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LECTURE ABSTRACTS

HS ONE HEALTH SCIENCE 1

HS PATHOGEN DISCOVERY

1 OHS A01 - PATHOGEN DISCOVERY - SALON AB

Plagiorchis sp. in small mammals of Senegal: an emerging food-borne trematodiasis?

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BACKGROUND: Trematodes of the genus *Plagiorchis* are cosmopolitan and characterized by low host specificity. *Plagiorchis* spp. infect lymnaeid freshwater snails as first intermediate hosts, a wide range of aquatic insects and freshwater fish as second intermediate hosts, and the intestinal tract of a variety of reptiles, birds and mammals, including humans, as definitive hosts. Whilst the zoonotic potential of *Plagiorchis* spp. has been documented across different countries of Asia, data on *Plagiorchis* spp. from Africa are insufficient and reports of this trematode remain anecdotal.

METHODS: Between May 2016 and November 2017, we trapped, humanely euthanized and necropsied 671 small mammals from sites in and around the town of Richard Toll and on the shores of Lake Guiers, Senegal. At post-mortem, organs were examined for helminths. DNA from individual worms was amplified for the complete internal transcribed spacer (ITS) region of the nuclear ribosomal DNA and for a segment of the cytochrome c oxidase subunit 1 (COI) gene of the mitochondrial DNA. Maximum Likelihood (ML) and Bayesian Inference (BI) were used to infer phylogenetic relationships and evolutionary lineages among *Plagiorchis* species.

RESULTS: *Plagiorchis* sp. was found in the liver and the proximal segment of the small intestine of 187/324 Mastomys huberti mice (57.7%), 7/22 *Crocidura* sp. shrews (31.8%), and 5/81 *Arvicanthis niloticus* rats (6.2%) from sampling locations around Lake Guiers. None of the 244 small mammal sampled from the Richard Toll area were found to be infected. Infection intensity was typically over-dispersed, with only 16.7% of the examined small mammals from Lake Guiers harbouring the majority of the parasites (≥ 60 worms). ML and BI analyses of the ITS (1159 base pairs) and COI (396 base pairs) regions strongly supported monophyly of this West African *Plagiorchis* sp. and its inclusion within a clade composed by other *Plagiorchis* spp. infecting rodents, sister to a lineage represented by *Plagiorchis* spp. of bats.

CONCLUSIONS: This study provides substantial molecular data to resolve the phylogeny of this newly described *Plagiorchis* sp. from Senegal. Its wide host spectrum and high prevalence in the Lake Guiers region raise concern about the zoonotic potential of this parasite, particularly when considering phylogenetic relationships with other *Plagiorchis* spp. recognized as agents of human infections. The occurrence of two divergent lineages suggests that the genus *Plagiorchis* has a complex evolutionary history, which may be the result of ecological specialization in different habitats and/or intermediate hosts. Trematode diversity and food- borne parasite transmission is a neglected public health issue in developing countries of Africa. Understanding the life cycle and epidemiology of this *Plagiorchis* sp. could have potential implications on the health of communities inhabiting regions where the parasite circulates.

2 OHS A01 - PATHOGEN DISCOVERY - SALON AB

Zika Virus Exposure In Malaysia; A Preliminary Study On Seroprevalence Among Local Population

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INTRODUCTION: Zika virus (ZIKV) is a zoonotic flavivirus transmitted via *Aedes* sp. mosquitoes and is known to cause mild disease. However, recent outbreaks linked ZIKV with congenital microcephaly and Gullain-Barré Syndrome alarming the public healthcare. In Malaysia, first isolation of ZIKV from mosquitoes was reported in 1969 while the first human case reported only in 2014. Subsequently, 8 cases of ZIKV were diagnosed using Real Time PCR (RT-PCR) during an outbreak in August 2016 where phylogenetic tree showed presence of both Micronesian and French–Polynesian strains. Meanwhile, a higher number of cases reported in the same year by the neighbouring countries; Thailand and Singapore, with 686 and 446 cases respectively. Infrequency in detection and diagnosis of ZIKV comparatively to flavivirus Dengue, provided limited information in assisting countries to tackle the disease. This study was conducted to measure the extent of ZIKV exposure in Malaysia by examining the seroprevalence of ZIKV among local population.

METHODS: A cross sectional study was conducted in Sabah, Malaysia and random sampling method was performed. All collected serum samples were tested for Anti-Zika IgG using the WHO approved commercial kit (Euro Imun Zika IgG ELISA) and for Anti-Zika IgM using the CDC Emergency Use Authorization (EUA) approved commercial kit (Inbios Zika IgM ELISA). Anti-Zika IgM reactive samples were then subjected to RT-PCR for detection of Zika viral RNA. All samples were subjected to Anti-Dengue IgG and IgM to eliminate cross-reactivity.

RESULTS: Out of 409 serum samples, 35.0% (143/409) were reactive for Zika IgG, and 4.9% (20/409) were reactive for Anti-Zika IgM. Following that, 10.0% (2/20) of Anti-Zika IgM reactive samples were detected for Zika viral RNA indicating an active ZIKV infection with viremia. Anti-Zika IgM reactive cases were detected from 9 different districts which were at least 30km apart. Analysis indicated that cases involved ranges from 12 to 80 years old, with the highest number of cases (30.0%) seen in above 50 year old age group. No significant gender and occupation groups showed inclination to ZIKV infection as the reactive cases were seen almost equally among farmers, students, housewife and other professions. All of them were asymptomatic. Seroprevalence of ZIKV in Sabah is estimated at 22.0% after correction for dengue cross-reactivity.

CONCLUSIONS: Approximately a quarter of Sabah's population have been exposed to ZIKV in their lifetime with a substantial number of active asymptomatic infection. Findings highlight the importance of ZIKV screening, especially among women of reproductive age due to risks of having foetal anomalies. A surveillance study on maternal ZIKV infections by monitoring foetal development is underway. This study also hints at the possibility of an existing large ZIKV natural reservoir among non-human primates triggering another research specifically targeting no-human primates.

3 OHS A01 - PATHOGEN DISCOVERY - SALON AB

A new concept for de-novo detection of viral pathogens with adaptive diagnostics and integrated data analysis approaches results in the recent discovery of two novel viruses

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BACKGROUND: New and reemerging viral infectious diseases cause frequent threats to both human and animal health. Diagnostic sequencing by unbiased next-generation sequencing is a key method for the identification of new pathogens. One major barrier for the use of this method in day-to-day diagnostics is often the lack of standardized workflows and data analysis tools in a user-friendly environment. The interdisciplinary project DetektiVir aims at closing this gap by deploying a new workflow which combines molecular nucleic acid-based virus detection by metagenomic sequencing with ad-hoc development of customized serological diagnostics, and integrates data in dynamic database applications.

METHODS: Central part of the new workflow is a novel diagnostic data hub application that combines raw sequence reads and metadata with the results from taxonomic classification software in a database environment. This core system offers flexible data interfaces and software algorithms in a user-friendly environment. The application was evaluated with samples from diseased animals infected with unidentified pathogens. Analyses comprised next-generation sequencing, data analysis and integration of data in the data hub. In case of sufficient data, full viral genomes were assembled and phylogenetically classified. Confirmation of the findings by RT-qPCR as well as attempts for virus isolation and electron microscopy were performed.

RESULTS: Applying the workflow, we were able to discover novel viruses. First, we identified a novel picornavirus, tentatively named ovine picornavirus, from 2-3 week old lambs in the UK, suffering with polioencephalomyelitis and ganglionitis. Phylogenetic analysis shows that the novel ovine picornavirus can be classified between the genera *Sapelovirus* and *Enterovirus* in the family *Picornaviridae*, and has 58 % overall pairwise sequence identity to a bovine picornavirus. Second, we identified a novel paramyxovirus, which was isolated from a diseased grizzled giant squirrel of Sri Lanka and is therefore preliminarily designated giant squirrel respirovirus. Interestingly, this novel virus has an overall pairwise sequence identity of 71 % with known murine respiroviruses and 68 % with human respiroviruses. Phylogenetic analysis suggests a novel branch between murine and human respiroviruses. The virus isolation was successful on primary porcine thyroid cells as well as electron micrographs of the virus particle.

CONCLUSIONS: The identification of the novel viruses proves the strength of the new workflow. By integrating the gathered information, including metadata, into the dynamic database the growing information will pave the way for earlier identification of associated outbreaks of a potential novel pathogen.

4 OHS A01 - PATHOGEN DISCOVERY - SALON AB

Novel orthobunyavirus identified in an African child with severe encephalopathy

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BACKGROUND: Non-traumatic coma is common in children in sub-Saharan Africa and causes considerable morbidity and mortality. Most children present with a suspected central nervous system (CNS) infection, but the underlying cause remains unknown in a majority of cases resulting in inadequate prevention and treatment strategies. Novel pathogens are a likely explanation for the unexplained encephalopathies as Africa is regarded as a hotspot for vector borne emerging infectious diseases. Orthobunyaviruses are of particular interest as they commonly cause outbreaks in Africa, can be zoonotic, are vector borne and are known to cause human encephalitis.

METHODS: Viral metagenomics was performed on pooled plasma and cerebrospinal fluid (CSF) of a three year old African child with fever, non-traumatic coma and prolonged convulsion for whom diagnostics on a wide range of common viral and bacterial causes were negative. Eleven inflammatory biomarkers were measured to determine the likelihood of a CNS infection

RESULTS: A novel orthobunyavirus was discovered. Sequences from all three viral segments were found (936 nt of the L-segment; 178 nt of the M-segment; 282 nt of the S-segment) which showed high diversity to known viruses (>29% on amino acid level) and clustered consistently within a clade of Anopheles mosquito borne orthobunyaviruses (Figure). The viral load was $3x10^2$/mL in CSF and the biomarker profile was typical of a CNS infection. Besides being present in CSF, the virus was also detected in plasma ($5x10^3$/mL).

CONCLUSIONS: We present a novel orthobunyavirus, present in the CSF of a three year old patient who presented with severe encephalopathy. A viral encephalitis, elicited by the novel virus, was the most likely cause of disease. This virus is probably transmitted by Anopheles mosquitos, highlighting that human contact may be common. Further screening in the same geographic area of the index case needs to be performed to determine the prevalence of this virus.

5 OHS A01 - PATHOGEN DISCOVERY - SALON AB

Seroprevalence of West Nile virus in wild birds in Bangladesh

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BACKGROUND: West Nile virus (WNV) is the most widespread arbovirus in the world capable of causing epidemics in both humans and animals. It is transmitted by a wide range of mosquitoes and multiple species of birds can act as amplifying hosts. Migratory birds are considered to be the main vehicle for introducing WNV into new regions. In humans, the pathogenicity of WNV varies from mild, self limiting, non-fatal, febrile illness to severe encephalitis. The status of WNV in Bangladesh is currently unknown. We conducted this study to assess the prevalence of WNV among resident and migratory wild birds of Bangladesh.

METHODS: During the period of 2010 to 2012 birds were captured using mist nets and noose traps, and blood samples were taken from wild birds landing on the coastal sandbars of Cox's Bazar, Hakaluki haor (seasonal wetlands) of Sylhet and Moulvibazar, Tanguar haor of Sunamgonj and the rice paddy fields of Patuakhali, Netrokona and Guibandha. Recovered serum was tested at 50% dilution for detection of WNV antibodies using a commercially available competitive ELISA following the manufacturer's instructions (ID Screen© West Nile Competition, IDVet, Montpellier, France).

RESULTS: Blood samples were obtained from a total of 888 birds comprising 21 families and 80 species; 250 (28%) of them were resident and 638 (72%) were migratory. Forty eight birds (5.4%, CI 0.04-0.07) tested positive for WNV antibody. The positive birds consisted of 45 common coots (*Fulica atra*), one ferruginous pochard (*Aythya nyroca*), one fulvous whistling duck (*Dendrocygna bicolor*) and one great crested grebe (*Podiceps cristatus*). Among those birds, two common coots, one fulvous whistling duck and one great crested grebe were from the Hakaluki haor, and 43 common coots and one ferrogionous pochard were from Tanguar haor. Only one positive bird, a fulvous whistling duck, was a resident species.

CONCLUSIONS: Both resident and migratory wild birds of Bangladesh demonstrated exposure to WNV infection. Most of the WNV positive birds were migratory common coots, which is similar to previous reports from India and Iran. Future isolation and molecular characterization of the virus will allow us to better understand the epidemiology of this virus in Bangladesh.

OHS DIAGNOSTICS

1 OHS A02 - DIAGNOSTIC - SALON AB

Recombinant techniques to address the challenges in development of assays for diagnosis and surveillance of emerging zoonotic diseases

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BACKGROUND: Emerging zoonotic diseases include pathogens that are newly recognised, newly evolved or known pathogens with an increase in incidence and/or change in their geographic distribution. Many emerging pathogens are viruses that require high containment facilities for culturing, limiting the number of laboratories with capacity to handle these viruses. Serological assays are essential tools for diagnosis and surveillance. Commercial assays for many of these viruses are expensive and not readily available. Crimean-Congo haemorrhagic fever (CCHF) virus is considered an emerging zoonosis. Most reagents are developed in house within BSL4 laboratories, however recombinant antigens could play a role in development of safe reagents and increase diagnostic and surveillance capacity. To address the challenge of developing assays in the absence of high containment facilities, epitope prediction and recombinant technology were investigated for preparing reagents for detection of CCHF.

METHODS: In this study mammalian cells were transiently transfected with a plasmid expressing CCHF nucleoprotein (NP). In-house antigen slides were prepared using cells transfected with pcDNA^{TM}3.1D/V5-His-TOPO.CCHFV.NP construct after confirmation that the construct could transiently express NP detectable in the cells by indirect immunofluorescent assays (IFA). A total of 14 serum samples from survivors of CCHF virus were screened for antibody. Negative samples were included to determine specificity. To confirm the in house assay results, the sera were tested using a commercial assay, CCHFV Mosaic 2 kit (EUROIMMUN AG). In addition, the samples were tested with an in house ELISA developed using bacterially expressed recombinant CCHF NP truncated to include epitopic regions identified using Bepipred Linear Epitope Prediction software.

RESULTS: Anti-CCHFV IgG antibody was detected in 14/14 serum samples using the commercial IFA and the in house IFA. Reactivity of sera with truncated NP antigens incorporating predicted epitopic regions identified an immunodominant region of the NP between amino acids 123 to 396. However there was limited reactivity of sera with a shorter truncated NP. A panel of CCHF IgG negative sera showed no reactivity.

CONCLUSIONS: The emergence in non-endemic regions and re-emergence in endemic areas that experienced long periods without CCHF cases emphasize the need for safe, validated, inexpensive assays. In house assays can also be readily modified for screening samples from other species. Prediction of potentially immunogenic epitopes in a given protein may reduce experimental efforts and cost for immunodiagnostics however functional assays are required to confirm the correlation between antigenic sites predicted using bioinformatics and biological activity. In summary recombinant proteins are a useful and safe alternative to native antigens and could have useful application in development of validated assays increasing capacity for diagnosis of medical and veterinary pathogens particularly in low resource environments.

2 OHS A02 - DIAGNOSTICS - SALON AB

Comparison of two RdRp PCR assays for the detection of MERS related Coronaviruses

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BACKGROUND: Coronaviruses (CoVs), specifically *Betacoronaviruses* (betaCoVs), are closely monitored in the context of emerging infectious diseases, as they are known to infect humans such as Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), and Middle East Respiratory Syndrome-coronavirus (MERS-CoV). Bats are the suspected source of these viruses. Multiple surveillance studies in bats have been conducted on different continents. Sensitive methods for detection of known and novel viruses are important for accurate surveillance data. RT-PCR amplification of the RNA-dependent RNA polymerase gene (RdRp) has been widely adopted to detect and identify CoVs in bats and other animals. We compared the results of two RdRp RT-PCR assays detecting MERS-related CoVs.

METHODS: Bat rectal swabs were collected from 9 study sites in Thailand during 2013-2015 and tested using one step RT-PCR followed by hemi-nested PCR and the results were compared. Two PCR protocols were used, including Watanabe's protocol (440 bp amplified target) and Corman's protocol (242 bp amplified target). Five µL of RNA template was used for both methods. Positive PCR specimens were confirmed by nucleotide sequencing.

RESULTS: Of the 376 bat rectal swabs, 30 specimens were positively identified using both methods; 12 and 24 samples were positive by Watanabe method and by Corman method, respectively. There was total agreement in the results of the two methods in 352 specimens (346 negative, 6 positive). Eighteen of 24 specimens positive by Corman method were negative by Watanabe method, and 6 of 12 positive specimens by Watanabe method were negative by Corman method. Of the 12 Watanabe positive samples, sequencing of viral DNA identified 2 as AlphaCoV, 6 as lineage C betaCoVs or MERS-related CoV, and 4 as lineage D betaCoVs. From 24 positive viruses by Corman method, 2 were lineage B betaCoVs or SARS-related CoV, 7 were MERS-related CoV, 1 was lineage D betaCoV, and 13 were of unclassified lineage betaCoVs. Combining the results from both methods, eight MERS-related CoV positive specimens were found; five specimens were positive by both methods.

CONCLUSIONS: Using two PCR primer sets for detection of MERS-related CoVs positively identified more samples than either method alone. The Corman method showed higher sensitivity than Watanabe, but there were some discrepancies between these methods, since different assays showed different detectability for the virus. To avoid any false negative results, more than one PCR method should be conducted.

3 OHS A02 - DIAGNOSTICS - SALON AB

The accuracy of pre-vaccination screening for Q fever and the extent of exposure – Bayesian latent class analysis

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BACKGROUND: Q fever is an acute febrile illness caused by infection with Coxiella burnetii that is most prevalent in occupational groups directly and indirectly exposed to livestock. The main method of prevention in Australia is vaccination of high risk individuals with Q Vax® (CSL, Melbourne). Since the vaccine has more side effects in persons who have already had the disease Q fever, so testing is necessary before vaccination is given to avoid unwanted vaccine side effects. However, there is lack of data on the diagnostic accuracy of the pre-vaccination screening tests: serology and skin tests. According to the Australian immunisation handbook, there is no information available on the accuracy of pre-vaccination Q fever screening tests.

OBJECTIVE: Therefore, the aim of this study was to assess the accuracy of pre-vaccination screening tests for Q fever. Methods: Bayesian latent class analysis (BLCA) used to determine the accuracy of the screening tests assuming that none of the serological tests is gold standard. Cohen's kappa used to assess the test agreement. We used data on the outcome of screening 79,414 individuals from Queensland, Australia tested between 1991 and 2016 obtained from the Q fever vaccination registry. We analysed the data using R Statistical Package: R-3.4.2 for Windows.

RESULTS: The posterior means of the sensitivity of blood and skin test, respectively, were found to be 67.3% and 77.0%. The posterior means of the specificity of blood and skin test, respectively, were found to be 99.0% and 95.6%. The mean posterior predictive positive values for blood and skin tests were, respectively, 85.0% and 59.7%. The mean posterior predictive negative values for blood and skin tests were, respectively, 97.2% and 98.0%. The posterior mean of the extent of the true latent Q fever exposure prevalence was found to be 7.9%. Agreement between serology and skin tests was only moderate (46%). The almost perfect agreement between the skin test and the health workers interpretation suggests they rely on this test for the overall decision.

CONCLUSIONS: The study confirmed previous findings of moderate agreement between screening tests (46%) and predictive value of history of vaccination/ exposure (immunity). In addition, the false negative rate was high (33% for blood test and 23% for skin test). The positive predictive value of the skin test found to be very low (59.7%) showing lower benefit of the skin test for ruling out previous immunity for Q fever. Moreover, up to 92% of new entrants in high-risk workplaces will be susceptible to Q fever and require vaccination. We recommend using serological tests for pre-vaccination screening in this high-risk population (i.e., phase out skin test). Further, follow up research in order to strength the current finding implicated.

4 OHS A02 - DIAGNOSTIC - SALON AB

Reproducibility of results and performance of TB diagnostics in East Africa Public Health Laboratory Networking Project sites in Kenya: Implication on Policy Resolution for Strategic TB Diagnosis

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BACKGROUND: Reproducibility of laboratory results and performance of diagnostic tools form major part of quality assurance in diagnosis, which is key to patient care. There no documented comparison of reproducibility of results and performance of TB diagnostics in different geographical settings.

METHODS: People presumed to have TB, aged 18 years and above were enrolled in a cross-sectional study between 2013 and 2016 at nine selected public health facilities in Kenya. Spot and morning sputum specimens collected from participants on two consecutive days with a total of 5715 specimens. At study site, a proportion of each specimen was processed for ZN, FM and GeneXpert MTB/RIF. The remaining portion was shipped to the Kenya Medical Research Institute (KEMRI) laboratory, Nairobi. ZN, FM, GeneXpert and Lowensen Jensen (LJ) culture were done according to standard procedures. KEMRI laboratory personnel were blinded of the study site results. Data processed with MySQL and IBM SPSS version 24 software. Reproducibility determined by Kappa values using specimen as unit of analysis and performance by diagnostic values (sensitivity, specificity, positive/ negative predictive values) using the patient as unit of analysis. LJ culture used as gold standard. Results at the study sites were compared with those from KEMRI.

RESULTS: GeneXpert had excellent Kappa value (0.855(95% CI:0.834-0.876) and was significantly higher than ZN microscopy (0.721(95% CI:0.708-0.734), FM Kappa value (0.749(95% CI:0.736-0.762), indicated substantial agreement. Specific results for the three diagnostic tools varied across the sites for microscopy but were not significantly different for GeneXpert. Marginal significant incremental sensitivity of microscopy at study sites for ZN (69.9% (95%CI:64.3-75.5); and FM (76.7% (95% CI:71.1-82.3); compared to KEMRI ZN (68.7% (95% CI:63.1-74.4); and FM (70.8% (95%CI:64.8-76.8). Sensitivity of GeneXpert at study sites (81.4%(95%CI:71.4-91.3); was not significantly different from that at KEMRI (81.4%(95%CI:71.4-91.3). Specificity of GeneXpert at site was not significantly different from KEMRI but significantly lower than microscopy both at site and KEMRI. Microscopy results varied across study sites but not significantly different for GeneXpert. Similar pattern was observed for positive/ negative predictive values.

CONCLUSIONS: GeneXpert indicated excellent reproducibility of results but not significantly difference in performance in study sites in Kenya suggesting that under ideal conditions GeneXpert is reliable irrespective of site setting. However, with higher specificity and positive predictive values, microscopy could compliment GeneXpert in strategic detection of mycobacteria especially in settings with inadequate capacity including infrastructure, human resource and high workload. The concept was adopted as a policy resolution in the East, Central and Southern Africa health Community – ECSA-HC 10th best practices Forum and 26th Directors Joint Consultative Committee Meeting April 2017 in Arusha, Tanzania.

5 OHS A02 - DIAGNOSTICS - SALON AB

Development of lateral flow immunochromatographic test for multiple detection of Salmonella Species in poultry food product

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BACKGROUND: *Salmonella* bacteria are facultative intracellular pathogens causing localized or systemic infections, in addition to a chronic asymptomatic carrier state. They have worldwide economic and public health significance. The largest number of food born illness cases attributed to poultry and poultry products are caused by the paratyphoid serotypes of *Salmonella*, namely S. enteritidis (group D) and S. typhimurium group (B) . In Egypt, diagnosis and control of avain salmonellosis depend upon the use direct bacteriological isolation and PCR This approach, however, is expensive, time consuming and require specialized laboratory and experienced personnel. Therefore, the need of a simple, sensitive, rapid and reliable test for detection of *Salmonella* Sp. sufficient to be applied on large scale of poultry is essentially required. Among the test candidates nominated to achieve this goal are the lateral flow immunochromatographic test (LFIT).

MATERIAL AND METHOD: The LFIT test for detection of SE and ST bacteria antigen in poultry and table poultry egg for human consumption. This work was planned to develop a simple rapid field test of high sensitivity, specificity, and accuracy that can improve and facilitates rapid field surveillance of salmonellosis. A rapid LFIT has been developed, in which rabbit antibodies against SE (somatic D) and ST (Somatic B) labeled with the gold chloride molecules laid on the conjugate pad. *Guinea pigs antibodies against SE and Guinea pigs antibodies against ST* were used as capture antibody at the test line 1 and test line 2 respectively of a nitrocellulose (NC) membrane and anti- rabbit antibodies were used as capture antibody at the control line (C) of the NC strip in the lateral flow layout .

RESULTS: The minimal microbial counts to be give positive of LFIT was 100CFU/100µl . The sensitivity, specificity and accuracy of LFIT as compared to PCR were calculated and was found to be 82.6%, 94.2 % and 90.6% respectively, The pretesting treatment of the test sample associated with pre-incubation in Tryptic soya broth for 4hr at 37°C increased significantly the sensitivity results and can detect 1CFU/100µl sample.

CONCLUSIONS: The developed test is a simple field rapid test of high sensitivity, specificity, and accuracy that control these pathogens from entering the food chain with subsequent reduction of the incidence of human salmonellosis transmitted through chicken and chicken food products

OHS SOCIAL SCIENCE AND POLITICS

1 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

Antimicrobials In Society: A One Health Approach in Kampala, Uganda

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BACKGROUND: The rise of antimicrobial resistance is a major challenge. A One Health framework has been adopted by WHO, FAO and OIE, articulating connections between humans, animals and the environment through the movement of antimicrobials and microbes. One Health approaches also emphasise wider social and political contexts. In this research, we explore and contextualise reasons for high levels of antimicrobial use in humans and their animals amongst vulnerable populations, with a specific focus in Kampala, Uganda.

METHODS: This research focuses on informal urban settlements and peri-ruban pig and poultry farms in Kampala, Uganda. Using ethnographic methods including direct observations and interviews, we explore the roles played by antimicrobials in everyday lives and livelihoods. Analysis is informed by anthropological theory including medicalisation and pharmaceuticalisation.

RESULTS: We find that antimicrobials – particularly antibiotics – perform important roles in productivity and protection in our setting. In a context of socioeconomic precarity, antimicrobials allow day wage labourers to continue to work, and farmers to maximise meat production. Antimicrobials provide protection against inadequate water and sanitation infrastructure, for people and their animals, and against infection risks posed by socio-economic structures that create high rates of transactional sex.

CONCLUSIONS: Antimicrobials are an important part of care. Rather than being used indiscriminately, our informants use them carefully to provide care to their children, animals and themselves. The context in which this care is required is one of poor infrastructure and acute precarity, rendering people's lives and livelihoods vulnerable. Antibiotics are one of a few tools available to respond within this context. Efforts to scale back use of antibiotics must therefore consider ways to support peoples' lives and livelihoods such that reliance on antibiotics is reduced.

2 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

(Re)Claiming Water Stewardship in a Changing Climate – Learning from the Margins

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BACKGROUND: As millions of people in low- and middle-income countries (LMICs) and recent experiences in South Africa and California can attest, access to sustainable, reliable water resources of suitable quality is not a sure thing. Resources are under threat from poor wastewater treatment, poor governance, competing uses for food, energy, and industry, and climate change impacts. But other dimensions to local water security are often overlooked – social, cultural, economic – that shape knowledge, attitudes, and practices around water and contribute to inequities. Given that local water security is essential to enable everyone to lead healthy, dignified, productive lives, we argue for a more nuanced framing of local water security and the development of tools that support comprehensive assessment and engagement at the community level. With a focus on health and wellbeing, systems, and feedback, the ecohealth and one health approaches lend themselves to this reframing of local water security considering both direct (e.g., water-related diseases) and indirect (e.g., nutrition and livelihoods) impacts on health.

METHODS: Mixed methods community-based assessments in East Africa and Canada have provided insight into the multiple facets of local water security. Focus groups, PhotoVoice, key informant interviews, community questionnaires, georeferencing, water point assessments, and water quality analyses have been employed to assess and understand knowledge, attitudes, and practices around local water resources and challenges.

RESULTS: A framework for local water security has been developed collaboratively with local community partners (Figure 1), to identify appropriate variables and develop, modify, and use local assessment tools that combine knowledge, human, and physical systems. Specific tools under development include the Community Water-Health Assessment Tool (C-WHAT) and WELLness, a tool for private well owners. The framing has also been applied to identifying and understanding the different water-related risks facing pregnant women.

CONCLUSIONS: Many communities have resources that can be brought to bear on local water security issues. This includes local knowledge and traditional interventions developed over time in response to challenges faced. Access to mechanisms for these communities to find a voice to share their stories and experiences enables them to (re) claim water stewardship and prepare for the uncertainties of a changing climate. The vulnerability and resilience of individuals, the cohesion and fragmentation of communities, and the capacity of governments to set standards, upscale successful development projects, sustain innovative approaches, and reinforce impacts of positive local strategies all require more flexible and responsive measurement strategies and tools. An age-old challenge for scientists is to find innovative and appropriate mechanisms to engage with communities to bridge research, policy, and practice for cohesive, reinforcing, sustainable difference on the ground. Reconceptualising and reframing complex systems using multiple knowledge systems in an era of big data and computational sophistication is not only possible, but essential.

3 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

MAN-IMAL: An experimental One Health degree program around animal-man-food

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In 2011, the French government began a vast experiment on pedagogical innovation by funding 37 projects experimenting creative, collective, and cross-disciplinary approaches to teaching.[1] One of these projects, MAN-IMAL, is the first France-based international higher education degree program exclusively founded on the “One World, One Health” initiative. MAN-IMAL experiments: i) the use of ICTE[2] ; ii) a multidisciplinary approach by its study content conceived by academics from Agricultural, Medical, and Veterinary Sciences; iii) as well as the interest of mixing students from various backgrounds (medical and veterinary studies, agricultural engineering, biological, and pharmacy studies). The created training courses include several Bachelor-level modules and an international One Health post-graduate degree taught entirely in English, the latter experimenting a multicultural approach. The teachers participating in the MAN-IMAL experiment have at their disposal a full-time support staff of 10 persons for 7 years, including pedagogical engineers, graphic designers, an audiovisual manager, education and studies assistants as well as a program coordinator. Today, almost 6 years after the beginning of the program, we are able to show results from multiple aspects of the project. Firstly, we present a successful multi-disciplinary cooperation between academics from different fields, secondly the particularities of coordinating a cross-disciplinary and multicultural class of students, and finally the importance of the close cooperation between the support staff and academics.

1. http://www.enseignementsup-recherche.gouv.fr/cid59599/37-projets-de-formation-labellises-idefi.html, http://www.man-imal.fr/en/home/introduction
2. Information and Communication Technology in Education

4 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

Human Behavioural Research at the Animal-Human Interface: Hunting and Trading of Bushmeat in Lao PDR

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BACKGROUND: Lao PDR is a major source of, and transit route for, wildlife that is hunted and traded for consumption or medicinal purposes. The livelihood of most Lao people in rural areas is based on non-timber forest products and bushmeat is an especially important source of their protein. However, hunting and trading of wild animals carries a risk of viral spillover from animals to humans.

METHODS: As part of USAID's PREDICT-2 program, quantitative questionnaires and qualitative interviews and focus groups which focused on human interactions with wild animals were conducted in Champasack province, which borders Cambodia, in southern Lao PDR. Interviews and questionnaires took place in the same location as ongoing viral surveillance of humans, wildlife, and livestock, in an effort to connect viral findings with human behaviours.

RESULTS: In Na Pa Kieb village, 34 quantitative questionnaires, 11 in-depth quantitative interviews, and 1 focus group with 9 individuals were conducted. The data collected indicated that villagers often cross the Lao PDR border to Cambodia to hunt animals like squirrels, giant flying squirrels, and bats, for household consumption and/or to sell to wildlife markets. As well, Khmer people from Cambodian villages near the border bring their bushmeat to sell to Lao people. Furthermore, quantitative interviews were conducted with a wildlife market vendor and a market supervisor, in order to gain knowledge on where animals originate, wildlife consumption habits, and hygiene or personal protective equipment used in the capture or slaughter of animals.

CONCLUSIONS: Data collection is ongoing and all behavioural information will be combined with biological and virological findings to produce a greater understanding of how viruses are shared between animals and humans, and what precautionary measures could be taken to reduce risk. With the government of Lao PDR as an integral partner in this research, the aim is to increase the awareness of locals of the potential for viral disease emergence and decrease the risk posed to people who rely on bushmeat as vital sources of protein.

5 OHS A03 - SOCIAL SCIENCE AND POLITICS - SALON AB

Evaluation of one health-ness: insights into interdisciplinary and cross–sectoral integration

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BACKGROUND: One Health (OH) is promoted as an approach for many current health challenges, particularly those arising from the intertwined spheres of humans, animals and the ecosystems constituting their environment. Adequate responses to these so-called wicked problems are achieved through interdisciplinary and cross-sectoral integration and participation, which must consider features of complex adaptive systems. The EU COST funded "Network for Evaluation of One Health (NEOH)" has identified characteristic features of OH initiatives and developed an evaluation framework to systematically assess the degree of OH integration associated with their outcomes.

METHODS: The NEOH framework hypothesises that, by definition, each OH initiative tackles complex problems at the animal, human, environmental interface. Therefore, OH initiatives require adaptive leadership to apply systems thinking, transdisciplinary working, and flexible planning to enable an appropriate response to unexpected outcomes. In addition, infrastructure providing opportunities for learning at individual, team and organisational levels is essential, which in turn requires sharing of data, information and experiences. The NEOH evaluation framework provides tools and metrics to assess these aspects systematically in a semi-quantitative way and summarizes them in a OH-index and OH-ratio. We illustrate its application in eight case studies and discuss the information it provides.

RESULTS: The assessment tools systematically identify areas in the six dimensions that are working well, and gaps that may hamper the progress or success of a OH initiative. Because the scoring is based on professional judgment by the evaluators, the summarizing OH-index currently only provides a rough indication of the degree of integration achieved by an initiative. In contrast, the OH-ratio illustrates quite clearly how intentions to tackle the complexity of a challenge are matched with infrastructure for learning and sharing, as well as adequate leadership.

CONCLUSIONS: The framework is useful to assess OH integration in initiatives that aim to tackle complex health challenges. The concept of the OH-index and OH-ratio produce insights into the comprehensiveness of a given OH initiative. Further implementation of the framework will provide benchmarking and best practices to minimize subjectiveness inherent in many evaluations.

OHS DRIVERS FOR EMERGING DISEASES 1

1 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

Quantifying the health, economic, and ecosystem impacts of land-use change as a driver of disease emergence in Southeast Asia

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BACKGROUND: Deforestation and land use change are occurring at an unprecedented rate in tropical countries. This activity has significant private benefits (e.g. industry profits) and social benefits (e.g. economic development, job creation) but also long-term negative effects on ecosystem services (e.g. loss of biodiversity, increased pollution, reduced capacity for disease regulation) that can impact social welfare. Our previous work shows that land use change is one of the most important drivers of disease emergence (31.5% of total emergence), and is involved in increased public health impacts from zoonotic diseases. Our research aims to: 1) describe the relationship between land use change and infectious diseases; 2) quantify an ecosystem's disease regulating value; and 3) build models of land-use change and economics of disease emergence that can be used by local and regional policy makers.

METHODS: We collated data on the conversion and production costs from the oil palm industry, on health impacts on society (i.e. malaria cases, mosquito control expenditure), and on land cover and land use change. We used this information to construct a spatially explicit model to estimate the effects of land conversion on the disease regulation capacity of forests in Sabah Malaysia, particularly the burden of malaria due to land use change. We combined these results with data on ecosystem services values, revenues from palm oil, and conversion costs to create a dynamic optimization model that seeks to optimize social welfare by accounting for private benefits and social costs (e.g. disease treatment) of oil palm development, allowing us to determine the economically optimal rate of palm oil development for each year after disease risk and ecosystem services cost are considered.

RESULTS: Our results showed that land use change, particularly deforestation and forest fragmentation, is associated with the increase of malaria cases in Sabah Malaysia. Our dynamic optimization model showed that since 1993, once the health and ecosystem services costs are considered, the pace of land clearing for timber and subsequent conversion to oil palm has outpaced what would be optimal, resulting in public costs for society and reduced profits for the plantations involved in land conversion.

CONCLUSIONS: Land use change is an important driver of disease and the failure to consider the disease regulation as another ecosystem service can lead to a reduction in both private and social welfare. Quantifying the impact of land use change on disease and the resulting economic benefits and costs allows for the development of targeted control strategies. We are using this approach to work with stakeholders in government, industry, and local communities to enhance planning approaches and develop more sustainable strategies for land use that benefit public health as well as economic development and conservation.

2 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

Impacts of urbanization and conversion of rainforests into large industrial oil palm plantations on the ecology of Aedes vectors in arbovirus foci, Côte d’Ivoire

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BACKGROUND: Arboviruses are zoonotic pathogens that have (re-)emerged from their enzootic reservoirs in Africa and the Americas, and caused many infections and diseases among humans worldwide, partly due to filtering effects of landscape anthropization forces on the ecology of *Aedes* vectors. We explored the effects of anthropogenic ecosystem disturbances such as urbanization and conversion of rainforests into large industrial oil palm plantations on the ecology of *Aedes* mosquitoes within yellow fever and dengue foci in Côte d’Ivoire.

METHODS: From January 2013 to December 2014, *Aedes* mosquitoes were sampled along an urbanization gradient (rural, suburban, and urban), and among four land-covers (rainforests, polycultures, oil palm monocultures, and rural-housing areas) using ovitraps, larval surveys, and human-baited double-net traps, coupled with socio-ecological surveys.

RESULTS: A total of 51,439 specimens of *Aedes* mosquitoes belonging to 20 species *(Ae. aegypti, Ae. africanus, Ae. albopictus, Ae. angustus, Ae. apicoargenteus, Ae. argenteopunctatus, Ae. dendrophilus, Ae. fraseri, Ae. furcifer, Ae. haworthi, Ae. lilii, Ae. longipalpis, Ae. luteocephalus, Ae. metallicus, Ae. opok, Ae. palpalis, Ae. stokesi, Ae. unilineatus, Ae. usambara and Ae. vittatus)* were collected. *Aedes* species richness was higher in rural (18 species), followed by suburban (7 species) and urban (3 species) areas. Conversely, the highest *Aedes* abundance was found in urban (n= 51,439; 50.7%), followed by suburban (32.6%) and rural (16.7%) areas. Ae. *aegypti* was the predominant species, and displayed higher abundance in urban areas (n= 26,072; 99.4%). *Aedes*-positive breeding site proportions were higher in urban (2,136/3,374; 63.3%), followed by suburban (1,428/3,069; 46.5%) and rural (738/2,423; 30.5%) areas. Rural areas exhibited a larger array of *Aedes* breeding sites ranging from natural containers (tree-holes…) to traditional containers (claypots…), and industrial containers (cans, tires, water receptacles…), while urban areas showed mainly industrial containers (2,129/2,136; 99.7%). Only four specimens of Ae. *aegypti* were collected in oil palm monocultures, whereas *Aedes* vectors showed higher abundance in polyculture (n= 28,276; 60.9%) and higher species richness (11 species) in rainforests. The anthropophilic Ae. *aegypti* and zoophilic Ae. *dendrophilus* and Ae. *africanus* vectors exhibited unexpectedly variable human blood-feeding behaviors according to human-disturbed land-covers, with high biting rates in polycultures (21.48 bites/human/day) and rural-housing (4.48 bites/human/day), and low biting rates in rainforests (0.62 bites/human/day).

CONCLUSIONS: In Côte d’Ivoire, anthropogenic ecosystem disturbances resulting from urbanization and conversion of rainforests into industrial oil palm plantations modify the ecology of anthropophagic and zoophagic *Aedes* arbovirus vectors. This suggests the coexistence of several arbovirus transmission cycles (enzootic: animal-to-animal; epizootic: animal-to-human; epidemic: human-to-human), with higher exposure of humans (citizen, villagers and farmers) to *Aedes* bites and yellow fever and dengue virus transmission risks in urban, rural-housing and polyculture areas. Arboviral disease control strategy should encompass integrated vector management (IVM), including landscape epidemiology, ecotope-based vector control, forestry, urbanism, water management, waste management and agricultural practices.

3 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

The use of a nationwide pig movement network to predict the spatial risk of Nipah virus outbreaks in Thailand

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BACKGROUND: Nipah virus (NiV) was first notified in pig populations in Malaysia in 1998. A total of 105 out of 265 infected human individuals died during the outbreaks and millions of pigs were culled to control the spread of the virus. NiV has never been reported in pigs in Thailand. However, the genetic evidence of the virus was detected in the flying foxes (*Pteropus* spp.) in the central plain of the country. High density of pig production as well as multiple colonies of flying foxes in the plain may drive the emergence of the disease. The present study therefore aimed to quantify the risk of NiV spread from the central plain to different regions of Thailand via the pig movement network.

METHODS: The national animal movement database was used in this study. We analyzed the pig movement data in May 2016. The month was previously identified as the highest recovery of NiV RNA viruses in bats. A directed one-mode network was constructed for the pig movement in the subdistrict level. The strongly and weakly connected component were examined. A Potential Surface Analysis (PSA) was applied to map the high-risk areas for bat-to-pig transmission. The map was then overlapped with subdistricts identified in the pig trade network to model the pig-to-pig transmission. The province with the highest number of high-risk subdistricts was chosen for further simulations. The NiV infection was mathematically seed into each subdistrict. The final epidemic size was observed and the infected probability was calculated. The programing language R was employed throughout analyzes.

RESULTS: The pig movement was identified in 1,627 subdistricts with 22,374 trade activities. A giant weakly connected component composing of 1,554 subdistricts (95.5% of the total nodes) was observed (Fig. 1). Based on our risk-based selection criteria, Chon Buri province was chosen. After simulations, 407 subdistricts across the country were identified as the NiV destinations. The highest risk was observed in Thai Ban Mai subdistrict, Mueang district, Samut Prakan province (Geocode: 110116) with the infection probability of 41.8%.

CONCLUSIONS: We suggested that the nationwide pig movement network in Thailand was vulnerable to the spread of NiV and other infectious diseases. Once the NiV emerges, it may spread to different regions of the country. The related authorities should strengthen the surveillance program on the network.

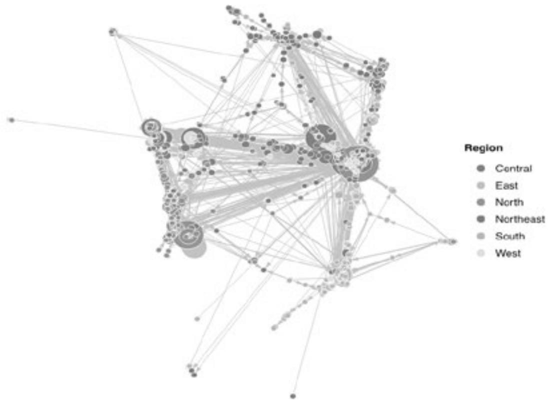

Fig. 1. A giant weakly connected component found in the nationwide pig movement network at subdistrict level (#node: 1,554, #tie: 3,424). The arrowhead indicates the direction of animal movements.

4 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

Ecosystem Change and Zoonoses Emergence

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BACKGROUND: Changes in land use change, animal populations and climate, primarily due to increasing human populations, drive the emergence of zoonoses. Force of infection (FOI), which for zoonoses is a measure of the ease with which a pathogen reaches the human population, can change with specific zoonoses and context.

METHODS: Here we outline three habitat classifications - domestic, peridomestic and sylvatic, where disease ecology alters the FOI of specific zoonoses namely *E. coli* O157, leptospirosis and *Echinococcus multilocularis*. In addition, we examine how the relationship between the vector, pathogens, reservoirs hosts, habitats and the potential for Lyme borreliosis in humans alters with different habitat contexts.

RESULTS: Human intervention has an overriding effect in the emergence of zoonoses therefore we need to understand the disease ecology, evolutionary capacity, virulence, resistance, stability, infectivity etc. of pathogens that are likely to interact differently within dynamic landscapes and the context is hugely significant. Biodiversity is just one factor of many that impacts the FOI.

CONCLUSIONS: Interdisciplinary collaboration, incorporating One Health land use planning, must appreciate that comparable empirical studies with powerful inference are difficult because of differences in local context. Further integration of additional explanatory variables that influence FOI such as human behaviour, economics and social dimensions will facilitate risk analyses to predict, manage and respond to zoonotic outbreaks.

5 OHS A04 - DRIVERS FOR EMERGING DISEASES 1 - SALON AB

Identification of molecular determinants of aquatic and terrestrial morbillivirus cross-species infections

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BACKGROUND: Members of the genus *Morbillivirus* are capable of infecting a wide variety of mammalian species, including humans, canines, felines, ruminants, and cetaceans. Cetacean morbillivirus (CeMV), canine distemper (CDV) and phocine distemper viruses (PDV) have in recent decades caused mass mortality events in both aquatic and terrestrial mammals. CDV is characterized by a broad host range, infecting not only carnivore and omnivore species, but also non-human primates, indicating that CDV may pose a zoonotic threat upon eradication of the closely related measles virus from the human population. In this study our primary aim was to identify molecular determinants important for intra- and inter-species transmission of aquatic and terrestrial morbilliviruses.

METHODS: CDV- and CeMV-infected wildlife tissue samples from terrestrial and marine mammals and cell culture adapted CeMV strains were processed and prepared for deep sequencing on an Illumina MiSeq system. The morbillivirus receptor CD150 from different phocid species was amplified, sequenced and cloned into an expression vector. New reverse genetics systems were generated for dog and Caspian seal CDV strains. Furthermore, the fusion (F) and hemagglutinin (H) glycoproteins from various morbillivirus strains were cloned for use in virus fusion and entry assays (pseudotyped-VSV) using cells expressing heterologous CD150 receptors.

RESULTS:
Aquatic morbillivirus
The CeMV strain, dolphin morbillivirus, infects a wide range of cetacean host species with minimal genetic adaptation. However, CeMV adaptation to growth in African green monkey (Vero) cells appears to require changes in the matrix protein.
Terrestrial morbillivirus
Phylogenetic analysis of the full genome of the CDV strain responsible for the mass mortality in Caspian seals in 2000 showed that this strain is a member of a novel lineage most closely related to the 'oldest' lineage: American I. Host molecular determinants regulating virus transmission were investigated by comparing CD150 receptors of different phocid and other terrestrial CDV host species. New reverse genetics systems based on viral sequences amplified from CDV-infected tissues from a dog and Caspian seal were used to assess the role of specific mutations in species tropism.

CONCLUSIONS: The combination of rapid full genome sequencing and *de novo* generation of recombinant morbilliviruses directly from wildlife tissue samples will enable more comprehensive analyses and risk assessment of future disease outbreaks caused by morbillivirus cross-species infections.

OHS DRIVERS FOR EMERGING DISEASES 2

1 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

Leveraging viral phylodynamics to inform spatiotemporal transmission of viral infectious diseases in Africa: 2009 Influenza A/H1N1 in Africa

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BACKGROUND: Emerging and re-emerging viral pathogens pose serious health threats to both humans and livestock. Although all global regions are at risk of viral infectious disease outbreaks, the African continent is disproportionately disadvantaged due to its weak health systems to mitigate, manage and prevent further spread of the pathogens in an outbreak situation. Molecular sequence data in combination with ecological, economic and demographic factors have proven to robustly describe phylodynamics of viral infectious diseases. Human mobility plays a central role in infectious disease transmission and due to economic constraints probably road transport networks are the key drivers of infectious disease spread in Africa rather than air travel, railway networks or Euclidean distances between sampling locations

AIMS AND OBJECTIVES: This study sought to unravel the introduction, the spatial dispersal pattern and to evaluate the contribution of genetic, ecological, and economic predictors of viral infectious transmission patterns using the case of 2009 Influenza A/H1N1 pandemic virus on the African continent.

MATERIALS AND METHODS: In this study, we combined ecological, economic and demographic data Bayesian phylogenetics to unravel the introduction, dispersal and test predictors of viral infectious diseases transmission patterns using the case of 2009 Influenza A/H1N1 pandemic virus on the African continent.

RESULTS, DISCUSSION AND CONCLUSIONS: Our study suggested that there were multiple simultaneous introductions of the 2009 H1N1 pandemic virus into the African continent and the phylogenetically inferred probable source populations existed in North America and Asia. Transmission predictor analysis suggested that proximity (geographical distance), air travel, and sampling location latitude might have contributed significantly to the spread of the 2009 Influenza A/H1N1pandemic virus in Africa.

2 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

Risk of pneumonia among residents living near goat and poultry farms

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BACKGROUND: The human health risks associated with industrial livestock production become increasingly clear. Recent research in the Netherlands suggests an increased risk of pneumonia among residents living close to goat and poultry farms, but the causes of this increased risk are unknown. For goat farms, specific analyses make it unlikely that the Dutch Q-fever epidemic of 2007-2009 is still responsible for the elevated pneumonia incidence reported over the years 2010-2013. Around poultry farms, the increased risk may be caused by the high particulate matter emissions from these farms, but additional evidence is required to support this hypothesis. Besides these uncertainties, there are some inconsistencies in results of previous analyses, which are hard to interpret because of the different measures of exposure and statistical methods used in different studies. More evidence and certainty is urgently needed since the risk of pneumonia would add to several other environmental and public health impacts of livestock production, such as chronic respiratory effects, odor annoyance, zoonotic disease transmission, eutrophication and greenhouse gas emissions. This multitude of effects influences political decisions, for example regarding the expansion of goat farms. More evidence may be obtained from analyses over more recent years than the 2007-2013 period on which previous analyses were based. In this study, such new analyses are performed to investigate whether the relation between general practitioner-diagnosed pneumonia and living close to goat and poultry farms can be confirmed for more recent years. In addition, the influence of more specific farm characteristics is studied, i.e. to distinguish between farms housing broilers or laying hens, thereby potentially providing more information regarding the causes of an increased pneumonia incidence.

METHODS: A cross-sectional analysis was performed, including about 100,000 patients registered in 23 general practices in a livestock-dense area in the south-east of the Netherlands, with on average about 35 goats, 130 cattle, 1,400 pigs and 8,000 chickens per km^2. Analyses are based on diagnoses of pneumonia from 2014-2016, as registered in electronic medical records. The association between pneumonia and farm proximity was analyzed using logistic regression models, which included several measures of distance of resident homes to goat and poultry farms as exposure variables, as well as variables to account for differences in sex, age and the presence of other farms.

RESULTS: Associations between pneumonia incidence and residential proximity to goat and poultry farms will be presented at the conference. This update over the years 2014-2016 should indicate whether the previously found associations (over the years 2007-2013) can be confirmed.

CONCLUSIONS: Previous studies show an increased risk of pneumonia among residents living within 1-1.5 km from poultry farms and 1-2 km from goat farms. The ongoing research will establish whether this association is still present in more recent years.

3 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

Effect of Habitat Modification on Risk of Scrub Typhus, An Emerging Infectious Disease in Bhutan

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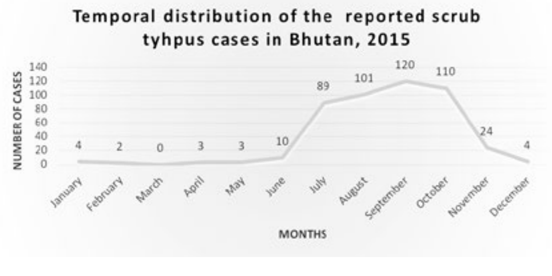
BACKGROUND: Scrub typhus or tsutsugamushi disease is an emerging zoonotic infection causing acute febrile illness in humans. The annual incidence of diagnosed scrub typhus in Bhutan has been increasing since first detected in 2008, reflecting significant public health impact. We conducted a nation-wide prospective observational study and a case-control study to measure the impact of this re-emerging disease in Bhutan and understand major environmental drivers.

METHODS: Three sources were used to recruit as many incident cases as possible occurring throughout Bhutan in the year 2015: (1) patients diagnosed in hospitals throughout Bhutan (Rapid diagnostic test RDT+ve); (2) notified cases to the Royal Centre Disease Control in Thimphu (RCDC) through national sero-surveillance (ELISA+ve); and (3) patients enrolled in the matched case-control study (78 cases and 205 controls from 11 districts, mainly located in southern Bhutan, between October and December 2015). In the case-control study, for each case, two controls were matched by village/location and a third was randomly selected from people visiting the same hospital. Interviews conducted using a standard questionnaire collected data on environmental and occupational exposures in the previous month.

RESULTS: The prospective study identified a total of 470 scrub typhus cases in Bhutan during January-December 2015, a 10-fold increase compared to cases identified through passive surveillance in previous years. The annual cumulative incidence was 60.5 new cases per 100,000. There was a clear seasonal pattern, with an epidemic peak between August and October, and a higher incidence in southern districts of Bhutan. In the case-control study, major risk factors identified for clinical scrub typhus included: harvesting cardamom (OR 10.6 to 18.7); clearing bush (OR 4.9); and sitting or sleeping on grass (OR 4.1).

CONCLUSIONS: Our study confirmed scrub typhus as an emerging disease in Bhutan. The seasonal pattern and increased risk associated with clearing bush and harvesting cardamom indicate an effect of habitat modification on the occurrence of disease emergence, and suggest scrub typhus may be an occupational hazard of this type of farming. Cardamom farming has recently been introduced to Bhutan and is becoming increasingly common. This study highlights the role of a change in agricultural practice as a potential driver for emergence of scrub typhus in Bhutan.



4 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

A One Health Understanding of the Rodent Meat Value Chain in the Mekong Delta, Vietnam: Implications for Zoonotic Disease Risk Mitigation (Wellcome Trust VIZIONS)

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3: Oxford University Clinical Research Unit in Vietnam

BACKGROUND: The Mekong Delta is a large floodplain in southern Vietnam and is one of the world's most productive rice and aquaculture zones. Agriculture expanded rapidly in the late 1980s and, as rice production increased, rodent populations expanded to fill a growing ecologic niche. By the late 1990s, the severity of rodent outbreaks prompted national policies aimed at controlling rodent populations through synchronized planting and live capture. In the last two decades, as a byproduct of increased live capture, the region has seen a booming market for rodent meat, estimated at 3,500 tons annually.

Rodents are of particular importance in the emergence of zoonotic diseases and have been associated with nearly 20% of new human pathogens since 1980. Given the intensity and scale of this rodent meat value chain, further research on human-rodent interactions may help better characterize the risk of zoonotic spillover and support the development of mitigation strategies.

METHODS: As part of the Wellcome Trust VIZIONS project, we conducted 92 in-depth interviews between 2014 and 2017 throughout An Giang and Dong Thap provinces, Vietnam with individuals involved in the rodent value chain. Interviews were recorded using digital audio recorders and then translated and transcribed into English by native speakers familiar with the value chain. Transcripts were analyzed in Dedoose using a grounded theory approach.

RESULTS: The rodent value chain involves distinct roles, with individuals often fulfilling one or more different activities. Common roles include: rodent hunting/trapping, transporting, small- to large-scale accumulation, slaughtering, and market sale. Rodents are mostly collected live in small metal cages along the perimeter of rice fields. Transporters typically shuttle stacks of cages between collection points and regional markets by motorbike for small loads and by truck or van for large loads. Rats are generally kept live until sold, at which point slaughterers will kill, skin, and butcher the rodent for consumers. In larger settings, rodents are butchered in mass and transported on ice to urban centers.

Throughout the value chain, rodent workers rarely utilize personal protective equipment, explaining that it makes the slaughtering too difficult or diminishes their dexterity at grabbing and manipulating live rodents. Rodent workers note frequent bites and slaughterers, in particular, are in constant contact with rodent blood and viscera. While some workers wear face masks, exposure to rodent hair and aerosolized urine and feces is ever-present. Despite the pervasive exposure, the population generally perceives field rodents to be “clean” and “healthy,” contrasting them to “city rats” or farmed livestock.

CONCLUSIONS: Rodent workers have an inadequate understanding of the health risks that rodents can pose; there is a poor understanding of how rodent-borne diseases can be transmitted to humans. Greater public health messaging innovative strategies to mitigate exposure risk are required.

5 OHS A05 - DRIVERS FOR EMERGING DISEASES 2 - SALON AB

Climate variability and infectious diseases nexus: Evidence from Sweden

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BACKGROUND: Many studies on the link between climate variability and infectious diseases are based on biophysical experiments, do not account for socio-economic factors and with little focus on developed countries.

METHODS: This study examines the effect of climate variability and socio-economic variables on infectious diseases using data from all 21 Swedish counties. Employing static and dynamic modelling frameworks, we observe that temperature has a linear negative effect on the number of patients. The relationship between winter temperature and the number of patients is non-linear and “U” shaped in the static model. Conversely, a positive effect of precipitation on the number of patients is found, with modest heterogeneity in the effect of climate variables on the number of patients across disease classifications observed. The effect of education and number of health personnel explain the number of patients in a similar direction (negative), while population density and immigration drive up reported cases. Income explains this phenomenon non-linearly. In the dynamic setting, we found significant persistence in the number of infectious and parasitic-diseased patients, with temperature and income observed as the only significant drivers.

HS VACCINES 1

1 OHS A06 - VACCINES 1 - SALON AB

Portfolio Approach, Development and Stockpile of MERS-CoV Vaccines: A Case Study

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CEPI, United Kingdom

BACKGROUND: CEPI was launched at Davos 2017 as a response to the emerging consensus following the Ebola and Zika outbreaks that a coordinated, international and intergovernmental plan was needed to develop and deploy new vaccines to prevent future epidemics. As such, CEPI's mission is to stimulate, finance and co-ordinate vaccine development against diseases with epidemic potential where market incentives fail. There is broad agreement that CEPI should avoid duplication and focus funding on the critical gap - the lack of capability to move vaccine candidates quickly from the preclinical stage through to proof of principle.

METHODS: This vaccine development requires funding the preclinical and clinical development required for proof of principle, facilitating early and frequent interactions between vaccine developers and regulators, and ensuring that a vaccine candidate can be successfully deployed in the event of an outbreak by working closely with clinical investigators, public health officials, and national regulatory authorities in at-risk countries. In addition to directly funding the development of specific vaccine candidates and platforms, CEPI will also fill gaps in developing biological standards, assays, animal models and other aspects of regulatory science for its funded projects and will coordinate with other institutional stakeholders to set priorities, develop pathogen specific road maps, and plan for accelerated clinical testing and regulatory review of products in epidemic situations. Finally, CEPI will coordinate with major institutional stakeholders such as Gavi and UNICEF on vaccine stockpiling and distribution.

RESULTS: In this paper, we will introduce the CEPI portfolio of MERS CoV vaccine candidates as an example of our work and discuss the technologies behind the vaccine programmes. We will also review manufacturing, stockpile, preclinical and clinical strategies deployed in emergency settings vs conventional vaccine development. We will present progress made on filling gaps on aspects of critical regulatory science and mechanisms of engagements of regulatory authorities for the enhancement of use of experimental vaccine candidates in emergency settings for efficacy trials in at-risk countries.

CONCLUSIONS: The CEPI portfolio approach for MERS CoV vaccine is an example for a coordinated, rapid development and deployment of vaccine candidates in emergency settings.

2 OHS A06 - VACCINES 1 - SALON AB

Protective non-specific effect of rabies vaccine in humans, dogs and cattle: One Health implications

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Non-specific effects of vaccines are defined as effects on recipient's health beyond those resulting from the vaccine's effect on its specific target agent. It has been proposed that the type of vaccine determines the nature of the effect, with live vaccines having beneficial non-specific effects and non-live vaccines having deleterious ones. To date, these effects have only been reported in human populations. We present the results of three separate studies (two published and one new study) reporting non-specific effects of rabies vaccine in humans, dogs and cattle, and discuss their implications.

The first study was a Phase 3 trial of RTS,S malaria vaccine in children in two age categories. Rabies vaccine was used as a comparator vaccine in the control group in the older age category. The low incidence of meningitis and cerebral malaria in this group relative to other study arms in both age categories is most parsimoniously explained by a protective non-specific effect of rabies vaccine. The second study was a population-based cohort study in free-roaming dogs in a high-mortality setting. During quarterly visits, heads of households were asked about owned dogs, including data on entry and exit events, demographics (sex and age) as well as rabies vaccination. Survival analyses using a piecewise exponential survival model by age group was performed, accounting for clustering within household. The study showed a reduced risk of death for vaccinated dogs (from 16 to 56%) in all age groups. The final study was a quasi-randomised controlled trial of non-specific effects of rabies vaccine on the incidence of bovine respiratory disease (BRD) in feedlot cattle. Following their arrival at the feedlot facility, 5,126 cattle from high-risk lots were allocated to receive a single intramuscular injection of rabies vaccine in addition to routine prophylactics, or to a control group that received routine prophylactics only. The risk of BRD within the first 60 days of arrival was reduced by 9% (95% confidence intervals 0% - 18%) in the rabies-vaccinated group, relative to the control group.

The three studies are consistent with the hypothesis of a protective non-specific effect of rabies vaccine, a non-live vaccine. This casts doubt on the proposition that non-specific effects of non-live vaccines are necessarily deleterious. Although rabies vaccine is known to be a safe and efficacious vaccine, its routine use as pre-exposure prophylaxis in children is not recommended as it is not cost-effective in most situations. A substantial non-specific protective effect against other infections would improve the cost-comparability of routine pre-exposure prophylaxis vs. post-exposure prophylaxis in areas where canine rabies is endemic. We therefore recommend further studies in animals and people to quantify this effect and understand the biological mechanism through which it arises.

3 OHS A06 - VACCINES 1 - SALON AB

Brucellosis in the changing peri-urban dairy systems of West Africa

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The dairy sector in West and Central Africa is evolving as demand for dairy products is growing and consumer preferences and behaviours are changing. High rates of urbanisation alter purchasing patterns and taste for value added and convenient products. The growth of the dairy industry in the region is undoubtedly positive in terms of increased nutrition and diversity in the diets of consumers, as a driving force for poverty alleviation amongst farmers and as an avenue for national and regional economic growth. However, this burgeoning demand is not without inherent risks in terms of the spread of zoonotic diseases and exposure to food borne pathogens. Of these risks, brucellosis is perhaps one of the most significant threats due to the potential impact on both human health and animal health and productivity.

In order to characterise this emerging sector and estimate the impact of brucellosis in West and Central Africa, a multi method approach was applied in six countries (Senegal, Cameroon, Togo, Mali, Burkina Faso and Ivory Coast). A cross sectional seroprevalence survey was carried out on bulk milk samples alongside a knowledge, attitudes and practices questionnaire administered to cattle keepers. Following this, focus group discussions with farmers and milk processors aimed to investigate opinions on barriers within dairy farming and attitudes regarding animal health care and vaccines. In general, those participating in focus groups had little knowledge about or access to vaccines for their livestock and felt that adequate healthcare as well as financial and land issues were the biggest barriers facing dairy farming at the present time.

This work lays the foundations for the next stages in estimating the farm level economic impact of the disease in this setting and assessing potential intervention strategies to inform policy within the region.

4 OHS A06 - VACCINES 1 - SALON AB

Evaluation of Rabies Post-exposure Prophylaxis Procurement and Delivery System in Vietnam

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BACKGROUND: Vietnam has made monumental progress towards reducing canine-mediated human rabies deaths. Within a 22 year time frame, cases have dropped 82%, from 505 cases in 1994 to 91 cases in 2016. This reduction was largely due to the expanded access to rabies biologics throughout the country. While an average of 400,000 vaccine doses are administered and 32,000 people receive equine immunoglobulin (eRIG) each year, limited data exists regarding the procurement, distribution, storage, and administration of rabies biologics at the provincial and district level medical centers.

METHODS: Between February through June 2017, Vietnam's National Rabies Control Program surveyed 191 medical centers that order biologics directly from vaccine manufactures in 2016. Questionnaires were emailed or mailed to all 63 provincial medical centers (PMC) and 130 district medical centers (DMC).

RESULTS: There was a 68.59% (63 PMCs and 69 DMCs, N=132 medical centers) response rate. 100% (131) medical facilities provided vaccine and 53.4% (70/131) provided eRIG. 43.5% (57) medical centers experienced delays in receiving vaccine or eRIG and 77 (58.8%) medical centers experienced a vaccine or eRIG shortage within the past year. Approximately 90% (118) medical centers used their internal funds to pay for biologics. Nineteen (15%) facilities depended on refrigerated space for other vaccines to store rabies biologics. Eight-seven medical facilities (66.4%) responded that lack of knowledge was the primary barrier for wound treatment after an animal exposure. Medical centers reported that financial cost (55%) to the patient, lack of vaccine/eRIG and the distance from health facilities (31%) were reported barriers to getting rabies biologics. 65% of prediction demand of rabies vaccine and immunoglobulin depended on amount of patients monthly.

CONCLUSION: Vietnam rabies system is inadequate VPs in district level. Provincial level did not have a VPs providing eRIG due to many problems, including population in that areas did not receive eRIG timely. The demand of VX/eRIG increase but not enough supply. The price of VX is still high. VP delays and shortages are from VX manufactures, solving policy and resource obstacles among VX manufactories to promote them producing more rabies vaccine. Integrated interventions between governments and vaccination companies that minimize administrative procedures and encourage pharmaceutical companies to subsidize vaccine/RIG cost could further reduce the price and increase VPs.

5 OHS A06 - VACCINES 1 - SALON AB

A systematic review of strategies for reducing missed opportunities for vaccination

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BACKGROUND: Missed opportunities for vaccination (MOVs) occur when persons eligible for vaccination visit a health facility and do not get the vaccines they need. We conducted a systematic review to assess the effects of interventions for reducing MOVs.

METHODS: We conducted a literature search in PubMed, Scopus, and the Cochrane Library. Three authors independently screened search outputs, reviewed full texts of potentially eligible papers, assessed risk of bias, and extracted data; resolving disagreements by consensus. We expressed study results as risk ratios (RR) with their 95% confidence intervals (CI) and assessed the certainty of the evidence using the Grading of Recommendations Assessment, Development and Evaluation (GRADE) tool.

RESULTS: Six studies (five trials and one cohort study) met our inclusion criteria, all conducted in the United States of America. All six studies had various limitations and were classified as having a high risk of bias. We found moderate certainty evidence the following interventions aimed at reducing MOVs probably improve vaccination coverage: patient education (RR 1.92, 95% CI 1.38 to 2.68), patient tracking and outreach sessions (RR 1.18, 95% CI 1.11 to 1.25), and patient tracking, outreach, and prompting (RR 1.24, 95% CI 1.18 to 1.31). In addition, we found low certainty evidence that education targeted at clinic and family settings concurrently may increase vaccination coverage (RR 1.25, 95% CI 1.08 to 1.46).

CONCLUSIONS: The currently available evidence supports the use of provider education; patient education; and patient tracking, outreach, and prompting as interventions to opportunities for vaccination and improve vaccination coverage. Rigorous trials are required to confirm these findings and increase the certainty of the current evidence base.

VACCINES 2

1 OHS A07 - VACCINES - SALONS AB

Development of a highly pathogenic avian H7N9 influenza disease model in mouse

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H7N9 influenza virus is a threat to public health because it has caused 1557 human laboratory-confirmed cases as of 25 July 2017, with 605 of them resulting in death. Although the avian origin H7N9 virus is currently unable to effectively transmit between humans, the potential of acquiring this trait through adaption poses an imminent pandemic threat to society. To better understand the pathogenesis of H7N9 virus and to ultimately develop and evaluate novel vaccine protection, we established a mouse disease model infected by the highly pathogenic avian influenza A/British Columbia/2015 (H7N9) virus. For this model, four groups of 12 mice each were infected intranasally with either different doses of the virus (10^3 pfu/mouse, 104 pfu/mouse and 105 pfu/mouse) or PBS which served as the mock control. Both body weight and survival rate were monitored daily for 12 days. Mice were sacrificed and organs collected when they fell below 20% of their total body weight. On day 2 and 5 post-infection, 3 mice from each group were sacrificed and the lung, spleen and brain were collected.

In the 10^3 pfu/mouse group, 50% of the mice fell below the body-weight cut-off by day 7 and were sacrificed, whereas the rest of the mice fell below the cut-off on day 8 and were also sacrificed. Similarly, in the 104 pfu/mouse group, 100% of the mice fell below the cut-off weight by day six and were sacrificed. In the 105 pfu/mouse group, 50% of the mice were sacrificed by day four, and the rest sacrificed at day five. On the last day (day eight) whereby the last mice of virus groups were sacrificed, the PBS mock group was also sacrificed and the trial was finished. Currently, cytokine and chemokine profiles as well as viral titres in the collected samples are being analyzed. For future studies 103 pfu/mouse will be chosen. This model will allow identification of viral virulent factors and evaluation of antiviral interventions.

2 OHS A07 - VACCINES - SALONS AB

A trial to assess the thermotolerance of an inactivated rabies vaccine

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2: MSD Animal Health, Netherlands;
3: Global Animal Health Tanzania;
4: University of Glasgow, UK;
5: MSD Animal Health, UK

BACKGROUND: Canine mediated human rabies is a neglected tropical zoonotic disease responsible for approximately 59,000 deaths and 8.6 billion USD in losses annually. The highest incidence is in rural Africa. Where annual mass dog vaccination (MDV) is implemented coverage of 70% will eliminate rabies. Teams in vehicles usually deliver campaigns, however this is expensive and, due to the requirement to refrigerate vaccines, reach is limited to areas in proximity to facilities with refrigeration units. Thermotolerant vaccines, storable at ambient temperatures for extended periods, could alleviate these constraints. The study's aim was to investigate the thermotolerance of the Nobivac® Rabies vaccine, commonly used in MDV around the world. Our objective was to determine whether the immunological response following non-cold-chain storage was not inferior to the response elicited by doses of the same vaccine following cold- chain storage (4°C).

METHODS: A controlled and randomized non-inferiority trial was carried out comparing the serological response at four weeks post vaccination in Tanzanian dogs inoculated with vaccine stored at elevated temperatures for different periods of time, with the response in dogs vaccinated with vaccine stored at 4°C.

RESULTS: The effectiveness of the vaccine at stimulating rabies neutralizing antibody was not inferior to cold-chain stored vaccine when it was stored for up to six months at 25°C or for three months at 30°C.

CONCLUSIONS: The neutralising antibody titre (a surrogate of protection) stimulated by the vaccine following extended storage at high temperatures is not inferior to cold- chain stored vaccines. These findings enable consideration of novel delivery strategies. For example vaccines could be stored in remote communities for extended periods allowing dogs to be vaccinated throughout the year, rather than annually. This could result in more consistent coverage (Figure 1) with less risk of herd immunity dropping below the critical threshold, below which rabies transmission is sustained. As with the successful smallpox and rinderpest eradication programs, a thermotolerant rabies vaccine that enables communities to manage their own campaigns could have a transformative impact on global rabies elimination plans ('Zero by 30').

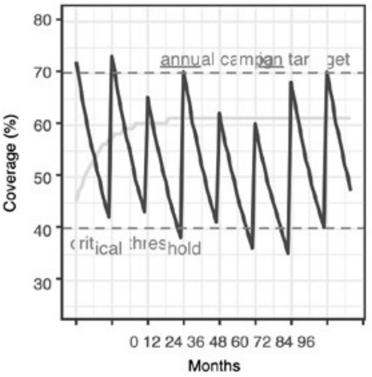

Figure 1: Blue line is hypothetical vaccination coverage, with peaks representing levels immediately after annual campaigns. Subsequent decline results from birth of susceptible pups and natural mortality of vaccinated dogs. Coverage is expected to remain above the critical threshold (lower red line) if the target of 70% (upper red line) is reached. The green line shows hypothetical coverage following community-managed delivery using vaccines stored locally and used throughout the year.

3 OHS A07 - VACCINES - SALONS AB

Acceptance of heterologous prime-boost vaccination regimens – an assessment

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BACKGROUND: Heterologous prime-boost regimens involve delivering antigens through different vaccine types, administered in a defined sequence. The approach is used to develop vaccines inducing both humoral and cellular immune responses as considered necessary against some major infectious diseases for which no efficacious vaccines are available, such as tuberculosis, HIV and Ebola virus disease. Additionally, the approach might become relevant for anti-cancer vaccines. Several vaccine candidates are in the development pipeline but none have reached licensure yet. An assessment has been performed to explore the potential future acceptance and uptake of the heterologous prime-boost vaccination concept.

METHODS: Following a literature review, 62 semi-structured key informant interviews were conducted with representatives of global and national stakeholders including National Medicines Regulatory Authorities, vaccination programs, health workers, academics and non-governmental organizations in 6 countries across 4 continents. Additionally, a quantitative online survey was answered by 50 respondents. It presented different scenarios in which the regimen might be introduced and asked respondents to indicate the expected benefits and challenges.

RESULTS: The majority of the respondents were unfamiliar with the heterologous prime-boost approach, despite belonging to the vaccine and public health community. Regional differences in knowledge and implementation considerations about the heterologous prime-boost vaccination approach were noted amongst respondents. While the overall first reaction to the approach was cautiously positive, familiarity and excitement grew the closer to research the key informant worked. Particularly appealing was the prospect of developing vaccinations against major public health threats. Respondents working on vaccine delivery and logistics expressed stronger reservations, mainly linked to the challenge of ensuring complete vaccination as per recommended schedule. A scenario in which a heterologous prime-boost vaccine was offered to adults to protect them against a disease for which currently no vaccine is available was considered the most likely, followed by a scenario in which such a vaccine, or an alternative to an existing vaccine requiring more than 2 appointments, was offered to children as part of the EPI schedule. Deploying heterologous prime-boost vaccines in anticipation of, or in response to, a disease epidemic was seen less favourably. With regard to licensure and uptake at country level, it was highlighted that such a product needed to be assessed holistically, taking safety, potential impact, delivery concepts, as well as communications into account.

CONCLUSIONS: Respondents were generally excited about a vaccination technology offering the prospect of controlling major diseases, but were conscious about the potential logistical challenges associated with its delivery. There is a need to prepare the public health community via proactive, transparent and scientifically solid communication.

4 OHS A07 - VACCINES - SALONS AB

Identifying Genomic Predictors of Vaccine Response in Swine

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Vaccination is recognized among the most effective tools for the control of infectious diseases, and is a widely-used disease-prevention strategy in the pig industry. However, response to vaccination can be highly variable between individuals, and the molecular events that lead to, or anticipate protective immunity are not well understood. We investigated gene expression patterns in whole blood and microbiome signatures in the gut as potential predictors of a protective immune response. The effect of raising pigs with or without antibiotics on these traits was also investigated.

Mycoplasma hyopneumoniae (M.hyo) vaccine was chosen as an exemplifier, because it elicits both humoral and cell-mediated immune responses. Healthy M.hyo infection free piglets (n=120) were used at the University of Alberta, Canada, swine research facility. At processing, 80 piglets received 0.5 ml Oxytetracycline, whereas the remaining were raised antibiotic free. Blood samples for RNA-Seq analysis were collected on experimental Day 0 (D0; 28 days of age) just prior to vaccination, D2, and D6 post-vaccination. A vaccine booster was given at D24. Fecal samples for microbial DNA sequencing were collected at 7 days of age, and on experimental D0 and D35. At D35, blood samples were collected, and M. hyo-specific antibodies in serum were quantified, and the results were used to classify pigs based on antibody titer levels, and groups of 'high' and 'low' responder pigs (n=15 each) were identified.

Biological activities including: leukocyte migration, recruitment, activation and migration of immune cells, adhesion of phagocytes, proliferation of T lymphocytes, inflammatory response, and movement of antigen presenting cells, increased in the 'high' group at D2. In contrast, cytotoxicity of T lymphocytes, synthesis of reactive oxygen species, and immune response of cells, decreased in 'low' compared to 'high' pigs. At D6, the 'low' group was associated with a decrease in migration of cells, phagocytosis, immune response of T lymphocytes, inflammatory response, proliferation of immune cells, and delayed hypersensitivity reaction. No significant changes were observed on D0. Secreted phosphoprotein 1 (SPP1), C-C Motif Chemokine Receptor 2 (CCR2), C-X-C Motif Chemokine Ligand 8 (CXCL8), were among the genes associated with these changes. Several genes that could be potential vaccine response biomarkers or predictors were also identified. Fecal bacterial profile revealed significant differences between the high and low responder pigs, and between pigs raised with or without antibiotics at different time points, suggesting a role of microbiota in vaccine response.

The results suggest that, the 'high' pigs had immunologically competent cells prior to vaccination, hence, were able to mount an effective and specific immune response following the vaccination, compared to the 'low' ones. Therefore, gene expression biomarkers and microbiota profile could be potential predictors of vaccine response, and thus, improve cost-effectiveness of vaccination, an important industry consideration.

5 OHS A07 - VACCINES 2 - SALONS AB

Q fever vaccine failure rate, duration of longevity of immunity and associated demographic factors in Australia

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BACKGROUND: Since its commercial availability in Australia in 1989, the Q fever vaccine (Q-Vax) vaccine is considered highly effective in adults and proven to be a complete and long lasting vaccine. Though there were studies and meta-analysis that reported 83% - 100% efficacy rate of the Q fever vaccine, there is limited understanding of the efficacy as a result of lack of well-designed follow up studies which utilize multiple source of data on Q fever. In this study, we presented a novel approach considering linked data from Q fever vaccination registry, Q fever notification and admission data reported between 1991 and 2016.

OBJECTIVE: The main aim of the study was to estimate the Q fever vaccine failure rate, determine the duration of vaccine immunity and identify demographic factors associated with duration of immunity of the Q fever vaccine.

METHODS: Retrospective cohort study with record review based on a linked and de-identified data from three large databases containing information on Q fever from 1991 to 2016 was conducted. Vaccine failure rate was computed as the number of Q fever cases per 100,000 person years of follow-ups. Multivariable Cox Proportional Hazard (CoxPH) model was fitted to estimate the duration of immunity of Q-VAX accounting for potential confounding demographic factors: age, sex, and job as covariates.

RESULTS: Lack of adherence to vaccination protocol was observed since 158 individual sought vaccination services after their notification/admission and 532 individuals with negative screening tests did not receive the vaccine. The incidence in vaccinated and unvaccinated individuals, respectively, were 5.40 [95% CI: 3.65, 7.72] and 89.50 [95% CI: 70.50, 112.00] per 100,000 person years of follow up. The duration of immunity of the Q fever vaccine found to be at least 20 years in vaccinated individuals. The hazard rate of Q fever infection was 0.07 (95% CI: 0.04, 0.10) in vaccinated individuals compared to unvaccinated individuals, i.e., vaccinated individuals were 93% less likely to be infected. The hazard was the highest from 25-54 years of age, i.e., 2.06 (95% CI: 1.18, 3.58) in 25-34 years, 2.21 (95% CI: 1.22, 4.01) in 35-44 years and 2.20 (95% CI: 1.11, 4.35) in 45-54 years. The hazard was 2.76 (95% CI: 1.11, 6.85] times higher among workers in a meat processing plant compared to other workers.

CONCLUSIONS: The vaccine is highly effective in protecting from Q fever infection. However, higher incidence was observed in unvaccinated individuals considered immune during the pre-vaccination screening. In addition, lack of adherence to vaccination protocol was observed. We pose questions on the effective implementations the Q fever vaccination program, especially, the pre-vaccination screening tests. How accurate the pre vaccination screening/or diagnostic tests in confirming prior exposure to Q fever? How adherent to vaccination protocol?

OHS ONE HEALTH SCIENCE 2

OHS SURVEILLANCE AND EARLY DETECTION

1 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

One Health-oriented outbreak response in Cameroon: A case study of the 2016 Monkeypox outbreak response in Cameroon.

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1: Mosaic, Cameroon;
2: Metabiota Inc

BACKGROUND: Monkeypox virus (MPXV) is an *Orthopoxvirus* that causes clinical disease in monkeys and appears to be hosted in either rodents and an unidentified host. It can infect humans, causing disease with potential secondary transmission. On August 14, 2016, a chimpanzee in a primate sanctuary at Mfou National Park, Cameroon, stopped eating and died the next day. Lesions consistent with Monkeypox infection (MPXV) were noted at the time of death. Government technical staff from the Ministry of Livestock (MINEPIA), Ministry of Defense, Ministry of Forestry and Wildlife (MINFOF) and Ministry of Health (MINSANTE) established a multi-sectorial team to manage the outbreak using a One Health (OH) approach to implement surveillance and control measures.

METHODS: MINFOF and MINEPIA staff collected specimens from the dead chimpanzee, additional animals with suspected MPXV infections, and took environmental swab samples from the enclosure housing the infected chimpanzees. Monkeypox reservoir surveillance was initiated by collecting samples from rodents captured around the enclosures of the chimpanzees infected with MPXV. All samples were sent to the Military Health Research Centre (CRESAR) in Yaoundé for analysis using a real-time PCR assay.

RESULTS: The outbreak occurred in a group of 23 healthy chimpanzees at a sanctuary that housed approximately 300 primates in 18 enclosures. The outbreak killed two chimpanzees, 19 additional chimpanzees had clinical signs consistent with MPXV infection, and 22 humans were exposed to the infected animals and enclosures. Within 24 hours of the first chimpanzee's death, MPXV was confirmed at CRESAR with support from the USAID PREDICT project and the results were reported to MINEPIA. An official report was sent to OIE 10 days after first symptoms were detected, in contrast to the 16 day reporting lag during the 2014 MPXV outbreak. Rodents sampled during the active surveillance were all negative. Control measures were put into place one day after lab confirmation of the first case; these included closing the sanctuary to the public, limiting access to the affected group, enhanced disinfection procedures, training of staff in the use of PPE, reduced animal contact, and temperature checks for exposed workers. The rapid mobilization of the multisectoral team allowed for rapid identification of the virus, deployment of response protocols, no spread of the virus beyond the one enclosure, and no human infection.

CONCLUSIONS: A OH multi-sectorial approach greatly improved the investigation and response capabilities which, in turn, enabled Cameroon to quickly detect, confirm, and report on MPXV. It also allowed Cameroon to implement successful control measures which resulted in containment of the outbreak. This decreased the risk of human exposure and the potential economic impact of this zoonotic virus.

2 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

Zoonotic Enteric Parasites in Humans, Animals, and Drinking Water in Mongolian Households and Their Associated Risk Factors

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BACKGROUND: Mongolians live in close harmony with their domestic animals through harsh weather and among rough, expansive terrain. But this contact puts herders and their families at risk for zoonotic disease. As part of a larger study on zoonotic enteric parasites, the current research aimed to determine of presence of Cryptosporidium spp., *Giardia lamblia*, and *Entameoba histolytica* in humans, animals, and drinking water from rural, peri-urban, and urban Mongolian households and to identify risk factors for zoonoses based on household survey data.

METHODS: A total of 250 households were enrolled from the rural provinces of Selenge, Zavkhan, and Dundgovi and from the capital city Ulaanbaatar, within Tov province. This cross-sectional study was carried out between April and October 2017 using a One Health framework. Following a survey on topics related to animal contact, water, sanitation and hygiene behaviors, diarrheal disease, and animal care practices, stool samples from household members and domestic animals were collected as well as a sample of the household drinking water. Multiplex real-time PCR was used to simultaneously detect the 18S ribosomal RNA gene for *Giardia lamblia* and Entamoeba histolytica and the COWP (Cryptosporidium oocyst wall protein) for Cryptosporidium spp. from all samples. Multivariate logistic regression was utilized to assess the association between the presence of zoonotic enteric parasites and household risk factors.

RESULTS: Initial analysis of household survey data shows that unimproved drinking water sources are common and adherence to drinking water treatment methods is inadequate. Self-reported hand washing is widespread after animal contact but does not often occur before preparing food, eating a meal or after visiting the toilet. Open defecation is the primary sanitation option for many rural and peri-urban households. All rural households report animal contact and cohabitation with livestock inside gers is not uncommon, especially during the winter or if an animal is sick. Many households reported diarrheal disease among their livestock in the past year with some describing a resulting herd die-off. Close contact during home slaughtering, butchering, milking, and birthing presents distinct exposure risks for rural Mongolian households. Laboratory analysis is forthcoming.

CONCLUSIONS: Our study uses a multidisciplinary One Health approach to study sectors of food, environment, animal and human health. It aims to study neglected enteric parasites in a holistic manner that will provide a more comprehensive description of the exposures and transmission pathways associated with human and animal infection from zoonotic enteric parasites. Resulting information on risk factors and the presence of pathogens in household members and the household environment will aid in developing unique messages for healthier human-animal interactions and the prevention of zoonotic diseases within Mongolia.

3 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

Evidence of silent infection of domestic pigs with Highly Pathogenic Avian Influenza H5N1 and H1N1pdm09 in ‘hot spot’ Nigeria: Is a pandemic virus already in the pipeline?

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BACKGROUND: Avian influenza viruses (AIV) potentially transmit to swine. Further reassortment in swine may contribute to the generation of pandemic strains. Associated risks of AIV inter-species transmission are greater in countries like Nigeria with recurrent epidemics of highly pathogenic AI (HPAI) in poultry and significant pig population.

METHODS: In a central slaughter house in Jos, Plateau state Nigeria, 129 tracheal swab specimens were collected from apparently healthy pigs in December 2015 to February 2016 during presence of HPAI virus H5N1 outbreaks in poultry. In addition, a total of 500 swine sera were collected as follows: 100 in 2013 when there were no cases of AIV; 300 in 2016 during AIV cases from the same slaughter house. Also, another 100 sera were obtained from another slaughter house in south west Nigeria in 2013. Swabs were analyzed by Reverse Transcriptase-Polymerase Chain Reaction (RT-PCR) and gene sequencing by Sanger methods. Sera were first screened for antibodies using competition Enzyme Linked Immunosorbent Assays (ELISAs) against influenza A virus nucleoprotein and subsequently H5 HA and thereafter subtyped by Hemagglutination Inhibition (HI) tests according to procedures described by kit manufacturer and the World Organization for Animal Health (OIE) manual.

RESULTS: Assay for influenza A by RT-qPCR yielded 43 positive samples. Twenty-two could be determined by clade specific RT-qPCR as belonging to the H5N1 clade 2.3.2.1c which was confirmed by partial hemagglutinin (HA) sequence analysis. Serologically, 222 (44.4%) and 42 (8.4%) sera were positive for influenza A virus NP and H5 antibodies, respectively. Selected sera reacted differently to H5N1 and A/H1N1pdm09 strains by HI.

CONCLUSIONS: We report for the first time in Nigeria of natural exposure of domestic pigs to H5N1 and H1N1pdm09 in the same population. This has implication for co-infection and gene reassortment in the mixing vessel and may result in the emergence of a novel, zoonotic or pandemic virus. The potential public health and pandemic risk requires further investigation and monitoring.

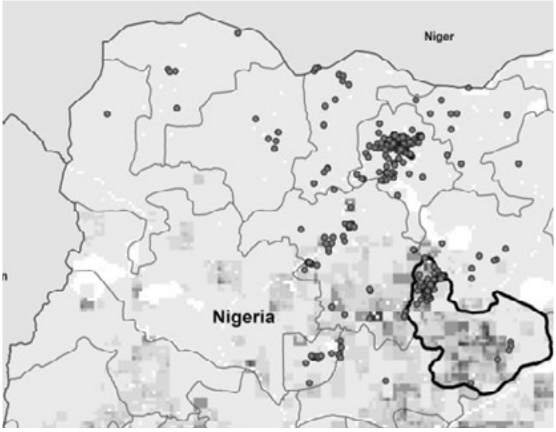

Figure 1. Map of Nigeria, Plateau state, source of pigs to the slaughterhouse. Color bar shows density of pigs in the state while dots indicate spatial distribution of HPAI H5N1 outbreaks in poultry in 2015-2016. Map generated with ArcGIS (Software: ArcGIS 10.3 by ESRI- https://www.esri.de/support-de/produkte/arcgis-for-desktop-10-3). Data source: Global Administrative Areas (http://www.gadm.org/) and Global Pig Density (2005) – GeoNetwork by FAO (http://www.fao.org/geonetwork/srv/en/main.home).

Table 1. Summary of NP (Nucleoprotein) and H5 influenza ELISA serology on three categories of sera collected from Jos (2013 and 2016) and Enugu (2013).

Sera collection	**ELISA serology**					
	NP			**H5 ELISA**		
	total	Pos	%	total	pos	%
Jos abattoir, 2016	300	183	61	183	42	22.9 (14)
Jos abattoir, 2013	100	15	15	15	0	0
Enugu slaughter slab, 2013	100	24	24	24	0	0
Total	**500**	**222**	**44.4**	**222**	**42**	**18.9 (8.4)**

Table 2. Sero-reactivity of swine influenza strains H1avN1av, H1huN2, H1N1pdm and H3N2 on selected NP-positive sera

Antigens		**Field sera ID (titre)**													
Sub-type	**Virus strain**	**353**	**186**	**30**	**24**	**100**	**202**	**15**	**56**	**286**	**72**	**48**	**129**	**204**	**293**
H1av N1av	A/sw/Germany/R1738/2011	80	40	160	20	80	40	20	20	160	40	160	160	40	40
H1hu N2	A/sw/Germany/R2107/2010	40	20	640	40	80	10	20	80	40	40	80	20	20	20
H1N1 pdm	A/sw/Germany/R26/2011	1280	1280	640	320	320	320	320	320	1280	640	1280	640	640	640
H3N2	A/sw/Germany/R96/2011	10	10	80	10	10	20	10	10	10	20	10	10	10	10

Table 3. Sero-reactivity of H5 strains to H5N1 2.3.2.1c, H5N8 2.3.4.4, H5N1 2.2. and H5N3 on selected NP positive sera

		Sera ID					
Subtype/clade	**Virus strain**	**106**	**192**	**229**	**294**	**232**	**242**
H5N1 2.3.2.1c	A/Dubai/AR/3435/14	640	640	1280	160	320	320
H5N8 2.3.4.4.b	A/Tufted duck/AR/8444/16	10	10	10	10	10	10
H5N1 2.2.	A/Whooper swan/Germany/R65/2006	40	10	10	160	20	80
H5N3	A/Common teal/England/7894/2006	80	80	640	320	160	320

4 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

Phylogenetic analysis of viruses detected in mosquitoes, horses and humans supports epidemiological data indicating two different geographical origins for epidemics of encephalitis due to Murray Valley encephalitis virus

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BACKGROUND: Murray Valley encephalitis virus (MVEV) is a member of the Japanese encephalitis serogroup of flaviviruses. It is maintained primarily in a mosquito-water bird cycle. Human illness varies from a nonspecific febrile illness to severe encephalitis, with a mortality of 20-25%, and persisting neurological deficits in 50% of survivors. Initial outbreaks occurred on the Australian east coast but, since 1975, activity has been almost completely confined to north-western (NW) Australia. An enzootic mosquito-water bird focus there leads to MVEV activity every wet season, and usually less than five human cases. Occasional larger outbreaks that spread beyond these areas, including uncommon instances of MVEV activity in central and south-eastern Australia, have been thought to represent spread from this enzootic focus. In 2011, extensive rainfall and flooding occurred over much of Australia, followed by the largest outbreak of MVEV encephalitis in humans and animals since 1974.

METHODS: Mosquitoes were collected from multiple sites within the Kimberley region at the end of the 2011 wet season using standard EVS-CO2 light traps. They were stored and transported on dry ice for speciation and virus culture, followed by sequencing of the E-gene of isolates.

RESULTS: Between March and May 2011, 16 confirmed cases of MVEV encephalitis occurred: 13 in NW Australia and three in south-eastern (SE) Australia. Cases were also reported in horses and ducks in SE Australia, and there were extensive MVEV seroconversions in sentinel chickens. We obtained partial or full E gene sequences for 17 MVEV isolates from mosquitoes collected in the Kimberley region. Phylogenetically, all the 2011 NW mosquito MVEV sequences plus a human isolate in GenBank formed a group within sub-lineage 1A of genotype 1 (G1-1A), which has been confined to NW Australia and Papua-New Guinea since 1951. In contrast the isolate from a Victorian (SE Australia) horse belonged to sub-lineage 1B (G1-1B), which has been widely spread across Australia since the 1960s.

CONCLUSIONS: The phylogenetic data combined with the epidemiology strongly suggest two simultaneous but separate epidemics: one due to G1-1A arising in NW Australia, the other due to G1-1B and having a separate origin which, as G1-1B is widespread in northern Australia, we could not determine where. However, the pattern of cases and historical records of outbreaks and sporadic cases of MVEV encephalitis suggest a reservoir within eastern Australia as well. Confirming this is important in better understanding how and when epidemics may occur, and how interventions should be directed. Ongoing human, insect and animal surveillance, with collective analysis of data, will be of great ongoing value.

5 OHS B01 - SURVEILLANCE AND EARLY DETECTION - SALONS CD

Prevalence and characterization of Brucella spp. in slaughter animals in Gauteng Province abattoirs and assessment of zoonotic risk factors posed to abattoir workers

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BACKGROUND: Brucellosis is a neglected zoonotic disease that affects humans, and domestic animals; a One Health concern. Globally, abattoirs are used for passive and active surveillance of diseases of both economic and public health significance. Surveys by serological assays of slaughter animals can detect newly introduced disease agents and monitor disease control and eradication programmes. This research goal was to determine the prevalence and characterize *Brucella* spp. in slaughter livestock in abattoirs in Gauteng Province, South Africa and to assess the zoonotic risk factors posed to abattoir workers.

METHODS: Fourteen abattoirs in the Gauteng province were visited and unclotted blood and lymph node samples were collected from 256 animals (199 cattle and 57 sheep). Rose Bengal test (RBT), complement fixation test (CFT) and indirect enzyme linked immunosorbent assay (iELISA), were used to determine the sero-prevalence of brucellosis in the slaughter animals. Lymph node samples were cultured for *Brucella* spp. using standard methods. AMOS PCR was used for molecular characterization; isolates were biotyped using standard methods. A structured questionnaire in Microsoft office was used to interview 143 abattoir workers to assess perceptions and risk factors that could predispose the workers to zoonoses. A 'One Health' approach was applied to produce educational materials such as brochures, mugs and posters, which were used to sensitize the abattoir workers and managers. Data collected were managed using Microsoft access, EpiData for questionnaires, and R CRAN was used for descriptive analysis.

RESULTS: The RBT screening revealed a sero-prevalence of 11.1% (22 of 199) for brucellosis. The CFT confirmed 2.5% (5 of the 22) as sero-positives and iELISA confirmed 5.5% (11 of 199) cattle as sero-positive for brucellosis. AMOS PCR characterized DNA of seven isolates from lymphatic tissues of the cattle as three *B.abortus* and four *B.melitensis*, of which five (5 of 7) were biotyped as two B. abortus biovars 1 and four as *B.melitensis*, of which one was biovar 2 and two were biovars 3. *Brucella ovis* iELISA revealed a sero-prevalence rate of 1.8% (1 of 57) in the sheep tested and AMOS PCR detected *B. ovis* DNA in the lymphatic tissues of the sero-positive sheep. Of the 143 abattoir workers interviewed, 78% were males and 22% were females. Of these workers, 37.1% believed they cannot contract zoonoses from working at the abattoir, 83.9% had hand cut injuries while on duty, 32.9% experienced fever and flu-like symptoms on duty and 88.1% do not seek medical attention when sick.

CONCLUSIONS: The combination of RBT and iELISA was more specific than RBT and CFT in this study. *Brucella* isolates were recovered from the cattle sampled. Brucellosis poses a potential zoonotic risk to abattoir workers. We recommend abattoir workers be tested to obtain baseline data to brucellosis exposure.

OHS INTERVENTION STRATEGIES

1 OHS B02 - INTERVENTION STRATEGIES - SALONS CD

Adapting the determinants of health perspectives to developing and implementing integrated priorities to address social and ecological expectations for fisheries and community health

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BACKGROUND: We hypothesized that a unified salmon health definition based on the determinants of health model from human population health could account for the socially and ecologically complex and cumulative nature of health in order to integrate information across scientific, social and management perspectives. Our objective was to adapt the determinants of health model to salmon and assess if that model could be used to foster dialogue to find common priorities between government and Indigenous fisheries management groups to meet community, fisheries and ecological needs.

METHODS: A systematic, thematic literature analysis was used to develop a draft socio-ecological model of salmon health. Themes were based on the human determinants of health. An expert opinion method determined if the draft model reflected expert perceptions, if the model could be used to detect shared priorities, and where human-animal and environmental interactions drove health. Experts from Fisheries and Oceans Canada and the First Nations Fisheries Council were identified using peer-referential techniques. A diagrammatic approach to network analysis using open-source network visualization and analysis software and the Fruchterman Reingold algorithm were used to visualize the relationships between the determinants. The Eigenvector centrality statistic was used to describe determinants' interconnections. The most negatively and positively important relationships identified by either group was determined by multiplying the mean score of the relationships by the number of times that experts mentioned relationships.

RESULTS: Both literature and expert opinion supported the validity of adapting the determinants of health model to describe salmon health as a cumulative effect of interaction abiotic, biotic and social determinants. The draft model was agreeable and understandable to both expert groups. These resource managers and researchers emphasized abiotic environmental determinants over pathogens, however, fish health policy emphasized pathogens as critical determinants of health. Human dimensions of salmon health were absent from expert opinion. The network analysis allowed visualization of critical relationships and comparison between groups; finding common ground between the regulators and fishing rights holders.

CONCLUSIONS: The One Health philosophy of integrating concepts of human and animal health lead to a useful approach to re-defining how to characterize and manage salmon health. The resulting conceptual model served as a useful tool to help regulators see how their various programs influenced health. It also was an understandable tool to visualize common priorities between a government and First Nations fisheries management agency. Further work to define and validate critical determinants and develop consensus on socially and biologically meaningful thresholds is needed to move the model from a planning and dialogue tool to a measuring and managing tool.

2 OHS B02 - INTERVENTION STRATEGIES - SALONS CD

Control versus elimination of Taenia solium in eastern Zambia: Preliminary assessment of a two-year interventional program in the Katete and Sinda districts in the Eastern Province of Zambia

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BACKGROUND: The zoonotic tapeworm Taenia solium causes significant health and economic burdens worldwide. A large-scale interventional study is currently underway in Zambia, to evaluate and compare the effectiveness of an integrated human- and pig-based T. solium elimination program versus a lower-intensity pig-only control strategy.

METHODS: A two-year intervention period was conducted in the Nyembe (Katete district), and Chimvira and Herode (Sinda district) communities in the highly endemic Eastern Province of Zambia, from March 2016 to November 2017. Integrated 'elimination' interventions were conducted in Nyembe on all eligible humans (praziquantel 10mg/kg PO or niclosamide 2g PO) and pigs (oxfendazole 30mg/kg PO and TSOL18 vaccine, 1mL intramuscular) at four-monthly intervals for six iterations (see Fig. 1.) In Chimvira, the 'control' study arm, eligible pigs were given oxfendazole (30mg/kg PO) once yearly for two iterations ('control' interventions).Herode was the 'negative control' study arm, in which no chemotherapeutic interventions were conducted. Health education was implemented in all three study arms. Monitoring and treatment will continue in the intervention study areas for another three years.

Sampling surveys determined porcine cysticercosis (PCC), taeniasis (TS) and/or human cysticercosis (HCC) prevalence in the various study arms at baseline (0 months), mid-intervention (+12 months) and post-intervention (+24 months) as outlined in Fig. 1.

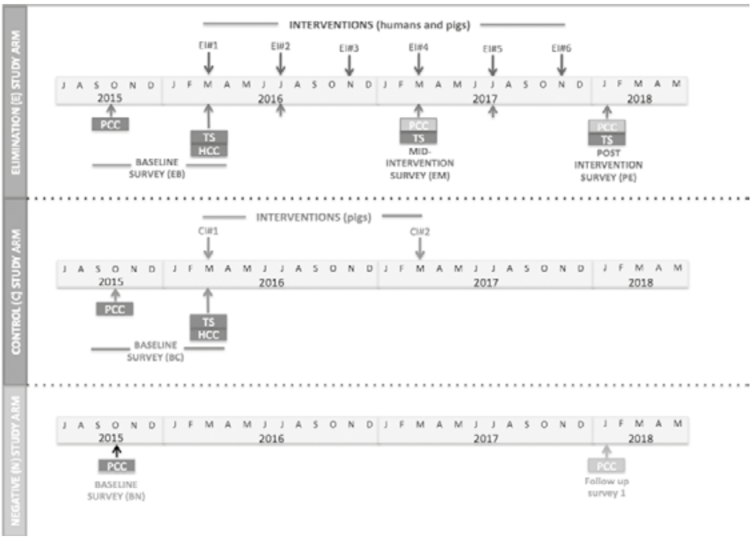
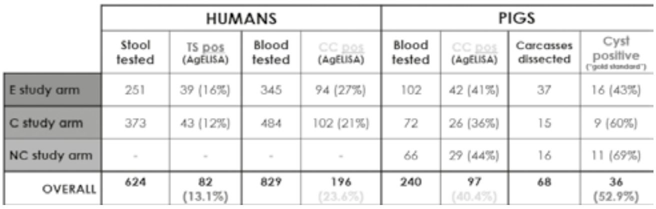


Figure 1: Timeline of project activities during the intervention period. EI#1-6 represent Elimination interventions; CI#1-2 represent Control interventions. The baseline, mid- and post-intervention surveys indicate which diseases are tested for at each time point (PCC, TS and/or HCC).

Preliminary results and **CONCLUSIONS:** Average baseline prevalence of TS was 13% (copro AgELISA), and of human CC was 24% (serum AgELISA). Average baseline PCC prevalence was 40% (serum AgELISA) to 53% (carcass dissection) (see Table 1.)



	HUMANS				PIGS			
	Stool tested	TS pos (AgELISA)	Blood tested	CC pos (AgELISA)	Blood tested	CC pos (AgELISA)	Carcasses dissected	Cyst positive ("gold standard")
E study arm	251	39 (16%)	345	94 (27%)	102	42 (41%)	37	16 (43%)
C study arm	373	43 (12%)	484	102 (21%)	72	26 (36%)	15	9 (60%)
NC study arm	-	-	-	-	66	29 (44%)	16	11 (69%)
OVERALL	**624**	**82 (13.1%)**	**829**	**196 (23.6%)**	**240**	**97 (40.4%)**	**68**	**36 (52.9%)**

Table 1: Results from Baseline survey conducted in study arms in October 2015 (pigs) and March 2016 (humans).

At mid-intervention (March 2017), TS prevalence was 6.8%, compared to 16% at baseline (E arm). This substantial reduction in prevalence is expected to continue throughout the remainder of the intervention period. (Mid-intervention PCC prevalence could not be determined due to low pig numbers following an African swine fever outbreak.)

Results of the post-intervention survey (to be conducted in January 2018) will be presented and discussed.

3 OHS B02 - INTERVENTION STRATEGIES - SALONS CD

An integrated human-animal health approach to reduce the disease burden of psittacosis

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BACKGROUND: Psittacosis is a highly underdiagnosed zoonotic disease linked to birds. Notified infections in humans mainly present as community-acquired pneumonia (CAP). For a timely response in zoonotic outbreaks such as psittacosis, a prompt exchange of epidemiological, clinical and laboratory data between the human and animal health chains is vital. The aim of this study is to reduce the disease burden of psittacosis via the establishment of a 'One Health' data exchange platform for psittacosis and to add essential information on C. *psittaci* in humans and animals.

METHODS: The research is organised in a five-year project with seven work packages: 1) develop an integrated human-veterinary information platform, 2) implement a 'One Health' typing method for C. psittaci, 3) determine the occurrence of C. *psittaci* in selected animal populations, including the poultry sector, 4) reduce the human diagnostic deficit, 5) determine disease burden in humans and identify the main animal reservoirs for zoonotic transmission, 6) perform improved source finding of reported human and animal cases, and 7) realise legally backed interdisciplinary cooperation. Nine Dutch partners and one Belgian partner are participating in the project.

RESULTS: An integrated, web-based information platform has been established in which human and animal case information, including OmpA genotyping information, can be uploaded and exchanged between the medical and veterinary domain. A digital source finding tool was developed and is now in use by the human and veterinary public health authorities. Disease burden from psittacosis in humans in the Netherlands was estimated at 222 (95% CI 172–280) Disability-Adjusted Life Years (DALYs) per year, highlighting the public health importance of psittacosis. Essential input for the burden estimate was provided by a meta-analysis of published CAP aetiological studies that indicated C. *psittaci* was the cause in 1.03% (95% CI 0.79–1.30) of CAP cases. To reduce the diagnostic deficit in humans, a PCR starter's kit was developed and offered to labs. To assess the presence of *Chlamydia spp*. on poultry farms, pooled faecal samples were collected from 151 layer hen farms, all testing negative for C. *psittaci* DNA. But, C. *gallinacea* DNA was detected on 47% of these farms. Exploratory spatial analysis of notified human psittacosis cases showed a large cluster that covered a highly poultry-dense area, and several smaller clusters. In multivariable analysis, the presence of chicken-processing plants and slaughter duck farms in a municipality were associated with a higher rate of human psittacosis notifications.

CONCLUSIONS: We show the three-year results of an integrated human-animal health project to reduce the disease burden of psittacosis. Research highlights include a relation between human psittacosis notifications and poultry density, and C. *gallinacea* but nót C *psittaci* detection on layer farms. Legal aspects of human-veterinary collaboration require further attention.

4 OHS B02 - INTERVENTION STRATEGIES- SALONS CD

Factors associated with improved uptake of Johne's Disease control mechanisms on Australian dairy farms: Regulatory insights from evolving control strategies

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BACKGROUND: Johne's Disease (JD), caused by *Mycobacterium avium ssp. paratuberculosis* (MAP), is a debilitating disease affecting dairy cattle in most countries with established dairy industries. Australia has a relatively low herd prevalence of infection (1.8%) yet a well-established livestock export industry relies on certification of freedom from numerous diseases including MAP. The convergence of animal welfare, farmer, industry, and government objectives for JD control presents an issue which has responded variably to different control policies globally. Over the last decade, there has been debate over the link between MAP and human gastrointestinal disease. Although recent evidence refutes this link, this perception contributes to the challenges of a complex One Health dynamic. Producer frustration with previous control programs implemented over the years, including various quarantine measures as well as subsidized and unsubsidized testing and culling, yielded unsatisfactory adoption of programs, prompting a review. As of 2017, JD in Australia remains a notifiable disease, though farms certify disease freedom through a voluntary, producer driven, risk assessment-based control program as part of integrated biosecurity planning intent on fostering increased participation for more successful JD control. We report on a study underway that aims to identify factors associated with choice of a JD control strategy on Australian dairy farms under the current regulatory climate and interpret these findings relative to JD control progress in other countries tackling this problem.

METHODS: Dairy farms in six Australian states are being surveyed proportionately using an online questionnaire capturing demographics, perceptions of JD control strategies, and control mechanisms in place. Assuming a 15% response, we are targeting > 2500 farms to obtain data from approximately 400 farms (6-7% of all Australian dairy farms), their veterinarians, milk processors, and state governments. The questionnaire covers knowledge of JD, attitudes and perceptions to JD control, and farm demographics. Choice variable regression methods will be used to identify associations between independent variables and choice of a control strategy. Tree and node diagrams coupled with joint probability functions and Bayesian statistics will be applied to estimate the likelihood of using a control mechanism under various scenarios of farm demographics, perceived benefits, and perceived barriers.

RESULTS: The relationship between demographics, knowledge, perceptions, attitudes to JD control policy, and choice of a control strategy will be described. We expect to identify key factors of a successful regulatory environment supporting JD control.

CONCLUSIONS: Considering the moderate success of Australian JD control programs admixed with some pitfalls over time, this evolution presents a valuable learning opportunity for understanding better the regulatory policy opportunities for all stakeholders to improve JD control. Identifying the factors influencing a successful participatory approach through integrated biosecurity may lead to healthier, more productive animals thereby improving sustainability and reducing the public health risk of MAP.

5 OHS B02 - INTERVENTION STRATEGIES - SALONS CD

Harm reduction: A strategy for One Health action in the face of uncertainty and conflict

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BACKGROUND: We hypothesized that harm reduction, effectively used in public health against complex, persistent problems such as addiction and homelessness, could promote collaboration and cooperation in cases where scientific uncertainty and social conflict stagnate action at the wildlife-society-environment interface.

METHODS: A scoping literature was supplemented with two qualitative case studies; (1) conflicts between community well-being and wild monkeys in St. Kitts and (2) aquaculture conflicts with marine conservation in Canada.

RESULTS: There is little evidence that harm reduction and its allied field of health promotion have guided risk management at the human-animal interface. The health belief model, theory of planned behaviour and other health promotion and harm reduction theories are rarely in the animal health lexicon. Case study #1 - Recommendations for Fraser River sockeye salmon recovery were consistent with harm reduction principles, but the current management approach focussed solely on hazard elimination. Debate over the attributable fractions of harm from specific hazards predominated the policy and science dialogue. It was no one's responsibility to integrate and coordinate the social and ecological dimensions of harms to identify opportunities for collaborative governance or action. Diverging values, scientific uncertainty, and multiple ideologies resulted salmon farming remaining a subject of public debate and source of social conflict that prevented harm reduction actions. The harm reduction approach was incorporated into recommendations by a multi-stakeholder government advisory panel as a new mechanism to motivate collaborative action. Case study #2 - Introduced vervets are impeding progress on three important areas of climate change adaptability in St. Kitts; (i) agriculture and food security; (ii) human health; and (iii) community livelihoods. There were strong divergent views on how to manage this issue. Lacking resources, only irregular attempts have been made to control this socio-ecological conflict, most often looking to biological controls. Harm reduction was seen as a viable approach to strategic collaboration to reduce social conflicts and climate vulnerabilities created by the vervets while protecting the cultural and economic benefits they bring.

CONCLUSIONS: A lack of awareness of the scope and uncertainty about the purpose of harm reduction impedes the animal health community's engagement with the human dimensions of community health and environmental risk management. There is little scholarship on how to enable people to increase control over and to improve their resilience to socio-ecological shocks by managing their relationships with animal health. Harm reduction approaches helped two intractable problems prioritizes issue(s) for which the group can agree progress can feasibly be made. It was seen as a means to reduce conflict by reorienting to collaborative governance and promoting a shared understanding of issues.

OHS PATHOGENESIS 1

1 OHS B03 - PATHOGENESIS 1 - SALONS CD

Cytokine patterns in Hemorrhagic Fever with Renal syndrome and Crimean-Congo Hemorrhagic Fever

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BACKGROUND: Two viral hemorrhagic fevers are present in the Balkans, hemorrhagic fever with renal syndrome (HFRS) caused by hantaviruses (mainly by Dobrava-Belgrade virus, DOBV) and Crimean-Congo hemorrhagic fever (CCHF) caused by CCHF virus (CCHFV). Even though the pathogenesis of these diseases is not fully understood, the activation of immune response system and the secretion of cytokines is thought to play a major role. Aim of the present study is to evaluate and compare the cytokine patterns in patients with HFRS and CCHF.

METHODS: The study included 6 serum samples from 5 HFRS patients (5 male) aged 25-68 years (median 35) and 6 serum samples from 6 CCHF patients (2 male) aged 25-62 years (median 44.5). One HFRS and two CCHF cases were fatal. All samples were collected 3-7 (mean 5.9) days after onset of the symptoms. Patients' samples were divided into groups according to the outcome of the disease. Serum samples from 16 apparently healthy individuals (9 males) aged 18-65 years (median age 45 years) were included in the study as control group. The quantification of 27 cytokine and chemokine serum levels was done using the kit Human Grp I cytokine 27-Plex-Panel in Bio-PlexTM Suspension Array system (Bio-Rad Laboratories, CA). The statistical analysis was performed using the software package IBM SPSS Statistics version 22 (SPSS Inc). Mann-Whitney U-test or Kruskal-Wallis test was used to evaluate the differences between groups. The significance level was set at p-value of < 0.05.

RESULTS: Compared to the control group, mean level of RANTES was decreased in both HFRS and CCHF patients ($p<0.05$). Similarly, in fatal HFRS and CCHF cases IP-10 was increased and IL-4 was decreased ($p<0.05$). Levels of IL-10 were increased only in fatal HFRS cases ($p<0.05$), while in fatal CCHF cases, MCP-1 and TNF-α were significantly increased and IL-12 was decreased ($p<0.05$). Mean levels of IL-6 and IL-8 were increased in all HFRS cases and in fatal CCHF cases ($p<0.05$). VEGF was increased only in HFRS survivors ($p<0.05$). No significant differences were found among fatal cases, while among survivors, mean levels of IL-8, IL-9, IL-10 and eotaxin were higher in HFRS patients ($p<0.05$).

CONCLUSIONS: Even though HFRS and CCHF are both hemorrhagic fevers, several similarities and differences were noticed in their cytokine patterns. The released cytokines may affect the course and the outcome of the disease. Understanding the role of cytokines may help to decipher the pathogenesis of viral hemorrhagic fevers, identify potential biomarkers and facilitate the development of new therapeutic approaches for these patients in the future.

2 OHS B03 - PATHOGENESIS 1 - SALONS CD

Replication of naturally occurring MERS-CoV protein 4a deletion variants in vitro and in vivo

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BACKGROUND: Middle East respiratory syndrome coronavirus originates from dromedary camels and ultimately from bats. Zoonotic infection of humans can cause a severe lower respiratory tract infection. Despite sequencing efforts, there is no substantial evidence for viral genome changes associated with human adaptation. However, viruses that contained a 48-nucleotide deletion in ORF4a were detected in humans in Jordan in 2015 (Lamers et al., 2015). Overexpression studies suggest that the protein encoded by ORF4a (p4a) is a dsRNA-binding protein that acts as an interferon suppressor by shielding viral dsRNA from recognition by either MDA5 or PACT (Sui et al., 2014; Niemeyer et al., 2013). Here, we aimed to assess the *in vitro* and *in vivo* replication of clinical isolates containing a naturally occurring deletion in p4a.

METHODS: Two viruses containing a deletion in p4a were isolated from clinical specimens obtained from the Jordan 2015 outbreak. Virus growth curves, comparing these novel isolates with the EMC strain (which contains an intact p4a), were performed on Vero, Huh-7, Calu-3 and primary normal human bronchial epithelial (NHBE) cells to assess *in vitro* differences in growth kinetics between isolates. Furthermore, *in vivo* differences in replication were assessed in the rabbit model.

RESULTS: *In vitro* replication kinetics of the p4a deletion viruses were similar to the EMC strain in Vero, Huh-7, Calu-3 and NHBE cells. *In vivo*, the deletion viruses replicated to similar levels as EMC until 2 days post inoculation. At day 3 and 4 post inoculation, deletion variants showed ~1 log lower titers in tracheal and nose swabs, respectively. This was in agreement with fewer infected cells in the nose of animals inoculated with the deletion variant as shown by immunohistochemistry.

CONCLUSIONS: The deletion in p4a appeared to have no effect on MERS-CoV replication *in vitro* in human and monkey cells, while only limited differences were observed in the rabbit model. Although we cannot not exclude the existence of compensatory mutations in the deletion viruses that may mask the effect of the p4a deletion, our data suggests that p4a is dispensable for replication in humans and may only be required in camels or bats. This hypothesis is currently under investigation.

3 OHS B03 - PATHOGENESIS 1 - SALONS CD

The effect of antiretroviral naïve HIV-1 infection on the ability of Natural Killer cells to produce IFN-γ upon exposure to Plasmodium falciparum- infected Erythrocytes.

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5: Department of biochemistry University of Dschang Cameroon;
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7: Department of Biological Sciences Alabama State University,;
9: Laboratory of Immunology Severance Biomedical Science Institute Yonsei University College of Medicine Seoul

BACKGROUND: In sub-saharan Africa intense perenial *Plasmodium species* transmission coincides with areas of high prevalence of human immunodeficiency virus type 1 (HIV) infection. This implies that antiretroviral naïve HIV infected people living within theses regions are repeatedly exposed to *Plasmodium species* infection and consequent malaria. NK cells are known to contribute to malaria immunity through the production of IFN-γ after exposure to *Plasmodium falciparum*-infected erythrocytes (iRBC). However in antiretroviral naïve HIV-1 infection these functions could be impaired. In this study we assess the ability of NK cells from antiretroviral naïve HIV-1 infected people to respond to iRBC.

METHODS: This study was approved by the National ethical committee of Cameroon with administrative authorization number 2015/08/631/CE/CNERSH/SP. Participant's enrolment was voluntary and each participant signed an informed consent. Twenty three (23) ARV naïve HIV-1 infected participants and eighteen (18) HIV-uninfected negative controls aged between 21 to 65 years were recruited to be part of this study. After venous blood drawing, Peripheral Blood Mononuclear Cells (PBMC) were isolated from the whole blood by density gradient centrifugation (using ficoll-hypaque). Magnetically sorted NK cells from anti-retroviral naive HIV-1 infected people were tested for their ability to response to iRBC following in vitro co-culture. NK cell IFN-γ production after coculture was measured through multiparametric flowcytometry analysis.

RESULTS: Our data show a significant reduction ($p=0.03$) in IFN-γ production by NK cells from antiretroviral naive HIV-1 infected people after co-culture with iRBCs. This was in contrast to NK cells response from healthy controls which demonstrated elevated IFN-γ production. NK cells IFN-γ production from untreated HIV-1 infected participants correlated inversely with the viral load ($r = -0.5$, $p= 0.02$) and positively with total helper CD4+ T cells count ($r=0.4$, $p= 0.04$).

CONCLUSIONS: The reduction of NK cells IFN-γ production observed in ARV naïve HIV-1 infected people was closely related to HIV disease progression, as we observed an inverse correlation between IFN-γ production and plasmatic viral loads. This is probably linked with an effective immune system as lower plasmatic viral load (<2 Log10) usually correlate with the ability of individuals to control the virus. This clearly indicates that anti-retroviral naïve HIV-1 infection impairs the ability of NK cells to respond to iRBC. In malaria intense regions there is need to consider people living with HIV as highly vulnerable to malaria and should therefore be offered prophylactic malaria treatment like in pregnant women and children.

4 OHS B03 - PATHOGENESIS 1 - SALONS CD

Inflammatory effects of glyphosate and endotoxin exposure on human alveolar epithelial cells

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BACKGROUND: Pesticides are commonly applied in both occupational or non-occupational settings. Exposure to pesticides at low concentrations has shown an ability to induce lung inflammation. Glyphosate is the most common active ingredient in herbicides and pesticides containing glyphosate are the most commonly applied worldwide. Despite the benefits for food production, exposure to glyphosate has been linked to health effects including respiratory symptoms in exposed workers. However, there is little information on lung inflammation related to glyphosate exposure. Moreover, endotoxin (LPS) exposure is common for agricultural workers and is a well-known stimulant for lung inflammation. Thus, we hypothesized that glyphosate can induce lung inflammation and that co-exposure to glyphosate and LPS can further enhance the inflammatory response.

METHODOLOGY: We studied the inflammatory effects of LPS and glyphosate exposure by using a human alveolar epithelial cell line (A549). Cells were treated for 24 hours with different concentrations of LPS and glyphosate individually and in combination. Supernatants were harvested and assessed for cytokines (interleukin-8 (IL-8)) using ELISA. RNA was isolated from treated cells and tested for expression of A20 (also known as tumor necrosis factor alpha-induced protein 3, TNFAIP3) with Real Time PCR to assess the potential for gene expression inhibition of NF-kB.

RESULTS: Glyphosate alone had no effect on IL-8 release at all concentrations (0.1 mM, 1 mM, 10 mM). However, there was a significant reduction in IL-8 in cells co-treated with LPS (100 µg/ml) and glyphosate (10 mM). Further, we found an increase in expression of A20 in cells co-treated with glyphosate and LPS, with no significant reduction in cell
viability.

CONCLUSION: Taken together, our results suggest that glyphosate co-exposure may inhibit the LPS mediated lung inflammation, and A20 may be an important regulator. Future experiments include evaluation of the inflammatory effects of glyphosate and LPS coexposure in an animal model.

5 OHS B03 - PATHOGENESIS 1 - SALONS CD

Dynamic interaction of rabies virus with endosomes and end binding partners (EB3 and p140cap) of Cytoskeleton

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BACKGROUND: The objective of the present study was to investigate the interaction of rabies virus (RABV) with proteins of early endosome (Rab5, EEA1) and late endosomes (Rab7 and LAMP1) in order to understand the earlier events of rabies virus (RABV) right after internalization in neuronal and SH-SY5Y cell lines. The fixed and street strains of RABV were used to see their effects on the localisation and quantifications of EB3 and p140cap genes which essentially regulate postsynaptic density, shapes of dendrites and overall neuronal morphology. It was hypothesized that RABV depend on endosomal proteins or engorge itself into vesicles through early and late endosomes for hijacking neuronal cell machinery. Furthermore, it was also hypothesized that RABV produces degenerative changes in the neurons by down-regulating EB3 and p140cap proteins which are essential end binding proteins of microtubule and actin.

METHODS: The study was carried out in the key laboratory of zoonosis, Jilin University, China. Fixed strain was used to observe the intracellular kinetic interaction of RABV with respect to endosomes using immufluorescence, western blotting, electron microscopy and RNA interference. On the other hands, both fixed and street strains were used to screen and quantify the gene expression using real time PCR and western blotting respectively, while immunofluorescence was also performed to see the localisation of EB3 in infected and fixed nerve cells at different time periods.

RESULTS: The findings propose validity to our hypothesis by showing that RABV colocalized with markers for early and late endosomes during different time intervals of fluorescence staining. The down-regulation of Rab5 and Rab7 hampered the normal trafficking of RABV inside the cells. Both strain of RABV significantly down-regulated the gene expression of EB3 and p140cap. Furthermore, both strains also demonstrated disfigured localisation of EB3 in different time intervals of staining.

CONCLUSIONS: RABV transport follows clathrin mediated endocytosis, in a favourable intracellular environment of low pH, via early and late endomes as transport vehicles. Rab5 and Rab7 are fundamental bioelements located on endosomes that regulate a sprawled network of endosomal trafficking with other organelles. The disfigured position of EB3 might predict the degenerative changes in the form of deformed dendrites and misshaped neuronal morphology.

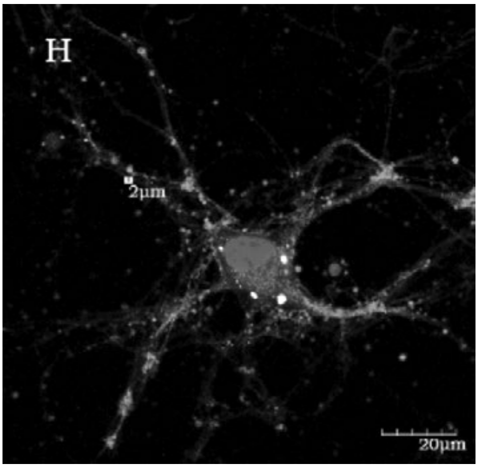

Fig: Localisation of EB3 in RABV infected neurons at 48 hours of post-infection (Green, blue and thick red spots indicate RABV, nucleus, and EB3).

OHS ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

1 OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES - SALONS CD

Molecular detection and characterization of Anaplasma phagocytophilum strains associated with different hosts in Bushbuckridge, Mpumalanga, South Africa

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5: Hans Hoheisen Wildlife Research Station, University of Pretoria, Pretoria, South Africa

BACKGROUND: *Anaplasma phagocytophilum* is a zoonotic, tick-borne, obligate intracellular bacterium capable of causing disease in diverse hosts, including humans, dogs, cattle and horses. It has not often been detected in Africa but recent research suggests its presence in the Mnisi community, a rural community nestled in the heart of a human/livestock/wildlife interface in Bushbuckridge Municipality, Mpumalanga Province, South Africa. The aim of this study was to explore the genetic diversity of *A. phagocytophilum* in different hosts in order to better understand its circulation in the study community.

METHODS: To achieve this, DNA extracted from blood samples from 282 wild rodents from five different habitat areas, 74 humans diagnosed with non-malarial undifferentiated acute febrile illness at the community clinics, 100 cattle and 56 domestic dogs, and 20 pools of *Rhipicephalus sanguineus* ticks collected from domestic dogs (1 pool=8 adult male ticks), were screened for *A. phagocytophilum* using a quantitative real-time polymerase chain reaction (qPCR) assay that targets the *msp2* gene.

RESULTS: Results revealed that 59% of wild rodents, 11% of humans, 10% of cattle, 82.9% dogs, and 85% R. sanguineus ticks were positive for *A. phagocytophilum*. Characterization of different strains by targeted sequencing of the 16S rRNA, msp4 and ankA genes from positive samples revealed the presence of different variants of *A. phagocytophilum* circulating within the community.

CONCLUSIONS: Sequence analyses confirmed the presence of *A. phagocytophilum* DNA in different hosts. *A. phagocytophilum* sequences identical to the *A. phagocytophilum* type strain Webster were obtained from a human patient, as well as from rodents, dogs and R. sanguineus ticks in the Mnisi Community. This serves as the first detailed report of the detection of *A. phagocytophilum* in humans as well as in other hosts in South Africa and highlights its importance as a possible cause of non-malarial AFI in South Africa.

as well as in other hosts in South Africa and highlights its importance as a possible cause of non-malarial AFI in South Africa.

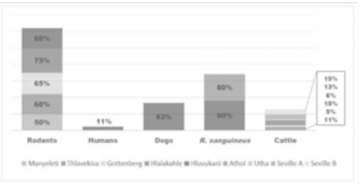

FIGURE 1: Percentage of samples from the different localities positive for *A. phagocytophilum* DNA using the *msp2* gene qPCR assay.

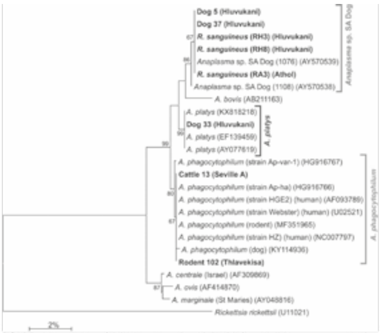

FIGURE 2: A neighbour-joining tree based on 16S rRNA nucleotide sequences showing phylogenetic relationships between the *Anaplasma* spp. The evolutionary distances were computed using the Kimura 2-parameter method and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated. There were a total of 596 positions in the final dataset.

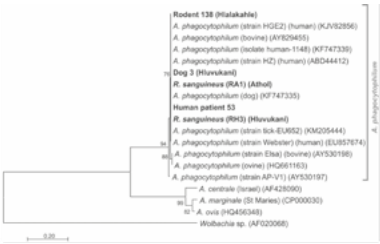

FIGURE 3: Maximum likelihood tree based on *msp4* deduced amino acid sequences showing the phylogenetic relationships between the *Anaplasma* spp. The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated. There were a total of 194 positions in the final dataset.

2 OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES - SALONS CD

Assessment of aerosolization of Avian Influenza A associated with market hygiene and practices and potential occupational exposure of live bird market workers in Bangladesh

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2: Royal Veterinary College, UK;
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6: City University of Hong Kong;
7: London School of Hygiene and Tropical Medicine, UK

BACKGROUND: Zoonotic avian influenza A virus subtypes H5N1 and H9N2 are endemic in Bangladesh where poultry consumption via live bird markets (LBM) is usual and popular. We aimed to assess the presence of aerosolized AIVs at LBMs and to evaluate association of AIV contamination with biosecurity practices and personal hygiene of LBM workers.

METHODS: A cross-sectional survey of 702 workers in 42 LBMs, with sampling probability proportional to market size, was carried out, collecting nasal and throat swabs and information on high risk practices. In each market, air samples were collected together with market-level hygiene assessments. A longitudinal study was also initiated in August 2017 to collect air samples and market level data every monthly from 10 LBMs for one year.

RESULTS: Most of the LBMs were retail markets (76.2%). While 61.9% had official weekly market closure day, all but one sold poultry every day. Birds not sold at the end of the day were kept in the same original stall. In 57.1% LBMs, wild birds were seen roaming freely. Only 3 LBMs had separate central slaughter house. All but 2 LBMs had daily market cleaning option. Less than two thirds of LBMs had systems in place for disposal of carcasses and offal. All but 3 markets had a hand washing station, and almost all (97.6%) had running water facility within the market. More than half (54.8%) had open drains. Dead birds were observed on the ground of
11.9 % markets. Laboratory testing of air samples is ongoing but initial findings from 23 LBMs suggested 39.1% of them were contaminated with Avian Influenza A. There was no obvious evidence of an association with market level hygiene on a preliminary analysis of 23 of the 42 markets and further analyses are being conducted.

Provisional results suggested 93.4% stalls were used for slaughtering or butchering of birds and 41.5 % used defeathering machines. At the individual level, most workers (93.3%) were involved in slaughtering and 79.9% in defeathering activities. Less than a quarter used masks during their work, only 0.7% used gloves, none used aprons, gowns or boots. Most of them (95.0%) reported they touched sick or dead poultry with bare hands. Only 21.8% washed their hand with soap after touching dead poultry and 17.3% washed their hand after touching sick poultry. With one step rRT-PCR, 14.4% LBM workers were tested Influenza A positive with nasal and/or throat swab.

CONCLUSIONS: The study provides evidence of aerosolization of AIVs in LBMs and its presence in respiratory passages of workers, thus risk of spillover infections. Longitudinal sampling will further inform periods of higher risk and relationship to changes in biosecurity over time. These findings support moving from emergency response to prevention of spillover.

3 OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES - SALONS CD

Transformation within Indigenous Lived Experiences and the Journey from a Pedagogy of Oppression to a Pedagogy of Hope and Freedom

Poelina, Anne

Madjulla Association, Australia

BACKGROUND: My career has focused on Indigenous Health and Wellbeing development using cultural, administrative and clinical actions; human and Indigenous rights; and environmental justice in the protection of environmental and public health. As an Indigenous researcher exploring and analysing within the Indigenous context, it is important that this research honours Indigenous science (knowledge making and adaptation) and culture from the beginning of time to modernity.

Description of the problem

A critical outcome of this research proposal is the imperative to frame Indigenous health and wellbeing as a set of practices within Aboriginal society that are complementary with, and act as a vehicle for reconciliation with, the Western deterministic view of health and its approach to research. Additionally what is the connection between the cultural, physical and emotional wellbeing of the individual and the health of the nation of which we are citizens.

Purpose and objective of the research

The purpose and objective of my research proposal is to emphasize and advocate a justice lens which explores the claim that Kimberly Aboriginal people in Australia continue to experience colonisation and its impact at different times and in different locations. This research is specifically aimed more generally into the emerging scholarship of ‘cultural as well as the socio-economic determinants of Indigenous health and wellbeing’.

METHODS: The context encompasses multiple methods and a trans-disciplinary approach through a critical research approach that champions both Indigenous methods and participatory action. The research approach and position embraces the convergence of Western and Indigenous science. Through this approach I plan to forge an ‘insiders’ understanding of contemporary context of colonization and its continuing aftermath.

CONCLUSIONS: This research frames the characteristics of colonisation not as an artefact of history rather it continues to be the lived experience of contemporary Indigenous Australian people acted out as personal, family and community and systemic violence. Freire theories apply to the construction of oppression from the viewpoint of its anti -dialogic actions regarding oppressive government policies towards Indigenous Australians. The Freire framework is based on mutual respect involving open and honest dialogue. This heightened sense of cooperation, has instruments known as ‘unity, organisation, [and] cultural synthesis’ which if undertaken leads to a process for a truly more positive life which enshrines the principles of human rights (Paulo Freire 1968).

The alternative put forward is a ‘strength based’ approach which is somewhat analogous to Freire’s dialogic action. It rejects narratives that promulgate inferiority. Strengths based education has a greater focus on innate ability, the advantages of Indigenous culture (rather than framing it as disadvantageous), dialogue, and ‘hopes and aspirations’ for ‘how we want to be’. A strengths based research approach to ‘reframe’ research: how problems are defined and how they should be solved.

4 OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES - SALONS CD

Tackling the second deadliest Neglected Tropical Disease: Predicting and reducing the impact of snakebite on human and animal health through One Health analyses of hotspots and access to care

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4: MSF

BACKGROUND: Snakebite is the second neglected tropical killer being responsible for over 100,000 human deaths and 400,000 victims of disability globally every year. It affects poor and rural communities in developing countries (e.g. farmers and agricultural workers), where snakebite is more frequent and access to healthcare is limited. Snakebite also affects livestock animals intensifying its burden on these communities through an indirect impact on livelihood. However, snakebite is dramatically under-reported and the snakebite crisis is first of all a crisis of data. Following the inclusion of snakebite in WHO NTDs list in June 2017 and the subsequent political and scientific momentum, we advocate for an innovative One Health approach to snakebite and we aim to quantify for the first time its double human-animal burden in snakebite hyper-endemic areas.

METHODS: To address this question, the *Swiss National Science Foundation* will support during the next four years our Swiss and international team of experts in tropical medicine, One Health, herpetology, and spatial analysis. We plan an unprecedented collection of data from 24’000 households through a regional and national human-animal health survey in Nepal and Cameroon. This survey will feed an analysis of the impact of snakebite on livelihoods and will be complemented with geo-spatial information on national infrastructures (e.g., roads), demography, environment, etc., to set the basis to map local and regional human and animal snakebite hotspots and develop predictive models of access to healthcare.

RESULTS: Using a One Health approach to snakebite, this project will first contribute to tackling the data gap on snakebite in human and animals, and provide a systemic understanding of its burden in rural communities, including an indirect impact through a loss of livelihood. Second, this project will predict and map local and regional snakebite hotspots and accessibility to life- saving healthcare, serving as an evidence-based tool to support local and national health policies.

CONCLUSIONS: This project will raise scientific, political and public awareness on snakebite in Cameroon and Nepal, and at the regional level in Sub-Saharan Africa and South Asia due to the potential for extrapolation of our results, tools and recommendations. The results of this project will reinforce the global political momentum on snakebite (e.g. January 2018, WHO’s Executive Board recommends the resolution of snakebite to the WHA).

This project will promote the recognition of lay knowledge and its integration in epidemiological investigations while giving political voice to neglected communities. The project will not only improve our understanding of the impact of snakebite, but also on other NTDs associated with poverty, opening an opportunity to tackle them in an integrated and locally adapted manner.

5 OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES - SALONS CD

What will it take to eliminate rabies in Africa?

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BACKGROUND: Every year approximately 59,000 people die from dog-mediated rabies globally. Each rabies death is vaccine-preventable and a global target for elimination of human rabies deaths has been set for 2030. The feasibility of this goal is supported by the existence of effective rabies vaccines for dogs and humans, epidemiological characteristics of the disease that support elimination, and evidence of elimination success across regions in developed and developing economies. Over a third of human rabies deaths occur in Africa.

METHODS: Using data from running contact-tracing programs to enhance surveillance for human and dog rabies, mass-dog vaccination programs reaching up to 30,000 dogs per single 10-day campaign, and working with the government to finance mass dog vaccinations and provision of post-exposure prophylaxis in Kenya, we address the question of what it will take to eliminate rabies.

RESULTS/CONCLUSIONS: We argue it will take five critical actions to catalyze progress towards attaining freedom from dog-mediated rabies by 2030; prioritization or rabies elimination in each endemic country, development and adoption of rabies elimination plans, domestic ownership and commitment to implementing the plans, innovations in the delivery of rabies interventions and integration of rabies elimination programs into national health systems.

OHS PATHOGENESIS 2

1 OHS B05 - PATHOGENESIS 2 - SALONS CD

Species specific binding of the MERS-coronavirus S1^A protein.

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BACKGROUND: MERS-coronavirus uses its spike protein to enter target cells. One part of this spike protein, the S1^B domain, attaches to dipeptidyl peptidase-4 (DPP4) to mediate entry during infection. Recently, using a nanoparticle-based approach, we found that another part of the spike protein, the S1^A domain, binds to α2,3-sialic acid. We showed that these glycotopes are involved in mediating MERS-CoV infection when expressed together with DPP4. The *in-vivo* relevance of this finding is currently unclear. In this study we tested the binding of the A domain to tissues of susceptible animal species.

METHODS: We obtained respiratory tract tissues from human, camel, llama, pig, and rabbit from previous experiments as well as intestinal tissues of Pipistrelle bat, Serotine bat, Gambian and Egyptian fruit bat. We performed DPP4 immunohistochemistry and nanoparticle displaying multivalent S1^A protein (np-S1^A) histochemistry on all these tissues. Additionally, we also performed lectin histochemistry and MERS-coronavirus nucleoprotein immunohistochemistry on camel, llama, pig, and rabbit tissues. To further evaluate the importance of MERS-coronavirus S1^A binding in human lungs, we used primary normal human bronchial epithelial (NHBE) cell culture as a model.

RESULTS: Consistent with our findings that MERS-coronavirus replicates better in the nasal epithelium of camel in comparison to llama, pig, and rabbit – the nasal epithelium of dromedary camels expressed DPP4 and exhibited S1^A binding. In humans, S1^A bound to type II pneumocytes in the lungs, which also expressed DPP4. In NHBE cells, we found that neuraminidase treatment could significantly reduce MERS-coronavirus infection. In bats, on the other hand, DPP4 is expressed in the intestinal epithelium of the four bat species included in this study, but S1^A only bound to that of Pipistrelle bat.

CONCLUSIONS: MERS-coronavirus S1^A protein binds specifically to camel nasal epithelium, human type II pneumocytes, and Pipistrelle bat intestinal epithelium, but not to similar tissues of other susceptible animals. Our results support dromedary camel and human as the host for MERS-coronavirus. Additionally, these data also support Pipistrelle bat as a potential host for MERS-coronavirus-like-viruses.

2 HS B05 - PATHOGENESIS 2 - SALONS CD

Using Bioluminescent Salmonella Strains to Study Host - Pathogen Interaction in Chicken will Allow One-Health-Approach

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Chickens (*Gallus gallus domesticus*) are asymptomatic carriers of Salmonella enterica serovar Enteritidis (SE), one of the main *Salmonella* serovars responsible for human salmonellosis globally. Here we have characterized putative virulence genes of SE using a bioluminescent imaging (BLI) model to investigate the role of each gene in colonization & infection in chickens. We hypothesized that BLI would provide insight into host-pathogen interactions between SE and the chicken and further our understanding of Salmonella infection, colonization and transmission within the avian host. To allow for continuous monitoring of SE during *in vivo* infection, the lux operon (*luxCDABE*) from *Photorhabdus luminescens* was integrated into the SE wildtype and mutant strains, and expressed under a constitutive promoter to generate a continuous light signal. Virulence genes of interest included: Salmonella Pathogenicity Island 1 (SPI-1), SPI-2, ferric uptake regulator (fur), pagN (i.e., PhoP/Q regulated genes) and tonB (which encodes the energy transducer to facilitate Fe^{3+} uptake). Using cell enumeration, we compared virulence-defective mutant strains of SE compared to wildtype cells for differences in their ability to colonize day-old birds following oral challenge. We did not see a significant difference in cecal colonization from either virulence-defective mutant strain compared to wildtype at day 4, 5 post challenge. This was confirmed by ex-vivo imaging where strong signals came through cecum from each reporter strain during the time frame. The cecum is thought to be the primary colonization site for SE in chicken and our finding is contrast to role of SPI-1, *pag*N in mammalian models which play an important role in gastrointestinal colonization. SPI-2 plays a major role in systemic infection in mammals, and similarly we observed a dramatic reduction in the bacterial load in spleen and liver. However, performing enrichment cultures at day 4, 5 post challenge showed that 100% of the birds were systemically infected (most of them at a very low level). Iron is thought to be critical for bacterial survival and TonB facilitates uptake of Fe^{3+} from host tissue. Our data show evidence that Fe^{3+} uptake may not be critical for colonization in the cecum of chicken during early life. Fur acts as a global regulator in regulating iron homeostasis in Gram negative bacteria. Here we provide evidence that disruption of *fur* didn't affect colonization in the cecum. Overall our approach using BLI has revealed new insights into the interactions between SE and chickens.

The development of a live imaging model using bioluminescent *Salmonella* strains is a first step in a true one-health approach as it will provide a powerful tool to understand host-pathogen interaction, and to investigate the effect of therapeutic strategies (e.g., vaccination) with benefits for human health and the environment.

3 OHS B05 - PATHOGENESIS 2 - SALONS CD

Influenza A viruses activate host PI3K/Akt survival pathway for pro-viral advantage in chicken but not in duck cells

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Avian influenza viruses (AIVs) are a major threat to millions of poultry farmers. Highly pathogenic avian influenza viruses (HPAIVs e.g. H5N1) metamorphose from its progenitors in poultry flocks causing high mortality and pose a significant human health risk. On the contrary, ducks are mostly refractory and reservoirs. Disparate disease outcome between AIV infected chicken and ducks suggest potential species differences in mounting an antiviral response. Mammalian studies indicate that AIV non-structural protein 1 (NS1) interacts with vital host proteins, to interfere and hijack cellular functions for replication advantage. NS1 has been shown to bind to PI3K/Akt (phosphatidylinositol-3-kinase) p85beta subunit resulting in pathway activation. The PI3K/Akt pathway regulates cellular differentiation, proliferation and survival through inhibition of pro-apoptotic factors. However, the regulation of PI3K/Akt signalling and its implications on AIV replication in avian hosts is yet unknown. Understanding host cellular response to AIV infections is key to develop control measures. Therefore, the present study investigated the regulation of PI3K/Akt and its implications on virus replication. Chicken or duck embryo fibroblast (CEF/DEF) cells were infected with wildtype (WT) LPAI H2N3/H6N1 or recombinant H5N1 (rH5N1) or H9N2 (6:2 system 6 genes from H5N1 (50-92 or Tky05 or H9N2 with PR8 HA, NA). Activation of PI3K/Akt IAV infected cells was determined by western blotting. Virus titration from infected CEFs or DEFs was performed by foci forming assay (FFA). Inhibition of PI3K/Akt was done using LY294002 or Wortmannin. Cell metabolic activity and caspase 3/7 activity was measured using commercial kits as per manufacturer's instructions.

The results demonstrated that AIV infected CEFs produced significantly ($P \leq 0.0001$) higher infectious virus compared to DEF cells at 9 and 24hrs post infection (hpi). Activation of PI3K/Akt only in infected chicken but not in duck cells. Post-infection PI3K/Akt inhibition significantly reduced virus titres at 6 ($P \leq 0.05$), 9 ($P \leq 0.0001$) and 24 ($P \leq 0.0001$) hrs post infection in CEFs. Differential PI3K/Akt activation was observed between LPAI and rH5N1 viruses. All three LPAI H2N3, H6N1 and H9N2 viruses activated PI3K/Akt at 6 and 9 hpi only. Whilst a prolonged PI3K/Akt activation was observed even at 24hpi in both rH5N1 virus infected CEF cells. Inhibition of PI3K/Akt in WT H2N3 virus infected CEF cells resulted in significantly ($P \leq 0.0001$) higher apoptosis induction compared to controls at 24 and 48 hpi. Counterintuitively, although duck cells exhibited potent apoptosis induction than CEFs, the level of induction was comparable (non-significant) across treatment groups at 24 and 48 hpi. Results imply novel differences in the activation of PI3K/Akt survival mechanism in AIV infected chicken and duck cells are responsible for underlying host differences. The study signifies host-specific viral replication strategy that may find potential use in disease control interventions in the future.

4 OHS B05 - PATHOGENESIS 2 - SALONS CD

Environmental CO2 Modification of Innate Immune responses to LPS and Organic Dust

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BACKGROUND: Exposure to immune stimulants in the lung potentially act in the context of environmental dusts and accumulated gases. Carbon dioxide is a commonly elevated gas in work and home environments that at extremely high levels (hypercapnia) has been shown to cause changes in immune responses. Little to no work has concentrated on possible immune system effects at levels seen in poorly ventilated home and work environments. Exposure to organic dusts in concentrated animal feed operations have been shown to cause chronic inflammation in the lungs of workers, leading to increased incidences of asthma, COPD, chronic bronchitis, and a general reduction in lung function over time. As these facilities also experience elevated CO_2 we investigated if CO_2 exposure altered immune responses to these dusts. We hypothesized that increased CO_2 could modify innate immune responses to organic barn dust extract (BDE).

METHODS: Mice were intranasally instilled with either LPS or BDE then exposed for six hours at 5000, 2500, or 1000ppm CO_2 gas levels before lung lavage and lung tissue sampling. Lung lavage was centrifuged for cells that were counted and identified, and fluid which was used for ELISAs. Lung tissue was used to extract mRNA for RT-PCR.

RESULTS: Few changes were detectable in animals given saline or saline with CO2. Conversely, LPS and BDE treated animals showed signs of inflammation by measures of cytokines (IL-8, MIP-2, MCP-1) and lavage cell counts. BDE exposed animals showed increases in these measures over saline, with 5000ppm CO_2 co-exposure increasing these measures over BDE alone. LPS conversely showed a trend to increased lavage cells, but a significant decrease in the same measured cytokines at all CO_2 co-exposure levels.

CONCLUSIONS: Exposure of mice to CO_2 with saline alone at workplace relevant levels had no apparent effect on immune responses in mouse lungs. When CO_2 exposure was combined with LPS or BDE challenge however there was an increase in lung lavage cells and inflammatory cytokines with BDE at 5000ppm CO_2, and a decrease in cytokine levels down to 1000ppm in LPS treatment alone. This suggests that increased CO_2, as low as 1000ppm may modify inflammatory responses in the lung to innate immune challenge. These changes due to CO_2 differed depending on the immune stimulus. Overall these results suggest that the local environment, in the form of gas buildup, may combine with innate immune stimuli to directly modify immune responses.

5 OHS B05 - PATHOGENESIS 2 - SALONS CD

Rabies virus interrupts cofilin pathway and induces depolymerization of actin in hippocampal region

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BACKGROUND: Rabies virus (RABV) is a neurotropic pathogen that produces severe encephalitis and terrifying neurological symptoms in humans and animals. The pathological mechanism of RABV is poorly understood, but the current studies show that the virus preferably causes neuronal dysfunction instead of cell death or necrosis. Proteins involved in synapse and postsynaptic density are integral sub-cellular components that maintain neuronal cell shape in multiple aspects. For example, p21-activated kinases (PAKs) regulate the phosphorylation of cofilin in neuronal cytoskeleton; Rac1 is a G signaling protein belonging to Rho family of GTPases and controls orientation of cytoskeleton and growth of neuronal cell; cell division control protein 42 homolog (Cdc42) also regulates cell cycle and related signaling events. The present study speculates the hypothesis that RABV hampers the cofilin pathway and depolymerizes the filamentous actin in hippocampal region of brain tissue.

METHODS: The study was carried out in the key laboratory of zoonosis, Jilin University, China. Western blotting, immunohistochemistry and real time PCR were carried out to determine the interaction of street and fixed strains of RABV with associated mediators and binding partners of cofilin mediated pathway.

RESULTS: Results showed that RABV inhibits the gene expression of PAK, phosphorylated cofilin and total cofilin that ultimately interferes with interacting partners such as Cdc42 and Rac1. These changes perhaps cause depolymerization of filamentous actin in neuronal cytoskeleton of hippocampus. Moreover, the street RABV infection also hampers the binding of GTP Rac1 and Cdc42 with PAKs. Street RABV also causes significant reduction in the content of active Rac1 (GTP binding form), while total Rac1 contents remain unchanged after 1 hour of infection. It can also inhibit the transformation of inactive Rac1 to active Rac1 without affecting the expression of total Rac1.

CONCLUSIONS: These findings suggest that the RABV may alter the structural and physiological architecture of dendritic spine as well as postsynaptic density by reducing the amounts of specific proteins involved in maintaining the shape of dendritic spines. The present study also helps us to interpret network of pathways involving PAKs and Cdc42.

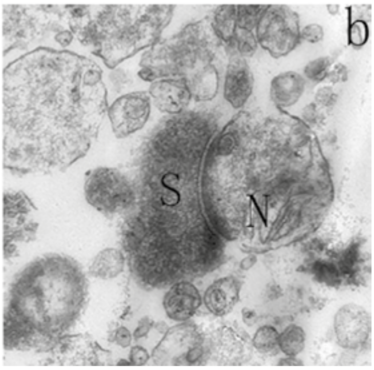

Fig: Close up view of a complete synaptoneurosome (10000X) showing Synaptosome(S) and neurosome

OHS INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1

1 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD

Integrating Ecosystem Approaches to Health: A One Health Investigation of Rift Valley Fever Virus

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BACKGROUND: Outbreaks of Rift Valley fever (RVF) can be devastating to livestock production sectors and have severe human health and high socio-economic impacts. The life cycle of RVF virus's presumptive primary vector, floodwater Aedes mosquitos, is influenced by environmental factors, and outbreaks have been associated with high levels of precipitation and subsequent rapid vegetation growth as measured by normalized difference vegetation index. Despite knowledge of these associations, the prediction of RVF outbreaks remains elusive. These factors necessitate a One Health approach to understanding and managing RVF, incorporating human, livestock, and environmental factors.

METHODS: We describe a case study in One Health research and the benefits of One Health study design, based on work conducted in South Africa on RVF. Our approach includes integrating experts in climate, soil science and vegetation ecology into our team of veterinary and public health epidemiologists, enabling us to study relationships among weather and climate, vegetation, the vector and the circulation of RVF virus in human and animal hosts.

RESULTS: We demonstrate how this integrated team used an ecosystems approach to conduct research on an infectious disease. We show the benefits of this approach and the importance of designing One Health studies *a priori* so as to assess and present the benefits of disease monitoring and investigations to policy makers and funders.

CONCLUSIONS: This RVFV example demonstrates a functional program design for One Health investigations as well as the scientific advantages in coordinated, *a priori* One Health investigations as compared to siloed investigations and *post-hoc* analyses.

2 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD

The Other Side of One Health: A Brucellosis story

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BACKGROUND: Reflections on zoonotic pathogens and associated diseases often focus more on the disease burden, pathogenesis, treatment, and control. In the analysis of the disease in a One Health perspective, however, it is essential to analyse indirect impacts of infectious diseases on the animal industry, particularly the affected farmers. A farmer may not be directly infected with a zoonotic pathogen, but the effects of losing a herd and the impact of the challenges faced post an outbreak on the farmers health, investments and psyche need to be explored and understood, bringing to fore the essence of One Health and the need to explore it on an interdisciplinary platform

METHODS: This research focused on *Brucellosis* in selected wildlife in South Africa, analysing data from farmers, veterinarians, researchers and other stakeholders. Using veterinary reports, farm records, and interviews, the indirect effects of *Brucellosis* on farmers were explored and analysed. A systemic review of published data on economic losses resulting from *Brucellosis* in Africa is also conducted. The diagnosis of *Brucellosis*, focusing on challenges in the system are further explored

RESULTS: A total of 42 research papers on the economic impacts of *Brucellosis* were retrieved after a comprehensive search and critical appraisal of published literature using search terms "*Brucellosis*" AND "Economic Impact". Unpublished reports, including farm records, veterinary reports and interviews with farmers were also analysed
Initial reports on *Brucellosis* in one wildlife farm perked losses at approximately 1 million rands (approx. $80,000), where the prices of Sable antelope have fluctuated between R 178 000 (Matetsi/ Southern Sables) and R 485 000 (Zambian Hybrids). Farm records documented the trauma of the farmer's loss of revenue and investments with records of depression and fatigue. The research built on that to discuss losses experienced by other farmers in the industry and this is being analysed. It was identified that gaining a "clean herd" reputation in the industry is a major hurdle farmers have to overcome, post-quarantine and outbreak and the strategies to ensure these are identified and discussed. The analysis also points to need for evidence- based research in diagnostics of pathogens as evasive as Brucella.

CONCLUSIONS: Within One Health, there is the need to look at indirect effects of disease outbreaks on human and animal populations, as well as systems and societal structures. A constant research- based control system is also important in addressing challenges posed by infectious diseases such as *Brucellosis*.

3 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD

One ring to rule them all: Uniting human, animal, and environmental data using the Checklist for One Health Epidemiological Reporting of Evidence (COHERE)

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WHY: Harmonizing and integrating the human, animal, and environmental data from One Health studies is complex and has not been adequately addressed by existing guidelines for scientific reporting. Improvement of the quality of reporting One Health literature is critical to demonstrate the value and integrity of this rapidly growing field.
WHAT: We created a Checklist for One Health Epidemiological Reporting of Evidence (COHERE) to assist authors to advance the quality of reporting interventional or observational epidemiological investigations that integrate data from multiple sectors and/or disciplines.
COHERE was developed by a core writing team, with guidance from an external, international and multidisciplinary panel of One Health experts.
WHAT: We present the peer-reviewed checklist that was developed and published, and demonstrate the checklist in action, using real-world examples to illustrate how COHERE is applied to One Health studies. We also show how COHERE helps to incorporate the Ecohealth perspective into One Health reporting. We aim to promote the idea that One Health studies should include all three domains (humans, animals and environment).
WHAT: This checklist can aid investigators at multiple points of a study, including study design, data analysis, and data reporting, and should facilitate the future generation of One Health meta-data that will allow higher level analyses.

4 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD

Ecohealth Project at the community level: Disease Research and development at the human-domestic animal and wildlife interface, Uganda

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BACKGROUND: Community capacity to manage health challenges at the human-domestic animal and environment interface has been limited due to lack of home grown solutions. Most of the research conducted in Africa does not go back to the community nor are there interventions to address some of the challenges the communities are facing. The purpose of the Ecohealth Chair project was to conduct research on human and animal disease at the human-animal and wildlife interface in and around a biosphere reserve.

METHODS: Using an Ecohealth approach, communities in and around Queen Elizabeth National Park, Western Uganda, participated in identifying, ranking and prioritizing health and environmental challenges in their population(s). Samples were collected from animals and analyzed using basic and molecular typing methods. In addition, surveys were conducted to understand knowldege and practices of community and health workers on animal and human diseases. Each community selected an intervention based on reults. More than 900 animals samples have been analyzed for Trypanasomiasis, Q-fever, and brucellosis and antihelminthic resistance.

RESULTS: Domestic animals had a prevalence of 13.6% for *Coxiella burnette*. Nearly 9% of the cattle were positive for *Trypanasoma brucei*. Farmers using communal livestock management system were more than 9 times at risk of helminth infection than those on paddocks system (OR=9.4, CI: 3.3-21.6, P = 0.001). The cattle that were sharing water points with wildlife were 14.7 times more likely to get helminth infection than those that were not (OR=14.7, CI: 3.6-23.5, P = 0.001). The cattle that feed on pastureland where wild animals visit daily were 6.1 times more likely to get helminths than those where wild animals never visited (OR=6.1, CI: 1.4-13.2, P = 0.031). Based on these results up to 5 communities selected interventions. These included training on zoonotic diseases, construction of spray race and provision of water for animals and cattle

CONCLUSION: This is the first study in the study area to report *T. brucei* and *C. burnette*. It also the first project to conduct research and development in the study area.

5 OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 1 - SALONS CD

“Whenever I see a fruit bat, I think Hendra” – Attitudes and risk perception of Australian horse owners towards flying foxes in relation to Hendra virus

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BACKGROUND: Hendra virus (HeV) is a zoonotic paramyxovirus that has threatened both equine and human health in Australia. It sporadically spills over from flying foxes (*Pteropus* spp.) to horses to humans causing neurological and respiratory disease with high mortality in horses (75%) and humans (57%). Prevention strategies, such as vaccination of horses and property management measures, are widely publicized, but hinge on initiative and action taken by horse owners as they mediate management and care of their animals. While outbreaks significantly impact the equine industry, they also propagate fear and misinformation amongst horse owners about flying foxes, leading to calls for more radical flying fox management approaches, including dispersal and culling. This study investigated knowledge and risk perception of horse owners towards flying foxes as reservoirs of HeV to identify common attitudes, knowledge gaps and misconceptions.

METHODS: Using a mixed method approach, data presented are derived from a two-year, online longitudinal survey as well as semi-structured face-to-face interviews with horse owners in Australia. Questionnaires comprised horse owner demographics, property management and mitigation measures, HeV risk awareness and knowledge, and attitudes towards flying foxes and their management. Uni- and multivariable analyses were performed to evaluate association of demographic, management and behavioral variables with perception of flying foxes as a direct threat to the health of horses. Interviews covered previous experience with HeV, HeV information-seeking behaviour, and risk perception and mitigation. All interviews were recorded, transcribed verbatim and analyzed with NVivo using thematic analysis.

RESULTS: Attitudes towards flying foxes and their management differed among the participants. Descriptive analyses revealed that the majority (73%) of respondents to the latest survey (N= 577) acknowledged the important role flying foxes play in the environment, yet 40% supported their culling if roosting in areas where they are causing a nuisance. Dispersal was not seen as an effective method of flying fox management because it just moves the problem somewhere else (73%). Interestingly, 59% considered flying foxes as a significant health threat to horses. Horse owners who saw flying foxes or believed that a HeV case was likely to occur in their area were more likely to perceive flying foxes as a threat.

CONCLUSIONS: The important ecological role of flying foxes in pollinating and dispersing seeds of native Australian flora was well recognized by the majority of horse owners as well as the need for them and support for their protection. However, there also was considerable support for their culling, potentially reflecting increasing human-wildlife interfaces and conflicts in urban and peri-urban areas due to anthropogenic changes. These findings facilitate a better understanding of horse owner perspectives and help to inform effective communication strategies.

OHS INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2

1 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

The role of mainland-island bat movement in the dissemination of viruses of public health concern in the Caribbean

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BACKGROUND: The Caribbean island of Trinidad, which lies just 7 miles off the northeastern coast of South America, has the highest bat species diversity of the Caribbean islands, with 69 bat species documented. Bats are recognized as reservoirs for many important zoonoses, including rabies, and are implicated in cross-species transmission of viruses to human and animal populations. Bat-transmitted rabies was first reported from Trinidad in the 1930s when the virus was transmitted from vampire bats (*Desmodus rotundus*) to humans and animals causing mass mortalities. Vampire bat rabies continues to cause sporadic outbreaks in livestock on the island, but it is unclear whether outbreaks reflect enzootic cycles or re-introductions of the virus from mainland South America and if so, the geographic origin of introductions. Therefore, the aim of this study was to assess the role of *D. rotundus* bats in the spread of rabies virus from the South American mainland to the island of Trinidad, as well as to identify other viruses of public health concern that these bats may transmit.

METHODS: Nucleic acid amplification and sequencing of the N gene was carried out for 37 rabies viruses isolated in Trinidad from 1997-2010. These N gene sequences were compared phylogenetically with pre-existing sequences from South America, to investigate viral evolutionary dynamics and geographic source. Microsatellite (DNA) analysis was performed to investigate genetic diversity and gene flow between *D. rotundus* bat populations from Trinidad, Guyana, French Guiana, Venezuela and Suriname (1910-2017) to determine mainland-island bat movement. Polymerase Chain Reaction (PCR) followed by Sanger and next generation sequencing (NGS) was also conducted on 83 bat fecal swab samples from seven species of bats sampled on the island of Trinidad during the period 2012 to 2016.

RESULTS: Trinidad rabies viruses were found to be bat variants and clustered with *D. rotundus* variant sequences from South America. Phylogeographic analyses indicated three successive viral introductions from the mainland during the period 1972-2004, from which Trinidadian rabies virus lineages arose. Microsatellite analysis revealed the presence of two distinct population groups of bats with varying levels of admixture, which suggested gene flow between the island and mainland bat populations. Bat herpesviruses and coronaviruses were identified by both Sanger and NGS sequencing methods, with an additional 5 viral families identified by the NGS platform.

CONCLUSIONS: These results suggested that bats move freely between Trinidad and South America, endorsing the role of *D. rotundus* bats in rabies virus translocation between the South American mainland and Trinidad. This work also highlighted the potential for the similar introduction of other viral diseases of public health concern by bat dispersal.

2 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

Nematode co-infections, environmental factors and weather impact infection with the zoonotic bacterium, Bartonella tribocorum, in urban Norway rats (Rattus norvegicus)

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BACKGROUND: Traditional zoonotic pathogen ecology studies in wildlife examine the interplay among hosts, their demographic characteristics and their pathogens. But pathogen ecology is also influenced by factors that traverse the hierarchical scale of biological organization, ranging from within host factors including co-infections at the molecular, cellular, tissue and organ levels, all the way to the host population within a larger environment. The influence of the environment and co-infections on zoonotic pathogen carriage in hosts may provide key information to create a holistic understanding of pathogen ecology in wildlife hosts, which are a major source of emerging infectious diseases in humans. Using wild, urban Norway rats (Rattus norvegicus) as a model species, the purpose of this study was to investigate associations among environmental factors, co-infections and *Bartonella tribocorum*.

METHODS: During a systematic trap and removal study of rats in Vancouver, Canada, between Sept. 2011 and Aug. 2012, city blocks were assessed for relative rat abundance and 48 microenvironmental characteristics. We also constructed 32 time-lagged temperature and precipitation variables. Rats were tested for the presence of *B. tribocorum* using culture and confirmatory PCR and the presence of invasive nematode infections using macroscopic assessment and/or histopathology. We then fitted multi-level multivariable logistic regression models with *B. tribocorum* status (positive/negative) as the outcome and city block as a random effect to account for clustering. For the environmental analysis, abundance, microenvironment and weather variables were potential independent variables, and for the co-infection analysis, nematode infections were independent variables.

RESULTS: Rats originated from 32 city blocks and the prevalence of *B. tribocorum* was 25.7% (101/393) and. The odds of a rat testing positive for *B. tribocorum* were significantly lower for rats in city blocks with one or more low-rise apartment buildings compared to blocks with none. Rats had significantly increased odds of being infected with *B. tribocorum* when there were high minimum temperatures for several time periods prior to rat capture and when rats had a nematode infection in one or more organ systems (Eucoleus sp. in the stomach, Capillaria hepatica in the liver, enteric nematodes, and/or Trichosomoides crassicauda in the urinary bladder or renal pelvis).

CONCLUSIONS: A baseline minimum temperature may be necessary for flea survival and *B. tribocorum* transmission among rats, which may lead to fluctuations in the number of infected rats and potentially, the risk to humans. Our results also suggest that nematode parasitism and the environment may have important roles in the ecology and epidemiology of *B. tribocorum* . Our approach may be applicable to future studies of zoonotic pathogens in rats and other wildlife hosts. A nuanced appreciation of how co-infections and specific environmental factors influence pathogen ecology in wildlife host systems may be particularly useful for surveillance and disease prevention activities.

3 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

Environmental Change Increases Human-Macaque Interactions and the Risk of Zoonotic Disease Spillover

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BACKGROUND: Environmental change is not a new issue in the study of public health. Many public health studies have been conducted that link environmental changes to emerging and re-emerging viruses. However, these studies rarely examine human-animal interaction in relation to environmental change. Zoonotic diseases have been considered a major public health concern, and one pathway through which disease risk is heightened is from environmental changes that increase interaction between humans and rhesus macaques (Macaca mulatta).

METHODS: Three sites of increasing local land-use change in Bangladesh-old Dhaka, Madaripur, and Chandpur were selected after preliminary key informant interviews and field observations.This qualitative study employed anthropological research methods including participant observation, ethnographic in-depth interviews (58) and focus group discussions (3) to understand local experiences of environmental change and patterns of humanmacaque interactions. Interviews and focus group data were coded using computational data analysis software (MaxQDA), and emergent themes were identified using a modified grounded theory approach.

RESULTS: Environmental changes are clear in each of the study sites, visible in the significant anthropomorphic landscape transformations.This qualitative study found that all the three areas went through significant landscape transformation due to the construction of roads or apartment buildings on open or agricultural land, to be used for both business and human settlement purposes.Disappearance of forestland has increased macaques' dependence on fruit trees of household backyards. As a result, residents often cut down fruit trees as macaque eat fruits from their trees and instead started planting woody trees so that macaques cannot disturb them. Natural water resources such as rivers and ponds were filled to support the development of roads and homes. As natural water sources were depleted, macaques became more dependent on human water sources, allowing possible water source contamination Macaques in all three regions have expanded their foraging areas and are now invading new areas where people are not culturally habituated to living with macaques. In response, many residents have reacted aggressively, leading to more frequent biting and scratching events. Many respondents accepted the presence of monkeys at their home, and few consider monkeys as a threat for disease transmission. As a result, they do not mind sharing food or water with macaques. Monkey bites/scratches are not always taken seriously, in some cases victims are not taken to the hospital.

CONCLUSIONS: Macaque-human interaction is on the raise in many areas of Bangladesh due to increased dependence on the same land, water, and food resources.This frequency of interaction increases the risk of zoonotic disease transmission. Human behavior is greatly responsible for human macaque interaction and zonootic disease transmission. Behavior change interventions should be developed to reduce zoonotic spillover by mitigating the risks associated with human-macaque interaction due to land use change.

4 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

Explaining variation in human and animal zoonotic infection risk in northern Tanzania: defining agro-ecological systems and their contribution to risk

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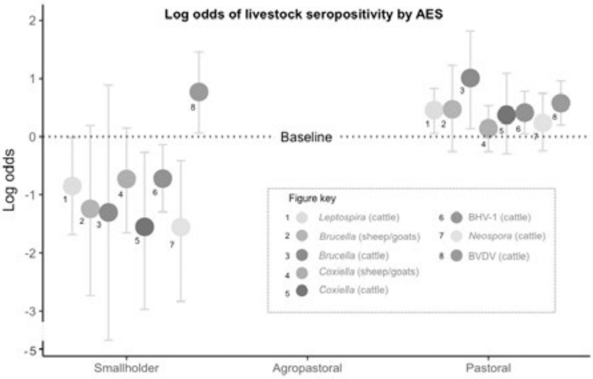
BACKGROUND: The risks of human infection with livestock-associated zoonoses depend on a complex interplay of factors, including local livestock infection prevalence, contact with animals and contaminated environments, and food preparation and consumption behaviours. Zoonotic disease risk is therefore highly context-dependent. Quantifying the degree to which social and environmental conditions shape variation in infection risk can help identify health inequalities, and provide targets for interventions to reduce them.

METHODS: We describe the outputs from a cross-sectional survey conducted in northern Tanzania in 2016. A mixed methods approach was employed, including household surveys (n=404) and serological testing of humans (n=351), cattle (n=3133), sheep (n=2178) and goats (n=2554) for a range of zoonotic pathogens. Prevalence of *Brucella* and *C. burnetii* exposure was generated for livestock and people, and *Leptospira borgpetersenii* serovar Hardjo for cattle. To explore variation in livestock infection risk more broadly, cattle sera were tested for exposure to several non-zoonotic pathogens, including bovine viral diarrhoea virus (BVDV), bovine herpes virus-1 (BHV-1) and Neospora caninum. A data-driven approach was used to classify livestock-keeping households into groups based on indicators considered to represent agro-ecological system (AES). These included livestock demographics, management, crop agriculture, and land use. Classification was performed using factor and hierarchical cluster analysis. Multi-level logistic regression models were built for each pathogen with a focus on examining relationships between individual seropositivity and AES.



RESULTS: The overall prevalence of cattle, small ruminant and human exposure to *Brucella* was 2.8%, 3.3%, and 5.1%, respectively. For *C. burnetii*, this was 4.1%, 24.4%, and 3.7%. Bovine *N. caninum, Leptospira*, BVDV, and BHV-1 seroprevalence was 12.6%, 23.6%, 36.1%, and 66.3%, respectively. Three household clusters were derived that corresponded with historical descriptions as smallholder (n=39 households), agro-pastoral (n=217), and pastoral (n=124) AES. Whilst relationships were not significant for all pathogens, a general trend for elevated livestock infection risk in pastoral systems and reduced risk in smallholder systems was apparent (Figure). There was no evidence for differences in the risk of human exposure to *Brucella* or *C. burnetii* between AES.

CONCLUSIONS: We demonstrate the value of using data-driven approaches for household classification in a setting with a range of livestock-based livelihoods. Important variation in livestock pathogen exposure risk was observed between systems, with the highest overall infection pressure in pastoral households. Further work is underway to identify correlates of human *C. burnetii* and *Brucella* exposure that may better explain variation in zoonotic disease risk in northern Tanzania.

5 OHS B07 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE 2 - SALONS CD

Building collaborative capacity to evaluate zoonotic viral sharing among bats, primates, and people in Tanzania

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BACKGROUND: As human populations expand, people are living in closer contact with wildlife, altering human-animal interactions and increasing the risk of disease transmission. Viruses traced to bats and primates have caused significant human epidemics and pandemics, but these animals also play critical ecological roles. In the biodiverse Udzungwa Mountains, one of Tanzania's last areas of undeveloped mountain forest, bats and primates live in close proximity to human communities, creating a high-risk interface for zoonotic disease transmission. Using a One Health approach to surveillance and capacity building, we investigated the presence of and risk factors for viral sharing among geographically overlapping bat, primate, and human populations.

METHODS: We built an interdisciplinary team to integrate human, animal, and environmental sampling in the Udzungwa Mountains of Tanzania. Partnering with four village-based human health clinics, we enrolled and collected samples from febrile patients (March 2016 – January 2018). Patients were screened for malaria using a rapid, field diagnostic test (mRDT), and a behavioral survey was conducted to assess contact with forest environments and wildlife. From neighboring town and forest habitats, we captured and sampled fruit bats and insectivorous bats and non-invasively collected feces and saliva from non-human primates (May 2016 – January 2018). Using data on bat movement and feeding patterns, we sampled fallen fruits discarded by foraging bats and used camera traps to assess connections to other species that contact these foods through scavenging or play. For biological samples (blood, oral swabs, feces or fecal swabs, and swabs or sections of fruit), we performed RNA extraction, cDNA synthesis, and viral family level consensus PCR screening (corona-, filo-, flavi-, influenza-, and paramyxoviruses) at laboratories in Tanzania. Confirmatory sequencing of suspect positive samples is currently being performed at University of California, Davis.

RESULTS: Our One Health team sampled 1,920 human patients, 1,037 bats, 339 primates, and 108 fruits discarded by foraging bats. Family-level PCR screening identified suspect positive samples from multiple viral families in human and wildlife samples. Confirmatory sequencing of these samples will be completed by May 2018 to allow for full analysis of viral sharing among people, bats, and primates in overlapping habitats. Following confirmatory testing, we will assess spatial, temporal, and behavioral risk factors for viral infection. During the project, our team trained 72 individuals, including veterinarians, human health professionals (clinicians and nurses), animal and human health students, and wildlife officers, building partnerships with diverse community, government, and university groups.

CONCLUSIONS: Preliminary evidence supports the potential for viral sharing among overlapping populations of bats, primates, and people in Udzungwa forest environments. Connections with communities, government, and interdisciplinary research partners allowed us to successfully integrate human, animal, and environmental sampling, enhancing capacity for future viral surveillance and One Health project implementation.

AMR ANTIMICROBIAL AGENTS AND RESISTANCE

AMR USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT

1 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

Reduced and responsible use of antibiotics in food-producing animal in The Netherlands

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BACKGROUND: In the period 2008-2011 the outline of the Dutch policy for a substantial reduction and a more responsible use of antibiotics in the livestock industry was drafted as a reaction to the persistent high level of antibiotic use in the livestock sector and public concerns about any transfer of antimicrobial resistance from livestock to humans. Sales of veterinary antimicrobials dropped by more than 64% between 2009 and 2016, and antimicrobial resistance levels decreased substantially as a result of the reduced use. These results are achieved by intensive collaboration between government, the veterinary association and stakeholders within the major livestock sectors.

However the main reduction was achieved in the first years whereafter the reduction leveled off. The idea was that a more targeted and sector specific approach should be developed. For this reason research was performed on the critical success and fail factors of a low usage of antibiotics in the different sectors.

METHODS: First of all the changes in usage on farm level were analysed to see whether there are structural high and structural low users and to define the farms to be incorporated in the study. After that different characteristics of the farms in the low and high users groups were further analysed e.g. farm type, farm size, farm management, construction of farm, health of the animals, education and knowledge of farmer etc.. Statistical analyses were performed to show possible associations between certain factors and high/low usage of antibiotics.

RESULTS: For all sectors certain associations were found e.g. for the veal calf and pig sectors the small farms have a lower usage where the association is the other way around for poultry, large farms have a lower usage of antimicrobials. In all 3 sector clear leads were found to decrease the usage in the high user group.

In the poultry sector associations were found with the different market concepts, slower growing breeds use less antimicrobials. Management practices like thinning the flocks increase the usage.

In the veal sector management, ventilation and feeding but also nationality of the calves are points of attention. In the pig sector associations were found with management, vaccination and the number piglets. Not all results can be clarified and not all associations are causal relationships. Further in depth research will be needed on certain aspects of the current results, however these results can be a basis for more sector specific plans to further reduce the antimicrobial usage.

CONCLUSIONS: The reduction targets for antimicrobial usage in livestock production in the Netherlands was -70% in 2015 with reference to the amount of effective substance sold in 2009. The last few years it became clear that the general approach would not lead to this reduction. By making an analysis of the critical success and fail factors of the different sectors, a sector specific approach can be developed. The outcomes of these studies will be presented.

2 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

Antimicrobial resistance in wildlife species: the potential for sentinel surveillance in a ONE HEALTH perspective

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BACKGROUND: Antimicrobial resistance (AMR) is an emerging problem worldwide, and is widely spread in many environments. The use of antibiotics and other drivers for AMR development in humans, livestock or agriculture may have a direct impact on wildlife, and wild animals may provide a biological mechanism for the spread of antibiotic resistance genes. The wild reservoirs of resistance remain poorly understood, even though its origins and mechanisms are of paramount relevance to human health. We have conducted several studies with different wildlife species in Norway to monitor AMR and understand the potential for these to both work as sentinels/bio indicators for AMR spread, and help explain the dynamics and driver for resistance in the environment.

METHODS: Between 2013-2017 faecal samples were collected from different wild species in continental Norway: wild birds (ducks and gulls) (n=357); red foxes (n=387); wild reindeer (n=265); roe deer (n=301). In addition faecal samples were collected from 27 wild reindeer from the arctic archipelago of Svalbard. Resistant bacteria were identified by culturing on selective media and/or by susceptibility testing of randomly chosen *E. coli* from the samples . Microbroth dilution were conducted to assess phenotypic resistance.

RESULTS: *Wild birds: E. coli* resistant to extended-spectrum cephalosporins (ESC) were detected in 31 samples (8.7%) and quinolone resistant *E. coli* in 74 samples (5.6%). Additional resistance to one or more agents was found in 45.9% of the isolates.
Red foxes: The occurrence of AMR was 9.2%, 6.3% and 14.7% in areas of low, medium and high human population density, respectively. A statistically significant difference in AMR occurrence was observed between medium and high population density areas. Resistance to fluoroquinolones occurred in 76 foxes (14.4%) with a statistical relevance between density areas.
Roe deer and wild reindeer: E. coli was isolated and susceptibility tested from 274 out of 301 (91%) roe deer, and from 230 out of 265 (86.8%) wild reindeer. Resistance to streptomycin was detected in 1.7% of wild reindeer and in 5.1% of roe deer. The overall occurrence of *E. coli* resistant to ESC was 0.3% in roe deer. This is the first finding of an ESBL from a wild cervid in Norway.
Svalbard reindeer: Fifteen isolates (55%) were resistant to more than one antimicrobial agent. Resistance regions with high homology to plasmid regions previously described in bacteria from swine in the Netherlands and poultry in China were identified.

CONCLUSIONS: Results from these studies demonstrate that AMR is present in the environment even in pristine ecosystems such as the Arctic. Longitudinal and spatial broad studies should be prioritized in order to better understand this problem and elucidate the role of wildlife species in the spread of AMR in a one-health perspective.

3 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

Comparative human exposure to antimicrobial-resistant Campylobacter species, Escherichia coli, Salmonella enterica from food animals using integrated assessment modelling: A farm to fork approach.

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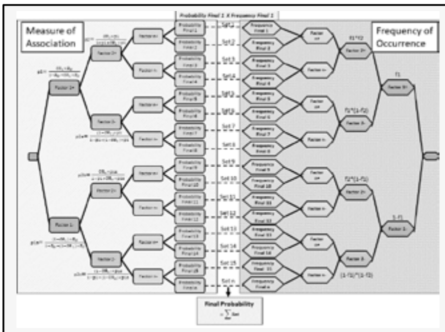
3: Population Medicine, University of Guelph

BACKGROUND: Antimicrobial resistance (AMR) is an important public health concern and there is a large body of research on this topic. To further understand AMR, there is a need to synthesize existing information and our objective was to develop quantitative models to synthesize existing data and assess human exposure to extended-spectrum cephalosporin-resistant E. coli (ESC-E. coli) and Salmonella enterica (ESC-Salmonella), and fluoroquinolone-resistant Campylobacter (FQ-Campylobacter) from chicken, beef or pork consumption in Canada.

METHODS: Individual farm-to-fork quantitative models for ESC-E. coli, ESC-Salmonella, and FQ- Campylobacter from beef cattle, chickens and pigs were constructed using data from the Canadian Integrated Program for Antimicrobial Resistance Surveillance and a comprehensive literature search. Using a branching probability tree approach, the models propagated a baseline probability of AMR modified by 1) the odds ratio between factors and the occurrence of AMR, and 2) the frequency of occurrence of the factors (Figure 1) through the agri-food chain. Estimates of Canadians' exposures to resistant bacteria through beef, chicken and pork were obtained by adjusting the calculated probabilities by Canadian consumption patterns and population.

RESULTS: All models included management system (e.g., organic) and antimicrobial use. The chicken models also included other factors (e.g., type of litter, chilling at abattoir, type of retail packaging). A FQ- Campylobacter model for beef cattle could not be constructed as there were no data about factors linked with AMR reported in the reviewed literature relevant to Canadian beef production. There was higher exposure to AMR through chicken when compared to beef or pork. The highest exposure was to ESC-E. coli, then ESC-Salmonella and lowest exposure to FQ-Campylobacter. There was comparatively lower exposure to ESC-E. coli and ESC-Salmonella from beef or pork and lowest exposure to FQ- Campylobacter from pork.

CONCLUSIONS: The comparative human exposure to antimicrobial resistant bacteria was highest from chicken. This observation was attributable in part to higher baseline probabilities of AMR from chickens, higher bacterial recovery rates at retail, and higher consumption rates. However, there are substantial data gaps in the models including factors such as animal density, factors affecting pathogen load, and vaccination. Filling these data gaps will enable us to build models that more adequately represent the agri-food system in Canada and identify plausible interventions to reduce exposure to AMR. Further development of this integrated assessment model includes filling data gaps, addressing other pathways of AMR (e.g., environment, human pathways) and incorporating whole genome sequencing resistance data.



[a]Factors are measured observation whose relationship with antimicrobial resistance was investigated (e.g., antimicrobial use, organic production)

Factor$_{n+}$: Presence of the factor (e.g., antimicrobial use);

Factor$_{n-}$: Absence of the factor (e.g., the absence of antimicrobial use);

Measure of Association: Probability tree to update probabilities using odds ratio; **p_n**: Updated probability of antimicrobial resistance; **B_O**: baseline or initial probability of antimicrobial resistance; **OR_n**: odds ratio of a specific factor and the occurrence of antimicrobial resistance;

Frequency of occurrence: Probability tree to update the frequency of occurrence of factors in the system; **f_n:** frequency of occurrence of factors; **f+**: frequency of factors occurrence (e.g., 30% of animals are exposed to antimicrobials); **f-**: frequency of factor non-occurrence (e.g., 70% of animals are not exposed to antimicrobials).

Figure 1. Branching probability tree of propagation of the probability of antimicrobial resistance (AMR) modified by the odds ratio between factors and AMR, and the frequency of occurrence of factors.

4 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

Assessing Impacts of Antibiotic Therapy in Neonatal Dairy Calves on Gut and Animal Health

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BACKGROUND: Diarrhea and pneumonia are commonly observed in pre-weaned calves on dairy farms and account for > 50% of all calf deaths. There is evidence that these diseases are over treated with antibiotics which may disrupt colonization of gastrointestinal tract (GIT) microbiota. The aim of this study is to better understand the impacts of intramuscular antibiotics on dairy calves' growth rate, health and microbiotic density of beneficial bacteria in the GIT. The study hypothesis was: antibiotics given to healthy calves created a GIT dysbiosis and subsequent negative health and productivity outcomes.

METHODS: The study was conducted on a commercial dairy farm in the Pacific Northwest USA. The farm milked 3000 Holstein and Holstein-Jersey mix cows and raised all their replacement stock. Study personnel worked with on-farm staff to conduct the study and identify animals to be included. The study was a clinical trial design with calves initially enrolled at the first sign of disease (usually diarrhea) and an age-matched calf with no clinical signs. This was determined by on-farm calf caretakers. Subsequently, calves in each group (healthy and unhealthy) were randomly assigned to be treated with a parenteral antibiotic or palliatives and oral electrolytes. Body weight at enrollment and weaning were recorded. Daily health scores (appetite, fecal consistency, fecal dry matter, pre-feeding attitude and body temperature) were recorded twice daily before, during and post treatment.
Calves were regrouped for analysis to reflect disease status based on daily health scores collected by study personnel. *Bifidobacteria*, an anaerobic Gram- negative bacteria associated with decreased *E. Coli* and overall good health was quantified from fecal samples before, during and after treatment using pPCR.

RESULTS: A total of 121 pre-weaned dairy calves were enrolled into one of four groups. An important finding was a disconnect between the decision made by farm personnel to identify a calf as sick and criteria based on clinical signs observed and measured by the investigators. Across the four groups, 26 percent of calves enrolled into groups by farm personnel did not accurately correspond to disease groupings based on daily health scores. Average daily gain was not significantly impacted by the use of antibiotics or by disease groupings Inappropriate use of antibiotics (treating healthy animals or not treating clinically sick animals) was associated with decreased *Bifidobacteria* quantities in the GIT.

CONCLUSIONS: Inappropriate antibiotic use had a negative impact on GIT *Bifidobacteria*. Also, these data illustrate the importance of effective communication between veterinarians and farm personnel to improve disease diagnosis and better promote understanding and definition of the on-farm treatment decision-making process and encourage appropriate antibiotic use protocols.

5 AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE LINK TO AMR AND ENVIRONMENTAL IMPACT - GALLERY CD

Prevalence and Antimicrobial Resistance profile of Salmonella spp. in retail meats of Super Shop: a food safety risk

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Salmonella spp has represented as the primary cause of foodborne diseases in human. Immunocompromised people and infants are mainly vulnerable to Salmonellosis. *Salmonella* spp can be found in many foods and food products including retail meat where multi-drug resistant *Salmonella* spp evolves a robust challenge to food safety. The aim of this study was to determine the prevalence and antimicrobial resistance profile of *Salmonella* spp in retail meat of super shop at Dhaka City, Bangladesh. During July 2015 and June 2016, a total of 476 samples were collected from 10 super shop of Dhaka city; categorized in chicken meat (n=170), beef (n=68), mutton (n=34) and environment (n=204). *Salmonella* spp. were isolated from the samples by using selective enriched media and confirmed by real-time PCR. Phenotypic resistance was determined by disk diffusion method. Extended-spectrum β-lactamases (ESBLs) and quinolone resistance genes were determined by PCR. The overall prevalence of *Salmonella* spp. was 18.5% (n=88; 95% C.I.15-22%) comprising in chicken meat 26% (n=44; 95% C.I.19.5-32.5%), beef 15% (n=10; 95% C.I.7-23%), mutton 18% (n=6; 95% C.I.6-30%) and environment 14% (n=28; 95% C.I.9.5-18.5%). In antimicrobial assay, 55% isolates were found multi-drug resistant (MDR). Among 22 tested antibiotics, extreme level of resistance was observed against Tetracycline and Erythromycin 99.1% (n=87, 95% CI: 94.5-99.9%), followed by Doxycycline 98%, Pefloxacin 93.9%, Azithromycin 92.2%, Enrofloxacin 91.2%, Moxifloxacin 89.7%, Nalidixic Acid 87.1%, Trimethoprim/Sulfamethoxazole 75%, Ciprofloxacin 53.4% and Streptomycin 49.6%. Nevertheless, only Ceftriaxone, Cefotaxime, Imipenem, Amoxicillin/Clavulanic acid showed good level of sensitivity as 82%, 73%, 73% and 68% respectively. In minimum inhibitory concentration (MIC) assay, high level of MIC50/MIC90 were observed against Amoxicillin (512/>1024), Flucloxacillin (512/1024), Cephradine (256/1024), Cefixime (2/512), Gentamycin (4/512), Chloramphenicol (32/512), Azithromycin (512/1024), Erythromycin (1024/>1024), and Sulfamethoxazole (512/ >1024). Among the phenotypically resistant isolates, ESBL encoding genes were observed as bla (TEM) 80% (n=40/50), bla (shv) 10% (n=5/50), bla (ctx) 34% (17/50), bla (cmy) 8% (4/50); and Quinolone resistance genes qnrA 10.63% (5/47) gyrA 57.45 %(27/47) and gyrB 23.40%(11/47). High level prevalence of MDR *Salmonella* spp in retail meat which could cause foodborne illness is a great alarming issue for public health.

AMR GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION

1 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

The human resistome within the Dutch pork production chain, a metagenome-wide study among farmers and slaughterhouse workers.

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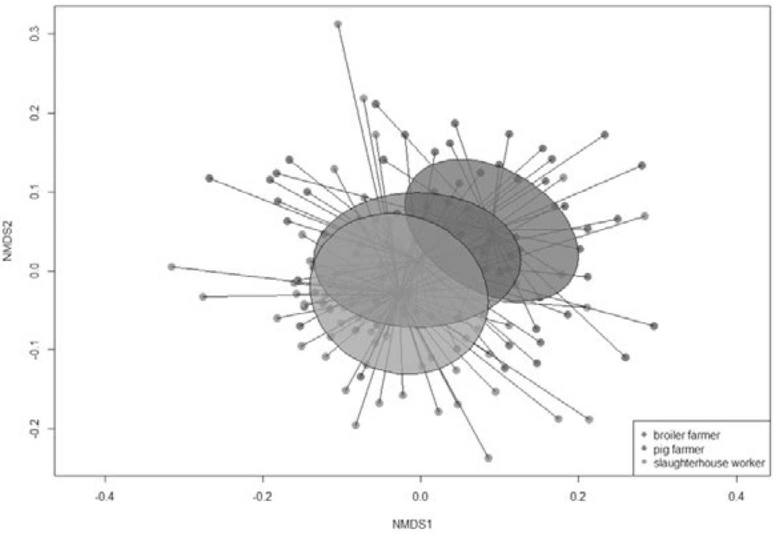
This study is part of the European EFFORT project (http://www.effort-against-amr.eu).

BACKGROUND: Studies investigating antimicrobial resistance (AMR) in humans working in the meat production chain have primarily focused on specific bacterial species and types of AMR. However, larger scale resistome and microbiome studies, to our knowledge, have never been reported. This study analyzes (dis)similarities in faecal microbiome and resistome composition within and between farmer (pigs and poultry) and slaughterhouse populations (pig slaughterhouse employees, pig carcasses and faeces).

METHODS: Between October 2014 and December 2015, faecal samples were collected from 79 Dutch pig and poultry farmers, their families and co-workers (age: 18-65 years). Subsequently in two sampling rounds (June 2015 and July 2016) within one slaughterhouse, we collected faecal samples from in total 70 pig slaughterhouse workers (age: 21-59 years), 60 pigs (colon samples) and 480 pigs (carcass: cork borer). The latter two sample types were pooled by slaughter step and sampling round (carcass: 12 pools, pig faeces: 2 pools). All participants filled out a personal questionnaire regarding past antimicrobial use, animal contact, travelling, hospitalization, and meat consumption. DNA was extracted from all 163 samples and acquired resistomes and microbiomes were determined by metagenome (Illumina HiSeq4000) sequencing to 40M PE150 clusters. Bacterial genome and antimicrobial resistance genes (ARGs) where classified by mapping to NCBI bacterial reference genomes and the 90% identity/AMR-class clustered resfinder database. Fragments Per Kilobase ARG per Million bacterial fragments (FPKM) was used for relative abundance comparisons. Finally, necessary data transformations (incl. outlier removal) and descriptive and multivariate analyses were performed (NMDS, PERMANOVA, SIMPER analysis).

RESULTS: Significant differences in relative ARG load (total FPKM) were observed between the three human populations (Kruskal-Wallis: $p<0.005$), with pig farmers (median: 782) and slaughterhouse workers (median: 768) carrying the highest relative loads, and broiler farmers (median: 433) the lowest. Relative abundance of tetracycline resistance was highest among all samples, followed by β-lactam (humans) and macrolide resistance (humans, carcasses, pig faeces). Within the farmers' group, significant differences were observed between the farmers' partners and the other family members/farmers/employees (Kruskal-Wallis: $p<0.05$). Furthermore, we observed differences between relative ARG loads along the slaughter line (humans) with higher abundances in samples at the beginning (lairage-scalding) and at high-risk positions (evisceration, removal heart-lung-tongue) (Kruskal-Wallis: $p<0.01$). Multivariate results indicate resistome composition differences between the different human populations (PERMANOVA $p<0.001$; Figure 1).



CONCLUSIONS: Differences in ARG abundances were observed within and between farmers and slaughterhouse workers populations. Further work on the microbiome and the comparison of the microbiome and resistome is forthcoming.

Figure 1: NMDS plot: Resistome clusters by human sample type. ARGs were used at the aggregated AMR class level (Bray-Curtis dissimilarity, data = square root transformed, stress=0.16). PERMANOVA on sample type: p<0.001, R2=0.056, after removal of outliers, 'R' software v.3.4.2.

2 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

Genomic and evolutionary analysis of Clostridium difficile sequence type 11: a genetically diverse lineage of significant One Health importance

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BACKGROUND: In the last decade, *Clostridium difficile* infection (CDI) has reached an epidemic state in some parts of the world with sources outside the healthcare system, particularly livestock, identified as potential reservoirs. *C. difficile* sequence type (ST) 11 is a diverse evolutionary lineage comprising at least 5 PCR ribotypes (RTs) that contribute considerably to the global burden of CDI in humans and production animals. Increasing evidence of a shared ancestry and genetic overlap of RT078, the most common ST11 sublineage, between these populations suggests that CDI may have a zoonotic or foodborne aetiology.

METHODS: Whole-genome shotgun sequencing and core genome phylogenetics were performed on a diverse collection of 207 ST11 isolates of clinical (n=150) and veterinary/environmental (n=57) origin from Australia and 12 countries across Asia, Europe and North America (16 RTs including major ST11 sublineages 078, 126, 127, 033 and 288).

RESULTS: Phylogenies based on core orthologous genes (1276 loci) showed clustering of clinical and veterinary isolates indicative of very recent shared ancestry. Core genome single nucleotide variant (SNV) analysis provided ultra-fine scale resolution of this lineage, identifying multiple intra- species and inter-species clonal groups (isolates separated by ≤ 2 SNVs in their core genome) in all the major RT sublineages. Many clonal groups comprised isolates spread over a vast geographic area (different states, countries, and continents), indicative of reciprocal long-range dissemination and possible zoonotic/foodborne transmission. Antimicrobial resistance genotypes and phenotypes varied across host species, geographic regions and RTs, and included macrolide/lincosamide resistance (Tn*6194*; *ermB*), tetracycline resistance (Tn*6190*; *tetM* and Tn*6164*; *tet44*), fluoroquinolone resistance (*gyrA/B* mutations) as well as several aminoglycoside resistance cassettes. *C. difficile* ST11 is defined by a large 'open' pan-genome (10378 genes) comprising a core genome of 2058 genes (remarkably, accounting for only 19.8% of the total gene repertoire) and an accessory genome of 8320 genes containing a large and diverse collection of clinically important prophages of the Siphoviridae and Myoviridae.

CONCLUSIONS: This study provides novel and critical insights on strain relatedness and genetic variability of *C. difficile* ST11, a lineage of significant One Health importance.

3 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

Whole genome sequencing reveals limited contribution of non-intensive chicken farming to extended-spectrum beta-lactamase producing Escherichia coli colonization in humans in southern Vietnam

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BACKGROUND: Overuse of antimicrobials in agriculture in Asia has been reported, but the risk of acquisition of extended-spectrum beta-lactamase (ESBLs) in humans through non-intensive chicken farming still remains unclear. We conducted this study to investigate the contribution of transmission of ESBL-producing Escherichia coli (ESBL-Ec) from poultry to ESBL-Ec colonization in humans.

METHODS: We collected faecal samples from 204 randomly selected farmers and their chickens, and from 306 community-based individuals who did not raise poultry in Vietnam. ESBL-Ec was isolated from MacConkey agar with and without antimicrobials supplemented. Logistic regression model was built to investigate risk factors associated with ESBL-Ec colonization in humans. A total of 486 ESBL-Ec isolates were sequenced to examine genomic relatedness of ESBL-Ec colonizing chickens and humans in Vietnam.

RESULTS: The prevalence of ESBL-Ec colonization was 20.0% in chicken farms, 31.1% in chicken farmers, 49.5% in rural individuals and 38.3% in urban individuals. Multivariable analysis showed that colonization with ESBL-Ec in humans was associated with human usage of antimicrobial drugs (OR=2.52, 95%CI=1.08–5.87) but not with involvement in chicken farming (OR= 0.71, 95%CI=0.43–1.19).
Whole-genome sequencing revealed that CTX-M genes were the most predominant ESBL genes, found in 468/486 (96.2%) of ESBL-Ec isolates. However, the distribution of CTX-M genes across chicken and human isolates was different (Figure 1). CTX-M-55 was identified as the most common ESBL-encoding gene in chicken isolates (72.1% versus 12.9% in human isolates, $p<0.001$), whilst CTX-M-27 was more prevalent in human isolates (44.2% versus 7.0% in chicken isolates; $p<0.001$).

On 16/204 farms (6.9%; 95%CI=3.4–10.3%) ESBL-Ec were detected phenotypically in both the farmers and their chickens. On 3/204 farms (1.5%; 95%CI=0–3.1%), ESBL genes of ESBL-Ec isolated from the farmers and their chickens were identical. However, we detected identical sequence types of ESBL-Ec between chicken and farmer isolates in only one farm. Isolates also revealed 0 pairwise SNP distance based on core genome alignment, indicating potential sharing of ESBL-Ec between the chickens and farmer on that farm.

CONCLUSIONS: The findings in this study suggest that non-intensive chicken farming is not a major source of ESBL-Ec colonization in humans and that human antimicrobial drug usage appears to be a more important driver of ESBL-Ec colonization in humans in Vietnam.

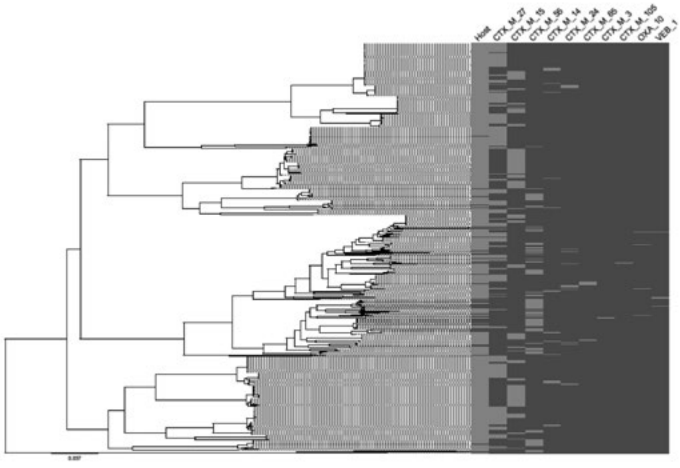

Figure 1 Distribution of ESBL genes across the phylogeny of ESBL-Ec isolated from chickens and humans in Vietnam. On the left is the maximum-likelihood phylogeny based on 230791 single nucleotide polymorphisms (SNPs) in the core genome of 486 ESBL-Ec isolates. The first column at the termini of the phylogeny represents the host of the isolates (red indicates human isolates, blue indicates chicken isolates). The presence (red) and absence (blue) of ESBL genes is shown in the next ten columns.

4 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

Associations between antimicrobial use and the fecal resistome on broiler farms in nine European countries

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BACKGROUND: Several studies have suggested that antimicrobial use (AMU) selects for antimicrobial resistance (AMR). The association has never been determined specifically for the resistome of broiler fecal samples on farm level though. The aim of this study is to determine associations between farm and flock level AMU and the

abundance of antimicrobial resistance genes (ARGs) in broiler fecal samples from nine European countries. Also the association between farm biosecurity status and ARGs is explored.

METHODS: In the cross-sectional pan-European EFFORT-study, conventional broiler farms were visited to collect feces and to record biosecurity and AMU. The resistome (all known resistance genes included in the Resfinder database) of a pooled fecal sample was determined by metagenomic analysis for 176 farms. To take a potential country effect into account, meta-analysis was used to relate total and class-specific ARGs to AMU. ARGs, clustered at a 90% identity level, were quantified by metagenome short read mapping expressed as Fragments Per Kilobase ARG-reference per Million bacterial fragments (FPKM). AMU is measured by Treatment Incidence per Defined Daily Doses Animal (TI-DDDvet) for group treatments of the sampled flock, or products purchased by the farm in the year before sampling. In a similar way, the association between biosecurity status of a farm (defined with Biocheck.UGent) and the resistome was explored. All associations were adjusted for multiple testing by controlling the False Discovery Rate.

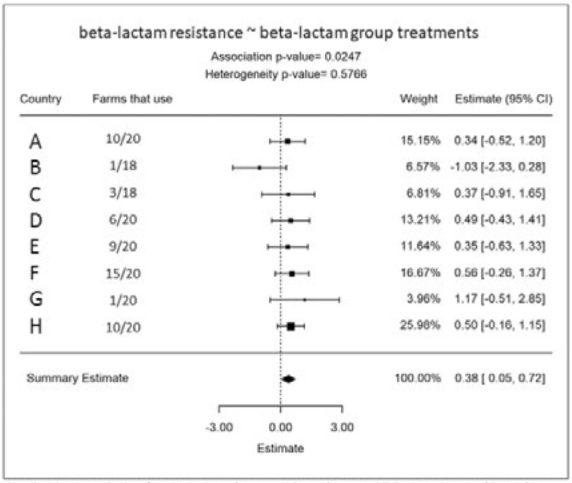

Fig. 1. Meta-analysis of associations between beta-lactam ARG presence and beta-lactam usage as group treatment in the sampled flocks, with number of farms that use AM, the weight of the individual association in the summary estimate and the 95% confidence intervals per country. At the bottom the summary estimate for the overall association. Country I reported no usage.

RESULTS: For 66 (38%) flocks there was no report of group treatments. These flocks show a similar resistome composition and roughly similar FPKM levels as AM-treated flocks. Nevertheless, we found significant positive associations between class-specific antimicrobial flock treatments and ARG clusters conferring resistance to the same class, for beta-lactams (fig.1), tetracyclines, macrolides, trimethoprim and aminoglycosides. Similar associations were found between ARG clusters and purchased products, which represent usage on farm level. In a gene level analysis for the class beta-lactam, a significant positive association was found for bla_{TEM} and bla_{ACT} gene clusters, which are in the top five most abundant gene clusters for this class. Little evidence was found for associations between resistance genes and biosecurity. No indications for confounding by age and biosecurity status were found.

CONCLUSIONS: The fecal microbiome in European broilers contains many resistance genes, even in the absence of current antimicrobial selection pressure. Despite this, the relative abundance of genes and composition of the resistome is positively related to the antimicrobial use in European broiler farms for several antimicrobial classes.

5 AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION - GALLERY CD

Epidemic clones of community-acquired methicillin-resistant Staphylococcus aureus in slaughter pigs, Cuba

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The WHO, FAO and OIE, promote a global action plan under the One Health approach for a rapid containment antimicrobial resistance (AMR). In 2011 in Cuba, human infections caused by MRSA were predominantly associated with the USA300 clone, and the Latin American variant (USA300-LV) was not identified. Although these lineages are generally not associated with nasal carriage in pigs, which usually harbor the livestock-associated MRSA (LA-MRSA) lineage ST398, the presence of human epidemic clones in pigs cannot be excluded. Following the One Health recommendation, the epidemiological MRSA situation in slaughter pigs from three Cuban provinces was investigated. From May to July 2015, 22 of 285 nasal swabs taken at one central slaughterhouse from fattening pigs raised in the provinces of Mayabeque (n=67), Matanzas (n=90) and Cienfuegos (n=128) were found to carry MRSA (prevalence 7.7%). Isolates were obtained after two-step of enrichment and selective cultivation in Müller-Hinton (MH) broth. MRSA were identified by matrix-assisted laser desorption/ionisation time of-flight mass spectrometry (MALDI-TOF/MS) and by detection of the methicillin resistance gene *mec*A by PCR. The minimum inhibitory concentrations (MICs) were determined by microdilution in MH broth using the Sensititre susceptibility plate EUST. Antibiotic resistance and virulence genes were detected using microarrays (Alere). Isolates were characterized using pulsed field gel electrophoresis (PFGE), multilocus sequence typing (MLST), *Staphylococcus* protein A (*spa*) typing, SCC*mec* typing, ACME typing and *mec*-associated direct repeat unit (dru) typing. PFGE revealed three groups of MRSA. The MRSA isolates gathering into PFGE cluster I shared the same PFGE profile as the USA300 epidemic clone as well as the same genetic properties (ST8 except one ST173, SCC*mec* IVa, dru dt9g, PVL+, ACME I +). The isolates belonged to *spa* type t024 also contained the *sek* and *seq* enterotoxin genes. The strains were resistant to β-lactams (*mecA, blaZ*), macrolides [*msrA, mph*(C)], aminoglycosides [*aph(3')-III*] and fluoroquinolones [GrlA(S80-Y) and GyrA(S84- L)]. MRSA clones of PFGE cluster II were characteristic to USA300-LV (ST8, *spa* t008, SCC*mec* IVc, *dru* dt7j, PVL+ and ACME–). These clones were resistant only to β-lactam antibiotics (*mec*A, *bla*Z). The third PFGE cluster (cluster III) contained clones belonging to ST5, *spa* t010, SCC*mec* IVc, dru dt10a. They were all PVL– and ACME–, contained the enterotoxin genes *sea*(N315), *seb, sel, selm, seln, selo, egc* and *selu*, and were resistant to β- lactams (*mec*A, *bla*Z) as well as to the aminoglycosides gentamicin and kanamycin [*aac*(6')-*Ie-aph*(2")-*Ia*]. These findings demonstrate that pigs from Cuba carry MRSA belonging to the same clonal lineages than those found in humans causing infection in the community. It is therefore of major veterinary and public health importance to take specific preventive measures and antimicrobial stewardship in both human and animal settings to limit the spread of MRSA.

AMR REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING

1 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

Comparative Genomics of Vancomycin-Resistant Enterococcus spp. isolated from Wastewater Treatment Plants

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BACKGROUND: Wastewater treatment plants (WWTPs) are considered hotspots for the environmental dissemination of antimicrobial resistance (AMR) determinants and receive antimicrobial residues and resistant microorganisms from a variety of sources. Vancomycin-Resistant *Enterococcus* (VRE) is a candidate indicator organism for gauging the degree of AMR contamination in water environments. The multi-drug resistant nature of vancomycin-resistant E. faecalis and E. faecium, their ubiquity in wastewater and the gastrointestinal tracts of mammals, and the use of the genus as an indicator organism for fecal contamination make these species ideal candidates for this purpose.

METHODS: Three hundred and thirteen presumptive VRE isolates from two WWTPs from the same municipality were selected using selective broth containing vancomycin (4mg/L). In this study, a total of 39 isolates were selected for whole genome sequencing based on source, species (determined by groEL loci) and AMR phenotype (disc diffusion antimicrobial susceptibility). These genomes included E. faecalis (n=24),
E. faecium (n=11), E. *casseliflavus* (n=2) and *E. gallinarum* (n=2). The presence of AMR genes, virulence genes, bacteriophage, and CRISPR/Cas arrays was determined using a variety of databases. Analysis of the phylogeny and the pangenome was also conducted with the inclusion of genomes of E. faecium, E. faecalis and E. *casseliflavus* from NCBI.

RESULTS: All but 3 isolates (2 *E. gallinarum* and 1 E. faecalis) exhibited resistance to three or more antimicrobials. The AMR phenotype generally aligned with genotype which confirmed the presence of multi-drug efflux proteins and specific resistance genes. Genes conferring vancomycin resistance were detected in 20 of the genomes. Vancomycin resistance was conferred by vanA (E. faecium), vanM (E. faecium), vanG (E. faecalis) and vanC (E. *casseliflavus* and *E. gallinarum*). A minimum of 18, 5, 6 and 3 virulence genes were detected in E. faecium, E. faecalis, E. *casseliflavus* and E.gallinarum genomes, respectively. Functional CRISPR/Cas arrays were detected in 10 E. faecalis genomes and 1 *E. gallinarum* genome. All of the E. faecalis genomes with CRISPR/Cas arrays also contained at least one prophage. The accessory genomes for each species show clear differentiation between isolates from wastewater, livestock, food products and clinical sources and could provide candidate biomarkers for microbial source tracking.

CONCLUSIONS: This study characterized the genomes of isolates from various species of VRE. It includes not only multi- drug resistant E. faecium and E. faecalis, commonly associated with humans, but also environment-associated E. *casseliflavus* and *E. gallinarum*. Analysis using additional genomes from the NCBI database demonstrated differential clustering of isolates from wastewater, clinical and other sources suggesting that these strains are specifically adapted to their environments.

2 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

Integrating whole genome sequencing data into quantitative microbial risk assessment modeling: a case study for Salmonella Heidelberg resistant to third-generation cephalosporins in Canadian broiler chicken production

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BACKGROUND: Salmonella Heidelberg resistant to third-generation cephalosporins (3GC) in chicken products has been identified as an important foodborne antimicrobial resistance concern by the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS). Primarily under the Genomics Research and Development Initiative on Antimicrobial Resistance (AMR) (GRDI-AMR), approximately 2,000 S. Heidelberg isolates collected in Canada were subjected to whole-genome sequencing (WGS). The objective of this study was to explore applications and added value of integrating WGS data into a farm- to-fork quantitative microbial risk assessment (QMRA) model for 3GC–resistant S. Heidelberg in broiler chicken.

METHODS: A QMRA framework was developed in accordance with the Codex Alimentarius guidelines for risk analysis of foodborne AMR (Figure 1). Using data from a literature review and consultation with WGS experts, we identified potential areas where WGS data could be integrated into the QMRA model through refinement of the hazard identification, exposure assessment and hazard characterization steps, in order to produce a more accurate estimate of the public health risk associated with the occurrence of 3GC–resistant S. Heidelberg in chicken in Canada.

RESULTS: Applications of WGS data were identified at each step of the QMRA model (Figure 1). For hazard identification, WGS data can refine the AMR profile of the hazard of interest by providing a comprehensive list of AMR genes present and describing their location on the chromosome or on mobile genetic elements. The latter is critical to determine whether horizontal gene transfer should be considered in the risk pathway and if so, at which steps along the farm-to-fork continuum. Additionally, WGS data can be used to determine the virulence profile of the hazard and any associations with AMR. By quantifying the relatedness of isolates collected along the agri-food chain using phylogenetic approaches, the proportion of hazards carried through each step (i.e., farm, abattoir, retail) can be integrated into the exposure assessment to better characterize how upstream events affect consumer exposure.

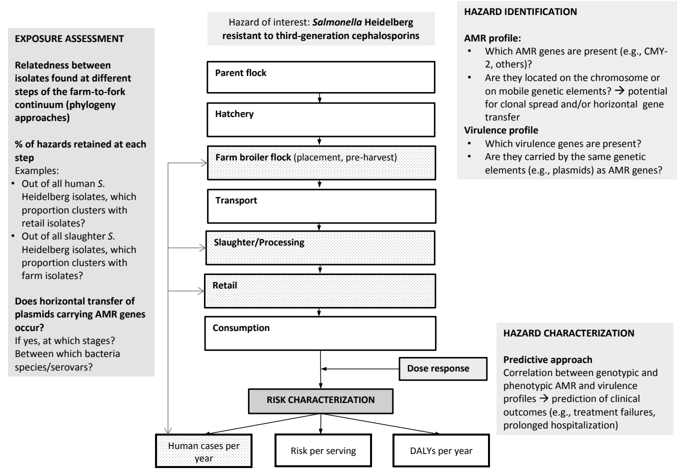

Figure 1. Potential added value of whole-genome-sequencing data to quantitative risk assessment of *S.* Heidelberg resistant to third-generation cephalosporins in broiler chicken

Colored boxes indicate key areas where whole-genome sequencing data could inform quantitative risk assessment steps as defined by the *Codex Alimentarius* guidelines for risk analysis of foodborne antimicrobial resistance
Dotted blue boxes: steps where *S.* Heidelberg isolates were sequenced via whole-genome sequencing primarily under the Canadian Genomics Research and Development Initiative on Antimicrobial Resistance

For the hazard characterization, virulence profiles can be integrated into novel dose-response models. As well, WGS data are expected to better predict clinical outcomes following exposure to the hazard, although correlations between genotypic and phenotypic profiles need to be validated first.

CONCLUSIONS: WGS data have the potential to make a huge improvement to QMRA modeling, which has been traditionally performed using phenotypic information. Some of the possible improvements described herein will be tested under the GRDI-AMR project using 3GC-resistant S. Heidelberg as a case study.

3 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

Whole Genome Sequence Profiling of Antibiotic Resistant Staphylococcus aureus isolates from Livestock and Farm Attendants in Ghana

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BACKGROUND: Recent studies in Ghana have indicated the presence of epidemic methicillin resistant *S. aureus* clones among carriage and clinical *S. aureus* isolates. Information on the epidemiology of *S. aureus* among livestock in Ghana is, however, not available. Therefore, the objective of this study was to characterize *S. aureus* isolates from livestock and farm attendants to determine the differences, if any, with respect to antimicrobial resistance, genotypic diversity and virulence gene content.

METHODS: Swab samples were collected from the anterior nares of cattle, pigs, goats, sheep and farm workers from selected farms. Identification of *S. aureus* was done by MALDI-TOF MS. Antimicrobial susceptibility testing was performed by VITEK (Biomerieux) and interpreted according to EUCAST guidelines. Whole genome sequencing was done using the illumina Miseq Platform.

RESULTS: Twenty-six (26) *S. aureus* isolates were recovered from a total of 401 nasal swab samples collected. Isolates were frequently resistant to penicillin (65%), tetracycline (42%), ciprofloxacin (31%), clindamycin (9%) and cefoxitin (7%). Genome sequencing of 15 out of the 26 isolates revealed that the isolates belonged to ST8 (n=1), ST152 (n=4) (humans); ST9 (n=1), ST97 (n=4) (Pigs) and ST133 (n=5) (Goats). Almost half (46%) of the isolates were multi-drug resistant. The two MRSA isolates detected (belonged to ST8 and ST152) were from humans; none was found among livestock. Panton Valentine leucocidin toxin gene was detected among 27% of the isolates (mainly from humans).

CONCLUSIONS: The detection of ST152 as MRSA was particularly interesting; although this clone was dominant in a collection of carriage and clinical isolates in previous studies in this country, none was MRSA. ST152 MRSA has been reported in Central Europe, the Balkan, Switzerland and Denmark as a community acquired MRSA. All isolates detected in this study belonged to global lineages (ST133, ST9, ST97, ST8, ST152). The finding of 46% multidrug resistant isolates is worrying as routine detection of resistant bacteria species are not performed on these farms due to limited microbiological infrastructure in Ghana. This calls for capacity building to prevent the spread of these resistant bacteria species in the country.

4 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

Phenotypic and genomic analysis of antimicrobial resistant E. coli isolated from ready-to-eat food in Singapore

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BACKGROUND: Antimicrobial resistance (AMR), especially multidrug-resistance, of bacteria is posing a great threat to public health. This study aimed to determine the phenotypic antimicrobial resistance (AMR) profiles of Escherichia coli isolated from ready-to-eat retail food in Singapore. *E. coli* is widely recognized as a food safety indicator and a high priority Gram negative bacterium for studying antimicrobial resistance. We then compared the phenotypic traits of these isolates with the antimicrobial resistant genes identified by next-generation sequencing (NGS) technique which can serve to support further work on elucidating the genetic mechanisms involved.

METHODS: A total of 99 E.coli isolates (77 were from poultry-related food, 22 were from fish-related food) from ready-to-eat retail food were included in this study. Disk diffusion was conducted to determine the phenotypic AMR profiles of isolates against 12 antimicrobials. Isolates resistant to ceftriaxone (30 μg) were subjected to double-disk synergy test using amoxicillin and clavulanate (20/10 μg), ceftazidime (30 μg), and cefotaxime (30 μg) for the phenotypic confirmation of Extended-Spectrum β-lactem (ESBL)- production. Isolates resistant to at least one antimicrobial were subjected to micro-dilution against 33 antimicrobials (including classes of β-lactem, aminoglycosides, tetracycline, fluoroquinolones, polymyxin et. al.). These isolates were also subjected to whole genome sequencing (WGS) using Illumina HiSeq2500 sequencer. Short reads were assembled by Velvet. Resfinder, an online tool, was used to analyze WGS data for the detection of AMR genes.

RESULTS: Based on disk diffusion results, 24.2% (24/99) of the E.coli isolates from ready-to-eat retail food were resistant to at least 1 antimicrobial agent, and 68.7% (68/99) isolates were sensitive to all 12 antimicrobials tested. Poultry-related *E. coli* isolates showed a higher resistance rate (29.9%, 23/77) to at least 1 antimicrobial agent than fish-related isolates (4.5%, 1/22). No resistance to amikacin, amoxicillin/ clavulanic acid and meropenem was observed. The most common resistance pattern observed was tetracycline resistance (17.2%), followed by ampicillin resistance (15.2%). Two ceftriaxone-resistant isolates were confirmed as ESBL-producing *E. coli*. Of 24 isolates subjected to micro-dilution, 70.8% (17/24) were resistant to tetracycline, followed by chloramphenicol (50%, 12/24), ampicillin and trimethoprim (41.7%, 10/24). Genomic analysis of 24 *E. coli* isolates revealed the presence of 9 classes of AMR genes; 20 isolates carried at least one AMR gene. High agreement (79.2% to 95.8%) between AMR phenotypes and genotypes across all antimicrobials was observed, with exceptions for aminoglycosides (79.2%) and colistin (79.2%). Differences observed between phenotypic and genomic findings of isolates could be due to unknown or noble resistance mechanisms of the bacteria or it could be due to the limited range of antimicrobials used in phenotypic tests.

CONCLUSIONS: The detection of *E. coli* harboring antimicrobial resistance traits in ready-to-eat food can be of potential public health concern. Although these are non-pathogenic *E. coli* strains and are unlikely to cause foodborne disease, they can still be good reservoirs for the acquisition and transmission of AMR genes in bacteria in retail food and the environment. This study illustrates the usefulness of WGS in supporting work for understanding the genetic mechanisms of antimicrobial resistance traits in bacteria. With the advancement in technology and the general declining cost in sequencing, WGS is a promising tool that can be applied even for routine surveillance for the monitoring of AMR trends in human pathogens and environmental bacteria.

5 AMR 03 - REAL LIFE APPLICATIONS OF WHOLE GENOME SEQUENCING - GALLERY CD

Antibiotic use and biosecurity in pig farming are determinants for antimicrobial resistance, a metagenome-wide association study in nine European countries.

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EFFORT GROUP: Haitske Graveland (UUVM), Alieda van Essen (WBVR), Bruno Gonzalez-Zorn (UCM), Gabriel Moyano (UCM), Pascal Sanders (ANSES), Claire Chauvin (ANSES), Julie David (ANSES), Antonio Battisti (IZSLT), Andrea Caprioli (IZSLT), Thomas Blaha (TIHO), Katharina Wadepohl (TIHO), Maximiliane Brandt (TIHO), Tine Hald (DTU), Ana Sofia Ribeiro Duarte (DTU), Dariusz Wasyl (NVRI), Magdalena Skarzyńska (NVRI), Magdalena Zajac (NVRI), Hristo Daskalov (NDRVI), Helmut W. Saatkamp (BEC), Katharina D.C. Stärk (SAFOSO). This study is part of the EFFORT project (http://www.effort-against-amr.eu).

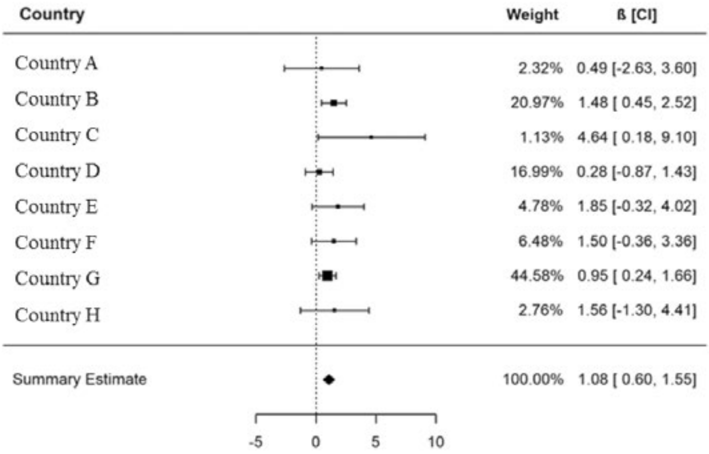
OBJECTIVES: Previous studies in food-producing animals have shown relationships between antimicrobial use (AMU) and resistance (AMR) in specifically isolated bacterial species. Multi-country data is scarce and only describes between-country differences. Here we investigate associations between the pig faecal mobile resistome (based on Resfinder, i.e. full collection of horizontally acquired antimicrobial resistance genes (ARGs)) and characteristics at farm-level across Europe.

METHODS: A cross-sectional study was conducted among 176 conventional pig farms from nine European countries. Twenty-five pig faecal samples were pooled per farm and acquired resistomes were determined by shotgun metagenomics and clustered. Normalized Fragments resistance genes Per Kilobase reference per Million bacterial fragments (FPKM) were calculated. Specific farm-level data (AMU, biosecurity) was collected. Random-effects meta-analyses were performed by country, relating farm-level data to ARG abundances (FPKM).

RESULTS: Total AMU during fattening was positively associated with total ARG (total FPKM). Positive associations were especially observed between widely used macrolides (e.g. Figure 1) and tetracyclines, and ARGs corresponding to the respective antibiotic classes. Significant AMU/ARG associations were not found for β-lactams and no colistin-encoding ARGs were found, despite being the antimicrobial classes used highest in younger pigs. An increased internal biosecurity was directly related to higher abundances of ARG mainly encoding macrolide resistance. These effects of biosecurity were independent of AMU in mutually adjusted models.

CONCLUSIONS: Using resistome data in associations studies is unprecedented and adds accuracy and new insights to previously observed AMU-AMR associations. The major components of the pig resistome are positively and independently determined by on-farm AMU and biosecurity conditions.

Figure I: Meta-analysis: A positive association was observed between macrolide and lincosamide use and macrolide resistance (FPKM) (forest plot)



Macrolide resistance = f(Macrolide and lincosamide use during the fattening phase)*

*Legend: q-value summary estimate < 0.01, p-value heterogeneity test > 0.5. Weight for country 'i' is dependent on the inverse of the sum of the within-country variance for country 'i', plus the between-country variance tau-squared. CI = confidence interval. *Includes lincomycin-spectinomycin antimicrobial use. One country couldn't be included in the above association as a consequence of no macrolide/lincosamide use during the fattening phase in the respective farms of this country.*

AMR PREVALENCE AND SURVEILLANCE OF RESISTANCE

1 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

Temporal Changes in Antibiotic Resistance in Common Bottlenose Dolphins (Tursiops truncatus), a Sentinel Species

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An increase in resistance to antibiotics among common bacterial pathogens is one of the most significant threats to public health. Increases in antibiotic resistance (AR) have been documented globally in isolates from humans, wildlife and the environment. To date, few studies have examined long-term trends in AR in organisms isolated from marine mammal populations despite the potential role of aquatic environments in the proliferation of resistance genes. The objective of this study was to examine temporal trends in resistance to antibiotics among pathogens isolated from common bottlenose dolphins (*Tursiops truncatus*) between 2003 and 2015. Individual dolphins, resident to the Indian River Lagoon, FL, an ecosystem with significant human impacts and a large coastal population, were sampled as a part of the Bottlenose Dolphin Health and Environmental Risk Assessment Project. Swab samples for microbiological analyses were taken from the blowhole, stomach and anus as a part of a comprehensive health examination. Isolates were identified using gram stain morphology and growth on selective media. Antibiotic resistance was measured using disc diffusion on Mueller Hinton agar. The multiple antibiotic resistance index (MAR) was calculated for each isolate. A total of 733 isolates were obtained from 171 individual dolphins. The most commonly cultured pathogens included *Aeromonas hydrophila, Escherichia coli, Edwardsiella tarda and Vibrio alginolyticus*. The MAR was compared between 2003-2007 and 2010-2015 for each organism and was significantly higher for *Pseudomonas aeruginosa* and *Vibrio alginolyticus* during the later period. For all bacterial isolates, resistance to cefotaxime, ceftazidime and gentamicin increased significantly between sampling periods. This represents the first study to use multiple antibiotic resistance indexing for bacterial isolates from a marine mammal. The significant increases in resistance for some bacterial species likely reflect shared environmental exposures to antibiotics and transfer of resistance from terrestrial sources, and animal or human populations to dolphins.

2 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

Antimicrobial Resistance in Salmonella enterica Isolates from Wildlife in Virginia

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BACKGROUND: A large majority of national surveillance efforts for enteric bacteria in the United States currently come from clinical isolates from humans or samples from the agriculture and livestock domain. However, there has recently been a drive to implement surveillance efforts with a more One Health approach and focus. Wildlife has the potential to serve a critical role in the dispersal and dissemination of antimicrobial resistance (AMR) genes. Wildlife may carry a wide array of AMR genes and can potentially introduce these genes into the soil and water through excrements. These genes may then proliferate in the environment and be transmitted to humans and domestic animals through indirect or direct exposures.

METHODS: A total of 65 *Salmonella enterica* isolates from two studies between 2010-2012 involving birds, reptiles, and mammals sampled in the Eastern region of Virginia were tested for AMR by two different methods. The first method performed antimicrobial susceptibility testing by the traditional Kirby-Bauer disk diffusion method (phenotypic resistance) following Clinical and Laboratory Standards Institute concentrations and guidelines against a panel of 12 antibiotics representing nine antimicrobial categories. Whole genomic sequencing (WGS; genotypic resistance) was also performed on the isolates. The CARD database in conjunction with the ARIBA platform tool was used to identify genes associated with the different antimicrobial categories.

RESULTS: The prevalence of AMR in the samples by Kirby-Bauer disk diffusion was 61/65 (94%) with most samples demonstrating at least intermediate resistance to streptomycin. Over 10% (7/65) of the isolates showed resistance to three or more antimicrobial categories; therefore, classifying them as multidrug resistant. An isolate of *Salmonella* Senftenberg from a bird was resistant to eight drugs. Overall, phenotypic resistance showed a high correlation with genotypic resistance for the 65 *Salmonella enterica* isolates. From an epidemiological perspective, an overall sensitivity of 86.8% and specificity of 87.0% were observed. The concordance between tests was categorized as ‘good’ as shown by the kappa value of 0.59. The overall agreement between all of the calls (9 antimicrobial categories* 65 isolates=585 total calls) was 87% (509/585).

CONCLUSIONS: Antimicrobial resistance was present in many of the wildlife samples likely indicating that AMR is present in their environment. Different measures for test performance demonstrate that WGS can be used to predict AMR phenotypic resistance for *Salmonella* in wildlife. It is highly recommended to pursue more research in this area as the numbers are small for any analysis performed by species or antimicrobial class and that a standard for be developed to compare WGS technology to current gold standards.

3 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

Antibiotic resistance and epidemiology of Campylobacter recovered from humans, animals and environmental sources in Ghana

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BACKGROUND: Antibiotic resistance is a major challenge in public health especially in developing countries where antibiotic use is widespread and poorly moderated. This study highlights the resistance trends in environmental water sources, human and veterinary public health.

METHODS: The research was carried out in the Kumasi Metropolis in Ghana from March 2013 to May 2016. *Campylobacter* were isolated using standard bacteriological methods and speciated on API CAMPY kit. Isolates were confirmed using multiplex PCR targeting the IpxA gene of *Campylobacter*. The antibiogram profile of species were determined by the CLSI's Kirby-Bauer disk diffusion method against 13 relevant antibiotics.

RESULTS: A total of 635 faecal and 595 carcasses of livestock and poultry, 241 farm and market vegetables, 188 water samples from different sources and 202 human samples were analysed. Prevalence of *Campylobacter* in the animals were 23.4%, 27.2%, 21.2%, 32.5% and 22.3% respectively in cattle, sheep, goat, pigs and poultry. In farm and market vegetables, prevalence was 23.9% and 41.9% respectively, as 17.3% and 22.3% were recovered from humans and water sources respectively. Species identified were C. *Campylobacter*, C. *Campylobacter sub sp. doylei*, C. coli, C. lari and C. hyointestinalis with C. *Campylobacter* and C. coli being the dominant specie (>80%). Resistance of the species from humans, animals, vegetables and water sources respectively were 34-46%, 17-74%, 33-49% and 48-69% to the quinolones, 9-43%, 4-29%, 20-31% and 45-55% to aminoglycosides, 97-100%, 80-100%, 95-100% and100% to β-lactams, 96-100%, 98-100%, 96-100% and 88-100% to erythromycin, 54-56%, 68-87%, 90-96% and 75-93% to chloramphenicol, 92-100%, 62-98%, 64-75% and 50-100% to tetracycline and 67-81%, 46-92%, 57-67% and 25-100% to trimethoprim sulphonamides.

Resistance to imipenem was 0%, but a proportion of the *Campylobacter* strains exhibited intermediate susceptibility from all sources.

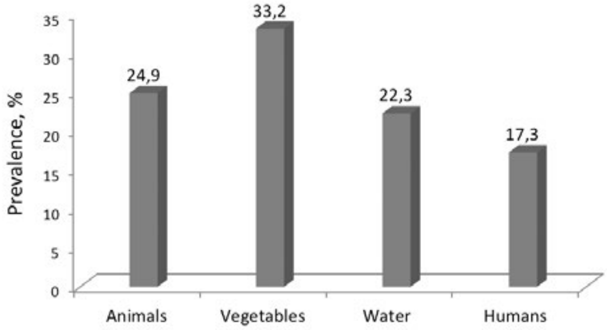

Fig. 1: Prevalence of Campylobacter isolated from animals, vegetables, water and humans.

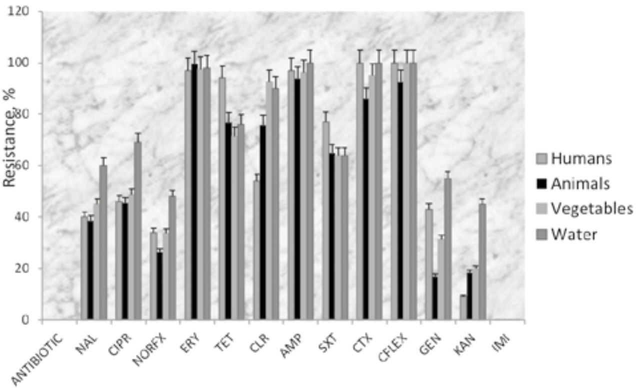

Fig. 2: Antibiotic resistance profile of Campylobacter species recovered from various sources

CONCLUSIONS: The study established multidrug resistant *Campylobacter* as widespread in the environment, present in the food chain and among patients presenting with gastroenteritis in Ghana. The high resistance rates observed against erythromycin and other commonly prescribed antibiotics is worrying, which necessitates the establishment of a national antibiotic resistance management team to monitor and control antibiotic use in agriculture, veterinary and human medicine.

4 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

A longitudinal evaluation of Salmonella Typhimurium AMR prevalence and transmission using whole genome sequencing and phenotyping in a poultry population with no antimicrobial selection pressure.

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BACKGROUND: Australia released its first National Antimicrobial Resistance Strategy in 2015 and the implementation plan for this strategy in 2016 (Commonwealth of Australia, 2016). The use of antimicrobials in food producing animals in Australia is strictly regulated and few antimicrobial classes are available for use in poultry. It is currently unknown what the long term impact of the reduction in use of antimicrobials will have on antimicrobial resistance in specific pathogens. An ongoing longitudinal study investigating the transmission of *Salmonella* Typhimurium within an "antibiotic free" vertically integrated chicken meat enterprise has been conducted. This study evaluated the impact of antimicrobial prescribing on the prevalence of antimicrobial resistance in *Salmonella* Typhimurium isolates in this poultry population.

METHODS: No antimicrobials have been used in the studied population for a period of 5 years. Three hundred and twenty-seven S. Typhimurium isolates were screened for antimicrobial susceptibility using the calibrated dichotomous sensitivity test (CDS) method. Four hundred and eleven isolates were whole genome sequenced using Illumina HiSeq and sequence reads were screened for the carriage of known antibiotic resistance genes using SRST2.

RESULTS: Two clonal lineages of S. Typhimurium were identified in this population. The phenotypic test identified 16.5% of isolates susceptible to all antimicrobials tested and three resistant phenotypes; sulphafurazole (68.5%), streptomycin (56.5%), and ampicillin (10.1%). No fluoroquinolone, cephalosporin or ESBL producing phenotypes were identified. Genotyping identified four TEM ß-lactamase resistance genes in 11 isolates (3.4%). Nine of the 11 isolates were resistant to ampicillin (MIC ≥ 8mg/L). These genes were identified on two occasions only. No transmissible genes conferring resistance to sulphonamides or streptomycin were identified in this population.

CONCLUSIONS: Two S. Typhimurium lineages were clonally disseminated through a vertically integrated poultry operation with their origin at the parent sites. Whole genome sequencing failed to identify the similar dissemination of antimicrobial resistance genes within this *Salmonella* population. The presence of phenotypic resistance (streptomycin MIC ≥ 16mg/L), in the absence of known resistance genes, at minimum inhibitory concentrations for antimicrobials not permitted nor available for use in poultry for nearly 20 years suggests factors other than direct antimicrobial use maintain phenotype presence in this S. Typhimurium population. These findings have important ramifications with regards to the current drive for the reduction in the use of antimicrobials in food producing animals and its’ impact on the prevalence of antimicrobial resistance and subsequent transmission via the food chain.

5 AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE - GALLERY CD

Antimicrobial resistance in Escherichia coli from dairy farms of Quebec, Canada, and identification of Extended-Spectrum-β-lactamase/AmpC resistance

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Passive surveillance of antimicrobial resistance (AMR) in dairy pathogens in Québec, Canada, has revealed resistance to various antimicrobials including third generation cephalosporins. Some studies have also suggested that calves may be a greater source of antimicrobial resistant bacteria than mature cows. Third generation cephalosporins are of very high importance in human health medicine in Canada and one of these, ceftiofur, is used in the dairy industry. This usage could contribute to the emergence of resistance due to bacterial production of AmpC beta-lactamases and extended-spectrum beta- lactamases (ESBL). In addition, the prevalence of AMR, other than to ceftiofur, at the dairy farm, which includes bacterial isolates from healthy and sick animals, is unknown in Québec because passive surveillance programs focus on pathogenic bacteria. The hypothesis of the present study is that the prevalence of AMR in enteric bacteria is higher in calves than in cows for Québec dairy farms. Thus, an objective of this study was to determine the prevalence of AMR in the enteric indicator bacterium *Escherichia coli* in adult cows and calves on farms in Quebec using faecal and manure pit samples. Dairy farms (*n*=102) were recruited randomly on a voluntary basis for the one-year study period between March 2017 and April 2018. For each farm, composite manure samples were collected from three different sources: up to five randomly chosen preweaning calves, five random lactating cows and two locations of the manure pit. Farms were visited twice at an interval of 6 months. Faecal samples (*n*=602) were stored at -80°C with a preservative medium for 2 – 6 months before processing. Each sample was streaked on MacConkey agar for isolation of up to 5 lactose positive colonies. Also, fecal samples from the first visit (*n*=302) were pre-enriched with buffered peptone water then streaked on MacConkey agar supplemented with 1µg/ml of cefotaxim for recovery of presumptive ESBL/AmpC colonies. *Escherichia coli* were identified by Matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-ToF MS). Minimum inhibitory concentration (MIC) was performed by the broth microdilution technique for one *E. coli* isolate per fecal sample (*n*=602). MIC results are presently being analysed. Following selective enrichment of samples, presumptive ESBL/AmpC *E. coli* were found in lactating cows (11/102; 0.11 [IC 95% : 0.06 - 0.18]), manure pit (24/102; 0.24 [IC 95% : 0.16 - 0.33]) as well as calves (53/98; 0.54 [IC 95% : 0.44 - 0.64]). Hence, our preliminary data indicate that calves may represent a greater risk for carrying ESBL/AmpC *E. coli* than lactating cows in dairy farms in Québec. Production of ESBL/AmpC by dairy commensal bacteria could contribute to the dissemination of this resistance and this warrants further investigation.

AMR NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS

1 AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS - GALLERY CD

Operationalising One Health Approaches to Surveillance for Antimicrobial Resistance

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3: Morvet Ltd, Masterton, New Zealand

BACKGROUND: Antimicrobial resistance (AMR) is a truly 'wicked' global health issue that requires a One Health approach to understand the complex range of interacting factors involving humans, animals and the environment that may be associated with its emergence. One Health is a fundamental principle of the WHO-FAO-OIE Global Action Plan for AMR and the UK Department of Health and Social Care's Fleming Fund Programme. The Fleming Fund Country Grant and Fellowship programmes are designed to strengthen collaborative and integrated surveillance in South and Southeast Asian and sub-Saharan African countries to produce data on AMR and AMU in humans, animals, farmed aquatic species, the environment and agriculture that over time will support development of evidence-based policies and programmes to mitigate AMR risks.

METHODS: The Fleming Fund Management Agent, Mott MacDonald, and technical partner, Massey University, are working with the Ministries of Health, Agriculture/Livestock and other related Ministries in multiple countries to design and implement integrated One Health AMR/AMU surveillance systems. Key design aspects that support integrated surveillance are:

- a common set of zoonotic bacteria/ antibiotic combinations
- standardised diagnostic approaches to antibiotic sensitivity testing
- equivalent laboratory quality assurance systems
- comparable recording of diagnostic results
- sampling strategies that facilitate comparison of AMR/AMU patterns in related human and animal populations

In addition to supporting implementation of the surveillance programmes through Country Grants, supporting the establishment of multi-sectoral technical and policy-making bodies, and facilitating collaboration within these, is critical to operationalisation of One Health. The Fleming Fellowship Scheme supports technical leaders share and interpret their surveillance results, identify epidemiological links and design future surveillance to strengthen the relatedness of the AMR/AMU information generated by each sector. Collaboration amongst members of policy-making bodies is supported through critical decision-making meetings throughout the Fleming Fund programme.

RESULTS: The extent to which a One Health approach to AMR/AMU surveillance is operationalised varies considerably amongst countries which have different cultural and political environments. A key influencing factor is the extent to which the national AMR committee leadership facilitates engagement and collaboration amongst the sectors within the committee, which guides implementation of the country's national action plan for AMR. Other factors reflect the extent to which professionals from different sectors know each other and have worked together in the past. Collaboration is most effective amongst people who respect each other and enjoy working together.

CONCLUSIONS: Moving from words to action in operationalising One Health is challenging as it involves engaging with increased complexity and requires building relationships, respect and trust amongst people from different sectors to work effectively together to address a common health issue. On-going facilitation is necessary to strengthen collaboration towards a transdisciplinary approach through building a shared vision and understanding of AMR, building relationships, understanding, respect and trust amongst the multidisciplinary teams.

2 AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS - GALLERY CD

#AMR: Exploring the role of social media in addressing antimicrobial resistance

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2: University of Frederickton

BACKGROUND: Despite the pervasiveness of social media (SM) today there is limited discussion about the value of these platforms in addressing issues of antimicrobial resistance (AMR). The Pew Research Center indicated the increasing use of SM in 2018, including significant advances in the 30-49 and 50-64 age groups. This trend aligns with producer demographics and animal agriculture organizations are increasingly promoting SM use to their members. However, there is little exploration of use of these media as a means for knowledge dissemination, community building, and/or intervention in the AMR literature. The aim of this research was to determine the volume, reach, and engagement of AMR discourse on SM in the four months immediately preceding the conference to deliver near real-time data on the potential role of these media as a mass scale AMR health information sharing platform.

METHODS: This study began with a comprehensive review of the existing literature on SM and AMR using a combination of related terms in the CABI, Medline, and AGRICOLA databases. This search resulted in limited relevant literature (N=10) and demonstrated a lack of SM AMR content analysis and analytics. To address this gap, a fit-for-purpose Twitter-stream monitoring application was created using Python and the tweepy library to collect AMR posts using predetermined SM hashtags. In the four months immediately preceding the conference the Python scraper will continue to retrieve AMR related tweets to populate a SQL database. Using Python and the natural language toolkit, the raw Tweets will be analyzed for trends and common themes, including separating original Tweets from re-Tweets, assessment of tone using sentiment scores, and the identification of the most impactful Tweets in terms of volume and reach.

RESULTS: The relative frequencies of the retrieved hashtags were evaluated over an initial two-week period allowing for refinement of the Python code to establish a robust tracking system. Within the first 24 hours 1625 posts were captured, with more than 15 000 at the conclusion of the two-week test period. There was a significant change in the hashtag capture during the test period, and the researchers will continue to refine the code as needed to elicit the most comprehensive dataset. In the week immediately preceding the conference a full suite of analytics, as previously detailed, will be completed.

CONCLUSIONS: This research will deliver a near-real time characterization of the current SM AMR discourse to attendees of the 5th International One Health Congress, a critical first step in determining the efficacy of SM in reaching knowledge users. There is an increasing volume of AMR data being exchanged through SM platforms and yet the role of these media in monitoring trends, influencing dialogue and producer practice, and for knowledge translation is largely uninvestigated.

3 AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS - GALLERY CD

Development of 2-Aminoimidazole Compounds that Enhance Antibiotic Activities to Reduce Antibiotic Usage

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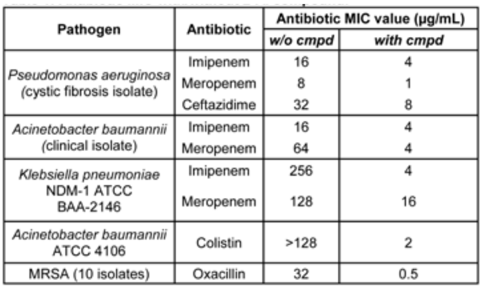
BACKGROUND: A novel strategy to reduce antibiotic usage is to develop 2-aminoimidazole (2-AI) compounds that enhance the activity of antibiotics. These compounds inhibit the response regulator of bacterial two component systems, so bacteria cannot sense and respond to their environment and are unable to turn on defense mechanisms (i.e. biofilm formation, efflux pump upregulation, and membrane modification). Here we present the efficacy of two compounds in increasing antibiotic sensitivity in vitro and in two rodent models in vivo.

METHODS: Minimum inhibitory concentration (MIC) were determined following the CLSI microdilution method.
CD-1 mice were infected with 106 CFU of Pseudomonas aeruginosa PAK, and administered the treatments *(Figure 1)*. Sprague-Dawley female rats were infected with 105 CFU of MRSA Xen30, and administered the treatments *(Figure 2)*.

RESULTS: MIC assays show 2-AI compounds lower the MICs of antibiotics *(Table 1)*.
The mouse lung infection model shows combination treatment with AGL-503 + colistin reduced bacterial counts versus colistin alone *(Figure 1)*.



Pathogen	Antibiotic	Antibiotic MIC value (µg/mL)	
		w/o cmpd	*with cmpd*
Pseudomonas aeruginosa (cystic fibrosis isolate)	Imipenem	16	4
	Meropenem	8	1
	Ceftazidime	32	8
Acinetobacter baumannii (clinical isolate)	Imipenem	16	4
	Meropenem	64	4
Klebsiella pneumoniae NDM-1 ATCC BAA-2146	Imipenem	256	4
	Meropenem	128	16
Acinetobacter baumannii ATCC 4106	Colistin	>128	2
MRSA (10 isolates)	Oxacillin	32	0.5

Table 1: Antibiotic MIC with/without 2-AI compound.

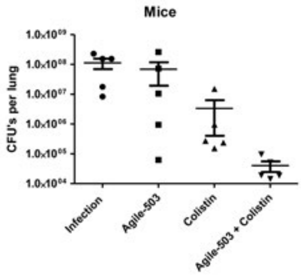


Figure 1. Bacterial burden after colistin, AGL-503, and combination treatments in a mouse lung infection model. Treatments started 2 hours after infection q12h for 36 hours.

The rat infection model show combination treatments with AGL-324 + antibiotic had statistically significant lower MRSA densities versus antibiotic alone *(Figure 2)*.

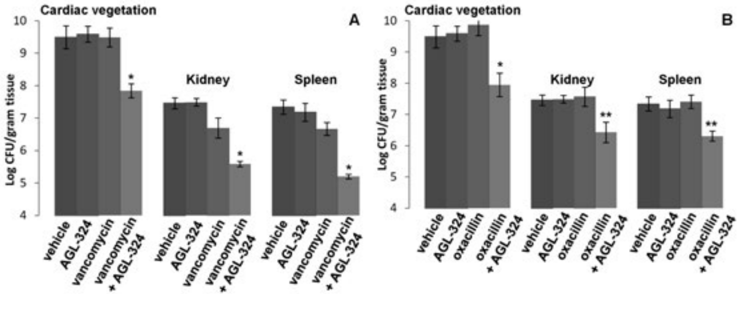


*Figure 2. Bacterial burden in target tissues after antibiotic (vancomycin panel A; oxacillin panel B), AGL-324, and combination treatments. Treatments started 24 hours after infection, twice a day for three days. * P < 0.05; ** P < 0.05 versus all other tissues*

CONCLUSIONS: These experiments display the activities of these novel 2-AI compounds in enhancing antibiotic activity and supports the development of these compounds to reduce antibiotic usage.

4 AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS - GALLERY CD

A novel participatory strategy to reduce antimicrobial use in agricultural systems

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BACKGROUND: Agricultural antimicrobial use (AMU) is recognized as being closely linked to the development of antimicrobial resistance (AMR) (Chantziaras et al. 2014). AMR is recognized as one of the greatest risks to human health globally (O'Neill, 2015), and agriculture uses the majority of antimicrobials globally.
The New Zealand Veterinary Association (Anon, 2015) has set an aspirational goal of reducing AMU to zero by 2030, and has embarked on a number of projects in an attempt to achieve this.
Participatory development (PD) has been used to help facilitate farmer projects previously (Reyher, 2016). This paper reports on the interim results of a three- year project using PD in farmer- led groups to help formulate AMU reduction strategies in New Zealand.

MATERIALS AND METHODS: This project is currently active in the lower region of New Zealand. Farmers and veterinarians across the lower South Island have been invited to participate in 4 strategic farmer groups comprising up to 12 farmers per group, from sheep, beef, deer (red meat) sectors, and from the dairy sector.
Each group has a facilitator, who is a trained agricultural consultant with a background in group facilitation. The groups are initially given a comprehensive AMR workshop, where they are introduced to the concept, to the risks and history, data around AMU and other background. This material is subsequently made available to them during the project in a variety of formats; and they are also given regular technical briefings.

RESULTS: The goal is for each group to develop separate novel AMU reduction strategies. The 4 groups to date have developed 10 quite distinct and quite varied strategies. These have been crystalised into a format for communicating to other farmers via presentations, social media and other vehicles. The strategies will then be implemented across a number of farms to effect change.

CONCLUSIONS: This study intends to facilitate farmers to create a range of strategies for reducing AMU which they will feel ownership of, and then to test these strategies in the field, with regard to ease of implementation, level of effect, consequences and other impact. From this, effective, simple strategies are hoped to be identified by farmer leaders and adopted by the farming community, because farmers will feel the ownership of these strategies themselves. The goal is to facilitate farmer uptake and effect reduction in AMU by farmer-led initiatives. Monitoring of AMU as part of this project will help determine the quantitative effect of the various strategies.
The ultimate goal is to reduce AMU on farm by 20% by 2020.

5 AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS - GALLERY CD

Can inhibition of transmission of KPC and CTX-M producing plasmids reduce the spread of AMR?

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2: School of Pharmacy, University College London, United Kingdom

BACKGROUND: Antimicrobial resistance (AMR), including resistance to carbapenem and extended spectrum beta-lactam antibiotics, poses a serious threat to modern medicine. Genes encoding resistance to these and other antimicrobials are frequently located on plasmids, which can be transmitted between distantly related bacteria. AMR plasmids and bacterial hosts can co-evolve, resulting in plasmids being maintained over long periods of time. Plasmid transmission occurs on a global scale. AMR plasmids can move between humans, domestic, livestock and wild animals, agricultural soil, and the wider environment. Furthermore, the global movement of people, animals and products such as food, provides a direct mechanism for AMR plasmids to traverse the globe. Some compounds have been identified which reduce plasmid carriage, however most are highly toxic. Therefore, alternative approaches to identify compounds that prevent transmission of large, complex, and clinically important plasmids could help reduce the global burden ofAMR.

MATERIALS/METHODS: Using cloning techniques developed for this purpose, we have engineered two clinically successful plasmids $pCT_{CTX\text{-}M\text{-}14}$ and $pKpQIL_{KPC}$ to encode fluorescent protein genes. The modified plasmids were inserted into *E. coli* and *K. pneumoniae*, respectively. Plasmid transmission within a population was monitored using flow cytometry and confocal microscopy. To validate this assay, we have previously shown it was able to identify characterized plasmid-inhibiting compounds, including chlorpromazine, ascorbic acid, and linoleic acid. Using this system, we have now screened one drug library plus natural products to identify novel and non-toxic compounds which inhibit AMR plasmid transmission and/or persistence. Identified compounds were tested for impact upon bacterial growth, and the optimal concentration using dose-response assays for anti-plasmid activity was determined.

RESULTS: Our screen of over 2,000 compounds has identified Compound E, which has novel and strong potential as an anti-AMR plasmid compound. Compound E is neither an antibiotic nor a biocide. Compound E inhibited transmission at concentrations which did not significantly impact upon bacterial growth. The dose-response experiments revealed the optimal concentrations for anti- plasmidactivity.

CONCLUSIONS: Using our fluorescent transmission assay, we have identified a compound which prevents the spread of “real-world” AMR plasmids amongst clinically relevant Gram-negative bacteria. Compound E has the potential to be used to reduce the prevalence of AMR plasmids found in critical priority antibiotic-resistant pathogens. This compound could be used in a variety of settings, including in humans, animals, and/or the environment. The use of non-toxic, transmission inhibiting compounds, such as compound E, could be a viable strategy to reduce the global spread and prevalence ofAMR.

AMR ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS

1 AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

Antibiotics usage by pastoralists in livestock in North-central Nigeria: The socio-cultural drivers for antibiotic resistance emergence and public health implications

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2: University of Ibadan, Nigeria 002

BACKGROUND: Improper use of antibiotics in food animals contributes to the development of antibiotic resistance, a global health threat. Exploration of pastoralists' local knowledge and practices towards antibiotics usage is crucial for development of antibiotics surveillance in extensive husbandry system and control of antibiotic resistance in food animals. Study objectives were: to assess pastoralists' local knowledge and practices regarding antibiotics usage and pathways for resistant pathogens transmission from animals to humans. Our Null hypothesis was that pastoralists' socio-cultural activities cannot influence antibiotic resistance emergence and spread through food chain.

METHODS: Interview structured questionnaire-based cross-sectional study was conducted in systematic randomly selected household heads in pastoral settlements of North-central Nigeria in 2015. Pastoralists' communities in Nigeria herd about 90% of ruminants and practice year-round nomadism in rural areas. Descriptive and multivariable logistic regressions analyses were performed at 95% confidence level.

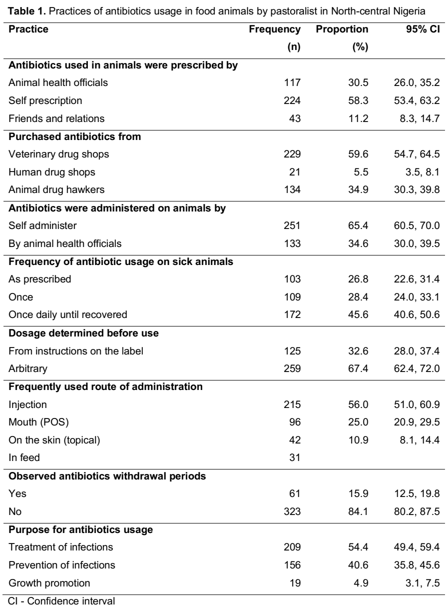

Table 1. Practices of antibiotics usage in food animals by pastoralist in North-central Nigeria

Practice	Frequency (n)	Proportion (%)	95% CI
Antibiotics used in animals were prescribed by			
Animal health officials	117	30.5	26.0, 35.2
Self prescription	224	58.3	53.4, 63.2
Friends and relations	43	11.2	8.3, 14.7
Purchased antibiotics from			
Veterinary drug shops	229	59.6	54.7, 64.5
Human drug shops	21	5.5	3.5, 8.1
Animal drug hawkers	134	34.9	30.3, 39.8
Antibiotics were administered on animals by			
Self administer	251	65.4	60.5, 70.0
By animal health officials	133	34.6	30.0, 39.5
Frequency of antibiotic usage on sick animals			
As prescribed	103	26.8	22.6, 31.4
Once	109	28.4	24.0, 33.1
Once daily until recovered	172	45.6	40.6, 50.6
Dosage determined before use			
From instructions on the label	125	32.6	28.0, 37.4
Arbitrary	259	67.4	62.4, 72.0
Frequently used route of administration			
Injection	215	56.0	51.0, 60.9
Mouth (POS)	96	25.0	20.9, 29.5
On the skin (topical)	42	10.9	8.1, 14.4
In feed	31		
Observed antibiotics withdrawal periods			
Yes	61	15.9	12.5, 19.8
No	323	84.1	80.2, 87.5
Purpose for antibiotics usage			
Treatment of infections	209	54.4	49.4, 59.4
Prevention of infections	156	40.6	35.8, 45.6
Growth promotion	19	4.9	3.1, 7.5

CI - Confidence interval

RESULTS: All 384 recruited pastoralists participated in the study. Majority (58.0%) of them had no formal education. Only 8.1% of the respondents knew antibiotics misuse to be when given under-dose, 7.3% indicated when given over-dose and 70.1% had no idea of what misuse entails. Nearly two-thirds (64.8%) of respondents did not know consequences of improper antibiotics uses in animals. More than half (58.3%) reported self prescription of antibiotics used in animals. Regarding antibiotics dosage determination before use, two-thirds (67%) of pastoralists reported arbitrary applications. More than half (54.4%) of participants used antibiotics mainly for therapeutic purposes, less than half (40.6%) of them for preventive purposes, and 4.9% of them as growth promoters (Table 1). Frequently used antibiotics by pastoralists were penicillin (94.0%), gentamicin (75.5%), streptomycin (93.0%), tetracycline (96.6%), tylosin (95.6%), neomycin (67.2%) and sulfonamides (92.4%).

Table 2. Identification of pathways for transmission and spread of antibiotic resistant pathogens to humans through food animals in North-central Nigeria

Pathway	Frequency (n)	Proportion (%)	95% CI
Contaminated food animal products			
Raw milk	96	25.0	20.9, 29.5
Raw cheese	101	26.3	22.1, 30.9
Under cooked meat	142	37.0	32.3, 41.9
I don't know	45	11.7	8.8, 15.2
Contacts: direct or indirect			
Humans with contaminated animals	294	76.6	72.1, 80.6
Humans with contaminated formites	32	8.3	5.9, 11.4
I don't know	58	15.1	11.8, 18.9
Environmental releases and wastes			
Discharged contaminated faeces (manure)	214	55.7	50.7, 60.7
Aerosols from herd facilities	56	14.6	11.3, 18.4
Flies attracted to the contaminated faeces	93	24.2	20.1, 28.7
I don't know	21	5.5	3.5, 8.1

CI - Confidence interval

Table 3. Factors that influence emergence and spread of antibiotic resistance through food animals to humans in pastoral settlements of North-central Nigeria

Factors	Poor influence (%)	Satisfactory influence (%)	Odds ratio (OR)	95% CI	P-value
Improper use of antibiotics					
No	28 (63.6)	16 (36.4)	1.00		
Yes	20 (5.9)	320 (94.1)	28.00	13.06, 60.02	<0.001
Non enforcement of laws regulating antibiotics usage					
No	37 (52.1)	34 (47.9)	1.00		
Yes	60 (19.2)	253 (80.8)	4.59	2.67, 7.91	<0.001
Weak financial status of pastoralists					
No	37 (56.1)	29 (43.9)	1.00		
Yes	68 (21.4)	250(78.6)	4.69	2.69, 8.17	<0.001
Low education and expertise of pastoralists					
No	46 (73.0)	17 (27.0)	1.00		
Yes	74 (23.1)	247 (76.9)	9.03	4.89, 16.69	<0.001
Mobile culture of pastoralists					
No	55 (73.3)	20 (26.7)	1.00		
Yes	68 (22.0)	241 (78.0)	9.75	5.47, 17.38	<0.001
Husbandry system: extensive system					
No	32 (54.2)	27 (45.8)	1.00		
Yes	91 (28.0)	234 (72.0)	3.05	1.73, 3.57	0.001

Statistically significant at p<0.05

Pathways for transmission of antibiotic resistant pathogens through food animals were identified as: consumption of contaminated animal products (raw milk); direct and indirect contacts with contaminated animals and formites; and environmental wastes (faeces) (Table 2). Factors that significantly influenced antibiotic resistance emergence and spread were: improper use of antibiotics (P<0.001), non enforcement of laws regulating antibiotics usage (P<0.001), weak pastoralists' financial status (P<0.001), pastoralists' low education and expertise (P<0.001), pastoralists' mobile culture (P<0.001), and extensive husbandry system (P=0.001) (Table 3).

CONCLUSIONS: The study revealed that the majority of pastoralists had low levels of knowledge and practices regarding antibiotics use in livestock. Antibiotic emergence and spread through livestock may not be unconnected with pastoralists' socio-cultural activities. To combat antibiotic resistance menace effectively, it is imperative to raise pastoralists' knowledge/awareness on effects of antibiotics misuse and promotion of prudent use in livestock through only registered veterinary services. Gradual reform of these socio-cultural activities through multifaceted strategies, in line with the 'One Health' approach, is recommended so as to assured food safety, food security, public and environmental health.

2 AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

Extent of dispensing prescription-only medications without a prescription in community drug retail outlets in Addis Ababa, Ethiopia: a simulated-patient study

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PURPOSE: This study was aimed at assessing the extent of dispensing prescription-only medications without a prescription in community drug retail outlets (CDROs) of Addis Ababa, Ethiopia.

METHODS: A descriptive cross-sectional observational study design was used to sample 31 pharmacies, 25 drug stores, and two rural drug vendors from August 11, 2015, to October 21, 2015, through a simple random sampling method. A simulated-patient method of visit was implemented to collect data. Requests of six tracer prescription-only medicines (amoxicillin + clavulanic acid capsule, amitriptyline, captopril, glibenclamide [also known as glyburide], omeprazole capsule, and sildenafil citrate) and upper respiratory tract infection were selected as the simulated clinical scenario.

RESULTS: Amoxicillin–clavulanic acid capsule was dispensed when requested in 87.93% of the dispensaries. All of the CDROs dispensed omeprazole upon request. Sildenafil citrate (Viagra) was in stock in 96.55% of the CDROs, all of which issued the requested number of tablets without asking why or for whom the drug was needed. Amitriptyline, captopril, and glibenclamide (glyburide) were dispensed in 84.48%, 89.65%, and 87.93% of CDROs upon the provision of an empty container. Antibiotics were obtained from 75.86% of CDROs for presentation of upper respiratory tract infection symptoms. Among the dispensed antibiotics, the most common was amoxicillin (93.18%), followed by amoxicillin–clavulanic acid capsule (72.72%), and azithromycin (50%). Only 4.5% of the dispensaries asked about drug allergies, and 15.9% of the CDROs informed the simulated patient about the possible side effects of the drugs.

CONCLUSIONS: This study revealed a very high rate of dispensing of prescription-only medicines without a prescription. Antimicrobials and drugs for chronic diseases were obtained with ease from almost all of the randomly sampled CDROs. Putting good dispensing practice into effect and adhering to the existing national laws and regulations regarding the same are necessary. It is also necessary to adopt a strong and explicit line of action, especially toward the irrational use of antibiotics.

3 AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

Towards a Global Database of Emerging Antibiotic Resistance

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BACKGROUND: Antimicrobial resistant (AMR) pathogens are on the rise globally, making infections harder to treat and cure. However, the underlying patterns and mechanisms in where and when AMR is emerging are not clearly understood, making control and prevention difficult. There is a need to better catalog the emergence of AMR to allow for targeted research into the drivers of emergence and assist in the development of a rigorous One Health approach to prevent future resistance. We have built a surveillance database of the first reported emergence in humans of a specific of an antibiotic-resistant bacterium and characterized these events by extracting information on the geographic, demographic, and temporal scale associated with their emergence.

METHODS: We conducted an extensive systematic literature review of all the publications contained in PubMed, Embase, and ProMed Mail databases ranging from 2006 to 2017. We then used this dataset to identify the first temporal emergence of an AMR in a human population. We used PRISMA guidelines to structure the review, with each abstract screened twice, and final inclusion as a “new emergence event” determined after full-text review and background corroboration that the event was the first recorded instance of a specific resistance type. Articles selected for inclusion were summarized in a database of emerging antibiotic resistance with available information on pathogen, drug or drug combination resistance, location, and event date.

RESULTS: Our initial search identified 22,770 publications to be reviewed for inclusion in our database. The majority of publications were from 2015, with an overall increase in publications from 2006 onward. To this date we have identified 882 publications that will be reviewed in detail. This database includes information on the location, bacterial pathogen, clinical disease, and drug resistance, which can be used to analyze trends in global emergence. The dynamic structure of the AMR database easily allows the systematic and continuously updated of new AMR disease events as they may arise.

CONCLUSIONS: To our knowledge, this is the first comprehensive review of the *first emergence* of antibiotic resistance and first database of this kind. Treating AMR as an emerging threat allows for targeted measures to *prevent* new resistance combinations from emerging. Coupled with existing measures to reduce current AMR, more targeted surveillance and prevention could be a key measure in reducing the burden of AMR on human health and increasing the longevity of current antimicrobial treatments. Our comprehensive database will act as a critical resource for evaluating the current state of emerging AMR bacteria and creating strategies to mitigate the impact of novel AMR, as well as support further research into the origins of resistance in people. Developing this database is an important first step in understanding the drivers of new resistance globally.

4 AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

Current Patterns of Antibiotic Resistance in High Density Livestock-Human Populations in Western Kenya

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Over the last 80 years, correlation between antimicrobial use and resistance has been observed, and extensive use of antimicrobials in human and veterinary medicine has resulted in the widespread emergence of multi-drug resistant bacterial infections. Kenya has a rapidly growing livestock industry; thus, various antimicrobials are used to maintain livestock health. The purpose of this work was to determine if there were similarities in the patterns of antimicrobial-resistant bacteria (AMR) in farmers, their animals and their immediate environment. This was undertaken in Western Kenya, representing an area with a high density of livestock and using *E. coli* as our sentinel organism.

Water, environmental swabs and human and animal faeces were collected from 70 mixed crop-livestock smallholder farms across Busia county, Western Kenya. A questionnaire regarding access to and understanding of antimicrobials was given to each farmer; up to 3 fresh faecal samples were collected from each species of animal and human volunteers. Water samples were collected from wells, boreholes or stored rainwater. Living areas were sampled using bootsocks to determine contamination with representative bacteria and their AMR patterns. Faecal samples were cultured on eosin-methylene blue (EMBA) agar, 5 colonies representative of *E. coli* were selected and susceptibility determined via antibiotic disc diffusion and using human EUCAST breakpoints; extended-spectrum β-lactamase-producing *E. coli* were selected on EMBA containing 1mg/l cefpodoxime, and then confirmed by double-disc test (cephalosporin with, and without clavulanic acid). Water samples and environmental swabs were pre-enriched in tryptone-soya broth for 24 hours and then processed as per faecal samples.

261 samples were processed and AMR *E. coli* was detected in 96.0% of samples with the following breakdown for other resistance outcomes: tetracycline (91.2%, n=238), ampicillin (83.1%, n=217), sulfathiazole (79.7%, n=208) trimethoprim (62.1%, n=162), chloramphenicol (9.6%, n=25), ciprofloxacin (3.4%, n=9) and gentamicin (2.3%, n=6). Multi-drug resistant *E. coli* (to 3 or more drug classes) was found in 77.4% samples. ESBL-producing *E. coli* was detected in 24 (9.3%) of all samples, and the majority of isolates were MDR. The most common resistance pattern (tetracycline, trimethoprim, and sulfathiazole) was observed in all three groups, indicating potential sharing of AMR-bacteria.

This study demonstrated a high prevalence of AMR and MDR *E. coli*. The high prevalence of tetracycline and sulfa-drug resistance is reflective of the antimicrobials which are commonly cited as being used in Kenyan livestock. Further investigation of isolates will include full genotyping by whole genome sequencing and the phylogenetic background of strains and resistance determinants and their genetic context determined. This further work should elucidate sharing of MDR bacteria and/or resistance elements between animals, people and their shared environment. Such data is important for informing veterinary public health and our methodology has already been shared with key Kenyan stakeholders for this purpose.

5 MR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS - GALLERY CD

Antimicrobial use behaviours, the economics of animal disease and perceptions of antimicrobial policy in pig production in Vietnam

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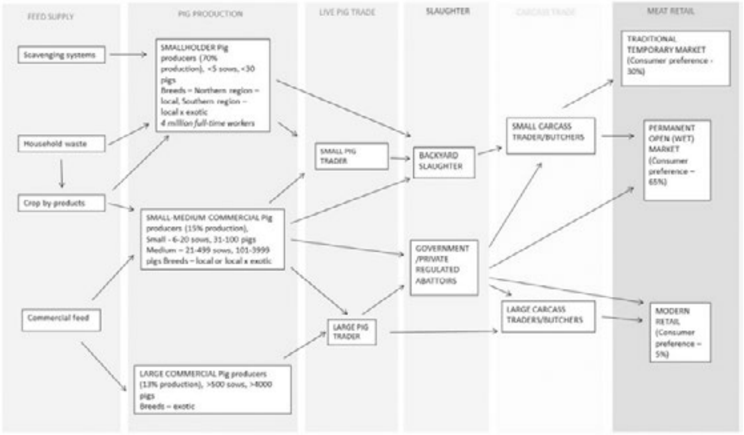
2: Agricultural and Resource Economic Consulting Services, Armidale, Australia

BACKGROUND: Antimicrobial resistance is influenced by antimicrobial use in the human and animal health sectors, exerting selection pressure on pathogen populations that encourage the development of resistance and exchange of resistance genes. The scale of antimicrobial resistance in Vietnam remains unknown, however, studies suggest that it is a major issue in both human and animal health.

Around three quarters of all meat consumed in Vietnam is pork identifying pigs as a priority species for further research. The limited data on antimicrobial use in pigs highlight high risk behaviours such as high overall antimicrobial use, large proportions of commercial feed containing antimicrobials and poor adherence of farmers to meat withdrawal periods.



Pork Supply Chain – movement of feed, pigs and pork

METHODS: The study explored antimicrobial use in 20 farms in the Nam Dinh Province (North) and 20 farms in the Dong Nai Province (South) of Vietnam. Data were collected through a structured interview and the collection of discarded antimicrobial packaging over a 6 week period. The study sought to explore how and why antimicrobials were used in pig production; including a focus on the economic costs and benefits of use for the producer.

RESULTS: Overall antimicrobial use was found to be high with frequent reported use of the World Health Organisation highest priority critically important antimicrobial classes and antimicrobials routinely used in combinations of two of more active ingredients. Farmer awareness of what constituted an antimicrobial was poor and there was little knowledge or understanding of policy to prohibit the use of antimicrobials as growth promoters (introduced on 31 December 2017). Overall, farmers perceived a low risk to human health from antimicrobial use in pigs. Economic assessment of the benefits of antimicrobial use was challenging as record keeping on productivity, health and veterinary costs was poor.

CONCLUSIONS: The study results provide insight into antimicrobial use behaviours by Vietnamese pig farmers and highlight areas such as poor farmer awareness of antimicrobial use and resistance, limited knowledge of antimicrobial use regulation and poor record keeping as areas of priority for future interventions to reduce antimicrobial use and promote responsible behaviours. These data may form the basis of further research to inform policy makers in supporting economically sustainable production systems, with minimum risk from antimicrobial use and which focus on food safety. The data collection framework will be made available for use in other countries to address similar antimicrobial use knowledge gaps.

AMR RAPID DIAGNOSTICS

1 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

Analysis of single nucleotide polymorphism in katg gene in isoniazid resistant mycobacterium tuberculosis

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Mycobacterium tuberculosis (MTB) is one of the most wide spread bacterial pathogens. The emergence of drug-resistant tuberculosis is a significant problem worldwide. Multiple drug-resistant tuberculosis (MDR-TB) results when *Mycobacterium tuberculosis* becomes resistant to most of the baseline anti-TB drugs such as isoniazid (INH) and rifampicin (RIF). Genetic alterations in the genome of MTB such as mutation in katG gene are involved in the development of resistance to INH. The present study aimed to explore mutations in KatG gene in *Mycobacterium tuberculosis* isolates resistant to isoniazid by sequencing.

The sputum samples (n=390) were collected from suspected patient for tuberculosis during the year 2015-2016. Collected samples were decontaminated using N-Acetyl-L-Cysteine-Sodium Hydroxide (NALC-NaOH) solution. All the samples were screened for *Mycobacterium tuberculosis* through GeneXpert MTB/RIF analysis, Fluorescent Microscopy and MGIT Culturing. The culture positive samples were then checked for antibiotics resistance using drug susceptibility test (DST).

Genomic DNA was extracted from *Mycobacterium tuberculosis* isolates resistant to isoniazid using QIAamp DNA Mini Kit(Qiagen Germany). The extracted DNA was amplified in Thermal cycler (Kyratec, Australia). The PCR products were run on 2% agarose gel (Thermo Scientific). The PCR products were then cleaned-up and sequencing was performed. Each sample was sequenced in both directions. Contig sequences were generated using Sequencher 5.3. KatG gene sequence of M. tuberculosis H37Rv (Accession No. NC000962.3) was used as a reference. Multiple alignment of the sequences was performed using BioEdit. Deduced amino acid sequences were generated from the nucleotide sequences using MEGA 6 software.

Of the 390 sputum samples from TB suspected patients 145, 110 and 119 samples tested positive in GeneXpert MTB/RIF, FM and MGIT Culturing, respectively. The relative sensitivity of GeneXpert on samples which were positive both in FM and MGIT culture was found to be 98.8% (80/81).

The culture positive samples (n=119) were checked for drug susceptibility test (DST) using first line antibiotics such as Streptomycin, Isoniazid, Rifampicin, Ethambutal and Pyrazinamide and second lineantibioticsi.e. Amikacin, Capriomycin and Oflaxacin. It was found that 29% (n=35), 53% (n=64), 38% (n=45), 19% (n=23), 11% (n=13) 6.7% (n=8), 8.4% (n=10), 37.8% (n=45) were resistant to the first and second line drugs, respectively. In DST 44 samples were also confirmed to be MDR-TB samples. Out of 64 Isoniazd, 20 selected samples were further preceded for direct DNA sequencing of KatG gene of which 10 isolates had substitution mutation at codon 315 (AGC=ACC) that resulted in change in amino acid from Serine=Threonine while mutation at codon 463 (CGG=CTG,) was detected in all the INH resistant *Mycobacterium tuberculosis* sequenced. This mutation resulted in change in amino acid from Arginine to Valine.

High resistance rates were found in MDR-TB against first-line and second-line anti-tuberculosis drugs. This study also shows high frequency of mutation in KatG gene in isoniazid resistant *Mycobacterium tuberculosis*.

2 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

Exploiting the potential of flow cytometry in rapid antimicrobial susceptibility testing

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INTRODUCTION: Conventional culture-based antimicrobial susceptibility tests (AST) are slow to deliver definitive results, forcing prescribers to counter the risk of antimicrobial resistance (AMR) with an excessive quantity and spectrum of antibiotics. Improved diagnostic methods have thus been identified as decisive AMR countermeasures, and rapid AMR detection has become a high priority.

METHODS: Recent attempts to solve this problem range from detection of specific AMR markers to broad-based genotypic and phenotypic characterisation of bacteria. We developed a flow cytometry-assisted susceptibility test (FAST) that combines reference method accuracy with unprecedented speed. FAST methods exploit reproducible changes in bacterial physiology during the early stages of antimicrobial exposure that predict the Minimum Inhibitory Concentration.

RESULTS: We have expanded our repertoire to a range of antimicrobial agent families and to additional multidrug resistant bacteria. The FAST method reduced the time to an accurate, objective AST result by one to three days and remained accurate across the wider range of antimicrobial agents and bacterial species we tested. These included ceftriaxone and gentamicin with multidrug resistant *Enterobacteriaceae*, and isoxazolyl penicillins and cefoxitin with *Staphylococcus aureus*. Accurate FAST results were completed for Gram negative bacteria without identification beyond Gram stain.

CONCLUSION: The FAST method addresses the trade-off between accuracy and time to result by using a rapid AST measurement technique. Alternative rapid AMR detection methods do not predict true susceptibility, and rely on prior identification of bacteria from pure culture. There are a few technical obstacles to translation of these FAST methods into standard laboratory procedures. The principal challenges are regulatory compliance, integration with existing clinical laboratory systems and upscaling for high laboratory throughput.

3 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

Novel and Rapid Multiplex Allele-Specific PCR (MAS-PCR) Test for Rapid Detection of MDR and XDR-TB from the Sputum of Lung TB Patients in Makassar, Indonesia

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BACKGROUND: Until now, Multi-Drug Resistant TB (MDR-TB) and Extended Drug Resistant TB (XDR-TB) are still difficult to rapidly detect, due to the length of time it takes (eight weeks) for the gold standard culture method to arrive at a diagnosis. In this research, we designed a rapid and accurate detection method applicable in developing countries such as Indonesia.

METHODS: The study was done in Makassar, Indonesia and sputum samples were taken from TB suspect patients and Mycobacterium tuberculosis (MTB) sample collection from the HUMRC-TB Laboratory, Makassar. The rapid and accurate detection method to detect MDR and XDR-TB pathogen types was designed using a PCR technique called Multi-Allele Specific Polymerase Chain Reaction (MAS-PCR) to detect a combination of specific genes encoding susceptibility to first and second line anti-TB drugs. The sequence of amplified PCR products was analysed with BLAST.

RESULTS: From 89 sputum samples tested with MGIT 960 culture method for first-line drugs, 43 samples (48.3%) were susceptible, 5 samples (5.6%) were mono-resistant R and 41 samples (46.1%) were MDR. Based on SLD-DST, amongst 46 samples resistant to FLD, 36 samples (78.3%) were susceptible to SLD, 5 samples (10.8%) were resistant to OFX, 4 samples (8.7%) resistant to KAN, and 1 sample (2.2%) were resistant to both OFX and KAN. The MASPCR test demonstrated 97.7% and 95.5% specificity in MDR-TB and XDR-TB detection, respectively.

CONCLUSIONS: The MAS-PCR technique allows rapid detection of TB pathogens that are resistant to INH, RIF, FQ, and KAN in a simple and costeffective manner to enable early diagnosis and treatment of MDR and XDR-TB patients, and in turn may prevent further spread to their surrounding contacts.

4 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

Presence of oqxA and oqxB genes in a multidrug resistant Salmonella Typhimurium isolate recovered from swine in Brazil

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BACKGROUND: Fluoroquinolones (FQs) are often first-choice antimicrobial agents used to treat adult salmonellosis. However, a global rise in the number of *Salmonella* with reduced susceptibility to the FQs has been observed in isolates recovered from food, animals, the environment and humans, thus confounding treatment options. Therefore, we designed this study to determine the molecular characteristics of *oqx*A and *oqx*B genes in *Salmonella enterica* isolated from swine in Brazil.

METHODS: In this study, 14 *Salmonella enterica* isolates (Typhimurium, n=8; Infantis, n=3; 4[5],12:i:-, n=2; and Panama, n=1) with known resistance profiles were analysed for the presence of plasmid-mediated quinolone resistance (PMQR) determinants and mutations in the quinolone resistance-determining region using PCR and sequencing techniques.

RESULTS: Only one *S.* Typhimurium isolate recovered from the stomach of one pig was positive for a plasmid carrying *oqx*A and *oqx*B genes (Table 1). A mutation in the *gyr*A gene (Asp87Asn) was observed in codon 87 with replacement of the amino acids asparagine (Asn) by aspartate (Asp). In addition to the PMQR genes, WGS analysis revealed the presence of resistance genes for aminoglycoside (*str*A, *aph*(6)-Id), β-lactam (*bla*$_{\text{TEM-1A}}$), phenicol (floR), sulphonamide (sul2) and tetracycline (tetB). Five of these genes (strA, aph(6)-Id, bla$_{\text{TEM-1A}}$, *flo*R and *sul*2) were located in the same plasmid identified as IncR. The sequence type (ST) was determined to be ST19. There was 99% concordance between *oqx*B, *oqx*A, *flo*R, *sul*2 and the backbone molecular structure of *S.* Typhimurium strains isolated from human and poultry samples reported worldwide.

CONCLUSIONS: Although other plasmid-types are most often harbored by S. Typhimurium, our results demonstrate multi-drug resistance associated with the IncR replicon type. Additionally, ST19 is a particularly virulent sequence type of *Salmonella* . The global spread of this plasmid-encoded multidrug efflux pump *oqx*A, *oqx*B and other resistance determinants represents an emerging resistance problem of great concern.

5 AMR 07 - RAPID DIAGNOSTICS - GALLERY CD

Inter-laboratory validation for antimicrobial susceptibility testing of highly pathogenic bacteria performed by an European laboratory network

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OBJECTIVES: The antimicrobial susceptibility testing (AST) of highly pathogenic bacteria is difficult due to incomplete breakpoint definitions and the lack of standardized regulations. Up to now, guidelines are only available from the Clinical and Laboratory Standards Institute (CLSI) and from WHO manuals for *Bacillus anthracis* and *Francisella tularensis*. The CLSI M45 3rd ed. document gives recommendations for testing conditions (microdilution), but breakpoints are lacking for several relevant antibiotics. Furthermore, the breakpoints are only available for the category susceptible. The AST working group from the European network EMERGE (Efficient response to highly dangerous and emerging pathogens at EU level) consists of 14 laboratories specialized in highly pathogenic bacteria in their countries and is working on a suitable standard operation procedure (SOP) for AST of highly pathogenic bacteria.

METHODS: The broth microdilution method with user-defined commercial microdilution plates was chosen and the tests were performed according to CLSI recommendations. The reproducibility was investigated in a multicenter study involving six European institutes, specialized in highly pathogenic bacteria. 35 bacterial isolates of *Bacillus anthracis*, *Brucella spp.*, *Burkholderia pseudomallei*, *Burkholderia mallei*, *Francisella tularensis* and Yersinia pestis from the EMERGE repository were tested via intra- and inter-laboratory-validation towards antimicrobial substances typically used for therapy of these agents.

RESULTS: Overall the broth microdilution method showed good practicability and concordance for all highly pathogenic bacteria. In the intralaboratory validation between 97,8% and 86,5% of the MIC results were within one log2 dilution step from mode. The lowest conformity was observed for slow growing bacteria *Francisella tularensis* and *Brucella spp*. For *Bacillus anthracis* and for *Brucella spp*. the method showed need for improvement due to differences between two categories.

CONCLUSION AND PERSPECTIVES: The microdilution method is applicable for AST of all highly pathogenic bacteria, but needs optimization for *Brucella spp*. Further interpretation of the variances observed during this inter-laboratory validation is difficult due to the small set of data for each stain/substance combination. Therefore, after adaptation of the SOP a follow-up inter-laboratory-validation using a set of clinical strains including only one strain per species and 10 replicates per site was conducted and the results are still pending. After validation, the SOP is planned to be used to get MIC distribution of wild type strains and to produce epidemiological cutoff values by testing the strain collections from all partners. These data can be used to complete the clinical breakpoints for all agent-relevant substances and to implement the method to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines.

Additionally to the presenting author listed above, the EMERGE AST working group consists of the following persons and institutions: Tscherne A, Zöller L, Georgi E, Hinz C, Vollmar P and Zange S (Bundeswehr Institute of Microbiology, Germany), Jacob D and Grunow R (RKI, Germany), Henczko J (National Public Health Institute, Budapest), Manzulli V, Fasanella A (IZSPB, Italy); Papaparaskevas J (NKUA, Greece); Pelerito A, Nuncio S (INSA, Portugal); Thomann S, Schürch N (SPIEZ, Switzerland); Nenova R (NCIPD, Bulgaria); Elschner M, Tomaso H (FLI, Germany); Jureen P, Boskani T (FoHM, Sweden); Feruglio SL, Johansen T, Jensen V (NIPH, Norway); Wojciech I, Kedrak-Jablonska A (NVRI, Poland); Bertolini B, Di Caro A (INMI, Italy); de Vries MC (RIVM, The Netherlands); Machoaizpurua M (BIOEF, Spain); Bolton PF (PHE, United Kingdom).

SPI SCIENCE POLICY INTERFACE

SPI

1 SPI - THE IMPACT OF ZOONOTIC DISEASES - WHY SHOULD ONE HEALTH BE OF IMPORTANCE TO POLICY MAKERS? LESSONS LEARNT FROM ONE HEALTH CRISES - GALLERY A-B

New World Screwworm Eradication in South Florida – A One Health Success Story

Lisa Conti

One Health Initiative

During October 2016, a foreign animal disease, New World screwworm (Cochliomyia hominivorax) was confirmed in endangered Key deer from a wildlife refuge on Big Pine Key in Monroe County, Florida. New World screwworms are fly larvae (maggots) that can infest livestock and other warm-blooded animals, including people.

Florida Department of Agriculture and Consumer Services worked closely with the U.S. Department of Agriculture and other One Health partners on control and response efforts to eradicate the screwworm. Eradication activities included sterile fly release, enhanced surveillance, and extensive public outreach in order to engage the public in early detection of the screwworm and treatment of infected animals.

With no new screwworm finds since January 10, 2017, sterile fly releases continued in the Infested Zone through April 25, 2017, and Florida was officially free of this pest January 2018.

CONCLUSION: Estimated cost benefit of US screwworm freedom is $4.5 billion annually.

2 SPI 01 - ADDRESSING ZOONOTIC DISEASES AT THE ANIMAL-HUMAN-ECOSYSTEM INTERFACE. WHAT ARE THE THREATS? HOW TO BE PREPARED? - GALLERY A-B

Avian Influenza Surveillance in Live Birds Markets in Thailand

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Thailand, located in Southeast Asia, has a history of one of the largest influenza A (H5N1) epidemics during 2004-2008. Given its relative close proximity to China where influenza A (H7N9) is currently endemic, and the nature of the regional poultry trade, Thailand is at risk of new outbreaks of avian influenza. In addition to H7N9, new risks are emerging as China reported the first human case of H7N4 avian influenza in mid-February 2018 and other viruses such as H5N6 continue to circulate. Of particular concern, some new strains of avian influenza viruses may cause asymptomatic infections in poultry but severe disease in humans. Without ongoing poultry surveillance, detection of these viruses could be difficult prior to human infection. Active surveillance for avian influenza in poultry is therefore critical to prevent transmission to humans.

Live Bird Markets (LBM) have been implicated in transmission of avian influenza viruses, particularly of influenza A (H5N1) throughout Southeast Asia and (H7N9) in China. With Support from United States Centers for Disease Control (U.S. CDC) Thailand Office, Bangkok Metropolitan Administration has been conducting monthly avian influenza surveillance in all (9) districts with active LBMs since 2013. During 2015-2016, influenza A (H1N1) was detected in 24 poultry samples. In 2017, 42 poultry and environmental samples were positive for 3 subtypes of low pathogenic avian influenza viruses: H3N8 (n=3); H4N6 (n=34); and H8N4 (n=5). No highly pathogenic avian influenza (HPAI) viruses were found.

Starting in March 2018, four provinces in Northern Thailand, namely Chiang Rai, Nakhon Phanom, Mukdahan, Ubonratchathani, will conduct monthly avian influenza surveillance programs to enhance the surveillance routinely performed by the Department of Livestock Development. The program will include poultry sampling at LBMs, backyard farms, fresh markets and border control points. In synergy, surveillance of influenza like illnesses and severe acute respiratory infections for humans will also be implemented in these 4 provinces. These complementary surveillance programs in animals and humans will help provide data of virus circulation to ensure that emerging pandemic threats might be contained before spreading.

CONCLUSION: Avian influenza surveillance is critical for monitoring virus circulation in poultry and facilitating early detection and response to an outbreak in order to prevent human infections. Resources in both human health and animal health sectors should be allocated for routine surveillance, as well as enhanced surveillance during an outbreak or in high-risk locations.

2 SPI 02 - ADDRESSING ZOONOTIC DISEASES AT THE ANIMAL-HUMAN-ECOSYSTEM INTERFACE. WHAT ARE THE THREATS? HOW TO BE PREPARED? - GALLERY A-B

Challenges in Complexity: How Brucellosis Thrives in the Science-Policy Interface Space

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Brucella abortus and Brucella melitensis present significant animal health threats to domestic and wild ruminants and economic losses for their owners. They also cause severe human disease and are the most common global zoonoses. First identified over 140 years ago and with more diagnostic tests than any other organism, nonetheless, brucellosis continues to defy eradication attempts in many countries. B. abortus has been eliminated from some developed countries through lengthy, expensive programmes, but B. melitensis persists in sheep and goat populations. Both diseases occur largely unchecked in the developing world where the prevalence and impact on human and animal health are generally unknown, leading to the disease being called a "neglected zoonosis" by the World Health Organisation.

Why is brucellosis so difficult to diagnose and eradicate? First and foremost, the organisms are able to evade the hosts' immune mechanisms and thus avoid detection by diagnostic tests - sometimes for many years. Second, there are few pathognomonic symptoms - in animals or people - leading to reliance on the very diagnostic tests that depend on the hosts' immune responses to work. Third, the incubation period may be long - often more than 18 months in cattle - significantly longer than the average quarantine period for affected herds or people's memories of putative exposure. Finally, and not least, effective control requires political will, substantial funding, stakeholder cooperation and close collaboration between affected government departments.

Brucellosis is the archetypal "One Health disease", traversing the human-wildlife-livestock interface and requiring collaborative initiatives for optimal control and eradication. It also creates tensions at the science-policy interface as it demands flexible policies, science-informed and adaptable legislation, application of the precautionary principle and multidisciplinary teamwork. Such approaches are usually foreign to policymakers who prefer once-size-fits-all policies and legislation, or to scientists who desire hard evidence for advice and decision-making. These are detrimental to efficient control of this "furtive" bug, which thrives in the absence of rapid, epidemiologically sound interventions.

In this presentation, brucellosis control is compared in two very different contexts: one a developed country, with its intensive cattle production, advanced animal health controls and substantial resources, and the other a developing nation with extensive production systems, wildlife involvement and limited resources. Examples are provided as to how the science-policy interface "space" can lead to persistence of the disease and recommendations are provided as to how it might be avoided. The principles are applicable to a range of other difficult-to-control diseases or zoonoses

CONCLUSIONS: Zoonotic diseases that traverse the human-livestock-wildlife interface require innovative, flexible and multidisciplinary approaches if they are to be effectively managed, especially under resouce-constrained conditions.

Zoonotic diseases that traverse the human-livestock-wildlife interface require innovative, flexible and multidisciplinary approaches if they are to be effectively managed, especially under resouce-constrained conditions.

2 SPI 03 - ADDRESSING ZOONOTIC DISEASES AT THE ANIMAL-HUMAN-ECOSYSTEM INTERFACE. WHAT ARE THE THREATS? HOW TO BE PREPARED? - GALLERY A-B

Achieving Rabies Zero by 2030

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Rabies has been regarded as one of the lingering and enigmatic public health issue of the developing state that has been taking innocent lives for the past several years. Untiring efforts are needed to implement the concept of educate, vaccinate and eliminate (EVE) in the developing nations. Studies pertaining to knowledge, attitude and practice (KAP) reveal multiple loop holes and problems which persist the prevalence of this disease in these countries including African states. The knowledge regarding the basic preventive measures against rabies is severely deficient in the communities and people are unaware of the disease that how it spreads. The attitude and practice of the health practitioners in Middle East and central Asia is also miserable which puts the people at constant risk. Most of the health and veterinary practitioners are unaware of the causes, signs and symptoms of the diseases and most importantly they usually mimic the diseases with any superstitions and pseudo psychological illness. Various KAP studies have been conducted in the Asian and African states which reveal drastic and a serious lack of information and awareness in health workers and community. There is a dire need to raise the concept of education and awareness among the people to fill the knowledge gaps and wipe out miserable human deaths due to rabies. The global alliance for rabies control, along with WHO and OIE has collaboratively launched the concept of EVE which enforces the one-health concept.

The second issue is poor recognition, reporting and diagnostic laboratories against rabies. The third issue is the lack of understanding the interactive behaviour of humans towards dogs. The layman and the community of developing states do not impart positive attitude towards free wandering or pet dogs. The dog has often been described as man’s best friend, but unluckily this animal has been considered notorious in developing states where responsible pet ownership (RPO) has been deficient and extensively lacks. There is also a dire need to explain the facts that how kids, a common person, pet owner and a pedestrian should interact with his dog. People must be educated regarding the prophylactic vaccination against rabies. They must also need to educate pertaining to a clean and hygienic environment that can facilitate and limit the wandering of stray dogs in trash.

Overcoming epidemiological constrains, passive and active community sensitization, mass dog vaccination, enhancing positive human-dog interaction, implementing RPO among pet owners and an active participation of the government heads along with legislative policies in the countries can eradicate this disease from developing countries. These are the risk factors of rabies which have been discussed in these presentations and narrative overviews of relevant solutions have also been discussed.

CONCLUSIONS: “Achieving Rabies zero by 2030” is only possible by overcoming poor surveillance, lack of community awareness, upgrading KAP among doctors and paramedics, depleting obsolete and ineffective sheep brain vaccine/nerve tissue vaccine, inadequate understanding and unavailability of cell culture vaccines, deficient dog population dynamic studies, inadequate veterinary services and lack of diagnostics.

2 SPI 04 - ADDRESSING ZOONOTIC DISEASES AT THE ANIMAL-HUMAN-ECOSYSTEM INTERFACE. WHAT ARE THE THREATS? HOW TO BE PREPARED? - GALLERY A-B

Future Earth's Top Ten Challenges for One Health

Peter Daszak and William B. Karesh

EcoHealth Alliance

Future Earth's oneHEALTH Global Research Project conducts an annual horizon scan review of hot topics for One Health that will profoundly change the future of health on the planet. We present 10 high-impact issues for global human, animal and environmental health, summarizing the evidence to date and showcasing needs and opportunities at the science-policy interface: 1.) Big data, artificial intelligence, and monitoring earth systems; 2.) Global collaborations on microbial diversity and phylodynamics; 3.) Mitigating the underlying drivers of emerging infectious diseases and disaster risk reduction; 4.) Gene editing technology; 5.) Human-driven evolution and synanthropic species; 6.) Mechanisms and manifestations of disease transmission; 7.) Crowdsourcing and private funding influencing future research; 8.) Mass mortality events; 9.) Economic optimum for land development; 10.) Financial risk-rating instruments for disease outbreaks. The multisectoral nature of these issues warrants a One Health approach to enhance understanding of future threats and opportunities and maximize progress across the Sustainable Development Goals and related initiatives for health security, disaster risk reduction, conservation, and economic development that can benefit from novel integration of disciplines. The goal of the horizon scan is to galvanize global thinking, knowledge and resources to translate these to policy action for a healthier planet.

CONCLUSIONS: Horizon scanning can help to anticipate future risks and opportunities. Applying a One Health approach can facilitate better understand of complex issues to identify trade-offs and synergies and engage a wider range of stakeholders to find multisectoral solutions.

3 SPI - THE DRIVERS OF EMERGING ZOONOTIC DISEASES - GALLERY A-B

The migration, climate change, and vector-borne disease nexus

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Humans and other animals are hosts for various vector-borne pathogens. As these hosts move and modify their environments, the distribution of arthropod vectors may also change, and, with it, the pathogens these vectors carry. The population displacements caused by the multiple and sometimes overlapping political and humanitarian crises that have occurred in various parts of the globe over the past decade will probably continue to be a feature of the human population, along with rapid urbanization. At the same time, vector-borne diseases are highly responsive to environmental change, and climate change is likely to provide new habitats for living organisms, including vectors. Climate change also increases pressure on food security because of reduced reliability of seasons and extreme climatic events such as droughts or heavy rains. These factors will also contribute to the emergence and spread of vector-borne infections.

Climate change, associated with increases in atmospheric CO2, may result in a significant increase in atmospheric temperatures by 2050; changes in abundance and distribution of rainfall will accompany this increase. Also by 2050, two-thirds of humans will live in urban areas, with infrastructure lagging behind migration into city margins. Finally, regional conflicts have led to the highest number of displaced persons in history (over 65 million in 2016), often leading to makeshift communities with high human densities, with people facing challenges similar to those in rapidly urbanizing areas. The international financial institutions and their partner development agencies work with countries to anticipate and address the effects of this nexus of migration, climate change, rapid urbanization, conflict, and violence on the emergence and geographic expansion of vector-borne diseases. Understanding these drivers in the emergence of disease is essential to preventing, preparing, detecting, and responding to vector-borne diseases. Conversely, a lack of understanding of the drivers that may lead to an outbreak, their spatial and temporal heterogeneity, and their interconnections across an affected region and beyond may hamper the ability of countries to prevent or prepare for outbreaks.

Specific examples, including climate change and Rift Valley fever, urbanization and dengue, and forced displacement and leishmaniasis, will be used to explore this nexus and its various dynamics in specific country contexts. As the development community and countries at risk plan for improved preparedness and response, the potential effects of multiple drivers on the emergence and spread of these diseases should be carefully considered. The diversity of drivers and their shared implications underscore the relevance of the ‘One Health’ concept, which calls for an integrated approach to human, animal, and environmental health. The One Health approach recognizes the need to take into account the interactions between environmental, epidemiological, and socio-economic factors. Strategies to mitigate disease, including surveillance for pathogens and drivers in new projects and the development of policies that impact multiple sectors, will be proposed.

CONCLUSIONS: Migrations due to climate change, economic, or political need will change the landscape of vector-borne diseases, which are highly responsive to environmental change. The development community and countries affected should consider this nexus and its impacts on the emergence and spread of vector-borne diseases to successfully address these growing challenges.

3 SPI 01 - RESISTANCE TO ANTIBIOTICS AND ANTIVIRALS: CHALLENGES FOR POLICY MAKERS AND SCIENTISTS GALLERY A-B

Antimicrobial Resistance and One Health solutions

Joergen Schlundt

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While infectious and foodborne diseases have a very significant health effect globally, an even more concerning development related to both human and animal health and food production must be considered: the increase in antimicrobial resistance (AMR). AMR results in microorganisms that cannot be treated with our standard antibiotics, and the increase in the number of multi-resistant bacteria (resistant to several antibiotics) threatens a return to the pre-antibiotic era, where a simple scratch or a sore throat could be life-threatening. It is estimated that 700,000 die globally every year from AMR microorganisms, and that this figure will increase to 10 million by 2050 (the global death toll from cancer is 8 million). It should be noted that the vast majority of antimicrobials used globally is actually used to make healthy animals grow faster (growth promoter), not to treat sick humans or animals.

Sensible action to deal with this problem and prevent the dramatic, stipulated increase must be based in efficient surveillance of use of antimicrobials and prevalence of AMR. Model surveillance systems have already been running for more than 20 years in some countries, but the vast majority of countries have no surveillance. Likewise simple, but necessary regulatory changes have been introduced in some countries, focusing on 1) all antimicrobial use governed by prescription, 2) ban/reduce all use of antimicrobial growth promoters, 3) disable the Veterinarians right to profit from sales of antimicrobials.

Any action to control these problems have to be based in science, and Next Generation Sequencing (NGS) gives us a potential to develop standardized global surveillance of all microorganisms as well as AMR, providing a basis for sensible 'One Health' interventions.

3 SPI 02 - RESISTANCE TO ANTIBIOTICS AND ANTIVIRALS: CHALLENGES FOR POLICY MAKERS AND SCIENTISTS
GALLERY A-B

Antimicrobial resistance: Canada’s science and policy challenges

Aline Dimitri

Canadian Food Inspection Agency, Canada

Antimicrobial Resistance and Use (AMR / AMU) is a complex issue that impacts health, agriculture, the global environment, and trade. Addressing this issue requires active collaboration among multiple partners in many sectors with a “One Health” approach. Coordinated action is needed in the human and animal health and the agriculture sectors to combat the spread of AMR and ensure the availability and the effectiveness of antibiotics in the future. Canada has been working to develop a national action plan. In the fall of 2017, the pan-Canadian framework on AMR and AMU was released to set out the high level policy and potential areas for action to be elaborated in the anticipated pan-Canadian Action Plan. The framework outlines four pillars where future actions are needed; Surveillance, Stewardship, Infection Prevention and Control, and Research and Innovation. Canada has also been an active participant in international fora to ensure harmonization between guidelines and policies internationally.

Antibiotics are a critical tool in a food producers toolbox. They are needed to ensure the health and wellbeing of animals and in return the production of safe and sustainable food for human consumption. While antibiotics have been an important tool in this toolbox, there is a need to develop and use alternatives in addition to antibiotic in raising food animals to ensure antibiotics remain effective and available in the future.

There are many science and policy challenges for those working on developing a national action plan and policies along with stakeholders who are in the field raising or treating food animals. While Canada has a comprehensive surveillance system, gaps remain that must be addressed to better benchmark the use of antibiotics and the spread of AMR. There is also a need to ensure alternatives, such as vaccines, are available and that the decreased use of antibiotics for prophylactic and growth promotion purposes have minimum economic impact on the agriculture and animal health sectors and ultimately the consumers. More research and development is needed in this field as well as well as on different husbandry practices to reduce the need for antimicrobials in food animal production. As the world’s population increases, safe and sustainable food is needed to enhance human health and quality of life while preserving antimicrobials for both human and animal medicine. Collaboration and investment amongst domestic and international partners is the only pathway to success in solving many of these science and policy challenges.

CONCLUSIONS: Collaboration in the human and animal health sectors is critical in combating the spread of AMR and increasing the prudent use of antibiotics under a one health umbrella.

Investments in research and innovation will ensure the availability of alternatives to antibiotics in the production of safe and sustainable food supply.

Canada will continue its actions domestically to elaborate a national action plan and will continue its international engagements to ensure a harmonized response to the threat of AMR.

3 SPI 03 - RESISTANCE TO ANTIBIOTICS AND ANTIVIRALS: CHALLENGES FOR POLICY MAKERS AND SCIENTISTS GALLERY A-B

The Nordic countries strategy for AMR: challenges at “high latitudes” for policy makers, scientists and society

Carlos Gonçalo das Neves

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The increased use of antibiotics in humans, livestock, agriculture has led to a global and growing challenge, in the form of antibiotic-resistant bacteria and microbes. This challenge is made even more complex due to the environmental accumulation/spread of resistant bacteria. Some studies forecast that by 2050, multi-resistant bacteria and microbes will kill up to 10 million people worldwide each year, with economic losses in the trillions of dollars. AMR has therefore grown to be one of the major global challenges for our planet, and has deserved the combined efforts of major key players such as UN, WHO, FAO, OIE.

AMR in Scandinavian countries is in general lower than most of its European counterparts, due to several factors, such as geographic location and lower human and livestock densities. That said in a globalized world, Scandinavia is affected by many drivers for resistance such as increased livestock production, import of food and animals, human migrations, use of heavy metals, climate change, tourism, etc…

Recognizing that the current AMR situation can change quickly in the near future, Scandinavian countries have tried to “team up” in efforts to fight AMR in a multi-level approach including the political, management, scientific and educational levels. Though often with similar problems on AMR, there are important differences and threats, which have been handled differently by Scandinavian countries (e.g. MRSA in livestock and humans).

In 2017 the Nordic Council launched a common road map for fighting AMR in Scandinavia through 12 different measures focusing on policy, research, education, internationalization among others. This document has been the focus of heated debates among countries and many options both pro and con have been considered. Also in 2017 a high-level ministerial meeting on AMR took place in Norway. At this meeting, there was a special focus on AMR and the environment. The inclusion of environmental aspects of AMR are considered central to achieve several of the roadmap goals, specifically the one focusing on “Collation of knowledge of distribution patterns and the spread of antimicrobial resistance.”

Scandinavian countries are also gradually investing in the internationalization of their research/management in AMR as a way to help developing and LMICs countries to fighting this threat. At EU level it is worth mentioning the new joint programme on One Health, where AMR has taken a central focus, in what is the Union’s biggest project ever on One Health with a budget of over 90M €.

This presentation will first briefly discuss the situation on AMR in Scandinavian countries (with a focus also on political and society aspects), as well as describe the major lines of ongoing national strategies. The presentation will then focus on some of the differences and threats that have highlighted difficulties at the political/ management level. To finalize the Scandinavian roadmap for AMR ongoing discussion will be presented and how its implementation is being thought at a multi-level approach (politicians, researchers, managers, educators and society).

CONCLUSIONS: Joining efforts across boarders to fight AMR is not "problem-free", but can enhance global capacity to address major threats. The Scandinavian example highlights some of these difficulties but also the major gains of such political/scientific strategies.

3 SPI 04 - RESISTANCE TO ANTIBIOTICS AND ANTIVIRALS: CHALLENGES FOR POLICY MAKERS AND SCIENTISTS
GALLERY A-B

Trade Implications of Antimicrobial Resistance in the International Food Chain

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Antimicrobial resistance (AMR) challenges the scientific and technical capacity of most national governments to deliver existing and new types of data which capture both the direct and indirect consequences of AMR, including social and economic consequences. From a public health perspective, AMR also raises complex governance and policy issues which neither national institutions nor their international equivalents have sufficiently addressed, particularly in collecting and testing relevant economy-wide AMR data.

For example, one significant transmission route for AMR is global trade but scrutinising this policy area has generally been surreptitiously avoided or placed at the bottom of the ‘things to do’ on One Health implementation plans. To examine why ‘trade’ is not actively at the forefront of AMR policy raises larger questions because even for the non-expert it would appear obvious that one of the most complex aspect of AMR transmission is its global dimension.

Globalisation of trade has long been promoted as an ‘enabler’ for achieving development goals and raising safety standards including in food production. Some improvements are generated from national based food import standards which can encourage adoption of safer practices in countries wishing to export food to, for example, the EU/US markets. The other major influence on setting food safety standards is Codex Alimentarious which is now re-examining its AMR guidelines but will not report till 2020. Overall, trade aspects of AMR do not seem to be addressed with the degree of urgency needed perhaps indicating a significant policy implementation gap that has both structural and political dimensions.

In relation to policy coordination, trade rules and obligations tend to be politically quarantined from health issues within bureaucracies. Trade obligations are often esoteric not well understood within key portfolios responsible for developing AMR policy, particularly the health/science focused areas. But with the level of threat from AMR, any policy barriers erected around trade need to be opened to scrutiny and ‘trade’ strategically integrated into AMR One Health Action Plans. Other interventions offering solutions to plug policy gaps include the powerful new science around the gut microbiome which links to antibiotics and AMR but is not yet strategically factored into AMR policy as a significant public health issue capable of also transforming public opinion on AMR.

Such strategies would also create strong linkages to consumer and investor priorities and could provide greater political impetus to prioritise, resource and implement AMR One Health Policies. Governments and international institutions have been slow to proactively respond to ‘trade’ as a significant conduit for AMR organisms but as consumers become more aware of the dynamics and spread of AMR they will demand action and investors are well attuned to concepts of brand damage.

CONCLUSIONS: AMR One Health Action Plans should substantially address the trade issues linked to the spread and development of AMR. Articulating the AMR linkages to other public health issues such as the gut microbiome and interests of consumers and investors could generate greater political support to fund and address AMR.

4 SPI 01 - MAKING ONE HEALTH OPERATIONAL: THE BARRIERS TO CHANGE AND GLIMMERS OF HOPE - GALLERY A-B

A decade of implementing One Health in Kenya: Translating research into practice

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BACKGROUND: More than 75% of emerging infectious diseases are zoonotic in origin. A transdisciplinary, multi-sectoral One Health approach is a key strategy for their effective prevention and control. In response to global advocacy for a One Health approach, Kenya created a coordination framework between public health and animal health sector to understand, prevent and control (re-) emerging and endemic zoonotic diseases. Here, we highlight milestones that have catalyzed the implementation of a One Health approach in Kenya and describe the key pillars of this approach including developing institutional capacity, strengthening surveillance for zoonotic diseases and expanding research capacity in Kenya and East African region. In addition, we highlight specific application of research findings into disease control policies, implementation challenges and recommendations to achieve the full benefits of the One Health approach.

RESULTS: Two events, the global expansion of highly pathogenic H5N1 and the 2006 East African multi-country outbreaks of Rift Valley Fever, catalyzed the Ministry of Health and the Ministry of Agriculture, Livestock, and Fisheries and other partners to establish a framework for multi-sectoral collaboration at national and county level and to establish a coordination office referred to as the Zoonotic Disease Unit (ZDU). The ZDU has provided Kenya with an institutional framework to address the public health importance of endemic and epidemic zoonoses including RVF, rabies, brucellosis, Middle East Respiratory Syndrome Coronavirus, anthrax and other emerging issues such as anti-microbial resistance through capacity building programs, surveillance, workforce development, research, coordinated investigation and outbreak response. These efforts have led to improved outbreak response, and generated data including discovered two new pathogens, and generated data that have informed disease control programs to reduce burden of, and enhance preparedness for, zoonotic diseases. Since 2014, the Global Health Security Agenda implemented in the country has provided additional impetus to maintain this effort and Kenya's achievement now serves as a model for other countries in the region. Significant gaps remain in implementation of the One Health approach at subnational administrative levels, including sustainability concerns, competing priorities and funding deficiencies.

CONCLUSION:

The adoption of the One Health approach in Kenya has led to better multisectoral collaboration among public health professionals, researchers and other stakeholders and generation of research and surveillance data for public health action. These achievements have allowed for advocacy and informed decisions to be made on the control and prevention of zoonotic pathogens and have identified gaps in diagnosis and surveillance. However, challenges remain in sustainability, veterinary laboratory diagnosis and resources to implement more comprehensive control and *prevention measures*.

4 SPI 02 - MAKING ONE HEALTH OPERATIONAL: THE BARRIERS TO CHANGE AND GLIMMERS OF HOPE - GALLERY A-B

One Health Secretariat: A Formalized coordinating Entity for Operationalizing One Health in Bangladesh

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Bangladesh has been encountering health problems at human, animal, wildlife interface and is considered as hot spot for the emerging infectious diseases (EID). High population density, deforestation, land use change, agricultural intensification, globally integrated animal production system, predominating small holding farming, rapid urbanization and industrialization drive emergence of infectious diseases. Zoonotic diseases like Highly Pathogenic Avian Influenza, Nipah, Anthrax, leptospirosis, Rabies, etc are common in the country. A multi-disciplinary team including physicians, veterinarians, environmental scientists, and civil society and development practitioners formed an organization, 'One Health Bangladesh (OHB)' in 2008 after experiencing avian influenza outbreak in the country that shattered the poultry industry and threatened public health. The forum started advocacy with the government, development partners, NGO, civil society organizations, professional bodies, research institutions, academic institution to promote One Health concept. As a result, Government of Bangladesh developed and endorsed a National One Health Strategy and Action Plan in 2012.The strategy emphasized the need for institutionalization of One Health and called for a coordinated multidisciplinary program management. While informal sectoral collaboration in the field of outbreak investigation, surveillance, workforce development, communication continued, strive to formalize the coordination mechanism also continued in parallel. The government thus took steps to institutionalize One Health within the government systems through creating One Health Secretariat (OHS) and, Inter-ministerial Steering Committee on One Health and the terms of reference of those platforms. The leadership of these entities will rotate among the Ministries at an interval of every three years. Government has already mobilized resources for the functioning of OHS. The OHS with seconded staff from three ministries has started functioning at Institute of Epidemiology, Disease Control & Research within the Ministry of Health and Family Welfare. OHS has assessed the performance of one health mechanisms for future planning, supported revision of One Health Strategy and prioritized zoonotic diseases. The secretariat has taken initiative to update Pandemic Influenza Preparedness and Response plan. As routine work, OH is coordinating zoonotic disease outbreak and response.

4 SPI 03 - MAKING ONE HEALTH OPERATIONAL: THE BARRIERS TO CHANGE AND GLIMMERS OF HOPE - GALLERY A-B

Making One Health operational within the Caribbean Region

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BACKGROUND: The Caribbean nations are connected by shared waters, culture and climates, yet the distance, diversity and various approaches to governance between nations complicates efforts to promote an integrated, holistic approach to problems. Overcoming this challenge is urgent because of the many significant One Health problems in the region, many of which are directly related to climate change. These challenges include more frequent and more severe tropical storms and hurricanes, water shortages, rises in sea levels, losses of fisheries, increases in mosquito-borne diseases and chronic non-communicable diseases linked to poor nutrition, poverty and environmental pollution.

METHODS: Through a European Union (EU) funded project, 'One Health, One Caribbean, One Love', tangible actions were implemented to make One Health operational across the Caribbean region. Firstly, a platform for change was developed through a regional One Health policy, which was endorsed by the human, agricultural and environmental health sectors of the region. Secondly, a road-map or strategic framework was developed through consultation with the relevant Caribbean organizations, allocating responsibilities for specific activities. Thirdly, the need for change was marketed to get buy-in from key stakeholders, through emphasizing the many advantages of following a One Health approach. Finally, a cadre of inter-sectorial One Health leaders with skills to be agents of change was created across the region.

RESULTS: Results are summarized in a freely accessible E-book entitled "Caribbean Resilience and Prosperity through One Health" (www.onehealthcaribbean.org). In brief, a regional One Health policy has been approved by the human health, agricultural and environment ministerial councils under the Caribbean community (CARICOM) structure. A six year Caribbean One Health strategic framework has been prepared and circulated. Its endorsement and roll-out is central to a follow-up project that is currently under development. A regional network of 29 One Health leaders has been developed across 12 Caribbean countries. Through the development of national One Health networks, the One Health leaders worked with technical mentors to carry out national projects, which demonstrated the value of a One Health approach to address priority health-related issues at the interface between human, agricultural and environmental health in their home country. Details will be presented on how the One Health Leadership series was set up and conducted, what challenges were faced, and what priority areas were selected for study in the national projects.

4 SPI 04 - MAKING ONE HEALTH OPERATIONAL: THE BARRIERS TO CHANGE AND GLIMMERS OF HOPE - GALLERY A-B

Characterizing the interventions of the private sector extractive industries during the Ebola virus disease crisis in West Africa

Susan Scribner

Vice President Health Systems Solutions, DAI Global Health

During the 2014-2016 Ebola outbreak in West Africa, the private sector were active participants in response efforts. The USAID Preparedness and Response Project surveyed 23 oil and gas and mining companies operating in West Africa to understand the actions/behaviors of firms during the response and to assess what they think industry's role should be in future outbreaks. Companies in Guinea and Ghana were selected because each has large extractive industries and mounted a response to Ebola. We also wanted to see the differences between a country that had to respond to Ebola and one that did not have to, but needed to be prepared. The survey was conducted in different ways: participants at a workshop took the survey and P & R also conducted in-person and phone interviews.

All companies surveyed reacted to varying degrees to the Ebola outbreak. All companies implemented compulsory handwashing at entry points to buildings and entry points to concessions. Thermal screening was used at entry points and at company offices. Most companies coordinated with non-governmental organizations (NGOs) to assist with the distribution of supplies, such as rice and sanitation kits (buckets, soap, and chlorine tablets). Many companies funded NGOs to sensitize communities on hand washing, feet washing, culturally appropriate risk mitigation measures, and screening.

Most companies had to adjust their supply chains, and some had significant disruptions, but the biggest social and economic challenge was due to closing of national borders and transportation routes.

4 SPI 05 - MAKING ONE HEALTH OPERATIONAL: THE BARRIERS TO CHANGE AND GLIMMERS OF HOPE - GALLERY A-B

Tripartite Guidance: Taking One Health Approaches to Address Zoonotic Diseases in Countries: A “Glimmer of Hope”

Elizabeth Mumford

World Health Organization

Zoonotic diseases continue to pose risks to both animal health and human health, and have far reaching impacts on economies and livelihoods. Collaboration across all sectors responsible for health - taking a One Health Approach - is required to effectively prevent, detect, and respond to, as well as to prepare for and assess both acute zoonotic disease events and endemic zoonoses and other health threats at the human-animal-environment interface.

However, most countries have no, or inadequate, mechanisms in place for administrative and technical collaboration among the animal health, human health, and environment sectors and other relevant sectors to address zoonoses and other health threats. Gaps in national multisectoral, One Health capacity are routinely noted during assessments under the International Health Regulations (IHR, 2005) Monitoring and Evaluation Framework and in OIE Performance of Veterinary Services (PVS) Pathway reports.

JUSTIFICATION: Countries have identified the need for standard operational guidance and tools as they strive to build multisectoral, One Health capacity among the relevant sectors and meet their obligations under IHR, PVS, and other frameworks including the United Nations’ Sustainable Development Goals (SDGs). In 2008, the Tripartite (WHO, FAO, and OIE) published guidance to support countries in establishing such multisectoral, One Health collaboration for zoonoses. Since 2008, countries and development partners have gained important experience in implementing multisectoral, One Health approaches which could be useful to other countries wishing to do so as well. Now, to improve practicality and relevance, the Tripartite are updating and expanding the 2008 guide. This new Tripartite Zoonoses Guide (TZG) (1) captures operational experiences, lessons learned, and good practices from countries and international experts and (2) has an expanded scope of topic areas relevant to prevention, detection, and response to zoonotic diseases at the country level.

This TZG is being developed collaboratively by technical experts in WHO, FAO, and OIE, and international, regional, and national experts from around the world. Input from countries is included in development of the content and guidance, and some specific countries’ experiences and lessons learned are included as vignettes.

SCOPE: The TZG is applicable to all countries and regions, and to all zoonotic diseases: endemic, emerging or otherwise. The guidance provided is not disease-specific so will be applicable to any zoonotic disease event or endemic zoonotic disease. While focusing on infectious hazards, the TZG is also flexible enough to cover multisectoral collaboration for other health threats at the human-animal-environment interface such as AMR and food safety/security.

The TZG focuses on multisectoral, One Health aspects of the seven topics below. Existing sector-specific guidance will be referenced. The TZG will also include guidance on national overarching topics, such as conducting a stakeholder analysis, national infrastructure mapping, financing, and multisectoral zoonotic disease prioritization. It will provide options for improving sustainability of the programmes and activities, and contextualisation of these activities within international frameworks.
- Multisectoral Coordination Mechanisms
- Strategic planning and emergency preparedness
- Surveillance and information sharing
- Coordinated investigation and response
- Joint risk assessment for specific threats
- Risk Reduction, Communication Strategies and Community Engagement
- Training and workforce development

USE OF THE TZG: The activities described in the TZG are meant to be undertaken jointly by the governmental sectors working on zoonotic diseases in the country. In most cases that includes the ministries, agencies, or departments responsible for human health, animal health (including livestock, wildlife, and pets), and the environment. In many situations, other sectors and disciplines are important to include as partners or advisors.

Countries may choose to use the TZG to build capacity to fill gaps identified through external assessments or identified during internal review of national experiences with zoonotic disease events, or to operationalise national health plans. Some countries may wish to use the TZG in its entirety; others may choose to undertake only certain activities to fill specific gaps in national capacity. The TZG also encourages countries to identify and use or expand existing national mechanisms and infrastructure when they already exist. Importantly, the TZG is an operational guide, not a standard or requirement. It offers a spectrum of options for countries to consider for implementation, and some experiences and good practices based on other countries' experiences. Activities are generally offered as operational "elements" within the topic areas that can be implemented based on countries' specific needs and the national context.

NEXT STEPS: Depending on funding available, the TZG will be expanded to include specific Operational Tools and technical resources to support each of the topic areas. For example, an Operational Tool detailing the processes and steps for conducting joint risk assessments has already been developed and piloted, and will complement the initial version of the TZG, set to be released in late summer 2018 in all six UN languages.

The timing of release of the guide coincides effectively with the 5th One Health Congress and fits exceptionally well in this session, as an operational "Glimmer of Hope" that will soon be available to support policy makers, development partners, and others in countries in taking multisectoral, One Health approaches to zoonotic diseases and other health threats at the human-animal-environment interface.

5 SPI - ONE HEALTH IN UNDERSERVED, RESOURCE-POOR AND MARGINALIZED COMMUNITIES -GALLERY A-B

One Health, rabies response and more-than-human considerations in Indigenous communities in Northern Australia

Chris Degeling

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BACKGROUND: Australia is currently rabies free; however, the spread of rabies in eastern Indonesia poses a risk to northern Australia. Dogs are numerous in East Arnhem Land (EAL) and the Northern Peninsular Area (NPA), usually unrestrained and living in close human-dog relationships. The response to any rabies outbreak on Australian territory will focus on dog vaccination, controlling dog movements and depopulation. A One Health approach to zoonotic disease control should seek to co-promote human and animal health, whilst also seeking to accommodate the preferences of affected communities.

METHODS: We report on 5 focus groups/workshops and 28 semi-structured interviews conducted with: (i) EAL and NPA community members; (ii) Indigenous Rangers in EAL and NPA; and (iii) residents of the city of Cairns Queensland, a local regional hub and service centre. We used storyboard methodologies to work with participants to explore the following questions:

1. What should and should not be done to prevent and control canine rabies in northern Australia?
2. What are the roles and responsibilities of government officers and members of the community in the event of a canine rabies outbreak?

RESULTS: We found that the capacity of community members in the NPA and EAL to contribute/adapt to a biosecurity response is likely to be limited by material disadvantage and cultural norms. Responsible ownership means different things within and across the study settings which has implications for management strategies. The cultural value placed on dogs/dingoes is variable and conditional; some dogs are totems and some are seen as being essential to food security. There is inadequate fencing to allow community compliance with key control measures such as enforcing restrictions on canine movements. However, even though dogs and dingoes can have great cultural and social importance, key interventions might be accommodated within cultural beliefs and long-standing norms of dog management if sufficient effort is expended on adapting them to local contexts and community preferences. Adopting a 'strengths-based' approach mandates that the communities at greatest risk need to be helped to prepare for and develop strategies to manage a biosecurity response to a rabies incursion. This would include attending to the educational needs and infrastructural means for supporting individuals and communities to respond appropriately.

CONCLUSIONS: Successful implementation of control measures for a rabies incursion in northern Australia will depend on broad community support and compliance among affected communities. The results of this study can inform control strategies that are consistent with community values.

LATE BREAKERS

LB

1 LB1 - LATE BREAKERS 1 - SALON AB

Coronavirus bio-surveillance of the insectivorous bats at the Matlapitsi cave in the Limpopo province, South Africa

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Bats host a large diversity of coronaviruses, many of which have been associated with a history of cross-species transmission and co-evolution. Several examples of coronavirus cross-species transmissions and adaptations to new hosts have been documented in the past 16 years. These include human coronaviruses such as severe acute respiratory syndrome coronavirus and Middle East respiratory syndrome coronavirus. Recently in Asia, a fatal enteric disease (porcine enteric alphacoronavirus) emerged in porcine populations from a novel bat-borne alphacoronavirus previously identified within the *Rhinolophus* bat genus. Continued coronavirus surveillance is thus essential to build on the known diversity of bat-associated coronaviruses and enable investigation into the emergence of viral species of public health and veterinary importance. We therefore aimed to expand on the known diversity of bat-associated coronaviruses from South African bat species. We focused on the species present at a specific cave-system (Matlapitsi) in the Limpopo province in South Africa, which is rich in species diversity, with high abundance of certain hosts. We analyzed samples collected from insectivorous bats from 2013 to 2017, such as fecal material (n=58) from caught-and-released bats as well as the rectal/intestinal samples (n=59) of bats collected as vouchers. The samples were investigated for coronavirus RNA with a hemi-nested RT-PCR assay targeting a conserved region of the RdRp gene. This region was extended with an assay from the literature for better phylogenic resolution. Of the 117 samples tested thus far, 44 were found to harbor coronavirus RNA. The high positivity rate (37.6%) identified from the bats at this site was mainly attributed to the high positivity encountered from the large number of sampled *Miniopterus natalensis* species that roost in the cave. Overall, nearly half of all sampled material from the species collected over five years were found positive for coronaviruses. The *Rhinolophus* spp., Myotis sp. and *Pipistrellus* sp. were shown to harbor coronavirus RNA with low levels of positivity. Preliminary analysis of the sequenced regions show three lineages of novel *Miniopterus* alphacoronaviruses as well as a novel lineage of a *Rhinolophus* alphacoronavirus. There is a significant lack of comparable sequence data for some of these lineages, and this study also constitutes the first reports of coronavirus sequences from South African *Rhinolophus* species. These preliminary findings show the presence of a large coronavirus diversity within just one site. These bats were sampled over five years, also showing persistence within these hosts. The *M. natalensis* species can be highlighted as a model to study the factors involved in the persistence, maintenance and shedding of coronaviruses that may be applied to investigating emerging coronaviruses among human and livestock populations.

2 LB1 - LATE BREAKERS 1 - SALON AB

Zika Virus Surveillance at the Animal-Human Interface in Brazil, Colombia, and Peru, 2017-2018

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BACKGROUND: Zika virus (ZIKV) was first discovered in 1947 in Uganda, but was not considered a public health threat until 2007 when found to be the source of epidemic activity in Asia. Epidemic activity spread to Brazil in 2014 and continues to spread throughout the tropical and subtropical regions of the Americas, where *Aedes aegypti* mosquitoes are abundant. Despite ZIKV being zoonotic in origin, information about potential vertebrate hosts and invertebrate vectors for ZIKV in the Americas and the role they play in virus maintenance and transmission is lacking.

METHODS: We conducted active surveillance of native primates, as well as other non-human vertebrates and mosquitoes to ZIKV virus in Brazil, Colombia, and Peru at established field sites up to 5 times per year, where there was evidence of recent or active ZIKV transmission in humans. Trapping efforts focused on abundant wildlife and domestic animals, as these would be candidate reservoirs or amplifiers if they are hosts. We screened whole blood and mosquito samples for ZIKV nucleic acid by a pan flavivirus real time RT-PCR and confirmed by ZIKV specific real time RT-PCR. We tested plasma samples for presence of anti-ZIKV antibodies by plaque reduction neutralization testing (PRNT).

RESULTS: From February 2017 to March 2018, we collected 4,727 animal and roughly 27,000 mosquito samples. Preliminary test results, for the subset of the samples from Brazil and Colombia with test results to date, reveal that 7.7% (144/1,863) of animal and 26.4% (146/554 mosquito pools; 1,115 total pools collected) of pooled mosquito samples are positive for flavivirus by RT-PCR and 8.9% (68/761) of animal plasma samples show evidence of anti-ZIKV antibodies by PRNT. Laboratory analysis for the remaining 70% (7,391/10,569) of individual and pooled samples is underway.

CONCLUSIONS: Results of this study will facilitate a better understanding of ZIKV's ability to establish a sylvatic cycle outside of human transmission, shape future surveillance strategies for ZIKV in tropical ecosystems, and inform the need for public health intervention efforts like vaccine development.

3 LB1 - LATE BREAKERS 1 - SALON AB

Avian-origin PB1 gene confers selective advantages to 2009 pandemic H1N1 virus RNA transcription and replication

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BACKGROUND: Polymerase functions of avian influenza viruses were restricted in mammals due to host restrictions. To overcome restrictions on heterotrimeric polymerase complex, diverse adaptive strategies has been deployed by viruses. PB1 gene originated from avian strains has been frequently observed in seasonal and pandemic strains. Nevertheless, the biological significance and corresponding molecular mechanism by which avian-origin PB1 emerged in these strains have long been elusive.

METHODS: To elucidate the effects of avian-origin PB1 on the functions of viral polymerase complex and pandemic formation, we introduced avian-origin PB1 into the background of 2009 pH1N1 virus, which naturally lacks avian-origin PB1 segment and the well characterized PB2 E627K mutation. Viral polymerase activities were measured using mini-replicon assay or primer extension assay. cRNA stabilization assay was used to dissect the influence of avian-origin PB1 on different step of viral RNA synthesis.

RESULTS: We showed that avian-origin PB1 can markedly elevate polymerase activity of pH1N1 in human cells. Notably, acquisition of avian-origin PB1 can assist pH1N1 polymerase to compensate the lack of PB2-associated adaptive mutations in a similar manner as overexpression of chANP32A, the recently identified major host factor underlying host restrictions on viral polymerase complex. Analysis of viral RNAs synthesis indicated avian-origin PB1 enhanced both replication and transcription of pH1N1 polymerase. Further cRNA stabilization assay results suggested that avian-origin PB1 facilitated the vRNA synthesis from cRNA template in a *trans*-activating manner.

CONCLUSIONS: Our results demonstrated that avian-origin PB1 can boost the viral polymerase activity, or even compensate the function of the canonical adaptive mutation in 2009 pH1N1 polymerase. These data implicated that avian-origin PB1 should be regarded as one of the adaptation markers in the surveillance for pandemic strains, especially in the frequent reassortment events occurred between avian and human strains. Moreover, the proposed mechanism used by avian-origin PB1 to facilitate vRNA synthesis might be applicable to other adaptive mutations such as PB2 E627K. Both of these findings will promote studies on host adaptation of influenza polymerase complex.

4 LB1 - LATE BREAKERS 1 - SALON AB

Learning form an evolutionary host: IRF3 signaling is critical to prevent Middle East respiratory syndrome (MERS) coronavirus propagation in big brown bat cells

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2: Vaccine and Infectious Disease Organisation-International Vaccine Centre (VIDO-InterVac)

Rationale: Insectivorous bats are speculated to be evolutionary hosts of Middle-East respiratory syndrome (MERS) coronavirus (CoV) and Jamaican fruit bats experimentally infected with MERS-CoV do not exhibit symptoms of disease. MERS-CoV causes disease in humans with a thirty-five percent mortality. MERS-CoV has evolved proteins that can counteract human antiviral responses that are mediated via interferon regulatory factor 3 (IRF3). Since bats experimentally infected with MERS-CoV do not develop classical signs of disease, we tested the hypothesis

that MERS-CoV cannot subvert antiviral interferon responses in bat cells. Methodology and results: We infected human and big brown bat cells with MERS-CoV and observed that the virus propagated significantly more in human cells. MERS-CoV effectively suppressed antiviral interferon beta (IFNβ) response in human cells, unlike in bat cells. By studying the response of IRF3 to poly(I:C), a synthetic analogue of viral double-stranded RNA, we observed that bat IRF3 responded to poly(I:C) by phosphorylation and nuclear translocation; hallmarks of IRF3 activation. The role of IRF3 in antiviral signaling is not known in bat cells. By knocking down IRF3 in bat cells by small interfering RNA (siRNA), we demonstrated that IRF3 is critical in poly(I:C) and MERS-CoV mediated IFNβ gene expression. We performed a kinome analysis on poly(I:C) treated bat and human cells and observed that similar pathways were up-regulated. We also infected IRF3 knocked-down bat and human cells with MERS-CoV and observed that MERS-CoV propagated to significantly higher levels in IRF3 knocked-down bat cells.

CONCLUSION: Our study was able to identify a unique IRF3 mediated antiviral signaling process in bat cells that is resistant to subversion by MERS-CoV. Future studies will enable us to adapt these strategies to restore antiviral signaling in coronavirus infected human cells.

FUNDING: NSERC Discovery, Saskatchewan Innovation and Opportunity and Dept. of Vet. Micro.

5 LB1 - LATE BREAKERS 1 - SALON AB

Anti-viral activity of HDAC6 against influenza A virus mediated via suppression of viral RNA polymerase subunit PA

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BACKGROUND: Influenza A virus can cause lethal disease in humans and animals. The virus can trigger severe pneumonia and lead to acute respiratory distress syndrome. The life cycle of influenza A virus (IAV) is modulated by various cellular host factors, which either promote or dampens virus infection at different stages. However, the precise mechanism of IAV infection eliciting the unique host response is still not well understood. Thus, it is critical to find new strategies to control IAV infection

METHODS: To obtain a better understanding of the molecular events of IAV replication, we used the IAV mini-genome construct to quantify the IAV RNA polymerase activity in 293T and MDCK cells. Results:
Our data revealed that HDAC6 plays an important role in fine-tuning IAV RNA replication and transcription. Specifically, we found that HDAC6 physically interacts with three subunits of the IAV RNA polymerase, PA, PB1 and PB2, as well as nucleoprotein NP. Interestingly, the protein stability of PA is preferentially decreased via HDAC6-mediated deacetylation. We also found that overexpression of HDAC6 attenuates the expression of PA protein during IAV infection, concomitantly with a decrease in synthesis of both viral genomic RNA (replication) and viral mRNA (transcription). In contrast, upon treatment with Tubacin, an HDAC6 specific inhibitor, IAV RNA replication and transcription are enhanced potentially due to elevated viral RNA polymerase activity. Consistent with this, we showed that depletion of HDAC6 increases the level of PA protein as well as IAV RNA replication and transcription.

CONCLUSIONS: Our study provides important mechanistic insight into the understanding of IAV replication via suppression of viral RNA polymerase. Taken together, our findings indicate that HDAC6 plays a negative role on IAV RNA polymerase activity via deacetylating PA protein and thus restricts IAV RNA transcription and replication. Thus, HDAC6 could be a potential candidate as the therapeutic target for treating IAV infection.

FUNDING: This work was supported by the Fundamental Research Funds for the Central Universities (KYHW201702), the National Natural Science Foundation of China (Grant No. 31472218), and the Priority Academic Program Development of Jiangsu Higher Education Institutions (PAPD).

6 LB1 - LATE BREAKERS 1 - SALON AB

Rapid and sensitive molecular detection of viruses, bacteria, and parasites without sophisticated laboratory equipment

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BACKGROUND: On-site rapid-diagnostic tests (RDTs) can have limited accuracy, whereas molecular genetics-based diagnostics such as real-time PCR can overcome accuracy limitations by offering high sensitivity, but require significant infrastructure with constant power requirements. We have developed a new low-resource molecular genetics workflow that enables accurate disease identification without any sophisticated equipment (not even a centrifuge). Only a battery-operated heating block is required for incubation at 39 °C. We demonstrated this work flow can be applied widely for detection of parasites, bacteria, and viruses in crushed tissue and whole blood.

METHOD: Malaria parasites were detected from cultured Anopheles mosquitoes (n=116) or red blood cells infected with Plasmodium falciparum. *Wolbachia* bacteria was detected from infected *Aedes* mosquitoes (n=79). Prawn hepatopancreatic parvovirus detection was demonstrated using fresh and wild-caught *Fenneropanaeus merguiensis* prawns (n=30). Analytical sensitivity was determined using dilutions of synthetic plasmid material. Our rapid detection workflow consisted of a simple three-step detection process (see Figure): (1) Mosquitoes, tissue, or blood were homogenized in a novel single-solution extraction buffer for 5 minutes, before (2) specific disease identification using recombinase polymerase amplification (RPA) and incubation at 39 °C for 10-30 minutes, followed by (3) a 5 minute lateral flow strip detection.

RESULTS: Analytical sensitivity of *Plasmodium falciparum* detection was 30 gene copies/µL, which was sufficient to detect a single oocyst within a single infected Anopheles mosquito, even when pooled with 19 uninfected mosquitoes, and when mosquitoes were left in traps for up to 8 days; diagnostic sensitivity and specificity for detection in Anopheles mosquitoes was 100% and 94% respectively. Pilot studies indicated detection of *Plasmodium falciparum* in cultured red blood cells could also be achieved, with a sensitivity down to 50 parasites/µL. Analytical sensitivity of *Wolbachia* detection was 200 gene copies/µL, which enabled detection of a single infected *Aedes* mosquito, even when pooled with 4 uninfected mosquito, and even when mosquitoes were left in traps for up to 7 days; diagnostic sensitivity and specificity for detection in *Aedes* mosquitoes was 96% and 97% respectively. Analytical sensitivity for detection of prawn hepatopancreatic parvovirus was 200 copies/reaction which enabled detection of homogenized *Fenneropanaeus merguiensis* tissue with PCR-determined viral loads of 34.8 copies/µg; diagnostic sensitivity and specificity for detection in *Fenneropanaeus merguiensis* were both 100%.

CONCLUSION: We demonstrated a rapid three-step detection workflow for sensitive and accurate pathogen detection with broad applicability for the detection of parasites, bacteria and viruses in a variety of different sample types. Our workflow could enable accurate on-site detection of pathogens for rapid and decentralised monitoring of diseases during elimination programs and outbreak management.

1 LB2 - LATE BREAKERS 2 - SALON CD

One Health in History: Bison, Parks Canada and the Emergence of Tuberculosis in the Canadian Arctic

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BACKGROUND: Tuberculosis has been described as the defining disease of the Canadian Inuit. By the mid 1940s, the Canada operated a mass evacuation program Inuit sick with TB to the south. While researchers have focussed on the experiences of TB patients and the operation of the evacuation program, this research focuses on the initial reports of tuberculosis in the eastern Arctic in the 1920s. Prior to the 1920s, tuberculosis was extremely rare in the region but by the mid 1930s, a TB ward was opened on Baffin Island, a sign of the growing threat of the disease. The emergence of TB in the region, marked by signs of extra-pulmonary infection, occurred as the Canadian government operated an emergency food ration program to alleviate periodic hunger among the Inuit. Dehydrated meat was provided from bison located at Wainwright, Alberta. Testing at the time of slaughter showed that the herd was seriously infected with disease. Infection from the Wainwright herd to other animal populations is well documented. This study is the first to link infection in the Wainwright herd with the outbreak of disease in a human population.

METHODS: This paper considers the relationship between TB among bison on the northern Great Plains and the emergence of the disease among the Inuit in the eastern Arctic. Data on the health of the bison herd was collected from veterinary records of Parks Canada, the organization that brought the species back from the brink of extinction. Canadian government correspondence was used to uncover the logistics of the food program including the distribution of the meat in the north and the debate over the use of the meat as food. Medical records and correspondence of officials in the north were used to illustrate the growing recognition of TB as a threat to human health in the Arctic.

RESULTS: This examines zoonotic disease transmission in the past. It establishes the presence of disease in herd of bison managed by the government of Canada. It considers the debate over the health of the animals and their fate along with their use in a program that provided meat to the Inuit at the same time that TB was first observed as a growing threat to human health in the region. It follows the chain of infection from an animal population to a new and susceptible human population a considerable distance away.

CONCLUSION: In detailing the relationship between infection in disparate populations of humans and animals in the past, this paper illustrates the value of applying principles of One Health to historical research.

2 LB2 - LATE BREAKERS 2 - SALON CD

Alveolar echinococcosis – An emerging zoonosis in North America?

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Alveolar echinococcosis (AE) is a life-threatening medical condition that occurs when people are infected by the zoonotic cestode *Echinococcus multilocularis*. In the northern hemisphere, this parasite cycles between wild canid definitive hosts and rodent intermediate hosts, and people are accidentally infected by ingesting eggs shed in the fecal matter of infected foxes, coyotes, wolves, or dogs. Until recently, the distribution of *E. multilocularis* was thought to be limited to two geographic foci in North America- the Northern Tundra Zone and the North Central Region; however, reports in dogs and wild canids from outside these regions suggests that the distribution is expanding. Cases of domestic dogs infected with the larval stage of *E. multilocularis* (rather than adult cestodes) have increasingly been reported since the index case was detected in 2009. Since then, AE cyst material from dogs across all 4 western Canadian provinces, and one human from Saskatchewan, have been genetically characterized. First, to confirm identity, parasite DNA was extracted from cysts, cyst fluid or free abdominal fluid, and amplified by a multiplex PCR designed to differentiate *E. multilocularis* from *E. granulosus* and *Taenia species*. Second, to identify haplotypes and analyze biogeographical origin, PCR was conducted at three additional loci - NADH dehydrogenase subunit 2 (nd2), cytochrome b (cob), and cytochrome c oxidase subunit 1 (co1). PCR products were purified, sequenced and aligned, and then compared to other *E. multilocularis* sequences by haplotype network analysis. Our analysis demonstrates that the genetic sequences of *E. multilocularis* causing AE in dogs and a person in Western Canada were more similar to European strains than North American strains. European strains appear to have greater zoonotic potential than endemic strains long established in the central region of North America. This work emphasizes the need to enhance North American capacity to detect and differentiate Echinococcus species in animals and people, and to develop enhanced AE surveillance and reporting in North America as the risk profile of AE might be changing. Finally, a One Health approach to risk mitigation and communication regarding AE is needed, involving (and not limited to) wildlife managers, urban planners, veterinarians, and medical professionals.

3 LB2 - LATE BREAKERS 2 - SALON CD

Students' experiences during One Health field attachment: A case study of One Health Institute in Makerere University, Uganda

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BACKGROUND: Increasingly, it is getting clearer that solving complex global health problems requires interdisciplinary, intersectoral expertise and cooperation i.e. One Health (OH). Recent global movements and supporting evidence, including the report of the commission on the education of health professionals for the twenty-first century, have argued for a redesign of health professional education systems to better match the population needs and to produce a workforce that can meet complex health challenges. Universities are testing sites for education where innovative transdisciplinary approaches to training professionals are constantly introduced and refined, including One Health approaches. Makerere University implemented an innovative One Health Institute (OHI) in 2016 where undergraduate students were selected from different disciplines. The students were first taken through theoretical principles in OH followed by a field attachment in the communities. The field attachment exposed students to experiential educational opportunities. In this paper, we present students experience and their contributions in solving communities' health challenges.

METHODS: This was a cross-sectional study, utilizing qualitative data collection methods, involving students who participated in the OHI-field attachment and community members in Eastern Uganda. Six focus group discussions (FGDs) and four key informant interviews (KIs) were conducted among the students, while four FGDs and 14 KIs were conducted among community members. All interviews were audio-recorded, transcribed and analysed manually.

RESULTS: Two themes were identified: Students' gains and students' contribution to communities. Regarding students' gains; they appreciated the training sighting gaining skills in communication, team work and collaboration. Through the multi-disciplinary teams, the students appreciated that each discipline had something to contribute towards achieving health in the community. Students also reported a feeling of gratitude and accomplishment. They felt that they made a positive impact to the community by coming up with interventions to some of the challenges that the communities were facing. The students reported participating in creating awareness on water, sanitation and hygiene, prevention of zoonotic diseases like bovine TB and rabies. They also helped in designing interventions such as briquette making by recycling waste and maintenance of safe water sources. The communities learnt and appreciated the concept of OH. The communities appreciated the students' contribution such as improving sanitation and hygiene in schools, abattoirs and markets. In addition, students were reported to raise awareness about general disease prevention and health promotion. Students were reported to exhibit a spirit of team work and collaboration in addition to showing love and care to the communities.

CONCLUSIONS: This exposure helped students experience working in interdisciplinary teams that value inputs from other disciplines and gained OH competencies like communication and collaboration. Adopting this model in university teaching system, is urgently needed as this kind of training imparts skills in disease detection, prevention and response including influenza.

4 LB2 - LATE BREAKERS 2 - SALON CD

A novel vaccine candidate for Salmonella gastroenteritis

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Gastroenteritis (enterocolitis) caused by non-typhoidal Salmonellae (NTS) is one of the most common food borne diseases worldwide. Current global estimates are 94 million cases of gastroenteritis with 150,000 deaths annually. We have characterized a surface-associated polysaccharide capsule that is conserved in pathogenic Salmonella strains, and cross-reactive between the three most common North American groups of NTS: Salmonella serovars Typhimurium, Enteritidis and Heidelberg. We used a combination of random and targeted mutagenesis to generate a Salmonella strain that produces high levels of the capsule antigen, and have established optimal purification conditions. We performed an immunization trial in mice showing that the antigen can induce an immune response when delivered alone, and that conjugating the capsule to an immune stimulatory carrier protein can boost the response. Future challenge experiments with Salmonella will allow us to assess the level of protection achieved.

5 LB2 - LATE BREAKERS 2 - SALON CD

Core Competencies in One Health Education: What Are We Missing?

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BACKGROUND: Today's public health challenges are complex and crosscutting, such as antimicrobial resistance, food insecurity, and outbreaks of emerging infectious diseases. An important step toward synergistically addressing these issues would be to apply consistent One Health core competencies in education, in order to optimally prepare future One Health leaders. It is unclear if and how core competencies are currently being employed in One Health education. We assessed the evolution of existing One Health core competencies, how they are being applied in academic programs, and identified gaps that could be filled through our recommendations.

METHODS: We conducted a literature search for core competencies in One Health education, as well as searches for One Health academic degree programs in the United States. Post- secondary degree programs were included if they were taught with an interdisciplinary approach linking human, animal, and environmental health disciplines. We reviewed all available information online and contacted administrators by e-mail for each program.

RESULTS: Three separate groups developed One Health core competencies between 2008 and 2011, which were later synthesized in 2012. Since then, core competency recommendations have not been updated and provided as a public resource. A competency domain related to health sciences was missing from previously recommended competencies.
We identified at least 45 One Health degree programs in the US, of which 27 (60%) were master's level, 10 (22%) were bachelor's level, and 8 (18%) were doctoral programs. The majority (83%) of academic programs were established after 2001. Only 14 (31%) had core competencies publicly available. Among key areas that were evaluated, plant biology, antimicrobial resistance, and law were underrepresented in the programs, whereas epidemiology and environmental health/ecology were well represented.

CONCLUSIONS: The One Heath approach has been embraced by a diverse and growing number of educational programs, but the product of such an education cannot be reasonably anticipated by prospective employers without consistency in One Health training objectives. We recommend One Health core competencies in (i) health knowledge, (ii) global and local issues in humans, animals, plants, and the environment, and (iii) professional characteristics, highlighting the importance of proficiency in health sciences, understanding complexities of real-life health challenges, as well as skills to apply scientific principles to solve them. One Health degree programs could be improved by voluntary commitments to core competencies, including proficiency in at least one health science, and to educating future professionals in disciplines that are both currently well represented as well as disciplines that are underrepresented. Furthermore, program administrators should continue to focus on practical training and communication. It is important to define, develop, evaluate, improve, and continue to refine One Health education, not only in One Health degree programs but also in existing public health, environmental, veterinary, and medical curricula.

6 LB2 - LATE BREAKERS 2 - SALON CD

West Nile disease: possible epizootic transmission cycle in Southern Pakistan

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BACKGROUND: West Nile Virus (WNV) genus *Falavivirus*; is a cause of seasonal fever with neurotropic findings in countries that share borders with Pakistan; however data from Pakistan is very limited. The magnitude and distribution of WNV disease is poorly understood as Pakistan. The human and vector related part of this study was published in Frontiers in Public Health, 2018. In this abstract we have additional findings of WNV seropositivity from Equine animals suggesting maintenance of epizootic transmission of virus in southern region of Pakistan.

METHODS: A cross-sectional study was conducted to determine which flaviviruses were agents of seasonal febrile and related neurological disease in southern region of Pakistan 2015-2017. Patient with acute febrile illness with or without neurological complications were recruited from six different field sites. In addition mosquitoes and equine blood samples were collected (over limited geographical distribution) to see evidence for animal / vector positivity, confirming the epizootic cycle of WNV in Pakistan. For animal samples multispecies competitive ELISA to detect antibodies against WN pr-E envelope protein (cELISA; ID Screen®, West Nile Competition, ID Vet, Montpellier, France) were used. Statistical analyses were performed on clinical data using MedCalc version 17.9.7—64-bit, Logistic regression for dichotomous independent variables was performed. Odds ratios were calculated with 95% confidence intervals.

RESULT: This is the first report of WNV causing neurological disease in human patients in Pakistan. Of 997 enrolled patients presenting with clinical features suggestive of arboviral disease, 105 were positive for WNV IgM antibodies, and 71 of these patients possessed WNV-specific neutralizing antibodies. Cross-reactivity of WNV IgM antibodies with Japanese encephalitis virus (JEV) occurred in 75 of these 105 patients. Patients with WNV infections were more likely to present with altered mental status, seizures, and reduced Glasgow Coma scores when compared with JEV-infected patients. Human WNV cases and vector numbers exhibited a temporal correlation with climate. Additionally we tested 39 equine sera (34 horse and 5 donkey) for West Nile seropositivity, using multispecies competitive ELISA to detect antibodies against WN pr-E envelope protein. The seropositivity in animal samples was 89.5% (34/39) from southern Pakistan.

CONCLUSION: The findings of WNV seropositivity from equine animals and temporal correlation of human WNV and vector numbers suggests maintenance of epizootic transmission cycle of virus in southern region of Pakistan, with horses/donkeys and humans infected in a spillover transmission as “dead-end” hosts. These findings are of great public health (both human and veterinarian) concern and alerts authorities for urgent initiation of one-health based control strategies to prevent epidemic outbreak in the country.

1 LB3 - LATE BREAKERS 3 - GALLERY AB

Genetic diversity of VCC-1 carbapenemase-producing Vibrio cholerae in costal waters of Germany

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BACKGROUND: Recently, we reported on seven VCC-1 producing *Vibrio cholerae* isolates that were recovered from coastal waters of the North and Baltic Sea in Germany. As *V. cholerae* non-O1/-O139 isolates are widely distributed in coastal waters with low salinity and sometimes are associated with wound infections and diarrheal diseases in humans, detailed information on the genetic background of these isolates is necessary to assess the risk for the distribution of this carbapenem resistance.

METHODS: In order to characterize the genetic diversity of the isolates, the genome of the reference strain VN-2997 was determined by PacBioRSII and MiSeq sequencing. PacBio reads were assembled using HGAP followed by mapping of the MiSeq raw reads against the PacBio genome. Bioinformatics, PFGE profiling, and DNA-DNA hybridization as well as conventional PCR were used to reveal the organization of the bla_{VCC-1} gene locus on other *V. cholerae* genomes. Furthermore, resistance testing of the isolates was performed by broth microdilution methods according to CLSI guidelines.

RESULTS: As initial MiSeq sequencing of all prevailing isolates did not reveal the genetic localisation of bla_{VCC-1} within the genomes, further dissection analyses were performed. PFGE profiling revealed that the isolates exhibit two distinct XhoI PFGE-patterns, which is in good agreement with the observed MLST-types of the isolates. DNA-DNA hybridization indicates that one or two copies of bla_{VCC-1} gene are present in different parts of the *V. cholerae* genomes. The presence of one or two bla_{VCC-1} genes did not correlate with the differences observed in the MLST-type or the observed MIC level. The organization of the bla_{VCC-1} harbouring genome region of the individual isolates will be presented in detail.

CONCLUSION: Our study indicates that VCC-1 carbapenemase-producing *V. cholerae* are frequently present in different regions of the German coastline. Despite of the close phylogenetic relationship of the two observed MLST-lineages the bla_{VCC-1} genetic context diverges from isolate to isolate.

2 LB3 - LATE BREAKERS 3 - GALLERY AB

6 years (2010-2016) lag phage of ESBL$_A$- to ESBL$_{Carba}$ in Enterobacteriaceae isolated from wild birds: Towards the start of the environmental spread of Carbapenamse producers in Bangladesh?

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BACKGROUND: The dissemination of extended spectrum beta-lactamases (ESBL$_A$ and ESBL$_{Carba}$) producing *S*, in clinical and environmental settings has become a global concern. ESBLA, (CTX-M-15) has been reported in humans, livestock and the environment, and their isolation frequencies are increasing rapidly worldwide, however, ESBL$_{Carba}$ (NDM, KPC, OXA-48) has not been reported as frequently yet, but hospital wastes are believed to be the source in Bangladesh. To explore the molecular epidemiology of ESBLs (A and Carba) in the environment, birds foraging on hospital wastes in Bangladesh were examined for a period of 6 years (2010-2016) as wild birds are considered as bio-indicator.

METHODS &MATERIALS: During 2010 to 2016, once in every year 110 fecal samples were collected from the crows foraging on hospital wastes in the Rajshahi medical college and hospitals area. Fecal samples were enriched and cultured for ESBL-producers (A and Carba) during 2010 only, but later we screened for only ESBLCarba as it was a serious concern globally during 2011. Isolates were tested for susceptibility to 13 antibiotics including carbapenems according to EUCAST. ESBL producing Isolates were identified and characterized by PCR, rep-PCR, sequencing and MLST.

RESULTS: During 2010, 55% of the crows were positive for ESBLA, however no ESBLCarba.was noticed. ESBL producers were belonging to several species of the Énterobacteriaceae family, for example, E. coli, K. pneumoniae, R. terrigena and E. cloacae. No ESBL$_{Carba}$ was found during the following years (2011-2015). The most common ESBLA-type was CTX-M-15, followed by CTX-M-55, CTX-M-1 and CTX-M-14. During 2016, ESBL$_{Carba}$ was found in 6% of the birds and E. coli, K. pneumoniae was the bacterial species so far recorded. NDM-1, NDM-5 and NDM-7 were found in E. coli and K. pneumoniae. Other than carbapenems and cephalosporins, E. coli and K. pneumoniae were resistant to broad spectrum antibiotics like ciprofloxacin, gentamycin, mecillinam, trimethoprim-sulfamethoxazole and chloramphemicols. Birds were sharing common clones closely related to clinical clones. Birds also shared clinically important sequence types with humans, including E. coli clone O25b-ST131.

CONCLUSION: In conclusion, ESBL$_{Carba}$-producing bacteria with multi-resistance have started to spread from 2016 into the environment of Bangladesh and hospital wastes are attributing to the spread. High level of carbapenem resistant bacteria in the bird population of Bangladesh is worrying, and there is no easy solution in sight.

3 LB3 - LATE BREAKERS 3 - GALLERY AB

Alternative Approaches to Managing Demand for Antibiotic Treatment in Dairying

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BACKGROUND: Regulations on antibiotics in animal agriculture have expanded over the past decade. Antibiotics have been administered to food production animals in feed to either prevent disease or improve feed efficiency, and also therapeutically. Our interest is in dairy farm use where purposes are therapeutic. Our focus is the managerial economics of farm-level antibiotics choices. Research in human medical practice reveals strong patient pressure on doctors to over-prescribe antibiotics (e.g., Linder et al. 2017). Evidence is also accumulating that agricultural decision-makers may, through rational inattention or irrationality, systematically mismanage their inputs (e.g., Perry et al. 2017). We seeks to understand whether opportunities exist for behavioral economics approaches to reduce antibiotics demand on dairy farms.

METHODS: During mid-2017, paper and web surveys were sent to dairy farmers in Wisconsin, Minnesota and Michigan, requesting information about, among other matters, antibiotics input choices on the farm. One question presented a stylized decision environment. Four contexts were provided where in each two parameters were given: probability a single cow can be cured with antibiotics, and loss reduction if cured. Subjects were asked to provide willingness to pay (WTP) to treat the animal. Four versions were sent out. We received 648 responses of which about 480 completed the WTP queries.

RESULTS: Letting p = cure probability and L = reduction in loss then pL = expected reduction in loss. Analysis reveals that mean WTP exceeds expected loss at low losses and approximately equals expected loss at higher losses while strong sensitivity to probability is expressed. Least squares regression estimates confirm that WTP is more probability sensitive than loss sensitive. Sensitivity of WTP to expected loss is about 50%. A separate question for factors importance in management corroborates the finding that probability is the variable that managers focus on managing.

CONCLUSIONS: Our findings should alleviate concerns that growers far over-apply antibiotics from the private optimization viewpoint. What is best for society is a different matter. Our results also suggest that research and outreach efforts and practical tools which seek to better inform growers on probability of infection will be more effective than those addressing loss (e.g., more stringent rules about milk withdrawal from market after treatment) or emphasizing cost, perhaps through user fees as currently implemented in several European countries.
Social Media: In managing antibiotics use, research and outreach efforts and practical tools that seek to better inform milk producers on probability of mastitis infection will be more effective than those addressing loss.

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4 LB3 - LATE BREAKERS 3 - GALLERY AB

Longitudinal field study in evaluating the ecological spillover of antibiotic-resistant Escherichia coli from poultry to humans in rural Ecuador

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Small-scale farming operations in rural communities often prescribe high amounts of antibiotics for industrial meat production breeds of chickens (e.g. broilers, Fig. 1A). In contrast, free- ranging local varieties of backyard chickens (Fig. 1B) receive almost no antibiotics. Recent evidence suggests that backyard chickens in proximity to broiler chickens have increased levels of phenotype and genotype antibiotic resistance. We conducted a seven-month longitudinal study aimed to examine whether backyard chickens and children serve as sentinels for detecting antibiotic resistance spread into the environment from broiler chickens in northwestern Ecuador. *Escherichia coli* isolates were identified from children (*n* = 1144), backyard chickens (*n* = 1323), and 1-day-old broiler chickens purchased from vendor sources (*n* = 253). Isolates were examined for their resistance phenotypes to 12 antibiotics and selected resistance genes. Phenotype resistance profiles fluctuated over time for human and backyard chicken samples. In contrast, broiler chicken resistance profiles remained high for all antibiotics tested. We also detected that households closest to households raising broiler chickens yielded significantly greater phenotype resistance levels among avian and human samples (general additive model; $p < 0.005$). The same *bla*CTX-M gene was detected in both human and chickens. These results likely suggest that small-scale broiler farming operations may function as sources of environmental antimicrobial exposure for the surrounding human and animal populations. Our results indicate that industrial meat-producing animals may introduce antibiotic resistance into other animal breeds, likely through horizontal gene transfer spillover events into backyard breeds and humans.

5 LB3 - LATE BREAKERS 3 - GALLERY AB

Non-prescribed use of antibiotics in peri-urban small-holder dairy farms: A cross-sectional study of 510 farms across 5 cities in India

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BACKGROUND: Non-prescribed use of antibiotics (NPAb) in dairy farms is long reported as a prevalent practice. It is perceived as a serious threat to antibiotic effectiveness in animals and humans and an inevitable challenge to the agroecology and sustainable production of 'healthy' dairy produce. However, the practices have not been adequately investigated. India is the largest milk producer in the world. Small holder dairy farms in peri-urban areas are a significant contributor to this production. This study investigated non-prescribed use of antibiotics by these farmers in India and determinants thereof.

METHODS: Using a multi-stage random cluster sampling, we selected small holder dairy farms (≤10 cows) in peri-urban ecosystems of five cities of India. For quantitative surveys, we used a 'dairy farmer questionnaire' capturing antibiotic usage, farm and farmer characteristics, farming practices and farm environment. For direct observation, we used a 47-item 'observation checklist' assessing dairy and milking area, milk storage area, and hygiene. Milk samples were collected randomly from selected 'wet' cows from each farm and investigated for antibiotic residues. NPU was defined as self-reported use of allopathic medicine within the past 1 year for any of pre-specified 10 animal conditions without advice from a qualified veterinarian and/or detection of antibiotic residues from any of the milk samples.

RESULTS: Total 510 farms were included in the study. The rates of NPU in the study cities were as follows: Bengaluru, 40.2% (30.5-49.9); Bhubaneswar, 35.3% (25.9-44.7); Guwahati, 43.1% (33.4-52.9); Ludhiana, 53.9% (44.1-63.8); Udaipur, 76.5% (68.1-84.8). Antibiotic residues were detected in 14.3% (11.3-17.4) of the total farm. The most commonly used antibiotics in these farms were tetracyclines [10.0% (7.6-13.0)] followed by fluoroquinolones [2.8% (1.5-4.6)] and sulphonamides [1.8% (0.8-3.3%)]. Overall, about 26.2% (22.0-30.8) of the farms reported using medicines (antibiotics/ non-antibiotics) for purposes other than treating disease. The proportion of self-administration was significantly different (p=0.002) between NPU farms (40.6%) and non-NPU farms (27.7%). Half of the NPU farm respondents said that they got advice from others on how to use these medicines as compared to 39.8% among non-NPU respondents (p=0.021). In multivariate analysis, NPU was significantly associated with age of the farm beyond 5 years, self-administration of the veterinary antibiotics by the farmer, ease of administration, popularity of the drug, if the famer had not visited the government veterinary hospital, and use of the drugs for diarrhea among specific conditions in the animal.

CONCLUSION: NPU was widespread across all the cities but rates varied from city-to-city. Antibiotic residues indicated that about 1 in every 7 farms were currently using antibiotics and for common conditions. Rates were likely to be higher in cities that were more likely to use intensified dairy farming. Such widespread use is likely to fuel AMR and reflects unsustainable farming practices.

6 LB3 - LATE BREAKERS 3 - GALLERY AB

Population wide assessment of antimicrobial use in companion animals using a novel data source – a cohort study using pet insurance data

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BACKGROUND: Antimicrobial use in veterinary practice is under increasing scrutiny as a contributor to the rising risk of multidrug resistant bacterial pathogens. Surveillance of antimicrobial use in food animals is extensive, but population level data is lacking for companion animals. Lack of census data means cohorts are usually restricted to those attending veterinary practices, which precludes aggregating data from large cohorts of animals, independent of their need for veterinary intervention. The objective of this study was to investigate the exposure of companion animals to antimicrobials at a population level.

METHODS: A retrospective cohort study was performed using a novel data source; a pet insurance database. The rate of antimicrobial prescribing, and the rate of prescribing of critically important antimicrobials, was measured in a large population of dogs (813,172 dog-years) and cats (129,232 cat-years) from 2013 - 2017. Factors affecting the rate of prescription were explored using Poisson regression.

RESULTS: There were 222,069 dogs and 37,732 cats registered in the database in 2013. This increased to 385,915 dogs and 60,807 cats over the study period to the end of 2016. A total of 611,788 courses of antimicrobial treatment were prescribed. The incidence rate of antimicrobial prescribing was 5.8 prescriptions per 10 dog years (95% CI 5.8-5.9 per 10 dog years) and 3.1 prescriptions per 10 cat years (95% CI 3.1-3.2 per 10 cat years). Claims were submitted on average for 35% of insured dogs and 21% of insured cats each year. Among animals that had an insurance claim submitted, other than for routine preventative health measures (vaccination, parasite control, desexing), 53% received systemic antimicrobials (48% of cats and 54% of dogs). Critically important antimicrobials accounted for 8% of all the antimicrobials prescribed over the 4-year study. With the exception of 3rd-generation cephalosporins in cats, no other CIA represented more than 5% of the antimicrobial use in a species. Cats were 4.8-fold more likely than dogs to be prescribed 3rd-generation cephalosporins. A seasonal influence on prescribing was seen for dogs and cats. There was a small, but significant, reduction in the year-on-year rate of exposure to antimicrobials, after adjusting for species (RR 0.99, 95% CI 0.986-0.997, P=0.002).

CONCLUSIONS: The level of antimicrobial exposure in dogs and cats was less than half that for the coincident human community. Data such as this provides a unique opportunity to monitor antimicrobial prescribing in veterinary medicine, which is a critical component of optimal antimicrobial stewardship. While restricting all off-label use of antimicrobials in animals in Australia is likely to be detrimental to antimicrobial stewardship measures, and animal welfare in general, it may be necessary to restrict the use of 3rd-generation cephalosporins in this manner to reduce the inappropriate use of this antimicrobial.

THE 5TH INTERNATIONAL ONE HEALTH CONGRESS

POSTER ABSTRACTS

ONE HEALTH SCIENCE

PATHOGEN DISCOVERY

P001 - OHS A01 - PATHOGEN DISCOVERY

Characterisation of Viruses in Australian Wild Birds using Metagenomics

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BACKGROUND: Birds can be infected or act as carriers for pathogens that can be transmitted to other species including humans. Migratory birds crossing national and international borders may provide long-range dispersal of pathogens to novel hosts. In addition, environmental factors, such as human encroachment or climate change, may modify the epidemiology of pathogens through changes in migration patterns. Australia is home to more than 800 bird species including endemic, introduced and migratory species. To date, there has been limited virus population (virome) studies in birds, and as such, there is little known about virome diversity and factors impacting virome ecology. Our research project aims to address this knowledge gap through method development for avian virome detection, characterisation and relative quantitation using a combination of novel techniques and ecological information.

METHODS: Fresh bird faecal samples were collected from Victoria, Australia. Samples were processed using different biophysical methods like filtration, ultracentrifugation for virus enrichment followed by nuclease treatment, nucleic acid extraction and cDNA preparation. Library preparation was then carried out and next-generation sequencing performed using IonS5 genetic sequencer. An optimum method was thus formulated for successful identification of viruses which also enabled an additional outcome by providing an insight into the gut biosphere of the bird.

RESULTS AND CONCLUSIONS: We successfully determined both DNA and RNA viruses from the bird faecal samples. For example, we characterised a total of 12 and 9 viruses in Pacific Black Ducks and Muscovy Duck, respectively. Among the 21 viruses, we found 9 avian host associated viruses belong to the virus family *Paramyxoviridae, Coronaviridae, Picornaviridae, Reoviridae, Caliciviridae, Adenoviridae* and *Parvoviridae*. We found 8 insect viruses from which 3 belonged to the virus families *Mesoniviridae, Dicistroviridae* and *Iridoviridae* and 5 unclassified RNA viruses. We also characterised 2 plant viruses belonging to *Partitiviridae* and *Endornaviridae* and 2 bacteriophages belonging to *Myoviridae* and *Podoviridae*. Some of the viruses were ~30% different in their genetic sequence to currently known viruses. Some viruses with relative high differences in their nucleotide sequence showed highly conserved amino acid sequences. Other
viruses were highly similar to viruses previously found in geographically remote locations suggesting that these may be more widespread than formerly thought.

In addition to viruses, the technique also characterised ribosomal RNA and host mitochondrial genes such as the COX1 and cytochrome B genes providing identification of the host species (if unknown), an insight into the “ribosomal activity microbiome”, food eaten such as plants or insects, and gut parasites such as tapeworms and thus provide correlation with non-avian host associated viruses found. This technique could, therefore, be used as an efficient and cost-effective screening tool for assessing the gut biosphere of wild birds and has application to other species including humans and other animals.

P002 - OHS A01 - PATHOGEN DISCOVERY

From SADS to STING: a story on bats

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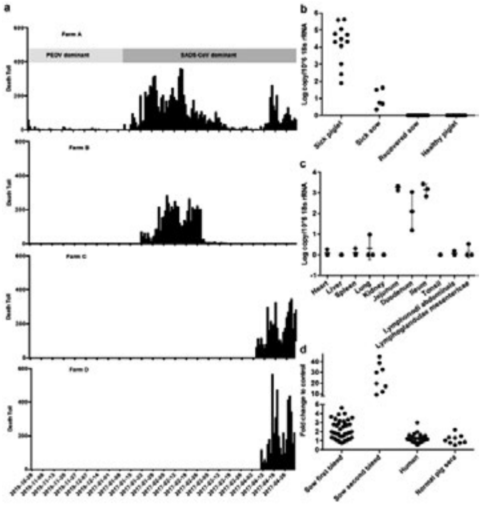
BACKGROUND: Cross-species transmission of viruses from wildlife animal reservoirs poses the greatest threat to human and animal health. Bats have been recognized as one of the most important reservoirs for emerging viruses. Jump of bat-origin coronaviruses into human population via intermediate animals was responsible for the high-impact emerging zoonosis like SARS, Ebola, Hendra, Nipah and Marburg viruses. The key questions are whether there will be new virus spillover from bats to human society? Why and how bats carry these deadly viruses?

METHODS: We answer these questions from two different angles: firstly, we did long-term molecular epidemiology on bats and their surrounding environments for known and unknown viruses; secondly, we tried to uncover the mystery of the coexistence of bats and viruses by studying bat innate immunology.

RESULTS: Here, we report virological, epidemiological, evolutionary and experimental infection evidence that a novel HKU2-related bat coronavirus, Swine Acute Diarrhea Syndrome coronavirus (SADS-CoV), is the etiological agent responsible for a large scale outbreak of fatal disease in pigs in China with the death of 24,693 piglets across four farms (Figure 1). Significantly, we identified SADS-related CoVs with 96-98% sequence identity in 11.9% (71/596) of anal swabs collected from bats in Guangdong Province during 2013-16, predominantly in Rhinolophus spp. horseshoe bats that are known reservoirs of SARS-related CoVs. We then ask why this spillover was from bats (again)? Our previous studies on bat innate immunity demonstrated that bat type I IFN locus was contracted but IFNα was constitutively expressed, which may contribute to a special ability of bats coexistence with viruses. Here we have another evidence of unusual bat immunity: we observed dampened STING-dependent interferon response in bats due to the replacement of the highly conserved serine residue (S358), while reverse mutation by introducing S358 restored their functionality in interferon activation and virus inhibition.

CONCLUSIONS: Another SADS-CoV spillover from bats to human society highlights the importance in identifying coronavirus diversity and distribution in bats to mitigate future outbreaks that threaten livestock, public health and economic growth. It also prompted us to study why bats can serve as deadly virus reservoir hosts. The nature of the weakened but not entirely lost functionality of STING and bat IFN system may have profound impact for bats to maintain the balanced state of "effective response", but not "over response" against viruses.



Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin; bat immunity is unusual.

P003 - OHS A01 - PATHOGEN DISCOVERY

Detection of MERS-related Coronavirus in Wrinkle-lipped free-tailed bats

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BACKGROUND: Middle East respiratory syndrome coronavirus (MERS-CoV) belongs to lineage C of *Betacoronavirus* (betaCoV), which can infect multiple host species including humans, camels, hedgehogs and bats. Thailand houses at least 140 different bat species, including *Tylonycteris* spp., *Pipistrellus* spp., and *Taphozous* spp. These species have been reported to carry MERS-related CoV in other countries. MERS-like CoV has previously been detected in unidentified dried bat guano from a cave in Ratchaburi province, where 14 bat species are known to roost. Of these, wrinkle-lipped free-tailed bat (*Chaerephon plicata*) population is the most abundant, with approximately 2.5 million bats. Because of the close contact between guano miners, bats and other small mammals, this site presents a significant risk interface for the transmission of bat-borne viruses. In this study, we describe the detection of two CoVs closely related to MERS-CoV from wrinkle-lipped free-tailed bat.

METHODS: Bats were harvested on three occasions from a cave in Thailand, in March and October 2013, and October 2017. Rectal swabs were collected from individual bats and immediately put into Lysis buffer. MERS-CoV was detected using Pan2c-heminested RT-PCR, through amplification of RNA-dependent RNA polymerase gene of betaCoV. Sequencing was performed from positive PCR specimens for confirmation, and phylogenetic analysis was used for characterization of viral species.

RESULTS: In March 2013, 102 wrinkle-lipped free-tailed bats were captured, while in October 2013, three bat species were captured for the study including 19 wrinkle-lipped free-tailed bats, 19 black-bearded tomb bats (*Taphozous melanopogon*) and 62 Horsfield's leaf-nosed bat (*Hipposideros larvatus*). There were no PCR positive CoV specimens collected in March 2013, while 18 PCR positive CoV were detected in October 2013 specimens (18/104=17.3%). Phylogenetic analysis of the 152 base pair amplicon revealed that all 6 CoVs detected from wrinkle-lipped free-tail bats belonged to lineage C of betaCoV or MERS-related CoV (6/19 = 31.6%). On the other hand, 12 CoV positive samples belonged to lineage D betaCoV, (1/19 black-bearded tomb bats ((5.3%) and 11/62 Horsfield's leaf-nosed bats (17.7%), respectively). MERS-related CoV were detected in 29 of 150 (19.3%) wrinkle-lipped free-tailed bats collected in October 2017.

CONCLUSIONS: This study reported betaCoVs closely related to MERS that were detected in wrinkle-lipped free-tailed bats, but not from other two bat species captured at the same time from the same cave. Higher CoV detection in October than March raises the hypothesis of seasonal infection of CoVs in bat.

P004 - OHS A01 - PATHOGEN DISCOVERY

Discovery of Ecologically Distinct Clades within Pathogenic and Non-pathogenic Bacterial Taxa

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BACKGROUND: Bacterial populations rapidly split into ecologically distinct lineages (ecotypes), yielding multiple ecotypes per recognized species taxon. In the case of pathogens, it is useful to identify all the ecotypes within a species taxon because this may allow us to characterize unknown pathogenic populations before they cause human disease. To help identify newly divergent ecotypes, we have developed the algorithm Ecotype Simulation, which discovers sequence clusters that are most likely to represent ecologically distinct populations. Our aim here is to discover the rate of diversification for some bacteria exemplifying different lifestyles (free-living phototrophs, free-living heterotrophs, and pathogens).

METHODS: We applied Ecotype Simulation to species exemplifying different lifestyles: free-living heterotrophs (*Bacillus subtilis* from Death Valley), free-living phototrophs (*Synechococcus* from Yellowstone hot springs), and pathogens (*Legionella pneumophila* clinical isolates and *Campylobacter jejuni* clinical, animal reservoir, and environmental isolates). We tested whether increasing the resolution of the analysis, from a single gene to the whole core genome, reveals more putative ecotypes. We tested whether the putative ecotypes demarcated by Ecotype Simulation were ecologically distinct, based on associations with different microhabitats, and whether each putative ecotype was ecologically homogeneous, based on genomic analyses.

RESULTS:
Synechococcus. Ecotype Simulation based on a single gene yielded dozens of ecotypes within each taxon, and these ecotypes were ecologically distinct from one another. Each hypothesized ecotype appeared to be ecologically homogeneous, indicating a slow rate of speciation.
Bacillus. Ecotype Simulation based on three genes yielded dozens of putative ecotypes per species taxon, and habitat associations indicated ecological diversification among hypothesized ecotypes, as for *Synechococcus*. However, genomic analyses revealed extreme ecological heterogeneity within each hypothesized ecotype, indicating that speciation was much too rapid to be revealed by low-resolution (single-gene) analysis.
Legionella pneumophila. Ecotype Simulation hypothesized eight ecotypes within *L. pneumophila*, and several were confirmed to be ecologically distinct by differing in their associations with different amoeba species.
Campylobacter jejuni. We are applying Ecotype Simulation to a set of 884 *C. jejuni* isolates from a diversity of sources. We will determine how the number of hypothesized ecotypes increases by including more genes, and will test whether the hypothesized ecotypes differ in their habitat associations.

CONCLUSIONS: Bacterial taxa can differ greatly in their rates of ecological diversification. For example, the obligate human and amoeba pathogen *Legionella pneumophila* has diversified into a modest number of ecotypes, while the free-living *Bacillus subtilis* has diversified into an astronomical number of ecotypes. Identifying and characterizing all the ecologically distinct groups within any pathogenic taxon will allow us to anticipate the transmission and symptoms properties of not yet characterized clades before they can cause human disease.

P005 - OHS A01 - PATHOGEN DISCOVERY

Geostatistical analysis of the density of primary reservoir of plague in Armenia

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BACKGROUND: The common vole (*Microtus arvalis*), is the primary and most numerous plague reservoir in the Transcaucasian high mountain natural plague focus in Armenia. This research sought to identify significant areas for epidemiological and epizootic research by using ordinary kriging to create a prediction map to identify areas where the common vole density, and thus plague risk, will be higher than normal.

METHODS: Using the Geostatistical Analyst module in the ArcGIS program and the Kriging method, the density of common voles across the entire territory of Armenia was analyzed. Year-long observations from 2017 throughout the territory of Armenia were used to calculate the density of common voles by the route method. Each area of the route lines was at least one hectare. All the inhabited colonies of a common vole were counted on these sites, and at least five of them were dug out, with the catch and counting of all the animals living in it. The density of common voles per hectare (D) was calculated by the formula:

$$D = \frac{N}{n} x\, n_1$$

where (N) is the number of caught animals, (n) is the number of excavated colonies, and (n_1) is the number of counted colonies on the route. A geodatabase was created from the collected data to facilitate geostatistical analysis.

RESULTS: The density of the common vole in spring varied from 0 to 19 animals per hectare and was more stable in the mountain meadow and sub-alpine zones, where the humidity is moderate and vegetation is varied. Summer data showed that the density fluctuated from 27 to 66 animals per hectare, and the voles were concentrated in mountain steppe zones to agricultural land. In the autumn, the density varied from 46 to 107 animals per hectare, and the index was higher than the average in the sub-alpine meadows of the high mountain zones. For a short-term forecast of the density of common vole, for the spring of the next year, geomorphological zones with a high and stable density were identified and mapped. Using the geostatistical analysis, maps were created with interpolated density data of the primary reservoir of plague in Armenia.

CONCLUSIONS: Under favorable climatic conditions for the wintering of the common vole, these areas will be the most optimal zones for the ecology of the common vole and for epidemiological research in the spring of the next year.

P006 - OHS A01 - PATHOGEN DISCOVERY

Towards bat coronavirus isolation – one cell culture at a time.

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BACKGROUND: Bats are known to carry numerous viruses that can potentially infect other animals and humans, resulting in what may range from harmless infections to severe global epidemics. Numerous coronaviruses (CoV) have been found in bats, including the progenitors of Severe Acute Respiratory Syndrome (SARS)- and Middle East Respiratory Syndrome (MERS)-CoVs. The outbreak of SARS-CoV in 2002/03 resulted in over 8 000 cases and a 10% fatality rate, followed by the MERS-CoV epidemic starting a decade later, causing over 2 143 infections and 750 deaths to date. SARS-CoV was transmitted to humans from civets and MERS-CoV from dromedaries. *Neoromicia capensis* CoV (NeoCoV), a novel bat-derived CoV, was recently discovered and is 85% genetically identical to MERS-CoV. Numerous research groups worldwide are involved in the detection and *in silico* analysis of CoV from bats and other animals, producing abundant sequence data yet there remains no data on the functional aspects of these potentially emerging viruses. Although virus isolation is inherently challenging, bat CoV are notoriously difficult to isolate and only two laboratories have succeeded. This study aims to develop tools for- and attempt the isolation of NeoCoV and related CoV in cell culture.

METHODS: Trachea, kidney and lung specimens from a *N. capensis* bat, the host species of NeoCoV, were used to create primary cell cultures using the explant method. Immortalisation was carried out by lentiviral transduction with the large T antigen of Simian Virus 40. Similarly, lung and trachea cell lines have been opportunistically generated from *Rhinolophus clivosus* bats. Bat feacal, urine and saliva samples collected across South Africa were screened for alpha- and beta-CoV by a panel of 3 PCRs per sample. Selected positive samples, with preference for co-infections, were homogenized and applied to various mammalian epithelial cell lines including the above-mentioned cultures and camel-, monkey (Vero e6) - and *Pipistrellus* kidney cells. Culture supernatant was passaged up to 5 times per specimen, cell type and parameter.

RESULTS: Five immortalized cell cultures namely *N. capensis* trachea, lung and kidney and R. clivosus lung and kidney cells were successfully established. After inoculation with virus-containing homogenates no discernible CPE was observed up to 5 passages in culture from two co-infected samples on Vero, *N. capensis-, Pipistrellus-* and camel kidney cells, both in pooled and individual approaches. A highly sensitive real-time RT-PCR has been developed in-house for the screening of passaged supernatants for future isolation attempts.

CONCLUSIONS: Host specificity plays a major role in virus infection. We have successfully produced 5 cell lines from 2 Southern African bat species for the isolation of NeoCoV and related CoV. Although CoV isolation remains a mystery that cannot be resolved in a single study, developing tools for- and reporting it's difficulties will aid in closing this critical knowledge gap.

P007 - OHS A01 - PATHOGEN DISCOVERY

DNA of human bocavirus origin detected in non-human primates in the Democratic Republic of the Congo

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BACKGROUND: Human bocaviruses were first described in 2005 in children with respiratory symptoms of unknown origin, and have since been found to infect people all over the world. DNA of related bocaviruses was also found in gorillas and chimpanzees and it was suggested that human and non-human primate (NHP) bocaviruses diverged from common ancestors and have since coevolved with their host species. The goal of the present study was to screen African NHPs in the Democratic Republic of the Congo (DRC) for the presence of bocaviruses and assess their relationship to known isolates based on their DNA sequences.

METHODOLOGY: Specimens from 20 species of NHPs (620 animals) were collected opportunistically between December 2010 and December 2013 in DRC as part of the global USAID funded Emerging Pandemic Threats (EPT) PREDICT-2 project that aims to increase global capacity for the detection and discovery of viruses at the human-animal interface. Whole blood samples (93%) were collected on filter paper by local hunters from freshly killed wild animals. Other samples were tissue (colon, liver, spleen, lung) from freshly killed wild animals and fresh blood from NHPs located in a bonobo sanctuary, the Kinshasa Zoo, and several touristic sites. Samples were subjected to DNA extraction and a semi-nested broad range PCR assay targeting the Non-Structural gene 1 (NS1) of human and other primate bocaviruses. On positive samples, a set of three additional nested PCR assays targeting NP1, VP1/VP2, and a different NS1 gene fragment were performed. Samples positive for viral DNA were additionally tested with a Cytochrome b PCR assay to confirm the host species. PCR product were assessed and analyzed phylogenetically. All laboratory analyses were performed in the DRC PREDICT laboratory, at the Institute National de Recherche Biomedicale, in Kinshasa, DRC.

RESULT: During NS1 broad range PCR screening, 99% of samples produced a negative result, while putative bocavirus DNA was amplified from 6 samples (1%). Amplified PCR products were sequenced and, following comparison with the GenBank database (BLASTN), were confirmed as bocaviruses. Four of the sequences exactly match the sequence of a published human bocavirus 3 isolate. A fifth positive sample shares 99% nucleotide identity with the same human bocavirus 3 isolate, and the sixth sequence resembles human bocavirus 2, sharing 100% of the nucleotide sequence with several HBoV2 isolates. Followup PCRs and phylogenetic analysis confirmed the clustering of the isolates with human rather than with known NHP bocavirus isolates.

CONCLUSION: Bocaparvoviruses like protoparvoviruses and potentially erythroparvoviruses are able to cross species barriers. Consequently, NHP species could be a source or reservoir for bocaviruses that have the ability to infect humans, regardless of whether these animals are the original source of the viruses or if the viruses have been introduced through human contact.

P008 - OHS A01 - PATHOGEN DISCOVERY

Ten year experience developing one health capacity in Africa

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BACKGROUND: Faced with the conundrum of a high burden of infectious disease yet low capacity for its risk management, representatives of academic and research institutions in 5 Member States of the Southern African Development Community (SADC) – Democratic Republic of Congo, Mozambique, South Africa, Tanzania and Zambia, formed in January 2018 the Southern African Centre for Infectious Disease Surveillance (SACIDS) to address infectious diseases in the endemic settings of Africa, through a collaborative effort between natural and social sciences to advance the understanding of interactions between humans, animals and the environment to improve public and animal health. This was a joint initiative between the public health and animal health universities and national research institutions dealing with infectious diseases of humans or animals. Our working hypothesis was a shared Mission for harnessing innovations in science and technology in order to improve Africa's capacity to detect, identify and monitor infectious diseases of humans, animals and their interactions in order to better manage the risk posed by them.

METHODS: Our core strategy encompasses 3 approaches: (i) functioning as a Virtual Centre pooling the best of human and physical resources across the participating African institutions; (ii) An African coordinated smart partnership of African and non-African scientists that shared the Mission of SACIDS; (iii) theme based research linking subject matter specialists, research students and postdoctoral fellows as a Community of Practice.

RESULTS: Our cohorts of scientists now undertake research programmes that address key aspects of the infectious disease burden in Africa e.g.
Emerging and vector-borne diseases – including developing diagnostic capability for Ebolavirus, risk modelling of mosquito-borne viral diseases;

- Viral diseases that constrain food security and livelihoods
- One Health focus on Mycobacterial infections and on the genomic surveillance of antimicrobial resistance
- Community-level One Health based participatory disease surveillance aided by in-house developed mobile technology applications (AfyaData http://afyadata.sacids.org/about)
- Health and Food Systems analyses.

Over the last 10-years we have enrolled: 19 Postdoctoral Research Fellows; 31 PhD students; 15 MPhil students; 77 One Health based MSc students

Our Smart partnership now includes 26 institutions drawn from within Africa, UK, Europe, USA, Brazil, South and East Asia.

CONCLUSIONS: Out of SACIDS we have generated 2 World Bank designated Africa Centres of Excellence for Infectious Diseases of Humans and Animals- in Zambia and Tanzania.

In the aftermath of the West African Ebolvirus Epidemic, our Theory of Change emphasizes Community Level One Health Security for national and global health security.

SOCIAL SCIENCE AND POLITICS

P009 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Environmental protection as an ethical requirement for community health

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BACKGROUND AND OBJECTIVES: Environmental ethics and sustainable development are inexorably bound together as the decline of environmental conditions affect the population health resulting in increase the morbidity and mortality rate. The objective of this paper is to analyze the different factors contributing to environmental protection identifying the roles and responsibility of government, community and individuals.

METHODOLOGY: To achieve our objectives in this paper, a bibliographic study was applied to collect information from different sources; books, journals and websites. The following key words were used in this search: Environmental factors, Responsibilities in environmental protection, Strategies of protection. The information obtained was organized in chapters covering each stated objective.

FINDINGS: The results were outlined showing the environmental factors affecting community health, the socioeconomic conditions and quality of life and the responsibilities for protection of the environment. The different strategies for environmental protection is outlined in this paper.

CONCLUSIONS: The conclusions of the study is that the main threats to the world health, to stability and even to mankind's existence itself comes from the synergetic interaction of the following three factors: poverty , population and environment.

RECOMMENDATIONS: The study recommended the application of some strategies for better environmental protection such as policy, changing organization behavior, education protection, promoting community educator and strengthen individual knowledge and skills.

P010 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Culling as a Public Health Measure

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BACKGROUND: Millions of non-human animals are killed yearly all over the world to control zoonotic disease outbreaks. Other than intuition, there is very little evidence that culling is effective in the long run or overall more cost-effective than other preventive measures. In fact, the Randomized Badger Culling Trial, the largest trial to date that compared no culling with proactive and reactive culling, persuasively established the ineffectiveness and/or cost-ineffectiveness of culling to control the spread of bovine tuberculosis. This has not deterred the UK government from continuing to kill badgers- 15,548 during 2013-2016 to be exact.

Culling as a public health measure reflects a ‘perfect One Health’ storm,’ as it potentially affects humans, animals, and ecosystems. As a public health policy, it is a meeting grounds for ethics, science, social science and politics. Badger culling in the UK is done in the guise of scientific justification, and has inspired a fair share of government reports, scientific articles, and public discussions. As such, many countries would surely learn from the UK experience, potentially putting their own wildlife at risk. Further, human stakeholders will suffer from direct and indirect consequences of culling of their livestock.

My goal here is to critically review the badger culling policy in the UK, continuing published work. By adopting a normative One Health approach, I hope to salvage the lives of voice-less populations in the UK, namely the badgers. Further, I argue that since culling has been shown largely to be ineffective in reducing disease in cattle, such a policy would mainly harm human stakeholders in the UK, mainly farmers.

METHODS: Analytic analysis

RESULTS: Culling as a public health measure is scarcely supported by scientific evidence and is thus ethically unjustified.

CONCLUSION: One Health aims to benefit humans, animals, and the environment. Public health policies ought to be scientifically justified and ethically defensible. Culling is neither.

P011 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Differential impact of inequity on elimination of HIV in Nigeria: the intersection of policy, programme design and social norm

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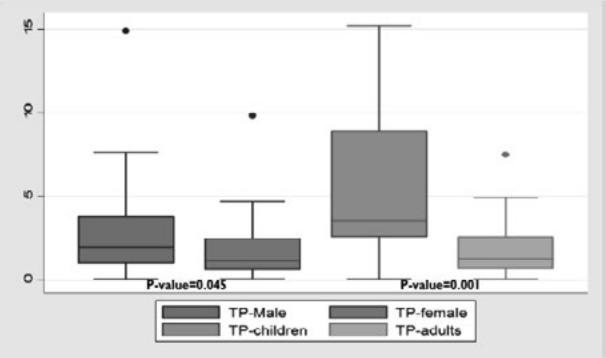
BACKGROUND: In resource-limited and high HIV burden country like Nigeria, women are a key target population for HIV prevention, treatment and support because they are disproportionately burden by HIV. However, health needs of their male counterparts are often neglected based on the assumption that their societal status should facilitate timely access to health care. Extant studies have shown that men are less likely to receive HIV testing, access and adhere to treatment. Despite the worsening health outcomes among men, this has received little global attention. Also, more efforts are concentrated on adults while children are often left behind. This age-gender bias continues to impede HIV control as countries strive to achieve the global Sustainable Development Goal target to end the HIV epidemic. This study measured the impact of age-gender disparity on HIV control in resource-limited setting by using Nigeria as a case study.

METHODS: We conducted trend analysis from 2010-2015 on HIV tipping point ratios (TPR) by using the validated National HIV programmatic data and spectrum estimates for the 36 states and Federal Capital Territory. A cut-off ratio of <1 was used to depict effective control of HIV infections by showing that the HIV incidence falls below rate of ART initiation. Differences in ratios across the years were assessed with Mann-Kendall test for trend. Mann Whitney U test was used to explore age and gender differences. We generated Choropleth thematic maps to visually inspect their distribution. The significance level was set at α=5%.

RESULTS: From 2010-2015, the national TPR has significantly declined from 2.2 to 1.1; [S= -11, p=0.03]. In 2015, Nigeria significantly achieved safe TPR of 0.9 for adults but not for children (3.6); [U= 288.5, p=0.0001]. Despite the yearly variations, the TPR for 2015 was marginally significantly lower for female than male, 0.9 and 1.5 respectively, (U=506, p=0.045). It was observed that 4(10.8%) of the states have reached a safe TPR for children, compared to 16(43.2%) observed for adults (z=-3.1, p=0.002). More (43.2%) states have attained safe TPR for females compared to males (24.3%) [z=1.7, p=0.09].

CONCLUSIONS: As is the case in Nigeria, age-gender bias has led to an undesirably slow decline in new HIV infections among men and children. This signals an urgent need to ensure that strategies for the attainment of the 90-90-90 global targets by 2020 adequately capture HIV prevention and treatment for these population-groups in particular men and children.



P012 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Expanding the umbrella of One Health – are there any outer boundaries or internal conflicts?

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BACKGROUND: The One Health approach has been expanding from a rather narrow approach combining veterinary medicine and human medicine to a wider approach comprising research from natural sciences, social sciences and humanities. Such a process of expanding the boundaries of the approach can cause shifts in core scientific areas and values involved. This study will analyse whether there are any outer boundaries or internal conflicts within this expanded One Health approach by a comparison with similar competing approaches such as EcoHealth, Planetary Health and One Welfare.

METHODS: The method is a study of underlying philosophical and scientific values, theories of science, and the core scientific fields included within these approaches. These aspects are compiled using the umbrella depiction tool once developed by One Health Sweden in collaboration with the One Health Initiative Autonomous *pro bono* team.

RESULTS: There are crucial differences between the approaches of One Health (in its wider sense), EcoHealth, Planetary Health and One Welfare, although the awareness of these differences and of the concepts from a theoretical angle appears quite limited among the researchers and stakeholders involved. Difference were found both in core scientific fields as well as in core values. 'Health', which is one of the most crucial concepts for all these approaches, differs considerably in characterization. Furthermore, the relative importance of veterinary and human medicine differs between the approaches. Planetary Health was found to have a distinct human-centred focus, while EcoHealth emphasizes the importance of all life on Earth, but also actively involves health care in underserved communities and indigenous traditional knowledge. The One Welfare concept, on the other hand, is focusing on the links between human and animal mental well-being.

CONCLUSIONS: While it is important to acknowledge that the One Health approach should not be strictly focused on medicine (human and veterinary) only, but also involve aspects such as the ecological aspects of disease transmission, health care systems for various species and also the prevention of non-infectious diseases, researchers involved may want to make sure that a common understanding of the outer boundaries is achieved. In expanding the One Health concept, scientists and others need to be aware of the risk of making it too broad, resulting in inner conflicts and also in a risk of ending up with a 'therory of everything', which will not be particularly useful as a concept in the long run.

P013 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Implications for the United States drawn from European Union experiences with antimicrobial use, policy, and resistance

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BACKGROUND: Spurred on by critical reliance on antibiotic use in healthcare systems worldwide, antimicrobial resistance (AMR) is a preeminent global health crisis. Antimicrobials are also economically important as antimicrobial growth-promotants (AGPs) for livestock being produced as sources of human foods. Due to potential connections between antimicrobial use in food animals and increased AMR identified in zoonotic pathogens, many governments worldwide have enacted or proposed legislation intended to restrict antimicrobial use for livestock production purposes. Starting in 2012, the United States Food and Drug Administration (FDA) began to release a set of industry guidance documents that proposed a phase-out of medically important antimicrobials as AGPs in food animals. Effective January 1st, 2017, these new regulations have left many questions as to their economic and logistical impacts on the food animal industry, as well as their effects on food animal and human health. The European Union and its member states have had similar regulations for several decades now, with the constituent nations of Sweden and Denmark being particularly strong examples. These nations and their data-collection infrastructures offer a wealth of information as to the possible economic and health effects of AGP restrictions in the United States. The purpose of this project is to propose possible implications of the recent AGP regulations in the United States, and make recommendations that alleviate the impact of any negative implications.

METHODS: Information was compiled from peer-review research, white papers, legislation, regulations, official reports, and position statements from a variety of European and United States governmental organizations, non-governmental organizations, independent researchers, scientific bodies, intergovernmental organizations, and interest groups.

RESULTS: Similar to the European Union, the new regulations in the United States will likely result in increased therapeutic use of livestock antimicrobials, increased weanling pig mortality, and decreased AMR prevalence in some bacterial species. The new FDA regulations are expected to have a negligible effect on the continually-increasing AMR bacteria prevalence in human populations. Economically, the new FDA guidance regulations will provide protection against negative trade impacts caused by food import markets that disfavor AGP use, while increasing appeal to niche AGP-free markets. A resultant 1-3% increase in food animal product prices will likely be observed in the United States.

CONCLUSION: To help mitigate AMR spread in bacteria, health and agricultural agencies and industries in the United States and the European Union need to continue advancing science-based judicious antimicrobial usage in both animals and humans. They also need to define comparisons between human and animal antimicrobial doses, and expand and standardize monitoring and surveillance infrastructures for antimicrobial usage and resistance prevalence in both humans, livestock, and other animals.

P014 - OHS A03 - SOCIAL SCIENCE AND POLITICS

International Circumpolar Partnerships in One Health; Role of the Arctic Council

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Complex impacts of climate change on the Arctic call for regional multidisciplinary stakeholder collaborations to advance understanding of emerging health threats and improve resiliency of Arctic communities and the ecosystem. Under the aegis of the Arctic Council's Sustainable Development Working Group (SDWG), Canada, Finland and the U.S., are collaborating on a project, *One Health- One Arctic* with the view to regionalize One Health approach in the Arctic. The project aims to develop a multidisciplinary One Health network of the Arctic to disseminate information between the Arctic states, regionally as well as locally. Our proposal is to assemble a panel of 5 speakers, including an Indigenous representative, to highlight recent accomplishments under the SDWG's One Health arena as well as Finland's plan to establish a circumpolar animal health network. We would also showcase the outcomes of a tabletop exercise carried out in Alaska (February 2017), as well as the roles being played by the Local Environment Observation Network (LEO) and the International Circumpolar Surveillance System (ICS) to improve the monitoring of diseases transmitted by animals to humans, animal health, food and water safety and adaptation to climate and environmental change.

P015 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Ensuring the viability and sustainability of One Health Platforms: Is Tackling Anti-Microbial Resistance the Answer?

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BACKGROUND: One Health Platforms come in many shapes and sizes, but share a common purpose of promoting cross-disciplinary and cross-sectoral collaboration among animal, human and environmental health stakeholders. Many of these platforms have been established and supported to address the threat of zoonoses with pandemic potential, such a Highly Pathogenic Avian Influenza, Ebola and MERS. However, during 'peace time', namely the absence of major outbreaks, these platforms struggle for national political and financial support. In addition, animal and environmental health professionals face difficulties in garnering scarce resources, especially in competition with human health priorities. Anti-Microbial Resistance, since it is a known, ubiquitous and cross-cutting threat, may be the ideal problem for One Health Platforms to address to demonstrate current and future value to diverse advocates and skeptics.

METHODS: The primary focus is on OH Platforms in Africa and Southeast Asia whose origins stem from either the HPAI outbreaks in the past 10 years or in reaction to the West Africa Ebola outbreak. Many of these platforms are being supported by the USAID Preparedness and Response (P&R) project, as well as other donors. A brief survey and follow up telephone interviews with Platform staff will be conducted. In addition, the paper will use the P&R project Platform Self-Assessment process and tool. It outlines a path to organizational maturity against six broad capacity categories—structure, leadership, multi-sectoral integration, communication and information exchange, planning/M&E, and funding. The output of the assessment results is an aggregate score between 0 and 4 for each country, corresponding to both a stage on the maturity model (Beginning, Developing, Expanding, or Mature) and progress toward functional multi-sectoral coordination mechanisms as defined by the Joint External Evaluation (JEE) initiative.

RESULTS: Currently, Indonesia, Bangladesh, Uganda, Kenya and Cameroon have incorporated AMR into their One Health Platform mandate. The paper will examine the basis for including AMR and the extent to which animal and environmental health professionals are directly involved in the AMR program. Scores from the P&R Self-Assessment tool will augment the information gained from the survey and interviews. Specifically, the results will show whether and how One Health Platforms are evolving beyond their original focus on pandemic threats.

CONCLUSIONS: The paper provides policy makers and One Health practitioners a better understanding of the type and scope of problems that One Health Platforms need to tackle to improve public health and well-being. This includes recommendations on how animal health and environmental health professionals and stakeholders can participate more equally and effectively with their human health counterparts.

P016 - OHS A03 - SOCIAL SCIENCE AND POLITICS

The Health Belief Model and water testing behaviour: A qualitative study of rural well owners

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BACKGROUND: In Alberta, over 400,000 residents rely on well water for domestic use. Private water wells are more vulnerable to waterborne disease outbreaks with more than 45% of waterborne disease outbreaks occurring in rural non-municipal water supply systems. This public health issue is exacerbated by the fact that low proportions of private well water owners adhere to water quality testing recommendations set out within their jurisdictions.
Studies across North America have reported a low compliance towards water testing recommendations. In Alberta less than 11% of well water owners test their water on an annual basis. Recommendations for well testing within Alberta state that well owners should conduct testing at least once per year for bacterial contamination and at least once every 3 to 5 years for chemical contamination.
Health theories play a role in explaining health behaviours. Well water quality testing can be contextualized as a preventative health behaviour. The Health Belief Model (HBM) has been used to explain health behaviour change. The aim of this study is to explore and understand factors influencing well water owners' decisions to conduct water quality testing as viewed through the theoretical lens of the HBM.

METHODS: In depth, semi-structured interviews were conducted with 20 well owners in Alberta. Participants had to be at least 18 years of age and must have had a water well which they used for domestic purposes. Interview sessions were conducted between May and August 2017. The major coding categories based on the HBM were developed though the questioning route with minor codes and sub-themes developed iteratively. Themes were developed according to the codebook and a framework analysis was used to populate the thematic categories based on the HBM with direct quotations from participants through indexing.

RESULTS: Thirteen male and seven female well owners participated. Participants statements were evaluated to assess how well they endorsed components of the HBM. The majority of well water owners had low perceived susceptibility towards well water contamination despite the severity of well water contamination being appraised as high. The benefits of well water testing were perceived as high despite there being notable barriers to conducting water tests. Finally, all participants had high self efficacy and were able to go through the process of water testing as a component of the study.

CONCLUSIONS: The major findings from this study revealed that overall perceived susceptibility to well water contamination was low, perceived severity of contamination was often viewed as high, barriers to water testing were low and the benefits to water testing were low. These findings are important in informing and tailoring messages delivered in well stewardship programs, as well as guiding policy for health agencies responsible for well water testing in Alberta.

P017 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Politics before the First Cooperative Clinical Cancer Trial in Canada and Policies Thereafter

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Clinical cancer research in Canada entered a new phase in 1971. That year, the National Cancer Institute of Canada agreed to launch and support a multidisciplinary cooperative clinical trials program. The first collaborative randomized controlled trial (RCT) for the treatment of advanced Hodgkin's disease got underway in medical centers across the country in December 1971. At the same time in the United States, the National Cancer Act came into effect. To what extent were these Canadian and American developments coincidental? I argue that the advent of cooperative clinical trials program in Canada was not a coincidence but a corollary of the US declaration of war on cancer. Evolution of the Hodgkin's disease trial serves as a good example to demonstrate how a growing collaboration among Canadian and American doctor-investigators brought about a large-scale national study. The latter became a prototype of further cooperative RCTs in Canada over the 1970s.

These developments also ushered in a systematic development of Canadian policies on optimal conditions for the organization of cooperative clinical trials. I analyze constituents of this program historically to explain why certain forms of cancer came into focus for leading Canadian therapeutic radiologists and chemotherapists in the process of their interaction with American colleagues and regional healthcare administrators. I conclude that particular professional interests and practices in radiotherapy and medical oncology became accommodated within one cooperative group owing to a nexus of national and local needs. Importantly, the design and implementation of clinical trial protocols reconciled contending evidential paradigms of physicians, radiotherapists and chemotherapists through epistemological and political means.

I build on the work medical historians and sociologists of medicine, like Peter Keating and Alberto Cambrosio, to show how the RCT method made it possible not only to sideline inter-professional disagreements on innovative cancer treatment modalities, but also to form clusters of investigators in a national network that induced a multi-level human subject research regulation. Drawing on archival records from the clinical trial committees, doctor-investigators' correspondence, and institutional papers from associated public health bodies, I trace the emergence of the cooperative clinical trials program and the related policy-making in Canada. It is instructive to draw a parallel between a contemporary organization of clinical cancer research and the past initiatives of medical professionals so as to appraise imbalances in and challenges of the domain that brings innovative treatments and procedures to the patient's bedside.

P018 - OHS A03 - SOCIAL SCIENCE AND POLITICS

High level of Pesticide Biomarkers among Bangladeshi villagers

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BACKGROUND: Pesticide use in Bangladesh increased over 13 times from 1977 to 2009. In 2008, 2009, and 2012, clusters of acute severe neurologic syndrome were suspected to have been caused by unintentional acute pesticide poisoning. Despite the potential morbidity and mortality, there is a lack of systematically collected data in Bangladesh on background pesticide exposure levels; this makes it difficult to assess the impact of pesticides on morbidity and mortality and determine the contribution of pesticides towards acute poisoning events. We aimed to assess biomarkers of pesticide exposure among individuals living in two rural farming villages near Dhaka where a previous outbreak occurred.

METHODS: During 2013-2014, we conducted four cross-sectional assessments (three months apart) in two villages with1,938 residents. Each time, we selected 80 participants from two villages (40×2) using a stratified (≤10 and >10years of age) random sampling technique, for a total of 320 villagers. We recorded information on demographics (age, sex, etc.) and 24 hours food and environmental exposure using a questionnaire and collected urine samples. Urine samples were analyzed by the U.S. CDC laboratory for commonly used pesticide metabolites using semi-automated solid phase extraction method. For each metabolite, we calculated the percentage of persons with concentrations greater than the limit of detection (LOD) and percentiles. We adjusted for variation in urinary dilution using creatinine concentration. We compared results to the United States National Health and Nutrition Examination Survey (NHANES) because it represents levels in a relatively un-exposed population and thus can serve as a reference group.

RESULTS: Respondents median age was11 years (IQR 6-34years) with 53% male. The participants with detectable levels was highest for the organophosphate-specific metabolites for Para-nitrophenol, PNP (100%), 3,5,6-trichloro-2-pyridinol, CPM (97%) and Diazinon, OXY2 (68%). Metabolites of synthetic pyrethroidconcentration greater than LOD of 3-phenoxybenzoic acid (OPM) was 77%, trans-3-(2,2-dichlorovinyl)-2,2-dimethylcyclopropane carboxylic acid –TCC) was 7% and 4-fluoro-3-phenoxybenzoic acid-4FP was 2(0.6%).15% respondents had Dichlorophenoxyacetic-24D acid above LOD. No significant variation exists in the distribution of village, age, sex for each the metabolite's exposure (>LOD) except for 24D which was more common among children. The creatinine corrected concentration(μg/g)of organophosphate metabolites(OXY2, PNP, CPM), pyrethroids (4FP and TCC) and herbicide-25T in the urine exceeded reference levels (above the US NHANES 95thpercentile), suggesting that residents of these villages were exposed to much higher levels of these pesticides metabolites in the environment than the general US population.

CONCLUSIONS: This study measured the baseline pesticide metabolite concentrations among Bangladeshi villagers over a full one-year period; six of eight metabolites were markedly elevated compared to the reference group. Data from this study can be used for comparison in future pesticide biomonitoring studies or for reference levels in future outbreaks in rural Bangladesh. Strategies to reduce these exposures should be considered.

P019 - OHS A03 - SOCIAL SCIENCE AND POLITICS

One Health surveillance for brucellosis in Armenia: Approaches and a path forward for veterinary services

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BACKGROUND: Brucellosis is one of the most widespread zoonotic diseases in Armenia. While the number of confirmed cases of brucellosis among livestock has remained stable in the past two years, there has been no observed improvement of the brucellosis epidemiological situation, and control efforts put in place thus far have been cost-ineffective. However, the true prevalence of brucellosis in animals and humans in the country is unknown, and the full epidemiological situation has not been properly evaluated. The main goal of this study was to identify the main gaps in the current brucellosis surveillance system among livestock in Armenia.

METHODS: As part of Phase 1 of the “One Health Surveillance for Brucellosis in Armenia” project, funded by the US Department of Defense, brucellosis surveillance systems in Armenia were qualitatively assessed. Information was gathered through in-person meetings with local authorities from the National Centers for Disease Control and Prevention and State Service for Food Safety and with other relevant stakeholders at central and peripheral levels. Relevant data and documents provided by local authorities or available in the literature were also reviewed. The assessment focused on available reporting systems, data flow aspects (including data ownership, responsibilities, legal context, data formats, and interfacing [e.g. paper to electronic]), available data management systems at all levels, and interaction and communications between Ministry of Health and Ministry of Agriculture authorities at various levels.

RESULTS: Multiple gaps, as well as opportunities for the development of a One Health surveillance system, were reported by the assessment team. The lack of an official real-time information exchange system between public health and veterinary health authorities is a major gap, and the revision of legislative framework to enable the official exchange of information is currently underway. Other major gaps identified include:

- One common surveillance scheme that does not account for the unique epidemiological situation and differing prevalence rates of each region.
- Lack of data on risk factors and epidemiological parameters. Lack of capacity for data analysis.
- Absence of animal identification and registration systems.
- Lack of surveillance in swine population, which is particularly important in rural areas with reported human cases of brucellosis.
- Lack of standardized epidemiological forms.
- The Electronic Integrated Disease Surveillance System (EIDSS) developed and customized to Armenia’s needs is not widely used.

CONCLUSIONS: The findings of this assessment will help in designing a new model for brucellosis surveillance in Armenia. The new model, based on One Health principles, will include regular communication between local veterinary services and public health representatives as part of official risk communication policy and procedure. Use of the EIDSS data management system will provide a structured process for data sharing to accompany this enhanced communication.

P020 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Compassion Fatigue and One Health: supporting our relationship with the animals we care for thru an integrated One Health approach

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This presentation will focus on Compassion Fatigue (CF) in the Laboratory Animal Professional community and how the One Health concept can be used to understand and support these personnel when they experience CF. The ultimate goal is to provide a program that can be utilized internationally to support Laboratory Animal Professionals in their important work caring for animals and supporting advancements in science.

Compassion Fatigue (CF) is the “cost of caring” for other beings and can result in emotional, mental and physical pain (Figley, 1982). The One Health concept takes a holistic approach to the relationship of humans, animals, and the environment and focuses on optimizing the relationship between the triad. Laboratory Animal Professionals (animal caregivers, researchers, veterinary technicians, animal care committee members, etc.) are in a unique situation where they are balancing their feelings and emotions to support advancements in medicine and science and the use of animals in experimental studies. One Health becomes critical in all aspects of this as it is combining the human and animal health improvements and the environmental stewardship with the balance of caring for the animals that are used to make new discoveries. In addition, post-traumatic disorders in Laboratory Animal Professionals after natural disasters have been mentioned but are still underreported and/or underdiagnosed. It is becoming more evident that Laboratory Animal Professionals need help in recognizing and coping with CF in their daily work life. Many programs have been introduced and attempts made to alleviate the effect of CF in these circumstances.
Most of these programs fail and are not sustained as personnel changes occur in a facility. The authors will share their approach to developing a sustainable CF program in a culturally diverse academic setting that can be applied and utilized in multiple environments. This has included a thorough needs assessment, a diverse committee composition with delegation of responsibilities, a focused mission of the team and a consistent appreciation for what everyone has to contribute. We will share our program ‘Dare 2 Care’ (D2C) and provide a checklist for institutions to take with them to develop a program in their own work environment. There should be clear incorporation and encouragement of D2C programs internationally to support One Health advances and acceptance and to help in the understanding of how people are integrated with animals and their environment.

P021 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Understanding the social lives of antibiotics and their policies in the UK dairy industry

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In the United Kingdom, the government has made the agricultural industry responsible for addressing antibiotic use in livestock and has set targets for the industry to reduce their overall antibiotic use by 2018. By transferring responsibility to the individual animal sectors, this has resulted in different approaches and results between animal sectors in controlling antibiotic use. Compared to the UK pig and poultry industry, the UK dairy industry has been relatively slow in taking up responsibilities. As such, this PhD has used a qualitative study design to explore how the UK dairy industry develops and implements antibiotic policy, and how this is perceived by veterinarians and farmers. A multi-sited ethnographic methodological framework has been used which includes policy document analysis, in-depth interviews with key dairy stakeholders, participant observation of veterinarians in practice and the observation of policy transfer during farmer meetings from retailers to farmers. With data being analysed through thematic coding in N-vivo software, initial results indicate that antibiotic policies in the dairy industry only partially address the complex network of people, animals and the environment in which antibiotics circulate. Although UK milk processors and UK retailers have taken up the lead to produce dairy antibiotic policies, the policies are fragmented and seem to rather benefit market purposes than address structural issues in UK dairy production systems. At the same time, the policies fail to assess the complex interplay of antibiotic exchange between veterinarians and farmers. Drivers such as the veterinary business model (that is still largely dependent on the sales of veterinary medicines), uncertain milk markets due to fluctuating milk prices, and farmers self-regulating their sick animals, have a large impacts on antibiotic dispensing and their use in practice. Some of the policies co-produce new travel routes of antibiotics between systems, such as for example by forbidding to feed antibiotic contaminated milk to calves, it is now disposed into the slurries through which it can end back into the environment and into the food chain. Hence, the former examples show how the governance of agricultural antibiotics entails more than accomplishing antibiotic reduction targets; it demands to explore how antibiotics are part of different worlds that co-produce the circulation of antibiotics and their effects. As such, the concept of One Health is not only about integrating leadership on animal and human level to produce antibiotic policies; it is about exploring both the heterogeneity as relationality of antibiotic realities, and the impact of those processes on antibiotic futures.

P022 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Mentored research experiences in One Health: Increasing science identity and self-efficacy among undergraduate students from rural backgrounds

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BACKGROUND: Culturally relevant and place-based education and training initiatives are important for recruiting and retaining students from under-represented populations in Science Technology Engineering and Math academic programs. We hypothesize that One Health, the premise that human, animal, and environmental health are inextricably linked, resonates with the cultural and life experiences of rural Alaskan and Alaska Native students, and provides a relevant context for recruiting and retaining students from these backgrounds.

METHODS: In the Alaska Biomedical Learning and Student Training (BLaST) program, we combined One Health and Social Cognitive Career Theory into an integrated biomedical research training and education program focused primarily on recruitment and persistence of rural Alaskans and Alaska Natives – two populations under-represented in the biomedical research workforce. We explore the impact of mentored undergraduate research experiences on science identity, science self-efficacy, and other indicators of student persistence between 2 groups of Alaskan students (rural and non-rural). We also assess the perceived relevance of One Health to Alaskan students and to students from urban backgrounds participating in a biomedical training program at an urban university.

RESULTS: Alaska BLaST students find linking human, animal, and environmental health more important, and assert that animal and environmental health research is more relevant to them, than basic human research compared to their urban counterparts. We also find that mentored research experiences increase science identity and science self-efficacy in undergraduate students participating in the BLaST program.

CONCLUSIONS: Our data suggest that a One Health context for biomedical research training can improve recruitment and persistence, into biomedical science, of rural and indigenous populations in which subsistence life experiences are common.

P023 - OHS A03 - SOCIAL SCIENCE AND POLITICS

The formulation of One Health policies: lessons from Burkina Faso

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INTRODUCTION: There is consensus on effectiveness of the One Health approach to promote a development that is sustainable from a human, animal and environmental perspective. The operationalization of One Health, however, has proved challenging, as it calls for human, animal and health practitioners to cross their disciplinary and institutional boundaries. This paper presents the approach followed by the Burkina Faso Ministries in charge of livestock, the environment and human health to operationalize, in collaboration with the FAO, the One Health concept. Their joint effort resulted in a report that quantifies the impact of the livestock sector on social, environmental and public health indicators, and highlights the trade-offs embedded in any policy supporting livestock sector growth and transformation.

METHODS: The core element to operationalize the One Health approach in Burkina Faso was a common definition of the different livestock production systems in the country, agreed upon by the Ministries in charge of livestock, the environment and human health. The lack of a common denominator, that is a common understanding of livestock production systems, was in fact a major constraint for operationalizing One Health. National stakeholders were consulted to statistically characterize and map cattle and poultry production systems in the country, using nationally representative statistics and data from the FAO Gridded Livestock of the World. The identified livestock production systems were linked to national datasets to assess the contribution of livestock to household income and nutrition. The livestock maps served as an input to quantity GHG emissions from the characterized livestock production systems using the FAO Global Livestock Environmental Assessment Model. An Expert Elicitation Protocol was implemented to assess the monetary impact of four zoonotic diseases on society, including estimating the value of animals and production lost and the cost of morbidity and mortality in humans, proxied by the willingness to pay for a disability adjusted life-year (DALY).

RESULTS: In Burkina Faso, cattle in all production systems support the livelihoods of about one million households and contribute between USD 71 and 115 million to their aggregate income; they generate about 16 million metric tonnes of CO2 equivalent, with brucellosis and bovine tuberculosis costing society a total of around USD 56 million per year. About 98 percent of rural households depend on chicken for their livelihoods, with birds raised in different production systems generating about 0.2 million metric tonnes of CO2 equivalent. Salmonellosis and HPAI in poultry cost society around USD 29 million per year. These estimates are performed for the different cattle and poultry production systems, such as extensive, semi-intensive and intensive, which allows simulating the different impacts of policies supporting livestock sector growth and transformation on people's livelihoods, the environment and public health.

P024 - OHS A03 - SOCIAL SCIENCE AND POLITICS

One Model for Generating Early Career Problem Solvers and Multi-Disciplinary Networks who place Global Issues in a One Health Framework

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BACKGROUND: This presentation introduces one model for introducing the One Health (OH) framework among an early career, multinational network. There must be communication and collaboration across multiple disciplines to effectively address health issues that now quickly escalate to a global scale. Today's worldwide trade and travel requires networks of expertise in the prevention of disease and health management. The sooner and more often we connect people from various areas of study to focus on the same problem while offering their unique perspective, the more likely the problem will be effectively addressed.

METHOD: The OH Challenge is a cross border partnership between two universities with multi-national enrollment. Student recruitment across a wide disciplinary spectrum builds a volunteer cohort interested in problem solving, network building, and health across human, environment, and animal sectors. Graduate students with faculty mentors facilitate the work of undergraduate interdisciplinary teams while they address a case study focused on a global health issue, such as antimicrobial resistance (2017) and water scarcity (2018). Each team is a mix of students from each university and various majors. Specific tasks are assigned and culminate in a presentation competition that includes how the problem fits into an OH framework. A panel of judges select a winner of $1000 towards a KIVA project of their teams' choosing. KIVA provides microloans to help alleviate OH problems associated with poverty.

RESULTS: There is a survey circulating among 2017 participants and by April, the feedback for 2018 will be analyzed. Responses from two program runs will reveal if participants continue to think in an OH Framework following participation. Do they continue to connect with their OH colleagues or an OH network? For now, we know former MSU participants have since traveled to Saskatchewan to present their work and participate in the OH Leadership Experience. Others have presented the cross border educational exchange at professional conferences. A few have had related internships abroad (ex. Tanzania Food Project). Thus far, students have had the opportunity to collaborate with colleagues from around the world to develop an understanding of OH that will be integral to their future studies and careers.

CONCLUSIONS: The 2018 OH Challenge cohort has 20 students representing 10 countries and 15 disciplines, including engineering, human biology, political science, and psychology. This diversity lends to interdisciplinary collaboration, while breaking down complex problems. The OH Challenge is prepared to take on more university partners to broaden its impact. Given additional funding resources and administrative support, the challenge of creating a global network of early career problem solvers who see an intersection of human, animal and environmental health will be further met.

P025 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Operationalizing One Health: Strengthening Interagency Coordination through Systems Mapping and Analysis

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The “One Health” concept attests that global challenges such as infectious disease, bioterrorism, antimicrobial resistance, and emergency response for health, conflict and natural disasters are complex and beyond the purview of any one discipline working in isolation. One Health has been largely developed and studied within the natural sciences, and has evolved in response to downstream implementation failures. However, despite a focus on individual and organizational collaboration, One Health has not pulled from the depth of organizational and crossboundary scholarship available in the social sciences.

The University of Minnesota (UMN), in partnership with the U.S. Department of Agriculture (USDA), has recognized the need to assess and improve the systems where human, animal and environmental healths interconnect through combining methods from both the natural and social sciences. As a result of an extensive research, discovery and prototyping process, the 6step One Health Systems Mapping and Analysis Resource Toolkit (OHSMART™) was developed. The OHSMART™ tool integrates business process improvement methods with policy and infrastructure assessment methods to enable visualization of a One Health network of partners and associated processes. The approach differs from hypothesis driven positivist investigation and instead focuses on understanding causal mechanism by asking ‘How?’ phenomena have come to be. This tool emerged largely from a heuristic, practice driven and qualitative approach, responsive to the challenges seen within collaborative health efforts.

The process has been used to support systems strengthening in over 12 countries, and tailored to fit different applications from zoonotic disease preparedness and antimicrobial resistance planning to workforce planning. Action plans formed through the OHSMART™ process have been used to improve national action plans on antimicrobial resistance, revise emergency response frameworks and create multiagency infectious disease collaboration protocols. OHSMART™ toolkit has proven to be robust and capable of fostering crosssectoral collaboration and complex system wide problem solving. Currently plans are underway to evaluate long term outcomes, in countries and within institutions where OHSMART™ has been implemented.

P026 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Power struggles, lack of leadership, and weak evidence on effective approaches are hindering collaboration between human, animal, and environmental health sectors

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BACKGROUND: While it appears that One Health has received growing attention and support in recent years from policymakers, funders, and practitioners, it remains unclear whether this support will translate into sustained political prioritisation and action. As such, this study investigates the extent to which factors necessary for sustained political priority for One Health are in place and examines key challenges impeding a shift from rhetoric to action in the One Health policy space.

METHODS: Semi-structured interviews were conducted with 25 high-level informants from the United States (9) and Europe (16) to gain insight into key challenges and opportunities facing the One Health policy community. Interviews were transcribed and analysed thematically, inductively and deductively, utilising Shiffman and Smith's (2007) framework on political priority to assess presence or absence of key determinants.

RESULTS: Regardless of the perception of growing attention to One Health as an issue, the policy community identified numerous challenges that were impeding action and resource mobilisation to support One Health. Notably, the lack of clarity on how to operationalise One Health has hampered the development of a robust evidence base on the added value of the approach. Relatedly, the perceived absence of indicators to monitor and evaluate One Health initiatives presented a major challenge for resource allocation decisions. As it is much easier to quantify their severity, human health issues have tended to be prioritised and, subsequently, the most salient frames mobilised for One health have been humancentric and focused on crisis narratives. This attention to catalytic human health issues, however, was perceived to exacerbate siloed and unstable interest towards One Health that has not been sustained during "peacetime". Global interest in antimicrobial resistance was seen as a key policy window for One Health. Inequitable power dynamics between human health and veterinary practitioners were hotly discussed, and there was no consensus amongst respondents as to who should assume a leadership role for moving One Health forward.

CONCLUSION: For the One Health 'policy window' to be effectively utilised, there is a need for improved clarity on how to best operationalise One Health, otherwise silo- and issue-based approaches are likely to persist. Power inequities within the One Health policy community need to be addressed and sectoral barriers must be overcome so that new indicators and political frames to advocate for One Health that are suitable to all relevant disciplines can be developed and mobilised.

P027 - OHS A03 - SOCIAL SCIENCE AND POLITICS

Themes from One Health Zoonotic Disease Prioritization Workshops in 18 Countries, 2014-2017

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BACKGROUND: Endemic and emerging zoonoses, those diseases shared between animal and humans, continue to have adverse global health impacts. This common health threat is an opportunity for human, animal, and environmental health partners to coordinate across sectors more effectively to protect human and animal health. A One Health approach recognizes the need for human, animal, and environmental health sector collaboration, and is needed to mitigate these impacts and advance global health security. An early step in the collaborative process is identification of diseases of greatest concern so that limited financial and personnel resources can be effectively focused. CDC has developed a One Health Zoonotic Disease Prioritization (OHZDP) tool and workshop process to improve multisectoral, One Health collaboration and selection of priority zoonotic diseases. Over a multi-day workshop, representatives from human, animal, environment, and other relevant health sectors develop criteria and questions that are used to rank zoonotic diseases of national concern through decision tree analysis. The typical workshop goal is to use a multi-sectoral, One Health approach to prioritize endemic and emerging zoonotic diseases of greatest national concern that should be jointly addressed by human, animal, and environmental health ministries within a country.

METHODS: OHZDP workshops conducted globally from 2014–2017 were analyzed by identifying workshop disease criteria, prioritized zoonoses lists, and further action items identified during the workshop. Zoonoses lists were standardized, and both criteria and action items were categorized around common themes.

RESULTS: From 2014 to 2017, CDC and partners facilitated OHZDP workshops in 18 countries in Africa (n=13), Asia (n = 4) and North America (n =1). All countries selected criteria that captured the epidemic or pandemic potential and the disease severity of each zoonosis. Other common criteria included ability to prevent or control the zoonosis (n = 17), economic impacts associated with losses in production, trade, or travel (n = 16), and the bioterrorism potential of the zoonosis (n = 6). Frequently prioritized zoonotic diseases were rabies (n=17); zoonotic influenza viruses (n=16); anthrax (n=12); brucellosis (n=12); and Ebola or Marburg (n=10). Finally, the most common follow-up action noted by countries was the need to strengthen multi-sectoral, One Health coordination (n =14; 78%).

CONCLUSIONS: The CDC OHZDP tool provides a method for prioritizing country-specific zoonotic diseases while fostering recommendations that utilize a One Health approach. During discussions of future actionable items, the majority of countries recognized that improving multisectoral coordination is necessary, which supports that adopting a One Health approach is critical to address the management of emerging and endemic zoonoses. Assessing workshop themes not only strengthens One Health at the national level, but is guiding the development of regional and global One Health guidance, tools, and resources, and is helping to identify common zoonosis concerns.

DRIVERS FOR EMERGING DISEASES

P028 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Reservoirs of Spillover Pathogens Exhibit Fast Life History Traits

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BACKGROUND: Pathogens that spill over from a reservoir species represent a significant threat to human and animal health. Prior work suggests that animals with fast life history traits exhibit higher reservoir competence. Life history traits include measures of developmental timing, reproductive output, mass, and longevity. These traits are largely correlated with one another. For example, species with large litter sizes can be expected to have small offspring. Large-bodied species will develop slower than small-bodied species.

METHODS: We expand upon this to ask if the relationship holds across all mammal species that act as reservoirs for spillover pathogens. We assembled a database of spillover pathogens, their targets, and their vertebrate animal reservoirs. After controlling for body mass, we used permutation tests to ask if reservoir mammals differed from all mammals with respect to gestation length, litter size, neonate body mass, interbirth interval, weaning age, and sexual maturity age.

RESULTS: Reservoir mammals exhibited exceptionally fast life history characteristics for four of the six traits examined.

CONCLUSIONS: A trade-off between immune system investment and pace-of-life may underlie this relationship. However, species with high reproductive outputs could include more common species and are thus sampled more frequently than rare species.

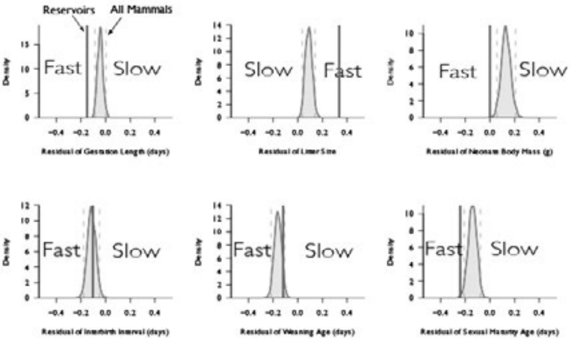

Figure 1. Results of permutation tests comparing the average mass-independent trait for 177 mammalian reservoir species with a distribution of 1,000 draws of 177 random mammals with the same distribution amongst orders. Average life history traits for reservoirs is shown with a thick blue line.

P029 - OHS A04 - DRIVERS FOR EMERGING DISEASES

A quantitative exploration of Rift Valley Fever knowledge and associated social drivers in Fulani nomadic pastoral communities of North-central Nigeria

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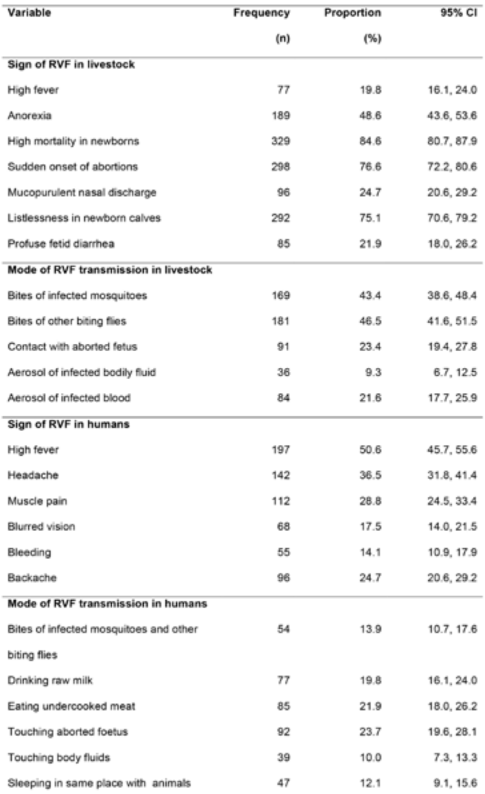
BACKGROUND: Rift Valley fever (RVF) is a mosquito-borne emerging viral zoonotic disease. Research into socio-cultural activities of pastoralists will add innovations to RVF control and prevention. This study was partly built on Health Belief Model foundation, in which knowledge and preventive practices are influenced by socio-demographically oriented factors. Study objectives were: to explore local knowledge and preventive practices regarding RVF among nomadic pastoralists. Our Null hypotheses were: that pastoralist's socio-demographic characteristics cannot influence their overall knowledge and preventive practices towards RVF in nomadic cattle herds; and their socio-cultural activities cannot influence emergence of RVF in herds.

METHODS: Interview questionnaire-based cross-sectional study was conducted in 403 systematic randomly selected household heads in Fulani nomadic pastoral communities of North-central Nigeria in 2015. Nomadic pastoralists live in some of the most underdeveloped environments in the world, with poor veterinary services. Descriptive and multivariable logistic regressions analyses were performed at 95% confidence level.

RESULTS: About 97% (389/403) of pastoralists participated in the study. Majority (65.3%) of participants had no formal education. All respondents interviewed (100%) had heard about RVF. Majorities (84.6% and 76.6%) of participants mentioned high mortality in newborns and sudden onset of abortions in pregnant cows, respectively, as signs of RVF in livestock, and about 43.4% of them knew that mosquito bites transmit RVF virus. About 51% of pastoralists mentioned high fever as RVF symptoms in humans, and 13.9% of them knew that RVF virus is transmissible humans through mosquitoes (Table 1). About 34% of pastoralists avoided mosquito sites during grazing as preventive measure, and 24.4% of them avoided contacts of healthy animals with aborted fetuses. Pastoralists' socio-demographic characteristics that significantly influenced their overall knowledge and practice of preventive measures towards RVF were: age ($P=0.001$), gender ($P=0.001$) and tertiary education ($P=0.010$) (Table 2). Pastoralists' socio-cultural activities that significantly influenced RVF emergence in nomadic pastoral herds were: extensive husbandry system ($P=0.001$), culture of borrowing and loaning of livestock ($P<0.001$), sharing watering points that led to animals concentration ($P<0.001$), mixed grazing and watering of large with small ruminants ($P=0.001$), keeping of healthy animals with sick ones within herds ($P=0.001$), introduction of new animals from markets into herds ($P<0.001$), and giving out livestock as gift or payment of dowry ($P=0.001$) (Table 3).

CONCLUSIONS: There were low levels of overall knowledge and preventive practices towards RVF among nomadic pastoralists. The existing gaps in knowledge and preventive practices call for pastoralists' sensitization through collaborative efforts of public health and veterinary authorities on the epidemiology of RVFe. Socio-cultural activities were identified as key social drivers that influenced RVF emergence in nomadic communities. Surveillance and preventive programmes that take these factors into consideration will be beneficial to public health and livestock industry in Africa.

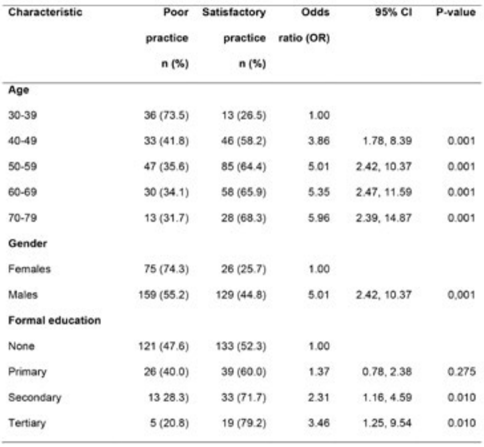
Table 1. Proportions of pastoralists with knowledge about RVF in Fulani nomadic pastoral communities of North-central Nigeria (n = 389).



Variable	Frequency (n)	Proportion (%)	95% CI
Sign of RVF in livestock			
High fever	77	19.8	16.1, 24.0
Anorexia	189	48.6	43.6, 53.6
High mortality in newborns	329	84.6	80.7, 87.9
Sudden onset of abortions	298	76.6	72.2, 80.6
Mucopurulent nasal discharge	96	24.7	20.6, 29.2
Listlessness in newborn calves	292	75.1	70.6, 79.2
Profuse fetid diarrhea	85	21.9	18.0, 26.2
Mode of RVF transmission in livestock			
Bites of infected mosquitoes	169	43.4	38.6, 48.4
Bites of other biting flies	181	46.5	41.6, 51.5
Contact with aborted fetus	91	23.4	19.4, 27.8
Aerosol of infected bodily fluid	36	9.3	6.7, 12.5
Aerosol of infected blood	84	21.6	17.7, 25.9
Sign of RVF in humans			
High fever	197	50.6	45.7, 55.6
Headache	142	36.5	31.8, 41.4
Muscle pain	112	28.8	24.5, 33.4
Blurred vision	68	17.5	14.0, 21.5
Bleeding	55	14.1	10.9, 17.9
Backache	96	24.7	20.6, 29.2
Mode of RVF transmission in humans			
Bites of infected mosquitoes and other biting flies	54	13.9	10.7, 17.6
Drinking raw milk	77	19.8	16.1, 24.0
Eating undercooked meat	85	21.9	18.0, 26.2
Touching aborted foetus	92	23.7	19.6, 28.1
Touching body fluids	39	10.0	7.3, 13.3
Sleeping in same place with animals	47	12.1	9.1, 15.6

n – Number of participants that gave YES responses;
CI - Confidence interval.

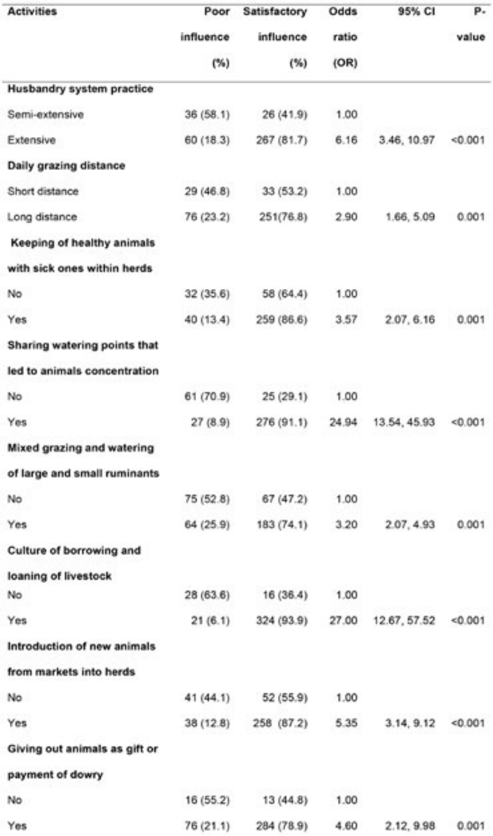
Table 2. Socio-demographic characteristics associated with pastoralists' overall knowledge and preventive practices towards RVF in Fulani nomadic pastoral communities of North-central Nigeria.



Characteristic	Poor practice n (%)	Satisfactory practice n (%)	Odds ratio (OR)	95% CI	P-value
Age					
30-39	36 (73.5)	13 (26.5)	1.00		
40-49	33 (41.8)	46 (58.2)	3.86	1.78, 8.39	0.001
50-59	47 (35.6)	85 (64.4)	5.01	2.42, 10.37	0.001
60-69	30 (34.1)	58 (65.9)	5.35	2.47, 11.59	0.001
70-79	13 (31.7)	28 (68.3)	5.96	2.39, 14.87	0.001
Gender					
Females	75 (74.3)	26 (25.7)	1.00		
Males	159 (55.2)	129 (44.8)	5.01	2.42, 10.37	0,001
Formal education					
None	121 (47.6)	133 (52.3)	1.00		
Primary	26 (40.0)	39 (60.0)	1.37	0.78, 2.38	0.275
Secondary	13 28.3)	33 (71.7)	2.31	1.16, 4.59	0.010
Tertiary	5 (20.8)	19 (79.2)	3.46	1.25, 9.54	0.010

n – Number of respondents; % - Row percentage;
CI – Confidence interval; Statistically significant at p<0.05.

Table 3. Pastoralists' socio-cultural activities that influenced RVF emergence in Fulani nomadic pastoral communities of North-central Nigeria.



Activities	Poor influence (%)	Satisfactory influence (%)	Odds ratio (OR)	95% CI	P-value
Husbandry system practice					
Semi-extensive	36 (58.1)	26 (41.9)	1.00		
Extensive	60 (18.3)	267 (81.7)	6.16	3.46, 10.97	<0.001
Daily grazing distance					
Short distance	29 (46.8)	33 (53.2)	1.00		
Long distance	76 (23.2)	251(76.8)	2.90	1.66, 5.09	0.001
Keeping of healthy animals with sick ones within herds					
No	32 (35.6)	58 (64.4)	1.00		
Yes	40 (13.4)	259 (86.6)	3.57	2.07, 6.16	0.001
Sharing watering points that led to animals concentration					
No	61 (70.9)	25 (29.1)	1.00		
Yes	27 (8.9)	276 (91.1)	24.94	13.54, 45.93	<0.001
Mixed grazing and watering of large and small ruminants					
No	75 (52.8)	67 (47.2)	1.00		
Yes	64 (25.9)	183 (74.1)	3.20	2.07, 4.93	0.001
Culture of borrowing and loaning of livestock					
No	28 (63.6)	16 (36.4)	1.00		
Yes	21 (6.1)	324 (93.9)	27.00	12.67, 57.52	<0.001
Introduction of new animals from markets into herds					
No	41 (44.1)	52 (55.9)	1.00		
Yes	38 (12.8)	258 (87.2)	5.35	3.14, 9.12	<0.001
Giving out animals as gift or payment of dowry					
No	16 (55.2)	13 (44.8)	1.00		
Yes	76 (21.1)	284 (78.9)	4.60	2.12, 9.98	0.001

n – Number of respondents; % - Row percentage;
CI – Confidence interval; Statistically significant at p<0.05.

P030 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Climate Change and Emerging Viral Threats in Canada: Modeling the Transmission Dynamics of Chikungunya Virus

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BACKGROUND: Chikungunya virus (CHIKV) is a globally reemerging pathogen occurring over 60 countries in Asia, Africa, Europe and the Americas. In 2016, Pan American Health Organization reported ~350,000 suspected and ~150,000 laboratory confirmed CHIKV cases in the region and is a major public health concern for Canada. The virus spreads through the bite of an infected *Aedes aegypti* or *Ae.albopictus* mosquitoe and was recently introduced to Europe by infected travelers returning from endemic countries. Many vector-borne diseases from tropical and sub-tropical regions are introduced into Canada by returning infected travelers. With anticipated climate change, local transmission within Canada is expected to occur. We hypothesize that risk (magnitude and geographic extent) of future Canadian CHIKV outbreaks due to autochthonous transmission will be strongly influenced by environmental factors. Our objective is to assess the risk of transmission of exotic mosquito-borne diseases in Canada under current and future climate scenarios, using CHIKV as an example.

METHODS AND ANTICIPATED RESULTS: We plan to develop a stochastic, compartmental model (Figure 1) to simulate CHIKV disease dynamics in humans in Canada using projected climate change scenarios. Examples of model-associated equations can be found in Figure 2 and a description of model variables and parameter values can be found in Table 1. To assess the current and future transmission dynamics of CHIKV in Canada, we will calculate R0 (average number of secondary cases generated from an initial case) to understand the viruses' ability to trigger epidemics under the current and future climate change scenarios and the potential attack rate for geographical regions at risk. These outcomes will be compared with a second model that will incorporate temperature-dependent EIP for the vectors and their survival beyond the EIP to assess the impact of vector's transmission potential affecting the R0 and attack rates in at-risk the populations. Similarly, to assess the effect of early case detection and isolation on reducing R0 and attack rate, we will introduce a compartment to capture the proportion of symptomatic human CHIKV cases (I_{HS}) and variations in vector densities to simulate different levels of vector control in the model. We will conduct wide-ranging sensitivity analyses on parameter values of interest and compare model outcomes to a base case model with no interventions.

CONCLUSION: We anticipate that modeling outcomes will contribute to an improved understanding of the future public health impact of CHIKV, allow for a systematic examination of health interventions, and quantify the resources required to manage the emergence of CHIKV in Canada. The outcomes will enable us to assess the risk of locally-sustained transmission of exotic mosquito-borne viruses and the efficacy of current interventions.

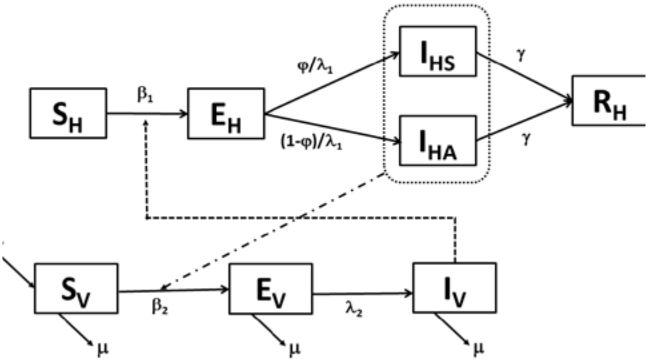
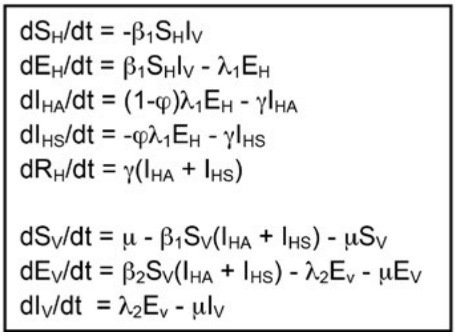


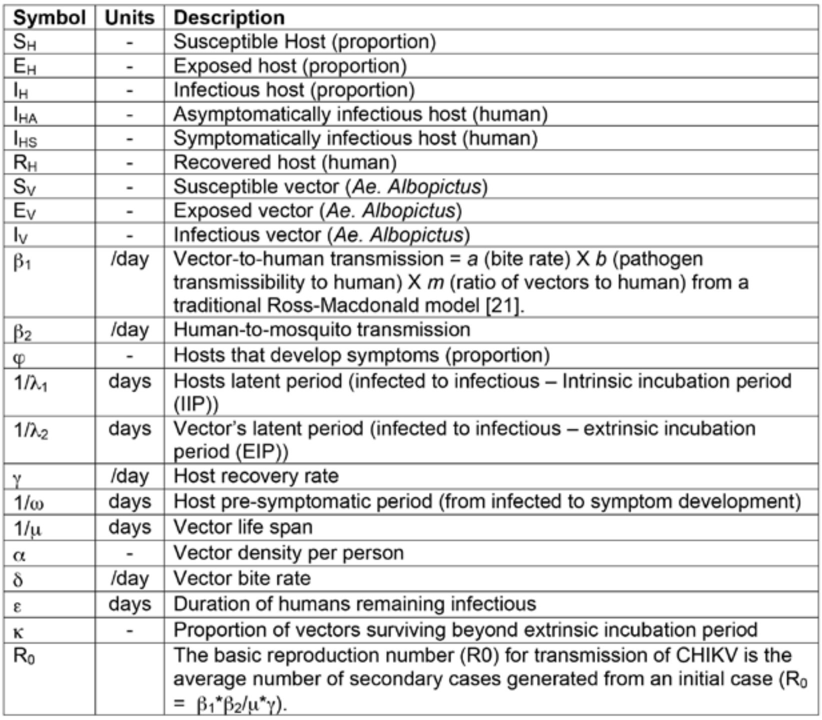
Figure 1: Compartments of the proposed epidemiological model for Chikungunya virus transmission in Canada. The human population will be divided into susceptible (S_H), exposed (E_H), infectious symptomatic (I_{HS}), infectious asymptomatic (I_{HA}) and recovered (R_H) epidemiological classes. Depending on the presence or absence of clinical signs, the infectious individuals will be considered either symptomatic (I_{HS}) or asymptomatic (I_{HA}). The vector population is divided into susceptible (S_V), exposed (E_V) and infectious (I_V) categories.



$$dS_H/dt = -\beta_1 S_H I_V$$
$$dE_H/dt = \beta_1 S_H I_V - \lambda_1 E_H$$
$$dI_{HA}/dt = (1-\varphi)\lambda_1 E_H - \gamma I_{HA}$$
$$dI_{HS}/dt = -\varphi\lambda_1 E_H - \gamma I_{HS}$$
$$dR_H/dt = \gamma(I_{HA} + I_{HS})$$

$$dS_V/dt = \mu - \beta_1 S_V(I_{HA} + I_{HS}) - \mu S_V$$
$$dE_V/dt = \beta_2 S_V(I_{HA} + I_{HS}) - \lambda_2 E_v - \mu E_V$$
$$dI_V/dt = \lambda_2 E_v - \mu I_V$$

Figure 2: Equations to be used to model CHIKV transmission dynamics Canada



Symbol	Units	Description
S_H	-	Susceptible Host (proportion)
E_H	-	Exposed host (proportion)
I_H	-	Infectious host (proportion)
I_{HA}	-	Asymptomatically infectious host (human)
I_{HS}	-	Symptomatically infectious host (human)
R_H	-	Recovered host (human)
S_V	-	Susceptible vector (*Ae. Albopictus*)
E_V	-	Exposed vector (*Ae. Albopictus*)
I_V	-	Infectious vector (*Ae. Albopictus*)
β_1	/day	Vector-to-human transmission = *a* (bite rate) X *b* (pathogen transmissibility to human) X *m* (ratio of vectors to human) from a traditional Ross-Macdonald model [21].
β_2	/day	Human-to-mosquito transmission
φ	-	Hosts that develop symptoms (proportion)
$1/\lambda_1$	days	Hosts latent period (infected to infectious – Intrinsic incubation period (IIP))
$1/\lambda_2$	days	Vector's latent period (infected to infectious – extrinsic incubation period (EIP))
γ	/day	Host recovery rate
$1/\omega$	days	Host pre-symptomatic period (from infected to symptom development)
$1/\mu$	days	Vector life span
α	-	Vector density per person
δ	/day	Vector bite rate
ε	days	Duration of humans remaining infectious
κ	-	Proportion of vectors surviving beyond extrinsic incubation period
R_0		The basic reproduction number (R0) for transmission of CHIKV is the average number of secondary cases generated from an initial case ($R_0 = \beta_1 * \beta_2/\mu * \gamma$).

Table 1: Chikungunya viruses in humans in Canada, compartmental model parameters and variables.

P031 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Drivers for Emerging Zoonoses in Pastoralist Communities in Northern Tanzania: Using a mixed methods approach to determine animal-human interaction and rural health-seeking behaviours of livestock-keepers.

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BACKGROUND: Zoonotic disease represents a major threat to the health and livelihoods of poor communities in Sub-Saharan Africa. However, there is limited data on human-animal interaction and the opportunities for transmission of zoonoses from animals to humans. Secondly, data on rural health-seeking behaviours that may impact uptake of preventive and curative measures for zoonoses such as vaccines is scarce, yet this could have implications for implementation of effective intervention strategies. My poster draws from data based on the 10 months of ethnographic study I conducted in four pastoralist sub-villages in Naiti, northern Tanzania, with the aim quantifying the human-animal interaction and exploring local knowledge of zoonoses and rural health-seeking behaviours and the implication for prevention of zoonotic disease.

METHODS: This study took place in remote wilderness pastoralists environments of northern Tanzania. A purposive sample was taken from four sub-villages, with an initial survey of 370 individuals examining their knowledge of zoonotic diseases and the range of treatment options that were most commonly used to treat febrile illness. Unstructured participant observation included observing human-animal interaction to quantify exposure to animals in a variety of settings, as well as observing diagnoses between febrile patients and clinicians within hospital settings. Data analysis is currently underway using Nvivo software, and preliminary findings are presented here.

RESULTS: Pre-teen boys have the most direct contact with animals followed by women and small children. The boys spent at least 10 hours each day herding animals while the latter often slept in the same hut as goats and sheep. Older men had the closest interaction with animal carcasses immediately after death. They handled raw blood and other fluids and they were involved in cutting up the animal and distributing meat for consumption. Therefore, these groups are the most likely to be exposed to zoonotic pathogens and should therefore also be the primary targets for interventions

In addition, the health-seeking behaviour study found use of at home treatment was widespread for an array of febrile conditions including potential zoonotic disease in both people and animals, due to lack of access to human and veterinary services in the community, and the exorbitant costs associated with seeking treatment in these scarce facilities, as a majority of the people that I spoke to emphasised that they would use health facilities more if these were available, well-equipped and affordable.

CONCLUSIONS: Control of zoonoses in pastoralist environments relies on availability of affordable veterinary and human health services. This includes availability of timely vaccination of animal hosts of pathogens especially sheep and goats, and working in collaboration with community leaders to identify risky behaviours that may expose people to zoonotic infections. Thus, limitations inherent in the health system has direct impact on effective control of zoonoses.

P032 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Pregnancy and Other Drivers of Viral Detection in Bat Hosts

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BACKGROUND: Understanding drivers of viral infection in wildlife reservoir species is critical to predicting pathogen spillover and, ultimately, managing and preventing human disease. Given their propensity to serve as reservoirs for viral pathogens of special public health concern, bats are particularly important reservoir host taxa. Therefore, characterizing natural viral dynamics in diverse bat host species is fundamental to disease management efforts.

METHODS: To further our knowledge of viral infections in free-ranging bats, we developed and fit hierarchical Bayesian models to leverage a multi-year, global-scale dataset from the PREDICT project's pathogen surveillance efforts. Biological samples were collected across numerous bat host species, and a consensus PCR testing method was used to detect viruses, both known and novel, across multiple viral families. Our statistical modeling techniques, implemented in the Stan programming language, explicitly controlled for sources of variation in the resulting viral detection data, including geographic region of data collection, specimen type, and specific testing protocol used. Consequently, our analyses address broad, general effects on bat viral dynamics using viral detection (positive or negative) as the outcome of interest. Our models also allowed for bat host species-specific seasonal trends in viral detection and incorporated influences of precipitation and important biological states, including pregnancy and lactation, as main effects. Models were fit separately for adult female and adult male bat data.

RESULTS: Although models could accommodate seasonal fluctuations in viral detection across all bat hosts, strong temporal trends were only apparent for well-sampled species like *Pteropus giganteus*, which showed a mid-year peak in viral detection. Our analyses revealed that, among the main effects tested, pregnancy had the most influence on viral detection in adult female bats. Intriguingly, pregnancy appeared to have a protective effect, reducing the probability that an individual female would test positive. In contrast, adult male bats were more likely to have virus detected when female conspecifics were pregnant. Precipitation and lactation variables had smaller, idiosyncratic effects on viral shedding across bats of both sexes.

CONCLUSIONS: Overall, our results reflect both individual- and population-level drivers of viral shedding in bats. During pregnancy, female bats may undergo immunomodulation or have protective physiological strategies that act to reduce their rate of viral shedding. Males may be more likely to have detectable virus during periods of pregnancy if reproductive activity coincides with communal roosting behaviors and increased interspecific contact rates that promote pathogen transmission. These findings move us closer towards understanding when and why bat host species have the opportunity for infection with viruses that may represent a spillover threat.

P033 - OHS A04 - DRIVERS FOR EMERGING DISEASES

One Health in Thailand: Multisectoral contributing towards success addressing zoonotic EIDs

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BACKGROUND: Most of harmful Emerging Infectious Diseases (EIDs) are zoonotic origins. Since 1992 Thailand has introduced human - animal interface by launching Rabies Act , the beginning of partnership between public health and livestock sector. Later become officially known as "One Health" and expand to cross-sectoral collaboration at national, regional and global level.

OBJECTIVE: To illustrate evidence of effort on multi-sectoral contributing towards success addressing zoonotic EIDs through One Health concept in Thailand

RESULTS: In 2004, having attacked with Avian influenza, multidisciplinary surveillance , capacity building in outbreak response team workforce such as FETP-V, joint SRRT and the 1st National Strategic Plan for EIDs were established. Up to now more than 10,000 joint SRRT teams, 14 one health provinces and multisectoral communicable diseases committee from central level to sub-district level under Communicable Diseases Act 2015 are covering EIDs detection, prevention and response countrywide while the national plan for EIDs which focused on One Health strategy will be moving forward by national committee mechanism in 2017-2021. 2 MoUs for cross-sectoral collaboration on One Health preparing and combating to EIDs have been signed at ministerial level among 8 organization included agriculture, natural resources and environment, Ministry of Interior, Social Development and Human Security, Labor, Education, Public Health, and Thai Red Cross Society . In addition, we also collaborate with partners in country eg. Thailand One Health University Network (THOHUN), research network and international community eg. SEAOHUN. Thai One Health Coordinating Unit has been also established to coordinate one health activities in Thailand.

CONCLUSION/DISCUSSION: Effective institutionalized cross-sectoral partnership and continuously strong commitment from high level policy are fundamental for success on preparedness and response to EIDs including IHR and GHSA achievement.

P034 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Prevalence of vector-borne diseases in the Republic of Armenia

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BACKGROUND: Several endemic vector-borne diseases (VBDs) are circulating or have circulated in Armenia, but the situation is changing. Malaria was endemic until the 1950s-1960s, and the World Health Organization certified Armenia as malaria-free in 2011. Leishmaniases were widespread in Armenia until 1969, with no further cases until a reemergence in 1999. Although plague natural foci comprise about 90% of Armenia's territory, only one case of plague has been detected since 1877. The surveillance system for VBD in Armenia is passive: cases are only detected when the patient is admitted to a health facility that reports them. This study describes trends in the emergence and prevalence of human cases of VBDs in Armenia.

METHODS: Population-based epidemiological surveillance data (monthly and annual reports on instances of reportable diseases) was reviewed. Healthcare facilities diagnose malaria using microscopy; tularemia and Lyme disease using ELISA; and leishmaniasis using microscopy, PCR, rapid test rK38, and ELISA. Entomological surveillance data and analyses of vectors from 2000-2015 were also reviewed. NCDC entomologists collect and inventory larval and adult mosquitoes and adult Phlebotomine sand-flies at sample sites across Armenia and collect ticks from animals and through flagging. Morphological and molecular methods are used for species identification. The results of 2015-2017 field studies on vectors were analyzed through Geographic Information System mapping and compared to locations of VBD cases.

RESULTS: Entomological surveillance suggests the ongoing presence of twelve sand-fly species, flies, fleas, lice, ticks, and *Anopheles, Aedes, Culex,* and *Culicinae* mosquitos across all regions in Armenia. Autochthonous *P. vivax* malaria cases were registered from 1994-2005, peaking in 1998 with 1156 cases; since 2006, there have been just thirteen cases of malaria, and they were found only in travelers and foreigners. From 1999-2017, 132 cases of visceral leishmaniasis were reported, confined mainly to Yerevan and the Syunik, Tavush, and Lori regions, but in 2017, cases were registered in Aragasotn and Kotayk where the competent vector, *Phlebotomus kandelakii*, was also found. From 1996-2017, 306 cases of tularemia were treated in Armenian health facilities. Lyme disease was first detected in Armenia in 2010 (6 cases, clinically diagnosed). It was added to the reporting system in June 2017, and since then, 22 clinically- and 19 laboratory-confirmed cases of Lyme disease have been registered.

CONCLUSIONS: The VBD situation in Armenia is dynamic: Lyme disease emerged, native malaria disappeared, and the geographical distribution of leishmaniasis cases broadened in correlation with the distribution of its main vector. Given the high diversity of vectors and the circulation of "new" and "old" diseases in the region, further investigation is required to determine the burden of VBDs in Armenia. Diagnostic and surveillance capacities should be improved, and new diseases should be added to the reporting system to increase detection rates.

P035 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Biological and anthropogenic drivers for emerging zoonoses from an interdisciplinary perspective

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BACKGROUND:

Over the last decades, several zoonoses emerged that had high impact on public health. Examples include highly pathogenic avian influenza, severe acute respiratory syndrome (SARS) and Ebola. Emergence of zoonoses is influenced by social, economic, environmental, and ecological factors. Hence, a multidisciplinary and transboundary approach is required to understand, predict, prevent and control the emergence of zoonoses. The aim of this study was to identify the main drivers of emerging zoonotic pathogens and to indicate targets for prevention and intervention from an interdisciplinary perspective.

METHODS:

Identification of drivers was based on three case studies to account for different disease agents, reservoir hosts, and socio-economical and climatic conditions. Case studies selected were Lyme disease and Q-fever in the Netherlands, and classical rabies in South-America. For each case a schematic diagram was drafted to depict drivers for emergence, and their correlations and interactions, based on literature review and expert knowledge.

Experts from different disciplinary backgrounds including veterinary medicine, human medicine, ecology, economy, and sociology, were asked to evaluate these diagrams, and to identify the five drivers that could best be targeted for effective prevention or control of these emerging zoonoses. The selected drivers were labelled as critical control points for intervention (CCPs). Two different methods were used for this expert consultation: an interactive workshop (12 experts) and a Delphi study with two mailing rounds (12 different experts).

RESULTS:

The schematic diagrams for the three case studies had different levels of detail. The case of Lyme disease was most complex with a total of > 60 drivers identified. Although individual drivers differed among the diseases studied, drivers could be grouped into nine generic clusters of which five were classified as biological (climate, landscape, vertebrate hosts, arthropod vectors, agent aetiology) and four as anthropogenic (human behaviour, nature management, living conditions, human and veterinary medicine).

Results of the expert consultation were consistent between the workshop and the Delphi study, and indicated that drivers related to human behaviour and awareness/knowledge are important CCPs for both Lyme disease and rabies. Although these were also selected as CCPs for Q-fever, drivers related to livestock farming and human and veterinary medicine were considered more effective CCPs for Q-fever. Human and veterinary medicine were also seen as important CCPs for Lyme disease and rabies, with a strong emphasis on early diagnosis and vaccination, respectively.

CONCLUSIONS:

The multidisciplinary approach of this study enabled a robust inventory of the most important biological and anthropogenic drivers for emergence of zoonoses and as such contributes to improved understanding. Targets for effective prevention and control of the case pathogens were mainly associated with anthropogenic drivers, with human behaviour, awareness/knowledge, and human and veterinary medicine identified as important CCPs.

P036 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Understanding emerging infectious disease at the human-wildlife-environmental interface in Africa

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BACKGROUND: A myriad of factors influence human use and alteration of landscapes and natural resources. As human populations grow, resource requirements increase, especially the need for land and access to water. In Africa, this interaction is increasingly intense, with human community expansion and development leading to growing levels of overlap and contact between human populations, their domestic animals, and wildlife. This interaction has led to escalating levels of contact with wildlife, vectors, and environmental pathogen reservoirs and has contributed to degradation of ecosystem services. How do these changes influence pathogen emergence and transmission potential at the human-wildlife-environmental interface? How will climate change, escalating poverty, and human landscape dependencies shape these interactions?

METHODS: Using various host-pathogen systems and sociocultural, environmental, and wildlife ecology data collected over the last 20 years in Botswana, Southern Africa, we evaluate interdependent pathways that lead to pathogen emergence and provide an overview of the ecology of disease invasions.

RESULTS/CONCLUSIONS: Using these systems, we provide compelling evidence that an ecohealth approach is necessary to understand emerging pathogen threats to human and animal populations living in complex socioecological systems.

P037 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Seasonal reproduction of the Egyptian fruit bat drives viral infection dynamics

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BACKGROUND: The Egyptian fruit bat (*Rousettus aegyptiacus*) has been implicated as a potential reservoir species for several fatal zoonotic pathogens including Marburg, paramyxo- and the rabies related lyssaviruses. Our surveillance has also confirmed the presence of these viruses in South African bats. *R. aegyptiacus* is a cave dwelling bat that is widespread in Sub-Saharan Africa, Middle East and Southwest Asia with roosting colonies numbering over 5 000 individuals. In South Africa, mating and fertilization take place between June to mid-September and births between October to December, in contrast with eastern Africa where births occur twice a year. Seasonal reproduction is characterized by physiological as well as behavioural stress factors and very few studies have investigated how this influences disease transmission and shedding patterns of pathogens.

METHODS: This study focused on a maternity colony of *R. aegyptiacus* in Matlapitsi cave, Limpopo province, South Africa where we did seasonal sampling to collect oral, urine and blood specimens and recorded the age class, sex, as well as reproductive condition. Urine samples were collected from individual bats as well as from plastic sheets placed underneath the colony inside the cave. Saliva were collected from captured bats by carefully swabbing the tongue, palate and inside of the lips with sterile cotton swabs. Sera were tested for the presence of MARV antibodies (n=1431) using an ELISA (Paweska et al., 2015). Urine samples (n=243) were tested using two nested RT-PCR assays targeting the Paramyxoviridae family (Tong et al., 2008) and saliva samples using a nested PCR for herpesviruses (VanDevanter et al.,1996).

RESULTS: MARV seropositivity in adult bats ranged from 43.7% in August to 100% in February and in juvenile bats from 1.3% in June to 77.3% in January. Excretion of paramyxovirus nucleic acids in urine was detected sporadically throughout the year (one/two samples per month), however two peaks were observed for both henipa and rubula paramyxoviruses during June-July as well as October. Only β-herpesviruses were detected in saliva samples. A peak in shedding was observed at the beginning of the reproductive season (September/October), followed by a decrease until January and then another peak in April which may reflect the progressive loss of maternal antibodies during the first months of life.

CONCLUSIONS: Our results for several viruses indicated that the gradual loss of passive immunity among juveniles increases the number of susceptible individuals, creating favourable conditions for virus spread. Seasonal reproduction also results in changes in virus shedding and seroconversion patterns which are driven by sex, age and reproductive condition of female bats. This study highlights the complexity of viral infection dynamics in potential reservoir species and the importance of longitudinal studies to understand risk of spillover.

P038 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Identifying Avian Flu (H5N1 & H1N1) as an emerging disease to threaten both human and animal health especially to immunologically naïve communities.

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BACKGROUND:
The recent spread of Avian Influenza has touched all 4 continents with just years in between, having reached USA, Africa, Asia and European countries between 2006 and 2017. This then calls for global collaboration in understanding the current spread and understanding its potential to further deteriorate the wellbeing of immunologically naïve populations and the reliability of the poultry industry. Despite the discussion on poultry vaccination process, the disease has reached human in all 4 continents. In understanding this pathogenic disease, one cannot exclude climate change and its impact on environmental changes that influences the spread of diseases. Increasing surveillance systems, exploring methods of preparedness is one of the key issues in epidemiology. An outbreak in China claimed more human lives, increasing cost and resulting in system failure. In as much as the risk of infection from human to human might seem very low, concerns around immunologically naïve populations and those living with HIV/Aids continue to threaten human life.

METHODS:
An analytical review of literature about the topic was done. 68 articles were systematically reviewed these included those with the key words relevant to climate change and Avian Influence (H5N1 as well H1N1). The processes included eliminating all articles that were not relevant to the topic. Furthermore some literature had no information on the effects of Avian Influenza on animal and humans.

RESULTS:
The spread of disease has a potential of spreading from human to human. This increase the risk for immunologically naïve people such as those living with HIV/AIDS, TB and those who work in the poultry industry especially those with backyard poultry farms and people whose main source of income is through selling poultry.

CONCLUSION:
Global multisector preventative and surveillance measures needs to be put in place. The potential of emerging diseases such as Avian Influenza should not be taken for granted. Various

stakeholders such as farmers, Epidemiologist, Food and drug Administrative representatives should be able to communicate about this potential pandemic. Innovative strategies should be explored. Human resources and capacity should be increased. Availability of medication, medical personnel as Nurses and Doctors should be prioritized globally in order to be able to tackle emerging diseases and treating current epidemics. Furthermore realistic plans to vaccinate and monitor that poultry industry should be in place, and these should include backyard farmers.

P039 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Recurrent crow (corvus spendens) mortality events linked to H5N1 influenza virus circulation in live bird markets, Bangladesh

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BACKGROUND: H5N1 avian influenza caused >500 reported outbreaks in poultry and wild birds in Bangladesh since 2007. Multiple crow mortality events occurred during the winter season (Nov-March) between 2016- 2018 within the same areas of Dhaka and Rajshahi in Bangladesh. A One Health approach was used to investigate the crow mortalities, identify the etiologic agent, assess the extent of the outbreak, and identify the possible source of infection.

METHODS: Cloacal and oropharyngeal swabs were collected from moribund and dead crows (N=375) and offal and environmental samples from nearby live bird markets (LBMs; N=430). All samples were tested using a pan-influenza A consensus PCR assay as well as specific q-PCR for influenzaA (M gene) H5/H7/H9/N1/N6.

RESULTS: The team observed crows feeding on poultry offal and waste in neighboring LBMs. Of the total, 61% (n=228) of crows and 22.6% (n=97) of LBM samples tested positive for H5N1. 20.5% (n=77) of crows and 15% (n=64) of LBM samples tested positive for H5Nx. Phylogenetic analysis based on a partial sequence of the HA gene of H5N1 subtypes suggests that the strain found in the crows is similar to the Bangladeshi 2.3.2.1a clade that circulated in 2011.

CONCLUSIONS: The findings suggest that multiple subtypes of H5 influenza viruses are circulating in LBMs without mortality in poultry. The virus may have been transmitted to crows while they were feeding on poultry waste in the LBMs. But when the virus spilled over to crows it become pathogenic and causes mortality creating a dead-end host. Crows may play a role in transmission between LBMs or to people. Improved LBM biosecurity measures are needed to reduce the risk of influenza virus spillover to wild birds or people in Bangladesh.

P040 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Epidemiology of Brucella sp. antibody in cows of Chittagong Metropolitan Area, Bangladesh: A Prioritized Zoonotic Disease

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INTRODUCTION: Brucellosis is endemic both in humans and animals in Bangladesh. However, little information regarding the prevalence of and risk factors for brucellosis is available in the dairy intensive Chittagong area is available.

MATERIALS AND METHODS: From February to November, 2015, 158 serum samples were collected from six randomly selected dairy farms of Chittagong Metropolitan Area (CMA) to understand the epidemiology of seroprevalence of anti-brucellosis. The Rose Bengal plate test (RBPT) and a competitive ELISA (cELISA) were used for screening and confirmation, respectively. Farm and animal-level demographic data and exposure to risk factors were collected. A mixed effect multiple logistic regression model was used to identify animal-level risk factors, with herd considered as a random effect and demographic and other explanatory variables as fixed effects.

RESULTS: Twenty percent (n=32, N=158) of animals were seropositive by RBPT and 9% (n=4) by cELISA. The farm level prevalence ranged from 10-26% and 5-21% by RBPT and cELISA, respectively. Multiparous cows had significantly higher seropositivity levels than heifers (22%;OR=5.76;95%CI:1.86-17.82;p=0.002). Cows in their first trimester were more likely to be seropositive (23%;OR:3.27;95%CI:1.17 -9.23;p=0.024) and cows with a history of reproductive disorders were 3 times more seropositive (38%;OR:3;95%CI:1-8;p=0.031) than those without reproductive disorders. The seropositivity of brucellosis varied significantly ($p<0.05$) according to the amount of milk production at the animal level and two-third of the farm owners were unaware about Brucellosis.

CONCLUSIONS: Occupationally exposed people in the study area may be at risk for this zoonosis. Control of brucellosis in dairy cattle and awareness building among the farm owners will reduce the exposure of people at high risk and thereby the disease.

P041 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Earth observation for environmental surveillance of pathogens

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BACKGROUND: Water- (cholera, shigella) and vector- (malaria, zika) borne infections continue to be a major threat to human population. Although environmental pathogenic niches are well established, yet the major challenge is to determine causal linkages of those niches with hydroclimatic processes (such as precipitation, temperature, salinity etc.). Regions with human communities having poor access to safe water and sanitation facilities remain at constant risk of interaction of water and vector borne pathogens, and lead to outbreak of infections. In addition, unavailability of hydroclimatic data from those regions limit ability to develop any prediction protocols for estimating risk of abundance of pathogens. The goal of this research is to highlight quantitative importance of use of earth observation in developing prediction algorithms for cholera and zika virus.

METHODS: Using data from several satellites (MODIS, VIIRS, GPM, LANDSAT), a new universal time invariant algorithm is developed that can provide estimates on risk of cholera and zika in a particular region.

RESULTS: Cholera can be predicted at least four to six months in advance using conditions of warm temperatures intersecting with heavy precipitation. Abundance of zika viruses can be predicted atleast five weeks in advance using thresholds on dew point temperature as risk markers.

CONCLUSIONS: The study demonstrates that water and vector-borne infections can be predicted using earth observation, provided appropriate hydroclimatic processes are identified and analyzed. The time invariant algorithm is able to predict trigger of an infections using only satellite data.

P042 - OHS A04 - DRIVERS FOR EMERGING DISEASES

Emergence of Extended Spectrum of β-lactamase (ESBL) producing Enterobacteriaceae in migratory birds

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Migratory birds, the drivers of pathogen emergence, move hundreds to thousands of kilometers, often spanning continents and spread pathogens around the world via migratory flyways. West Nile virus and the highly pathogenic avian influenza H5N1 virus offer the best evidence of emerging, zoonotic diseases spread over long distances by migratory birds. Approximately 325 types of migratory birds visit Bangladesh every year and may play a role to transmit antimicrobial resistance (AMR) bacteria from one region to another. Considering this facts, the study undertaken to evaluate the occurrence of extended-spectrum-β-lactam resistance in enterobacteriaceae in migratory birds.

A total (n=1620) non-invasive fecal samples of migratory birds were collected from different hot spots of Bangladesh during 2016-18 at winter time. Most significant bacteria of enterobacteriaceae family, *Escherichia coli* and Salmonella *spp* were isolated and confirmed with qPCR. Kirby bauer disk diffusion method and microdilution technique were used to determine phenotypic resistance and minimum inhibitory concentration (MIC) of antibiotics respectively. Prevalence of important ESBL producing genes were also investigated in the isolates through PCR.

Out of 1620 samples, 90.1% (n=1460,95%CI:88.7-91.6) and 9.26% (n=150,95%CI:10.7-7.9) samples were *E. coli* and *Salmonella spp* positive respectively. Among the tested isolates, 51.5% (n=201,95%CI:47.3-55.8) *E. coli* and 93.3% (n=140,95%CI:89.5-97) Salmonella spp were multi-drug resistant (MDR) according to the CLSI guideline 2015 and the breakpoints 2017. In case of E. coli, 48.5% isolates showed phenotypic resistance against β-lactam antibiotics where highest resistant was against ampicillin 26.9% (n=105,95%CI:21.7-33.5) followed by cefotaxime 25.4% (n=99,95%CI:20.4-31.9), cefixime 20% (n=78,95%CI:15.7-25.1), ceftriaxone 18.5% (n=72,95%CI:14.4-24.5), cefepime 17.7% (n=69,95%CI:13.8-23.6), imipenem 17.7% (n=69,95%CI:13.8-23.6) and most effective one was amoxicillin/clavulanic acid with 73.1% (n=285,95%CI:70.4-78.7) sensitivity. Among the other tested antibiotics (n=15) most resistant one was azithromycin (59.2%, n=231,95%CI:55.2-62.6) and most sensitive was chloramphenicol (79.2%, n=309, 95%CI:76.2-83). In case of *Salmonella spp*, 75.3% (n=113) isolates showed phenotypic resistance against β-lactams where ampicillin, amoxicillin/clavulanic acid, cefixime and cefotaxime resistance pattern has no significant variation (20%, n=30,95%CI:11.7-33.5). Nonetheless, cefepime was fully sensitive against all *Salmonella* isolates. In antimicrobial activity assay, higher MIC_{50}/MIC_{90} (μg/ml) was found in sulfamethoxazole (≥2048/≥2048), azithromycin (128/1024), and amoxicillin (32/≥2048) where ceftriaxone (≤1/2) was the most effective one. Results also revealed, 30.2% (n=57) phenotypically resistant *E. coli* harbor ESBL encoding genes including bla_{CTX}(n=36), bla_{TEM}(n=21), bla_{SHV}(n=12), bla_{CMY}(n=9), bla_{PSE}(n=9), bla_{OXA}(n=3) where 11.1% isolates (n=21) carry more than two genes. *Salmonella spp* also persist high ratio (53.3%, n=80) of ESBL encoding genes including bla_{TEM}(n=70), bla_{CTX}(n=20), bla_{SHV}(n=20) and bla_{OXA}(n=10).

β-lactam antibiotics resistance with ESBL encoding genes in enterobacteriaceae in migratory birds might be due to close interaction with native wild life or sharing the contaminated environment which is alarming for control of emergence pathogens. Continued surveillance of AMR pathogens in local and migratory birds will improve the understanding of prevalence and transmission patterns.

VACCINES

P043 - OHS A06 A07- VACCINES

Development of a mouse model for highly pathogenic avian H5N1 influenza virus

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Influenza A viruses are responsible for annual seasonal epidemics, causing 250,000-500,000 deaths worldwide. The viruses naturally infect a wide range of species, including human, avian, swine, equine and other mammals. The genome of influenza A virus is composed of eight segmented RNA molecules of negative polarity. The nature of the genomic composition and the wide range of host species enable influenza A viruses to reassort their genetic elements between different strains, thus generating novel virus strains with the pandemic potential. Influenza pandemics happened every 30-50 years.

Wild aquatic birds are the natural reservoir of influenza A virus. In January 2014, the first North American case of human fatal infection with avian H5N1 was reported in Canada, calling for the research on understanding how the avian virus crossed the species barrier and caused human disease and new vaccine development. Here we report the establishment of the mouse disease model infected by highly pathogenic avian influenza H5N1 isolated from human sample in Canada. Group of 12 mice were divided into four groups and were either PBS infected or A/Alberta/2014/01 (H5N1) infected intranasally with three different doses (10^3PFU/mouse, 10^4 PFU/mouse or 10^5PFU/mouse, designated low-, medium- and high- dose). Body weight and survival rate were documented daily for ten days. Mouse lung, spleen and brain were harvested at predetermine time or when mice succumbed from the disease. All the experiments were conducted in containment level 3 labs in InterVac. The results showed that mice that were mock infected steadily gained weight over time, however, three groups of mice infected with H5N1 virus had significant weight loss. By day 5 all the mice in medium and high dose groups succumbed. The mice infected by low dose virus all died on day 7 post infection. Virus titres, cytokine profiles and histopathology are being assessed. The low dose will be chosen for the further animal experiment. The establishment of this model will allow the study of the H5N1 virus pathogenesis, test for new vaccine and antiviral design.

SURVEILLANCE AND EARLY DETECTION

P044 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Investigation and monitoring of Brucellosis associated abortion in a dairy cattle farm in Bhutan

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National Centre for Animal Health, Bhutan -

INTRODUCTION: Bhutan is essentially an agrarian country with about 56.7% of the population engaged in agriculture and livestock farming forms an integral part of the agriculture system with about 62% of the households rearing livestock. In late 2014, one of the cattle breeding farms - the National Jersey Breeding Centre which supplies breeding stocks reported unexpected rate of abortion (54.17%, 13/24) among the pregnant animals within a short period of time. The cause of abortion was suspected to be due to Brucellosis. The veterinary authority immediately investigated the cause of abortion.

MATERIALS AND METHODS: Series of sampling and laboratory testing at five different time points were conducted over a period of two years to initially identify the cause and monitor the status of infection. Serum samples were tested for antibody using Rose Bengal Test (RBT), Enzyme Linked Immunosorbent Assay (ELISA) and Complement Fixation Test (CFT). Abortion materials and milk samples were cultured and isolates confirmed by conventional polymerase chain reaction (PCR) test. Test results were considered positive for 1+ and above agglutination in RBT; SP% ≥ 80 in ELISA; titre of IU ≥ 20 in CFT and detection of 450 bp amplicon of *bp26* gene in PCR.

RESULTS: The 1st time point test results from serum samples were 31.67% (38/120) RBT positive and 39.17% (47/120) ELISA positive. 30.30% (10/33) of milk samples were positive by culture/PCR. The 2nd second time point test results from serum samples were 32.23% (39/121) RBT positive and 49.59% (60/120) ELISA positive. 16.67% (8/48) of milk samples were positive by culture/PCR. The 3rd time point test results from serum samples were 25.00% (32/128) RBT positive and 35.94% (46/128) ELISA positive. 29.27 (12/41) of milk samples were positive by culture/PCR. The 4th time point test results from serum samples were 36.92% (48/130) RBT positive, 37.69% (49/130) ELISA positive and 36.15% (47/130) CFT positive. 13.33% (6/45) milk samples were positive by culture/PCR. The 5th time point test results from serum samples were 38.18% (42/110) positive by RBT, ELISA and CFT. Culture of abortion materials yielded to Brucella organism. The mean (M ± SE) detection rates over the period of two years were 32.8 ± 2.32 (RBT), 40.11 ± 2.42 (ELISA), 37.17 ± 1.01 (CFT) and 22.39 ± 4.32 (culture/PCR).

CONCLUSION: The investigation confirmed that the abortion was due to *Brucella abortus* infection and the infection was consistently maintained in the farm for a long period of time.There is an urgent need to control and prevent the spread of infection. To prevent the spread of infection to human, personal protections of farm workers are enhanced and sale of unpasteurized milk banned. To prevent the spread of infection to other animals, distribution of breeding stock is put on hold. Public health authority is in the process of screening risk group humans for possible exposure.

P045 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Contact tracing of dog-bites, disability-adjusted life year score and associated risk of rabies in four Government hospitals of Pakistan.

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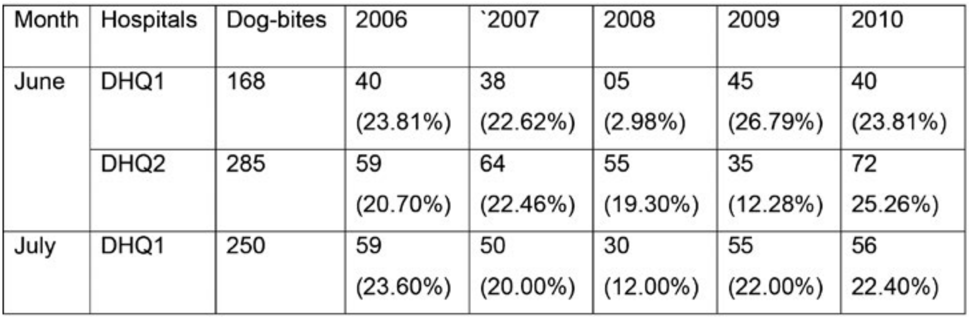
BACKGROUND: Rabies is an underestimated, lingering and neglected tropical disease in Pakistan. The present study was designed to investigate the burden of bite cases in humans, associated disability adjusted life year score (DALYs) and risk of rabies. The risk of rabies can be correlated with the number of bites caused by different species. This formulates the basis of our hypothesis and objective behind the data collection. The data were obtained from 4 district headquarter hospitals (DHQs) of Punjab, Pakistan which are maintained by the government and considered as an easy access health facility for the public.

METHODS: The data were manually procured from the outdoor patient department from 2 hospitals during 2006 to 2012, while similar method was carried out to obtain the data from remaining 2 hospitals during 2012 to 2017. It was manually categorised into number of total bites to male, female and children with specie causing the bite. Analysis of variance was carried out to statistically analyse the data obtained.

RESULTS: Results showed that the dog is the principal reservoir in causing almost all the bites in humans. The highest cases (n=310) were recorded in 2017 carrying the maximum number of male patients in one DHQ. The monthly distribution of bites were higher in summer with highest figure (>80%) of DALYs caused by category II bites, while limited number (>10%) of DLAYs was reported due to category III bites. The case of dog bite with essential requisites from a single patient was neither uniformly composed in hard form nor it was stored in soft form for future surveillance or national control plan.

CONCLUSIONS: Rabies is still endemic in Pakistan due to various epidemiological constraints including inadequate and insufficient prophylactic measures in basic health units of Pakistan, increasing population of unvaccinated stray dogs, lack of responsible pet ownership. Most importantly, lack of proper diagnostics and higher economic cost towards the prevention and elimination of rabies are the barriers behind legislative negligence. Moreover, lack of public awareness, and poor perceptions of health practitioners towards rabies are also causing higher number of dog bites in population.



Month	Hospitals	Dog-bites	2006	`2007	2008	2009	2010
June	DHQ1	168	40 (23.81%)	38 (22.62%)	05 (2.98%)	45 (26.79%)	40 (23.81%)
	DHQ2	285	59 (20.70%)	64 (22.46%)	55 (19.30%)	35 (12.28%)	72 25.26%)
July	DHQ1	250	59 (23.60%)	50 (20.00%)	30 (12.00%)	55 (22.00%)	56 22.40%)

Table 1: Total number of dog-bites in humans from 2 DHQs of Punjab, Pakistan.

P046 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Flaviviruses detected in wildlife and livestock in South African

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BACKGROUND:

Many Flaviviruses (family Flaviviridae) are arboviruses of medical and veterinary importance. The Flaviviruses genus consists of over 70 viruses including Zika-, Dengue-, West Nile- (WNV) and Wesselsbronvirus (WSLV). Many Flaviviruses have a zoonotic component in their life cycles, although the reservoir or amplifying hosts are not clearly defined. Previous studies have shown WNV as a cause of neurological disease in horses with a fatality rate of 35.0% in South Africa. The Emerging Arbo- and Respiratory Virus Programme (EARV) has been doing passive surveillance since 2010 to determine the aetiology of unexplained neurological-, febrile- or respiratory disease as well as sudden unexplained death in animals. Furthermore, sero-surveillance on healthy animals was conducted on wildlife from three provinces in South Africa to detect specific antibodies to WNV and WSLV. This study, as a follow up to surveillance in horses, aims to investigate Flaviviruses as cause of disease in wildlife, livestock and domestic species in South Africa and to identify possible reservoir hosts.

METHOD:

Veterinarians across Southern Africa send specimens from animals with unexplained neurological-, febrile- or respiratory disease or sudden unexplained death (SUD) to EARV. All specimens were tested with a Flavivirus genus nested real-time PCR. An epitope blocking ELISA (eb-ELISA) was used to detect specific antibodies against WNV and WSLV in healthy wildlife. The panel of sera comprised of 360 giraffes from Limpopo- and KwaZulu–Natal Province and 50 white rhinoceros and 45 buffaloes from Kruger National Park, Mpumalanga Province.

RESULTS:

Flaviviruses were detected in 13/504 (2.8%) sick or fatal animals. WNV was detected in 4/308 (1.3%) wildlife (2/22(9.1%) roan antelope, 1/8(12.5%) lion and 1/3 (33.3%) exotic deer), 3/128 (2.3%) livestock (2/77(2.6%) cattle and 1/6(16.7%) goat) and 1/21 (4.8%) domestic dogs. Bagaza virus was detected in 5/47 (10.6%) exotic pheasants. Phylogenetic analyses confirm WNV lineage 1 in the lion and the remainder as lineage 2. Flavivirus PCR positive cases were mostly associated with neurological signs (7/13, 54.0%) followed by respiratory signs (3/13, 23.1%), SUD (2/13, 15.4%) and fever (1/13, 7.7%).

Flavivirus antibodies were identified in white rhinoceros: 12/50 (24.0%) WSLB and 22/50 (44.0%) WNV and 3/50 (6.0%) WNV co-infections (WSBV, MIDV or SHUV). No WNV or WSBV antibodies were detected in buffalo. WSLV virus antibodies were present in 11/360 (3.1%) giraffes.

CONCLUSION:

From 2010-2017 we detected three Flaviviruses (primarily WNV) in various wildlife, livestock and bird species with neurological or respiratory signs by PCR. Sero-surveys identified WNV and WSBV antibodies in rhinoceros and giraffes but not in buffalo. This study suggest wildlife, livestock and domestic animals may also be affected by WNV and less well known flaviviruses in Africa and investigation of reservoir or amplifying host species are required.

P047 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

OHPIK (One Health Photography In Kinshasa)

Levy, Etienne; Antoine-Moussiaux, Nicolas; Desmecht, Daniel

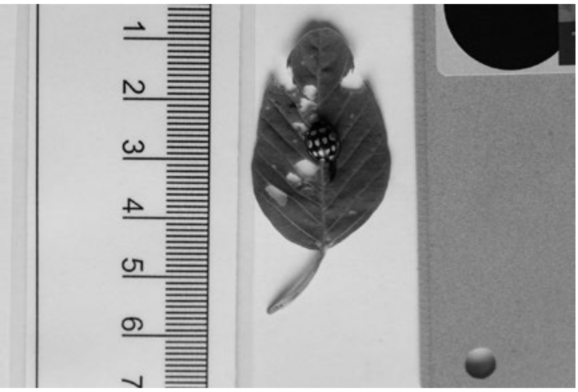
Uliege, Belgium -

BACKGROUND: Recent technological progresses have led to cheaper, easier to use and weather resistant cameras, of which performances equal those of human vision. These improvements pave the way to the emergence of a new discipline: One Health Photography.

METHODS: The project consists of a teaching in scientific photography to a multidisciplinary audience (human, animal, insect and vegetal specialists). It included an on-line step spread over 3 months firstly, followed by a one-week long practical teaching on the field. The first course was given in Kinshasa (Democratic Republic of Congo) in October 2017, thanks to a collaboration between CAVTK and ULiege and under the auspices of WBI and Ricoh-imaging.

RESULTS: The project is expected to provide sufficient knowledge and skills to the students for rendering them able to make high-resolution (36 Mpixels) images of macroscopic lesions that can be exchanged through the internet or printed for efficient remote diagnosis of local diseases even in very remote and poor locations. By doing so, medical and/or veterinary stakeholders benefit of an easy and cheap access to reference pictures of specific diseases, which efficiently complete the listings of known symptoms. Moreover, the time-, and GPS-tags associated to each picture adds an epidemiological dimension to the pictures collected, which will provide a new means to follow human and animal diseases in real time. The Kinshasa team has already produced several pictures useful for their area of expertise:

- Creation of a guideline concerning the management of water regarding the cholera epidemic
- Creation of a guideline concerning the housing of animals, with the aim of decreasing the needs of antibiotics.
- Creation of a database of healthy and unhealthy seeds to improve the farmers yield.
- Creation of a database of the edible insects, the crop pests, and the insect vectors of plant diseases.



Learner's picture after 2 days of training:

CONCLUSION: This type of course is adapted to both developed and developing countries. In the former, the sharing by internet pushed to a standardization of picture taking. For the latter, the course leads to the production of visual data with a high information value, that can be widely shared and evoke massive feedback and discussions with only cheap equipment. The final objective is to generate a world, multidisciplinary, standardized and geolocalized data base of human, animal and vegetal characteristic lesions.

P048 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Environmental Sampling for the Surveillance of Swine Influenza Virus.

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1: Sunnybrook Research Institute, Canada - 2: Canadian Food Inspection Agency - 3: Public Health Agency of Canada - 4: University of Toronto -

BACKGROUND: Swine influenza virus is a pathogen of significant public health importance. Environmental sampling techniques that prove to be practical and effective to detect influenza viruses would benefit efforts in disease surveillance and thus enhance early detection of potential zoonotic diseases The objective of this study was to demonstrate the feasibility of bioaerosol and surface sampling to detect and analyze influenza virus in swine barns while piloting a mobile application for data reporting using the Canadian Network for Public Health Intelligence (CNPHI) On the Go application.

METHODS: Sampling was conducted at a large farrow-to-finish swine operation. A barn containing 8 weaner rooms with pigs ranging from 3 to 11 weeks of age was sampled on 14 occasions in 2016 and 2017. Negative controls were collected from an experimental pig population and a dairy research barn. Oral fluids from rope media and surface swabs were collected from each pen and pooled. Five aerosol samplers were also tested, including a polytetrafluroethylene cassettes (PTFE) filter, a cyclone sampler or the National Institute for Occupational Health and Safety (NIOSH sampler), a 2-stage Anderson impactor, and two high volume cyclonic samplers. Sample interrogation was performed by PCR for the influenza virus matrix gene. Bioaerosol samples were sent to Fusion Genomics for sequencing using the EnviroScreen assay for swine influenza. Statistical analysis was performed using fisher's exact test and univariate logistic regression. All data and results were reported using the mobile data application.

RESULTS: A total of 90 pooled oral fluid samples, 74 environmental swabs, and 134 bioaerosol samples were collected and analyzed. Seventy-one percent (54/76) of swine barn oral fluid samples were positive by PCR. Analysis revealed a statistically significant relationship between detection of influenza virus RNA from PTFE cassettes and oral fluids by fisher's exact test and univariate logistic regression (p-values 0.0007 and 0.0014 respectively). Statistically significant results were also obtained for environmental swabs and oral fluids by fisher's exact test (p-value 0.0063) and univariate logistic regression (p-value 0.0085). Swine influenza virus subtype H3N2 was identified by Sanger sequencing on an oral fluid sample and by EnviroScreen on a bioaerosol sample. All but one set of negative control samples were negative. Use of the mobile application for data reporting allowed real-time reporting of samples and results.

CONCLUSIONS: We demonstrate the feasibility of environmental sampling for swine influenza virus. Bioaerosol sampling using PTFE cassettes and environmental swabs are predictive of influenza virus activity among swine; further study is required to leverage this approach with genetic sequencing of influenza virus in bioaerosols for surveillance and risk assessment of circulating swine influenza viruses. In addition, mobile data collection and reporting was piloted and stands to be an invaluable tool in data collection and reporting in the field.

P049 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Identification of cereulide producing strains of Bacillus cereus group by MALDI-TOF MS

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1: Chair of Food Safety, Veterinary Faculty, Ludwig-Maximilians University, Germany - 2: Chair for Hygiene and Technology of Milk, Veterinary Faculty, Ludwig-Maximilians University, Germany -

BACKGROUND: The *Bacillus (Bac.)* cereus group is genetically highly homogenous and consists of six recognized species. *Bac. cereus* strains play an important role for food intoxications by producing different toxins. The heat stable peptide cereulide causes severe emetic syndromes immediately after ingestion. However not all strains are able to produce cereulide and are therefore of minor relevance for food safety.

Currently, only time-consuming cell bioassays, molecular methods and tandem mass spectrometry are applied for the differentiation between emetic/non-emetic *Bac. cereus* strains. Thus, the aim of the present study was to set up a fast and reliable method for the differentiation between emetic/non-emetic strains by MALDI-TOF MS.

METHODS: Selected isolates of *Bac. cereus* group strains (n = 112) were cultured on sheep blood agar overnight. The cultures were directly analyzed by MALDI-TOF MS (Autoflex, Bruker Daltoniks) without prior extraction steps (direct smear method). The samples were measured in linear positive ionization mode in the mass range of *m/z* 800 – 1,800 Da.

RESULTS: Using ClinProTools 3.0 statistical software of Bruker Daltoniks, a differentiation between emetic/non-emetic isolates was possible with a rate of correct identification of 99.1 % by means of the evaluation of two specific biomarkers (*m/z* 1171 and 1185 Da).

CONCLUSION: In the presented approach, *Bac. cereus* cultures were directly measured from the agar plate and the detection of cereulide positive/negative samples was performed within 5 minutes. Thus, it is possible to differentiate fast and reliably between emetic and non-emetic strains by MALDI-TOF MS.

P050 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

A scoping review of Middle East respiratory syndrome coronavirus in natural animal hosts

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1: University of Guelph, Canada - 2: Food and Agriculture Organization of the United Nations -

BACKGROUND: Middle East respiratory syndrome coronavirus (MERS-CoV) is an emerging zoonotic pathogen discovered in 2012. The early implication of livestock (and dromedary camels in particular) in MERS-CoV transmission rapidly led to a number of experimental and field studies that aimed to improve our understanding of the epidemiology of this virus in animal hosts. The evidence base that builds from these experimental and field studies provides the foundation for more complex epidemiological analyses, and for designing effective early detection strategies. The purpose of this scoping review was to summarize the empirical evidence for MERS-CoV in animals in order to map knowledge gaps which can be used to inform future studies and surveillance.

METHODS: The review was guided by the five phases outlined by Arksey and O'Malley's (2005) framework for scoping reviews: Defining the research question; identifying relevant studies; study selection; charting the data; collating, summarizing, and reporting the results. In order to better assess the evidence base, and to more accurately identify research and knowledge gaps, a quality assessment of the articles was conducted by including key methodological questions adapted from the Critical Appraisal Skills Programme (CASP) checklist. A review protocol was developed a priori according to the research question "What are the general, epidemiological, and methodological characteristics of MERS-CoV in natural host populations?" The initial search was conducted on 26 April 2017 using five electronic databases.

RESULTS: Ninety-nine publications were identified for full review out of 1368 unique records. Of these publications, 71 were refereed, 26 were outbreak report entries in the EMPRESi database, and two were conference proceedings. Ninety of the studies were observational and the remaining nine were experimental. Prevalence of infection and seroprevalence were the most frequently reported outcome (69.7% and 39.4% of observational studies, respectively). Dromedary-level data reported included age and sex (52.8 % and 30.6% of observational publications, respectively). Seventy percent of the publications sampled dromedary camels at primary production points, while 20.8% sampled at abattoirs. Other characteristics summarized included species sampled, sample sizes, variables measured and outcomes of interest. Methodological characteristics and challenges were discussed.

CONCLUSIONS: In general, gaps in the evidence base of MERS-CoV in animals include epidemiological field studies with internal and external validity, and studies that examine questions of immunity in dromedary camels, especially long-term immunity. Tackling these two challenges would greatly advance our understanding of zoonotic risk and improve our ability to develop sound surveillance and disease prevention strategies.

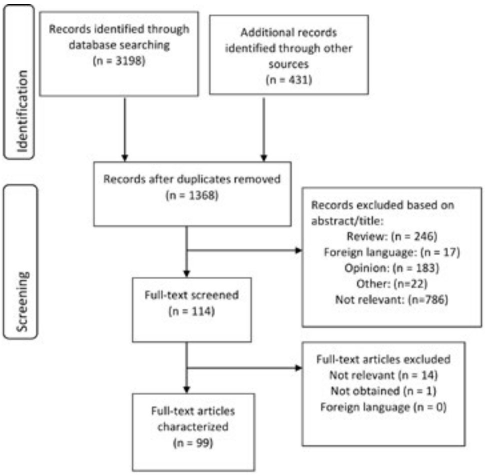

Figure 1 Review flowchart according to PRISMA template (http://prisma-statement.org/prismastatement/flowdiagram.aspx).

P051 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Synchronized surveillance at the wildlife-livestock-human interface in Thailand: a novel approach to early detection of viral transmission across species interfaces

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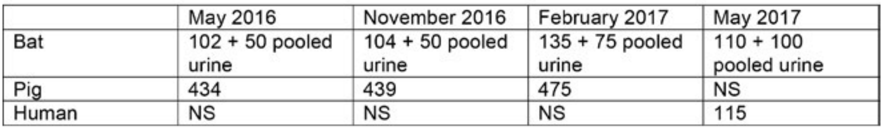
1: Ministry of Agriculture and Cooperatives, Thailand - 2: Faculty of Medicine, Chulalongkorn University, Thailand - 3: Regional Office for Asia and the Pacific, Food and Agriculture Organization of the United Nations (FAO), Thailand - 4: Wat Luang Health Promoting Hospital, Chonburi, Thailand - 5: Department of Forest Biology, Kasetsart University, Thailand - 6: Department of National Parks, Ministry of Natural Resources and Environment, Thailand - 7: EcoHealth Alliance, United States of America - 8: Cooperative Biological Engagement Program, U.S. Department of Defense, United States of America - 9: U.S. Agency for International Development, United States of America -

BACKGROUND: Current strategies for detecting emerging viral zoonoses of epidemic and pandemic potential are reliant upon event-based or indicator-based surveillance in select populations of humans or animals. Such approaches are challenged in documenting viral sharing across species interfaces, a pre-requisite for emergence, limiting their utility in early detection of emerging disease threats at source. Previous studies have documented Nipah virus and SARS-like coronaviruses in bats in Thailand. We present here the results of geographically- and temporally-synchronized viral zoonoses surveillance conducted across the wildlife-livestock-human interface in Thailand.

METHOD: A longitudinal study was conducted in Chonburi, Thailand. Sampling of 451 *Pteropus lylei* at one bat colony where Nipah virus has been identified; 1349 swine at 36 commercial farms; and 115 healthy community volunteers were conducted in May and November 2016, and February and May 2017 (table 1). Swine farms were within the 30 km radius of the bat colony sampled, and healthy human subjects were those living within proximity to the bat colony. At each occasion, sampling of all human and animal subjects was conducted within the span of one week. Whole blood, serum, oral or nasal and rectal swabs were collected and screened by consensus RT-PCR against five viral families with known epidemic/pandemic potential—paramyxovirus, coronavirus, flavivirus, filovirus, and influenza—using USAID PREDICT protocols. Pooled urine collected from under bat roosts was screened using paramyxovirus family and Nipah virus-specific RT-PCR assays. Data was uploaded into a secure, common data sharing platform for analysis.

Table 1: Synchronized surveillance sampling framework and number animals/humans sampled



	May 2016	November 2016	February 2017	May 2017
Bat	102 + 50 pooled urine	104 + 50 pooled urine	135 + 75 pooled urine	110 + 100 pooled urine
Pig	434	439	475	NS
Human	NS	NS	NS	115

NS: not sampled

RESULT: Bat rectal samples from May 2016 were positive for a novel betacoronavirus; pooled bat urine was positive for a novel paramyxovirus and a known Nipah virus with 99% homology to a strain detected in Bangladesh. Swine nasal, rectal and urine samples across all four sampling events were variously positive for known paramyxovirus (porcine parainfluenza virus); known coronaviruses (porcine epidemic diarrhea virus, porcine hemagglutinating encephalomyelitis virus, and transmissible gastroenteritis); and known influenza A. Other data—including results from oral swabs, whole blood and urine specimens from enrolled healthy humans—are under review and expected to be available by May 2018.

CONCLUSION: Although viral detection was not comparable across species surveilled, this study demonstrates the feasibility of—and provides a model for—synchronized viral zoonoses surveillance across species interfaces. Further risk-based refinement of animal population targets, syndromic surveillance in high-risk human populations focused on respiratory and acute encephalitis syndrome, addition of serology to guide surveillance targets, and enhanced temporal alignment, extended seasonal profile and expanded sample size may yield viral detection comparable across species. Such a platform holds promise of delivering upstream detection of spillover events, enabling earlier response and control, with benefits to human and animal health.

P052 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Collaborative multiagency approach to melioidosis biopreparedness in Western Australia

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INTRODUCTION: Melioidosis, a potentially fatal bacterial infection of humans and animals, is endemic in tropical Western Australia. In recent decades there have been case clusters in human and animal inhabitants of the temperate southwestern part of the state. Only one such cluster was restricted to humans and was attributed to contamination during health care procedures.

METHODS: Close collaboration between state human and veterinary pathology services enabled a coordinated approach to bacteriological investigation, exchange of bacterial isolates, a sharing of other laboratory resources and generated an evidence base for melioidosis countermeasures.

RESULTS: Two other melioidosis case clusters were epizootics in livestock from the same district, and were linked by a common *Burkholderia pseudomallei* genotype. Sporadic, culture-confirmed human cases were noted during both epizootics, but no direct epidemiological link to livestock was established, though human cases may have been exposed to the same environmental source as animal infection. The recent epizootic occurred shortly after unusual wet weather caused flooding of property used for the affected livestock.

CONCLUSION: A multiagency approach to surveillance and early laboratory guided response has strengthened our understanding of the changing disease distribution. Better access to bacterial whole genome sequencing in future will improve case cluster confirmation. A timely laboratory response to unexpected and unfamiliar bio-threats is best served by inter-agency cooperation.

P053 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Recurrent Anthrax Outbreaks in Human, Livestock and Wildlife in the same Locality, Kenya, 2014-2017

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BACKGROUND: Although epidemiologic data support a global distribution of anthrax outbreaks associated with certain ecological factors that promote survival and viability of *Bacillus anthracis* spores, these factors are not fully elucidated in the diverse African ecosystems. Here, we characterized three anthrax outbreaks involving humans, livestock and wildlife in the same locality between 2014 and 2017 in Kenya.

METHODS: Clinical and epidemiologic data on the three outbreaks were collected using standard active case finding, and review of human, livestock and wildlife records; whereas chronology and spatial distribution of prior outbreaks in the areas were collected through participatory epidemiological (PE) approaches (participatory mapping and focus group discussions).

RESULTS: The 2014-2017 outbreaks in West Nakuru sub-county affected 15 of 71 people that had contact with infected cattle (attack rate = 21.1%), including seven (46.7%) with gastrointestinal, six (40%) with cutaneous, and two (13.3%) with oropharyngeal forms of the disease. Two (13.3%) gastrointestinal human anthrax cases died. Of the 54 cattle in 11 households affected, 20 died (attack rate = 37%). Of the 768 wildlife animals that died at Lake Nakuru National Park, 747 (97.3%) were African buffalos with a species-specific mortality rate of 17% (747/~4500), while 8 (1%) were black and white rhinoceros with a species-specific mortality rate of 10% (8/78). The species-specific mortality rate ranged between 1%-5% for the other wildlife species affected; elands, impalas, Thompson gazelles, and Rothschild giraffes, warthogs, and waterbucks. Participatory epidemiology conducted at Soimet village affected by the 2017 outbreak indicated occurrence of prior anthrax outbreaks in 1973, 1979, 1982, 1986, and 2011 in the village.

CONCLUSION: Among the cultural practices that increased the risk of anthrax outbreaks were slaughter and consumption of infected animals, skinning livestock carcasses before burial, and lack of routine vaccination.

P054 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Zoonotic and vector borne agents causing disease in adult patients hospitalized due to fever of unknown origin in Thailand

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BACKGROUND: Early detection of infectious diseases in high-risk populations is also vital for limiting the spread of EIDs. Disease surveillance by gathering and generating data on disease incidence and prevalence in high-risk populations, as proposed here, can provide the basis of evidence for early detection and prompt response to EIDs in Thailand. The objectives were to determine etiologic agents of fever of unknown origin (FUO) among populations in agricultural communities and to assess the possible risk factors for zoonotic infections

METHODS: We conducted the study from November 2013 to August 2015 in agricultural communities in three provinces with a total of seven participating community hospitals. Hospitalized patients with fever of unknown (FUO) etiology were asked to participate After a written informed consent was obtained, all participants answered a standardized questionnaire. A direct person-to-person written informed consent was obtained at enrollment. Occupational exposure to livestock or wildlife was assessed by project staff at the participating hospitals through patient interviews. The participants were collected blood samples, cerebrospinal fluid, or nasopharyngeal swabs for laboratory tests at each hospital. Initial screening for endemic diseases including influenza, dengue, leptospirosis, scrub typhus, salmonellosis, typhoid, and malaria was done at the surveillance hospitals. Undiagnosed specimens were transported to a central laboratory where testing for several infectious agents were performed by molecular technique.

RESULTS: We were able to identify the etiologic agents in 24.6% of the 463 enrolled patients. Zoonotic and vector borne agents were confirmed in 59 cases (12.7%). Dengue virus (7.3%) was the most frequently detected disease followed by scrub typhus (3.2%). There were two cases of comorbidities of scrub typhus and dengue fever. The other six cases of zoonoses were leptospirosis, melioidosis, and Streptococcus suis infections. Patients with zoonotic/vector borne agents noticed rats in their houses and reported having contact with livestock feces more frequently than those patients without zoonotic/vector borne agents.

CONCLUSIONS: Dengue virus and scrub typhus were most frequently detected in the study populations. The number of cases of FUO, from dengue fever, scrub typhus and other zoonotic diseases including leptospirosis and melioidosis detected in our study were highest in the rainy season from July to October. Clinicians should be aware of those diseases when patients are admitted to the hospital with fever of an unidentified etiology, especially during the rainy season, to give a proper clinical management before the disease progresses.

P055 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Environmental Sources of Zoonotic Enteric Parasites in Mongolia

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BACKGROUND: Across Mongolia, there are over 61 million livestock that roam freely across the steppe. These domestic animals are predominantly made up of horses, goats, sheep, cattle, camels, and yaks and depend upon seasonal movement to find pasture and water throughout an extreme climate. Nomadic herding families relocate their homes with their livestock and often depend upon the same water sources as their animals. As part of a larger study on the presence of zoonotic enteric parasites, the objective of this research was to determine the presence of *Cryptosporidium spp., Giardia lamblia,* and *Entameoba histolytica* in and around environmental water sources utilized by domestic animals and herding households. Additionally, the potential role of fly vectors in the transmission of zoonotic enteric parasites was examined through the analysis of filth flies collected from inside herding households.

METHODS: Environmental water sources used by herding households were identified in the rural provinces of Selenge, Zavkhan, and Dundgovi and in the peri-urban district of the capital city of Ulaanbaatar in Tov province. Approximately 500mL of water was collected from each site during the spring and fall of 2017. Fresh stool from wildlife and domestic animals at the water site was also collected. In 250 rural, peri-urban, and urban households, fly strips were placed for 24 hours before flies were collected. Real-time PCR was used to detect the 18S ribosomal RNA gene for *Giardia lamblia* and *Entamoeba histolytica* and the COWP (Cryptosporidium oocyst wall protein) for Cryptosporidium spp. from all samples of environmental water, wildlife and domestic animal stool from the water site, and household filth flies.

RESULTS: Water was sampled from rivers, streams, deep wells, and springs and each site had evidence of recent usage by animals. Fourteen samples from environmental water sources and over 60 stool samples from wildlife and domestic animals at the shared environmental water site were collected for analysis. Flies samples were gathered from 115 households and identified as primarily from the families of *Muscidae, Calliphoridae,* and *Sarcophagidae*. Laboratory analysis on the presence of zoonotic enteric parasites is currently being conducted.

CONCLUSIONS: Zoonotic enteric parasites can be transmitted from domestic animals, wildlife, humans, contaminated water sources, and fly vectors. Our study on the association of these parasites with shared human and animal environmental water sources and proximal household filth flies demonstrates a holistic One Health approach to the identification of potential exposure pathways for zoonoses in rural and peri-urban herding families and areas for public health interventions. Results of this study will be used to develop recommendations for the prevention of zoonotic enteric parasite transmission among people and domestic animals of Mongolia, particularly in herding households that share drinking water sources with livestock, wildlife, and the environment.

P056 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Community event–based Surveillance by using One Health approach in communities of livestock farmers

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BACKGROUND: An outbreak notification program, called a routine program, has been routinely initiated in Thailand since 2013. Most public health agencies reported diseases and abnormal events via this program. Source of information about the abnormal events mostly found in human populations and few reports from animal populations. Since 2017, strengthening the surveillance and investigation of zoonotic diseases has been implemented by using One Health approach at a community level. Local public health officers, livestock officers and livestock farmers in three districts from two pilot provinces were trained to understand an essential component of event-based surveillance and asked them to notify the abnormal events on our Mobile app development.

METHODS: Suspected zoonotic diseases were extracted from all submitted events that were reported on the Mobile app and the routine program. Source of reporter was stratified by occupations. Timeliness was measured as the difference between the date occurs and the reporting date. Differences in timeliness and number of joint investigation units were evaluated by comparing between two data sources from the Mobile app and the routine program using a generalized linear model with Pearson's goodness of fit statistic.

RESULTS: We assessed 63 reports in the Mobile app and 40 reports in the routine program. 90.5% of the reporter from the mobile app was farmers in communities while only 10% in the routine program coming from people in communities. The Mobile app reports were received, on average, 1.7 days were the timeliness if the event was observed at people in communities versus 12.3 days for reports in the routine program (p =0.0001) and 2.1 days versus 17 days if the event occurring in poultry farms (p =0.002). There were 17 reports in pig farms from the Mobile app and there was none of pigs' event in the routine program. There was 30.2% of events in the Mobile app that describedan activity of joint diseaseoutbreak investigation for zoonoses (human and animal health sectors) while only 12.5% reporting this activity in the routine program.

CONCLUSIONS: The event-based surveillance when using a One Health approach and implementing into the community level can show more efficient capabilities of early detection and responding to threats in local communities.

P057 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

The seropositive of influenza A (pH1N1) in Thai cat

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BACKGROUND: Influenza virus is a single-stranded RNA virus and belongs to *Orthomyxoviridae* family. This virus is able to classify as 4 types including A B C and D. In 1918, the influenza pandemic H1N1 was first reported in human and caused 40 million people died. After that the novel influenza pandemic H1N1 outbreak occurred again in North America, 2009 and was declared by WHO in June in the same year especially in young children, pregnant women, or people of any age with certain chronic lung or other medical conditions. The monitoring of influenza should be investigated closely for next upcoming pandemic prevention.

METHODS: Cats were chosen randomly in this study. Blood samples were collected into plain tubes and were centrifuged within 12 hours at 3,000 rpm for 10 minutes. Supernatants were stores at -20 degree Celsius before testing. Totally 79 serum samples from 79 unvaccinated cats including 45 females (n= 45/79, 56.96%) and 34 (n=34/79, 43.04%) males were collected during December 2011 to September 2014 from 14 provinces. All serum samples were screened for influenza A nucleoprotein antibodies detection as well conserved region using a commercially available multi-species competitive NP-ELISA assay (ID Screen®, ID Vet, France) and were confirmatory tested with Hemagglutination inhibition assay (HI) using 3 positive virus subtype including canine H3N2, human pandemic H1N1 and human H3N2 viruses.

RESULTS: All samples showed negative when tested by NP-ELISA method. A sera sample (n=1/79, 1.27%) from Nakorn-Pathom province was positive when tested by Hemagglutination inhibition assay (HI) showing the antibody against pandemic H1N1 but showed negative against human H3N2 and canine H3N2, the S/N value from NP-ELISA showed 83.00 (negative).

CONCLUSION: The NP-ELISA assay should not be only used for influenza testing. Hemagglutination inhibition assay is more specific than NP-ELISA as previous papers described. The seropositive of influenza A pandemic H1N1 was demonstrated in cat sera by using Hemagglutination inhibition assay but the origin of the virus needs to be investigated more in the next experiment by using the viral isolation method for describing the original species of the virus. Moreover, the inter-transmission should be monitored closely especially to human because it might able to have pandemic potential in other species particularly in human.

P058 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Risk of chronic Q-fever in patients with cardiac valvulopathy, after a large epidemic in the Netherlands: a one-year cross-sectional study

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BACKGROUND: From 2007 through 2010, a large epidemic of acute Q-fever occurred in the Netherlands, in which dairy goats were implicated as the source. About 5% of the acute Q-fever patients develop chronic infection, a life-threatening complication of this zoonotic disease, which mainly presents as endocarditis or vascular infection. Patients with pre-existing cardiac valvulopathy have a high risk to develop chronic Q-fever after a symptomatic or asymptomatic acute infection. This patient group was not routinely screened during and after the epidemic, so it is unknown whether all chronic infections among patients with valvulopathy have been diagnosed. The objective of this study is to investigate how many chronic Q-fever patients can be identified, by routinely screening patients with valvulopathy, to establish whether the policy of not routinely screening should be adapted.

METHODS: This is a one-year cross sectional study (2016-2017) in a hospital in the epicentre of the Q-fever epidemic. One blood sample was taken from patients 18 years and older, who attended the hospital for cardiac valvulopathy. The blood sample was tested for IgG antibodies against phase I and II of the *Coxiella burnetii* bacterium, with an immunofluorescence assay. An IgG phase II titre of ≥1:64 was considered serological evidence of a previous Q-fever infection. An IgG phase I titre of ≥1:512 was considered suspicious for a chronic Q-fever infection and these patients were referred to the Internal Medicine Department for further examination.

RESULTS: Of the 904 included patients, 133 (15%) had serological evidence of a previous *C. burnetii* infection. Six (5%) of these 133 patients had a chronic infection after further medical examination.

CONCLUSIONS: In a high-risk group of patients with a heart valve defect, we diagnosed new chronic Q-fever infections, seven years after the end of the epidemic. This suggests that screening of this patient group is still meaningful in order to prevent further complications of those who were not yet diagnosed in areas that were affected by the Q-fever epidemic. It also shows the long-term impact of an epidemic of the zoonosis Q-fever.

P059 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Characterizing ecological traits of wildlife hosts of zoonotic flaviviruses to identify geographical hotspots for sylvatic transmission

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BACKGROUND: Recent emergence of Zika virus (ZIKV) and recurring outbreaks of West Nile virus (WNV) and yellow fever virus (YFV) indicate that flaviviruses represent a significant public health threat with high pandemic potential. Zoonotic flaviviruses are known to circulate among a wide variety of mammalian and avian hosts, and spillover from sylvatic cycles can thwart efforts at disease control. Identifying potential undiscovered non-human vertebrate hosts for flaviviruses will help to recognize geographic areas and high-risk interfaces likely to be involved in future spillover events. This study characterizes macro-ecological host traits of zoonotic flaviviruses to advance our understanding of host propensity of flaviviruses and geographic regions with increased risk.

METHODS: A systematic search of the peer-reviewed literature was undertaken to identify non-human vertebrate hosts of zoonotic flaviviruses. A hierarchical cluster analysis was done to identify flaviviruses that share similar vertebrate hosts using data collected on all recognized hosts for flaviviruses. We evaluated ecological and climatic trait profiles of these hosts using generalized boosted regression tree methods. Presence of mosquitoes and tick vectors across the geographical distribution of hosts were also included in host trait features as a proxy for interaction between hosts and vectors. We ran multiple models for virus clusters and individual viruses to highlight traits distinguishing hosts from non-hosts and to predict potentially new, undiscovered wildlife hosts.

RESULTS: Preliminary analyses revealed distinct clusters of flaviviruses among recognized hosts, including: 1) ZIKV and YFV; 2) WNV, St. Louis encephalitis virus, Usutu virus, and tick-borne encephalitis virus; and 3) Rio Bravo virus, Dakar bat virus, and Entebbe bat virus. The generalized boosted regression tree model for YFV and ZIKV (AUC 0.972) indicated that out of 71 modelled host traits, traits of highest importance were related to host distribution, habitat propensity, and foraging behavior (Figure 1c). Primates showed significantly higher probability of becoming hosts than species from other orders. Models identified novel hosts with geographical distributions wider than the currently understood distribution of confirmed hosts (Figures 1a and 1b). Similar model results were found for the other virus cluster models.

CONCLUSION: We present a novel modeling framework for predicting potentially new and as-yet-unrecognized sylvatic hosts of flaviviruses which can be applied to groups of viruses having similar host propensity. Our findings can inform on needed investments in targeted wildlife surveillance to identify wildlife reservoirs and their role in the re-emergence and propagation of flaviviruses.

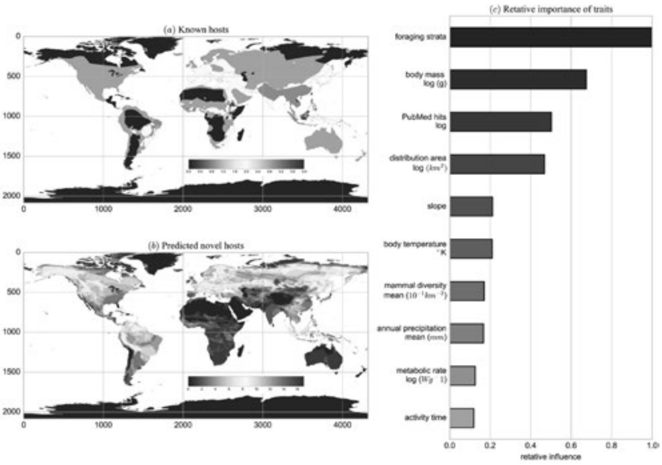

Figure 1. Results for the Yellow Fever virus (YFV) and Zika virus (ZIKV) model: (a) overlapping geographical ranges of known sylvatic hosts; (b) overlapping geographical ranges of model-predicted novel hosts in the 95th percentile probability for YFV and ZIKV; (c) bar plot showing the relative importance of the top 10 host traits discerning hosts and non-hosts for YFV and ZIKV.

P060 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

One Health in China——From SARS to H7N9

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BACKGROUND: Emerging infectious diseases (EIDs) are always major issues that threaten global health: the damage caused by SARS-CoV is still impressive to people throughout the world in 2013; since 2009, starting in China as the source of the epidemic, the influenza A H1N1 virus has gradually spread 206 countries or regions; similarly, causing five epidemic waves in China since 2013, avian influenza A(H7N9) virus brought a heavy blow to China's public health. China's health system has made great strides in its concepts, strategies and effects of coping with public health issues, which suggests that China surely play a key role in safeguarding global health with the striking economic growth.

METHODS: Taking the disposal of SARS epidemic and H7N9 outbreak as examples, the characters of the response of Chinese health system of public health issues were analyzed by descriptive research approach, to illustrate the change of China's health system and the urgency of implementing One Health strategy.

RESULTS: During the SARS outbreak, China's approach to the disposal of EID was built on the principle of "maintaining social stability", which challenged the reaction to emergency event of Chinese public health system, and revealed its insufficiency of reformation. China has gradually made a series of transformation in this field: The response to the outbreak of human infection of avian influenza H7N9 are commendable for the effective prevention and control measures; the "Chinese Model" has successfully assisted Africa in the fight against the Ebola outbreak, and provided precious experience in the prevention and control of EIDs worldwide. Another lesson learned from the SARS outbreak is the indispensability of rapidly identifying the source of infection and routes of transmission. In order to improve the ability of monitoring and early warning and evidence-based decision-making capacity, China has gradually established a new system and a better disease model. These products have been applied to pathogen detection, rapid diagnosis and treatment of infected person. For major infectious diseases, such as AIDS, tuberculosis, etc, it is proposed the joint prevention and control strategy in China. However, there are some shortcomings in Chinese public health system. The question how to coordinate regional or local interests to reach consensus is still hard to answer, and the proposal of "the Belt and Road initiative" also poses a challenge for public health in China.

CONCLUSIONS: In order to further improve Chinese public health construction, One Health strategy is an effective and imperative measure to meet the health and safety challenges of both China and the international community after considering the animals, the environment and other factors that could affect human life. In the future, we're anticipating that China will make greater achievements in the field of One Health practice.

P061 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Atlantic Bottlenose Dolphins (Tursiops truncatus) as A Sentinel for Exposure to Mercury in Humans: Closing the Loop

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Mercury (Hg) is a global contaminant with important public health implications. Much of this Hg enters the oceans through atmospheric transport and rainfall deposition. In the marine environment inorganic Hg is converted to the toxic form of the element, methylmercury, and biomagnified through the food web. The bottlenose dolphin (*Tursiops truncatus*), an apex predator with a long life span, bioaccumulates high concentrations of contaminants including Hg, thus making them an important sentinel species for ecosystem and public health. Concentrations of Hg in blood and skin of bottlenose dolphins of the Indian River Lagoon, FL (IRL) are among the highest reported world-wide. In previous studies, we demonstrated associations between concentrations of total Hg in the blood and skin of IRL dolphins and markers of endocrine, renal, hepatic, hematologic and immune system dysfunction. In humans, the predominant manifestation of exposure to mercury is neurotoxicity. During the 1950s and 1960s, residents of Minamata bay, Japan were exposed to high concentrations of methyl mercury as the result of ingestion of fish and shellfish contaminated in this infamous environmental disaster. Affected adults had severe motor and sensory abnormalities. Methyl mercury crosses the placenta during pregnancy. Children exposed in *utero* were born with congenital anomalies and suffered from neurologic disorders. Significantly, local cats that consumed Hg contaminated fish developed severe signs of neurotoxicity which led to their subsequent description as the “dancing cats of Minamata bay”. Unfortunately, the cause of these strange manifestations in cats was not recognized in time to prevent additional cases from occurring. More recent studies have demonstrated exposure to mercury as a result of seafood consumption during pregnancy may result in multiple cognitive and neurodevelopmental effects in children. The levels of mercury found in bottlenose dolphins and the health effects we identified alerted us to the possibility of an important public health hazard. The IRL occupies 40 percent of the east coast of Florida and is bordered by counties with approximately 2.5 million human inhabitants. Therefore, we hypothesized that local inhabitants in communities bordering the IRL could be at risk of exposure to Hg from the consumption of fish and shellfish. We measured hair Hg in 135 local residents and found a mean concentration of 1.53 μg/g which was higher than previous studies of sport fishermen and coastal residents in other states. Over 50% of participants had a hair Hg concentration which exceeded the U.S. EPA exposure guideline. Hair Hg concentration was directly related to the frequency of seafood consumption and to the proportion of fish and shellfish obtained from local recreational sources. This study clearly exemplifies the importance of an animal sentinel in identifying a public health hazard and is virtually unique in “closing the loop” between animal and human health.

P062 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Insights Gained for Surveillance and Biosecurity from the 2015 High Pathogenicity Avian Influenza (HPAI) Outbreaks in the Midwestern U.S.

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There is a need to maintain the food supply, implement biosecurity, provide data for surveillance, monitor virus evolution of HPAI, and develop response strategies for both animal and human health. In the U.S., the USDA National Poultry Improvement Plan (NPIP) requires testing for low pathogenicity avian influenza (LPAI), especially since LPAI H5 and H7 can mutate to HPAI H5 and H7. USDA-APHIS has Foreign Animal Disease Preparedness and Response Plans (FAD PReP). The Center for Food Security and Public Health (CFSPH) has developed a number of Secure Food Supply (SFS) Plans to facilitate movement of animals and/or animal products from premises with no evidence of infection for specific FADs. SFS Plans were developed with multi-disciplinary partnerships, funded by USDA-APHIS Veterinary Services, for a rapid decision making process to facilitate business and food continuity during an outbreak. SFS Plans' common components are: voluntary pre-outbreak preparedness, biosecurity, surveillance, epidemiology questionnaires, movement permits, risk assessments, and pre- and post-outbreak training. SFS Plans evolve with emerging science and capabilities, and serve as guidelines, since final decisions are made by the responsible officials. A SFS Plan for poultry, the Secure Poultry Supply (SPS) Plan, was developed based on an HPAI outbreak with the assumption of a zoonotic strain. SPS Plan objectives are: to minimize the risk of exposure of poultry flocks to HPAI, limit the spread of HPAI during an outbreak, and provide a high level of confidence that poultry products entering the food supply are free of HPAI virus via RT-PCR testing. During the 2015 H5N2 HPAI outbreak, Iowa had the catastrophic loss of 32 million poultry, an estimated $1.2 billion loss to the economy, and a $1 billion cost to the federal government. Fortunately, the H5N2 strain was not zoonotic. USDA-APHIS FAD PReP and SPS Plans were in place and used. Outcomes identified that surveillance monitoring worked well to demonstrate the lack of infection, to issue movement permits, and to prevent destroying unaffected healthy birds and eggs while preventing further spread of HPAI, facilitated by rapid RT-PCR results. The HPAI outbreak also identified areas for improvement. First, biosecurity that is adequate for an endemic disease is not adequate for an outbreak of a highly contagious novel disease, which lead to the adoption of new more rigorous biosecurity protocols for the commercial poultry industry as part of NPIP. Second, there was an essential need to depopulate entire infected flocks within 24 hours of virus confirmation. Failure to do so resulted in high virus production and disease spread. Third was efficient prior planning of environmentally acceptable and biosecure carcass disposal of large numbers of poultry, which is critical for containment. Poultry industry and regulatory officials have collaborated to implement important changes.

P063 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Surveillance on Crimean-Congo Hemorrhagic Fever in Georgia

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BACKGROUND: Crimean-Congo Hemorrhagic Fever (CCHF) is a zoonotic disease which is endemic for many European and Asian countries. The surveillance system of Georgia has detected an increase in numbers of CCHF cases over the past years, which stresses the importance of strengthening early detection and prevention systems by enhancing One Health approaches.

METHODS: Case-based data was extracted through the Electronic Integrated Disease Surveillance System (EIDSS) by using the following selection criteria: final diagnosis – CCHF; and final classification – confirmed (clinically compatible case with laboratory confirmation). A period between 2009 and 2017 was chosen.
Results: A total of 56 cases were identified. The median age was 48.5 (range 4-77 years); 34 (60.7%) were male. Cases of CCHF have occurred throughout the year, however, most of them have been registered in the summer (71.4%). The vast majority of cases were registered in the eastern part of the country (91%). 7 (12.5%) cases have had a lethal outcome, and interestingly, none of them received antiviral drugs at the time of notification. Out of selected cases, only 7 (12.5%) received specific treatment on time. Most of the cases (89.3%) were reported by the physicians on the same day of having clinical suspicion. The average number of days between onset of symptoms and admission to hospital was 3.4 (range 0-15 days). CCHF was frequently reported as an initial diagnosis (92.8%), however, some of the doctors suspected Hemorrhagic Fever with Renal Syndrome (3.6%), fever of unknown origin (1.8%), and Leptospirosis (1.8%) at first. Disease transmission was predominantly linked to tick bites (48.2%) and tick exposure (41.1%), as well as to close contact with livestock (8.9%). One case of nosocomial transmission was also registered (1.8%).

CONCLUSIONS: Despite the capability of identifying CCHF in Georgia, the data obtained through current surveillance system shows only one side of the problem and it lacks the ability to prevent avoidable epidemics, and predict focal outbreaks. Even though all three important segments are present (surveillance in humans, vectors, and animals), they lack a comprehensive and joint – One Health approach for determining CCHF epidemiology and transmission ecology. National Center for Disease Control and Public Health of Georgia will provide evidence-based information in the future for strengthening surveillance system by developing and implementing a risk assessment tool, capable of identifying local risk-factors for CCHF transmission, and use this data to effectively prevent future outbreaks.

P064 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

First study of Enterovirus typing by partial sequencing of VP1 gene in Georgia

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BACKGROUND: The most sporadic cases and outbreaks of aseptic meningitis worldwide are associated with enteroviruses (EV). In order to determine public health significance of enteroviral meningitis and to characterize associated etiologic agents in Georgia we decided to investigate hospitalized aseptic meningitis cases and environmental sewage samples from eight different regions of country.

METHODS: We investigated 36 Fecal, 18 CSF from hospitalized patients and 91 sewage samples from different regions of Georgia. Firstly, we inoculated them on RD and L20B cell lines, one tube of each cell type where used as a negative control. After 2 week observation for cytopathic effect 35 of them where positive. Further we performed Real-time PCR. RT-PCR positive EV amplicons were gel purified using QIAGEN Gel Extraction Kit and sequenced in both directions to assure accuracy. EV68 where used as positive control. Sequences were edited using Sequencher 5.0. NCBI BLAST.

RESULTS: As a result we typed by partial sequencing of VP1 gene epidemiologically interesting 8 samples and got five different strains of Enteroviruses CVB5, E9, E14, E18, A71. CVB5 strains where closely related to strains isolated from Australia, A71 Sequence analysis demonstrated 97% identity to strains isolated from Human meningitis cases in Germany, Strain E9 caused last outbreak of viral meningitis in 2006 in Georgia.

CONCLUSION: Study revealed EV diversity in Georgia in relatively short observation period in 2016-2017. Findings from molecular studies will determine rates and risk factors for having enteroviral aseptic meningitis in future in Georgia. Conducted research will be important for public health, as they will be used for developing and implementing appropriate diagnostic and control strategies for meningitis caused by EV in the country of Georgia.

P065 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Diversity and potential risk of dissemination of zoonotic pathogens associated with insectivorous bats in Georgia

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BACKGROUND: Bats are hosts of a wide range of zoonotic pathogens. *Bartonella, Brucella, Leptospira,* and *Yersinia* are zoonotic pathogens causing diseases in domestic or companion animals and in humans in Georgia. Human activities that increase exposure to bats are raising the opportunity for these infections to cross species barriers from bats to humans in the future.

OBJECTIVES: In view of this, a bat survey was conducted in Georgia, which identified ecologically interesting species and pathogens.

METHODS: Totally 218 bats, eight different species were obtained from attics of human dwellings and caves. A real-time PCR assay was performed in a triplex for detection of *Brucella* (IS711), *Bartonella* (tmRNA), and *Yersinia* (pal) from bat spleen tissues. An individual real-time PCR assay was used for detection of *Leptospira* (LipL32) in bat kidney tissues. Conventional PCR targeting the 16SrRNA gene was performed for detection of multiple strains of other bacteria in spleen tissues.

RESULTS: *Bartonella* DNA was detected in 77 of the 218 tested bat kidneys, giving the overall prevalence of 35%. *Brucella* DNA was detected in spleens of four bats, first time in the world. *Leptospira* DNA was amplified from kidneys of 25 bats, giving the overall prevalence of 11%. *Yersinia* DNA was detected in none of the bats, neither in spleen, kidney, nor intestine. Eighteen bats were co-infected with *Bartonella and Leptospira*, One *Miniopterus schreibersii* bat *from Tskhaltubo* cave was positive fro three different pathogen for *Bartonella, Brucella,* and *Leptospira.*

CONCLUSION: Investigated caves recently become an attraction place for tourism about 80 000 visitors per year, colonies of insectivores bats come out from the caves for feeding. The high prevalence observed pathogens suggest that these bats might p lay a possible role in the maintenance of *Leptospira* spp. and *Bartonella* and emerging *Brucella* in the environment, which can reflect possible spillover of pathogens in caves and new places.

P066 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Monitoring of zoonotic agents along the food chain - a valuable risk management tool

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BACKGROUND: Directive 2003/99/EC requires all member states of the EU to *“ensure that zoonoses, zoonotic agents and related antimicrobial resistance are properly monitored”* and therefore to collect relevant and comparable data along the food chain. Under German national legislation, these requirements are implemented through an annual program, known as “Zoonoses Monitoring”.

METHODS: An annual sampling plan is agreed upon by the *Laender* (German states) according to the requirements of Directive 2003/99/EC and Decision 2013/652/EU, as well as with regard to current areas of interest from the view of risk management.

The sampling plan contains specifications concerning the zoonotic agents to be monitored, the respective animal populations and/or stages of the food chain, such as primary production, slaughterhouses or the retail level.

The program regularly includes *Salmonella, Campylobacter, Listeria,* STEC and MRSA. Moreover, commensal *E. coli* of various production systems (broilers, layers, fattening pigs etc.) are regularly monitored for their resistance patterns, including identification of ESBL-, AmpC- and Carbapenemase-producing *E. coli.*

Apart from the most important food chains of animal production, food of non-animal origin and feed have been included in the program as well to gain an overall picture.

RESULTS: The “Zoonoses Monitoring” has been conducted annually since 2009. As a result, an extensive set of data on the prevalence of various zoonotic agents in animals, food and feed as well as their respective antibiotic resistance profiles has been obtained.

Results show that there is a significant decrease of *Salmonella* detection rates in broilers in recent years, probably as a result of compulsory control programs, whereas detection rates for *Campylobacter* have seen a constant increase.

Moreover, contamination rates along the food chain for both, *Salmonella* and *Campylobacter*, seem to be much higher in poultry compared to pork.

Regarding resistance patterns of commensal *E. coli*, the program revealed the highest rates in poultry and pork. In various cases (e.g. broilers and milk production) antibiotic resistance seemed to be less pronounced in organic as compared to conventional production.

CONCLUSIONS: Based on the requirements of Directive 2003/99/EC, comparable data on various zoonotic agents and their respective antibiotic resistance patterns are collected along various food chains. This has proven to be an invaluable tool to initiate risk management measures and/or to follow up on their results.
The results showed a decrease in *Salmonella* prevalence in broilers in Germany, most likely as a result of control programs, whereas in future the possible effect of a new process hygiene criterion for *Campylobacter* may be monitored through this program.

Moreover, the monitoring of the dynamics of antibiotic resistance in pathogens and commensal bacteria may lead to risk management decisions in the future.

P067 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Territorial model of integrated epidemiological surveillance

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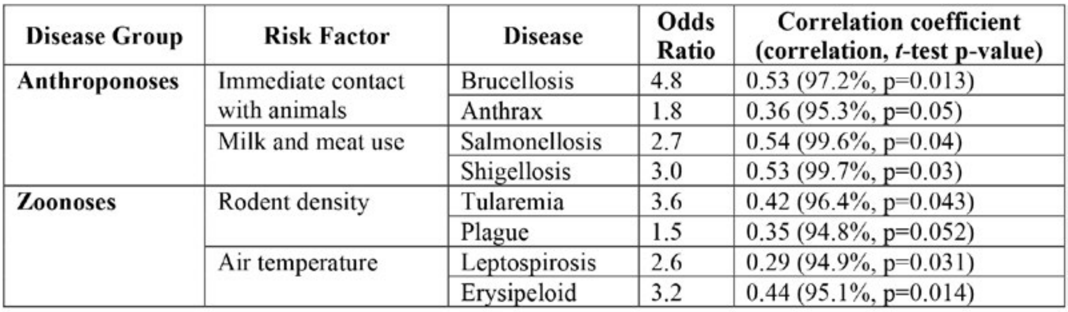
BACKGROUND: Public healthcare programs must ensure an optimum distribution of tasks and an integrated analysis of incoming information. An integrated epidemiological risk management model for infectious diseases in Armenia was developed.

METHODS: The National Center for Disease Control and Prevention has tracked epizootic data since 1954 and human infectious disease since 1977. Records from 1977-2017 included 16,540 cases of infectious diseases (including brucellosis, tularemia, anthrax, salmonellosis, and shigellosis) from 12 human and 40 animal outbreaks. All cases were analyzed by retrospective cohort epidemiological and statistical methods to determine correlation between disease severity and natural factors, including air temperature, humidity, outbreak location, and carrier and vector prevalence. Correlation coefficients and odds ratios for risk factors for each disease were calculated, and “high risk” was defined by correlation coefficient (correlation >95%, p-value <0.05) and odds ratio (OR >1). Establishment of the database, assessment of geographical risks, and mapping were accomplished using Arc-GIS10.1.

RESULTS: Outbreak records were integrated with entomological, parasitological, agricultural, veterinary, meteorological, climatic, and geographical data; risk factors impacting infectious diseases; and demographic and household data. Changes in risk factors affected disease emergence (OR=1,5-4,8). For example, though there were zero tularemia epizooties in the last ten years in Shirak Province, the integrated analysis predicted that the epidemiological threshold had been surpassed and pinpointed the at-risk population, based on increases in rodent and vector populations, warmer temperatures, and increases in agricultural field work. In 2017, four cases of tularemia were recorded in field workers, confirming the prediction. Similarly, risk factors for other infections were mapped against outbreak time and location to identify the dominant risk factor. In many cases, the same factors influenced multiple diseases (e.g. diseases transmitted by the same vector). Examples of risk factors affecting various diseases are shown in the table below.



Disease Group	Risk Factor	Disease	Odds Ratio	Correlation coefficient (correlation, *t*-test p-value)
Anthroponoses	Immediate contact with animals	Brucellosis	4.8	0.53 (97.2%, p=0.013)
		Anthrax	1.8	0.36 (95.3%, p=0.05)
	Milk and meat use	Salmonellosis	2.7	0.54 (99.6%, p=0.04)
		Shigellosis	3.0	0.53 (99.7%, p=0.03)
Zoonoses	Rodent density	Tularemia	3.6	0.42 (96.4%, p=0.043)
		Plague	1.5	0.35 (94.8%, p=0.052)
	Air temperature	Leptospirosis	2.6	0.29 (94.9%, p=0.031)
		Erysipeloid	3.2	0.44 (95.1%, p=0.014)

CONCLUSIONS: Forty years of data were analyzed to assess dominant risk factors and create a territorial model for integrated epidemiological surveillance. Based on risk factor, locality and timeframe characteristics of infection transmission pathways were determined, revealing cause-and-effect relationships. Aggregation and integration of long-term data identified high-risk regions where epidemiological surveillance must be strengthened by making it rational, operative, and targeted, and making the analysis comprehensive and multifunctional.

P068 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

The Canadian Food Inspection Agency strategy to face potential contamination of raw shellfish and associated illnesses

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Canadian Food Insepction Agency, Canada -

BACKGROUND: Microbial hazards such as *Vibrio parahaemolyticus* (Vp) and Norovirus (NoV) have been identified in outbreaks linked to consumption of raw shellfish. Considering the potential impact of climate change and increased ocean water temperatures, the likelihood of Vp illnesses could increase over the next years. In addition, a number of illnesses linked to Norovirus (NoV) contaminated shellfish have been reported last year in Canada.

This presentation highlights the integrated strategy that the Canadian Food Inspection Agency (CFIA) has been implementing to better control potential hazards. This strategy includes having early detection signal of potential outbreaks through food product surveillance at various levels, improved laboratory detection methodology for Vp and specific risk management framework in the context of outbreak situations linked to NoV.

METHODS: Surveillance activities have been designed specifically to detect contamination of products as early as possible in the distribution chain and during high risk periods. These activities include sampling and testing of product taken at the processor and retail level.

The CFIA developed a rapid identification method for Vp that has been published in the Compendium of Analytical Methods which is the repository of reference methods to determine compliance with standards and guidelines relative to microbiological material in foods.

The CFIA worked with government and industry partners to develop a specific response framework to be able to quickly react to NoV outbreak and ensure the appropriate management of risks based on scientific information.

RESULTS: Approximately 1100 samples are planned at the processor and retail level on a yearly basis. For fiscal year 16-17, results indicate some non-compliance for the presence of Vp in samples taken at the processor level (prevalence of 3,7%). This led to a number of recalls and notifications.

The presence of NoV RNA in oyster samples indicates that NoV could potentially represent a concern. However the determination of viability of this hazard also poses challenges in terms of risk determination.

The method developed allowed CFIA to reduce its turnaround time to 48 hours for reporting any confirmed Vp positive result. This allowed for the CFIA and industry to take risk management action on products faster.

The framework that was developed for outbreak response allows the CFIA and its partners to manage NoV outbreak situations and ensure that harvest areas are closed and re-opened based on specific criteria.

CONCLUSIONS: With this integrated approach, the Canadian Food Inspection Agency, in collaboration with its federal, provincial/territorial and industry partners is well positioned to detect and manage potential contamination of raw shellfish. By being able to quickly react to these situations, it is expected that risk management actions can potentially play a role in reducing the numbers of illnesses linked to the consumption of this raw shellfish.

P069 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Wildlife influences on the social determinants of health - key to climate change preparedness

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BACKGROUND: Early warning systems for climate change adaptation, preparedness and response will need to take into consideration the range of factors that can drive risk and vulnerability. While most attention has focussed on wildlife as sources or signals of changing zoonotic disease risk, community resilience to climate change will come from retaining capability to maintain an acceptable level of function, structure, and identity in the face of changing relationships with their natural and built environments. Wildlife impact many determinants of human health through both direct and indirect mechanisms, several of which are strongly interconnected.

METHODS: A scoping literature review using PubMed, Google Scholar, and Web of Science searched for evidence to elucidate the role of wildlife as climate change sentinels for public health, with emphasis on Canada. Additional literature was identified through forward and reverse citation searching.

RESULTS: We found no data from which to nominate the most effective, efficient and reliable wildlife health signals of public health risk or vulnerability related to changing climate. This reflects; (i) the challenge of deciding the proportional contribution of climate change to health and resilience outcomes, as many of the outcomes of concern are influenced by other macro and micro-factors; (ii) the dearth of assessments of the utility of climate change sentinels or early warning surveillance; and (iii) insufficient time for surveillance systems to have been operating to determine if wildlife health changes precede climate change effects on communities. There are, however, expectations and experience supporting the use of wildlife to forecast changing public health risk from food-, water- and air-borne infections; particularly on the use of wildlife as environmental markers of the introduction, distribution and abundance of infectious hazards. However, much of the vulnerability to effects of climate change for rural and northern communities will come from effects on social determinants of health including impacts on; aboriginal food security; fish and wildlife related economic activity; social relations; and freedom of choices and actions. The contributions of traditional activities on the land are difficult to extract from other determinants of health but reduced access to environmental resources can be viewed as drivers of reduced determinants of health and lack of access to critical social resources to build resilient communities. Vibrant wildlife populations provide people positive lifestyles choices related to outdoor activity, food sources, community activity, occupational options and cultural belonging.

CONCLUSIONS: The potential for people to make changes to address the consequences of climate change is influenced by the quality of their environment and the choices people have. Maintaining abundance, accessible and safe wildlife populations will sustain their contributions to the social determinants of health and community resilience. A wildlife health intelligence system could collect both data on incidents of disease and hazard discovery; information on social and environmental conditions that affect risk perception and likelihoods of human harms; and changing options for evolving our interactions with nature to protect the natural and social capital derived from wildlife.

P070 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

A One Health Approach Arbovirus Surveillance in the Atlantic Forest, Brazil

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In the past 100 years, five arboviruses infecting humans (*Yellow fever, Dengue, West Nile, Chikungunya and Zika*) have re-emerged. Many other arbovirus are zoonotic, infecting arthropods and wildlife in their sylvatic habitats, as well as humans as incidental hosts. Agriculture, deforestation, human movement patterns and human population densities have all intensified, resulting in altered patterns of virus-vector-host interactions. In this study, we monitored arthropods, wild animals and humans to assess the risk of arboviral infection in fragmented areas in the Atlantic Forest, Brazil. Between 2006 and 2014, we collected 196 blood samples from primates (*Leontopithecus chrysomelas* and *Sapajus xanthosthernos*) and 47 blood samples from sloths (*Bradypus torquatus* and *Bradypus variegatus*). In the same sites where mammals were sampled, we used dip nets and CDC traps to survey around seven thousand mosquito vectors. In 2014, we obtained blood samples from 523 humans from 11 communities that lived nearby wildlife monitoring sites. The blood samples were analyzed using

serological tests (Neutralization test, Hemagglutination inhibition test), cell cultures (C636 and Vero) and molecular tests (RT-PCR, Nucleotide sequencing). We investigated antibodies for 26 arboviruses in four genera: *Flavivirus, Alphavirus, Orthobunyavirus* and *Phlebovirus*. Prevalence of arboviral infection for wild mammals was 26.8%, with the highest value in *B. torquatus*(41%), followed by *L. chrysomelas*(25.4%), *S. xanthosthernos*(14.3%) and *B. variegatus*(14.3%). Using a generalized linear model, we found that arboviral infection was not associated with sex or age, but it was higher in sloths than in lion tamarins. In humans, the prevalence was 70.3%. Of the virus genera, *Flavivirus* had the highest prevalence in both animals (21.1%) and humans (69.8%). According to serological tests, wild mammals and humans were exposed to 13 and 5 species of arbovirus, respectively; four of which were shared in both hosts (*Iheus, Caraparu, Dengue virus* serotype 3 and *Eastern Equine Encephalitis virus*). Using multivariate logistic regressions, we found that people living close to forest fragments and nearby to free-living monkeys had a decreased risk of infection. This could be explained by the dilution effect, through which increases in local biodiversity tend to decrease the risk of diseases. Finally, we identified 49 arthropod taxa and culicids had the highest abundance and richness. We evaluated a RT-PCR test with genera-specific primers for viral detection in arthropods. Followed by sequencing, we detected *Rocio, Mayaro, Kamiti* and *Mosquito flavivirus virus*. The high sero-prevalence in wild mammals and humans, added to the presence of vectors infected with arboviruses, suggest viral circulation and risk of transmission across species in the sampled areas. We shared these data with universities, health and environmental services, zoos and local communities, in order to integrate people, wild animals and environment in a One Health framework to improve necessary actions on behalf of all involved.

ACKNOWLEDGMENTS: Saint Louis Zoo WildCare Institute (USA), The Wild Animal Fund, from the American Association of Zoological Veterinarians (USA), CNPq (Brasil), the Center for Research and Conservation of the Royal Zoological Society of Antwerp (Belgium), Lion Tamarins of Brazil Fund, National Lottery of Belgium, Primate Action Fund, Zoological Society of London, Conservação Internacional, Fundação o Boticário de Proteção a Natureza.

P071 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Characterizing the performance of avian influenza A(H9N2) surveillance from fecal samples and drinking water in live poultry markets

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BACKGROUND: Live poultry markets (LPMs) continue to operate in many Asian countries. Low pathogenic avian influenza (LPAI) viruses are often endemic in the poultry, and LPM presents the opportunity for human-poultry interactions and potential human infections with avian influenza viruses. This study assessed the performance of LPAI surveillance using fecal and drinking water samples in LPMs.

METHODS: We analyzed 7,321 paired fecal and drinking water samples from a longitudinal surveillance programme in Hong Kong LPMs. There were 2 monthly rest days during the study period, allowing consecutive poultry trading for about 14-15 days. Drinking water samples were collected from the trough shared by chickens in the same cage. The samples were cultured and positive isolates were subtyped by hemagglutination-inhibition tests and neuraminidase inhibition test. Data were aggregated by sampling occasion and days after the rest days.
A mathematical transmission model which incorporated turnover and overnight stay of poultry, virus contamination and decay in drinking water was fitted. Based on the parameterized model, we simulated H9N2 isolation rates from fecal and drinking water samples respectively over time, with different baseline prevalence.

RESULTS: Overall, H9N2 isolation rates ranged from 0-25% for fecal samples and 0-56% for drinking water samples. Based on the simulation, a clear increasing trend can be seen over days after the rest-days (Figure 1). Drinking water samples were more sensitive than fecal samples to detect H9N2, except for the first few days after the rest-days. The isolation rates from fecal samples were more stable over time. Other simulation results show that transmission via drinking water plays a major role in the amplification of LPAI in the LPMs.

CONCLUSIONS: Fecal and drinking water samples have their own advantage for different surveillance objectives in LPMs. Drinking water samples are more sensitive but less stable, and should perform better in the detection of emerging viruses which shed efficiently via the oral route. Fecal samples are more stable and should perform better performance for the monitoring of known endemic viruses. Lastly, avian influenza viruses (e.g. H5N1) may differ in their pattern of virus shedding via oral versus fecal routes and thus extrapolation of these results to other viruses needs to be done with caution. However, H7N9 viruses are similar to H9N2 viruses by being shed primarily via the respiratory / oral route and it is reasonable to assume that these conclusions would apply to H7N9 virus which is of major public health concern.

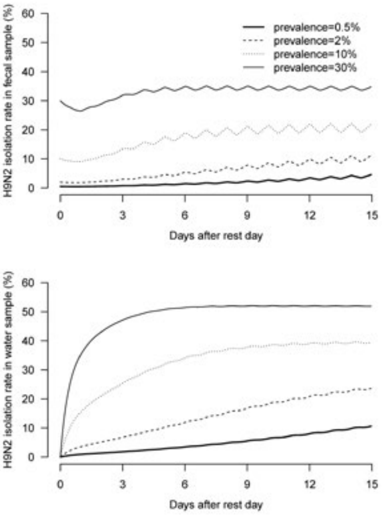

Figure 1. Simulated H9N2 isolation rates from fecal (top) and water (bottom) samples by days after the bi-monthly rest days, based on the dynamic transmission model with different background virus prevalence rates.

P072 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Implementation of One Health approach in Sciensano a new Belgian research centre for public and veterinary health

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1: CODA-CERVA, Belgium - 2: WIV-ISP, Belgium -

BACKGROUND: The fusion of the federal Public Health Institute (WIV-ISP) and the Veterinary and Agrochemical Research Centre (CODA-CERVA) into one institute, named Sciensano created the opportunity to set up a transversal cooperation in a One Health perspective. One of the key tasks of both institutes is supporting the authorities in scientific risk assessment and surveillance. Sciensano aims to be the scientific partner for one health surveillance.

METHODS: A questionnaire was discussed with 20 senior scientists and directors of both institutes, with 10 stakeholders and academics and with representatives of international organisations including the European commission; EFSA; OIE; WHO; Worldbank; CDC.
A proposal was discussed within the board of directors of Sciensano and is now still under construction.

RESULTS: The board of directors stated that Sciensano recognizes that human health is connected to animal health and to our shared socio-economic and physical environment. From all the previous discussion a priority list of topics was proposed to the board of directors and approved. These priorities are: Antimicrobial resistance; Zoonosis (Influenza, vector borne diseases and foodborne diseases) and risk evaluation and health risks of mixed exposure.
A structure is set up with a coordinator who ensures the One Health process and advocates One Health internally and externally, a focal point for each topic, who is an expert in that specific topic and leads a panel of in house scientists concerning this topic. This internal panel will work in close cooperation with the crisis unit of Sciensano in order to prevent, detect and cure early signals. Additionally an external platform on the topic will be created since most of the representatives of stakeholders and other organisations emphasized the role of Sciensano as a mediator for One Health at the federal level. This external platform consists of other scientists working on the topic and policy makers.

CONCLUSIONS: The aim of the internal panel is to integrate One Health into strategic research; to provide a harmonized answer concerning a specific topic in a One Health perspective; to have a single view on the resources available to provide scientific support to the stakeholders; to disseminate new knowledge, tools and material to the stakeholders including policy makers. Sciensano can have a coordination role in the external panel by getting signals and proposing response to specific issues together with key partners in the public health and veterinary fields. Regular meetings will be organised to discuss signals between veterinary and public health partners. Strategic focus on research activities in the field of the animal-human-environment interfaces will be discussed. With this approach the internal panel will provide a scientific transversal answer including both public health and animal health aspects. The external platform will function as a science - policy interface.

P073 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Factors associated with willingness to test drinking well water for E. coli in rural Alberta.

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1: University of Calgary - 2: Alberta Agriculture and Forestry - 3: University of Alberta -

BACKGROUND: Most rural residents of Alberta, Canada rarely or never test their drinking well water quality, leaving more than 450,000 Albertans at risk of consuming water of unknown quality. We sought to understand the perceptions of rural Albertans with respect to the quality of drinking well water and the association of those perceptions with the presence and management of livestock in order to inform water testing and livestock management policies for rural Albertans.

METHODS: We implemented a questionnaire mailed to more than 2000 rural Albertans and made available online, collecting data on attitudes and preferences relating to water testing, livestock management, manure storage, water quality, and demographics. More than 350 questionnaires were completed. We encouraged participants to also submit a drinking well water sample to test for *E. coli* and total coliforms using presence/absence enzyme substrate tests, pairing results with the questionnaire.

RESULTS: Of 82 water samples submitted, only one tested positive for *E. coli*. The majority (79%) of farm owners stated they test their drinking well water compared to 56% of non-farm owners. About 40% of each group stated they treat their water. Livestock owners were more likely than non-owners to treat their water (44% vs. 35%) and to test their well water (77% vs. 66%).
Regression analysis identified the following significant predictors of willingness to test drinking well water for bacterial contamination: owning a farm; history of treating well water; awareness of potential drinking water contaminants; and stated contentment with drinking well water. Well owners with the following characteristics were more likely to believe their wells were free from bacterial contaminants: have tested their wells; are content with drinking water from the well; and believe that presence of livestock on a neighboring farm is a risk for contamination. This implies awareness that a hazard exists but that mitigating actions are possible. We did not show significant differences based on age, education, or income of respondents.

CONCLUSIONS: Our results show that the majority of respondents are content with the quality of their drinking well water, feel there is low risk of susceptibility to microbial hazards contaminating their drinking water, feel that risk increases with the presence of livestock but can be mitigated, and participation in drinking well water testing would increase with improved access. Farm owners and livestock owners in particular are more likely to be engaged with drinking well water testing and mitigating activities than other rural drinking water well owners. Incorporating well water testing as a part of structured livestock manure management programs may increase participation rates and serves as an affirmation to non-livestock owners of the important role agriculturalists play in mitigating risk of contamination from livestock.

P074 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Investigation of Middelburgvirus, an African alphavirus, as cause of febrile and neurological disease outbreaks in horses, wildlife and humans following unusual high rainfall in South Africa, 2017

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BACKGROUND: Alphaviruses in the family Togaviridae have mainly been associated with febrile disease and arthralgia in humans in Africa and few animal cases have been described. New World Alphaviruses such as Eastern, Western and Venezuelan encephalitis viruses on the other hand are known zoonoses that may cause severe and fatal disease in horses and humans in the Americas. In 2015 we described Middelburg (MIDV) and Sindbis (SINV) viruses as previously missed causes of neurological disease in horses in South Africa. Syndromic surveillance for febrile and neurological disease in susceptible animals may act as an early warning system to detect arboviral outbreaks in Africa.

In January –June 2017 a rise in neurological cases was reported in horses following unusual high rainfall in South Africa and an outbreak of Sindbisvirus was reported in humans. This prompted us to investigate arboviruses in animals using an established surveillance program as well as in unsolved neurological cases in humans in hospitals in Gauteng where most horse cases occurred.

METHODS: An established surveillance network of >150 veterinarians across South Africa submitted cases with febrile or neurological disease to the Centre for Viral Zoonose (CVZ), University of Pretoria for arbovirus investigation[s]. Specimens were screened for flavi, alpha and orthobunyaviruses by real-time Polymerase chain reaction (RTPCR) and WNV also by IgM ELISA. Cerebrospinal fluid (CSF) specimens from human patients submitted to the National Health Laboratory Service virology laboratory from public sector hospitals in Pretoria and *ad hoc* cases of unsolved neurological disease from veterinary students submitted to the CVZ between February and June 2017 were also selected for arbovirus investigation.

RESULTS: In total, 404 cases from animals with febrile and neurological disease were submitted (January-June 2017). Horses tested positive for West Nile virus (WNV), (45/342, 11.4%); MIDV (41/342, 10.9%) and equine encephalosis virus (EEV)(49/342 12.1%). Positive cases were from Gauteng, KwaZulu Natal, Northern Cape, Free State, Mpumalanga and North West provinces. WNV (36/45)(80%)) and MIDV(25/41 (60%)) cases presented mainly with neurological signs relative to 21/49(42.8%) EEV cases. Of 64 other animals species submitted, 1 dove, 1 buffalo calf and 1 rhino were positive for MIDV, all being fatal. Of 2 veterinary students with unexplained neurological signs, 1 tested positive for Middelburgvirus. Of 189 CSF specimens submitted for general viral investigation, 3 tested positive for Middelburgvirus: a 49 year old HIV + male; a 30 year old HIV negative female and a 2 year old child, all with unexplained neurological signs.

CONCLUSION: Established One Health surveillance networks allowed for rapid identification of Middelburgvirus as a cause of neurological disease outbreaks in animals in South Africa in 2017 and identification of MIDV positive neurological cases in humans which would otherwise have been missed. Middelburg should be investigated as a potential cause of unsolved neurological disease in humans and animals in Africa and monitored as a potential emerging pathogen elsewhere.

P075 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

A One Health approach to detection of contamination in private well water systems in Western Canada

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BACKGROUND: In rural western Alberta, Canada approximately 600,000 people rely on private groundwater or stored water for drinking purposes. Current practice for testing of water quality parameters from private wells in Alberta includes testing for the presence of total coliforms (TC) and *Escherichia. coli* (EC) indicators of the potential presence of fecal contamination. Up to 25% of such water systems fail current drinking water quality parameters. This study aims to better understand rural well water quality and its relationship with environmental and agricultural factors in Alberta.

METHODS: Six-hundred-ninety-three well water samples collected from 104 premises (15 feedlots, 36 cow/calf farms, 14 poultry farms and 39 acreages in southern rural Alberta from 2015 - 2017 were tested for the presence/absence of TC, EC and Enterococcus (ET) using Colilert* (TC & EC) and Enterolert*(ET) (IDEXX Laboratories Canada Corp., Ontario, Canada) bacteriological procedures. Fifty of these premises undertook 12 monthly samples. Samples were also tested using a molecular prescreen to detect the presence of *Enterococcus* spp. (mET), *E. coli* (mEC), general *Bacteroides* (mGB), *Arcobacter butzleri* (mAR), *Campylobacter* spp. (mCA) and *Salmonella* spp. (mSA). Agreement between the bacterial and molecular tests was evaluated using McNemar's test to take into account the paired nature of the tests.

RESULTS: Twenty-three premises had no well water contamination. TC only were detected on 29 premises. EC was present on six premises. Thirty-nine premises had molecular contamination without the detection of contamination using standard methods. mET and mGB were detected without the presence of bacterial contamination on 51 and 38 premises respectively. Contamination with mET was persistent, with 37 premises having tests positive for mET for between two and eight sample-months. Contamination with concurrent mET and mGB was detected on one to four sample-months on 39 premises. On 33 premises, combinations of bacterial and molecular contamination were detected, with the most frequent (n = 18 sample-months) combination being TC and mET positive samples. An odds ratio of 3.32 (95% CI: 2.49, 4.50) with the associated McNemar's chi^2 probability of <0.0001 indicates that using mET as the indicator for contamination is more sensitive compared to TC. This was also true for mGB when compared with TC (OR 1.57 (95% CI: 1.16, 2.11)), McNemar's chi^2 probability of 0.0025). There was no significant differences when considering the presence of any contamination between the four premises types.

CONCLUSIONS: Results indicate that molecular level contamination with mET and mGB is frequently encountered in private well water samples, and can persist in water for long periods of time. These results give an insight into modes of contamination of rural groundwater, and tentatively indicate that the use of molecular methods of detection of well water contamination may be more sensitive than bacteriological methods.

P076 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Environmental Suitability and Predicted Distribution of Aedes Albopictus Mosquitoes in Canada and the United States: Assessing Arboviral Risks in North America

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BACKGROUND: *Aedes* species of mosquitoes, particularly *Aedes aegypti* and *Ae. albopictus*, are known vectors of more than 20 arboviruses of global public health importance including Chikungunya, dengue, Zika, and Yellow fever viruses. *Ae. albopictus* is considered to be more invasive to new geographic regions compared to *Ae. aegypti*. Chikungunya virus was recently introduced to parts of Europe by infected travelers returning from endemic countries and the virus is currently being autochthonously transmitted by local *Ae. albopictus* vector populations. *Ae. albopictus* was also recently reported in southwestern Ontario, Canada. The goal of this study was to apply a machine learning approach to assess the current environmental suitability and probable distribution of *Ae. albopictus* in Canada and the United States (US).

METHODS: We utilized *Ae. albopictus* occurrence data (n=2939) from 2001 to 2016 in Canada and the US from sources that included peer-reviewed literature and public access repositories. Four random pseudo-absence data-points were generated for each occurrence data-point and constrained to below 60°N. We modeled *Ae. albopictus* occurrences using ecological and anthropogenic predictors including mean, minimum and maximum temperature, total numbers of days in the year with mean daily temperature of 10°C or higher, total monthly precipitation averaged over a year and an annual mean enhanced vegetation index from 2001 to 2016, and urbanicity. We used boosted regression tree analyses to assess the relative contribution of each predictor, determine the predictive performance of the model and to map the ecological niche of *Ae. albopictus* in Canada and the US.

RESULTS: The probable distribution of *Ae. albopictus* in Canada and the US was primarily associated with: i) an increasing number of days with an average temperature ≥10°C (Relative contribution (RC): 45.2%), ii) urban locations (RC: 17.6%), iii) increasing amount of total monthly precipitation (RC: 9.7%), iv) enhanced vegetation index (7.2%) and v) rising minimum temperature (7.1%). The model-predicted niche of *Ae. albopictus* ranged from southeast regions of the US to the southwestern borders of Ontario, and from the east coast of the US to the Central US (Figure 1). Some small regions of the west coast also appeared suitable for *Ae. albopictus* (Figure 1). We validated the model fit with independent evaluation data and achieved an area under the ROC curve: 0.96 (standard error: 0.002).

CONCLUSION: A large extent of North America appears to be suitable for the establishment of an *Ae. albopictus* vector populations which increases the chance of local transmission of several arboviruses of public health significance. Many of these pathogens are foreign to this region. Continued surveillance for the vector in the high-risk regions might enable us to effectively use resources to identify circulating pathogens and the geographical range expansion of the vectors population in a more timely manner.

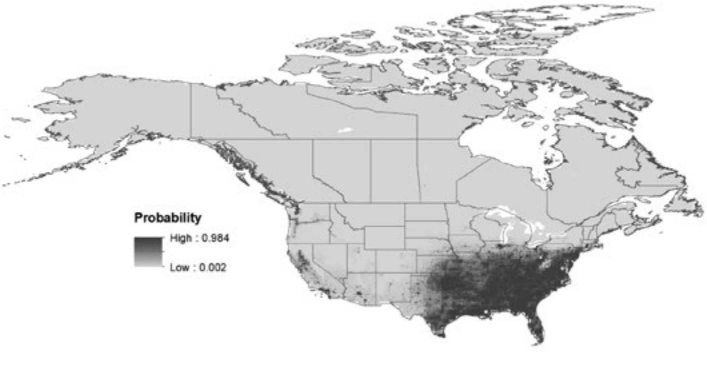

Figure 1: Model predicted ecological niche of Ae. albopictus vectors in Canada and the United States.

P077 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Formation of a national task force in response to the emerging infectious diseases in uganda: a case of the CCHF outbreak in Kiboga district.

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BACKGROUND: Uganda has experienced various outbreaks of Emerging Infectious Diseases (EIDs) including serious haemorrhagic fevers like RVF, EVD and CCHF that are associated with high case fatality among human victims. All these are zoonoses whose natural hosts are in the animal sector, both domestic and wild.

In August 2017, Uganda experienced a CCHF outbreak in Kiboga, Luweero and Nakaseke districts. This and earlier outbreaks led to the formation of a National Task Force. The objective of NTF formation by the Ugandan government was to manage and contain such outbreaks at source.

In this submission we describe how the NTF successfully brought together teams from various stakeholders to sample blood from domestic animals, collect data from the victims' homes and health centres where the victims received treatment, and support the created isolation centres with materials and reagents in the Kiboga CCHF outbreak.

METHODS: The National Task Force comprises of several professionals from various disciplines of Health, Veterinary, Wildlife, Defence who work together as a whole and this was recently witnessed during the August 2017 CCHF outbreak in Kiboga district. This time the response team comprised of Ministry of Health (MOH) and Ministry of Agriculture, Animal Industry and Fisheries (MAAIF) members who went to the field at the same time as opposed to earlier occurrences where the teams visited at different times. The MOH team collected patient data from the hospitals while the MAAIF team collected whole-blood samples and ticks from cattle that were being looked after by the CCHF victims.

RESULTS: Rapid response to ensure containment at source from a multi-disciplinary national team of professionals that is always ready to make investigations and share findings. This same team has periodic meetings from either the MOH headquarters in Kampala or the MAAIF headquarters in Entebbe, with the purpose of having up-to-date information on the happenings in each field of public health concern. Much as the two ministries take lead, there are colleagues from wildlife, Research and academic institutions who get involved as well especially during crises or outbreak periods.

CONCLUSION: NTF comprising multi-sectoral teams has effectively helped Uganda (as a country) manage and control the spread of zoonotic diseases by ensuring containment at source. The Kiboga team effectively handled the situation and there were no reported fatalities or further outbreaks in the district. The NTF should have pooled contributions from all stakeholders to ensure readiness at all times for effective interventions.

P078 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Investigation of Aedes mosquitoes as arbovirus vectors at sentinel sites in Gauteng, Limpopo, Mpumalanga and Kwazulu-Natal provinces, South Africa (2015-2017)

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BACKGROUND: Recent epidemics have increased the importance of the Aedes species globally as arbovirus vectors and raised awareness of the risk of international spread of African arboviruses. There is limited recent data about the vectors of arboviruses endemic to South Africa. To investigate *Aedes* species as potential arbovirus vectors, entomological surveillance was conducted in 3 different provinces (Gauteng, Limpopo and Mpumalanga) in South Africa. From 2017, an additional site was included in Kwazulu-Natal (KZN) province.

METHODS: Sampling was conducted for 2 consecutive nights per month, from January 2015 to May 2017, using 3 types of CO_2 baited traps: Tent, CDC light and BG sentinel. Mosquitoes were morphologically sorted according to species and pooled in groups of 50 for laboratory testing. Female aedine mosquitoes were screened by RT-PCR for 3 viral genera associated with zoonotic arboviruses in the families Flaviviridae (Flavivirus), Togaviridae (Alphavirus) and the Bunyavirales (former genera Orthobunyavirus and Phlebovirus).

RESULTS: A total of 30,531 adult mosquitoes were collected and identified morphologically, 3446 in 2015 (7 genera), 6286 in 2016 (10 genera) and 20,799 in 2017 (9 genera). Potential vectors for zoonotic arboviruses in South Africa were found at all the sites. *Culex* was the most abundant in all provinces although important *Aedes* spp were identified in all sites. *Ae aegypti,* the major vector for several of the globally most important arboviruses, together with *Ae mcintoshi*, which is a key vector for Middelburg, Wesselbron and Rift Valley fever, were commonly found at the collection sites, except for KZN. Between February and April 2017, *Ae mcintoshi* was the most common aedine found in Limpopo and Mpumalanga, *Ae quasiunivittatus* and *Ae dentatus* group in Gauteng, and *Ae durbanensis* in KZN.

In 2015, only one *Ae aegypti* pool from Limpopo tested positive for an unidentified Flavivirus. In 2016, one pool of *Ae. aegypti* tested positive for cell agent fusing virus and a pool of *Ae. hirsutus* from Gauteng for another unidentified Flavivirus. Two pools from Mpumalanga tested positive for the Orthobunyavirus Shuni virus (SHUV): one *Ae. mcintoshi* and one *Aedes* spp. According to the literature SHUV was previously only detected in *Cx theileri* and *Culicoides*.

For 2017, preliminary data identified 3 pools (*Ae quasiunivittatus, Ae mcintoshi* and *Ae aegypti*) in Gauteng and 2 pools (*Ae durbanensis* and *Ae aegypti*) from KZN that were positive for unidentified Flaviviruses. One positive pool of *Ae dentatus* group tested positive for Middelburg in Gauteng.

CONCLUSION: Identification of Shuni and Middelburg virus coincided with neurological disease outbreaks of these viruses in animals in the respective regions. Further investigations are needed to determine the importance of the unidentified flaviviruses. This study highlights the importance of continuous entomological surveillance to define arboviruses ecology and predict potential outbreaks in Africa.

P079 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Detection of novel reassortants of highly pathogenic avian H5 influenza strains in an outbreak situation

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BACKGROUND: Highly pathogenic avian influenza viruses (HPAIV) H5 of Asian origin (goose/Guangdong/96) evolved into numerous geno-types, subtypes and various phylogenetic clades. Some of these lineages contain strains with enhanced zoonotic properties causing fatal human infections. Starting in November 2016, HPAIV H5 was prevalent in Germany, causing high mortality in wild and domestic birds.

METHODS: Sequences of HPAIV-H5 viruses from wild birds, poultry and zoo birds were generated and used for reassortment analysis. For a global analysis of HPAIV reassortment events, influenza virus sequences were collected from public databases and included in the analysis.

RESULTS: More than 1200 cases of HPAIV H5-infected wild birds were detected across Germany from November 2016 until December 2017. In addition to wild birds, captive birds in commercial farms, small holdings and zoos or wildparks were affected. The outbreaks were mainly caused by HPAIV of subtype H5N8, while H5N5 and H5N6 were only rarely detected. Sequencing of the viral genomes confirmed relationship to viruses detected in China, Mongolia and Russia in summer 2016, but also revealed reassorted genomes. The reassortments were detected in a fast and efficient way by a combined approach applying network analysis on segment-based phylogenetic trees. At least six different genotypes were identified in Germany. They show a distinct spatio-temporal distribution that point to independent incursions. The analysis was expanded to sequences of global H5 viruses from 2016-2017. At least eleven distinct reassortants were identified with this method.

CONCLUSIONS: HPAI H5N5, H5N5 and H5N6 detected in birds in Germany 2016-2017 represent several distinct reassortants of H5 viruses, indicating multiple entries of globally occurring HPAIV H5NX reassortants into Germany. Phylogenetic supernetworks provide an efficient tool for the identification of reassortants in an outbreak situation.

P080 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Linking Human and Animal Notifiable Zoonotic Disease Data in Washington State

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Zoonotic diseases pose an increasing risk to human and animal health around the world. Although the ‘One Health’ initiative has spurred calls for integrated zoonotic disease surveillance, most human and animal disease surveillance systems continue to operate independently, including those in Washington (WA) State, USA. Because there are no laws detailing notifiable zoonotic disease data sharing between the Washington State Department of Agriculture (WSDA) and the Washington State Department of Health (DOH), zoonoses surveillance data from these agencies never have been analyzed jointly. The objective of this project is to compare trends in the number, incidence, and type of zoonotic diseases reported in humans and in animals (both companion and food producing) over time in WA State. We abstracted notifiable animal zoonoses data reported to WSDA from 1993 to present from paper and email records, and abstracted notifiable human zoonoses data reported to DOH over the same time frame from publicly available online reports. We focused our analyses on leptospirosis and psittacosis incidence because these were two of the most commonly reported zoonotic animal diseases from 1993-present that also are notifiable in humans, and because both diseases have associated public and/or veterinary health actions. We will present the results of these comparisons, as well as the identification of possible disease clusters, and the results of exploratory analyses of the relationships between environmental variables such as rainfall and temperature and zoonotic disease cases in both humans and animals. This project identifies barriers to implementing integrated surveillance, including the lack of a common data tracking, analysis, reporting, dissemination, and communication platform, in addition to the lack of a standardized system of disease nomenclature. It also explores the challenges of correlating climate data with human and animal cases of weather-sensitive zoonoses, such as leptospirosis. Data sharing and other communications between human and animal health agencies may be essential to improving integrated zoonotic disease surveillance and response. Integrated disease surveillance is an important step toward better understanding of zoonotic disease outbreaks in both animal and human populations (including occupational risk in animal workers), improved prevention, and more timely zoonotic disease outbreak detection and effective response. Furthermore, there may be sentinel value in animal health agency awareness of zoonoses in humans (i.e. humans as sentinels for animal disease risk), and vice versa.

P081 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Mobile phone based surveillance for animal disease in rural communities: implications for detection of emerging zoonoses

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BACKGROUND: Improving speed of detection and reporting of infectious diseases at onset of an outbreak in communities is a critical step in managing the threat of emerging infectious diseases, many of which are zoonotic, and enhancing global health security. Whereas implementing community-based surveillance systems has been difficult or too expensive, mobile phones have been postulated as potentially effective tools for real-time surveillance of infectious diseases. Here we test the effectiveness of mobile-phone based animal syndromic surveillance for infectious diseases in a rural community in Kenya, determine the individual and household correlates of their use, and examine the broader implications for surveillance of zoonotic infectious diseases.

METHODS: We use 4-year (2013 - 2017) longitudinal data collected from 1500 households participating in a linked human and animal syndromic surveillance platform in rural western Kenya. The syndromic surveillance covers illness in cattle, sheep, goats, and chickens. We compare data on animal illness and death collected at least monthly through household surveys with data reported directly from the community by animal owners through a toll-free number, and verified through veterinary response visits. We determine reporting patterns by surveillance method, animal species affected, type of syndrome, household demographics, and social-economic status.

RESULTS: A total of 14,935 illness and death events in livestock were reported through the two surveillance systems, half of which were confirmed as valid disease events by veterinarians. The mobile phone surveillance system outperformed household visits in the total number of reports captured and was 5.2 times (95% CI 4.8, 5.7) more likely to capture valid disease events compared to routine household surveys by trained community interviewers. Illness events were more likely reported through the mobile phone surveillance system [OR 10.9 (95% CI 9.3, 12.9)], while death events were less likely [OR 0.16 (95% CI 0.14, 0.19)] to be reported through the system. Disease syndromes with severe presentations were more likely to be captured through the mobile phone system. Phone ownership was not a determinant of using the mobile-phone surveillance system, but being older, male, and having formal education was associated with increased likelihood of using this system.

CONCLUSION: A mobile phone-based animal health surveillance system can contribute to enhanced global health security as an effective tool for rural community level detection and reporting of infectious disease events. Our study suggests the system will sufficiently detect outbreaks of zoonotic diseases such as Rift Valley Fever that present with severe clinical signs in high value livestock; however in the absence of additional reporting incentives it may miss early outbreaks of diseases such as avian influenza that present primarily with mortality.

P082 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

A near real-time livestock-wildlife syndromic surveillance system for early detection and response to biological threats in Kenya

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BACKGROUND: Early detection of animal disease outbreaks including zoonoses is critical to mitigate impact on human health. However, the animal health surveillance system in Kenya lacks a real-time disease reporting mechanism, which would enhance early detection of a public health threat. To address this, we developed and deployed an electronic syndromic surveillance system for livestock and wildlife for use by national authorities. The system, called the Kenya Animal Biosurveillance System (KABS), integrates a mobile-phone application that facilitates data collection by field officers, and a web-based dashboard that receives data in near real-time with automated data analysis and feedback.

METHODS: The KABS mobile app has separate livestock and wildlife reporting forms, with access based on field officer role. The KABS-Livestock form reports nine syndromes (abortion, sudden death, hemorrhagic, neurologic, respiratory, gastro-intestinal, cutaneous, animal bites and oral/foot lesions) in seven animal species (cattle, sheep, goats, chicken, camels, dogs, and cats) whereas the KABS-Wildlife form reports nine similar syndromes in five animal categories (herbivores, carnivores, avian, aquatic, and non-human primates). Data on number of animals affected and clinical diagnosis is reported. KABS was piloted in three counties (Makueni, Nakuru and Siaya) and all wildlife regions, with training of field officers in April-July 2017, and data collection launched in June for livestock and September for wildlife. Frequency data is analyzed using the web-based dashboard and shared with the counties.

RESULTS: A total of 117 livestock Thirty-seven wildlife and 37field officers were trained on KABS. By December 31st 2017, 88 (75%) of livestock officers had downloaded the app and of these, 79% sent a report. A total of 1445 syndromes were reported – 26% from Makueni 28% from Nakuru and 46% from Siaya county. Respiratory and gastrointestinal were the most commonly reported syndromes in cattle and goats. For 1138 (78%) syndromes with a clinical diagnosis, the most common were east coast fever (15%), rabies (7%), foot and mouth disease (6%), and helminthiasis (6%).

Of 37 wildlife field officers, 19 (51%) downloaded the app and 8 (42%) submitted a report. By December 2017, 30 reports were submitted from all wildlife regions. Deaths (52%), severe emaciation (29%) and cutaneous lesions (29%) were most commonly reported. Of the reports, 25%, 19% and 16%% were of zebras elephants and buffalos, respectively.

CONCLUSIONS AND FUTURE WORK:
KABS was adapted, deployed and used for reporting of animal disease events to the national authorities. Notably, the KABS pilot represents the first ever routine surveillance in Kenya wildlife populations. Further enhancing the system to incorporate algorithms to identify potential zoonotic disease events for data sharing with the human health sector as an early warning system and laboratory diagnosis of the reported syndromes will increase its utility.

P083 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Seroprevalence and Risk Factors of Toxoplasma gondii Exposure in Small Ruminants in Ontario, Canada

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BACKGROUND:

Toxoplasmosis is prevalent in most areas of the world and is of veterinary and medical importance, because it may cause abortion or congenital disease in its intermediate hosts including humans, sheep and goats. The objectives of this study were to determine the seroprevalence of *Toxoplasma gondii (T. gondii)* exposure in sheep and goats, and associations between *T. gondii* seropositivity and farm-level management risk factors in Ontario.

METHODS:

Sera and questionnaire data utilized here were collected from a previous study. Multi-stage random sampling was used to select farms and animals for participation. Serum samples and questionnaire data were collected from August 2010 to January 2012, and stored at -70°C. Participants in the original project were contacted between May and July 2017 by mail, email or telephone to obtain consent to test the stored sera for *T. gondii* antibodies, and to examine associations between *T. gondii* seropositivity and farm-level management factors. Overall, 48 sheep and 59 goat farms agreed to participate. On each farm, sera from up to 25 of the randomly sampled sheep or goats were analysed.

Sera were tested for antibodies to *T. gondii* using an indirect fluorescent antibody test (IFAT) with a dilution cut-point of ≥ 1:80 to indicate seropositivity. Two mixed logistic multivariable models were constructed for sheep and goat data using individual seropositivity as the outcome and controlled for clustering by farm.

RESULTS:

Overall, the animal-level seroprevalence was 71.4% (795/1114) in sheep, and 41.5% (490/1181) in goats. At the farm-level, 100.0% (48/48) of sheep farms and 88.1% (52/59) of goat farms had at least one seropositive animal. Risk factors for sheep included having cats on farm. For goats risk factors included: purchasing female animals under one year of age, and feeding milk from other species. Protective factors for goats included having a spring breeding season, using traps for rodent control, purchasing replacement animals from a dealer or broker, exposing replacement animals to adult goats or their manure, and burying aborted fetuses and placenta in the manure pile.

CONCLUSIONS:

The high seroprevalence among sheep and goats suggests a significant human risk of exposure to *T. gondii* in people who consume undercooked meat or unpasteurized milk from sheep or goats in Ontario. Additionally, results suggest the risk of abortion and neonatal loss due to *T. gondii* infection is high in Ontario sheep and goats. Risk factors associated with sheep and goat seropositivity highlighted the importance of farm hygiene and biosecurity measures. This information can guide public health and veterinary efforts in the development of prevention strategies including development of a livestock vaccine.

P084 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Evaluation for One Health in action – Enhancing animal disease surveillance systems in Africa

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BACKGROUND: In the era of One Health, a strong surveillance system incorporating multi-disciplinary collaboration is the first line of defense against diseases that pose significant threats to humans, animals and the environment. In developing countries, uncontrolled animal diseases can severely impact people's livelihoods, ranging from lack of access to international livestock markets at a country level, to food insecurity in the smallest communities. To enhance national animal disease surveillance systems, the Food and Agriculture Organization of the United Nations (FAO) developed the Surveillance Evaluation Tool (SET), with support from the United States Agency for International Development (USAID). SET provides a standardized method for assessing systems' strengths and weaknesses, culminating in the development of meaningful recommendations to improve countries' animal disease surveillance system.

METHODS: SET was adapted from the Oasis toolkit, developed by French agency "Agence Nationale de Sécurité Sanitaire de l'alimentation, de l'environnement et du travail" (ANSES).[1] Additional components from other FAO tools were incorporated, as well as Joint External Evaluations (JEE) indicators[2] related to zoonotic diseases, workforce development and real-time reporting. The current version of the tool assesses systems along seven main themes, divided into nineteen categories and ninety indicators, including components of intersectoral collaboration and One Health. Information entered into the tool is gathered during evaluation missions where official documents are reviewed, followed by interviews with actors and stakeholders of the system ranging from ministries, the private sector all the way to local livestock owners. Graphical outputs are automatically generated, visualizing strengths of the surveillance system, as well as areas needing improvement – a unique feature. From this, a participatory approach involving all main actors of the system is used to develop specific, realistic, time-bound and agreed-upon recommendations to improve animal disease surveillance. A written mission report is then distributed to all major stakeholders of the system.

RESULTS: To date, SET missions have been implemented in five African countries in phase 1 of the Global Health Security Agenda (GHSA), and more evaluations are planned. Results of SET assessments conducted in East and West Africa will be presented, including an overview of existing strengths and gaps identified during evaluations, with a focus One Health capacities.

CONCLUSIONS: SET differs from other evaluation tools by its in-depth focus on animal disease surveillance. It can be used following assessments such as the JEE to further characterize gaps in surveillance from an animal health perspective. The tool also evaluates and promotes the establishment of inter-agency surveillance strategies in line with One Health principles. Several countries are already applying the recommendations identified during SET missions, and the tool may be also used for follow-up self-evaluations to measure progress on all indicators. FAO is currently developing a roadmap for measuring the SET's long-term impact at country-level.

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P085 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Microbial diversity analysis for pollution source tracking of a Michigan sub-watershed

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BACKGROUND: Microbial contamination in watersheds has been a clear threat to humans and animals over the years. Pathogens carried by microbial contamination may impair the quality of drinking and recreational water, and cause infectious water-born or water-related disease. Nearly 75 percent of all emerging human infectious diseases in the past three decades originated in animals, transferred mainly through water or food route.

The Great Lakes basin is the biggest fresh water body on the planet, and it is facing various problems. In order to obtain healthy watershed and control microbial contamination, communities throughout the Great Lakes basin are developing and implementing watershed management plans to address non-point sources of pollution such as surface runoff, and meet Total Maximum Daily Load (TMDL) requirements. Investigating sources of microbial contamination in key streams and creeks is critical for the development of effective watershed management plans.

METHODS: This work aims to present an approach that will facilitate microbial contamination source identification. In addition to conventional indicator analysis, the approach includes molecular analysis of species-specific markers and microbial community diversity analysis. We characterized microbial pollution in the Sloan Creek subwatershed in Ingham County MI, one of the impaired areas located in the Great Lakes Basin. To identify pollution sources (human or animal) and major sites of origin (tributaries with highest pollution loads) water samples were collected from three locations in the subwatershed representing the main creek upstream, main creek downstream, and tributary. A fecal indicator *(E. coli)* and host-specific human and bovine-associated *Bacteroides* genetic markers were quantified in all water samples.

RESULTS: Results indicated that 54 percent of the samples from the three locations exceeded the recreational *E.coli* water quality guidelines. High concentrations of both human and bovine associated-*Bacteroides* indicated influence of multiple sources of fecal contamination. Statistical tests showed significantly different water characteristics between two of the sampling locations. Whole genome shotgun sequencing indicated fecal and sewer signatures, wastewater metagenome, human gut metagenome, and rumen gut metagenome in the water samples.
Conclusions: Probable sources of contamination were leakage from septic systems and runoff from agriculture activities nearby Sloan Creek. The studied area was under a high risk of endogenous disease and zoonotic disease. Placed in a One Health framework, this study offers a proposed MST methodology path to assess water quality at a sub-watershed level that will facilitate watershed management planning efforts for a TMDL site, and protect the health of humans, animals, and the environment.

P086 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Exploring the zoonotic risk in the general population, and among farmers and veterinarians in Western France: what are the prevalence and risk factors for Coxiella burnetii infection (Q fever)?

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BACKGROUND: Q fever, a zoonotic disease caused by *Coxiella burnetii*, is known to be endemic among cattle in Western France. However, studies assessing the risk of human infection in such areas are lacking in France to date, while such studies may provide key information for better targeting surveillance. This study aimed to assess the prevalence of antibody-carriers to *Coxiella burnetii* in the general population and in two populations at risk of occupational exposure to *Coxiella burnetii* (farmers and veterinarians) in Western France, and to identify related risk factors.

METHODS: A cross-sectional study was conducted in two districts (Finistère and Loire-Atlantique) during the 2017/18 winter. Nearly 600 sera were collected from blood donors (sampling with predetermined quotas for age, sex and residency), cattle farmers and veterinarians (volunteer samplings). Human sera were tested for antibodies against phase I and phase II *Coxiella burnetii* antigen using an indirect immunofluorescence antibody assay. Each participant was asked to complete a questionnaire containing socio-demographic characteristics, occupational and non-occupational risk exposure, history of Q fever infection and vaccination, and risk factors associated with chronic Q fever. Simultaneously, in the two districts, the status of each cattle herd with regard to *Coxiella burnetii* infection was determined by testing bulk tank milk samples (from dairy herds) and pooled sera (from beef cattle) using ELISA.

RESULTS: Preliminary results showed that the seroprevalence of antibody-carriers against *Coxiella burnetii* seems higher among the high risk groups (farmers and veterinarians) compared with the general population. Statistical analyses (generalized linear models) were also performed to assess the association between possible risk factors and human *Coxiella burnetii* seropositivity for each studied group. Spatial correlation analyses were used to assess the potential link between cattle and human seroprevalences.

CONCLUSIONS: Using Q fever as an example, this original study quantifies the zoonotic risk at the human-animal-environment interface and identifies practices at-risk in an area with a high livestock density in France. Given the growing and global threat of emerging and re-emerging zoonotic diseases, the acquisition of such new knowledge should help to improve surveillance strategies by developing collaboration between medical doctors and veterinarians.

P087 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Using satellite imagery and GIS data to help predict disease spread

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BACKGROUND: Innovative tools for modeling infectious agents are essential in the complex landscape of emerging infectious diseases and changing ecological, environmental, and demographic factors. Furthermore, to control or mitigate disease outbreaks, it is important to understand how they may spread geographically, which areas are at higher risk, and how control strategies may either reduce the probability of an outbreak in the first place or hinder further expansion if one were to occur. To address these challenges, we present a novel approach, which leverages fine-scale satellite imagery, GIS datasets, and population mobility models to simulate regional disease spread via road transportation.

METHODS: We used fine-grained satellite data on urban areas and high-resolution population data to build a metapopulation network upon which to model disease spread. Using the resulting geospatial network and the population attributes of its individual components (network nodes or vertices), we estimated the commuting rates between road-connected urban areas and incorporated mobility patterns in the network. We demonstrate the above process for Rwanda, and simulate Influenza A H1N1 (2009 pandemic strain) on the generated network using a discrete stochastic metapopulation model. We compare our forecast with the observed spread of the disease in 2009-10 and also determined the effects of vaccination campaigns on outbreak spread and impact.

RESULTS: Incorporating the fine-scale network allowed for more accurate forecasting of disease spread in terms of outbreak length and the order in which areas were infected: the results of our simulations were comparable to data collected during the actual outbreak of pandemic influenza in Rwanda. The probability of outbreak occurrence reduced when areas of infection origin were vaccinated, especially with increasing vaccination coverages and efficacies up to 80%. At the same time, outbreak impact, defined by the number of individuals were infected with influenza, was lower when larger urban areas were vaccinated.

CONCLUSIONS: Our modeling approach predicted influenza comparably to the actual outbreak and can be valuable for future planning and control purposes in real-time disease situations for which pre-outbreak data are unavailable or haven't yet been collected. We highlight the effectiveness of controlling outbreaks by targeting mitigation efforts at their points of origin, a process that can be made possible by increased surveillance and quicker outbreak response times. While we modeled influenza, this framework can readily be applied to other infectious diseases, such as Ebola in West Africa, where high population mobility promotes rapid disease propagation.

P088 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Bats and viruses in Western Asia: a model for One Health surveillance using research coordination networks

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BACKGROUND: Bats are critical components of ecosystems around the world and natural reservoir hosts to several emerging viruses with pandemic potential, e.g. henipaviruses, filoviruses, and SARS-related coronaviruses. However, current research on the distribution of bats, diversity of their viruses, and potential for zoonotic disease emergence is limited in many parts of the world. To fill this gap for Western Asia, we have launched a new collaborative One Health research project that will leverage regional expertise to characterize bat and coronavirus diversity and assess the risk of bat-borne zoonotic disease emergence. The research project, across multiple countries, will test key hypotheses related to the ecological, life-history, and evolutionary drivers of bat-associated viral diversity.

METHODS: Methods include extensive non-lethal field sampling of bats, screening and characterization of CoVs from bat samples, collection of associated ecological and site data, and modeling emerging disease risk by combining viral data with host, geographic, and ecological data. Over the 5-year duration of the project, we will collect over 20,000 samples from bats which will be prioritized for testing in regional laboratories (R. Lugar Center in Tbilisi, Georgia and Royal Scientific Society in Amman, Jordan). A second primary aim of the project is to create the Western Asia Bat Research Network (*WAB-Net*), a regional initiative to bring together bat ecologists and conservationists and public health representatives from >12 countries to strengthen regional capacity for zoonotic disease research. The WAB-Net will host annual workshops, in-service training opportunities, and One Health research exchanges to give students field-to-lab training in disease surveillance.

RESULTS: Since October 2017, when the project began, we have identified key personnel in each high engagement country (Georgia, Jordan, Turkey, and Pakistan); established standardized protocols for biosafety practices and bat sampling; identified field sites and obtained necessary permissions; established an initial database for the project; and developed preliminary spatial models of bat distribution in the region to prioritize surveillance. Preliminary viral testing results from Georgia and Jordan indicate that unique lineages of CoVs occur in bats.

CONCLUSIONS: Our recently-funded Western Asia project has two complementary goals: 1) to promote zoonotic disease awareness and risk reduction for bat-borne viruses, and 2) to foster scientific collaboration and proficiency among wildlife biologists, ecologists, public health specialists, and virologists. Our model is both cost-effective and sustainable because it leverages existing, regional expertise in wildlife research and laboratory diagnostics for One Health surveillance. The WAB-Net will also promote transboundary conservation of bat populations in this politically volatile region. We present examples of how this approach could be expanded to other research coordination networks globally.

P089 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Using microbiome community structure analysis to characterize zoonotic microbial transmission at the human-macaque interface in Northeast Thailand

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BACKGROUND: Traditional zoonotic disease research efforts centered on detection of high profile pathogens may miss opportunities to understand broader microbial transmission dynamics between humans, animals, and the environment. The Global Assessment of Zoonotic and Environmental Risks (GAZER) platform seeks to address this knowledge gap by examining overlaps of bacterial microbiome communities between humans, animals, and environments in settings where interaction with animals is high and potential for human health impacts of this contact are greater. We present data from Maha Sarakham, Thailand, where a growing population of long-tailed macaques (*Macaca fascicularis)* in the Kosumpee Forest Park interface with residents of the adjacent village. In particular, community members working in or near the park experience a high level of direct and indirect contact with macaques through feeding as well as aerosols of macaque feces during cleaning.

METHODS: Workers were surveyed to characterize tasks that contribute to exposure and other dietary or lifestyle factors that influence gut microbiome composition. We employed comparative microbiome analysis based on the V4 region of the 16S rRNA gene to assess the degree of similarity between gut bacterial communities and potential for pathogen transmission between macaques and workers. Fecal samples were collected from humans (exposed, n=12; control, n=6) and macaques (exposed, n=8; control, n=4) using the OMNIgene.GUT kit and sequenced on the Illumina HiSeq platform.

RESULTS: Alpha and beta diversity analyses between humans (exposed, n=12; control, n=6) and macaques (exposed, n=8; control, n=4) shed light on compositional changes in gut microbiota that may occur as a result of their increased level of contact. Bray-Curtis distance metric was used to assess degree of sharing based on the relatedness of microbial communities between groups. Variance and dispersion patterns detected in PCoA visualizations were tested using PERMNOVA and PERMDISP to investigate the role of the "Anna Karenina principle," a signature of dysbiosis characterized by increased variation in profiles of individuals in a disease state.

CONCLUSION: Alterations in gut microbiome composition of exposed worker and macaque populations and highlight the potential for increased susceptibility to other diseases.
By characterizing these exposures and resulting gut microbial community shifts, we can inform development of protective measures and training recommendations to reduce occupational hazards. It can also be used to mitigate negative aspects of contact between humans and macaques in order to optimize the health of both populations.

P090 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Developing an Animal Exposure History Tool for Physicians-In-Training to Improve Detection of Zoonotic Disease

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BACKGROUND: Zoonotic diseases are a vital public health issue, and about 75% of emerging infectious diseases are zoonotic in origin. (1) It is imperative to have a robust surveillance system that is able to detect these diseases in a timely and accurate manner. Data show that 33.7% of zoonotic disease outbreak reports originate from physicians and veterinarians, with clinicians detecting outbreaks more quickly than state departments or laboratories. (2) Since physicians and veterinarians are the first line of defense, it is important to ensure that clinicians are educated on how to detect zoonotic disease outbreaks. Currently, medical schools may lag behind veterinary schools in teaching clinical skills related to zoonoses. We report on a new clinical One Health elective for medical students at the University of Washington School of Medicine. One of the objectives of the rotation is to train medical students to take animal exposure histories, which would better equip physicians to identify and diagnose zoonotic infectious diseases.

METHODS: We performed a literature search to determine the extent of training that medical students currently receive on taking animal exposure histories. A script for taking an animal contact history was developed in collaboration with veterinarians and infectious disease experts through an iterative process. The tool was then piloted with standardized patients during the clinical elective.

RESULTS: The animal exposure history questionnaire was successfully piloted, and feedback was solicited from the standardized patients. The questionnaire addresses not only domesticated animals in the home, but also occupational and recreational exposures. The next phase will be to test its effectiveness among patients in outpatient and inpatient settings to verify its utility and ease of use. This could be achieved by comparing the detection rate of zoonotic infectious diseases between physicians who have been trained and use the animal exposure history, and those who have not, given similar patient populations. A subsequent phase would be to incorporate the history taking techniques into standard clinical skills curricula for medical students.

CONCLUSIONS: It is important to train physicians who are competent in taking animal exposure histories, to promote early and accurate detection of zoonotic infectious diseases. If the questionnaire were to be validated, it could then be disseminated and incorporated as part of the pre clinical curriculum at medical schools across the country. This would ensure seamless integration of One Health concepts as part of medical history taking. The early introduction of One Health in medical education, through teaching the animal contact history to better detect zoonotic infections, will shape a healthcare workforce that is sensitive to the changing patterns of zoonotic disease in human, animal environmental health systems, and propel them to find inter professional solutions to such health threats.

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P091 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Investigation of a Bonobo die-off Event of unknown origin at the “Lola ya Bonobo” Sanctuary IN Kinshasa, DRC, 2015-2016

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BACKGROUND: Emergence of new or unknown pathogens in animals may present a threat to human health. Animal keepers and veterinarians, because of very close and regular contact with animals, are especially at risk of infection. Assistance from the PREDICT-2 project, funded by the United States Agency for International Development, was requested by the "Lola ya Bonobo" sanctuary in Kinshasa, Democratic Republic of Congo (DRC), to help identify the pathogen(s) causing the death of 4 female bonobos between April 2015 and May 2016. Affected bonobos presented with neurologic symptoms without fever and respiratory distress, with a rapid evolution to death within four days.

METHODS: Biological specimens from two sick animals, and during necropsies, were collected by the Sanctuary staff. Suspicion of encephalitis (viral and bacterial encephalitis, encephalomyocarditis virus (EMCV), toxoplasmosis, and/or oesophagostomum) was investigated by biochemical, bacteriological, parasitological, serological (IgM/IgG anti-toxoplasma and anti-trypanosome antibodies) and hematological analyses at the Institut National de Rescherche Biomedicale (INRB), in Kinshasa, DRC. Slides for histopathology were prepared from brain tissues and sent to the Mountain Gorilla Veterinary Project team in Goma, DRC, for analysis. Oral swabs and tissue samples (lung, liver, spleen, kidney) were tested for with a variety of conventional broad range PCR assays at the PREDICT lab at INRB. Targeted viruses included filoviruses, flaviviruses, bunyaviruses (in general as well as hantaviruses specifically), paramyxoviruses, influenzaviruses, coronaviruses, enteroviruses, picornaviruses and herpesviruses).

RESULTS: Herpesvirus DNA was obtained from a cerebral-spinal fluid sample from one of two animals tested. The herpes virus strain was closely related to *Pan paniscus* lymphocryptovirus, in the Gamma herpesvirinae subfamily, found in bonobos and previously described as a novel simian homologue of human Epstein-Barr virus. None of the other PCRs amplified any viral DNA or cDNA.

CONCLUSIONS: The close collaboration between the institutions and the rapid testing for a variety of potentially dangerous viruses with different broad range assays allowed appropriate containment measures and ruled out many known zoonotic threats. It remains unclear if the bonobo die-off, could have been caused by the detected herpesvirus. The event appeared to be contained to the “Lola ya Bonobo” sanctuary, where the staff has since implemented increased biosafety measures in dormitories, cages, enclosures, and feeding areas.

P092 - OHS B01 - SURVEILLANCE AND EARLY DETECTION

Mapping the Distribution and Abundance of Major Zoonotic Diseases in South Tigray, North Wollo and Ab’ala (Afar), Ethiopia

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BACKGROUND: In developing countries every year 2.4 billion human infections with origins in animals (zoonotic) occur, causing widespread illness and 2.2 million human deaths. These diseases are often endemic and include brucellosis, tuberculosis, salmonellosis, leptospirosis, rabies, and others that are under diagnosed, underreported, and which disproportionately affect those who live nearest to animals. In Ethiopia neglected zoonotic diseases (NTZD) were not given the required attention at various levels. Data on their burden and distribution is incomplete and not updated periodically; access to preventive and curative services is inadequate and not well integrated.

METHODS: A cross-sectional and retrospective study was conducted from December 2016 to May 2017 in selected districts of Southern Tigray, North Wollo zone of Amhara region and Abala district of Afar region to map the distribution and abundance of major zoonotic diseases. Secondary data, informants’ interview and questionnaire survey were methods employed. The burden and intensity of four major zoonotic diseases (helimenthiasis, TB, rabies and schistosomiasis) was mapped using qGIS software.

RESULTS: Retrospective data (2012-2016) results indicated that, out of a total 1,273,145 observed human diseases cases, 53614(4.2%) of them were potential zoonotic diseases that include: helminthiasis (51192), TB (2085), rabies (227), schistosomiasis (105) and Visceral leishmaniasis (7) cases. The highest burden of TB (29%) and rabies (34%) were recorded in Gubalafto/Weldya followed by Raya Kobbo (26%) and Raya Azebo (21%) for TB and rabies, respectively. The highest burden of schistosomiasis was in Raya Alamata 71% followed by Gubalafto/Weldya 24%. Three cases of VL were recorded in Gubalafto/Weldya and 2 cases each in Abala and Raya Azebo. The highest disease cases were in age group above 15 and in male individuals. Rabies and TB showed in decreasing trend within the data recorded years. In animals only 31 rabies cases and 15 anthrax cases were recorded from 2012 to 2016. Key informants interview indicated rabies, anthrax, brucellosis, bovine tuberculosis and cysticercosis as major zoonotic diseases that need priority attention in the study areas. Animal management practices and product usage habits were indicated as the major risk factors for transmission of zoonotic diseases from animals to humans. Questionnaire survey result further indicated that about 91.1%,70.4%, 23.5%, 62.7%, 8% and 2.2% respondents heard about rabies, anthrax, BTB, taeniasis, brucellosis and hydatidosis, respectively. However, only 16.1% of respondents have an overall good KAP on those diseases.

CONCLUSION: The present study highlighted the burden and distribution of some major zoonotic diseases in the study area that need attention from responsible authorities. Further systematic and detailed research should be conducted to map the distribution of major zoonotic diseases at regional level so as to make an informed decision.

INTERVENTION STRATEGIES

P093 - OHS B02 - INTERVENTION STRATEGIES

Should ecological approaches be used to manage the risk of Hendra virus spill-overs? - A report on two citizens' juries

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BACKGROUND: Hendra virus infection is endemic in Australian flying-fox populations. It causes rare, but catastrophic, human infection. Loss of habitat has driven flying-foxes into agricultural and peri-urban areas, promoting viral 'spill-overs' into horses and people. An equine vaccine is available and horse-husbandry practices that minimize the risk of Hendra exposure are encouraged. However, vaccine uptake is suboptimal, horse owners find behavioral change burdensome, and some veterinarians are refusing to attend unvaccinated horses. Broader ecological approaches could usefully complement vaccination and behavioral strategies. Habitat creation and linkage could reduce stress on flying-foxes, and thereby, the amount of virus shed into the environment. However, the adoption of ecological approaches is controversial because they restrict the rights of landholders for the benefit of flying-fox populations.

METHODS: We convened citizens juries in Rockhampton (Queensland) and Lismore (NSW) to elicit the views of well-informed community members on:

- the acceptability of adding ecological approaches to current interventions that mitigate the risk of Hendra spill-over
- what obligations veterinarians might have to attend unvaccinated horses

These communities are both in areas affected by Hendra outbreaks. Participants of diverse background of mixed genders and ages were recruited from by random-digit-dialing; people who interact with horses and non-horse owners were equally represented. Each jury was presented with balanced factual evidence supporting different expert perspectives on the feasibility, benefits and potential cost of different strategies for managing Hendra risk, and given the opportunity to ask experts questions.

RESULTS: The juries were unanimous that ecological strategies should be part of the approach taken to manage Hendra virus risk. The key reasons for supporting the adoption of ecological approaches were: (i) they address underlying causes of disease emergence, (ii) they help to prevent the spill-over of other bat-borne pathogens, (iii) there would be broader benefits for the community. Of the potential mechanisms discussed, the Rockhampton jury preferred direct government action to create a habitat network, whereas the Lismore jury preferred to incentivise farmers to create and maintain flying-fox habitat. Both juries rejected placing further restrictions on land clearing. A majority in both juries held that veterinarians are not obliged to attend unvaccinated horses, because the consequences of the owner's decision not to vaccinate should not be borne by others. A minority held that veterinarians should attend because if a horse has a Hendra infection, as health professionals they are best placed to manage the public health implications.

CONCLUSIONS: These informed citizens acknowledged the importance of addressing the drivers of bat-borne infectious risks, while also seeking to reduce the burdens placed on veterinarians. Their overarching aim was that policy interventions should be directed towards creating collective actions and broad social support for improving habitat for flying-fox populations, while not transferring costs to landholders.

P094 - OHS B02 - INTERVENTION STRATEGIES

Impact of nutrition therapy program on the global acute malnutrition in three counties- an experience in a war-torn lakes state of South Sudan.

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BACKGROUND: The objective of this study was to determine the impact of nutrition therapy program on the Global Acute Malnutrition (based on the prevalence pattern) and to determine the feeding practice and perception of the mothers/caregivers regarding the nutrition therapy program in three counties (Cueibet, Yirol West and Rumbek North) in Lakes State of south Sudan.

METHODS: A combination of retrospective cohort and descriptive cross-sectional survey study designs was used. Data was obtained from District Health Information software (DHIS) across the three years 2014, 2015 and 2016, and structured questionnaire. Sample size was calculated using Leslie and Kish formula. Data analysis was done using the Statistical package for Social Science (SPSS) version 21 using Friedman Analysis Of Variance (ANOVA), Wilconxon Signed Rank test, Kruskal Wallis test, Man Whitney U test, Kruskal Wallis, and inferential statistics of Chi-square was used to test for significant associations between socio-demographic variables and the practices of the mothers/caregivers towards administering the food supplements on their children, and their perception on the efficacy of the nutrition therapy program in the three counties. Statistical level of significance was set at P-value <0.05

RESULTS: Findings revealed statistical significant differences in SAM and MAM within each county and among the three counties across the three years. The results further revealed that there was rising median values of SAM and MAM among the counties across the three years. More than 90% of mothers/caregivers in Cueibet and Yirol West counties have varying degrees of poor feeding practices and perceptions about the nutrition therapy programme, while in Rumbek North county, over 50% of the mothers/caregivers have good feeding practices but more than 50% of them also have varying degrees of poor perception about the nutrition therapy programme. Among suggestion for improvement include; intensive health education of mothers/caregivers, training and re-training of CNVs and CHWs, timely availability of food supplements, enactment of every possible policy to ensure food security, unwavering adherence to the principle of neutrality and impartiality on the part of INGOs and government, and conduct of pre and post-intervention surveys- all may serve as the panacea towards the present state of the nutrition therapy programme in the war-torn Lakes State of south.

CONCLUSION: It can be deduced that, espite the huge investment by all stakeholders in the intervention programme to ameliorate the status of the global acute malnutrition in the three counties, in Lakes state of south Sudan, there is a need for a comprehensive re-evaluation of the programme for effective and efficient nutrition therapy interventions.

P095 - OHS B02 - INTERVENTION STRATEGIES

Brazilian initiative to guarantee the Human Right to Adequate Food with sustainable food production

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The Earth faces a challenge to ensure Food and Nutrition Security for its entire population. Technological and scientific advances of major food manufacturing companies promotes extractive production that degrades environmental and animal health, besides contributing to increasing obesity and related complications, through the offer of high calories foods, damaging humans health. On the other hand, this production system is also related to socioeconomic disparities, undernutrition and lack of access to quality and healthy food, which remains a serious problem in many developing countries, including Brazil.

The Human Right to Adequate Food is defined as: food availability, adequacy, accessibility and stability of access to food produced and consumed in a sovereign, sustainable, dignified and emancipatory way. With this in mind, the National School Feeding Program was created in Brazil. The Program aims to transfer financial resources to partially meet the nutritional needs of Brazilian students in public schools, diminishing malnutrition risk in this population. Also, it requires that at least 30% of financial resources be invested exclusively in community agricultural products, preferably organic and/or agroecological foods. It guarantees the Human Right to Adequate Food and support sustainable development, through the production of regional, seasonal foods, in a sustainable production model, with lower environmental impact.

More than 80% of the productive units belongs to community agriculture, which besides feeding the 47 million students from Brazilian public schools, is also responsible for approximately 70% of the food consumed in Brazil.

The PNAE works in a sustainable production to guarantee Food and Nutrition Security and the Human Right to Adequate Food. It is considered one of the largest programs in the field of school feeding in the world, being praised by several nations.

P096 - OHS B02 - INTERVENTION STRATEGIES

One Health National Programme for rabies control and eradication 2017-2021

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Dog rabies is a pressing problem in the Northern provinces of Viet Nam and gradually spreading to other areas which has no or very few cases for many years. Between 2007-2016, approximately 90 people died from rabies annually in the country. During the past five years, approximate of 400,000 people received Post Exposure Prophylaxis (PEP) including bite wound treatment and vaccine preventing human deaths (Ministry of Health's report 2016). The main factors contribute to the disease spread including limited dog vaccination coverage, low trust in PEP and lack of effective inter-sectoral outbreak response and coordination.

During 2010-2015, Viet Nam had two separate national progarmmes for rabies control, one was implemented by Ministry of Agriculture and Rural Development (MARD) and one led by Ministry of Health (MOH). The programmes' implementation revealed critical gaps including overlapped interventions, under resource capitalization and inconsistent and conflicting messages. These gaps demanded for application of One Health (OH) approach that facilitate better coordination of resource and interventions especially in the public and animal health sectors.

The Food and Agriculture Organization (FAO) of the United Nations together with the World Health Organization (WHO) assisted Viet Nam to develop the OH National Programme for rabies control and eradication (NPRCE) 2017-2021. The NPRCE identified six specific objectives including i) 95% of towns can develop database of dog population; ii) Increased dog vaccination coverage of 85%; iii) No dog rabies outbreaks in 70% of all provinces nationwide for two years consecutively; iv) 60% decrease of the identified high risk provinces and v) 60% decrease of rabies human deaths in 2021 compared with the average during 2011-2015.

The progamme set out 12 strategic interventions including 1) To improve inter-sectoral outbreak investigation and response; 2) To revise the existing regulations of both public and animal health; 3) To enhance risk communications; 4) To increase inter-sectoral surveillance 5) To improve dog management, 6) To enhance dog vaccination coverage; 7) To increase PEP coverage; 8) To strengthen laboratory capacity; 9) To improve dog movement control; 10) To increase qualification of manpower resource; 11) To build up a rabies free zone and 12) To improve research capacity.

MARD and MOH are co-leading the NPRCE implementation in collaboration with the participating agencies including Ministry of Planning and Investment, Ministry of Finance, Ministry of Education and Training and Ministry of Information and Communication. Whilst the funding for the NPRCE come from both the national and provincial budgets, Viet Nam is calling for external assistance from international development partners.

The NPRCE serves as the strategic action framework for multi-disciplinary collaboration among research institutes, development organizations and private sector to control rabies effectively in Viet Nam.

P097 - OHS B02 - INTERVENTION STRATEGIES

An integrated health delivery platform, targeting soil-transmitted helminths (STH) and canine mediated rabies, results in cost savings and increased breadth of treatment coverage for STH in remote communities in Tanzania

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BACKGROUND: Achieving reduction in neglected tropical diseases (NTDs) requires cost-effective strategies that attain comprehensive coverage.

Objective 1: Investigate impact on coverage and cost of an *integrated intervention strategy*: deworming humans *and* vaccinating dogs against rabies; 2: Quantify the reach of the deworming intervention and compare with the national primary schoolbased deworming program (NSDP); 3: Evaluate community perceptions about integrated health interventions.

METHODS: Objective 1 & 2: The trial (in remote Tanzanian communities) comprised 24 villages allocated to Arm A (deworming and vaccination), Arm B (deworming only) or Arm C (vaccination only) (Figure 1).

Objective 3: Interviews with a range of participants investigated attitudes about integrated delivery.

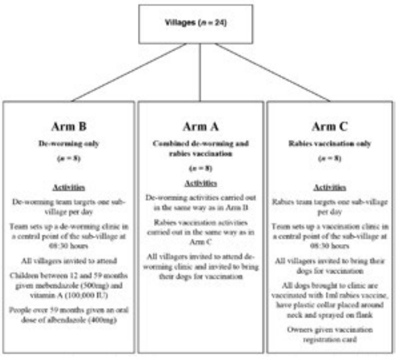

Figure 1: Diagram indicating treatment arm allocation and activities

RESULTS: Objective 1: The percentage of people dewormed in Arms A and B was 63% and 65%, respectively ($x^2 = 1$, $p = 0.32$). Integration did not result in coverage decrease. The percentage of dogs vaccinated in Arm A and C was 70% and 81%, respectively ($x^2 = 9$, $p = 0.003$). Despite a reduction in coverage in Arm A, both achieved the target threshold of 70% required to eliminate rabies. It took 33% less time to attend the integrated delivery than two separate events. Integrated delivery was cheaper, with deworming and vaccination reduced by $0.13 (54%) and $0.85 (19%) per dose respectively.

Objective 2: The percentage of *enrolled* primary school children reached by the NSDP and this trial was not different (F = 0.9, p = 0.36). However, of the primary school age children treated in this trial 46% *were not enrolled in school* and were out of the reach of the NSDP.

Objective 3: Opinions of combined human – animal health programs were overwhelmingly positive with support (in terms of time and cost savings and receiving multiple health benefits at once) for integrated approaches.

CONCLUSIONS: Integrated delivery platforms for health interventions are feasible, locally acceptable, result in cost / time savings, don't result in a reduction of humans treated or constrain the ability to achieve a target 70% threshold for dog rabies vaccination. These results indicate the utility of integrated One Health delivery platforms and suggest a role in the global campaign to reduce NTDs. The level of recorded school non-enrolment suggests that, in hard-to-reach areas, *school-based* delivery strategies miss a large fraction of school-aged children. Changing intervention location to be close to, rather than within, school grounds allows all children (enrolled or not) to benefit from treatment.

P098 - OHS B02 - INTERVENTION STRATEGIES

Community Perceptions on Integrating Animal Vaccination and Health Education by Veterinary and Public Health Workers in the Prevention of Brucellosis among pastoral Communities of South Western Uganda

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Brucellosis is a zoonotic disease of veterinary, public health and economic significance in most developing countries, yet there are few studies that show integrated human and veterinary health care intervention. The study aim was to explore community perceptions on integration of animal vaccination and health education by veterinary and public health workers in the management of brucellosis in pastoral communities. This study used a qualitative design where six Focus Group Discussions (FGDs) were conducted, two from each sub-county; one with the local leaders, and another with pastoralists and farmers. Five Key Informant Interviews (KIIs) with two health workers and three veterinary officers from three sub-counties in Kiruhura district were conducted. Latent content data analysis was used. All the groups mentioned that they lacked awareness on brucellosis commonly known as brucella and its vaccination in animals. FGD and KIIs respondents perceived improvement in human resources, facilitation of the necessary activities such as sensitization of the communities about the brucellosis, and provision of vaccines and diagnostic kits as important in the integration process. Community participation was believed crucial for sustainability and ownership of the process. Mass animal vaccination in combination with health education about the disease was mentioned as possible if collaborations are fostered by government and all other stakeholders as a One Health approach.

P099 - OHS B02 - INTERVENTION STRATEGIES

Estimation of the cost of rabies to society in West and Central Africa and elaboration of the cost of rabies elimination in Africa

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BACKGROUND: Around 99% of rabies infections in humans are due to dog bites and, 3.6 deaths per 100 000 individuals in rural Africa occur yearly. Unlike for most zoonoses, relevant and efficient vaccines for humans and animals are available. Unfortunately, these are frequently inaccessible and non-affordable in low-income countries where the rabies burden is greatest. However, the World Health Organization recognized that human rabies can be controlled by dog mass vaccination. However, in Africa, such intervention failed because of the low political engagement and fund allocated for rabies control, even if, studies in urban and rural settings in Chad and Tanzania show that interventions vaccinating dog populations are cost-effective and a sustainable way to control rabies in the long-term. To enable Africa to reach the target goal of rabies elimination by 2030, strategic plans must be developed. To reach this goal, the aim of this study is to identify the best financial and logistical option to control rabies in Africa based on its burden and cost-evaluation. To be able to implement interventions at a large scale, quantitative data on the economics of rabies vaccination campaigns and the cost of rabies cases and deaths to the country are necessary to show its impact on public health and its benefit to animal and human health systems through the control of vector populations.

METHODS: Data of the current Global Alliance for Vaccines and Immunizations (GAVI) project on the estimation of the burden of rabies (dog demography, human and animal incidences, post exposure prophylaxis, several costs) in Mali, Côte d'Ivoire and Chad and those from Tanzania will be used to parametrize a probabilistic model. This model of cost-effectiveness analysis, in addition of several costs, will combine data on phylogenetic, geographic, sociological and logistical information as input. The outcome will be the Quality Ajusted Life per Year (QUALY) which means the number of lives added in case of intervention for human.

EXPECTED OUTCOMES: Experience in East, Central & West Africa are capitalized to elaborate a regional predictive model to proof that canine rabies elimination is feasible (as rinderpest), cost-effective & sustainable. Importance and effect of intersectoral partnership for disease control like rabies are perceived especially for health and veterinary workers, Governments. A national and overarching strategic action plans for African rabies elimination is prepared and can be adapted for other infectious diseases.

P100 - OHS B02 - INTERVENTION STRATEGIES

Describing and modelling livestock movements in northern Tanzania and the implications for the transmission of endemic zoonoses

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BACKGROUND: Livestock and livelihoods are intimately entwined in northern Tanzania. Infectious diseases of livestock have important impacts on household welfare; impairing productivity, hindering economic growth and stability and threatening food security. Additionally, endemic zoonoses such as brucellosis, coxiellosis, leptospirosis and Rift Valley fever have direct impacts on human health, burdening individuals and societies with febrile illnesses.

Movements are recognised as a major contributor to disease transmission in farming systems across the world and effective control in livestock relies on understanding these movements. There is a paucity of data on livestock movements in northern Tanzania.

METHODS: This study focusses on describing and modelling livestock movements in the Arusha, Manyara and Kilimanjaro regions of northern Tanzania. Three classes livestock movements are investigated: i) herd and flock movements to grazing and watering points; ii) livestock movements between households (sales, purchases, gifts); and iii) livestock movements to/from markets. Data has been gathered using household and market-based questionnaires. Focus group mapping has been conducted within a range of smallholder, agro-pastoral and pastoral villages to describe grazing and water point movements and 59,000 government movement permits have been collected to explore livestock flow across the broader landscape.

RESULTS: A range of methods will be used to describe and model the livestock movement network. These methods include: gravity based generalised linear mixed models using movement permit data to simulate livestock trade movements (Fig.1); network analysis of the simulated network and agent-based modelling to describe temporary and indirect contacts which occur at watering and grazing locations.

The livestock movement networks will be used to identify high risk pathogen transmission routes and locations. The data will also be linked to serological data describing human and animal zoonotic pathogen exposure collected as part of the wider Social, Economic and Environmental Drivers of Zoonoses (SEEDZ) study.

CONCLUSION: Models will be used to explore the impact of specific behaviors and interventions, such as targeted vaccination, increased active surveillance or movement restrictions during outbreaks, on zoonotic disease epidemiology in northern Tanzania.

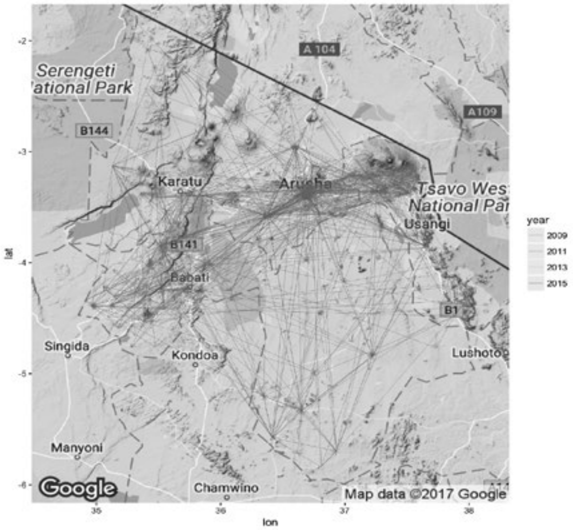

Figure 1: Map showing the results of a livestock movement simulation model built using 10% of livestock movement permits from 2009, 2011, 2013 and 2015 across Arusha, Kilimanjaro and Manyara regions in Tanzania.

P101 - OHS B02 - INTERVENTION STRATEGIES

Evaluation of a one health response to an outbreak of highly pathogenic avian influenza in the Western Cape province of South Africa

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BACKGROUND: As the primary responders to an animal health emergency, a great deal of the responsibility of considering all aspects of one health in the control of an animal disease outbreak rests on state veterinary services. This study explores the response to an outbreak of highly pathogenic avian influenza that mainly affected the Western Cape Province of South Africa in 2017. Infected poultry farms experienced high mortalities and were expected to destroy and dispose of all birds on their properties. We record to what extent aspects of a one health response were considered and could be practically implemented as well as what barriers exist to an effective response.

METHODS: Veterinary Services officials whose work was affected by the outbreak were interviewed and their perspectives and experiences recorded, including which aspects of the outbreak response they felt could be improved in the future.

RESULTS: While a contingency plan for outbreak response exists, it is not widely available or updated. Utilisation of existing government networks resulted in the involvement of agencies covering several important aspects of a one health response, including human health surveillance, environmental considerations regarding the disposing of infected material, social relief to affected farmers and farm workers, animal welfare during culling and communication with the public through the media. However, the delay in response for some of these aspects was a challenge, often due to bureaucratic procedures and under-resourcing.

Lack of a streamlined communication strategy both within and from veterinary services was identified as an issue. Consequently, there is a lack of education amongst farmers regarding their responsibilities and what actions to take in the event of a disease outbreak.

No psychological support for farmers, farm workers, their families and government officials during the outbreak was provided. A need for training of veterinary officials in responding to people affected by traumatic situations was identified.

Adequate collection of data or facilitation thereof during the outbreak was lacking. As a result, useful analyses of the outbreak could not be performed to their full potential, such as economic evaluation of the impact of the outbreak as well as research to inform disease control decisions in the future.

CONCLUSIONS: Although many aspects of a one-health approach were adequately considered, there is room for improvement to increase the efficacy of outbreak response. Recording and evaluation of actions is an important part of outbreak response. This should facilitate the production of comprehensive, frequently updated and well-communicated contingency plans for improved response to animal disease outbreaks in the future.

P102 - OHS B02 - INTERVENTION STRATEGIES

First “Global Flipped Classroom in One Health”: From MOOCs to research on real world challenges

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BACKGROUND: MOOCs are changing public/global health education offering free quality learning materials and gathering online global communities of learners and experts. In 2016 and 2017, we launched two MOOCs addressing One Health: *One health: Connecting humans, animals and environment* (University of Basel on *FutureLearn*) and *Global Health at the Human-Animal-Ecosystem Interface* (University of Geneva, Institute Pasteur, University of Montreal and Centre Virchow-Villermé on *Coursera*). These MOOCs raise awareness on One Health and support scientists, health professionals and decision-makers through specialized education.

However, MOOCs’ pedagogy is debated and blended approaches such as “flipped classrooms” promote more active learning and capacity building combining MOOCs with on-campus interactions with experts. We organised in Switzerland the first “Global Flipped Classroom on One Health” gathering learners from our MOOCs to test and promote a new educative model based on MOOCs and research-oriented learning in One Health.

METHODS: Twelve performant learners were selected from our MOOCs and granted by the *Swiss School of Public Health* to come to Geneva and Basel during 10-14th July 2017. Learners ranged from undergraduate students to senior researchers from a diversity of fields/interests and origins. The programme included: project pitching and interdisciplinary research mentored by experts from academia and IOs (e.g. WHO, FIND); visit to WHO and Swiss TPH and discussions on projects; final defence of projects.

RESULTS: Research projects selected addressed: 1) online primate trade and zoonotic risks using digital epidemiology; 2) boots to protect from snakebite in Nepal; 2) mapping urban wildlife and health risks using citizen science; 4) One Health communication campaign to tackle AMR in Kenya. Project 1 should result in a publication in 2018 and project 3 was integrated as a students’ research project in the UNIGE’s Master in Global Health.

According to a final survey, the satisfaction by participants was high, stressing on the benefits from interdisciplinary teams of peers and support received by experts. MOOCs gave learners knowledge basis and/or promoted innovative research approaches (e.g. digital epidemiology, citizen science).

CONCLUSIONS: This is the first MOOC-based and research-oriented flipped-classroom on One Health gathering interdisciplinary and international learners and experts. Learners benefited from this event through the reinforcement and extension of their knowledge in One Health, capacity to perform innovative and interdisciplinary research, interactions with experts etc. More widely, this event has reinforced links between Swiss and international One Health groups, and with *International Geneva* (e.g. WHO). This model illustrates new applications of MOOCs in general and particularly in One Health for a more direct and practical impact in research and problem-solving using interdisciplinary collaborations and available expertise within massive and global communities online.

P103 - OHS B02 - INTERVENTION STRATEGIES

The first MOOC on Global Health at the Human-Animal-Ecosystem Interface: Two years of innovative activities since the International One Health Congress 2016

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BACKGROUND: The MOOC on *Global Health at the Human-Animal-Ecosystem Interface* was first presented during the *International One Health Congress* 2016 (Melbourne) and launched on *Coursera* in March 2017. It was co-produced by University of Geneva (UNIGE), Institut Pasteur, University of Montreal and Centre Virchow-Villermé, and had contributions by 37 experts from 20 institutions including IOs such as WHO. This MOOC addressed emerging zoonotic diseases, neglected zoonotic diseases, antimicrobial resistance etc., and highlighted the need for One Health to tackle Global Health challenges.

UNIGE and other Universities are active producers of MOOCs, but in general they rely on passive models of online dissemination and utilization, only partly exploiting their full potential. During the last two years, we have tested new educative models based on our MOOC going beyond the pure online experience and interacting with learners more closely for an improved impact on education and research. We present here some of these activities.

METHODS: Using our MOOC and involving its global community of learners and experts, we developed several blended-learning and research-oriented activities in One Health during 2017-2018:

10-14th Jul. 2017, Geneva and Basel - First “Global Flipped Classroom on One Health” bringing together 12 learners from our MOOC and from that produced by the Swiss TPH on *One health: Connecting humans, animals and environment*, to do interdisciplinary and collaborative research activities on One Health.

Autumn-Fall semester 2017, Geneva - Blended-learning course on *Global Health at the Human-Animal-Ecosystem Interface* as part of UNIGE’s Master in Global Health involving 27 international students.

Oct. 2017- Feb. 2018, Geneva and Kakuma Refugee Camp (Kenya): Blended-learning course on *Global Health at the Human-Animal-Ecosystem Interface* combining distant mentoring of 15 refugees by 15 students from UNIGE’s Master in Global Health, and project-based learning in Kakuma mentored by two UNIGE’s experts.

RESULTS: Today our MOOC has over 2400 enrolled learners from across the globe. Besides the comments from the online community, our activities have given us the opportunity to meet some of these learners and obtain a more precise feedback. These activities have resulted on a more complete learning experience and tangible impact of our MOOC for a diverse group of learners, including students from the UNIGE, from other Universities and from Kakuma Refugee Camp (Kenya). Collaborations between our team and both learners and other researchers have emerged from these activities to bring new content to the MOOC and to develop collaborative research in One Health.

CONCLUSIONS: MOOCs gather massive and global communities of learners. Based on our experiences, we believe that, in addition to passive models of dissemination, Universities should further develop and test innovative ways to use MOOCs for more tangible interactions with participants for an improved impact on their learning experience and the society.

P104 - OHS B02 - INTERVENTION STRATEGIES

Assessmnet of IHR core capacities to prevent, detect and respond to zoonotic diseases in South Africa

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BACKGROUND: The International Health Regulations requires that all WHO Member States develop core capacities to prevent, detect and respond to priority public health threats including zoonotic diseases. The majority of emerging human pathogens are zoonotic, therefore the Department of Health (DOH) in South Africa established mechanisms to prevent, detect and respond to zoonotic disease threats through a One Health approach. This involved the collaboration of animal health, human health and the environmental sectors. We describe South Africa's progress in tackling zoonotic diseases, through the One Health approach, as shown by the WHO Joint External Evaluation (JEE).

METHODS: The JEE tool was used to independently assess the country's core capacities to prevent, detect and respond to zoonotic diseases. A Zoonotic Diseases Sub-committee was formed to conduct a self-evaluation and provide information on national capabilities based on indicators and technical questions in the JEE tool. The sub-committee reported on the status of South Africa to address zoonotic diseases in terms of the following indicators: surveillance systems, veterinary or animal health workforce and mechanisms for responding. A score (no capacity = 1, limited capacity = 2, developed capacity = 3, demonstrated capacity = 4, and sustained capacity = 5) was awarded for each indicator. The JEE team comprising 7 international subject matter experts and a multi-sectoral national team jointly discussed and agreed upon the score, strengths/best practices, areas which need strengthening, challenges and priority actions.

RESULTS: A score of 4 was awarded to each of the 3 zoonotic diseases core capacity indicators. Overall there is highly effective information sharing and coordinated activities between DoH, Department of Agriculture, Forestry and Fisheries, Department of Environmental Affairs and other stakeholders. Effective strategic fora at national level include a One Health Steering Committee, One Health Forum, government, academia and private sector. At the technical leadership level the Multi-sectoral National Outbreak Response Team (MNORT) is the key mechanism for coordinated zoonotic disease information sharing, analysis and action.

Zoonotic diseases surveillance is carefully prioritized and officially legislated. Training was conducted for animal and human health workforce, however further training was recommended. Mechanisms for responding include close to real-time reporting across sectors. Zoonotic disease reporting was provided at monthly MNORT meetings by both human health and animal health staff, providing opportunity for joint discussion, analysis of risks and response measures. Effectively coordinated One Health responses to zoonotic disease events include: Crimean Congo haemorrhagic fever, Rift Valley fever, anthrax, bovine brucellosis and avian influenza.

CONCLUSIONS: Key recommendations emanating from the JEE include: developing a policy for One Health and conducting a major joint zoonoses simulation exercise. South Africa has made excellent progress in implementing a One Health approach to zoonotic diseases and can be regarded as a model country within Africa.

P105 - OHS B02 - INTERVENTION STRATEGIES

Brucellosis in northern Tanzania: insights into human disease prevalence, multi-species transmission processes and the design of sustainable interventions

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BACKGROUND: Brucellosis, caused by multiple *Brucella* spp., is an important cause of human febrile illness in northern Tanzania but cases are often mis-diagnosed. Despite widespread awareness of this disease in the study area key knowledge gaps persist. The *Brucella* species present in and transmitted between different hosts are poorly described. Data defining the roles of different animal host species in transmission of infection between livestock species or to humans are scarce.

METHODS: Surveillance of outpatients presenting at Endulen Hospital in the Ngorongoro Conservation Area was conducted to estimate brucellosis prevalence in this population and identify the *Brucella* species responsible for human disease. Individuals presenting from August 2016 to October 2017 with reported fever within the past 72 hours, or a tympanic temperature of ≥38.0°C were eligible for enrolment. Blood culture was performed. A *Brucella* genus-level qPCR detection assay was used to test vaginal swab samples collected from livestock sampled in pastoral areas of northern Tanzania. A latent process model based on serology data collected across northern Tanzania was used to reconstruct *Brucella* transmission dynamics.

RESULTS: Eight patients with acute brucellosis were identified among 218 (3.7%) febrile study participants. Seven of eight *Brucella* isolates have been typed as B. melitensis and one preliminarily typed as *B. abortus*. Several other important bloodstream infections have been identified through this surveillance platform. Swabs from 8 of 252 (3.2%) cattle, 5 of 216 (1.9%) sheep and 10 of 260 (3.9%) goats were qPCR positive revealing *Brucella* infection (potentially including zoonotic and non-zoonotic species) in multiple livestock species. One qPCR positive swab collected from a sheep has been SNP typed as B. ovis. Modelling results identify goats & sheep as the most likely source of human *Brucella* exposure in northern Tanzania.

CONCLUSION: The data from this study reveal that *B. melitensis*, *B. abortus* and *B. ovis* are present in this northern Tanzania system. *B. melitensis* is the predominant zoonotic *Brucella* species causing acute human brucellosis in the febrile hospital population. In 2017, brucellosis was ranked as one of six priority zoonoses of greatest national concern in Tanzania. Our data indicate that control strategy developments for this setting should span *B. melitensis* and *B. abortus* control in goats, sheep and cattle. Our data, combined with existing data from Tanzania, suggest regional variation in the prevalence and human illness impacts of brucellosis. Areas with different epidemiological patterns or disease risks (e.g. pastoral systems as compared to commercial dairy systems) can be selected for next step research and intervention development projects.

P106 - OHS B02 - INTERVENTION STRATEGIES

The role of West African rodents in the transmission of zoonotic schistosomes: spillover or reservoir hosts?

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BACKGROUND: Schistosomiasis is a neglected tropical disease (NTD) of profound medical and veterinary importance caused by dioecious trematodes of the genus *Schistosoma*. This NTD currently affects over 240 million people, with the highest burden in sub-Saharan Africa. *Schistosoma* parasites are characterized by complex multi-host disease dynamics and interspecific interactions leading, under certain conditions, to viable hybridizations between human and animal schistosomes with subsequent zoonotic transmission. Anthropogenic land-use changes and the progressive loss of ecological barriers may have also favoured interactions between different *Schistosoma* species. Our study elucidated the role of wild small mammals as reservoir of zoonotic *Schistosoma* species and hybrids in a region of northern Senegal facing dramatic anthropogenic change.

METHODS: Between May 2016 and November 2017, we trapped, humanely euthanized and necropsied small mammals from sites around Lake Guiers and the town or Richard Toll, Saint-Louis Region, Senegal. At post-mortem, organs were examined for schistosomes. Multi-locus molecular analyses of *Schistosoma* spp. from rodents, in addition to specimens from humans, livestock, and snails, were followed by Maximum Likelihood (ML) and Bayesian Inference (BI) phylogenetic analyses. These datasets were used to infer evolutionary relationships and lineages among the circulating zoonotic *Schistosoma* species and hybrids.

RESULTS: A total of 671 small mammals were captured over 4089 trap nights. *Schistosoma* spp. were isolated in the portal system and mesenteric vessels of 24 out of 367 *Mastomys huberti* mice (prevalence 6.6%; intensity range 2-64) and 6 out of 257 *Arvicanthis niloticus* rats (prevalence 2.3%; intensity range 1-44). Infection prevalence was highly focal among study sites, with relatively high rates in the villages of Gueo (52.6%) and Temey (28.6%). Based on molecular ML and BI phylogenetic analyses, lineage support indicated shared transmission of zoonotic *Schistosoma* species and hybrids between humans and wildlife.

CONCLUSIONS: Our study emphasizes the role of rodents as important zoonotic reservoirs of *Schistosoma* species and hybrids. The breakdown of ecological barriers seems to support the life cycle and interspecific interactions between human and animal schistosomes. Therefore, a One Health, multi-host framework would better tailor local control programmes for schistosomiasis disease, enhancing public health interventions in many endemic areas of sub-Saharan Africa.

P107 - OHS B02 - INTERVENTION STRATEGIES

One health based Outbreak investigation of unknown diseases linked to consumption of raw wild boar meat in Guto Gida district, East Wollega of Western Ethiopia in 2017.

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1: Jimma University, Ethiopia - 2: Cornell University ,USA -

BACKGROUND: Multidisciplinary team made an outbreak investigation linked to consumption of wild boar meat on December 24\2016. The source of infection was meat of wild boars that were illegally hunted.The outbreak affected (n=50) people all of whom had consumed raw or under cooked of wild boar meat and 5 of them were died. They were referred to the nearby hospital and had treatment for anthrax and brucellosis by the physician but they did not respond.

METHOD: Across-sectional study design was used to conduct outbreak investigation. An integrated One Health team were established for this outbreak investigation and to save the life of the community. This outbreak investigation was conducted in guto gida district East Wellega of Oromia region. All the cases (n=50) were identified using a house-to house visit using structured questionnaire to collect information on the clinical features, date consumption of wild boar meat, onset of symptoms, consumption of meat products, and dates and places of meat consumed. Investigation of the first cases quickly revealed that they had consumed wild boar meat. A case definition was established based on quick descriptive epidemiological investigation made in our visit to the site and information obtained from some health facilities on their clinical history. Accordingly, suspected case is defined as any person who lived in Horro Haleltu kebelle and who has suffered from at least one of the two of the following symptoms: Abdominal pain, vomiting, diarrhea, fever; and muscle pain, swelling of the leg and/or faces, difficulty moving with the onset of the illness after December 24\2016. Those who consumed raw form develop clinical sign.

RESULT: Patients were categorized based on the type of meat they consumed (raw& undercooked), diseases onset and clinical sign. The onset of clinical signs after consumption mainly within 1-3days.The odd of infection and risk were higher in those who consumed raw meat but the clinical signs and the outcome of infection depends on the individual resistance and treatment. The multidisciplinary teams provide consultation to the physicians and changed the regimen. From total (15) who consumed raw meat, 5 died (33.33%) and 9 (60%) peoples had been treated with mebendazole and pridazone and recovered but 1(6.66%) did not get treatment remained paralyzed.Almost all showed the some kind of clinical signs: diarrhea, abdominal pain, difficult of breathing, vomiting, nausea, facial and legs swelling and loss of sensitivity. Age and sex were not associated with the outcome but raw consumption highly associated with the outcome.

CONCLUSION: A collaborative effort of multiple disciplines responds to this deadly outbreak and saves the lives of many communities living in under poverty. One health is a tool for the threats posed by epidemic and epizootic outbreaks of emerging and re-emerging diseases.

P108 - OHS B02 - INTERVENTION STRATEGIES

Generating evidence for one-health policies: An expert elicitation to assess the monetary impact of zoonotic diseases on society in Ethiopia

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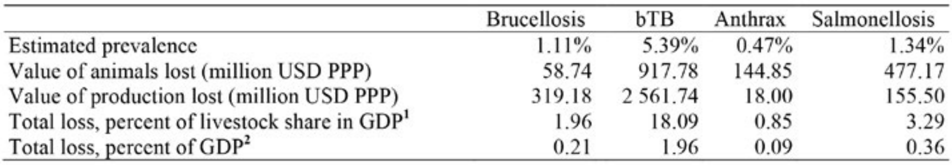
BACKGROUND: Designing and implementing one-health (OH) policies require stakeholders jointly assess the returns on investments made to tackle zoonotic diseases, AMR, other public health and environmental issues. In developing countries, two major constraints prevent the successful formulation and operationalization of OH policies: inadequacy of data and lack of common unit of measure to assess the returns on investments in livestock, public health or environmental domains. This paper presents an assessment of the monetary impacts of zoonotic diseases in Ethiopia based on information collected using expert elicitation protocol.

METHODS: We used a benefit-transfer methodology to transfer the yearly value of a statistical life calculated by the US Deparment of Health and Human Services to Ethiopia to generate a proxy for the willingess to pay for a DALY. We designed and implemented an expert elicitation protocol to assemble information and estimate costs of brucellosis, bovine tuberculosis (bTB), anthrax and salmonellosis in humans and cattle. A snowball sampling approach was employed to identify respondent experts. The final sample comprised 14 human and 28 animal health experts. Monetary impact of the diseases on society was determined as the sum of losses in USD PPP due to morbidity and mortality in infected animals and humans over one-year period.

RESULTS: Prevalence estimates of the diseases in animals were within reported levels. Overall animal mortalities estimated in this study were 9.03%, 10.46%, 80.68% and 43.38% for brucellosis, bTB, anthrax and salmonellosis, respectively. Economic impacts measured as value of animals lost and value of foregone production, are indicated in Table 1. bTB caused ~18% loss in the contribution of livestock to GDP or 1.96% loss in GDP. The loss due to salmonellosis and brucellosis were 3.29 and 1.96% of the livestock value added in GDP or 0.36 and 0.21% of GDP, respectively. Anthrax and brucellosis caused the highest DALY losses (193 642 and 107 343, respectively) in humans amounting 0.23 and 0.13% loss in GDP when converted to monetary values (Table 2). The total economic costs of bTB, salmonellosis and brucellosis were more pronounced in cattle than in humans (Fig. 1).

CONCLUSIONS: The formulation and implementation of OH policies are challenging because of limited reliable information as well as because methods to assess the cost and benefits of alternative interventions are not comparable among livestock, public health and environmental stakeholders. We tested a new methodology to implement an expert elicitation protocol and assessment of the monetary impact of zoonotic diseases on society. Results suggest impacts of zoonotic diseases are high, both from a livestock and human health perspective, and provide indications on how to possibly distribute the costs between livestock and human health authorities implementing OH policies to tackle zoonotic diseases. Stakeholders may consider refining and expanding the protocol to other diseases to provide information base for decision makers.

Table 1. Prevalence of selected zoonotic diseases and estimates of their economic costs in cattle (total of different production systems).

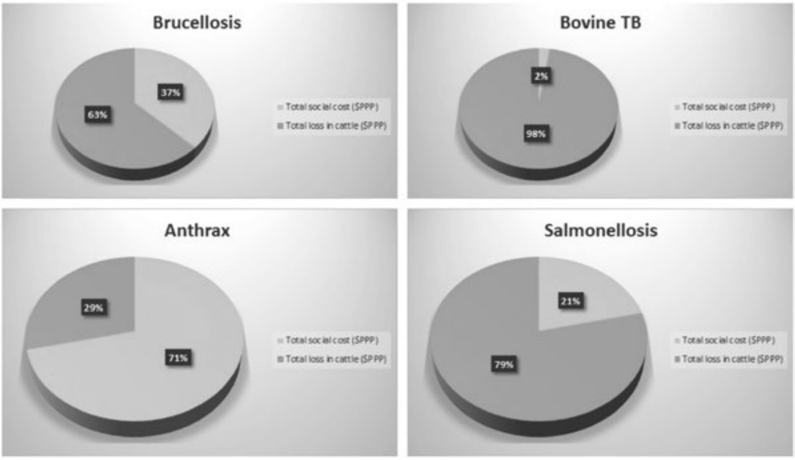


	Brucellosis	bTB	Anthrax	Salmonellosis
Estimated prevalence	1.11%	5.39%	0.47%	1.34%
Value of animals lost (million USD PPP)	58.74	917.78	144.85	477.17
Value of production lost (million USD PPP)	319.18	2 561.74	18.00	155.50
Total loss, percent of livestock share in GDP[1]	1.96	18.09	0.85	3.29
Total loss, percent of GDP[2]	0.21	1.96	0.09	0.36

Table 2. Estimates of the annual public health costs of selected zoonotic diseases in Ethiopia.

	Brucellosis	bTB	Anthrax	Salmonellosis
Years of life lost due to mortality (YLL)	106 576.17	41 575.85	193 641.02	81 617.43
Years lost due to morbidity (YLD)	767.04	101.44	1.13	66.85
DALYs (YLL + YLD)	107 343.21	41 677.28	193 642.15	81 684.28
Total social cost (million USD PPP)	225.420	87.52	406.64	171.53
Total social cost as percent of GDP (USD PPP)	0.13	0.05	0.23	0.10

Figure 1. USD cost of four zoonotic diseases in humans and animals (percent)



P109 - OHS B02 - INTERVENTION STRATEGIES

A realist review of the impact of sterilisation in canine rabies control programs: What works, for whom and under what circumstances?

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University of Nottingham, United Kingdom -

BACKGROUND: The management of free-roaming dog populations and the control of rabies are integrally linked. Therefore many organisations carrying out rabies control have wider objectives in improved animal health and welfare. Rabies control using canine vaccination has been well documented, however in practice many organisations carrying out these programs also perform sterilisation. While it is argued that sterilisation improves the health and longevity of dogs, thereby reducing population turnover and making vaccination coverage easier to maintain, direct evidence for the effect of sterilisation on rabies control is lacking.

This study aims to identify, appraise and synthesise the evidence regarding the contribution of sterilisation to rabies control interventions by comparing the outcomes of vaccination and sterilisation programs with those of vaccination-only programs.

Rabies control programs are complex interventions acting in complex social-ecological systems, and the impact of a program is dependent, to a large extent, on context and the way it is implemented. The addition of sterilisation and/or other dog population management tools complicates things further, making it difficult to assess the individual impact of each component. Therefore a ‘realist synthesis’ will be performed with the aim of identifying what works, for whom and in what circumstances.

METHODS: A systematic search was carried out in Medline, CAB Abstracts and Global Health, along with a search for grey literature. Included studies must have measured one or more of the following outcomes: number of dog bites (including confirmed or suspected rabid bites); doses of post-exposure prophylaxis administered; numbers of dog and/or human rabies cases; dog population turnover; health and welfare of dogs; human behaviour changes. Included studies will be synthesised and appraised and theories identified that explain relationships between the context in which the program is carried out, the mechanisms by which it works and the outcomes produced.

RESULTS: Twelve studies describing vaccination-only programs and five studies describing vaccination and sterilisation programs met the inclusion criteria from peer-reviewed literature. Grey literature is still being screened. Findings will be reported according to the publication criteria outlined by the realist and meta-narrative evidence synthesis (RAMESES) group.

CONCLUSIONS: Preliminary results suggest that the role of sterilisation in rabies control may differ with context. Many interacting factors affect the planning, implementation and impact of a rabies control program. Many programs, particularly those which include sterilisation, are not collecting data or reporting outcomes. Reasons for this will be explored and potential solutions discussed. The aim is to enable organisations to gain a more comprehensive understanding of their interventions and how they can be implemented most effectively.

P110 - OHS B02 - INTERVENTION STRATEGIES

Global One Health Research, The Future

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BACKGROUND: Health is crucial for quality of life, human health, animal health as well as health of the environment. Good health is very much related to our capability of preventing and controlling both chronic and acute diseases. Infectious diseases and their vectors can easily be transferred from environment to plants, animals and humans (One Health). Healthy nutrition is related to urbanisation and social and economic prosperity, poverty and inequalities in different parts of our world (Global Health). Both abundance, undernutrition, malnutrition an infectious diseases show that issues are complex, covering many disciplines, different regions, different niches in biology, and different time scales. It is by the integration of all these domains that the most appropriate actions can be achieved.

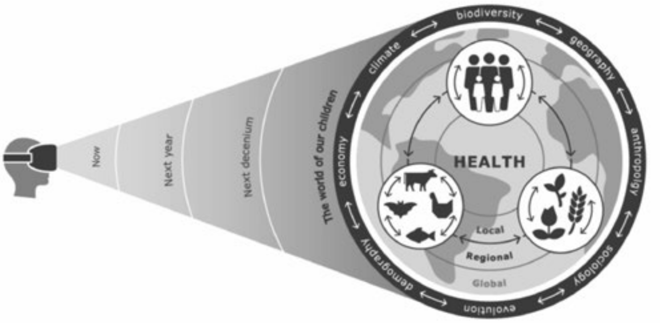
METHODS: Collectively, health issues ask for a systems approach, to study complex issues with various disciplines and at various scales. Hence, we need to consider important interactions in a globalizing world between, for example, human and animal diseases, the environment and human diseases, domestic animal and wildlife diseases, social changes and disease burden, economic development and diseases, and trade and diseases.

Therefore, Wageningen University decided to choose the wider Global One Health (GOH) approach, to emphasize the interdependence of human health under pressure of globalization with the health of animals, plants and sustainable ecosystems from a global perspective. This GOH approach uses multiple disciplines, both natural sciences and social sciences, to seek transnational solutions for improving the health of humans, animals and plants, and ultimately, the sustainability of the ecosystems of system Earth.

RESULTS: At Wageningen University the Global One Health research program was established in 2016. Within two years at least nine multidisciplinary research projects were started, covering themes like emerging infectious diseases, antibiotic resistance, food system sustainability, obesity, vector borne diseases, societal impacts on diseases, zoonoses and others.

To start implementing a Global One Health education programme a summer course was organised in 2016 and currently a GOH minor is developed. For development of a GOH module within MSc programmes a working group of Wageningen University scientists and teachers has been established in 2017. In spring 2018 an international Global One Health symposium is organised in which two main international university partners namely Nanjing Agricultural University, China and University of California Davis, USA, participate. Together with main stakeholders, including industry and funding bodies, the needs for global one health research are discussed.

CONCLUSIONS: Wageningen University and research has established a Global One Health research and education program based on interdisciplinary cooperation and using a systems approach. Innovative global one health research and training help to make better use of scientific knowledge of all health related disciplines and bring transnational solutions for improving the health of people, animals, plants and the environment.



P111 - OHS B02 - INTERVENTION STRATEGIES

Multi-Sectoral Involvement in Joint Cross-Border Disease Control Program in East Africa

Were, Willy Abwoka (1); Matu, Martin (1); Mushi, Benedict (1); Makayotto, Lyndah (2); Lubwama, Bernard (3); Kagirita, Atek (3); Ndayikunda, Claudette (4); Mbaga, Vida (5); Sonoiya, Stanley (6); Schneidman, Miriam (7)

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BACKGROUND: The East African region has been afflicted by many epidemics due to emerging infectious diseases. The East African Integrated Disease Surveillance and Response Network supported by the World Bank funded East Africa Public Health Laboratory Networking project aim at strengthening cross-border disease surveillance to reduce disease burden in the region. The borders have been demarcated into surveillance zones. These comprise districts on either side of the border in a defined locality. Officials from human, animal and environmental health, immigration, port health, and local administration are invited to participate in disease control activities including outbreak investigations and planning consultations to review the status of animal and human diseases in the zone. We evaluated the attendance of the cross-border meetings held to estimate the level of engagement by the different sectors.

METHODS: In a desk review, records of cross-border meetings were examined. Participants' details including district, country, work designation and meeting attendance were entered in an Excel worksheet. Frequencies and proportions of attendance at the meetings were calculated.

RESULTS: In all, 639 officials have attended 18 cross-border meetings since March 2012. Burundi districts participated in 8, Kenya in 11, Rwanda in 2, Tanzania 13 and Uganda 9 meetings. Human health was represented by 429 (67%) participants, animal health 77 (12%), environmental 51 (8%), and Immigration/customs by 8 (1%). Local administration/information collection teams contributed 57 (9%) of the participants, and port health 16 (3%). In 5 meetings the environment sector was not represented at all. Burundi districts did not send representatives of the environment and animal sectors in 6/8 meetings they attended; Kenya did not send animal health experts in 5/11 meetings attended and environmental health officials did not attend 3 meetings; for Tanzania delegations, animal health delegates missed in 5 meetings, and environmental health missed in 6 out of the 13 meetings attended by Tanzania delegations. Uganda districts did not send environment and animal health officials in 6 and 3 meetings respectively, of the 9 meetings they participated in.

CONCLUSIONS: Human health officials have been the vast majority in attending the cross-border disease control meetings. Greater effort is needed to sensitize national and sub-national leadership about the need to have greater participation by animal, environmental, wildlife, immigration, port health practitioners, as well as administrators, social scientists and other development actors in cross-border disease surveillance activities. To improve the effectiveness of the One Health approach in trans-boundary regions, there is a need to establish a better Sectoral balance among stakeholders.

P112 - OHS B02 - INTERVENTION STRATEGIES

Building an Operational One Health Competency Based Education Framework

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BACKGROUND: Global public health threats are increasingly complex and require the combined skills of multidisciplinary teams, particularly during response to large-scale epidemics. While multiple sets of sector-specific competencies exist, there remains a primary gap in competencies that bridge across sectors. Improved training and education that meets discipline-specific and cross-disciplinary competencies at an individual level, and international standards within and across sectors at an international level, will create a more capable and effective workforce that collaborates and coordinates efficiently for improved prevention, detection and response to global threats.

METHODS: Since 2015, a University of Minnesota (UMN) based team, consisting of representatives from the USDA, USAID One Health Workforce and UMN Food Protection and Defense Institute, has been working to build out a comprehensive One Health Competency Based Education Framework (OH-Frame). A scoping review was conducted and the results were used to conduct a landscape assessment of previous efforts to draft One Health core competencies. The data was analyzed and synthesized using a modified thematic analysis to report key patterns and themes. A formalized comprehensive competency based education and training framework was then developed inclusive of the previously accomplished work, and a focus group convened to test the concept and gain subject matter expert input.

RESULTS: A One Health Competency Based Education Framework has been developed to link various sector-specific competencies with One Health core competencies to create a workforce that is trained appropriately and is prepared to respond. This flexible workforce management tool and multidisciplinary competency framework will help individual workers from across sectors identify and link to training to meet professional goals and also support national governments to develop a multidisciplinary workforce that meets international standards. OH-Frame builds on existing workforce planning and assessment tools and aligns workforce development and training with country needs and measures that cut across all sectors, supporting a summative workforce that can be called upon to address national threats of concern. The ultimate goal is to help countries meet WHO International Health Regulation core capacities, the OIE's Tool for the Evaluation of Performance of Veterinary Services critical competencies, the Joint External Evaluation Tool – International Health Regulation indicators, and other nationally defined needs that measure and promote a capable and strong workforce.

CONCLUSIONS: OH-Frame provides a unifying architecture that workforce projects and national governments can follow as they develop and build skills, expertise and competencies for operationalizing a One Health workforce. Additionally, it can provide a platform for ministry officials to monitor and progress their country's workforce toward meeting international standards. This can lead to more strategic and targeted implementation of training, and ultimately creation of a workforce with the skills and competencies to work across sectors efficiently and effectively to address infectious disease and other public health threats.

P113 - OHS B02 - INTERVENTION STRATEGIES

Causal inference and One Health interventions: the need for epidemiologic methods

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BACKGROUND: Reporting guidelines now exist for One Health epidemiologic research (COHERE), and veterinary epidemiologic research (REFLECT). While these guidelines advance the tracking of One Health interventions, recent epidemiologic methods development—particularly causal inference methods—hold promise for further development of One Health interventions.

Most researchers limit conclusions from observational studies to associational statements, yet such conclusions often form the basis for intervention design, and underlying any intervention is a causal hypothesis. Thus, the design of effective interventions requires estimation of causal effects, necessitating rigorous epidemiologic methods. Furthermore, some causal questions necessitate use of newer and/or more advanced methods.

To evaluate the need for advanced epidemiologic methods in identifying optimal One Health interventions, we consider the role of livestock density in the eradication of human African trypanosomiasis (HAT). Coordinated control efforts have recently reduced the number of HAT cases reported, and elimination of the gambiense form (gHAT) is targeted for 2020. As targets exclude the rhodesiense form (rHAT) and unexplained focal persistence of gHAT has been documented, a more refined understanding of HAT epidemiology is required to achieve and sustain elimination of both forms.

METHODS: We reviewed hypothesized causal pathways for HAT that have One Health relevance. Next, we identified which features of these pathways require advanced methods for their estimation (“pathway-specific effects”). Finally, we considered where gaps in traditional epidemiologic methods require newer methods.

RESULTS: Wild and domestic animals are known reservoirs for rHAT, however the importance of animal reservoirs for gHAT is debated. Furthermore, there is evidence that the tsetse fly vector prefers non-human hosts—zooprophylaxis—and that grazing activities reduce brush and thus vector habitat.

Several features of these pathways complicate attempts to disentangle their effects, requiring advanced methods. First, livestock density is temporally dynamic, requiring exposure measurement at multiple times and longitudinal design. Second, estimation of the “reservoir” pathway requires adjustment for “zooprophylactic” and “environmental change” pathways, i.e., a mediation analysis.

Newer epidemiologic methods are required to separate the zooprophylactic and environmental change pathways. Isolation of the zooprophylactic pathway requires adjustment for environmental change, however environmental change is both a consequence and a result of livestock density, necessitating marginal structural models or g-methods.

CONCLUSIONS: Trypanocidal treatment of domestic animals will only be effective where the animal reservoir pathway dominates, while insecticidal treatment of domestic animals will be effective where the reservoir and/or zooprophylactic pathways predominate. Where the environmental pathway predominates, interventions on grazing management, alongside of aerial spraying, deployment of tsetse traps, and other vector control efforts, will be most effective. Due to the complex and non-linear nature of the livestock distribution-HAT association, understanding of path-specific causal effects is required to identify optimal integrated control strategies, and estimation of these effects requires advanced epidemiologic methods.

P114 - OHS B02 - INTERVENTION STRATEGIES

Afrique One-ASPIRE: Bridging the gap in translation of One Health research to public policy in Africa

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BACKGROUND: Afrique One-ASPIRE (African Science Partnership for Intervention Research Excellence) is funded under the DELTAS Africa initiative and focuses on zoonotic endemic diseases through building One Health research capacity in West and East Africa. This will be achieved through structured scientific training across five Thematic Training Programs (TTPs): Control of (i) canine rabies, (ii) brucellosis, (iii) zoonotic tuberculosis and buruli ulcers, (iv) food borne diseases and (v) surveillance-response. This program will prepare African scientists in planning, monitoring and evaluating control of zoonoses using a One Health approach. The program will ultimately improve both human and animal health. To achieve this however, will require translation of this scientific evidence to public policy. Multiple efforts to generate evidence-informed policy have attempted to teach policymakers how to understand and apply scientific research findings in their decision-making. These efforts have had limited success, because policymakers generally do not understand scientific methods and vice versa. Afrique One ASPIRE therefore aims to train the scientists in engaging and communicating this evidence to the public and policymakers.

METHODS: We plan to conduct workshops focusing on public and policy engagement strategies, research design and methods and the policy making process with the scientists on training, civil society groups and policy makers. We will code and analyze participant responses regarding their confidence in interpreting research findings and assess research credibility, and the extent to which their knowledge about research findings change after completing the workshops and if they comprehend the policy making process.

RESULTS: Our findings will determine the level of interest in understanding scientific research, scientific research methods and policy making process among the target groups.

CONCLUSION: Our results should show the benefits of empowering scientists in the process of translating scientific findings to public policy and public policymakers on the scientific process of generating credible evidence.

P115 - OHS B02 - INTERVENTION STRATEGIES

Educating children about One Health

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1: National Veterinary Institute, Sweden - 2: Uppsala University, Sweden -

BACKGROUND: We strive to improve ways of communicating biosecurity from a One Health perspective to the young public, with the youth organisation 4H of Sweden being the main partner. This organization has both visitor farms and other activities where food safety and animal welfare perspective can be communicated.

METHODS: Veterinarians, medical officers and microbiologists collaborate with pedagogic and psychologic experts to create an educational material covering four areas, zoonotic disease prevention, food safety, animal welfare and One Health. A training package, including educational movies, texts, as well as games, was developed in collaboration with employees, leaders and young visitors at the 4H farms. Since our target group is children 7-12 years of age we focus on hand washing as it is an important measure to minimize pathogen transmission between animals and humans. To communicate this, we designed hand washing information signs which were placed on the 4H farms. Follow-up studies have been performed to evaluate the outcome of different communication methods, including a small hand wash survey.

RESULTS: The follow-up studies suggested that the knowledge about hygiene and behaviour around hand washing in a farm context has improved over the years. In addition, the hand wash survey indicated that hand washing increased after the introduction of hand washing information signs. The training material developed so far, includes a game about hand washing and antimicrobial resistance, a “question bank” and a collection of key messages that can be used in different educational situations.

CONCLUSIONS: As a result of the project, hand washing was observed to increase at the farms. Additional educational material, including various One Health-related activities, are under development.

P116 - OHS B02 - INTERVENTION STRATEGIES

ONE HEALTH – A Practitioner's Viewpoint

Love, David Moody

DM & J Love, Switzerland -

The links between animal and human health are clear and have been discussed for decades. Human health problems are frequently blamed on animals and the management of their health – this could be a myth.

A JOINT APPROACH MAKES A LOT OF SENSE.
Diseased animals have reduced production performance and often die. Optimal health in livestock depends on appropriate feed and wholesome water - without it, life is unsustainable.

Similarly, without adequate food and clean water human patients succumb to illnesses resulting in lost school & work days and frequently death.

A predictable outcome is food shortages, famine, inter-community fighting and widespread insecurity.

HEALTHY LIVESTOCK PRODUCE HEALTHY FOOD TO SUSTAIN HEALTHY PEOPLE IN SECURE COMMUNITIES.
INTERVENTION STRATEGIES must address the needs of humans and animals and implement the BASIC PRINCIPLES of livestock production and human health & nutrition to deliver a sustainable future.

Despite 30 years of international aid (MDGs - 1990-2015 and SDGs 2016-2030 – Agenda 2030) and the investment of billions of US$, we still face the same global problems (poverty, hunger, health, education, climate change, gender equality, water & sanitation, energy, the environment & social injustice and insecurity).

High Tech solutions for Low Tech problems are a mismatch leading to unrealistic expectations and unachievable targets – such interventions are UNSUSTAINABLE.

There are too many 'white elephants' bearing witness to well-intentioned but misdirected projects and the "we have always done it this way philosophy" is no longer an acceptable excuse

IT IS TIME TO RETHINK THE STRATEGY.
To understand the links between animal and human health one must also understand the management systems for both species.

A 'back to basics strategy' with appropriate technology and support can provide a secure and sustainable foundation for the future.

- Identify the 'real needs of the people' and deliver appropriate aid to provide
    - Clean water and wholesome food
    - Hygiene, medical care advice and management
    - Gender equality & education
- Train farmers & veterinarians in livestock, feed & food production.
- Train health personnel to optimise appropriate medical and nutritional interventions
- Promote health & hygiene awareness
- Promote strategies for a sustainable population

INTERVENTION STRATEGIES MUST OFFER WHAT IS NEEDED NOT ONLY WHAT THE DONOR COUNTRY HAS AVAILABLE.

- Many agencies are offering 'clean' drinking water to local populations – regrettably, in many cases they are simply making 'dirty' water more easily accessible.
- 'Super Cows' are an option but only if they also have super feed
- Improving native breeds and feeding them – works!

P117 - OHS B02 - INTERVENTION STRATEGIES

The growth and functioning of One Health Networks: A systematic analysis

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1: London School of Hygiene & Tropical Medicine, United Kingdom - 2: Chatham House (the Royal Institute of International Affairs), United Kingdom -

BACKGROUND: As political and financial support have grown, an increase in One Health-related activities has occurred, with actors from public, private, academic, and non-profit sectors uniting to organize and facilitate multiple disciplinary collaborations at global, regional, and national levels. Although some initial work towards this has been conducted, the breadth of One Health Networks (OHNs) operating globally has not yet been documented in a systematic and comprehensive way, and diverse stakeholders including doctors, veterinary professionals, environmentalists, and researchers have expressed concerns about the lack of coordination and possible resultant inefficiencies. In light of the dearth of information on the growing global One Health activities, and the need for coordination and communication between initiatives to support efficient use of resources, this study systematically identifies OHNs and analyses trends and gaps with respect to their geographical focus, engagement across human, animal, and environment health sectors, key activities, stakeholder involvement, and accountability structures.

METHODS: We defined OHNs as an engagement between two or more discrete organizations with at least two of the following sectors represented: animal health, human health, and environment/ecosystem. We systematically searched for OHNs in PubMed, Google, Google Scholar, and 11 One Health conference websites. Data about OHNs, including activities conducted and stakeholders involved, was extracted using a standardised template and analysed descriptively.

RESULTS: After screening 2,430 search results, we identified and analysed 100 unique OHNs, of which 86% were formed after 2005. Academic institutions and government bodies were engaged in the majority of OHNs, with private for-profit organisations and community groups involved in only 23% and 10% respectively. We also found that 32% of OHNs covered only human and animal health. There was a paucity of south-south collaborations and of information presented about activities covered and monitoring and evaluation.

CONCLUSIONS: Along with increased political attention and investments in One Health – which is illustrated by the growth in OHNs that we documented since 2005 – there are concerns about a lack of strategic direction, coordination, and true operationalisation of One Health principles. A critical challenge has been a weak evidence base to indicate what practical steps can be taken by OHNs to improve their functioning. While there is no normative definition of how to operationalise a One Health approach optimally, our study provides empirical evidence of gaps in terms of the types of activities conducted, the involvement of stakeholders from the community and for-profit sector, south-south driven collaborations, and transparency in reporting goals and monitoring plans. This information can inform the strategic direction of new and existing OHNs, as well as funders investing in this space, ensuring that efforts to operationalise One Health are harmonised and appropriately coordinated.

P118 - OHS B02 - INTERVENTION STRATEGIES

Creating a network of emerging One Health leaders from Rwanda: Tufts-UGHE-UR One Health Fellowship Program

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1: Cummings School of Veterinary Medicine at Tufts University, United States of America - 2: University of Global Health Equity, Rwanda - 3: University of Rwanda -

BACKGROUND: The University of Global Health Equity (UGHE) in Rwanda, University of Rwanda (UR) and Cummings School of Veterinary Medicine at Tufts University have created a One Health Collaborative (OHC) that serves as an interdisciplinary framework to anchor UGHE's and URs health science training around One Health (OH) principles. This effort puts the universities at the forefront of a training paradigm shift that aims to graduate global health leaders with technical fluency in One Health. The One Health Fellowship (OHF) Program, one initiative of the OHC, is a two-way global exchange program that is designed to enhance One Health leadership and professional skills while building lasting partnerships between Fellows, Rwandan institutions and partners in the United States.

METHODS: Six fellows from Rwanda are selected from UGHE and UR graduates, faculty as well as government and private sector. They come from multiple disciplines and backgrounds including medical, veterinary, policy, gender, media, community organization, social and environmental sciences. They are young professionals who play vital supporting roles in strengthening their communities' resilience in the face of complex health challenges. The six-week Fellowship is comprised of 3 primary components: One Health Leadership and Advocacy training (OHLA); Fellowship placement and Follow-on project. The week-long OHLA training is designed to equip Fellows with multi-disciplinary, cross cutting leadership and advocacy skills. The Fellowship placement is the defining element of the program and attaches Fellows to different organizations in the US for a four-week individually tailored work-integrated learning experience. The placement provides an opportunity for Fellows and US mentors to work together, and to share ideas and strategies to address global health challenges. Fellow are encouraged to recognize their role as One Health leaders and active global citizens and to build strategic partnerships with individuals from other disciplines. With support from their US mentors, the Fellows develop a post-fellowship project to be implemented in Rwanda through which they can apply the skills they acquired in their home setting to address global health challenges.

RESULTS: The OHF Program contributes to a growing network of One Health leaders who, through targeted One Health leadership training, deliberately crafted fellowship placements, and creation of strategic and sustainable partnerships, will use their vital roles within their Rwandan communities to minimize public health threats. The program has adopted One Health as its core concept, and strategy for collaboration, sustainability and coalition building.

CONCLUSION: This Fellowship will create a robust and sustainable global network of One Health leaders who are change makers, continuously networking with each other, sharing resources, reaching out and impacting lives of future colleagues and increasing awareness of the role of non -traditional health care professionals in creating sustainable health systems and building resilience in their communities against public health threats.

P119 - OHS B02 - INTERVENTION STRATEGIES

Strengthening capacity of bio-risk management in Central and Eastern Africa Using a One Health approach

Naigaga, Irene (1); Wakabi, Timothy (2); Yawe, Agnes (3); Bokaako, Winnie (4); Kabasa, John David (5); Bazeyo, William (6)

1: One Health Central and Eastern Africa, Uganda - 2: One Health Central and Eastern Africa, Uganda - 3: One Health Central and Eastern Africa, Uganda - 4: One Health Central and Eastern Africa, Uganda - 5: Makerere University - 6: Makerere University -

BACKGROUND: A number of countries in East, Central and West African regions are hotspots for numerous biological agents that occur naturally in the environment. These regions continue to suffer epidemic outbreaks of diseases such as Ebola, Marburg, Avian influenza, Yellow Fever, Rift Valley Fever, to mention but a few. Under adverse conditions, these and other agents put human and animal health at risk. In order to prevent such diseases that can jeopardize public health, economic stability and the lives and livelihoods of the people there is need for preparedness not only in terms epidemiologic surveillance, detection and diagnosis capabilities, but also in biosafety and biosecurity. Measures to strengthen biosafety and biosecurity are necessary given the need for fast detection, pathogen containment and safety of laboratory professionals. The objective of this paper is to share One Health Central and Eastern Africa's (OHCEA's) intervention to strengthen laboratory capacity in her eight member countries – Cameroon, Democratic Republic of Congo, Ethiopia, Kenya, Rwanda, Senegal, Tanzania and Uganda. OHCEA an international university network in eight countries in East, Central and West Africa has been building bio-risk management capacity using a One Health approach since 2014.

METHODS: The capacity building method took on a two pronged approach of first building a pool of local trainers who were mentored by master trainers to deliver the same trainings to their colleagues. This approach was deemed sustainable as it focused on building local capacity. OHCEA in partnership with Sandia National Laboratories started by building a pool of trainers in five OHCEA member countries, i.e. Kenya, Uganda, Tanzania, Rwanda and Ethiopia through the "Trainers' Development program". These were later supported through mentoring to train other participants. Under the same partnership, trainings on Policy and Bio-risk Management targeting participants from government ministries who have influence on policy development and implementation was conducted.

RESULTS: Results include expansion of capacity building to francophone countries in the OHCEA network, namely, Democratic Republic of Congo, Senegal, and Cameroon under the ongoing One Health Workforce Project. Bio-risk management trainings targeting in-service health professionals continue to be conducted in other OHCEA member countries, specifically Kenya and Rwanda. Over 150 participants have been trained through these efforts, and they continue to practice bio-risk management measures at their respective institutions. A number of individuals trained have improved bio-risk management measures at their places of work.

CONCLUSIONS: Building local capacity in Bio-risk Management has continued to ensure expansion of the Bio-Risk Management skills, even after the end of support from the Sandia National Laboratories.

P120 - OHS B02 - INTERVENTION STRATEGIES

One Health @ University of Florida

Munoz, Olga; Agnelli, Sara; Gollakner, Rania; Mavian, Carla; Prosperi, Mattia; Salemi, Marco; Sabo-Attwood, Tara; Capua, Ilaria
University of Florida, United States of America -

BACKGROUND: The One Health Center of Excellence at the University of Florida (UF), housed at the Emerging Pathogens Institute, was created in 2010. With the arrival of a new team in mid-2016, we have redesigned the goals and activities of the Center to bring One Health, which is the interdisciplinary care of animal, environmental and human health, to a novel dimension: the One Health 2.0 vision. Previously, the center was focalized on infectious diseases; now we aim to embrace the broad array of different lenses of focus by expanding the disciplines and topics engaging with One Health. This new approach differs from many One Health initiatives around the globe which are mostly focused on specific interfaces within the biomedical realm.

METHODS: In order to propel this endeavor, we became an independent Center at the end of 2017. The Center's mission is to address complex problems related to the health of the biosphere by seeking novel solutions originating from interdisciplinary and lateral thinking. The Center's vision is to capitalize on and exploit existing fields of excellence within and outside UF by creating novel areas of intersection, leading to an expansion of research and intervention spheres within the One Health paradigm. The Center aims at placing One Health as a perfectly suited philosophy and tool for the community to reach the United Nations Sustainable Development Goals. The Center is engaged on two fronts to accomplish this: training and interdisciplinary activities.

RESULTS AND CONCLUSIONS: The One Health Graduate Certificate, a collaborative effort with the College of Public Health and Health Professions, represents the training component. This certificate will gather students from high and low-middle income countries and with diverse professional backgrounds around complex topics pertaining to health. It will be composed of four courses and will have four suggested tracks: communication and behavior; ecosystems; urban development; and, pathogens and contaminants. The interdisciplinary activities component is represented by a series of seminars: monthly seminars, One Health talks and Ladies4Ladies, and, a yearly seminar, One Health International. The activities also involve bridging with different departments through research project development and dialogue. Current projects and interests span topics from influenza and diabetes type I, Zika epidemics prediction, human-animal bonding, to plant health. As one of the pillars of the Center, in collaboration with the National Science Foundation Center for Big Learning at UF, the center is currently creating frameworks and pathways to use Artificial Intelligence for analyzing current and future wicked One Health problems.

P121 - OHS B02 - INTERVENTION STRATEGIES

Students' leadership in breaking disciplinary silos

Wakabi, Timothy Waiswa; Naigaga, Irene; Alunguru, Elizabeth; Bikaako, Winnie; Nitumusiima, Sarah; Nattimba, Milly

One Health Central and Eastern Africa, Uganda -

BACKGROUND: Whereas recent zoonotic disease outbreaks in Africa have highlighted the need multi-disciplinary collaboration in addressing in addressing such disease threats, many Universities have continued training students in a siloed manner. Since 2013, One Health Central and Eastern Africa (OHCEA), a network of 24 schools of Public Health and Veterinary Medicine has been supporting creation and nurturing of Students One Health Innovations Club (SOHIC). SOHIC is a student-led strategy that OHCEA uses in pre-service training to support experiential learning and promote breaking of disciplinary silos among the future One Health workforce (OHW). It is imperative to evaluate the effect of SOHIC on building the future OHW.

METHODS: This was a multi-site evaluation using mixed methods. Focus group discussions were conducted in addition to an online survey for SOHIC members and alumni from Uganda, Rwanda and Tanzania. Qualtrix online survey tool was used and involved sending emails with a survey link to all SOHIC members with email addresses. Reminders to complete the survey were sent through social media, OHSC leadership, and emails. 122 participants responded to the survey. Data analysis involved producing descriptive statistics for the qualitative data using SPSS computer package. Qualitative data relevant to each category was identified and examined using constant comparison.

RESULTS: Multi-disciplinary students responded to the survey i.e. veterinary medicine (38%), public health (17%), wildlife (14%), nursing (9%), human medicine (5%), zoology and conservation (3%), and others (5%). All clubs have well established leadership structure. Notwithstanding a reasonable percentage of SOHIC members being female (31%), only 8% of the leadership positions are occupied by female students. Students have collaboratively applied skills to conduct community sensitization, research, health education, communication, and training.

CONCLUSIONS: Student clubs have leadership structures that have facilitated implementation of student driven One Health activities which have facilitated breaking of the disciplinary silos. These students appreciate the value of multi-disciplinary collaboration in addressing complex challenges. SOHIC has played a crucial role in building the students One Health core competencies in areas like systems thinking, community health, multi-disciplinary networking, communication, and collaboration. Deliberate efforts should be made to ensure that more female students take up leadership positions in the clubs.

P122 - OHS B02 - INTERVENTION STRATEGIES

Human Interactions with Bat Populations in Bombali, Sierra Leone: Implications for Zoonotic Disease Risk Mitigation among Bat Hunters and Residents with Household Infestations (USAID PREDICT-2)

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1: Metabiota, United States of America - 2: UC Davis -

BACKGROUND: While non-human primates have been implicated in many outbreaks of Ebola virus disease, it is unlikely that they are the ultimate reservoir for the virus. Surveillance and modeling evidence suggests that bats are the most likely reservoir for the virus. During the 2013 West African Ebola outbreak, observational and interview data from the outbreak site suggested that bat contact was the likely origin of the event.

Further research on human-bat interactions in West Africa may help better characterize the risk of zoonotic spillover and support the development of mitigation strategies.

METHODS: Ethical approval for the USAID PREDICT-2 Ebola Host Project was obtained from the Sierra Leone Ethics and Scientific Review Committee. Two semi-urban communities in Bombali, Sierra Leone with significant bat interfaces were targeted for human behavioral investigation. One community was known locally for its fruit bat hunting, while the other struggled with pervasive domicile infestations of insectivorous bats.

Behavioral data was collected by trained field staff using the PREDICT-2 interview guides from 30 participants in March, 2017. Interviews and focus groups were recorded using digital audio recorders, then translated and transcribed. Transcripts were analyzed in Dedoose using the PREDICT Universal Codebook.

RESULTS: Eidolon fruit bat hunters reported direct and indirect exposure to bats. Hunting frequency varied, with some hunting bats in the community grove daily and others weekly. These adolescent male hunters described using catapults to hunt bats from fruit trees, noting occasional bites and scratches when collecting fallen bats. Hunters indicated that bat urine and feces fall on them while hunting. Most slaughtered the bats they captured. Nearly all hunting and slaughtering occurs without the use of gloves or other PPE. Though most knew about the association between bats and Ebola, very few thought their activities posed significant risk.

Residents with domicile insectivorous bat infestations reported daily direct and indirect exposure to bats. Though the bats have always resided in the area, their intrusion into human spaces only began in the last several years. Residents described bats flying into them at night, recalled crawling into confined spaces to physically remove bats from their ceilings, and mentioned occasionally handling bats without gloves or other PPE. Residents explained that their homes smell of bat urine, that feces falls from the destroyed ceilings, and that bats consume uncovered sources of food and water. Though residents expressed concern about diseases bats harbor, very few understood how they were transmitted.

CONCLUSIONS: While hunters and residents were aware of the association between bats and human disease, more public health messaging is required. Participants do not have an adequate understanding of the health risks that bats can pose, nor do they understand how animal-borne diseases can be transmitted to humans.

P123 - OHS B02 - INTERVENTION STRATEGIES

Workforce planning using the OHSMART tool in five One Health for Central and Eastern Africa (OHCEA) countries in Africa

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1: University of Minnesota, United States of America - 2: One Health for Central and Eastern Africa - 3: Tufts University - 4: United States Department of Agriculture -

BACKGROUND: Public health requires a multi-disciplinary and comprehensive approach to adequately address disease control and prevention in the face of emerging and re-emerging infectious diseases. The link between human, animal and ecosystem health cannot be over-emphasized and the devastating outbreaks of zoonotic diseases further highlight this. Working across disciplines helps to address these challenges that affect all sectors leading to loss of lives and huge economic impacts like the recent Ebola and Avian Influenza outbreaks. Despite this, the veterinary, human and environmental health sectors continue to work separately yet there are key areas of overlap where resources and expertise can be harnessed in a One Health approach to address these critical challenges. The USAID One Health Workforce project is working with two regional university networks in Africa - OHCEA (One Health for Central and Eastern Africa) and SEAOHUN (South East Asia One Health University Network) with the goal of strengthening institutions, multi-sectoral engagement, education and training. With OHCEA, workforce capacity gaps were identified and mapped in 6 of the 8 OHCEA countries (Uganda, Tanzania, Rwanda, Ethiopia, Senegal and Cameroon) using the OHSMART® tool (One Health Systems Mapping and Analysis Resource Toolkit) which provides a framework to visualize systems holistically enabling a focused dialogue to arrive at practical solutions.

METHODS: Workforce capacity gaps were identified after extensive review of key documents from the Ministries of livestock, health, environment and wildlife; the results were shared with stakeholders in government, academia and the private sector. Consultants used government research and policy documents to identify gaps in human resource capacity, finance and collaboration. The outcome, a synthesis report, included each country's self and external evaluation of its emergency preparedness and response to hazards. Using the CDC Prioritized Zoonotic diseases for each country, stakeholders from government, academia and the private sector enriched the synthesis report by identifying and mapping critical capacity gaps with the OHSMART® tool. The results have been validated in the OHCEA countries of Tanzania, Cameroon, Senegal, Ethiopia, and Rwanda by the government ministries and policy makers.

RESULTS: The OHSMART® tool led to multi-sectoral outbreak response maps that showed various sector specific, institutional, and cross-sectoral gaps between sectors which are potential areas for increased collaboration with government ministries and other stakeholders in the event of a disease outbreak.

CONCLUSIONS: Synthesis reports from different countries were enriched with the output from the OHSMART® process and shared with high-level government policy makers to promote their uptake for government implementation and partnerships. The importance of university-government partnerships were identified as key for workforce planning and government officials pledged to support training institutions through new legislation, funding, and strategic workforce development plans to provide needs-based training and education for the current and future workforce around infectious diseases.

PATHOGENESIS

P124 - OHS B03 B05 - PATHOGENESIS

Immunopathological variations in brain tissues of mice and dogs infected with street and fixed strains of rabies virus

Ahmad, Waqas (1,2); Maolin, Zhang (2); Liu, Zengshan (2); Khan, Iahtasham (1); Awais, Muhammad (1)

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BACKGROUND: The objective of the present study is to observe and characterise the different lesions and viable antigen distribution in different parts of brain tissue, and to compare the accuracy of diagnosis in both methods. It is hypothesized that distribution of antigens associated with rabies virus (RABV) and different microscopic lesions are not uniformly present in different parts of the brain tissue.

METHODS: The study was partially carried out in the department of pathology, University of Agriculture Faisalabad, while partial experiments were conducted in the institute of zoonosis, Jilin University, China. Fixed strain was experimentally inoculated in mice, and naturally infected rabid dog brains were collected. Both types of brain tissues were processed through immunohistochemistry (IHC) and histopathology using control and experimental groups.

RESULTS: Street and fixed strains of RABV produce variable number of lesions and rabies antigens in naturally infected rabid dog brains, while negligible lesions were seen in mice brain infected with laboratory strain. Grossly, the brain tissues of dogs were edematous and slightly congestive. Salient lesions included rod-shape neurons, cavernous lesions (cytoplasmic vacuolation), perivascular cuffs of multi or single layer of mononuclear cells, Babe's nodules, satellitosis, necrosis and neuronal degeneration in Purkinje cells of cerebellum and granular cell layers of cerebrum. Moreover, IHC showed discrete antigens of variable size in cell bodies and along the axons of hippocampus, cerebellum and cerebrum of dogs and mice, while histopathology of the same brain tissues in mice did not reveal any significant lesions.

CONCLUSIONS: RABV may produce tangible lesions in paraffin embedded frozen sections that may lead us to refer the sample as suspected positive. However, the IHC proved to be highly sensitive method to diagnose rabies as compared to the histopathology but the cost of IHC is relatively higher and needs expertise in experimentation. On the other hand, the histopathology technique is better for resource limited settings as it is cheap and easily performable, but this technique is not as sensitive as IHC. The IHC can be used to establish confirmatory diagnosis of rabies infected samples in countries where ordinary labs and high ambient temperature also exist along with inconvenience in the transportation of sample.

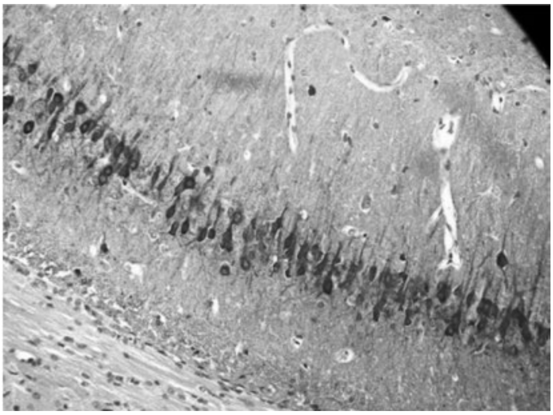

Fig: Characteristic amount of stained viral antigens in hippocampus of dog (DAB substrate, X-200).

P125 - OHS B03 B05 - PATHOGENESIS

Fluorescent Isothiocyanate Dextran evaluates the permeability of blood-brain barrier in rabies infected brain of mice

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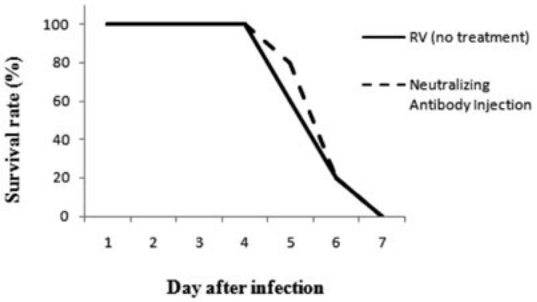
BACKGROUND: Acute encephalitis develops as the rabies virus (RABV) enters to the central nervous system by crossing the blood brain barrier (BBB) which is a tight junction of endothelial cells. In this study, three different molecular weight (70 kDa, 150 kDa and 200 kDa) of fluorescent isothiocyanate dextrans (FITC-Dextrans) were used to measure the extent of BBB damage and subsequent leakage patterns in brain tissues of rabies infected mice which were post-immunized with neutralizing antibodies to observe whether it has positive effect on infected mice by decreasing the death ratio.

METHODS: The brains were processed for immunofluorescence to observe the neutralizing antibodies and its relevant compatibility with the leakage of FITC-Dextrans.

RESULTS: Results showed that 70 kDa and 150 kDa FITC-Dextrans efficiently crossed BBB, and produced fluorescent illumination mainly in the cerebral cortex of brain. The enhancement of BBB permeability was significant at 5th day of post-immunization, while the neutralizing antibody neutralized some particles of RABV by crossing BBB, but it did not present enough treatment effect to the dying mice.

CONCLUSIONS: Taken together, these findings suggest that FITC-Dextran is an important fluorescent marker to investigate the integrity of BBB permeability in severe neurodegenerative diseases like rabies.

Fig: Survival percentage of RABV infected mice with or without neutralizing antibody injection.



P126 - OHS B03 B05 - PATHOGENESIS

Screening and distribution of different genes related to cytoskeleton and neuronal transmitters in hippocampus under rabies infection

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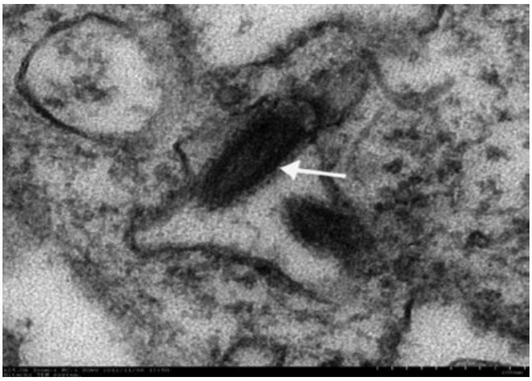
BACKGROUND: The pathogenesis of rabies remains elusive and carries hug economic losses. The objective of the present study was to illuminate the findings of neuronal dysfunction associated with rabies virus (RABV) infection by observing genes elated to neurotransmitters and cytoskeleton. In addition, the distributions of rabies glycoprotein antigens in the different areas of brain tissues were also observed through immunohistochemistry.

METHODS: Real time PCR and immunohistochemistry were employed to interpret the difference in the signal peptide sequence of amino acid among fixed strains (3aG, CVS) and street strains (SX, PB3) strains of RABV. Moreover, the neuronal structures of hippocampus were also observed under electron microscope.

RESULTS: The results demonstrated full similarity between SX and P B3 strains, while 84.2% similarity of signal peptide exist between CVS and 3aG. It is well known fact that stathmin1 (stmn1), katna1, adenomatous polyposis coli (APC) control neuronal cell differentiation, while glycogen synthase kinase 3β (gsk3β) regulate stability of intracellular microtubules; myosin light chain kinase (mylk) regulates intracellular filamentous actin; kinesin family member 5B (kif5) and kinase light chain 1 (klc1) hold the responsibility of transport events involving neuronal factors and vesicles, while mylk regulates actins and releasing of neurotransmitters. An up-regulation in genes expression of katna1, apc, gsk3β, mlck and gelsolin was observed, while down-regulated expression was seen for klc1 and Stmn1. The order of glycoprotein antigens were highest in cerebral cortex followed by hippocampus, brain stem, cerebellum, thalamus and olfactorybulb which was consistent with RABV distribution observed through immunohistochemistry. The electron microscopy demonstrated swelling of mitochondrion, disappearance in mitochondrial cristaes, hyper function of golgi complex and expansion of perinuclear cisterna.

CONCLUSIONS: These findings peep into the correlation of different genes associated with cytoskeleton and synapse which maintain neuronal shape and structure. Perhaps, RABV induce neuronal dysfunction by interrupting normal functioning of these genes.

Fig A: Infected nerve cell of mouse hippocampus showing rabies virus (arrow head) inside synaptic vesicle.



ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

P127 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Critical Evaluation of Maternal Health Program in Balasore District, Odisha (India)

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Goa Institute of Management Panaji, India -

BACKGROUND: India has still the largest number of maternal deaths which is estimated to be roughly 50,000 out of the 2, 89,000 deaths in the entire world. Odisha is classifieds as a 'high-focus' state by the National Rural Health Mission for the significantly high mortality of mothers. Odisha constitute 23% of tribals where the maternal mortality is very high. The study assess the provision of necessary health services for pregnant women in tribal pockets.

METHODS: The study was conducted in Jaleswar block of Balasore district, Odisha (India) where more than half of the population belongs to various tribes. More over the said area is geographically inaccessible due to rivers and rivulets. *Parijata tool* was used to assess various health care various facilities which was developed by UNICEF. By this availability of basic things like manpower, drugs and consumables are assessed along with laid down clinical practices and procedures. Further, a them list was used to assess the efficiency of grass roots level workers which was based on guidelines of government. The study looked into the promotion of health services by grass roots level workers in accordance with the tribal features. Further, data from health information system was analysed for the year 2013–2014 and compared with the field observations.

RESULTS: The study found that the health centres catering services to the tribals are not complying best practices on maternal health services. Both District hospital at Balasore and health facility at Hatigarh lacks the basic services recommended by WHO. Further the effort of government to implement a uniform program across the state hinder the tailoring of services for the tribal pockets. This is well marked from the guidelines and field observations in the tribal pockets. The grass roots level workers do not cater the need of tribal women for improvement of critical health conditions. The existing health information system is not catering to the decision making process and merely act as a data reporting system to the higher levels of administration.

CONCLUSION: The study raises critical issues about the potential of maternal health program to deliver effective care of pregnant women in tribal dominated Jaleswar block. Given the fact that the tribal community under consideration is considerably poor, gets isolated during the rainy season and has to out-migrate for earning opportunities, new ways of tracking pregnancies and reaching out to women are necessary. The study provides remedial measures for improving the role and functioning of grass roots workers, integrating indigenous medicine with biomedicine, and revamping health information system to incorporate cultural features, thereby improving its utilization in Jaleswar.

P128 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Economic analysis of zoonotic diseases in Bangladesh

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BACKGROUND: Zoonotic disease emergence events have increased in Bangladesh recently due to changing agricultural practices, demographic trends, and landscape and other environmental changes. This emergence causes health problems as well as economic loss to human populations and spans across sectors, threatening food safety, poverty alleviation and economic growth of the country. Assessment of the economic burden through a One Health lens of several high-priority pathogens are limited to date in Bangladesh. The objective of the present study is to determine the direct and indirect cost associated with human and animal cases of zoonotic diseases in Bangladesh. Quantifying total economic losses from important zoonotic diseases in Bangladesh can help shape multisectoral plans and actions for health security.

METHODS: The study is collecting economic data at household, government, private sector, and general population levels for cases reported within past 2 years for key priority zoonotic pathogens (Primarily, Anthrax, Avian influenza, Nipah and Rabies). Human and animal outbreaks are identified through respective official government institution. Approximately 10% of reported cases are targeted for sampling through random selection for household surveys that assess demographic information, direct medical spending, and indirect costs (e.g. lost wages, special caretaking services). Costs will be evaluated for both case and control households to identify costs above routine medical spending. Public program costs for control and prevention of these diseases will be collected from relevant government institutes and their partners. A questionnaire will be administered to private sector entities along the value chain (e.g. animal production) and indirectly impacted entities (e.g. tourism, environment) to collect loss data related to outbreaks and disease management. A general population survey will also be administered to identify costs of disease avoidance behavior.

RESULTS: The study will generate a total societal cost of priority zoonotic disease epidemics as well as the cost per case, estimated by summing direct medical costs, direct non-medical costs, and indirect costs borne by government, households, the private sector and the general population. It will generate the first assessments of economic impact of zoonotic diseases across sectors in Bangladesh.

CONCLUSIONS: By quantifying losses due to direct disease burden and indirect reactions to disease events across multiple sectors, we will help to identify key stakeholders like farmers, consumers, traders, policy makers and researchers for investments in prevention and control of disease to promote health and overall economic wellbeing. This study has the potential to inform country action as well as encourage wider multi-sectoral accounting of disease outbreaks to inform One Health approaches to emerging and endemic zoonotic disease management elsewhere in the region and world.

P129 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Preliminary insights on tuberculosis transmission between and among mahouts and captive elephants

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BACKGROUND: Humans are the only reservoir hosts of *Mycobacterium tuberculosis*, a unique multi-host pathogen, which is known to cause spillover infection in many other mammalian species. We gathered empirical data and examined the epidemiology and public health significance of tuberculosis transmission from mahouts to cohabiting captive Asian elephants (*Elephas maximus*). With the help of evidence based results, we intend to formulate specific policy guidelines to help mitigate the risk of cross-species infection.

METHODS: During the different components and phases of the collaborative research project, which spanned almost a decade, we screened nearly a thousand captive elephants and almost an equal number of mahouts in the southern Indian states of Kerala, Karnataka and Tamil Nadu. By isolating *M. tuberculosis* by sputum culture and also by undertaking a one-to-one questionnaire survey, we identified nearly 30 mahouts with either current or history of active pulmonary tuberculosis. By isolating *M. tuberculosis* from lung nodules obtained during post-mortem examinations, we identified nearly 50 elephants with active disease. A systematic identification and testing of the traceable mahout and elephant contacts of each of the diseased mahout and elephant were also done.

RESULTS: Two of the mahouts with pulmonary tuberculosis were identified to have cared for two of the diseased elephants. Almost all of the diseased mahouts had familial history of tuberculosis. In many such cases, the families' history superseded the mahouts' contact with diseased elephants. Cutaneous tuberculosis was identified in two mahouts associated with two diseased elephants. Prevalence of positive tuberculin skin test results were almost the same in mahouts who attended diseased elephants and in those who did not. Very few live elephants in contact with the diseased elephants tested positive for tuberculosis infection.

CONCLUSIONS: Almost all of the mahouts come from underprivileged families and along with their elephants follow nomadic lifestyles. Hence, locating the subjects for contact tracing and follow-up testing were difficult. Under the tropical climatic conditions in southern India, while the evidence is strong to suggest intra-species transmission among mahouts and inter-species transmission between mahouts and elephants in both directions, it appears weak to suggest intra-species transmission among elephants. Further study and analyses are needed to better understand the risks of anthropozoonosis and zooanthroponosis. Preliminary insights seem to suggest that the risk of cross-species *pulmonary* tuberculosis infection to a captive elephant from a diseased mahout outweighs the risks to a mahout or another elephant, from a diseased elephant. Formulating as well as implementing policy guidelines for the prevention and control of cross-species tuberculosis transmission, in the existing cultural and religious contexts of captive elephant management systems in southern India is a significant challenge.

P130 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

National early infant diagnosis coverages and socio-health indicators: an ecological regression analysis of 33 low and middle-income countries.

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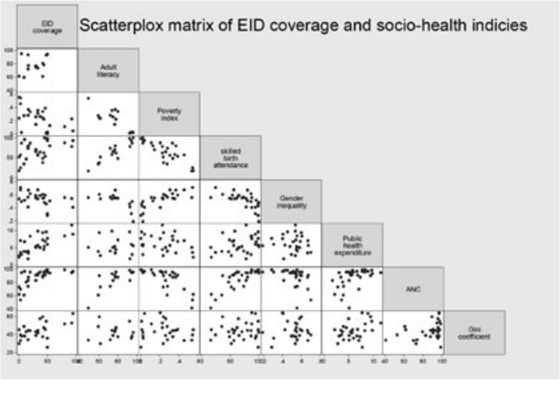
BACKGROUND: Pediatric HIV continues to be a global health challenge and a major contributor to under-5 mortality, especially in the low and middle-income countries (LMIC). Early infant testing is crucial in identifying HIV-infected children prior to disease progression so that treatment and other interventions could be started during the first months of life. Although early infant diagnosis (EID) services are available in most countries, EID coverage still stalls. The suboptimal coverage continues to hamper progress towards eliminating AIDS-related deaths in resource-limited countries. The relative contributions of governance and income inequality to EID coverage; and efficacy of maternal and child health systems in accelerating national EID coverage, are currently unclear. The objective of the study is to examine the influence, direction of and identify the critical social and structural indicators for EID coverage across the global priority LMIC for fast-tracking HIV elimination.

METHODS: We estimate cross-sectional, ecological regression models with data from 33 low and middle income countries on early infant diagnosis coverage from the UNAIDS; governance index and corruption control from Transparency International; and economy, behavioral factors and health service system indicators from World Bank and WHO database. Non-parametric regression models were performed. We computed covariates that were associated with EID at p-value≤0.20 from univariate analyses. In multivariate regression, adult literacy and poverty index were fitted into separate models to avoid multicollinearity (r>0.7). A p-value of 0.05 was considered statistically significant.

RESULTS: EID coverage was 33% [Range 1%, Pakistan and South Sudan; 95%, South Africa]. Countries with significantly higher EID coverage have controlled corruption (β=0.5;95% CI: 0.4,0.6;p< 0.001), increased adult literacy rates (β=0.5;95%CI:0.45,0.49; p< 0.001), increased income inequality (β=0.96;95%CI:0.9,1.0; p< 0.001), lowered HIV-related stigma (β=-0.8;95%CI: -0.9,-0.8;p< 0.001) and improved government spending on health (β=7.3; 95%CI: 0.4,0.6,p< 0.001). We observed that association between EID coverage and income inequity might be partly due to ecological fallacy.

CONCLUSIONS: Countries with better corruption control, adult literacy, government expenditure on health, income inequality and decline in HIV-related stigma experience higher EID coverage. Our findings indicate that improving EID coverage will require not only investment in strengthening HIV control programmes, but community and population health strategies that accelerate EID coverage.



P131 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Anti-rabies vaccination campaign for pets in a community living below the poverty line in poor neighborhoods in Lubumbashi, Democratic Republic of Congo

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BACKGROUND: Democratic Republic of Congo is a country where 88% of the population live below poverty line (< 2 $ US/day) in poor neighborhoods. This reflects financial inability to vaccinate animals. As a result, animals and humans are exposed to rabies. In the city of Lubumbashi 34 cases of mortality due to rabies were reported in 2017. Serological tests on samples of dogs and cats in wealthy communities showed an acceptable antibody level (n= 15; > 0.5 IU / mL). This finding supports the need to vaccinate to stop rabies transmission chain.
The objective of this study was to: 1) communicate with the public about the danger of rabies, 2) immunize pets (dogs and cats) to avoid loss of life given the gloomy prognosis of rabies. The study was conducted by a multidisciplinary students' club from the University of Lubumbashi.

METHODS: The rabies sensitization and vaccination campaign was conducted in July 2016 in Tabacongo area a poor neighborhood of Lubumbashi. The awareness campaign was led by a well-known local comedian who drained a large number of people to the event. Media coverage amplified the rabies control message. The population brought dogs and cats for a free vaccination.

RESULTS: Communication by the comedian was understood and well received by the community. Health risks and the need to vaccinate against rabies was accepted. The interest for vaccination expressed by people from neighboring community attested to the impact of the sensitization. This was as well facilitated by local media coverage. In total, 168 pets, including 153 dogs and 15 cats, were vaccinated under the supervision of qualified veterinarians and faculty.
At the end of the media coverage of the campaign, feedback from people from other neighborhoods reflected the importance of local Radio-TV stations for optimal community awareness.

CONCLUSION: Future campaigns to control rabies have to include a strong component off sensitization using local influential people such as comedians and should involve the media for large sensitization.

P132 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Multi-Sectoral prioritization of zoonotic diseases in Uganda, 2017: The perspective of One Health experts

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Ministry of Health, Uganda -

THE EPIDEMIOLOGY OF MARBURG VIRUS DISEASE OUTBREAK IN KWEEN AND KAPCHORWA DISTRICTS IN UGANDA, OCTOBER 2017

BACKGROUND: Marburg virus is feared due to the dramatic and highly fatal illness they cause. Though Marburg outbreaks rarely occur in humans, Uganda experienced an outbreak in October 2017, We describe the epidemiology of the Marburg outbreaks of Uganda in 2017 and explore the possible factors for the escalading frequency of the VHF outbreaks in Uganda

METHODS: A case series outbreak investigation was conducted to describe the initial cases with the aim of determining the definitive diagnosis to allow appropriate care to be initiated and to develop a working case definition for identifying additional cases. Additional assessments were taken to evaluate the potential high risk exposures prior to the onset of the illness and to identify all the contacts. Outbreak case definitions were disseminated country wide and hotlines were established to receive alerts from communities and health facilities. All suspect cases were verified by rapid response teams and all confirmed or probable cases were entered into Epi Info case data base

RESULTS: One Marburg virus disease outbreak was reported in the eastern region. The outbreak occurred during the period October and December 2017. A total of 48 Marburg cases with a case fatality rate (CFR) of 54% reported. The majority of the Marburg cases were females (60-80%) aged 20-29 years (46-50%). Though bleeding was reported in 36% of the Marburg cases most cases initially presented with non-specific symptoms. The Marburg outbreaks were linked to mining activities in caves infested with bats that later tested positive for the virus.

CONCLUSION: Uganda experienced for Marburg outbreaks with adults being more affected and the Marburg outbreak linked to mining. We recommend enhanced capacities for surveillance and response to allow prompt detection and response. Also, the mining sector should be regulated to avert the public health risk

ANTHRAX OUTBREAK IN A RURAL COMMUNITY IN BUSIA DISTRICT, 2017

BACKGROUND: Anthrax is a zoonotic disease caused by Bacillus Anthracis. Globally, it is estimated that between 20.000 and 100.000 human cases occur annually. The disease can present as cutaneous, gastrointestinal or inhalational lesions. It is an endemic disease among wildlife in Uganda. The medical superintendent reported two deaths suspected to be due to anthrax. We investigated to verify the diagnosis, determine the magnitude of the outbreak, identify sources of infection and determine if there was concurrent outbreak in animals

METHODS: We conducted a descriptive study. We received medical records at the district hospital to identify cases and conducted active search in the communities for both animal and human cases. Two abdominal fluid samples from the two human cases that died and two meat samples from the carcass of a cow that died and shared to the community members were taken and sent to the laboratory for testing. Data on human cases were analyzed by person place and time using Epi Info7. Anthrax cases were also classified as cutaneous or gastrointestinal.

RESULTS:

26 cases of human anthrax including two deaths from 11 communities were identified, two were laboratory confirmed and 24(94%) were epidemiologically linked cases. The mean age was 32 years, 15(58%) were males and the overall case fatality rate was 8%. The case was a 62 year old woman who was admitted to the district hospital. She died the same day. PCR tests on the human samples were positive for virulent Bacillus Anthracis, protective antigen and capsule. Bacillus Anthracis was also isolated from animal samples taken from the dead cow.

Twenty (77%) of the cases were cutaneous anthrax and six (23%) were gastrointestinal anthrax. 77% of patients had skinned dead animals and had handled raw beef and or consumed the meat of dead animals

CONCLUSION:
Anthrax outbreak in human and animals occurred in Busia district. Contact or consumption of the meat of infected animals was probably the cause of human cases. Most human cases were cutaneous anthrax. We recommended quarantine and vaccination of animals in the district, case management and prophylaxis for those exposed. A total of 6288 persons received ciprofloxacin prophylaxis and 16952 livestock were vaccinated against anthrax.

P133 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Anthrax impacts on the health and livelihoods of impoverished communities

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BACKGROUND: Neglected zoonotic diseases (NZDs) are responsible for half a million deaths yearly. These diseases are under-reported because they largely affect poor, rural and remote communities, so the true impact is likely higher. Apart from the health implications of these diseases, many affected communities suffer losses to their livelihoods. One such disease is anthrax, caused by the bacterium *Bacillus anthracis* and considered one of the major poverty-related diseases by the World Health Organization. Anthrax is endemic in many parts of Africa, but accurate estimates of disease occurrence and its impacts on people and their livestock are lacking. This study aimed to address some of these data inadequacies.

METHODS: This study was carried out in the Ngorongoro Conservation Area (NCA) of northern Tanzania, with an estimated human population of 80,070. The NCA is a multiple land use area where livestock and wildlife live in close proximity to people, and is therefore an ideal system for studying zoonoses in a One Health context. Data were obtained from two sources. First, a cross-sectional survey was applied to collect data from 209 households across seven wards. Second, investigations of suspected animal anthrax cases and outbreaks were carried out between August 2016 and March 2017 (n = 54) and samples were collected for confirmation. Case definitions were based on results from polymerase chain reaction (PCR) or microscopy, or on reports of human cases linked to handling/consumption of anthrax-infected animal carcasses. All analyses were carried out in the R0.99.484 Software.

RESULTS: The proportion of households reporting anthrax cases in livestock in the previous two years was 30.4% [$CI_{95\%}$, 24.0 – 37.0], but reached 100% in the most affected wards. Human anthrax cases were reported by 16.7% [$CI_{95\%}$, 11.7 - 21.9] of households and by 40.0% [$CI_{95\%}$19.0 – 61.0] of households in higher-risk wards, with 3.8% reporting a history of at least 2 cases. In a 2-year period between mid-2014 and 2016, as many as 4.8% of households reported the loss of between 100 and 200 animals due to anthrax, and 2.4% lost over 200 animals. Thirty-six of 54 investigated incidents were confirmed, involving a total of 464 livestock deaths. This amounted to a median loss of $250 per household involved, which exceeds monthly household income of up to $183 for 80% of households. The middle 50% of losses fell between $125 and $509. The maximum loss was $9910. Moreover, during these investigations, livestock owners reported past losses of an additional 2000 animals.

CONCLUSIONS: This study demonstrates the severe impacts that anthrax has on livestock-dependent communities. These data are expected to increase the visibility of an important, but neglected zoonotic disease, providing incentive for its prioritization and control in vulnerable communities.

P134 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Innovation of an improved tippy tap

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One health central and eastern Africa, Uganda -

INTRODUCTION: Hand washing with soap is believed to be a high cost effective means of reducing diarrhea incidence. However, global rates of hand washing with soap are frequently low.
In Uganda , a tippy-tap is a commonly used hand washing facility especially in rural areas because it is simple and economical, but has a very small Capacity of water ranging from 3-5 liters hence making it less feasible.

ABOUT THE INNOVATION: An improved tppy tap is a hand washing facility with a larger-water capacity tank, making it more feasible to use in large populatons. This was an innovaton that was funded by One Health Central and Eastern Africa (OHCEA) and was implemented by a multdisciplinary team.

RATONALE: While working with schools in Iganga District, most of the schools there had non-functoning ordinary tppy taps (without water). The improved tppy tap was aimed at improving the rate of hand washing in public places including schools.

OBJECTIVES: To improve hand washing practces in schools - To reduce on the prevalence of diarrheal
diseases among children - To utlize rain water and reduce on the
constant reflling of the hand washing facility

FUNCTONALITY OF THE TAP: The hand washing facility has a peddle on which the user steps, the bucket fips and water fows through the outlet. Afer washing hands, the bucket is returned to its normal positon when the user removes the foot from the peddle and the foatng ball inside the bucket drops to allow in more water from the reservoir through the inlet valve.

CONT........: The improved tppy tap has a water reservoir tank of 1500ltrs. This tank can be connected to a rain water catchment area during the wet season and can be reflled during the dry season.

PILOTING OF THE FACILITY: The hand washing facility was piloted in Itanda Secondary School located in Iganga District.

RESULTS AND BENEFITS: Since the facility was placed next to the wash rooms and play ground, 467 pupils were observed washing hands within one hour without refilling the reservoir. The hand washing facility was permanently given to the piloting school and monitoring is ongoing.

P135 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Evidence of exposure to Brucella among humans and cows in Shahjadpur sub-district, a high milk-producing area in Bangladesh

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BACKGROUND: Brucellosis is a zoonotic disease caused by *Brucella* spp. that can cause abortion, reproductive problems and reduced milk production in cattle and undulant fever, arthritis, and orchitis in humans. Transmission from cattle to humans occurs mainly by contact with infected animals or by ingestion of contaminated dairy products. Seroprevalence in Bangladesh is estimated to be as high as 21.6% in goat farmers and 9.7% in cattle. As brucellosis causes huge economic loss in dairy cattle and is a public health threat, and seropositivity and risk factors are not yet known in the dairy regions of Bangladesh, our objective was to identify the prevalence of *Brucella* antibodies and risk factors among cattle and humans in Shahjadpur sub-district, one of the highest milk-producing areas in Bangladesh.

METHODS: A cross-sectional study was conducted from September 2015 to February 2016. We identified 303 milk producing villages in this sub-district and randomly selected 25 villages. From each village, we randomly selected 5% of the total households. From each household, we randomly enrolled up to three humans (≥ 15 years old). If the households had cows (> two years old), we randomly enrolled up to three cows. We tested cow's milk and human and cow serum to detect anti-*Brucella* IgG using indirect ELISA. We used a standardized questionnaire to collect the following information: demographics, livestock raising practices, history of raw milk consumption, exposure to cattle, and history of reproductive problems for enrolled cows. We conducted multiple logistic regression, adjusting for household/farm-level clustering effect to evaluate the risk factors for human and animal *Brucella* seropositivity.

RESULTS: We enrolled 647 households, 1,313 humans and 698 cows; 360 cows were lactating. Of enrolled households, 443 (69%) had livestock. IgG antibodies to *Brucella* were detected in sera from 27 (2.1%, 95%CI: 1.2-2.9%) humans. Among the sera and milk specimens collected from cows, 11 (1.6 %, 95% 0.6%-2.4%) cows had at least one positive specimen; 6 (0.9%, 95% CI: 0.2%-1.5%) had positive sera and 9 (2.5%, 95% CI: 0.1%-4.6%) had positive milk. About half (53%) of the enrolled cows were reported to have at least one reproductive problem within the past 12 months; of these, 7 (2%) had anti-IgG antibodies to *Brucella*. No significant association was found between cattle-raising practices and the presence of IgG antibodies to *Brucella* among cattle. Also, no significant association was found between the presence of IgG antibodies to *Brucella* in humans and demographic variables, history of raw milk consumption and respondents' livestock exposure history.

CONCLUSION: Though the prevalence of *Brucella* seropositivity was low in this study area, the public health importance of this disease cannot be ruled out. Further in-depth studies throughout the country would help define the countrywide prevalence and risk factors associated with the disease.

P136 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Exploring agropastoral health seeking behaviour and attitudes towards animal vaccination in Arri, Northern Tanzania

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BACKGROUND: The burden of endemic zoonoses disproportionately affects those in underprivileged communities and has significant impacts on rural livelihoods. The problem is further exacerbated by lack of appropriate health care and entrenched structural barriers, inhibiting individuals from pursuing effective remedial actions in response to animal and human febrile illnesses (many of which are zoonotic). My research is concerned with how agropastoralists in Northern Tanzania engage with and negotiate different health seeking strategies in order to pursue optimal health outcomes for themselves, their families and their livestock. Included in this is an evaluation of knowledge, attitudes and acceptance of animal vaccination as a means to safeguarding animal and human wellbeing.

METHODS: All fieldwork was undertaken in the Babati district of Northern Tanzania, over a period of 8 months. A mixed method approach was adopted, whereby I conducted 100 health seeking behaviour surveys across two sub-villages, asking people to detail all the remedial actions they took in response to their most recent episode of febrile illness. Subsequently, I conducted further interviews with 50 of these respondents to assess their knowledge, attitudes and acceptance of animal vaccination. Throughout the fieldwork period I also conducted 20 key informant interviews with animal and human health professionals at various health facilities, as well as focus groups to attain general information relating to the main challenges and issues people face in accessing appropriate health care. This mixed method approach allowed me to triangulate my results whereby I could asses concurrence or divergence of responses.

RESULTS: Emerging results reveal the long-term and reiterative nature in which people experience and contend with animal and human febrile illness. Barriers at health service providers impede ability to pursue effective remedial actions that can keep illness at bay. As such, people are often left to negotiate between lesser effective remedies at the community level until the illness returns. This lack of agency also extends to vaccination, where people acknowledge its importance but are not in the habit of administering it to their animals themselves, believing it to be the responsibility of the government to do so. However, willingness to use vaccination is high if certain conditions are met such as; knowledge shared beforehand and administered by ‘experts’ i.e. official vaccinators.

CONCLUSIONS: Wider systemic and structural barriers in the Tanzanian health system constrain individual agency when pursuing remedial actions in response to febrile illness. As such, there is opportunity for animal vaccination to play an important role in safeguarding animal and human wellbeing. However, attention to local attitudes and perceptions towards vaccination must be taken into consideration for any future interventions to be effective.

P137 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Epidemiology and evolution of zoonotic schistosomiasis in West Africa

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BACKGROUND: Schistosomiasis is a Neglected Tropical Disease caused by parasitic worms of the *Schistosoma* genus, which represents a significant burden on humans, the majority of which in sub-Saharan Africa. Schistosomiasis is also a disease of substantial veterinary importance, thought to infect millions of livestock worldwide, often in the same underprivileged communities most affected by human schistosomiasis. The burden of animal disease has remained largely unquantified, and furthermore both domestic and wild animals can potentially act as zoonotic reservoirs for human infection. Whilst human schistosomiasis has attracted increased focus and funding in recent years, challenges remain and novel challenges have emerged.

Recent environmental changes, through both natural phenomena and human interventions, affect the distribution and availability of suitable definitive and intermediate hosts for schistosomes, increasing opportunities for mixing and subsequent hybridization between human and animal schistosomes. This is likely to have a substantial impact on the dynamics and distribution of this disease, with further challenges and constraints for effective control.

METHODS: Extensive and systematic parasite sampling from humans (children and adults), livestock (cattle, sheep and goats, both non-invasive live sampling and post-mortem abattoir surveys) and intermediate snail hosts, were performed over three years across key transmission sites under contrasting levels of recent anthropogenic change within Senegal and Niger. We applied novel diagnostic tests and conducted multi-locus molecular analysis to elucidate the epidemiology of novel zoonotic hybrid schistosomes and the consequences of parasite hybridisation on host spectrum, praziquantel efficacy, host morbidity and ultimately transmission potential.

RESULTS: Our large-scale epidemiological and molecular studies have demonstrated that schistosomiasis in humans and animals remains a massive burden in West Africa. Disease within human adults and animals in general is largely ignored, despite the often very high prevalence and intensities observed. We confirmed evidence of extensive viable hybridization within and between *Schistosoma* species of both humans and animals, indicating the zoonotic potential of animal schistosomes.

CONCLUSIONS: We have demonstrated a significant risk of ongoing schistosomiasis transmission through viable hybridization between human and livestock schistosomes especially in areas under strong anthropogenic changes. We now have a better understanding of the evolution, ecology and transmission dynamics of this potentially emerging disease threat of paramount important to the health of humans and their livestock, particularly amongst the poorest of the poor. This will provide decision-makers and health services at both national and community levels with improved tools for the implementation of a One Health framework for schistosomiasis control in people and animals living in high zoonotic transmission zones.

P138 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Cameroon One Health Response to HPAI (H5N1) Outbreaks (2016 -2017)

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National Veterinary Laboratory (LANAVET) Annex in Yaounde, Cameroon -

BACKGROUND: High pathogenic avian influenza is an important disease which affected domestic birds in Cameroon from May 2016-2017. 24 outbreaks of H5N1 (clade 2.3.2.1c) were in domestic birds. The aim was to Use a multi-sectorial One Health response to control and rapidly eliminate the H5N1 infection in the country.

METHODS: Birds samples were collected and sharing for laboratory (National Veterinary Laboratory (LANAVET), Military Health Research Center and Centre Pasteur of Cameroon. They were tested and results were communicating among human and animal sectors. Animal health specialists were in charge of poultry farms while investigation of contact persons was carried out by human health specialists. Stamping out of infected birds was carried out by field veterinarians and environmental specialist with help of civil engineer military staff. Animal movement control in and out of infected zones was conducted by veterinary check points assisted by the police, gendarmes and customs controls. Disinfection of infected areas was carried out by the fire brigade personnel in the presence of human, animal and environmental health staff. Daily multi-sectorial coordination meetings were organized all over the country from regional to remote areas under the supervision of administrative and traditional leaders.

RESULTS: All samples were of H5N1-HP-AIV of clade 2.3.2.1c. The investigation of contacts person reported no human case. The collaboration of the arms forces help to know about the disease, to avoid the extention of infection and outbreaks the disease in the country. The conference and epi- surveillance by government authorities and international organization permit to sensibilize everyone.

CONCLUSION: Collaborative response action of Multiple One-Health Sectors allows the elimination of the disease in less than a year; no human case has been reported and no spread to the neighboring countries.

P139 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

The genesis of one health activities and operationalisation in Tanzania: opportunities and challenges

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BACKGROUND: Despite the term "One Health" is fairly new, the concept has long been recognized both nationally and globally. One Health [OH] in Tanzania was informally realised in 1990's when research activities started involving disciplines from both veterinary and medical backgrounds. Research and training institutions were the pioneers to initiate OH in Tanzania. With the rapidly changing nature of public health threats (from infectious diseases to antimicrobial resistance, and disease events of unknown aetiology) involving the animal-human-environment interface, the value and need to institutionalize the One Health approach in Tanzania has become more imperative now than ever before. Drivers that enhance this process in Tanzania includes having 20% of its land occupied by wildlife, high population of livestock, increased agricultural activities, prevalent zoonotic diseases and the global threats of emerging and re-emerging infectious diseases such as Ebola and Highly Pathogenic Avian Influenza.

METHODS: This document on genesis of One health in Tanzania was compiled using information extracted from different sources and consultations. Previous projects that were implemented under One health approach were identified and listed. Documents including meeting documents were retrieved from One Health Coordination Unit. Also, international documents such as WHO/FAO/OIE were consulted.

RESULTS: Though the road map to OH was not straight, further momentum was triggered by recent outbreaks of Rift Valley Fever, Anthrax and projects that had OH components. Responsible ministries for human and Livestock health decided to meet and develop a road map to OH strategic plan. In collaboration with Prime Minister's Office and development partners the OH strategic plan was developed [2015-2020]and will be launched on 13th February, 2018 by the Prime Minister of the United Republic of Tanzania. Despite the challenges in managing and operationalize the plan several milestones were achieved. These include, OH Strategic Plan, establishment of One Health Coordination Unit under the Prime Minister's Office, formation of technical working groups to address specific objectives and prioritizing zoonotic diseases in Tanzania. A clear evidence of one health activity was the management of Anthrax outbreak that occurred in Monduli district, Tanzania.

CONCLUSION: Despite the fact the road map has been developed in the strategic plan, there are short to long term challenges in implementing the strategy including, resource mobilization, policy harmonisation and mainstreaming into local governance context. However, the approach is very relevant in countries where livestock production is the main means of livelihood where interaction between animals, human and wildlife is inevitable.

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Promoting one health in the community

Baldrias, Loinda

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When people feel engaged and accountable for solutions, they are more likely to rally around common objectives and work together to achieve them. Community engagement is indeed an important strategy for sustainable development (Schiavo, 2016).

The One Health approach upholds the collaboration of multiple disciplines and groups working locally, nationally, and globally to attain optimal health for people, animals, and the environment. This concept is an emerging field in the area of health sciences and is the basis for the One Health Worker Project Philippines. This project is an international research undertaking between the University of the Philippines System and the University of California Davis, which seeks to develop and utilize mobile communication technology to detect health problems and promote proactive surveillance of illnesses surrounding humans, animals and plants. The project stimulates a dynamic and co-equal interdisciplinary collaboration in the fields of human, animal, and plant health, recognizing that the health of human beings is very much linked to the health of animals and the environment we live in. Crucial to the success of the project is communication among stakeholders to foster the acceptance of the One Health worldview and its application at the grass root community for the improvement of health care in rural and urban villages locally known as Barangays.

P141 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Sero-epidemiological study on human brucellosis and associated risk factors in occupationally exposed population of Punjab, India.

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BACKGROUND: Brucellosis has emerged as one of the most important and neglected zoonotic diseases in northern India. It is a major threat to animal handlers, livestock workers and dairy farmers. The present study was undertaken to determine seroprevalence of brucellosis and to identify the associated risk factors in occupationally exposed high risk population in Punjab, India.

METHODS: Multistage random sampling plan was designed to select districts, sub-districts, villages and household in Punjab state. Out of 50 selected villages, four households from each village rearing with livestock were interviewed and in total 394 occupationally exposed human blood samples were collected. Serum was separated from blood and subjected to serological investigation comprising Rose Bengal Plate test (RBPT), Standard tube agglutination test (SAT) and IgG and IgM ELISA.

RESULTS: The results revealed overall prevalence of 7.6% in the high risk occupationally exposed population of the state. On basis of the questionnaire, six statistically significant ($p<0.05$) risk factors were identified. Sex of the respondent ($p=0.02$), direct involvement in milking/handling of animals ($p=0.01$), animal husbandry as primary occupation ($p=0.006$), handling of veterinary cases ($p=0.001$), knowledge of disease ($p=0.03$) and duration of animal contact ($p=0.001$) were all significantly associated with seropositivity. The odds of brucellosis seropositivity among livestock workers and farmers was about 6.5 ($p=0.01$) times higher, followed by about 5.8 times higher in veterinary practitioners than individuals involved primarily in agricultural farming. The odds of brucellosis seropositivity among individuals who had been in contact with livestock for more than 10 years was about 2.5 ($p=0.01$) times higher as compared to those who had less than 5 years of contact. The knowledge, attitude and practice study related with brucellosis indicated poor knowledge and brucellosis risk related practices leading to this issue. Although 39% of high risk individuals knew about the disease, merely 21% were aware of it being a zoonotic threat. Eighty per cent of individuals used burial as a method of disposal for aborted fetus and placenta while 20% discarded it in open fields and water bodies. Almost 72% of total sampled individuals showed eagerness and wanted to gain more knowledge about the disease. Fifty nine per cent of individuals readily sold their animals if they were suspected of brucellosis thus, contributing in endemicity of the disease in the state.

CONCLUSIONS: The study strongly suggests that the need of hour is to create awareness amongst workers via local veterinarians and media in order to efficiently manage this problem. Strict formulation and implementation of policies for vaccination and biosecurity measures should also be assembled.

P142 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

A multi-sectorial successful (One-Health) response to the 2016 HPAI-H5N1 outbreaks in domestic birds in Cameroon

Wade, Abel

LANAVET, Cameroon -

BACKGROUND: Highly pathogenic avian influenza virus (HPAIV) is a zoonotic pathogen of great public health importance worldwide. Cameroon was infected with A/H5N1 clade 2.3.2.1c in domestic poultry from May 2016 to March 2017. In total, 21 outbreaks were confirmed with losses estimated to 138,252 birds. The objective was to use One Health concept in these outbreaks management.

METHODS: Following first reports of high mortality of chicken at Complex Mvog-betsi farm, the Government sent in forces of law and order to secure the farm. Samples of dead chicken were collected and confirmed H5 positive few hours later by the National Veterinary Laboratory (LANAVET) Annex Yaoundé. Samples were also sent to laboratories of Centre Pasteur du Cameroun (CPC) and to the Military Health Research Center (CRESAR) for additional testing. Results from these 3 national laboratories gave room to international reporting. A press conference involving the Minister of livestock, fisheries and animal industries, the Minister of Public Health (MINSANTE), and the Minister of Communication was organized to inform the national and international communities about the outbreaks in the presence of various diplomatic bodies and journalists. Contact persons involved in outbreaks and all those involved in outbreak investigation, sampling, diagnosis or stamping out were systematically subjected to medical care by medical personnel of MINSANTE. Similarly, birds form infected farms were systematically stamped out, burned and buried with the help of environmental specialists and civil engineer military staff. Infected places were disinfected by the fire brigade personnel. Inter-ministerial coordination meetings were organized daily up to remote areas where outbreaks were confirmed. Public sensitizations using TV, radio, leaflets, journals or magazines were organized in official and local languages. Movements of poultry and related products were restricted with the help of forces of law and order (police, gendarmerie, custom services and veterinary check points). Coordination meetings involving all administrations (Governors, regional Delegates, and local authorities), human & animal health specialists and technical public/private sectors including traditional leaders were organized on a regular basis.

RESULTS: This first ever multi-sectorial (One Health) collaboration coordinated from the Prime Minister's Office allowed this success story.

CONCLUSIONS: These multi-sectorial efforts allowed containment of HPAIV spread, and enabled total elimination of the disease in few months, with no human case and no spread to and reintroduction from neighboring countries. This excellent achievement was the results of perfect technical preparedness of the professional teams by USAID, IAEA, FAO, WHO and DTRA. Most importantly, laboratory equipment and reagents given to LANAVET, multisectorial (One-Health) regional training courses organized in Cameroon by IAEA under RAF0042 and RAF5073 where human, animal and environmental health experts were trained on biosafety and biosecurity on field sample collection and laboratory analysis, detection and differentiation of various diseases including HPAI.

P143 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Investigating Zoonotic Parasites in Dogs in the Remote Northern Indigenous Community of Iqaluit, Nunavut, Canada.

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BACKGROUND: Recent studies indicate that residents in the Canadian North have the highest rates of self-reported acute gastrointestinal illness (AGI) in the literature. Recent publications have reported *Cryptosporidium spp*., and *Giardia spp*., in the feces of patients with gastrointestinal illness in Iqaluit, Nunavut. As such, these communities may be at an increased risk, when compared to more southern environments, for exposure to certain zoonotic intestinal parasitic infections. While these parasites may be shared between animals and humans, current epidemiologic research on the role dogs may play in their transmission is lacking.

The objectives of this study were to determine the fecal prevalence of *Cryptosporidium* and *Giardia* in dogs and examine their molecular characteristics.

METHODS: The community-based “People Animals Water & Sustenance” (PAWS) project to which this study contributes, was developed with a One Health approach to better understand and address the unique transmission pathways for gastrointestinal illness in the Canadian North.

A pilot study of sled dogs was conducted in July 2016. In September 2016, environmental fecal samples were collected from sled dogs (each sampled daily for three days); dogs housed temporarily at the Iqaluit Humane Society, and from fecal samples identified during transect walks of randomly selected areas of Iqaluit and the surrounding area. Samples were analyzed using IDEXX SNAP Giardia and Xpect™ *Giardia/Cryptosporidium* tests, and microscopy. Polymerase chain reaction (PCR) and sequencing of target genes, was performed on positive samples for zoonotic evaluation. Statistical analyses including prevalence estimates and regression analyses were performed using statistical software, STATA Intercooled 15.

RESULTS: The dog-level prevalence of shedding at least one parasite was 8.16% (CI:5.52-11.92), and of *Giardia* spp., and *Cryptosporidium* spp. was 4.42% (CI:2.58-7.49) and 6.12% (CI:3.88-9.53) respectively. The dog-level odds of fecal *Giardia* spp. shedding varied significantly across dog groups sampled in September ((LRT) *p-value x2* = 0.04). There was no association between dog group and fecal *Cryptosporidium* spp., shedding for the same period ((LRT) *p-value* x2 =0.81).

Sequence analysis of the amplified 18S gene targets revealed 6 samples were *Giardia intestinalis*, assemblages B (*n=2*), D (*n=3*) and E (*n=1*); and 5 samples were *Cryptosporidium canis*.

CONCLUSION: This is the first study of its kind to describe the prevalence and molecular characteristics of these parasites in dogs in Iqaluit, Nunavut, and sheds some light on the role dogs may play in their zoonotic transmission: *Cryptosporidium canis* is rarely found in humans and when present is usually in immunosuppressed individuals; Dogs may be a source of human *Giardia intestinalis* infection, but they may also acquire these parasites from humans. The results of this study are intended to increase our understanding of the source of enteric illness in humans and to help inform public health messaging in Nunavut, and other Indigenous communities in Northern Canada.

RESUBMISSION STATEMENT: This study was conducted in 2016. Preliminary data related to this study has been presented in poster format at the: 1) ArcticNet Annual Scientific Meeting in Winnipeg Manitoba, 5 -9 December 2016 and, 2) Centre for Zoonoses and Public Health’s One Health Day, at the University of Guelph, on October 31, 2017. Reasons for submitting the abstract to the 5th International One Health Congress include substantially updated information (i.e. final data will be presented) that is relevant and will contribute original information to the themes of “Pathogen discovery” and “One Heath in underprivileged communities”. The authors intend to submit this study for publication prior to the start of this conference.

P144 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Mycobacterium bovis infection in cattle and communal resource-constrained farmers living at the wildlife-livestock-human interface in South Africa

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University of Pretoria, South Africa -

BACKGROUND: Cattle are the reservoir of *Mycobacterium bovis (M. bovis)* but many other domestic and wild animals s including humans can be affected by bovine tuberculosis (Btb). In South Africa, bTB in cattle is only partly controlled and the African buffalo *(Syncerus caffer)* is the reservoir of *M. bovis* in several ecosystems infected with M. bovis and gives rise to a complex wildlife/livestock/human interface which increases the risk of *M. bovis* transmission, yet the significance of *M. bovis* in human TB is currently unknown. A One Health strategy was designed to assess the role of M. bovis at the interface of cattle, humans and wildlife in a resource-constraint rural community in the northern region of KwaZulu/Natal province in South Africa.

METHODS: In the first phase of this multi-disciplinary study a cross-sectional study was done to determine the prevalence of *M. bovis* infection in 659 cattle from a total of 192 herds using a modified BOVIGAM® interferon gamma assay (IFN-γ). Infection was confirmed by post mortem examination and *M. bovis* isolation from three test positive cattle. In phase 2, a collaborative study with the Department of Health was conducted to investigate the occurrence of *M. bovis* in members of 75 households associated with bTB infected herds. The initial screening was done using the GeneXpert for the *Mycobacterium tuberculosis* complex (MTC) followed by speciation using molecular techniques. In Phase 3, a socioanthropological study is being conducted to investigate the communal farmers' risk practices to bTB transmission among cattle and to humans as well as to assess their awareness of bTB. A structured questionnaire was administered and focus group discussions were facilitated in the study community. Opportunistic sampling of wildlife in game reserves in the study area is ongoing for the isolation and genotyping of *M. bovis*.

RESULTS: The apparent *M. bovis* prevalence rate in cattle at animal level was 13.5% (95% C.I =11.1- 13.3) with a true prevalence rate of 8.5% (95% C.I. = 3.9-13.8). Overall, 27.6 % of the farmers had at least one test positive animal. Out of 70 respondents 50 (71%) of the individuals did not know about bovine tuberculosis in wildlife and 55(79%) of the respondents were aware of bTB in cattle. Frequent, regular contact of cattle from different herds during grazing on communal pastures inside and outside the study area and contact with wild animals were identified as important risk factors in the ongoing study.

CONCLUSION: The confirmation of a high prevalence of *M. bovis* in cattle poses a risk to human health. The One Health approach is hence a suitable approach to investigate risk factors of *M. bovis* infection in cattle, humans and wildlife at the interface.

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Waste not, want not: Turning latrine waste into profit on northern Vietnamese rice farms

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Human waste is rarely considered a commodity, but it contains valuable nutrients required to optimize crop yields, and thereby, combat food insecurity in low resource areas. Excreta can also contain pathogens, such as soil transmitted helminths (STHs), which are detrimental to human health and development. We estimated the relative risk of STH infection for Vietnamese farmers who apply fresh excreta versus composted excreta and/or inorganic fertilizer to rice fields by conducting a systematic review and meta-analysis. As well, we quantified the cost-savings for such farmers by comparing the costs of fertilizing with excreta and/or inorganic nutrients in four application scenarios. Our analysis indicated that farmers are 1.24 (95% CL: 1.13-1.37; p-value <0.001) times more likely to be infected with STHs when they handle fresh excreta versus composted excreta, but that the relative risks of infection by specific helminths (i.e. hookworms, *Ascaris lumbricoides*, and *Trichuris trichiura*) were not significant. Our economic analysis indicated that farmers could save up to 22% of their average income by processing latrine waste for agricultural purposes. Farmers who reused fresh excreta had the highest cost-savings (847 000 VND) when compared with those who composted excreta for six months according to World Health Organization guidelines (312 000 VND), or those who accelerated the compost period using with lime (37 000 VND). This study offers a fresh perspective on nutrient reuse, pathogen risk reduction, and agricultural economics in low resource regions where food insecurity occurs, and identifies practical strategies for poverty reduction in northern Vietnam.

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Strengthened Cross-Border Disease Surveillance is Valuable for Control of Disease Outbreaks in East Africa

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BACKGROUND: Strengthened cross-border disease surveillance systems could achieve disease prevention, early detection and effective response to epidemics of infectious diseases – aspirations of the Global Health Security Agenda (GHSA) and International Health Regulations (IHR), and therefore lessen the disease burden in East Africa. We offer a case where a prepared multi-sectoral team helped to contain an outbreak of Marburg virus disease at the Uganda-Kenya border in East Africa.

METHODS: In its collaboration with the East African Integrated Disease Surveillance and Response Network (EAIDSNet), the East Africa Public Health Laboratory Networking Project approved by the World Bank in 2010, supports 5 central and 37 peripheral laboratories in peri-border areas by construction/renovation of laboratories, provision of equipment/essential reagents, capacity building, and enrollment in the quality improvement process towards accreditation. The project has supported the training of over 13000 health workers on specimen management, novel laboratory testing, and continuous quality improvement. In addition, the project has supported the formation and functioning of 9 surveillance committees in trans-boundary zones comprising officials selected from districts on either side of the border from the sectors of health, environment, security, immigration, wildlife and livestock to enhance cross-border disease surveillance. The surveillance committees and health workers have held 5 table-top and 2 field simulation exercises to test the available contingency plans and also improve their emergency preparedness. In the cross-border region along the Kenya- Uganda border, the hospitals supported are Busia and Kitale (Kenya) and Moroto and Mbale (Uganda).

RESULTS: An outbreak of Marburg virus disease was reported by the Ugandan government on 19th October 2017. The index case died before diagnosis; two

close contacts with symptoms were confirmed by the Uganda Virus Research Institute. Before their death they had extensively moved within the trans-boundary districts in Kenya and Uganda and made many contacts. Contact tracing of over 155 persons in the remote mountainous terrain and follow-up needed a lot of resources. The already strengthened laboratories in the trans-boundary zone and the capacitated multi-disciplinary teams provided the expertise for infection prevention and control, contact tracing, specimen collection and conduct of essential tests. The outbreak was declared over on 8th December 2017.

CONCLUSION: Enhancing cross-border disease surveillance including strengthening peripheral laboratories and multi-sectoral preparedness and response mechanisms offers a ready-to- use system in the remote cross-border regions in EAC and is an important investment for cross-border disease control, and therefore implementation of GHSA and IHR.

P147 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Building multi-sectoral One Health emerging infectious disease and zoonosis surveillance and response capacity in Indonesia: so much more than a training exercise

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BACKGROUND: Since 2005, Indonesia has become one of the Asian epicentres for human and animal H5N1 avian influenza infections. The re-emergence of the Ebola virus and the Middle East Respiratory Syndrome Coronavirus as well as the detection of Nipah, West Nile and Zika viruses in Indonesia, emphasizes the importance of strengthening Indonesian capacities to prevent, detect and respond to new, emerging, or re-emerging animal health threats and spill-over events.

The Indonesian Ministry of Agriculture, Ministry of Environment and Forestry, and Ministry of Health, together with the Coordinating Ministry of Human Development and Cultural Affairs are working with the Food and Agriculture Organization (FAO) on an pilot research and development program to identify sustainable strategies for strengthening capacities for One Health-focused, effective and sustainable prevention and control of targeted zoonoses and emerging infectious diseases (EIDs).

METHODS: The establishment of an agreement between the four collaborating ministries to support appropriate officers to participate in training and follow-up field activities, and the sharing of surveillance and response data between partners was a crucial foundational activity.

Four pilot districts were selected covering different agro-ecological zones: Boyolali, Central Java, Ketapang, West Kalimantan, Bengkalis, Riau, and Minahasa, North Sulawesi. A needs assessment on technical and practical skills of district officers across participating technical ministries in all four districts was conducted followed by workshops to strengthen commitments and encourage cross-sectoral collaboration.

Cross-sectoral workshops and trainings have been conducted focusing on increasing technical capacities to prevent and control targeted zoonoses and EIDs, providing field inputs to a national web-based platform for zoonoses and EID information-sharing between the agencies, and building cross-sectoral networks. The work is also supported by zoonoses and EID communication activities.

RESULTS: The zoonotic diseases prioritized in the workshops for One Health capacity building were avian influenza, rabies and anthrax. They represent national priority endemic diseases of varying prevalence across the country are present in all pilot districts and provide important opportunities for the different sectors to collaborate in support of human communities, animals and wildlife. The workshops and trainings resulted in the development of six One Health training modules. In total, 48 One Health Master Trainers and 234 field officers from the three sectors have been trained on the integrated OH approach since 2016. New cross-sectoral networks have enabled field officers to start communicating and sharing information, as well as improving their technical capacities for rapid risk assessments and integrated outbreak investigations.

CONCLUSIONS: This program illustrates a real-world approach to establishing sustainable and effective EID surveillance and response by building robust and functional collaboration between the key frontline ministries, civil society and the private sector. The focus on existing zoonotic disease accommodates the immediate needs of communities and frontline officers while simultaneously building effective disease prevention and control systems.

ACKNOWLEDGMENT:

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Knowledge, attitudes and behavioral practices of urban communities towards neglected zoonotic diseases in Addis Ababa, Ethiopia

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BACKGROUND: The World Health Organization has identified a subgroup of eight neglected zoonotic diseases (NZDs): anthrax, bovine tuberculosis, brucellosis, *Taenia solium* cystercercosis, cystic echinococcosis, leishmaniasis, rabies and human African trypanosomiasis. Neglected zoonotic diseases are found throughout the developing world, wherever people live in close proximity to their animals, affecting not only the health of poor people but also their livelihoods through the health of their livestock. Many of these NZDs impact the food safety of vital animal source foods needed for nutrition and development. The objective of this study was to ascertain the knowledge, attitudes and behavioral practices of three different demographics regarding neglected zoonotic diseases in Addis Ababa, Ethiopia.

METHODS: A cross-sectional knowledge, attitudes and practices study was conducted between April and June 2016 in Addis Ababa, the capital city of Ethiopia. A questionnaire was administered to 384 participants from three different demographics (livestock owners: n=268, milk vendors: n=85 and butchers: n=31). Stratified random sampling was used to select participants from appropriate sampling frameworks identified for each of the demographics. The questionnaire included questions on participant knowledge of NZDs, and attitudes and practices related to NZD prevention strategies. Data were entered into Microsoft Excel and analyzed using SPSS. This study was granted ethical approval from both the City Government of Addis Ababa Health Bureau Institutional Review Board (IRB) and the North Carolina State University IRB.

RESULTS: Animal ownership amongst the participants was high (82.8%) in addition to a low education level in the majority of participants (55.7% had either no formal education or primary school education). Only 36.6% of participants could correctly describe a zoonotic disease. Rabies was named by 83.9% of participants whilst brucellosis was named by only 2.1% of participants. The majority of participants could name <2 NZDs and there were significant differences in knowledge across the demographic groups. Participant's knowledge of the routes of transmission for NZDs identified significant differences across demographic groups, with 'being bitten by an animal' the most frequent response (97.1%) and 'consuming unpasteurized cheese' the least frequent response (13.3%). Participants had poor knowledge regarding the risk of bTB and brucellosis risk from unpasteurized dairy products. Additional data will be presented on participant's knowledge regarding routes of disease transmission, attitudes and risky behaviors.

CONCLUSIONS: This study identified variable knowledge levels amongst participants regarding neglected zoonotic diseases and routes of transmission for diseases, with specific differences across diseases and food products. The control of NZDs requires integrated action from both human and animal health sectors alongside support and consultation from other sectors and industries. Intervention strategies should take into account the economic, sociological and cultural issues related to NZDs as well as community knowledge, attitudes and behavioral practices.

P149 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

One health implementation for the prevention and control of intestinal parasites in underprivileged communities near theThai-Myanmar border

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BACKGROUND: Underprivileged communities at country borders are prone to infectious diseases due to unfavourable socio-economic and political circumstances. Located at the Thai-Myanmar border, communities in Tha Song Yang district, Tak Province, Thailand have limited access to health services and facilities. Our previous study identified high prevalence of intestinal parasitic infections in this area. Unfortunately, owing to its low fatality, this problem has been neglected. This study aimed to utilize the One Health approach to measure the burden of intestinal parasites, assess risk factors, and formulate specific and sustainable plans involving multiple sectors and community participation.

METHODS: Cross-sectional surveys were carried out to assess human, zoonotic and water-borne transmission of parasites. Specimens included stool samples from villagers and domestic animals, and water samples from upper, middle, and down-stream locations. Water treatment practices and waste management facilities were also determined. With assistance from the Ministries of Interior and Public Health, villagers, health volunteers, sub-district administrative officers, health-care providers, and public health authorities were mobilized to administer questionnaires to assess existing knowledge and attitude related to intestinal parasites. Multi-disciplinary and multi-sectoral brainstorming was done to explore current perceptions and identify target-specific solutions.

RESULTS: Risk factors were classified into human, animal, or environmental origins. Intestinal parasites were found in 70% of human and 90% animal stool samples with 7 and 8 unique parasite species, respectively. Among the parasite species identified, 6 are zoonotic. Questionnaire data indicated 70% of the respondents lack knowledge on associated risk factors. These findings raise concerns on potential zoonotic transmission, since domestic animals live in proximity to villagers together with existing poor waste management. In the environment, 44% of the water samples collected had free-living forms of parasites that can cause human infections. Water treatment infrastructures were inadequately maintained, while 41.8% of the villagers consume untreated tap water. The results were presented to stakeholders from different sectors, disciplines, and administrative levels. The brainstorming process identified water-related problems as the priority followed by improper waste management, unclean food, and poor personal hygiene, while highlighting the need to seek assistance from local authorities to improve water quality and waste management within the communities.

CONCLUSIONS: Anchored on the One Health approach, we successfully determined the burden of intestinal parasitic infections in the area and local risk factors by ensuring multisectoral and multidisciplinary collaboration. This enabled the formulation of targeted and participatory solutions elevated into a policy brief that was forwarded to local administrative and public health authorities, which in turn, can be used for policy planning and sustainable solutions to reduce the burden of intestinal parasites in the area.

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Pesticide application practices and knowledge among local rice growers and community in muvumba valley ofNyagatare district-Rwanda

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BACKGROUND: Rice production is a new and rapidly growing activity across Rwanda. Moreover, has grown in importance and is now one of the staple crops. The Muvumba rice scheme project was created in 2011 under the support of the Ministry of Agriculture and Rwanda Sector Support (RSSP) to improve on the well-being and food security of the community, and the country at large. Increased diseases and pests' effects rice production. Pesticides are widely used to control and kill insects/pests. Pesticide application has raised concerns about potential risk to humans, animals, and the environmental health. The concerns are mostly observed in low-income and developing countries where laws and regulations are not followed. There's lack of policy that governs the handling and usage of pesticides. Moreover, far too little attention has been paid to farmers' pesticides application practices and knowledge.

OBJECTIVES: This study aims on assessing the pesticide application practices and knowledge among the rice farmers in Muvumba valley of Nyagatare District Rwanda. The specific objectives were to identify and quantify gap(s) in farmers' knowledge on pesticide use, and discrepancies vis-à-vis established standards and recommended practices; to document the frequency, and the types of all commonly used pesticides in Muvumba rice scheme; and to identify factors affecting pesticide use among the rice growers in Muvumba.

METHODS: The study was conducted in Nyagatare district of eastern Rwanda. A cross sectional study was performed on 206 study participants. For ten days' data was collected using an observation tool recording farmers' behaviors while mixing and spraying the pesticide. A semi-structured questionnaire was then used to gather information on knowledge and perception through face-to-face interviews. The data collected was analyzed using SPSS version 16.

RESULTS: All 206 of the intended study participants participated in the survey. The mean age of study participants was 43, with minimum of 19 years, and maximum of 64 years. Of all the participants 81.6 % were males, 18.4% were females, and 100% of the study participants were the head of their families. Storage of pesticides in the home was reported by 80% of farmers. More than 95% of observed farmers do not comply with good pesticides practice during formulation and application. Over 90% of study participants reported to have observed animals (cows/ birds and fish) affected after consuming water or feeding on fruit/feed contaminated with pesticides. The reported repercussions of improper use of pesticides on health of animals included death in birds and fishes, dizziness observed in cows.

CONCLUSION: The study revealed high potential for pesticide exposure in the Muvumba rice scheme valley of Nyagatare district, Rwanda. Farmers' knowledge levels appeared to be unrelated to the risk. Rather than simply focusing on knowledge based strategies, comprehensive interventions are needed to reduce both exposure and health risks, such as access to personal protective equipment (PPEs), training, adequate warning descriptions in local language, improvements in labeling, and measures to reduce cost barriers to the adoption of safe behaviors.

P151 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Building Capacity in Trichinella Testing of Country Foods in Canada's North

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There are 12 recognized species or genotypes of the zoonotic nematode *Trichinella*, responsible for causing the disease known as trichinellosis in humans. Transmission can occur via consumption of raw or otherwise ineffectively treated meat harbouring infective first stage larvae from a wide variety of carnivorous or omnivorous mammals, as well as some birds and reptiles. Although not associated with clinical manifestations in animals, infection with *Trichinella* spp. can cause severe, occasionally fatal, disease in humans. Historically, most outbreaks of trichinellosis have been linked to infected pork, and to a lesser extent wild boar and horsemeat. However, in Canada and elsewhere where pigs are commercially raised under controlled management conditions, *Trichinella* has essentially been eradicated from domestic pork. Thus, current regulatory control measures are aimed primarily at continued demonstration of negligible risk of infection in the national swine herd for domestic food safety assurance and international trade purposes. However, consumption of harvested wildlife continues to constitute a food safety risk for trichinellosis, particularly to Canada's northern indigenous populations which rely on these 'country foods' for sustenance. The main commodity of concern is walrus (*Odobenus rosmarus*) meat, which is often consumed raw or fermented, and can be infected with the sylvatic species *T. nativa*. This has prompted food safety initiatives, such as the Nunavik Trichinellosis Prevention Program in northern Quebec, to establish community engagement and diagnostic testing capacity to screen harvested walruses for *Trichinella* prior to consumption. Our CFIA laboratory, a national and international (OIE) reference laboratory for trichinellosis, has been invited in recent years to provide guidance and on-site training on *Trichinella* testing of walrus to laboratory staff in both Nunavik and the neighbouring northern territory of Nunavut. This week-long training was adapted from a national certification program previously established to qualify industry laboratories to test pork and horsemeat for export, and incorporating quality assurance principles based on the ISO 17025 standard, including use of a validated method (magnetic stirrer digestion assay) and proficiency testing of samples spiked with known numbers of *Trichinella* larvae. Demonstration of effective training and ongoing competency of analysts to generate reliable results is key to informing defensible food safety decisions by public health authorities. This, combined with the faster turnaround times afforded by such regional testing, will hopefully further enhance community commitment to these efforts to mitigate zoonotic *Trichinella* transmission in the North.

P152 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Filling the healthcare professional gap in East Africa through a One Health focused education: the UGHE-UR-Tufts One Health Collaborative

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INTRODUCTION: To effectively empower local communities to identify and respond equitably to public health threats, risks caused by infectious diseases and harmful environmental changes, universities must play a key role in building student capacity to support communities through experiential learning and strengthening community frontline responder training. In Rwanda, a One Health Collaborative (OHC), has been formed between University of Global Health Equity, the University of Rwanda, and Tufts University, whose mission is to train the next generation of global health leaders through a One Health approach. This entails utilizing systems thinking to equitably improve the health of humans, animals and the environment, using multidisciplinary training, research and implementation science.

METHOD: This endeavor began with a One Health strategic planning process, which pooled together faculty and think masters across different institutions from academia, government and private sectors in Rwanda. Through this process, a dynamic structure (with provisions for extension from 3 founder institutions) was developed to identify concepts that would be systematically pursued, either as quick wins or long-term investment proposals. A critical analysis of Rwanda's system pointed out the need for leadership training skills and experiential learning as starting points for linking universities with local communities. The need to build a robust research agenda was recognized with key issues such as zoonotic disease management, antimicrobial resistance, disease surveillance, biosecurity, climate change, environmental degradation and sustainable agriculture-livestock being highlighted. Cross institutional teams were created that developed detailed plans on the key themes of One Health education and training, research and community engagement.

RESULTS: As an outcome of the strategic planning process, the OHC was born and a Memorandum of Understanding created between the three institutions. Processes for inter-institutional collaboration and decision-making were agreed upon. Technical plans for building out the three initiatives were laid out and initiated. Together these outputs allow the OHC to develop and to manage programs at institutional and community level that sustainably promote the One Health approach through; education and training, a robust One Health multidisciplinary research agenda to strengthen research and training, and student engagement and community outreach programs that will use a One Health approach to transform the communities the programs partner with.

CONCLUSION: By bringing the varied strengths and visions of these organizations together, the OHC gives students and faculty opportunities to transform their ways of thinking in providing public health support to the communities they serve, and a chance to apply hands-on field research, clinical practice, or policy recommendations in nearby under-served communities. The end goal is a locally based program that harnesses the best practices in higher education and integrates cutting-edge technology platforms to produce the next global health leaders and create community resilience to public health threats.

P153 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Balzac: One Health in action in Bangladesh

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BACKGROUND: Interventions to prevent zoonotic disease transmission requires research at biological, epidemiological, socio-economic and cultural levels. Rising incomes enable rising demand for fresh poultry meat around the world. In Bangladesh, several strains of avian influenza (AI) viruses are endemic, and the growing poultry trade network is very important in AI transmission between birds. *Behavioural adaptations in live poultry trading and farming systems and zoonoses control in Bangladesh* (BALZAC) is an ongoing project (2014-2018) studying these zoonotic pathogens and their associated networks. BALZAC is pioneering interdisciplinary methods, demonstrating collaborative capacity building across global north and south, thereby generating valuable evidence for effective interventions. Policy consultations seek to translate this evidence to action.

METHODS: BALZAC situates virological and epidemiological factors of AI within their social, economic and cultural contexts through:

- Virological and serological surveys at 40 live bird markets;
- National scale network analysis with 2000 poultry traders;
- Ethnographic studies of poultry trading, biosecurity, and risk perceptions with 144 informants at 33 sites, with further social norms analysis with 57 live bird market operators and 28 community stakeholders;
- Experimental behavioural epidemiological game experiments with 130 poultry farmers; methodology from behavioural economics was employed to understand epidemiologically significant decision making to inform AI modelling through novel methodology developed specifically by BALZAC team;
- Policy options and stakeholder analysis for AI.

Policy consultations with key poultry industry, research, and government stakeholders will be scoping barriers and opportunities to policy recommendations supported by findings from above investigations.

RESULTS: Live bird markets in Bangladesh are highly contaminated, with high H5 and H9 prevalence in marketed ducks and chickens respectively. Poultry transaction chains differ according to poultry breeds and farming systems; chains intermingle into a network within which all breeds and geographical origins are mixed, promoting spread of AI. Fluctuating prices and credit system influence network dynamics. Feed dealers act as “market makers”. Business risk and disease risks are perceived differently according to position in network. Competing norms coexist in markets: biosecurity, Islamic food ethics, and market rules interact. Detailed analysis of the network of actors in the poultry industry supported the mapping of targets for effective AI control and surveillance.

CONCLUSIONS: Social analyses contextualise and enrich biological investigations of AI with a view to improved intervention in Bangladesh. Collaborative capacity building was employed throughout: veterinary epidemiologists were trained in ethnographic methods. Innovation was delivered through developing and implementing novel methodology of experimental behavioural epidemiology. BALZAC identifies and promotes new avenues for collaboration between researchers, demonstrating potential to inform effective interventions for AI and wider zoonotic control. This develops the One Health concept in Bangladesh, and builds foundations to develop beyond.

P154 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Rural, East African, Poor, and Female – the fourfold climate change water-related liability for health

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BACKGROUND: While broad population-based burdens exist as a result of inadequate water quality or quantity, the multifaceted relationships between water and women mean that a significant portion is borne by women and girls. Climate change threatens the physical, social, economic, and political systems that affect the health of women and girls. Using Moser's triple role framework (reproductive, productive, and community management) and a lifecycle approach, we are able to expose pathways through which burdens are created and exacerbated.

METHODS: Several projects have been undertaken using mixed methods approaches (literature reviews, case studies, focus groups, semi-structured interviews, and key informant interviews) to better understand health, wellbeing, knowledge, practices, and burdens of women in rural communities in East Africa.

RESULTS: As a poor woman in a rural community, your life is constricted by water and the related elements of sanitation and hygiene, collectively referred to as WaSH. Direct burdens are time spent collecting water and poor health as a result of water-related diseases. Indirect burdens include costs of clinic visits and medicines; lack of WaSH in healthcare facilities that burdens both patients and providers; food security and nutrition; physical and sexual assault; women-to-women violence when queuing for insufficient water resources; the means by which a woman has to pay for water in lieu of cash; caregiving for the young, elderly, and sick; and, education and employment, which impact productivity, livelihoods and health. Pregnancy is a particularly vulnerable period. WaSH burdens are amplified by increased physical demands and decreased physical resources. Poor women cannot afford to pay for others to collect their water. The inability to secure adequate water increases the likelihood of partner violence. Poor hygiene prevents women from seeking prenatal care, opens them to discrimination by health staff, and increases the risk of maternal and newborn infection.

CONCLUSIONS: Women bear the burden of negative, water-related health impacts. When they are sidelined in terms of decision-making authority, they become more vulnerable. Exploring the interaction of social and physical systems using a gendered lens supports identification and understanding of water-health burden pathways.
Child development, economic growth, social development, and environmental integrity depend upon healthy, educated, productive women. The safeguarding of women's health, particularly at times of greatest vulnerability, requires that practice, policy and research are inextricably linked to and informed by each other. The One Health approach is particularly useful in making these linkages and supports the requisite transdisciplinary approaches to solving real-life problems. It calls forth the multi-stakeholder participation of governments, NGOs, the private sector, communities and research institutions, in the service of evidence-informed decision-making. Finally, it requires us to walk alongside women in communities, in schools and in health care facilities, asking the questions and seeking solutions together.

P155 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Attitudes and behaviors toward free-roaming dogs in marginalized urban communities in the Los Rios Region, Chile

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BACKGROUND: Free-roaming dogs are a pervasive health and human safety issue in urban areas throughout Latin America. They are known for their carriage of zoonotic infections including helminths, leptospirosis, and rabies, in addition to wounds and infection from dog bites. However, mobilizing resources to spay/neuter, vaccinate, and provide adequate food and shelter for these animals is difficult, particularly in marginalized communities. The purpose of this work was gather information on the attitudes toward and treatment of free-roaming dogs in marginalized urban communities as well as perceived self-efficacy of specific preventive measures against the diseases they may harbor.

METHODS: This study was conducted in two marginalized urban communities (53 households) the Los Rios Region of Chile in November, 2013. These communities were selected based on their participation in a concurrent study on the eco-epidemiology of leptospirosis in the region. A survey was designed in partnership with staff from the leptospirosis study who were local residents that addressed the perceptions of free-roaming dogs, interactions between humans and free-roaming dogs in the communities, self-efficacy in methods to protect against disease transmission, and acceptable costs for vaccination and sterilization of canines. Surveys were conducted via interview at the participant's household by study staff who were already known to the residents of the community. Frequencies and proportions were reported for survey responses.

RESULTS: The majority of participants reported negative perceptions toward free-roaming dogs in their community with 93% reporting that they are a nuisance and 74% reporting that they caused problems for the respondent and their family. Most common reasons given for free-roaming dogs being a nuisance included that they are aggressive and attack (27%), they bite (25%), and that they dig through the trash (19%). Even though few respondents reported petting free-roaming dogs (22%), opportunities for contact between free-roaming and owned dogs were common. Seventy-two percent of respondents reported free-roaming dogs on their property, and of the households who owned dogs (n=37), 78% reported their dog stayed outside, and 63% reported that the dog was permitted to roam without restraint. When assessing self-efficacy in reducing human contact with free-roaming dogs, 71% of respondents reported that they already do not touch free-roaming dogs, and another 21% perceived they could avoid touching dogs for at least a few weeks. In contrast, only 10% of respondents walk in areas without free-roaming dogs, and 37% of them perceived it to be impossible to avoid walking near the dogs.

CONCLUSIONS: Free-roaming dogs are a perceived nuisance in marginalized urban areas. Even though survey respondents suggested they could take some measures to protect themselves from diseases carried by the dogs, those who owned dogs did not prohibit their animals from interacting with the free-roaming dogs allowing for potential disease transmission.

P156 - OHS B04 - ONE HEALTH IN UNDERPRIVILEGED COMMUNITIES

Using a user-friendly tool to promote utilization of One Health M&E Data to support decision making

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One Health Central and Eastern Africa, Uganda -

BACKGROUND: One Health Central and Eastern Africa (OHCEA) is a network of 24 schools of public health and veterinary medicine in 8 African countries. OHCEA has been implementing a USAID funded One Health Workforce (OHW) project under the Emerging Pandemic Threats (EPT 2) program. The project supports development of a workforce that has the technical competencies needed to support national governments to achieve international standards and the essential cross-sectoral competencies needed to prevent, detect and respond to infectious disease threats efficiently and effectively. A major concern by OHCEA management and its partners was the poor implementation as reflected by project's low implementation rate.

METHODS: We designed a user friendly activity implementation tracking tool with a dashboard that tracks the implementation rate and provides a summary of implementation status of each activity. The tool was updated on a monthly basis at country and regional level. Consolidated reports were shared across the network and with other partners. Using information generated by the tool, OHCEA Board members on a quarterly basis discussed and came up with recommendations for improving activity implementation efficiently and effectively.

RESULTS: The tool enabled different stakeholders to easily relate and compare funds utilized with activities implemented. Implementation of activities in all countries improved following the deployment of the tool. Contrary to previous periods before introduction of the tool, majority of countries implemented all planed activities and utilized most of their funds. Over a period of 6 months following introduction of the tool, implementation rate increased from 20% to 60%.

CONCLUSION: Use of a user-friendly tool that can be used and understood by the various stakeholders coupled with OHCEA management's commitment to utilization of data resulted into more effective implementation of One Health activities. Sharing performance data across countries promoted positive competition among countries in implementing their activities.

INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

P157 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

Dog bite cases in Veterinary Hospitals of Narayanganj of Bangladesh

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BACKGROUND: Dog bite is fairly common in livestock in Bangladesh and prevalence of rabies is also high in humans and animals in this country. Bangladesh ranks third in the world in the number of rabies cases. The estimated disability-adjusted life years due to canine rabies globally in over 3.7 million live years and economic losses is more than eight billion USD annually. Here, we plan to estimate the occurrence of dog bite among hospital admitted animals in two above mentioned hospitals of the study area.

METHODS: A retrospective study was conducted on dog bite cases on the basis of the registers of Veterinary Hospitals in Narayanganj, Dhaka, Bangladesh from 2013-2017. Narayanganj Sadar Upazila Veterinary Hospital and Narayangonj District Veterinary Hospital receive animals with dog bite wounds from different areas of Narayanganj. In the registers we recorded the name and address of the owner, date of admission, species and breed of the animal, type of wound and details of treatment provided. Since July 2017, we recorded the mobile number of the animal owners in the register aiming to follow up the consequences. We used descriptive statistics to analyze the data.

RESULTS: We received a total of 242 dog bite cases from 2013 to 2017, of which 22 were cattle, 186 goats, 17 sheep, 12 dogs, 1 monkey and 4 cats. We found that 26 animals were admitted in the year 2013, 101 in 2014, 72 in 2015, 18 in 2016 and 25 in 2017. The median age of the admitted cattle was 13 months (IQR: 7-39) and that of goats was 12.50 months (IQR: 8-24). 19 animals were admitted on and after July 2017 and four of those (20%) were suspected to be infected with rabies: three were goats and one was a cow. The signs of the infected animals included inappetite, excess salivation followed by death within 10-12 days. Dog bite wounds in animals were managed by antiseptic wash and dressing of wounds along with antibiotics and post-exposure rabies vaccine. We recommended three intramuscular doses of commercially available anti-rabies vaccine immediately: at day 0, at day 7 and at day 21 following the instruction of the manufacturer.

CONCLUSIONS: Dog bite was observed in all principal domesticated animals of Bangladesh such as cattle, sheep and goats. Few pet animals like dogs, cats and monkeys also become victims of dog bite. The biting dogs were either normal or rabid. Though we could not follow up all the cases, one fifth of the animals during 2017 became infected with rabies. Few steps by Government authority such as awareness build up among animal owners, population control of dogs and vaccination of dogs with rabies vaccine might be able to reduce the occurrence of the disease in Bangladesh.

P158 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

The Development of a One Health curriculum for Universities in Vietnam

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Emerging pandemic threats such as highly pathogenic avian influenza, SARS, Ebola, Middle Eastern Respiratory Syndrome, Zika, coupled with other complex global challenges such as climate change, urbanization, food safety and antimicrobial resistance (AMR), have fueled the One Health movement in recent times. As such, a large number of academic institutions, with support from the public sector, have adopted this collaborative approach to prevent or prepare for the next high consequence event. However, the speed of operationalization of such a transformative process has varied, and has necessitated the need for illustrative regional "success stories."

With support from the US Agency for International Development (USAID) Emerging Pandemic Threats program, the Southeast Asia One Health University Network (SEAOHUN) has promoted One Health capacity-building based on a common, regional set of core knowledge, skills, attitudes and behaviors relevant to building successful One Health professionals. These "One Health Core Competencies" were designed by SEAOHUN faculty in partnership with University of Minnesota, Tufts University and Training Resources Group, Inc., and they have served as the basis for designing a robust framework for One Health educational platforms for university training as well as career development programs.

One Health (OH) curriculum for students is one of the most important conditions to build a new generation with strong knowledge, ability to respond with emerging and re-emerging diseases. In Vietnam, the medical, public health and veterinary training program are gradually improved along with the development of science and technology. OH approach has been partly incorporated into their curriculum in different subjects. However, this curriculum has not met the needs of OH core competencies. Therefore, Vietnam needs building new subjects or strengthening the integration of OH modules into existing subjects. In recent years, we were implemented different activities for building the training program bases on OH approach, included review current curriculum, create framework, develop training materials, test the teaching tools and apply to the training programs. A total of 17 universities belong Vietnam One Health University (VOHUN) were reviewed all current training programs, based on 7 OH core competency modules, 8 OH technical modules. Utilizing this competency-based framework, VOHUN has created a portfolio of educational OH modules to more effectively teach these competencies to undergraduate and postgraduate students. This presentation will focus on key outcomes and achievements of VOHUN in transforming veterinary and other health institutions and curricula across Vietnam.

P159 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

IN PURSUIT OF A SEROLOGICAL SCREENING TEST FOR MYCOBACTERIUM ULCERANS EXPOSURE

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INTRODUCTION: Buruli ulcer (BU) is a subcutaneous necrotic infection of the skin caused by *Mycobacterium ulcerans*. It is the third most common mycobacteria disease after *Mycobacterium tuberculosis* and *Mycobacterium leprae*. BU affect both humans and animals and *M. ulcerans* is believed to have an aquatic niche. The disease has been reported in the tropics and subtropics, mainly in West Africa. Some cases are also found in Australia where koalas (*Phascolarctos cinereus*), common ringtail possums (*Pseudocheirus peregrinus*), long-footed potoroo (*Potorous longipes*), alpaca (*Vicugna pacos*) have been observed to have BU as well as in horses, dogs and cats. The exact mode of transmission is unknown. Currently, the most common methods for diagnosis of the disease are PCR, histopathology and culture of the organism. However, these methods have their infrastructural and resource challenges in remote areas in West Africa. Additionally, BU has a 1.5-4.5 months incubation period. The infection rate is believed to be under reported due to lack of a rapid and easy to use screening test. Development of a serological screening test would be beneficial to more accurately assess *M. ulcerans* exposure as well as determine the natural history of infection in humans and animals. However, this requires dedicated antigen preparations reproducibly derived from *M. ulcerans*.

METHODOLOGY: This study has used a standardized protocol to produce and characterize 10 antigenic preparations from *M. ulcerans* (Batches: A, B, C, D, E, F, G, H and homogenate) and *M. smegmatis*. We have also expressed and semi-purify four *M. ulcerans* recombinant proteins (HSP_65, MUL 2232, MUP_057 and AT-propionate). Protein composition of produced protein extracts were determined by mass spectrometry. Sera from 10 confirmed BU patients, 20 healthy controls from same endemic region (Bellarine, Victoria) and 20 non-endemic controls from Tasmania were screened for antibody responses to these protein preparations by ELISA.

RESULTS: Mass spectrometry identified a total of 733 *M. ulcerans* proteins. A number of proteins were detected in all preparations, including known *M. ulcerans* antigens: chaperonins 1 and 2. Serum antibody responses to the 10 antigen preparations were highly variable, however Batch D and recombinant protein HSP_65 showed a significant difference between BU patients and healthy controls. Batch D had 90% sensitivity (CI = 55.50- 99.75%) and a specificity of 95% (CI = 75.13% - 99.87%). Using HSP_65 as test antigen had 50% sensitivity (CI = 18.71% - 81.29%) and 95 % specificity (CI = 75.13% - 99.87%).

CONCLUSION: There is prospect for this protocol to be used for disease surveillance and potentially exposure in at “risk communities” although more work is needed in particular including more BU cases and endemic and non-endemic controls.

P160 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

Cutting costs by cutting DNA: Economic molecular tools for One-Health studies of ticks and tick-borne diseases associated with wild birds in Brazil

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BACKGROUND: Brazil has a diverse ixodofauna, including 32 representatives of the genus *Amblyomma*; many of which use wild birds as hosts for immature stages, with some species confirmed/implicated as vectors of human and animal pathogens e.g. *Rickettsia parkeri*. Despite substantial progress in the last decade, lacunas exist in our knowledge of the bio-ecology of bird ticks, their role in pathogen transmission and the influence of environmental factors upon tick distribution and pathogen prevalence. Filling those gaps requires extensive field studies, resulting in the collection of hundreds of samples. Morphological identification of immature ticks and their associated pathogens, to the species level, requires recourse to nucleotide sequencing which may be financially and technically impractical for researchers in the developing world, representing a barrier to the development of this important line of One-Health research.

METHODS: *In silico* alignment and restriction digestion was performed with a fragment (460 bp), of the 16S rRNA gene of *Amblyomma* species recognized in Brazil. *In vitro* digestion of PCR amplicons from DNA of tick species previously identified by molecular sequencing, was performed using the enzymes VspI and DraI to evaluate the accuracy of *in silico* data. Rickettsial infections were detected and characterized using a PCR-RFLP technique, reported and validated by our research group in 2013.

RESULTS: *In silico* analysis indicated that the novel, dual enzyme PCR-RFLP method allowed differential identification of the 19 species of *Amblyomma* ticks known to infest Brazilian birds; a result subsequently confirmed *in vitro* with control DNA´s. Application of the PCR-RFLP method to field samples (n=300), allowed the correct, species level, identification of 100% of the ticks, as confirmed by sequence analysis. Infections, with members of the spotted fever group (SFG) of *Rickettsia* including *R. parkeri*, were detected in 45% of the samples and successfully identified, to the species level, using PCR-RFLP.

CONCLUSION: The present study reports the development of a simple, cost effective, sequencing-independent, molecular identification method based on PCR-RFLP for the classification of *Amblyomma* ticks associated with Brazilian birds and the rickettsial agents carried by them. The economy conferred by this method, relative to sequencing, was approximately 95%. Thus, by cutting the DNA rather than sequencing, it was possible to process large numbers of ticks generating high quality genotyping data. It is our hope, that the development of these techniques will result in a wider implementation of molecular analyses, particularly in developing countries, culminating in the development of improved One-Health epidemiological and ecological databases. Increased surveillance, will revert deficiencies in our comprehension of the bio-ecology and distribution
of these ectoparasites, permitting evidence-based conclusions in relation to pathogen transmission, host-parasite interactions, the detection of endemic areas and even the impact of environmental factors, including climate change, based on robust long-term comparisons.

P161 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

A collaborative masters degree training program dealing with health challenges at the human/animal interface

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BACKGROUND: The collaborative MSc in Tropical Animal Health [MSc (TAH)] is a postgraduate training program that provides tools to researchers and professionals to incorporate a One Health strategy in health challenges at the people, livestock and wildlife interfaces. The joint program was launched in January 2016 and builds on the expertise of the Institute of Tropical Medicine in Antwerp and the Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria in South Africa. This training program aims to support the building of capacity to control health challenges at the people, livestock and wildlife interfaces on one hand but also builds capacity that can influence policy to use an integrated One Health approach in health on the other hand. The overall objective of the program is to link animal and human health, with a focus on the relationship between infectious and parasitic diseases of animals and humans (zoonoses), diseases and ecosystem health in order to improve disease control strategies, ecosystem sustainability, food security and rural development.

METHODS: The MSc (TAH) is offered as a blended programme of e-learning and face-to-face teaching to create a tailor-made curriculum that fits into their daily work routine. It has a modular structure in order to ensure flexibility, with continued assessments throughout each module. It also includes a ten day compulsory induction/field-workshop that takes the participants to the interfaces in a South African context and brings them into contact with peers, faculty, local experts, and community members.

RESULTS: Group discussions and field observations are geared to give participants a first-hand experience with the health challenges at the interfaces and illustrates how One Health can be used in practice to improve health. Additionally, participants coming from all continents exchange their own experiences and build a multidisciplinary network of health researchers/professionals.

CONCLUSIONS: This program is unique as it goes beyond the theory of One Health and fosters the creation of a multidisciplinary community of practice of open-minded health experts in local and global contexts.

P162 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

Q fever exposure risk set: application of multiple correspondence analysis (MCA)

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BACKGROUND: Information that characterizes risk of Q fever based on the enhanced Q fever exposure from the notification surveillance data lacks. We therefore, conducted risk classification analysis based on the enhanced Q fever exposure data for which completed data on individual cases were available.

OBJECTIVE: The aim this study was to identify high-risk groups based on the notification characteristics on abattoir exposure using multiple correspondence analyses.

METHODS: Multiple Correspondence Analysis (MCA), which is the generalization of simple correspondence analysis for two categorical variables was employed to identify risk groups from the Q fever notification enhanced exposure information. The Q fever notification data consists of data on individuals regarding previous screening and vaccination for Q fever along with occupational associated exposures and whether or not they reside near areas where Q fever infection risk were considered high. Eigen values, scree plot and correlation plots have used in order to identify the risk sets from the enhanced Q fever exposure surveillance data.

RESULTS: We identified two principal dimensions, that is, dimension 1 and dimension 2, respectively, explained 16.98% and 10.80% of the variability within the enhanced Q fever exposure data thereby explaining 27.78% of the total variability. The categories EXPOSURE_TO_PADDOCK_DUST_ETC_YES, WORK_WITH_WOOL_YES, ASSIST_OBSERVE_ANIMAL_BIRTH_YES and WORK_IN_SHEARING_SHED_YES are the most important in the definition of the first dimension. In addition, WORK_INSIDE_ABATTOIR, ABATTOIR_EXPOSURE_YES, PREV_SCREENING_YES and PREV_VACCINATION_YES contribute the most to dimension 2.

CONCLUSION: Those workers who were exposed to paddock dust, worked with wool, assisted and observed animal birth, and worked in shearning and shed were the most at higher risk groups. In addition, those workers who worked inside abattoir, had abattoir exposure, previously screened and vaccined for Q fever were the second most at risk for Q fever. Working in the above types of work and exposure to dust, wool and shearing and shed lead to Q fever infection. In addition, being previously screened and vaccined for Q fever was also found to be an other risk set. Especial treatment of the work force that are occupationally exposed for Q fever such as using personal protective device (PPE) may help mitigate the risk of Q fever infection in occupationally exposed workers.

P163 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

Detection and characterisation of coronaviruses in Australian wild birds

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BACKGROUND: Coronaviruses (CoVs) cause significant disease in both humans and animals such as severe acute respiratory syndrome (SARS) virus and Middle Eastern respiratory syndrome (MERS) virus in humans, infectious bronchitis virus (IBV) in chickens, porcine deltacoronavirus (PDCoV) in pigs. Several coronavirus diseases have arisen as a result of cross-species transmission e.g. SARS-CoV and PDCoV. It is therefore important to know which animal species carry CoVs, and to characterise these viruses to better understand how these viruses switch hosts and to identify the origin of viruses in future outbreaks.

Wild birds are mobile hosts which travel across physical boundaries (e.g. oceans and mountains). They play an important role in the spread of viruses such as avian influenza virus. CoV's have been found in wild birds on all inhabited continents but there are no published reports of CoVs in wild birds in Australia. This project aims to address this gap in current knowledge and determine the extent of CoV in Australian wild birds and how these may evolve and potentially be a threat to other species.

METHODS: Combined cloacal and oropharyngeal swabs were collected from 918 birds, captured as part of avian influenza virus surveillance. Virus RNA was extracted and 3 different PCR assays used to screen for the presence of coronaviruses. Approximately half of all coronavirus positive samples were genetically sequenced and a ~ 300 nucleotide fragment of the RNA dependent RNA polymerase gene was compared to existing coronavirus sequences in the Genbank database.

RESULTS: Coronaviruses were present in 15.4% (141/918) of all birds sampled. No single PCR could detect all coronavirus positive samples. Coronaviruses were found in 4 non-migratory species of ducks (Pacific black duck *Anas superciliosa*, grey teal *A. gracilis*, radjah shelduck *Tadorna radjah*, Australian wood duck *Chenonetta jubata*), 3 migratory shorebirds (curlew sandpiper *Calidris ferruginea*, red-necked stint *C. ruficolis*, ruddy turnstone *Arenaria interpres*) and a pied heron *Ardea picata*.

Both gamma- and delta-CoV's were identified, with gamma-CoV's identified more frequently. Australian gamma-CoV's clustered with duck CoV's from China, Hong Kong, USA and Sweden. Ruddy turnstone gamma-CoV's clustered with gull CoV's from the Bering Strait. curlew sandpiper gamma-CoV's clustered with duck CoV's from Sweden.
Pacific black duck and pied heron delta-CoV's were ~20% different to their nearest relatives. Australian ruddy turnstone delta-CoV's clustered with a ruddy turnstone delta-CoV identified in the USA.

CONCLUSIONS: Given that Australian duck gamma-CoVs are highly similar to those found in other regions, and Australian ducks rarely come into contact with migratory Palearctic duck species, we hypothesise that migratory shorebirds are an important vector for moving wild bird coronaviruses into and out of Australia. Future studies should consider using multiple PCR assays or next generation sequencing to detect and characterise the diversity of CoV.

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Modelling multiple transmission routes of campylobacteriosis in Ontario using a One Health perspective.

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Campylobacteriosis (infection from the bacteria *Campylobacter*) is the most common gastrointestinal illness in Canada. This pathogen has complicated dynamics with many routes of transmission. Due to the seasonal fluctuations in disease incidence and complex relationship with the environment, this pathogen has yet to be modelled from a One Health perspective. The objectives of this study are to 1) expand a basic "SEIR" model to capture the seasonal fluctuations in disease incidence in Ontario, Canada by incorporating a seasonally fluctuating environmental compartment (B), 2) incorporate flies into the model as a mechanical disease transmission vector, and 3) use these models to identify the potential impact of changing weather patterns on human case occurrence. Using results from previous work on environmental drivers of campylobacteriosis in Ontario as well as supplementary literature, we have developed an SEIR model that includes an environmental reservoir (*B*). The "*B*" compartment is a proxy for different potential routes of transmission including; contaminated water, contact with animals, and other environments contaminated by human and animal fecal matter. This compartment was seasonally forced to represent the changing levels of *Campylobacter* found in these reservoirs. A second model, based off the Ross MacDonald model theory, was developed to incorporate flies as potential mechanical vectors of *Campylobacter*. In this model, flies can pick up *Campylobacter* on their bristles from the contaminated environmental reservoir. When flies land on human food, they can transfer the pathogen to the food. This can then be consumed by susceptible humans, thus infecting them. These models were fit to human case data from between 2007 and 2013, provided by Public Health Ontario (PHO). We will use these models to examine how the different model outcomes vary depending on the relative contributions of the different disease transmission pathways under consideration (environmental reservoirs and insect vectors). The models will also be used to explore how the human burden of disease changes in response to changing environmental conditions that can influence the pathogen in the environment as well as fly population dynamics. Modelling campylobacteriosis transmission from a One Health perspective permits an improved understanding of the transmission of this pathogen and how it may change in the future.

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Zoonotic disease research in Eastern Africa

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BACKGROUND: The Eastern African region is endemic with multiple zoonotic diseases and is one of the hotspots for emerging infectious zoonotic diseases. Here we present a systematic assessment of published research on zoonotic diseases in the region and thesis research in Kenya to understand the regional research trends, characteristics of publications, and estimate proportion of theses research transitioning to peer-reviewed journal publications.

METHODS: We searched PubMed, Google Scholar and African Journals Online databases for publications on 36 zoonotic diseases identified to have occurred in the Eastern Africa countries of Burundi, Ethiopia, Kenya, Tanzania, Rwanda and Uganda, for the period between 1920 and 2017. We searched libraries and queried online repositories for masters and PhD theses on these diseases produced between 1970 and 2016 in five universities and two research institutions in Kenya. All the data were entered into an Excel spreadsheet, and imported into R statistical software for analysis.

RESULTS: We identified 771 journal articles on 22, and 168 theses on 21 of the 36 zoonotic diseases investigated. Research on zoonotic diseases increased exponentially with the last 10 years of our study period contributing more than half of all publications 460 (60%) and theses 102 (61%). Endemic diseases were the most studied accounting for 656 (85%) and 150 (89%) of the publication and theses studies respectively, with publications on epidemic diseases associated with outbreaks in the region or elsewhere. Epidemiological studies were the most common study types but limited mainly to cross-sectional studies, while socio-economics were the least studied. Only 11% of the theses research transitioned to peer-review publications, and took an average of 2.5 years from theses production to manuscript publication.

CONCLUSION/SIGNIFICANCE: Our findings demonstrate increased attention to zoonotic diseases in Eastern Africa but reveal the need to expand the scope, focus and quality of studies to adequately address the public health, social and economic threats posed by zoonoses.

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The possible impact of the climate change on the Trans-Arax plague focus

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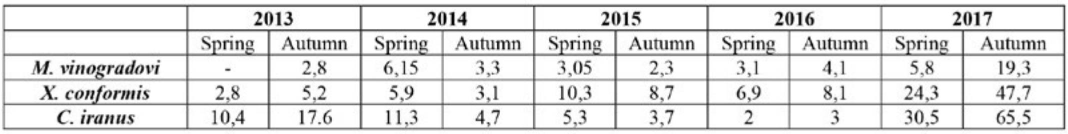
BACKGROUND: The polyhostal, polyvector Trans-Arax plague focus (TAPF) in Armenia covers semi-deserts, dry mountain steppes, and mountain steppes with a total territory of 450,000 hectares. The major carriers of the plague in the TAPF are Vinogradov’s jird (*Meriones vinogradovi*) and the Persian jird (*Meriones persicus*), while the main vectors are *Xenopsilla conformis* and *Ctenophtalmus iranus*. The objective of this survey is to observe the density dynamics of carriers and vectors of plague over the last 5 years, clarify the influence of climactic conditions on carrier and vector density dynamics, and estimate biological risks in region.

METHODS: Gero-type traps and live traps were used for trapping Vinogradov’s jirds, and aspirators were used to trap *X. conformis* and *C. iranus* in three regions of Ararat Province, located within the TAPF. About 500-600 mammals and 700-800 vectors were trapped annually in early spring and late autumn. Trapping location coordinates and type of material collected were entered into the Reference Laboratory’s database of TAPF data. Blood and tissue samples from collected organisms were tested to identify *Yersinia pestis* (polymerase chain reaction, indirect immunofluorescence assay, classical bacteriological method, infection bioassays, microscopy, etc.).

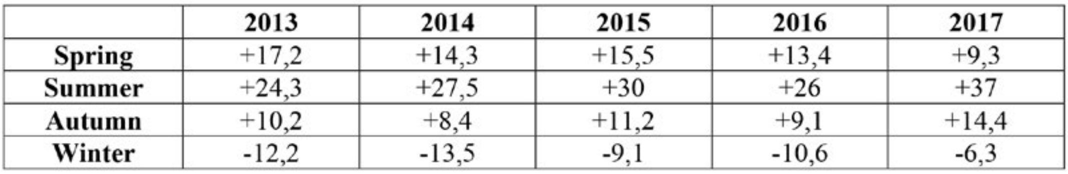
RESULTS: Density of both carriers and vectors depended on climate conditions: Vinogradov's jirds and their associated vectors increased in density in the seasons following hot summer and warmer winter conditions (spring and autumn, respectively). An absolute high temperature of +42.5°C and absolute absence of precipitation was recorded for summer 2017, which was not the case for other years of study.

Table 1: Density of M. vinogradovi, X. conformis, and C. iranus per hectare, by year and season



	2013		2014		2015		2016		2017	
	Spring	Autumn	Spring	Autumn	Spring	Autumn	Spring	Autumn	Spring	Autumn
M. vinogradovi	-	2,8	6,15	3,3	3,05	2,3	3,1	4,1	5,8	19,3
X. conformis	2,8	5,2	5,9	3,1	10,3	8,7	6,9	8,1	24,3	47,7
C. iranus	10,4	17.6	11,3	4,7	5,3	3,7	2	3	30,5	65,5

Table 2: Recorded average temperature, by year and season



	2013	2014	2015	2016	2017
Spring	+17,2	+14,3	+15,5	+13,4	+9,3
Summer	+24,3	+27,5	+30	+26	+37
Autumn	+10,2	+8,4	+11,2	+9,1	+14,4
Winter	-12,2	-13,5	-9,1	-10,6	-6,3

CONCLUSIONS: The significant increase in both carriers and vectors of plague in 2017 directly correlates with an unusually warm summer and mild winter. The TAPF of Armenia is mainly located in Ararat valley, where most of the population spends the year working in the fields, where direct contact with both carriers and vectors of plague is possible. Additionally, Ararat Province is located within the boundaries of greater Yerevan, which increases the epidemiological and epizootological danger to the capital and its population. Thus, systematic epizootological studies should be carried out among plague carriers and vectors to allow a timely forecast of the epizootological situation.

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Epidemiology of Human Rabies Death in Vietnam 1994-2016

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BACKGROUND: Human rabies deaths are preventable through prompt administration of post-exposure prophylaxis (PEP) after exposure to rabid animals. In Vietnam, imported and domestically produced equine rabies immunoglobulin are made available at all provincial medical centers and four regional institutes. Bite victims can go to any center for care, and are responsible for PEP associated costs. While PEP is widely available, approximately 91-300 dog-mediated rabies deaths still occur each year.

METHODS: Physicians in Vietnam diagnose and treat people with rabies according to WHO guidelines. We examined investigation forms of probable cases (clinical definition and documented animal exposure) reported to the Ministry of Health between 1994-2016. Patients and their families are interviewed with standard questionnaire. Cerebrospinal fluid samples are collected for laboratory testing by RT-PCR. Epi-Info was used to describe of epidemiology characteristics of all human rabies reported to VRCP.

RESULTS: There were 2,862 human rabies cases over the 22 year period. The average median age was 33 years old (range: <1-86). 99% of these deaths involved a dog exposure. 51% of families reported that the case-patients did not believed rabies vaccination was needed. 28% of families reported the case-patients seeking care from a traditional healer to treat rabies. Only 3% of families reported money was a reason for not seeking PEP
The median of incubation time was 54 days (range 7-420 days), but was significantly shorter for head and neck wounds (32 days, $p<0.05$). The clinical signs were agitation (80%), confusion (83%), hydrophobia (90%), hypersalivation (82%), and dyspnea (74%). All 8 cerebrospinal fluid samples tested were positive with lyssaviruses by RT-PCR.

CONCLUSION: Most rabies fatalities occur in mountain provinces in the North. Most deaths were in remote areas and in poor people who had little knowledge of rabies. The VRCP should focus interventions in the high risk areas and vulnerable groups.

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A Cross-Sectional Study Investigating Human Exposure to Dog Bites: Applying a One Health Philosophy to a Public Health Challenge in Rural and Urban communities in Ontario, Canada.

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BACKGROUND: Human exposure to dog bites is an important and often serious public health issue.

Some of the more important concerns surrounding the issue of dog bites include the repercussions of physical and emotional trauma experienced by bite victims, and less commonly, though no less importantly, the potential risk of transmission of the fatal, yet preventable zoonotic disease, rabies.

Undeniably, the human-animal-bond provides companionship and psychological benefits to humans through contact with pets; however, pets are known reservoirs of zoonotic diseases. The main reservoir for canine rabies transmission to humans is the domestic species of dogs. Primarily, rabies is transmitted to dogs through bites from foxes, raccoons, skunks, and bats. In Ontario in 2014, there were no cases of rabies in terrestrial mammals; in 2016 there were 288 confirmed cases in racoons, bats, and foxes.

The objectives of this study were to describe the proportion of households in which dog bites have occurred; the profile of biting dogs and, determine if a significant difference in dog bites exists between rural and urban households in Southern Ontario.

METHODS: This study comprises a subset of data from a larger cross-sectional observational study utilizing an on-line questionnaire administered to 2006 residents – 1004 urban and 1002 rural, in Southern Ontario between August 21 to September 2, 2014. In-keeping with the One Health philosophy, questionnaire design was the collective effort of stakeholders from academia, private organizations and government institutions within Ontario; and included veterinarians, epidemiologists and, zoonotic disease specialists with knowledge and expertise in One Health and quantitative survey design.

A series of statistical analyses were performed including descriptive statistics and regression analyses, using statistical software, STATA 14 S/E.

RESULTS: Overall, 975 (48.75%) households owned one or more dogs. During the 12-months prior, (September 2013-September 2014), in 12.54% of dog-owning households, at least one family member was bitten. The data also include who was bitten (age, sex), type of dog (age, sex, and rabies vaccination status), circumstances surrounding the bite (e.g., play, provoked), victims' healthcare-seeking behaviour following the bite, and whether it was by an owned or unowned dog.

CONCLUSION: Arguably, our long-term ability to mitigate public health risks associated with dog bites and the risk of rabies, is underscored by collaborative efforts informed by studies such as these which quantitatively describe the nature of human-dog interactions.

By examining these data, we present novel information relevant to multiple stakeholders and allow greater understanding of the value of differences in interaction between humans and dogs in rural and urban Ontario communities. We believe these data will provide a solid foundation for informed decision-making and enable community-specific public health strategies that can contribute to health capacity and sustain healthy communities for pets and people living in Ontario.

RESUBMISSION STATEMENT: This study was conducted in 2014. Preliminary data related to this study has been presented in poster format at the: 1) Canadian Association of Veterinary Epidemiology and Preventive Medicine Conference in May 2016 and, 2) Ontario Veterinary College (OVC) Graduate Student Research Symposium, in November 2017. Reasons for submitting the abstract to the 5th International One Health Congress include substantially updated information (i.e. final data will be presented) that is relevant and will contribute original information to the theme of "Infectious Diseases from an Ecohealth Perspective". The authors intend to submit this study for publication prior to the start of this conference.

P169 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

Leptospirosis in Slaughter Livestock in Gauteng Province, South Africa: Isolation, Serological and molecular Studies.

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BACKGROUND: Leptospirosis, caused by the pathogenic serovars of the Genus *Leptospira*, is considered a re-emerging zoonosis of global importance and it is responsible for morbidities and mortalities in humans and animals, particularly in developing countries. Gauteng Province, the study area, is in the Highveld and it is the smallest province in South Africa that accounts for only 1.5% of the land area (18.178 Km^2) of the South African total area of 1,220.813 km^2. The province is a well-developed with the largest and industrialized cities, Johannesburg and Midrand/Vanderbijil respectively. Abattoirs, although primarily used for animal slaughter, also provide invaluable facilities for both active and passive disease surveillance. In South Africa, there is a dearth of current information on leptospirosis with the last report on the isolation rate for *Leptospira* spp. was in 1999. This cross-sectional study employed convenience sampling method. The population of livestock considered for this study are cattle, pigs and sheep with the population per million in 2014/2015 of 13.7, 1.5 and 11 million respectively, in the Gauteng Province. The objectives of the study were to determine the prevalence of *Leptospira* spp. in slaughter livestock by isolation, serology and Polymerase Chain Reaction (PCR) for sequence analyses.

METHOD: A total of 646 samples (341 sera and 305 kidneys) were collected aseptically, from livestock slaughtered in 14 randomly selected low and high throughput abattoirs in Gauteng Province. These samples were transported in a cold chain to the laboratory immediately. Isolation of *Leptospira* spp. was achieved in EMJH media with 5-Flourauracil added and incubated at 29°C for 3 to 6 months using standard procedures, 237 kidney tissues were further subjected to quantitative PCR (qPCR) for quantification of *Leptospira* spp., and the presence and titres of serovars were determined by the microscopic agglutination test (MAT) with a panel of 25 serovars using standard techniques.

RESULT: Twelve (3.9%) of the 305 kidneys cultured were positive for pathogenic *Leptospira* spp. but qPCR revealed 29.1% (69/237) of pathogenic *Leptospira* spp. with the highest frequency of detection in ovine 54.5 % (19/35) and the seroprevalence of leptospirosis was 23.8 % (81/341). A total of 9 serovars were detected in the sera of which serovars Bratislava (6.5 %), Hardjo (6.2%) and Swazijak (2.1%) were predominant.

CONCLUSIONS: The data provided in this study reflects a great potential for human spillover infections to leptospirosis based on the frequency of detection by isolation and qPCR, the seroprevalence of Pathogenic Leptospira spp. and the infecting serovars in slaughter livestock may be vital for developing strategies to prevent and control leptospirosis in South Africa.

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A model of inter-market livestock movement in northern Tanzania: exploiting routinely collected data to investigate infectious disease transmission

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BACKGROUND: Movement of livestock between populations is a major factor in the spread of many livestock infections. In particular, inter-market livestock trade can mediate long-distance transmission, making markets prime targets for surveillance and control strategies. However, effective implementation of such strategies requires integration of knowledge of the trade network into disease transmission models. An obstacle to constructing such models is the lack of available data on livestock movements in developing countries. We aimed to address this problem by using routinely collected livestock movement permits to infer inter-market movement networks for cattle, sheep and goats in northern Tanzania, in the context of a study focussing on the zoonotic pathogens *Brucella* spp., *Coxiella burnetii,* and Rift Valley fever virus.

METHODS: We collected all available livestock movement permits (n ≈ 59,000) from the years 2009, 2011, 2013, and 2015 in the Arusha, Manyara, and Kilimanjaro regions. We used data (numbers of animals moved; origin and destination; date) from a 10% subsample of the permits to create monthly networks of recorded livestock movements between 398 wards (administrative areas holding ~12 thousand people), for both cattle and small ruminants (sheep and goats). We used a gravity model to identify predictors of livestock movements and infer movement networks while accounting for subsampling and non-random missingness. Movements between wards were predicted as a function of ward characteristics (including: inter-ward distance; human and livestock population sizes; area; market type). The model-predicted networks were used to simulate complete dynamic networks of monthly livestock movements.

RESULTS: The cleaned data subsample consisted of 4601 readable permits recording the inter-ward movements of 42,096 animals (65% cattle, 35% small ruminants). Cattle journeys (mean 116 km) were longer on average than those by small ruminants (mean 88 km). The model represented real movements realistically, as evidenced by the close match between recorded and simulated movement data. Similar seasonal trends were detected in movements of both cattle and small ruminants. Inter-ward distance (contributing 49% of explained variance; $P < 0.001$), destination human population size (30%; $P < 0.001$), and the presence of a secondary (large) market at origin and/or destination (23%; $P < 0.001$) were the strongest predictors of cattle movement. Distance (64%; $P < 0.001$) and destination human population size (14%; $P = 0.004$) were also strong predictors of small ruminant movement.

CONCLUSIONS: Our analysis demonstrates the feasibility of using routinely collected data to infer livestock movement networks in developing country settings. Further refinement of the model will incorporate climate, land use and economic data. The inferred networks will underpin models of disease dynamics that will allow us to address a range of questions around livestock movement and zoonotic disease risk, such as how pathogen dynamics might respond to interventions or social, economic and environmental change.

P171 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

Where do bats go? Tracking bats sheds light on virus exposure pathways and guides surveillance

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BACKGROUND: The straw-colored fruit bat, *Eidolon helvum*, is a highly gregarious species which is widely distributed in Africa. This species plays a critical role in the pollination of flowering plants and the dispersal of seeds, with some plants being almost entirely bat pollinated. Bats are also important reservoirs for many zoonotic infectious agents, such as paramyxoviruses, and understanding the dynamics behind possible spillover events of viruses between bats and other species, including humans, is important if we are to prevent and control future outbreaks. We sought to track the movements of these bat species in Tanzania to study their foraging patterns and implications for disease transmission to humans.

METHODS: GPS data loggers were deployed on 25 adult *Eidolon helvum* bats captured near their roosting locations in two areas: Morogoro Municipal and Kilombero district near the Udzungwa Mountains of Tanzania. The loggers were of two kinds, satellite (n = 15) and UHF (n = 10), and their weight did not exceed 5.5% of bat bodyweight. Foraging and roosting sites were determined from collected movement data and characterized according to their proximity to urban and protected areas via geostatistical analyses. Areas for environmental sampling using bat movements and virus shedding were determined, as were potential locations for setting up camera traps to record the presence of other animals near bat foraging sites.

RESULTS: Tracking data from 7 of the 10 UHF tags revealed variability between individual bat movements and a fidelity to foraging areas on consecutive nights. While the majority of the foraging areas were in or near urban areas, bats fed in protected areas as well, Udzungwa Mountains National Park (UMNP) being the most frequented out of these. The GPS information from the satellite tags led to researchers identifying specific types of orchards for environmental sampling and setting of camera traps.

CONCLUSIONS: The movement patterns of *Eidolon helvum* bats in Tanzania reveal that there is the possibility of contact between bats, non-human primates, livestock, and humans in bat foraging areas around human dwellings and horticulture, as well as an opportunity for viral sharing to occur between bats and other wild species in protected areas. Thus, while these bats are important for pollination and seed dispersal within protected areas, they may also serve as bridges for interspecific viral transmission.

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Future One Health workforce preparation for effective prevention and control of emerging infectious diseases

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BACKGROUND: Thailand remains a hotspot of various emerging infectious diseases including malaria, leishmaniasis, dengue and food- and water-borne diarrhea. The identification of any disease's origins, early detection and blocking transmission and spillover of pathogens, and preparing competent health workforces are promising ways for effective prevention and control. This study aimed to develop and evaluate a field-based training platform to prepare multidisciplinary graduate students as proficient future One Health (OH) workforce.

METHODS: Moh Tao village located in Thailand's Kanchanaburi province faces diseases and OH issues rooted in complex links between the environment, domestic and wild animals, and humans, hence its establishment as an OH demonstration site. Students were grouped into multidisciplinary teams and instructed to identify, investigate and formulate solutions to existing public health problems by integrating domestic and wild animal, environmental, human behavior and social factors. With 3 main issues (i. human-elephant conflict, ii. food and water, iii. Vector-borne diseases) identified by the residents in the OH village, students were assessed by measuring improvements in OH Core Competencies (OHCCs), level of knowledge, and technical skills including problem investigation, disease diagnosis, risk detection and analysis, proper risk communication and social innovation through self-evaluation and observations by multidisciplinary facilitators.

RESULTS: An average improvement (defined as change from moderate or less competency levels to high levels before and after the course) in 71.6% of the students was observed. The improvements were highest in Culture and Beliefs (88.9%) followed by Systems Thinking (84.2%) and Collaboration and Partnership (71.4%). Improvements in the Leadership (70.0%), Management (70.0%), Communication (66.7%), and Values and Ethics (50.0%) domains were also observed. Despite the conservative criteria for improvement, increases in competency levels were observed across all the OH domains. The students directly engaged the stakeholders (villagers, local health and administrative authorities, and schoolchildren) to gain a better understanding of the OH village. The students also formulated three sustainability-oriented innovative solutions: 1) landscape redesign proposal to prevent elephants from invading residential areas; 2) water filtration system model and advocacy campaign to improve practices; and 3) novel calendar for vector control. After presenting these ideas to the local stakeholders, the outputs from one of the groups were immediately taken up by the local Promoting Health Care Center for monitoring *Aedes* mosquitoes in the OH village including all neighboring villages within the Chong Sadao District.

CONCLUSIONS: With the successful development of a holistic training platform to prepare future OH workforce equipped with OHCCs, related knowledge, and vital skills required for multidisciplinary collaboration and formulation of innovative solutions, brings us a step closer towards OH-oriented professionals ready to face not just emerging infectious diseases, but also emerging complex problems.

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Assessment of Shiga Toxin-Producing Escherichia coli (STEC) in Private Well Waters in Western Canada with a One Health approach

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BACKGROUND: Shiga toxin-producing *Escherichia coli* (STEC) are a zoonotic pathogen with the potential to cause significant illness in people. Human exposure can occur through foodborne, waterborne and direct contact with infected animals (wildlife and livestock) or people. Exposure through waterborne pathways is not well described for groundwater sources in Canada where up to one sixth of the rural population depends on untreated groundwater sources for drinking water. This study examined the patterns of STEC in rural drinking water from groundwater sources and associations with agricultural, environmental and human factors in southern Alberta, Canada.

METHODS: Rural drinking water samples from groundwater sources were voluntarily submitted for routine water quality testing to the Alberta Provincial Laboratory for Public Health between 2004 and 2016. Qualitative testing for total coliforms and *E. coli* was performed using Colilert* (IDEXX Laboratories Canada Corp., Ontario, Canada). *Escherichia coli* positive water samples from the southern half of the Province of Alberta, Canada, were archived for future study. A quantitative polymerase chain reaction analysis for the stx gene was performed to characterize *E. coli* positive samples as STEC if stx positive. STEC-specific chromogenic growth media was used to isolate and distinguish STEC serotypes. Temporal and spatial patterns of STEC were described and seasonality assessed with Edwards' tests. Kulldorff spatial scan statistics were used to assess spatiotemporal clustering (SaTScan™ v 9.4.2, M. Kulldorff and Information Management Services Inc., 2015, Boston, USA).

RESULTS: Of all private drinking water samples tested, 0.2% were identified as STEC, amounting to over 7% of all *E. coli* positive water samples. Clinically relevant serotypes of STEC in Alberta were isolated from the water samples. A seasonal pattern of STEC occurrence was detected, as was a spatiotemporal cluster during a flood in 2005.

CONCLUSIONS: Shiga toxin-producing *E. coli* is present with a seasonal pattern in untreated groundwater used as drinking water in Alberta, Canada. A cluster of STEC positive drinking water samples was found related to a flooding event in 2005. Patterns of STEC occurrence in drinking water correlate with patterns of human illness in the region suggesting the importance of further research into the epidemiology of STEC in humans where waterborne exposure could be a significant risk factor. STEC in southern Alberta, Canada is a risk to public health highlighting the need for mitigation strategies for untreated drinking water systems.

P174 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

Specifying EcoHealth Pathways of Zoonotic Disease Through a Unifying Biopsychosocial Ecological Framework and Geospatial Mapping

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BACKGROUND: EcoHealth (EH) has heuristic value for its ability to convey the interdependence of ecosystem, human, and animal health. However, integrated approaches to infectious disease are needed to fully understand zoonosis pathways and mechanisms. The biopsychosocial (BPS) model is broadly applied in medicine to understand causes and optimize management of mostly non-communicable disease. A recent ecological extension of the BPS model (Figure 1) applicable to infectious disease outlines determinants of health in a broad, ecological context of the human microbiome (Maier & al'Absi, 2017). The BPS ecological framework identifies general biological/physical, psychological/behavioral, and social pathways that interact temporally across levels, from microorganisms to distal environments and socio-economic constructs. The high resolution of BPS pathways may add value to EH in elucidating zoonosis mechanisms.

METHOD: A selective literature review was conducted for "proof of concept" of the BPS ecological model adding specificity to the EH approach. A geospatial approach was used to visualize associations across selected aspects of the BPS model in relation to Lyme disease, a significant vector-borne disease in the US with widely available data.

RESULTS: There is extensive literature reflecting general zoonosis pathways suggested by the BPS ecological model across domains and levels. More novel are studies using a geospatial approach. Applied to human infection by *Borrelia burgdoferi* (Lyme disease agent), Nicholson and Mather (2014) developed a geographic information system (GIS) model to predict associations between disease incidence, blacklegged tick density, and *Borrelia burgdorferi* tick prevalence. More recently, Seukep et al. (2015) used GIS to observe correlations between Lyme disease incidence rates, land cover, income and age. Yet, Eisen et al. (2012) in identifying conceptual areas where increased knowledge could enhance prevention and control strategies, highlighted the need for deeper understanding of how human behavior influences Lyme disease risk. Accordingly, data visualizations of Lyme risk will be provided in a BPS ecological framework representing multiple pathways.

CONCLUSIONS: The BPS ecological model specifies likely mechanisms and pathways across the relevant disciplinary domains of biology, psychology/behavior, and other social sciences, and represents a unifying framework for a range of EH stakeholders to better conceptualize zoonosis prevention and intervention. The utility of this ecological framework may be enhanced using geospatial techniques that visualize the intricate and dynamic pathways of zoonoses in concrete terms that easily translate for broad use in various research, educational, and public health policy and outreach efforts.

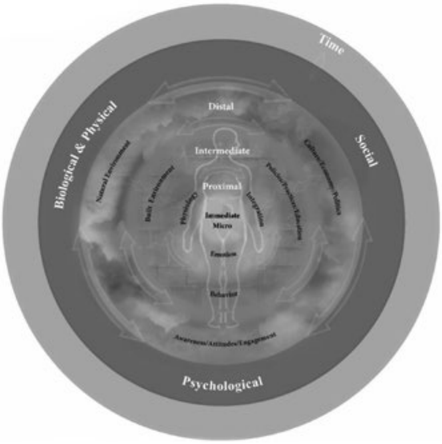

Figure 1: Biopsychosocial Ecological ModelAdapted.

P175 - OHS B06 - INFECTIOUS DISEASES FROM AN ECOHEALTH PERSPECTIVE

Surveillance of Zoonotic Viruses and Population Genetics of Confiscated Sunda Pangolins (Manis javanica) from Malaysia

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BACKGROUND: Sunda pangolin (*Manis javanica*) is listed as critically endangered and is the most illegally traded mammal in the world. Emerging and re-emerging zoonotic virus outbreaks in the past two decades have raised major public health and economic concerns globally. Since 2010, USAID Emerging Pandemic Threats: PREDICT project in Malaysia has identified 60 novel viruses (including a novel SARS-related CoV) and 28 known viruses from wildlife. During the 2002 SARS outbreak, the Chinese government closed the wildlife markets for the first time in history to control the outbreak; yet legal and illegal wildlife trade still actively occurs and threatens global health security. Therefore, it is crucial to identify the potential of pangolin carrying any public health concerned pathogen to create an early warning system.

METHODS: Through the USAID-funded PREDICT and Infectious Disease Emergence and Economics of Altered Landscapes projects, a total of 35 were confiscated and rescued by Sabah state authorities. All the samples were screened for 5 viral families (paramyxoviruses, filoviruses, orthomyxoviruses (influenza viruses), coronaviruses and flavivirus) using consensus PCR. In addition, the genetic variability of these pangolins was determined using 15 dinucleotide microsatellite markers. The levels of heterozygosities were calculated and cluster analysis were then performed to determine the genetic relatedness of these samples.

RESULTS: PCR test results were negative for all five viral families from the 35 pangolins from Sabah. Microsatellite results showed the values for the observed heterozygosity ($H_{o)}$ ranged from 0.194 to 0.727 (mean = 0.509) while the expected heterozygosity (H_e) ranged from 0.834 to 0.937 (mean = 0.877). The proportion of total genetic variance, $F_{ST,}$ was 0.738 and the FIS value was positive (-1.000) indicating an excess in heterozygosity. The dendrogram showed that the specimens were clustered into two main distinct groups.

CONCLUSION: The F_{ST} and F_{IS} values suggest that the population is not currently facing inbreeding pressure due to its diverse genetic variances. However, the observed heterozygosity was much lower than the expected heterozygosity ($H_{o<}$ H_e). This could be due to the small sample size or it may be indicative of a possible pressure in the genetic diversity of the species. Meanwhile, the dendrogram that was obtained can serve as a reference for forensic and smuggling investigation by comparing the confiscated pangolins with reference individuals of known origins. The current population status of the specimens in Malaysia is still unknown; hence, the dendrogram provides a representation of the genetic diversity information for the pangolins in Sabah. In addition to the Sabah pangolins, viral screening, serological testing an population genetics of pangolins from Peninsular Malaysia is currently ongoing to provide a comprehensive picture of the status of the species.

ANTIMICROBIAL AGENTS AND RESISTANCE

USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

P176 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Epidemiology of Antimicrobial Resistance pattern of Salmonella spp. isolated from Small Mammals of Bangladesh

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BACKGROUND: Antimicrobial resistance is a global concern that many of the antibiotics get resistance against some specific species of bacteria, which can hamper diseases recovery even though it can be fatal. Over the past decade, millions of people and animal become infected and die with bacteria that are resistant to antibiotics globally. Small mammals live with garbage and environmental wastage and may act as a bio indicator for the environment. Small mammals of Bangladesh may contaminated through their food and habitat with antimicrobial in human-animal interface.

METHODOLOGY: The aim of our research is to identify the ecology and epidemiology of *Salmonella* spp. isolated from small mammals with their antimicrobial resistant pattern. From a six month long study, we have captured small mammals (N=350), from both rural and urban settings which included *Bandicota* sp. (n=96), *Mus musculus* (n=100), *Rattus rattus* (n=112), *Suncus murinus* (n=42) from three districts namely Chittagong, Dhaka and Madaripur of Bangladesh. Oral and rectal/urine swab samples were collected in buffered peptone water (BPW) and tested on selective media, biochemical identification and finally, molecular identification was done by PCR. For AMR profiling 12 antimicrobials were selected to determine the AMR pattern by disc diffusion method.

RESULTS: The overall prevalence of *Salmonella* spp. were 27.4% (n=96; 95% CI: 22.8-32.4), sampling in different settings. There was no significant difference (p=0.34) was found among locations. Moreover, significant differences were found between species (p=0.01), age group (p=0.02), and sex (p=0.02). *Suncus murinus* 47.6% (n=20; 95% CI: 32-63.5) was more infected than other species. In case of sex group, female 33.1% (n=55; 95%CI: 26.1-40.9) were more infected with the salmonella infection. Small mammals from adult age group 32.2% (n=74; 95% CI: 26.2-38.6) were mostly infected than other age groups. We found Salmonella spp. (n=96) were resistant to Azithromycin (100%) followed by Nalidixic acid (88.9%), Sulfamethoxazole-Trimethoprim (83.3%), Tetracycline (80.6%), Cefotaxime (80.6%), Ciprofloxacin (75%), Chloramphenicol (72.2%), Ceftriaxone (63.9%), Gentamicin (69.4%), and Amoxicillin (47.2%). However, we also detected Salmonella spp. sensitive to Cefixime (52.8%) followed by Imipenem (50%) and most of the cases we found multi-drug resistant *Salmonella* spp.

CONCLUSION: The results indicated that most of the antimicrobial was resistant to *Salmonella* spp. isolated from small mammals. Close proximity to human dwellings, food animal, and agriculture increases the likelihood that microorganisms isolates from small mammals are resistant to some antimicrobials. Presence of resistant bacteria in small mammals possibly from livestock and human due to incriminated use, or to antimicrobials through contact with animal feed. However, these findings suggest that further study and attention needed for genetic analysis of these pathogens in small mammals and proper use of the antimicrobials in food animals and agricultural products to reduce multi-drug resistant pattern and transmission of resistance pathogen from human animal to the environment and vice versa.

P177 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Antimicrobial resistance of Escherichia coli associated with urinary tract infections and food poisoning at two main hospitals in Bujumbura, Burundi

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BACKGROUND: Urinary tract infection (UTI) is a common bacterial illness in adults and a common indicator of antimicrobial resistance. Antibiotic use in hospitals, the community and agriculture have contributed to selection pressures that have encouraged emergence of resistant bacterial strains. Treatment without appropriate diagnosis and antibiotic susceptibility testing contributes heavily to antibiotic resistance. Confirmation of pathogens associated with various illnesses and antibiotic susceptibility testing plays an important role in ensuring appropriate treatment is administered while contributing to surveillance of antimicrobial resistance.

OBJECTIVE: Determine the rate of resistance of strains of *Escherichia coli (E. coli)* isolated from patients with urinary tract infection and cases of food poisoning at two main hospitals located in the capital of Burundi (CHUK and Prince Regent Charles Hospital) against antibiotics commonly prescribed as first line as part of the studies under the East Africa Public Health Laboratory Networking Project.

METHODS: This prospective study was conducted over 6 months; from January 2015 to June 2015), in 535 patients with symptomatic acute lower urinary tract infection (white cells > 10^4 / ml, monomicrobial culture *E. coli* account colonies> 10^5 cfu / ml) and 14 patients with food poisoning. Culture of the urine specimen and community-type stool cultures was performed using conventional methods and identification of *E.coli* was done using biochemical tests including API 20E. Sensitivity to antibiotics commonly used was performed using the diffusion method. Detection of beta-lactamase extended spectrum (ESBLs) was also carried out using the recommended techniques

RESULTS: Among the sampled patients with a urinary tract infection and food poisoning , E.coli was isolated in 75% of women and 25% of men. Among these, 61% were in the age group of 15 to 65, 27%,were 0-15 years and 12% over 65 years. The rate of resistance to the antibiotics were as follows: amoxicillin (76%), amoxicillin + clavulanate (57%), ticarcillin (64%), ceftriaxone (5%), cefuroxime (5%), ceftazidime (10%), gentamicin (51%), trimethoprim + sulphamethoxazole (38%), nalidixic acid (23%), ciprofloxacin (11%), and fosfomycin (2%).

CONCLUSIONS: The study found increasing resistance of *E. coli* to commonly used antibiotics and emergence of resistance to ciprofloxacin. The study further showed that *E.coli* is a common pathogen associated with UTI and food poisoning in the population.

P178 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Antibiotics Use on Small and Medium Scale Broiler Farms in West Java, East Java and South Sulawesi Provinces, Indonesia

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Poultry production has been expanding rapidly in recent years in Indonesia to keep up with increased demand for animal protein by the fast-growing human population. Small and medium-scale (< 10,000 birds) commercial broiler flocks dominate this poultry sector and antimicrobial use (AMU) is said to be widespread on farms, although reliable data are not available.

To gain insight into antibiotics use patterns in poultry production, an AMU survey was conducted by the Directorate General of Livestock and Animal Health Services, Ministry of Agriculture on 360 small and medium scale commercial broiler farms in three provinces (West Java, East Java and South Sulawesi) of Indonesia. Most of the farms (86%) operated under a supply contract with a major integrated poultry company. The survey was conducted in September 2017 by 36 district level Veterinary Service Officers (VSO). The VSOs were trained in the administration of questionnaire surveys and data entry using a web-based application. The questionnaires, which were answered by owners (66.2%), farm managers (12.3%) and workers (21.5%), captured the farm profile, antibiotics used, patterns of usage, and compliance with withdrawal times.

The decision on which antibiotics to use is influenced by technical staff of the poultry farm supply contract company, who also provide the antibiotics for farmers (75%), followed by farmers' previous experiences (9%), and sales staff of drug/feed/day-old-chick suppliers (7%). Most farm supply contract company technical staff (86%) and drug/feed/day-old-chick suppliers' staff (50%) do not have a veterinary background. Enrofloxacin (49.4%), amoxicillin/colistin (35.3%), trimethoprim/sulfadiazine (14.1%), and doxycycline (13.3%) are the antibiotics most used on broiler farms.

Results reveal that 81.4% of farmers routinely give antibiotics as a prophylactic. Most farmers (61%) believe that antibiotic usage on their farms is necessary to raise broilers successfully. Only 2% of farmers performed antibiotic susceptibility tests to select antibiotics for flock treatment purposes.

Failures of antibiotic therapeutic treatment in broilers were experienced by 57% of farmers surveyed; when failures occurred at marketable age, 80% of farmers would sell the broilers to the market. The survey found an average antibiotic withdrawal time of 10 days before broiler harvesting, but 19% of farmers reported a withdrawal time of less than 5 days.

The survey showed that antimicrobials are widely used by broiler farmers mainly for disease prophylaxis. The most commonly used antibiotics are all categorized as either the highest ranked critically (colistin, quinolones), critically (amoxicillin) or highly (doxycycline, sulfadiazine, trimethoprim) important for human use. These survey results can form a baseline for comparison with future AMU surveys that are needed to monitor trends in the type of antibiotics being used and their indications in poultry production in Indonesia, especially as enactment of new regulations on antimicrobial growth promotors comes into effect.

P179 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Antibiotic residues in Raw Milk and locally produced dairy products in Ghana

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BACKGROUND: Antibiotic usage in animal husbandry to treat infections is a well-known practice, however non-adherence to guidelines often results in the presence of antibiotic residues in some animal products such as milk and milk products. Regular consumption of such products could lead to resistance against the antibiotic, sensitivity and allergic reactions in humans or interfere with the production of products like yoghurt and cheese where bacteria activity is required. It is therefore important to regularly monitor the levels of residues in animal products. In 2011, we reported a low antibiotic residue prevalence of 3.1 % of bulk raw milk samples from 224 kraals along the Coastal savannah regions of Ghana. In this study, we determined the prevalence of antibiotic residues in raw milk marketed in the Northern region of Ghana as well as some milk products sold in Accra.

METHODS: Seven districts in the Northern Region of Ghana were selected because of their high milk production and supply chain to the local community and nearby milk processing companies. In consultation with district Veterinarians, 30 kraals in each district were purposively selected based on the size of kraal, accessibility and proximity to market sites. The samples were collected in 2016 during the peak milk production season between March and September. From bulk raw milk containers, in each of the 210 Kraals, 50 ml of milk was drawn into 50ml Falcon tubes and transported to the lab on ice. The samples were kept frozen until the time of testing when they were thawed. Milk products comprising 15 yoghurt and 15 Burkina (a local milk and millet beverage) were also purchased from retail outlets in Accra for testing. The Charm® blue Yellow II Test which detects antibiotics in raw commingled and ultra-pasteurized cow milk was used according to manufacturer's instructions.

RESULTS: Antibiotic residues above the maximum EU residue limit were detected in 18.1% (38/210) of bulk raw milk samples and 4 milk products; two yoghurt and two burkina samples. The frequency of positive samples ranged from 2 to 10 out of 30 per district, indicating a general problem with antibiotic usage within the cattle rearing communities in all the seven districts.

CONCLUSION: Cattle owners and herdsmen need to be educated on the importance of adhering to withholding period after antibiotic administration and there should be regular tests done with sanctions applied for noncompliance.

P180 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Presence of Salmonella spp. And escherichia coli in eggs, chicken meat and pork in phnom penh market city and kandal market province in Cambodia

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Food of animal origin such as eggs and meat are implicate as the most common cause of foodborne infections which lead to morbidity and mortality, and a significant impediment to socioeconomic development. Enteropathogenic agents, *Salmonella* Typhi and *Escherichia coli (E. coli)* are foodborne diarrheal disease agents which contribute to the global burden. The study was aimed at counting the total number of bacteria colonies and checking for *salmonella* spp. and E. coli in eggs, chicken meat and pork. The samples of 9 chicken eggs and 18 chicken meat were randomly collected from various markets in Phnom Penh and of 36 pork were from Kandal (peri urban) province. The collected samples were tested using Bacteria cell counting technique, Bacteria cell culture, biochemical test (Gram-staining, Catalase test & TSI test) and those with the presence of *Salmonella* were tested by API 20E test in order to identify *Salmonella* as well as to study its adaptation to antibiotics (Antimicrobial resistance). The results showed that the mean values of the total bacteria colonies were 6531 CFU/g, $1226x10^3$ CFU/g and $8318x10^2$ CFU/g for the eggs, chicken meat and pork respectively. *Salmonella* spp. and *E. coli* were found in all samples (38.4%). *Pseudomonas* spp. were found in pork (16.7%) while Enterobacteriaceae was found in the eggs and chicken meat (19.5%). *Salmonella entirica* serovar *arizonae* was particularly found in the eggs (11.1%) and according to the test of adaptation to antibiotics (antimicrobial resistance), it was susceptible with Genamicin Ceftazidime and Cefoxitin and was intermediate with Ciprofloxacin and Enroloxacin. The bacterial burden in eggs, chicken meat and pork in this study was not significant different ($p > 0.05$). The contamination might be due to eggs or/and meat production or preparation chains, and thus proper cooking can prevent the foodborne enteropathogens. These results may contribute to the availability of document of foodborne pathogens in Cambodia.

P181 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Antimicrobial resistance profile of Escherichia coli and E. coli O157:H7 in raw milk produced and marketed in the Northern region of Ghana.

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BACKGROUND: Consumption of raw milk, an excellent protein source for humans, comes with several health concerns due to the level of contamination that can occur at the production chain. As a result, raw milk has been implicated as a vehicle for most foodborne pathogens. Farmers engaged in milk production administer antibiotics to cattle to boost feeding and milk production. The indiscriminate use of drugs in animal husbandry has contributed to the growing challenge of antibiotic resistance. This study investigated the prevalence and antimicrobial resistance profile of *Escherichia coli (E. coli)* and *E. coli* O157:H7 in raw milk produced in the Northern region of Ghana.

METHODS: Bulk raw milk from 224 cattle farms (Kraals) were analyzed. *Escherichia coli* and *E. coli* O157:H7 were detected using colony morphology, biochemical and agglutination tests. Antimicrobial resistance tests were performed using the agar disc diffusion method according to Clinical and Laboratory Standards Institute (CLSI, 2007) guidelines.

RESULTS: *Escherichia coli* and *E. coli* O157:H7 were detected in 40/224 (19.0%) and 5/224 (2.4%) samples respectively. *E. coli* 0157:H7 showed 100% resistance against nalidixic acid, gentamycin, chloramphenicol and cotrimoxazole while the resistance pattern of the other *E. coli* spp was nalidixic acid (95.7%), cotrimoxazole (95.7%) ceftriaxone (83.0%), gentamycin (80.9%) chloramphenicol (78.7%) and tetracycline (72.3%).

CONCLUSION: Raw milk marketed in the Northern region is contaminated with pathogenic *Escherichia coli* O157: H7 which is highly resistant to many antibiotics used to treat infection both in humans and farm animals. This calls for continuous education of cattle farmers on the adverse effects of indiscriminate use of antibiotics on both human and animal health.

P182 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Prospective evaluation of Ceftriaxone use in medical and emergency wards of Gondar university referral hospital, Ethiopia

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PURPOSE: This study aimed at evaluating the appropriateness of ceftriaxone use in medical and emergency wards of Gondar university referral hospital (GURH), Northwest Ethiopia.

METHODS: A prospective, cross-sectional study design was employed to evaluate the use of ceftriaxone. The medical records of patients who received ceftriaxone were reviewed prospectively between January 1 and March 30, 2017. Appropriateness of ceftriaxone use was evaluated as per the protocol developed from current treatment guidelines.

RESULTS: A total of 390 patients' medical records were reviewed. The utilization rate of ceftriaxone was found to be high with a point prevalence of 59%. Ceftriaxone was empirically used in 79.5% of cases. The most common indications of Ceftriaxone were respiratory tract infections (29.3%), central nervous system infections (24.1%), and prophylactic indications (16.4%). The mean duration of ceftriaxone therapy in our study was 11.47 days, with a range of 1-52 days. More than two-thirds (80.2%) of ceftriaxone use were found to be inappropriate and majority of unjustified ceftriaxone use emanated from inappropriate frequency of administration (78.3%), absence of culture and sensitivity test (68.7%), and duration of therapy (47%). Empiric treatment with ceftriaxone and the presence of coadministered drugs was significantly associated with its inappropriate use.

CONCLUSIONS: The present study revealed a very high rate of inappropriate use of ceftriaxone which may potentially lead to emergence of drug-resistant microorganisms and ultimately exposes the patient to treatment failure and increased cost of therapy.

P183 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Factors that drive antimicrobial use practices of beef cattle producers in Tennessee, United States

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BACKGROUND: Over the recent years, there has been increased awareness of antimicrobial resistance (AMR) in both human medicine and veterinary medicine. This increased awareness has triggered concerns over the issue of non-judicious use of antimicrobial drugs in animals especially due to the perceived risk associated with the zoonotic transfer of resistant pathogens from animals to human beings. To ensure judicious antimicrobial use (AMU) in animals, the U.S. Food and Drug Administration is implementing the Veterinary Feed Directive (VFD), effective January 1, 2017. The objectives of this study were: to determine the most common factors that drive AMU among beef cattle producers in Tennessee; to identify the common perceptions of Tennessee beef producers regarding the VFD.

METHODS: Tennessee beef producers with characteristics relevant to this qualitative study were purposively selected. A total of 5 focus group meetings were conducted in East, Middle and West Tennessee. Each beef producer focus group had 5 to 9 participants. A semi-structured interview guide was utilized. Each focus group was video recorded. To identify emerging themes, thematic analysis was performed using Nvivo, a qualitative data analysis tool.

RESULTS: In total, 39 Tennessee beef producers participated in this study. The factors that participants considered to drive AMU were: economic factors, disease epidemiology and outcomes, type of operation (management factors), veterinarian consultation, producer's self-perceived level of knowledge and experience, animal welfare, aggressive marketing by pharmaceutical companies, peer support from other producers, efficacy of the antimicrobial drug, season and consumer pressure. The VFD was perceived: to be a top-down government policy that has created additional costs for producers, to have affected small producers, to create more black-market access to antimicrobials, and to lead to increased use of injectable antimicrobials. Vaccination was considered an alternative to AMU. To encourage vaccine use among small producers, packaging of vaccines into small quantities was suggested by participants. The producers suggested that more education for cattle producers on prudent use of antimicrobials is needed.

CONCLUSIONS: Several factors drive the use of antimicrobials among cattle producers in Tennessee. Participants generally perceived their use of antimicrobials to be prudent. To reduce the burden of AMR, continuing education on prudent use of antimicrobials is needed for beef producers.

P184 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Antimicrobial use practices of veterinary clinicians at a veterinary teaching hospital in the United States

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BACKGROUND: Indiscriminate use of antimicrobial drugs is suggested as one of the modifiable factors contributing to the development of antimicrobial resistance (AMR). To reduce indiscriminate antimicrobial use (AMU), veterinary practices are encouraged to develop and implement antimicrobial stewardship (AMS) programs. The objectives of this study were: to identify factors influencing AMU practices of veterinary clinicians at The University of Tennessee Veterinary Medical Center (UTVMC); to evaluate the opinions of these veterinary clinicians concerning AMU, AMS, and AMR.

METHODS: A survey software was used to send a questionnaire to 121 eligible participants, who were all UTVMC faculty members with clinical appointments and house officers. Cumulative logit models were fitted to investigate associations between the demographics of these clinicians and AMU practices or concerns about AMR.

RESULTS: Response rate was 51.24%. Among the 62 respondents, culture and susceptibility test results and pressure from clients were the most and least important factors in their antimicrobial prescription decision-making, respectively. Compared to clinicians who obtained their veterinary degree from 1970–1999, those who graduated from 2000–2009 and 2010–2016 were 3.96 ($P = 0.034$) and 5.39 ($P = 0.01$) times less concerned about AMR, respectively. Clinicians' primary patient load (small animal, food animal, equine, mixed animal and exotics) confounded with the effect described above.

CONCLUSIONS: The findings suggest a critical need to evaluate AMU practices across other veterinary hospitals in the United States. In the interim, there should be an increased emphasis about AMR in the present veterinary teaching curriculum. Improvements in AMS are needed, through continuing education, especially among veterinary clinicians in this institution who graduated after 1999. Educational practices that target modification of AMU practices of veterinary clinicians would likely lead to improved AMS and possible reduction in the burden of AMR within veterinary medicine and public health.

P185 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

One Health and Antimicrobial Stewardship in the Pork Industry

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BACKGROUND: Antimicrobial resistance is an emerging global health issue that affects people and animals alike. Drivers of resistance are multifactorial and span the sectors of human, animal, and environmental health. Given the broad reach of this phenomenon, a One Health approach is needed to protect antimicrobial efficacy. In the U.S. swine industry, producers have taken an active role in curbing the trend of antimicrobial resistance such as funding research on antimicrobial alternatives and promoting judicious use among fellow producers through educational programming. Through these and related efforts, America's pig farmers, represented by the National Pork Board, demonstrate their commitment to protecting people, pigs and the planet.

METHODS: In order to assess the commitment of the organization to antimicrobial stewardship, a review of Pork Checkoff-related activities and research funding on antimicrobial use and alternatives was conducted. Annual summaries of funding support for antimicrobial related research and projects were calculated from 2000-2017. A numeric and descriptive summary of meetings and presentations either attended or led by Pork Checkoff funded staff were compiled and summarized. Industry buy-in of the Pork Quality Assurance® Plus (PQA Plus®) program, the flagship training and certification program of the National Pork Board, was assessed by determining its total enrollment value and overall representativeness of the industry.

RESULTS: More than $6 million in Pork Checkoff funds have been dedicated to antimicrobial resistance research efforts since 2000 with $1.4 million being dedicated in the past two years, i.e. 2016-2017. Policy changes within the organization reinforce the organization's commitment to responsible antibiotic use with the goal of protecting the health and welfare of pigs produced in these systems as well as pork safety and public health. PQA Plus® boasts buy-in from all major production systems and processing facilities in the country. The program has over a 20-year history of promoting key food safety and public health principles as it relates to antimicrobial use. It currently has 70,000 producers, veterinarians, and other stakeholders listed as certified in its database. These individuals represent nearly 60 percent of all production in the country. Furthermore, Pork Board staff remain actively engaged in collaborative efforts to improve antimicrobial stewardship with all major food-producing species. In addition, they work closely with federal and state agency representatives, academics, and individuals employed by NGOs on stewardship related efforts.

CONCLUSIONS: U.S. pig farmers remain dedicated to producing safe and healthy pork products while simultaneously protecting animal health and welfare. The National Pork Board assists farmers in upholding the pillars of public health through education and outreach. The organization will continue to strive toward continuous improvement in the realm of antimicrobial resistance, thereby protecting the health people, pigs, and the planet.

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Use of a stochastic production frontier approach to examine the impact of GIN management in beef cow-calf herds in Canada.

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BACKGROUND: Cattle are often treated for gastrointestinal nematode (GIN) parasites using anthelmintic drugs with a blanket approach at set times of the year, regardless of actual parasite burden. While this method is relatively cheap and simple, indiscriminate use of anthelmintics is not without consequences; there is strong evidence that this leads to anthelmintic resistance, and this approach may have unforeseen effects on the environment due to anthelmintic buildup. Furthermore, extensive long-term overuse could lead to toxicity in humans. A better understanding of how producers make decisions about anthelmintic use and GIN control is an important part of this problem and would be useful for effecting change.

METHODS: To better understand the impact of more prudent anthelmintic use, we first modelled beef cow-calf production. A basic stochastic production frontier (SPF) approach was applied for cow-calf herds using data from records in Western Canada. Functional form was imposed using a standard Cobb-Douglas approach, and anthelmintic usage, production demographics, and ecozone data were collected using an online questionnaire. An interactive website was then created to both inform producers about GINs and anthelmintic use, and to continue collecting data to further refine the SPF model.

RESULTS: Previous use of an SPF approach to cow-calf herd GIN management was not located in the literature. We were able to build an SPF model and apply it to various hypothetical GIN management options. This approach accepted modest deviations from perfectly efficient expectations and allowed producers to enter their own production details to estimate the economic gains from changing GIN management. Assuming a low-level GIN burden, we were able to show negligible economic impact from changing to more prudent use of anthelmintics. These results are by design speculative; estimating impact through field trials would be far more reliable, though costly in time and other resources. However, we were able to show proof-of-concept by developing and applying an SPF approach.

CONCLUSIONS: An interactive tool, like the website created as part of this project, is helpful both for engaging producers in discussions about the use of GIN anthelmintics and for refining an economic model of how cow-calf producers use anthelmintics. This will contribute to a long-term effort to shift cow-calf producer behaviour away from indiscriminate anthelmintic use toward a more prudent approach, helping reduce the risk of drug resistance and potential long-term harm to humans, animals, and their environment.

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Understanding disincentives to antibiotic use in Singapore’s food fish farming: A qualitative study

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BACKGROUND: Antimicrobial resistance (AMR) is one of the biggest threats to global health and its spread is accelerated by the extensive inappropriate use of antibiotics in humans and animals, including veterinary medicine, agriculture and aquaculture. However, information on factors that influence fish farmers’ decisions of whether and when to use antibiotics in the aquatic environment remains limited. We present preliminary findings from an ongoing qualitative study to understand decision making in relation to antibiotic use in Singapore's aquaculture industry.

METHODS: In-depth interviews were conducted with a purposive sample of food fish farmers in Singapore, who were asked about the characteristics of their farming operation, the use of antibiotics and other infection control measures in their farm, and factors influencing the choice of infection control measures. The interviews were transcribed, coded and analysed to identify incentives and disincentives related to the use of antibiotics in Singapore's food fish farming industry.

RESULTS: Preliminary thematic analysis indicated little incentive for antibiotic use in food fish farming in Singapore. Rather, the data revealed strong disincentives related to governance, economic and individual level factors. At the governance level, strict monitoring from regulatory agencies and stringent quality requirements for antibiotic-free products by fish suppliers and exporters were reported as major deterrents to antibiotic use. At the economic level, antibiotic use was reported as making little financial sense due to the relatively high price of antibiotics, particularly among farmers raising low value food fish such as tilapia and milk fish. At the individual level, personal knowledge and experiences related to the efficacy of antibiotics gained through individual farming experimentation also influenced farmers' decisions about antibiotic use. Some examples given byfarmers included noticeable impaired growth of fish post antibiotic consumption and the futility of feeding antibiotics to sick fish because of their lack of appetite. In place of antibiotics, alternative strategies to increase fish survival included the purchase of better quality fish fry, increased hygiene practices, the use of probiotics, as well as other non-conventional forms of disease management.

CONCLUSION: Although food fish farming industries differ significantly across countries, lessons learnt from the preliminary results in Singapore’s food fish farming industry show the importance of an environment in which multi-dimensional factors can come together to discourage the irrational use of antibiotics in food animal production. In addition, our results allow greater insight into food fish farmers’perspectives on infection control and forms a basis from which further research work can be undertaken.

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Antibiotic-resistant pathogens in wastewater inside poultry slaughterhouses and their fate in in-house wastewater treatment plants

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BACKGROUND: The aim of this study was to investigate the occurrence of antibiotic-resistant pathogens (ARP) in wastewater from the poultry slaughterhouses and after treatment by in-house wastewater treatment plants (WWTPs).

METHODS: Wastewater samples were taken inside two poultry slaughterhouses in Germany with slaughtering capacities of 125.000 (S1) and 440.000 (S2) chickens/day (Fig. 1) and at a farm (S3) with slaughtering capacity 30 chickens/month (Fig. 2).

Samples were semi-quantitatively screened for the presence of ARP using CHROMagar selective media. When applicable, up to 6 colonies of appropriate morphology per sampling point were selected. The final identification was done by MALDI-TOF MS and resistance was confirmed by determining of MICs using the ID/AST testing system. The resistant strains were further characterized by different molecular typing approaches. The colistin-resistant strains were screened for the presence of *mcr-1/ mcr-2* by rt-PCR.

RESULTS: A total of 201 resistant strains were isolated from S1 and S2, and 142 strains were isolated from S3. 88% of all strains from S1 and S2 were represented by *E. coli,* MRSA and *A. baumannii* complex, whereas their abundances in the outflows from in-house WWTPs were the lowest. *E. coli* and *A. baumannii* complex were the most widespread (93% of isolated strains) in S3. Species distribution and occurrence at the sampling points are shown in Figures 1 and 2. No VRE were detected.

37,1% of the isolated strains from S1 and S2 (n=170) were MDR and 18,8% colistin-resistant, whereas 37,5% thereof were *mcr-1* positive and none *mcr-2* positive. 6,3% of the isolated strains from S3 were MDR and 2,6% colistin-resistant (*mcr-1/mcr-2* negative). All isolated strains were carbapenem susceptible.

Phylogenetic typing of *E. coli* showed that 4,1% of strains from S1 and S2 (n=73) as well 3,0% from S3 (n=33) belonged to the pathogenicity-associated extraintestinal groups B2 and D. The MRSA strains tested (n=15) were known livestock-associated types.

CONCLUSIONS: Antibiotic-resistant pathogens are widely spread in the wastewater inside the investigated poultry slaughterhouses. Despite the considerable bacterial reduction by the WWTPs, they could still be found in the outflows. This could pose a threat to human health, and needs to be further investigated.

FIGURE 1: SPECIES DISTRIBUTION AND OCCURENCE OF THE ISOLATED STRAINS AT THE SAMPLING POINTS IN S1 AND S2

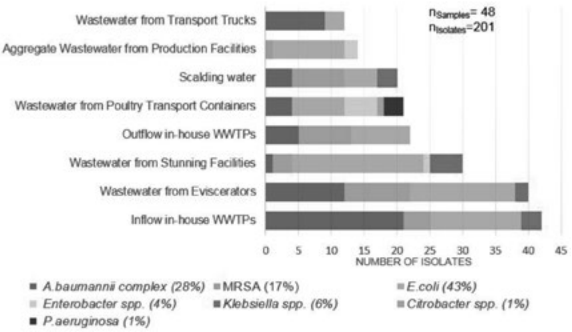
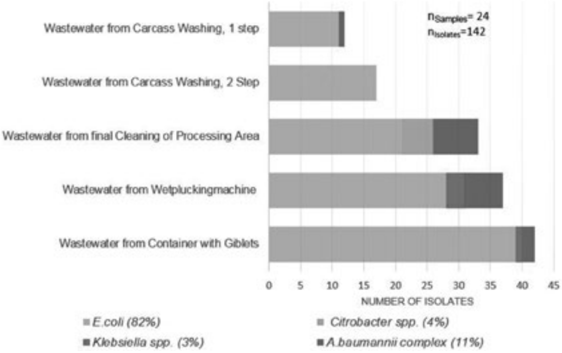


FIGURE 2: SPECIES DISTRIBUTION AND OCCURENCE OF THE ISOLATED STRAINS AT THE SAMPLING POINTS IN S3



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Informing our knowledge on AMR through the use of risk assessments: a scoping review

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BACKGROUND: Antimicrobial resistance (AMR) is considered a global threat to human health that requires a one health approach to its mitigation. Risk assessments are a component of risk analysis used to understand and evaluate the risks associated with foodborne antimicrobial resistance. They provide a transparent, systematic evaluation of relevant scientific knowledge to inform decisions regarding risk management activities. There are however, numerous approaches to risk assessment. Standardization of risk assessment protocols is necessary to make the best use of the data generated from these informative processes.

METHODS: A scoping review was undertaken which aimed to identify and describe the literature on risk assessments for the study of foodborne AMR in humans. Screening of 1822 abstracts and 57 full text articles was undertaken in duplicate.The definition of what constituted a risk assessment from a methodological perspective was based on the Codex Alimentarius *Guidelines for Risk Analysis of Foodborne Antimicrobial Resistance*. The Codex guidelines address the risk to human health associated with the transmission of AMR microorganisms from animals through the food chain or in animal feed, in a structured risk assessment framework. The content of each article identified was assessed using a series of questions categorised under the four components of a risk assessment: hazard identification, exposure assessment, hazard characterization and risk characterization.

RESULTS: Twenty-eight English language articles produced between 1989-2017 were identified following a comprehensive search strategy. All articles originated from North America or Europe. Most articles (22/28) were quantitative risk assessments. Fifteen articles made no reference to any relevant international documents for setting priorities for risk assessment or risk management activities. The sources used to identify hazards included scientific literature (n = 28), reports from government organisations (n = 20), expert opinion (n = 5), surveillance reports (n = 15) and data from non-governmental/industry organisations (n = 10). Microorganisms of concern included *Campylobacter* spp. (n = 13), *Salmonella* spp. (n = 9), *Enterococcus* spp. (n = 10), and *Escherichia. coli* (n = 5).

CONCLUSIONS: Just 28 articles relating to the use of risk assessments for foodborne AMR were identified following a comprehensive search strategy. It is possible that limiting the search to articles in English language only limited this number. All articles identified were published in North America or Europe indicating that research from countries in which regulation and control of antibiotics is not so stringent is not forthcoming. There is the potential for articles to consider a broader scope when the reviewing literature used for hazard identification. Codex guidelines provide a structured framework by which to conduct a risk assessment relating to the microbiological hazards and AMR and should be addressed in every risk assessment on these topics.

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A critical evaluation in the implementation of antimicrobial resistance sustainable control plan in Brazil: what is being done, challenges and perspectives to control its effects

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The antimicrobial control with some kind of antimicrobial resistance (AMR) has become a major challenge for the food industry. The domestic animals used for this purpose have been identified as keys to the development of AMR and the main reservoirs of bacteria carrying the resistance genes. Therefore, gradual changes had been implemented in the food production chain in the world; however, changes in the prescription of antimicrobial uses in production animals can also reduce food production perspectives for the future, and consequently result in the decrease of food supply for humans and animals.

Brazil is a major producer and exporter of animal food products. A year report 2015 of the United Nations Food and Agriculture Organization (FAO) and the Organization for Economic Cooperation and Development (OECD), points to Brazil as a major food exporter in the world in the next decade.

The Ministry of Health and Ministry of Agriculture Livestock and Food Supply in Brazil (MAPA) developed a National plan of action on antimicrobial resistance, it encompasses the concept of One health and has the collaboration of FAO and OIE. However, in addition to MAPA unilateral measures, there is still a poor integration between research centers (universities), other government entities and lack personnel training to monitor, performer approaches and scarce resources.

The aim of this paper is to discuss the programs implemented in Brazil for reducing the AMR levels, the problems in the implementation of these programs and perspectives for the future of a more sustainable animal production. In addition, presenting data of other countries in Latin America in antimicrobial usage.

Brazil has implemented measures with the (MAPA) as The National Program for the Prevention and Control of Antimicrobial Resistance in Agriculture (2017), the prohibition of the use of colistin sulphate in animal production in the year 2016, and other programs, such as the National Plan for animal production waste (1999). Notwithstanding, the implementation of unilateral measures by MAPA may not have the desired effects, since there is a lack of integration among the entities.

Some results of analyzes of foods such as meat, milk and of animals affected by diseases, obtained at the Federal University of Viçosa (UFV), have shown that there is a wide range of AMR microorganisms (*Yersinia enterocolítica, Escherichia coli, Staphylococcus aureus*, family *Enterobacteriaceae*) to various antimicrobials used not only in animal production environments, but in foods fed directly to final consumers.

Therefore, Brazil is a developing country that is implementing measures to contain the advance of ARM microorganisms. Nevertheless, there are still shortcomings and challenges in national strategies for the short, medium and long term, for prevention and containment measures that must be applied locally, nationally and regionally in cooperation with other entities.

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Using a one health approach - understanding antibiotic resistance and coupling points across complex African landscapes

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BACKGROUND: Antibiotic resistance has historically been considered an emergent problem in high-income countries. The tide is changing with antibiotic resistance now a rising phenomena in low and medium income countries struggling to address complex health threats. Globalization provides a conduit for movement of microbes and resistance that crosses ecosystems, threatening global health.

METHODS: In Chobe District, Northern Botswana, we take a unique, one-health approach to evaluating the phenotypic expression of antibiotic resistance in *Escherichia coli* among patients presenting to the primary hospital from 2007-2017 (n=1190), wildlife by life history strategy (water dependent, water associated, human associated, carnivores/herbivores, n= 900, 19 species), cattle (n=20), and river water (n=2003) and sediment (n=526).

RESULTS: Antibiotic resistance was widespread in humans, wildlife, and the environment. Among hospital patients, cultured isolates were resistant to multiple antibiotics (mean= 2.84 ±1.84, range=0-9) with 31% of isolates (95% CI=29.4-33.6%) demonstrating multidrug resistance (MDR≤3). For a number of antibiotics, levels of resistance among humans increased significantly over the study period and were comparable to that found in surface water, wild animals, and soil, albeit at higher levels. In this system, MDR was greatest in the urban land area but was found in all land use types including the protected areas where human disturbance was minimal. No resistance could be found in the limited number of *E. coli* isolated from the small population of cattle used in subsistence farming. MDR accumulation among water isolates was highest in areas where humans and wildlife overlapped at the aquatic-terrestrial interface. Across wildlife species, MDR was greater in those species that were water adapted, lived in close association with humans, or were carnivores.

CONCLUSIONS: In our study, drug resistance was wide spread independent of the presence of intensive livestock production systems, hospital waste, and inputs from wastewater treatment plants. Wildlife life history strategy provided important insights into exposure routes. AMR patterns in the environment mirrored those found in the human population reporting to the local hospital. This study highlights the need to take a one health approach and broaden our focus beyond livestock and sewage as the main culprits in this growing global threat.

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Knowledge, attitudes and behavioral practices of antimicrobial usage and resistance within rural communities in central Ethiopia.

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BACKGROUND: Antimicrobial resistance (AMR) and drug resistant infections are being recognized as a crosscutting threat to global health, with high rates of resistant infections documented in healthcare and community settings. Social determinants of health like poverty, education, infrastructure and access to health services are an important driver of antimicrobial usage and a comprehensive understanding of these issues would aid intervention programs. The objective of this study was to ascertain the knowledge, attitudes and behavioral practices of rural villagers regarding antimicrobial usage and resistance in Ethiopia.

METHODS: A cross-sectional knowledge, attitudes and practices study was conducted between April and June 2016 in rural Ada'a district within the Oromia regional state of Ethiopia. The study population were rural individuals residing in nine Peasant Associations (PA), and both households and PA were randomly selected from appropriate lists. A questionnaire was administered to 392 participants and included questions on knowledge and attitudes towards antibiotic usage both for humans and animals, and usage practices of antibiotics both for humans and animals. Data were entered into Microsoft Excel and analyzed using SPSS. This study was granted ethical approval from both the Oromia Health Bureau Institutional Review Board (IRB) and the North Carolina State University IRB.

RESULTS: The majority of the 392 participants were famers (81.1%) and 27.3% of participants were classed as illiterate or having only received informal education. Of the 392 participants surveyed, 26.8% reported being ill in the last month, with 65.1% reporting a sick animal in the last 12 months. When participants were asked about the purpose of antibiotics, 60.5% responded they did not know. Only 15.6% of participants could name the antibiotics they used for treatment in their household with 83.7% unable to name the antibiotics used in their animals. The antibiotics named for use in humans were Ampicillin, Penicillin and Amoxicillin. Only 45.7% checked the expiry date of the antibiotics prior to use. Additional data will be presented on participant's knowledge, attitudes and risky behaviors.

CONCLUSIONS: The use of antimicrobials in animal agriculture and their potential impact on human health has been widely debated. In recent years, there is increasing consensus that there are links between veterinary drug use and drug resistance in human pathogens, and that it is desirable to reduce antimicrobial use in agriculture. This study identified variable knowledge levels amongst participants regarding antibiotics and AMR. To tackle the grand challenge of AMR requires integrated action from both human and animal health sectors alongside support and consultation from other sectors and industries. Intervention strategies should take into account the economic, sociological and cultural issues related to antimicrobial usage as well as community knowledge, attitudes and behavioral practices.

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A scoping review of psycho-social factors influencing food animal producers' use of antimicrobials

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BACKGROUND: In many developed countries current food animal production practices result in higher rates of antimicrobial (AM) consumption by livestock than by humans. Livestock consumption of AMs has been identified as a major potential source for development and transference of AM resistance across the human-animal-environment interface. Appropriate AM use is critical in minimizing emergence of resistance, tasking food animal producers with the complex role of AM stewardship. In recognizing the complex decision-making process producers engage in to determine AM use, the purpose of this scoping review (SR) was to determine the psycho-social factors of influence on food animal producers' use of AMs.

METHODS: A rapid single-author scoping review was completed using Arskey & O'Malley's SR framework. A comprehensive search was implemented using three databases up to June 2017: AGRICOLA (ProQuest), CABI (Web of Science), and Medline (Ovid). Each database required a separate search strategy including a variety of terms that captured the following four concepts: food animal producers, food animals, antimicrobials, and influencing factors. A reference list search of articles meeting the inclusion criteria was completed to identify additional relevant literature. Braun & Clarke's thematic analysis, a qualitative content analysis approach, was used to identify, report, and analyze themes within the literature.

RESULTS: A total of 23 articles were included from 253 identified citations. The majority of the articles were published since 2010 (19, 82.6%), and conducted within the European Union (15, 65.1%). Cattle producers (14, 60.9%), particularly dairy producers (12, 52.2%), were the most frequently investigated population regarding AM use. Concerning the explored context of AM use, the majority of the articles discussed general AM use (12, 52.2%) rather than focusing on a specific disease or issue.

Four overarching themes were identified: (1) veterinarians as major (limited) influence, (2) experiential knowledge, (3) practice complacency, and (4) disconnect. Veterinary advice was identified as the largest external influence on producers' AM practices, however this influence was limited given veterinary advice was sought only in times of uncertainty. Producers relied on experiential knowledge believing their experience provided the necessary knowledge for sound AM use. Producers believed they could reduce their overall AM use if required, however there was a sense of contentment amongst producers regarding their current AM practices with producers believing that they were using "the right amount." The final theme highlighted disconnect around knowledge translation, trust of research findings, and government organizations.

CONCLUSIONS: AMR is a pernicious global health threat requiring multi-faceted approaches to make significant gains. This SR identified potential target areas for interventions and policies to improve AM practices including development of an actionable AM resistance framework. Identification and exploration of the psycho-social influences on food animal producers AM use is an emerging area that warrants further exploration.

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Production animal antimicrobial use in New Zealand

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BACKGROUND: The NZVA has stated its aspirational goal that *'by 2030, NZ Inc will not need antibiotics for the maintenance of animal health and welfare'* (Anon1).

New Zealand already has one of the lowest rates of antimicrobial use (AMU) in the world (Hillerton et al, 2017). However, there are few data available in New Zealand describing AMU in production animals to the level of detail required to both adequately monitor, and effect change, around AMU. In particular, the WHO has deemed it is important to be able to determine actives used at a species level.

This paper reports on a pilot project to assess and analyse all production animal use (sales) data from six key clinics across New Zealand.

MATERIALS AND METHODS: This project was co-funded by the NZVA and by XLVets in New Zealand.

Data were requested and gathered for all farm clients serviced by participating businesses during this period.

Antimicrobial sales data was married with ACVM data and classified according to route of treatment, class, and active. Total biomass was calculated for each farm.

Data were then combined to calculate mg active/kg PCU, for reference against existing data and for summary analyses.

RESULTS: Data were gathered from a total of 1462 dairy farms and 707 other (general) farms representing 623,430 adult milking cows, 27,399 mixed age beef animals, 706,035 mixed age ewes, and 12,107 mixed age hinds and stags.

Mean PCU for all dairy farms was 8.54 mg/kg. The lowest mean by clinic was 4.72 and the highest 11.91. Mean PCU for all general farms was 0.57 mg/kg; with a minimum by clinic of 0.32 and a maximum of 0.94.

For dairy farms, 56.3% of all AM used (by weight of active) was injectable, followed by intramammary dry cow (33.4%) and then intramammary lactating cow (8.9%) (Figure 1). The majority of active used was Penicillin (77.6%), followed by Macrolides (9.04%) and then Cephalosporins (5.1%) (Figure 2).
For general farms, 59.0% of all AM used was oral, followed by injectable (39.2%). The majority of active was Tetracyclines (66.0%), followed by Penicillin (19.2%) and then Sulphonamides (7.1%) (Figure 3).

CONCLUSION: These data confirm that the use of AMs amongst production animals in New Zealand is very small, and that routes of administration and actives vary between dairy and red meat sectors.

The data also confirm that the use of (3rd generation) cephalosporins and macrolides is very low amongst general farms and low amongst dairy farms. Fluoroquinolone use is virtually negligible across all species.

The data presented here provide a far greater level of analysis by providing for species used, active, PCU, region and route of administration.

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Understanding the differences in antimicrobial use in dairy cows in New Zealand and in the UK

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BACKGROUND: Antimicrobial resistance (AMR) is recognized as one of the greatest risks to human health globally (O'Neill, 2015). There have been links made between antimicrobial use (AMU) and AMR in agriculture (Chantziaras et al. 2014); and, by volume, the majority of AMU globally is in agriculture. Therefore, it is important for the agricultural sector to both monitor and manage AMU.

The authors have gathered data on AMU from both the UK and New Zealand for comparative purposes in this paper.

MATERIALS AND METHODS: Reliable dairy AMU data, using sales as a proxy for use, and measured in mg per population correction unit (mg/PCU), were available from recent, large scale nationwide studies in both New Zealand and the UK. The studies reflected similar 12- month periods (2015/2016 and 2016 respectively), and were both gathered using AM sales data from veterinary clinics and animal denominator data from farms.

There were a total of 358 dairy farms and 81,640 dairy cows represented from the UK, and 1462 dairy farms and 623,430 dairy cows from New Zealand. The UK data was collated from 4 large veterinary clinics and the New Zealand data from 6 veterinary clinics.

RESULTS: Mean AM use (sales) in New Zealand and the UK was 8.54 and 22.11 mg/PCU, respectively. At a farm level, the range in the UK was 0.36 to 97.79mg/PCU; whilst at a clinic level, the range in NZ was 4.72 to 11.91.

For both countries, the greatest route (by weight) used was by injection (78.1%, 56.3%, UK and NZ respectively). In both countries, this was followed by either intramammary lactating cow therapy (6.5%, 8.9%), or by DCT (6.0%, 33.4%).

Beta lactams made up the bulk of antimicrobial actives in both countries, totaling 42.8% and 77.6% of mg (UK and NZ respectively). The second highest actives in the UK were aminoglycosides (20.9%), and in NZ were macrolides (9.0%).

CONCLUSION: These data highlight the challenges in assessing AMU across different countries and farming systems. However, they also highlight that the gathering and analysis of this information is critical to better understand the societal role of AMU in a one health setting.

Although animal disease may be similar between countries, expectations around disease management and treatment vary. More significantly, societal approaches to animal welfare and production vary. There may be opportunities to intervene to utilize different management and mitigation strategies in some country situations, that may reduce AMU.

Furthermore, there are structural differences between agricultural sectors in different countries that could be leveraged where appropriate to create a more globally sustainable agriculture.

P196 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Analysis of antibiotic residues and metabolites in wastewater from Hospital, livestock and treated water in Kigali City, Rwanda

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INTRODUCTION: Antibiotics improve human, animal and plant health, and increase life expectancy. They are among the most important medicines commonly used for human, animal treatment. However, they must be considered as important pollutants as well since they can challenge microbial populations. Residues from human and livestock environments may contain antibiotics and antibiotic resistance genes that can contaminate natural environments.

METHODS: This is an experimental study that was conducted at three sites in Kigali city sites (Kigali University Teaching Hospital, Rubirizi livestock and Kacyiru water treatment plant) in Kigali city, Rwanda between July1-September30, 2017.

After acidification to pH=3 with phosphoric acid, 25ml of effluent samples were enriched by solid phase extraction. A combination of anion-exchange cartridges was used in the solid-phase extraction. A Liquid chromatography MSMS triple quadrupole system (Agilent 1260 series) was used and MS analysis was performed on TSQ quantum ultra triple stage quadrupole mass spectrometer with an electrospray ionization source.

RESULTS: Nineteen different antibiotics from six therapeutic classes of antibiotics namely aminoglycosides, beta-lactams, fluoroquinolones, sulfonamides, phenicols, and tetracyclines were assessed. Higher concentrations of Chloramphenicol (4,607.3µg/L) were detected followed by Sulfadiazine (79.6µg/L), Tetracycline (36.3µg/L), Chlortetracycline(26.1µg/L) and Sulfathiazole(20.2µg/L) in wastewaters from Kigali University Teaching Hospital. Cephalexin (645.9µg/L) was the most prevalent antibiotic in municipal wastewaters of Rubilizi hatchery followed by Sulfadimethoxine (48.5µg/L), Ofloxacin(38.1µg/L) and Tetracycline(31.3µg/L). In water from Kacyiru water treatment plant, Oxytetracycline(65.3µg/L) was the highly detected antibiotic followed by Cephalexin(48.5µg/L) and Streptomycin(44.2µg/L).

CONCLUSION: Regular assessment of antibiotics concentration levels in treated water, hospital and livestock wastewaters will help to identify specific medicine use problems, provide healthcare providers, veterinarians, environment scientists and policy makers with relevant information that could be useful in reviewing policies related to proper disposal of pharmaceuticals, treatment of wastewaters in order to contain the transmission of antibiotic resistance genes.

P197 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

ANTIMICROBIAL RESISTANCE PROFILES IN ESCHERICHIA COLI AND SALMONELLA SPP. ISOLATED FROM SLAUGHTER HOUSES IN CAMBODIA

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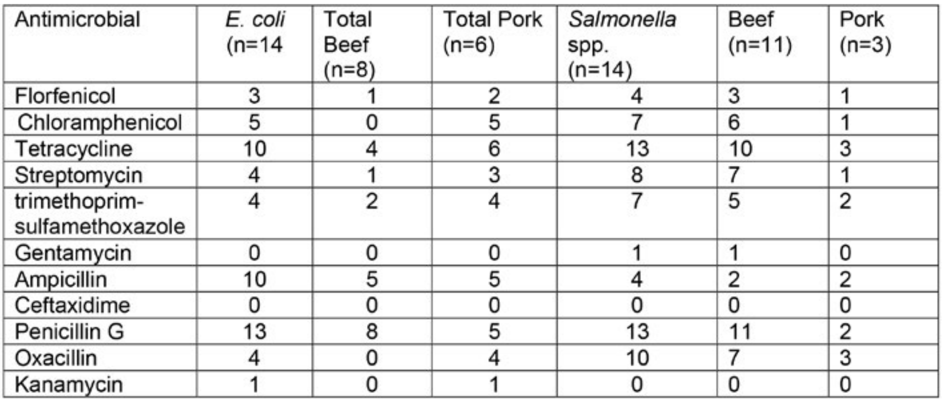
BACKGROUND: The commensal bacterial contamination in meat and their resistance profiles has cause public concern. The aim of the study was to isolate *E. coli* and *Salmonella* spp. from beef and pork in slaughter houses contamination in 2 provinces in Cambodia in part of the bacterial and hygiene monitoring in meat from slaughterhouse around Cambodia.

METHODS: A total 40 specimens of beef (n=20) and pork (n=20) were collected from slaughterhouses in 1 from Siem Reab and 1 from Kampong Thom Province (20/20) and considered the contamination on slaughtering processes. Bacterial contamination *E. coli* were 14 and *14 Salmonella* spp. tested on 11 antimicrobial susceptibility profiles using disk diffusion method based on CLSI standard VET01A4 and interpreted result following CLSI VET-01S and M100-S26.

RESULTS: The preliminary result of AMR profiles has showed in Table 1 below.

Table 1. Number of isolate of E. coli and Salmonella spp. that resistance to antimicrobial from slaughter house in Siem Reab and Kampong Thom in each specimen.

Moreover, multi-drug resistance was found both E. coli and Salmonella isolates.



Antimicrobial	*E. coli* (n=14	Total Beef (n=8)	Total Pork (n=6)	*Salmonella* spp. (n=14)	Beef (n=11)	Pork (n=3)
Florfenicol	3	1	2	4	3	1
Chloramphenicol	5	0	5	7	6	1
Tetracycline	10	4	6	13	10	3
Streptomycin	4	1	3	8	7	1
trimethoprim-sulfamethoxazole	4	2	4	7	5	2
Gentamycin	0	0	0	1	1	0
Ampicillin	10	5	5	4	2	2
Ceftaxidime	0	0	0	0	0	0
Penicillin G	13	8	5	13	11	2
Oxacillin	4	0	4	10	7	3
Kanamycin	1	0	1	0	0	0

CONCLUSIONS: The AMR profile were found higher among the major use of antimicrobial in livestock including tetracycline, penicillin G and ampicillin. This result has raise risk concern on AMR to public health in Cambodia. This is result is one part of the picture of AMR monitoring in both species and the further study on the specimen from pig production system and antimicrobial use are required.

P198 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

ANTIMICROBIAL RESISTANCE PROFILES IN SALMONELLA SPP. DETECTED IN DIARRHEAL CHICKEN IN CAMBODIA

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BACKGROUND: One of the most common health problems in Cambodian broiler chicken production is diarrhea, which results in slow growth rate and secondary infections. In Cambodia, a majority of broiler farmers use antimicrobials to prevent and control infections such as diarrhea in their chickens, without any prior veterinary consultations or confirmed diagnosis. The objective of this study was to determine the presence of antimicrobial resistance in *Salmonella* spp. isolated from diarrheal broiler chickens reared in a semi-commercial farm in Cambodia.

METHODS: This cross-sectional study was conducted on faecal swabs in a farm with 100 broiler chickens in Kandal province in southern Cambodia. *Salmonella* spp. was isolated from 13 chickens with clinical signs of diarrhea and susceptibility testing was performed against 10 antimicrobial agents, using disk diffusion CLSI VET01-A4 method with the results evaluated based on CLSI VET 01S and M100-S26.

RESULTS: High presence of *Salmonella* spp. was confirmed among the diseased chickens. Of the 13 chickens sampled, six (46%) were detected with *Salmonella* spp. All six *Salmonella* spp. isolates were susceptible to ampicillin, chloramphenicol, ceftazidime, fosfomycin, gentamicin, kanamycin, and streptomycin. In contrast, all isolates were resistant penicillin and tetracycline, and one isolate (17%) was resistant to trimethoprim-sulfamethoxazole.

CONCLUSIONS: The results show that resistance to antimicrobial agents, in particular to penicillin and tetracycline, is common in *Salmonella* spp. isolated from chickens with diarrhea raised in a semi-commercial farm. Although further studies are required with the inclusion of a larger number of chickens and farms, the results indicate that resistance to frequently used antibiotics is common in Cambodian broiler chickens. By educating farmers on improved chicken management and prudent antimicrobial use, further resistance may be prevented.

P199 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Variation in airborne DNA concentrations of various antimicrobial resistance genes and livestock-related bacterial indicator organisms measured at residential level at 61 sites in a livestock dense area

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BACKGROUND: Microbial air pollution from livestock industry has raised concerns about potential public health and environmental impact. Various bio-aerosols can be emitted by livestock farms including AMR bacteria. Elevated concentrations of airborne bacteria and their constituents have been reported at close proximity to farms. Knowledge on concentrations at further distances is limited, while this is important regarding public health relevance. Therefore we performed a study aimed at measuring DNA concentrations in ambient air at residential level of AMR genes against antimicrobials widely used in livestock production, and of livestock commensal bacteria used as indicator organisms for livestock farm emissions. Our objectives were to gain insight in airborne concentrations over time, to assess spatial variation, and to explore associations with livestock-related characteristics of the surroundings.

METHODS: Measurements were performed from May 2014 till December 2015 in a livestock dense area in the Netherlands. Ambient fine dust was collected repeatedly at 61 sites (residential gardens) representing a variety of nearby livestock-related characteristics. Furthermore a reference site was included, which was sampled continuously. Samples were analyzed by means of qPCR for DNA of AMR genes (tetW: tetracycline, mecA: narrow spectrum penicillins) and bacterial DNA of livestock-related indicator organisms (*Escherichia coli, Staphylococcus spp*). Mixed models were used to explore associations with livestock-related characteristics of the surroundings using detailed farm information.

RESULTS: Clear differences over time in bio-aerosol concentrations were observed, especially for *Staphylococcus spp* and tetW. Patterns of temporal variation were comparable for the measured components (range in Spearman correlations:0.8-0.9), concentrations peaked in the period around May 2015. Clear differences in bio-aerosol concentrations between sites were observed (fold change from 10th to 90th percentile of: *Escherichia coli*=10, *Staphylococcus spp*=11, tetW=4.8, mecA=31). Correlations in spatial variation for the different bio-aerosols were considerable (range in Spearman correlations:0.7-0.9). Univariable analyses showed generic livestock characteristics of the surroundings (e.g. distance to nearest farm, number of farms in buffers ranging from 500-3000m) to be significantly associated to bio-aerosol concentrations measured at residential level. When taking animal-species specific information into account; associations were strongest with pig farms and poultry farms especially when including animal numbers.

CONCLUSIONS: Presence of livestock-related bio-aerosols including AMR genes at residential level in a livestock-dense area was shown. AMR genes concentrations correlated highly with livestock commensal bacteria concentrations, strengthening the link with livestock farm emissions. Observed clear variation over time may be related to non-constant emissions and/or dispersion processes, additional research including temporal data is needed to increase insight in this. Pig farms and poultry farms showed strongest associations with AMR genes concentrations. This is consistent with the usage of penicillins and

tetracylines being highest (on average) at these types of farms in the Netherlands. Health implications of observed airborne concentrations are not yet known, and should be studied further.

P200 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Dairy calf treatment decisions by farm personnel compared to veterinary observations of clinical signs

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BACKGROUND: Antimicrobials are frequently administered to calves with diarrhea, despite evidence suggesting questionable efficacy. Even an efficacious treatment requires accurate disease detection to ensure that it is properly applied. The study hypothesis was: on farm treatment decisions are often not appropriately matched to disease symptoms.

METHODS: Four farms in the western USA, three farms that reared preweaned dairy heifer and bull calves and one dairy farm that raised their own replacement heifers were enrolled in the study. The study was a longitudinal design and calves were enrolled on the day they were placed into calf housing. A veterinarian evaluated calves on each farm daily for 28 days and worked with on-farm personnel to observe and document daily treatment decisions made by calf care workers. Veterinarian observations included: morning appetite and attitude, fecal and hydration scores, and respiratory signs. Treatment decisions were based on farm protocols and all treatment decisions were independent of the veterinary observations. Data were analyzed using contingency tables and multivariate GLM methods.

RESULTS: A total of 460 calves were enrolled in the study and accounted for 12,101 observation days. Abnormal clinical signs were observed on all farms with the most common abnormal clinical observation being diarrhea with an incidence risk of 0.85 and noted across 10% of the observation days. This was consistent across all farms. Dehydration was the next most commonly observed abnormal clinical sign with an incidence risk of 0.33 and noted across 3% of the observation days. The incidence risk for a calf being treated with an antibiotic was 0.7. Electrolyte therapy was the next most common therapy but this was often in conjunction with an antibiotic. The most important finding is the mismatch between clinical signs and treatment decisions. In a multivariate model controlling for farm effects, calves without signs of clinical disease were just as likely to receive an antibiotic as their first treatment as calves with clinical signs. In contrast, calves first observed with diarrhea or dehydration were more likely to be treated than calves who had no evidence of disease.

CONCLUSIONS: In this study, it is clear that a high proportion of preweaned dairy calves were observed with diarrhea and to a lesser extent as dehydrated. It was also observed that on-farm personnel treated a high proportion of calves with antibiotics. The important finding was the mismatch between first treatment decision by farm personnel and observation of a clinical sign. Two opportunities to address these findings are to better understand the significance of an observed diarrhea event and to develop more effective approaches to support on-farm decision making.

P201 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Our story of modelling antimicrobial resistance: broadening the scope, finding new tools and lessons learned.

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BACKGROUND: *Modelling antimicrobial resistance: Our motivation.*
The epidemiology of antimicrobial resistance is complex with multiple populations, reservoirs and mechanisms of transmission. We wanted a more comprehensive understanding of this complexity in Canada and in general. To accomplish this goal, we constructed quantitative models describing the exposure of Canadians to antimicrobial resistant bacteria through various pathways (e.g., agri-food chain, human pathways, and environment), and our initial focus was on the of consumption of beef, chicken and pork.

Broadening the Scope: A more comprehensive approach.
The relationships between antimicrobial use in livestock and the occurrence antimicrobial resistance in human bacteria have been reported. Most studies investigated a single resistant bacteria in a specific a population (e.g., fluoroquinolone-resistant *Campylobacter* jejuni in broiler chickens). We wanted to use a quantitative modelling approach that included multiple bacteria (e.g., *Campylobacter*, *E. coli*), multiple resistances (e.g., fluoroquinolones, tetracycline) in multiple populations (e.g., broiler chicken, pigs), and factors that may alter the occurrence of antimicrobial resistance (e.g., antimicrobial use, organic production).

METHODS: *Finding New Tools: Methods for a complex system.*
Our quantitative approach was guided by integrated assessment modelling: a method for modelling complex and dynamic systems (e.g., climate). Our quantitative models propagated through the Canadian agri-food chain the probability of antimicrobial resistance modified by the relationships between factors and the occurrence of antimicrobial resistance described by measures of associations (e.g., odds ratio, risk ratio) (see *Lessons Learned*). Estimates of Canadians exposed to resistant bacteria through beef, chicken and pork were obtained by adjusting probabilities by Canadian consumption patterns and population.

RESULTS: *Lessons Learned: Profiting from perseverance.*
There are many measures of associations describing relationships between factors and antimicrobial resistance. We explored several measures of associations and approaches to modelling to modify the probability of antimicrobial resistance propagated through the agri-food chain. These investigations were particularly challenging requiring lengthy, iterative discussions (research team and external consultants), and model modifications to resolve problems encountered during model development and construction. Following these activities, we constructed a functional integrated assessment model that models antimicrobial resistance along the agri-food chain using odds ratio and the frequency of occurrence of factors using a branching probability tree approach.

CONCLUSION: *Next chapters: The story continues.*
Our overall goal is to have a better understanding of antimicrobial resistance in Canada, including the contribution of on-farm antimicrobial use to antimicrobial resistance affecting Canadians. After multiple discussions and revisions, we constructed models estimating Canadian's exposure to antimicrobial resistant bacteria through uncooked beef, chicken and pork. Other aspects of the epidemiology of human exposure will be addressed through additional models. The contribution of on-farm antimicrobial use to antimicrobial resistance in Canadians will be better understood by linking to and understanding other exposure routes to resistant bacteria.

P202 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

Quantification, Antimicrobial Susceptibility Testing and Speciation of Vancomycin-Resistant Enterococci Isolated from Two Wastewater Treatment Plants using Different Treatment Processes

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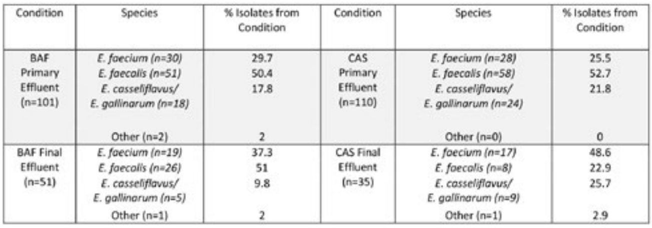
BACKGROUND: Wastewater treatment plants (WWTPs) receive wastewater from multiple sources and are considered a possible point of control for the environmental spread of antimicrobial resistance (AMR). The objective of this study was to determine how biological aerated filter (BAF) and conventional activated sludge (CAS) treatment processes influenced the presence and characteristics of vancomycin-resistant enterococci (VRE).

METHODS: Culturing methods for Enterococcus and VRE combined with quantitative PCR for total bacterial load, *van*A (vancomycin resistance) and class I integrons (*IntI-1*), were used to quantify enterococci and VRE in the primary (PE) and final effluents (FE) from the WWTPs over a 2-year period. The relationships between the removal of enterococci/VRE and the chemical and environmental factors (using principle component analysis) and land use information for the municipality were also assessed. *Enterococcus* spp. (n=1200) were isolated from the biomass, primary and final effluents of the WWTPs and screened for vancomycin resistance using broth-based susceptibility testing (MIC 4mg/L). Presumptive VRE isolates (n=313) were speciated (using groEL loci) and underwent disc susceptibility testing for 12 antibiotics. Relationships between species, frequency of resistance, and sampling location were determined using the chi-square test.

RESULTS: The BAF system removed more enterococci from the waste stream than the CAS system. This was associated with the alkalinity and total suspended solid content of the wastewater. VRE was not selected for through treatment and was removed at the same efficiency as the overall enterococci population regardless of treatment process. Service areas of the WWTPs did not impact the relative proportion of *Enterococcus* spp. or relative frequency of resistance to the antibiotics tested in the PE, which was similar in both WWTPs. A shift in species, through treatment by the CAS system, (Table 1) could account for increased nitrofurantoin resistance (NTRO^{R}, p<0.001) and decreased quinupristin/dalfopristin resistance (QUIN^{R}, p=0.003) through treatment and also accounted for the higher frequency of NITRO^{R} (p=0.012) and lower frequency of QUIN^{R} (p=0.007) and streptomycin resistance (p=0.022) in the CAS FE compared to BAF FE. Multidrug resistant isolates were common (45.7% to 62.4%) in both systems. In total, 73 unique AMR phenotypes were characterized; many of which were shared among PE and FE from both WWTPs.

CONCLUSIONS: VRE was removed at the same rate as the total enterococci population in both the BAF and CAS systems. The BAF system removes enterococci more efficiently. The relative frequency of resistance to a particular antibiotic may be more indicative of the relative proportion of species in the wastewater influent rather than the capacity for VRE to acquire AMR genes through the treatment process.

Table 1: Summary of the number of isolates analyzed in this study, origin of each isolate and the relative proportion of each species isolated from each sample types.



Condition	Species	% Isolates from Condition	Condition	Species	% Isolates from Condition
BAF Primary Effluent (n=101)	*E. faecium (n=30)*	29.7	CAS Primary Effluent (n=110)	*E. faecium (n=28)*	25.5
	E. faecalis (n=51)	50.4		*E. faecalis (n=58)*	52.7
	E. casseliflavus/ E. gallinarum (n=18)	17.8		*E. casseliflavus/ E. gallinarum (n=24)*	21.8
	Other (n=2)	2		Other (n=0)	0
BAF Final Effluent (n=51)	*E. faecium (n=19)*	37.3	CAS Final Effluent (n=35)	*E. faecium (n=17)*	48.6
	E. faecalis (n=26)	51		*E. faecalis (n=8)*	22.9
	E. casseliflavus/ E. gallinarum (n=5)	9.8		*E. casseliflavus/ E. gallinarum (n=9)*	25.7
	Other (n=1)	2		Other (n=1)	2.9

Table 1: Summary of the number of isolates analyzed in this study, origin of each isolate and the relative proportion of each species isolated from each sample types.

P203 - AMR 01 - USE OF ANTIBIOTICS IN HUMAN AND ANIMALS, IN FOOD AND AGRICULTURE AND THE ENVIRONMENTAL IMPACT

The role of benchmarking the use of antimicrobials at the farm level: the Dutch experience

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BACKGROUND:

The Netherlands Veterinary Institute monitors and analyses antimicrobial usage data from more than 40 000 livestock production farms in the Netherlands. In 2011, benchmarking was introduced by defining benchmark values. These values reflected levels below which use was considered acceptable, and levels above which attention should be given to the usage patterns or action was required to reduce the usage pattern immediately. In addition, 3rd and 4th generation cephalosporins and fluoroquinolones got a benchmark value of 0, which meant in practice that they could only be used after sensitivity testing and when alternatives were considered not adequate or effective. The effect of benchmarking over the years is being evaluated and changes in usage patterns are explored and described.

METHODS:

Annuals antimicrobial usage data were available for all registered farms in the Netherlands. Antimicrobial usage was described by calculating Defined Daily Dosage Animal (DDDA) for different species and age categories at the farm level. Changes is DDDA were calculated for different species (broilers, cattle, pig, veal calves) across farms over the observation period from 2011-2016 (data will be extended to 2017 for the presentation). The change in shape of the distribution of DDDA across farms was compared over the years for each of the species. Mixed models were used to explore variation between and within farms over the years.

RESULTS:

Use of antimicrobials greatly reduced between 2009 and 2016 with 38% (veal calves) to 72% (broilers).

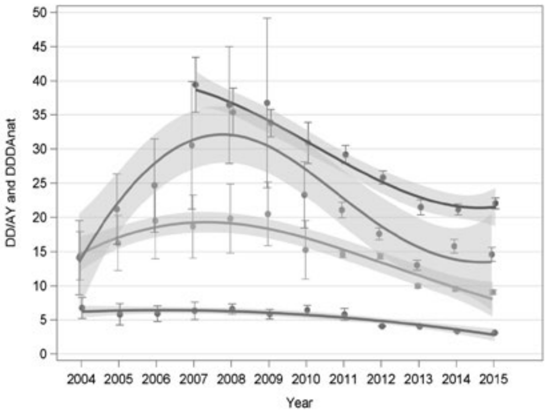

Figure. Long-term developments in antibiotic use based on a spline with 95% CI point estimates for each year. Data before 2010 based on samples, 2010 and following full coverage. Blue: veal farming sector; orange: broiler farming sector; light green: pig farming sector; dark green: dairy cattle farming sector.

The distribution of DDDA across all farms changed from very broad distributions with extremely high DDDA values (from 100-250 DDDA/year, depending on the animal species) to narrower distributions skewed to the right with long tails but clearly less extreme high values. Generally, exceedance of signaling and action level benchmark values reduced over the years. Introduction of benchmark values for use of 3rd and 4th generation cephalosporins and fluoroquinolones led to a change from regular to only incidential use. Systematic high usage over two or three consecutive years involved fewer farms in more recent years.

CONCLUSIONS:

Introduction of benchmarking supported farmers and veterinarians with antimicrobial reduction strategies and resulted in considerable reductions in antimicrobials.

GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION

P204 - AMR 02 - GENOMIC EPIDEMIOLOGY / EVOLUTION OF AMR TRANSMISSION

AMR Markers in Non-Pathogenic Bacteria Isolated From Food

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Canadian Food Inspection Agency -

BACKGROUND: Antimicrobial resistance (AMR) is recognized as a serious threat to global health and food security. The resistance to antimicrobials can develop due to the potential misuse or overuse of antibiotics. Due to the movement of genetic elements between microorganisms, resistance can spread between bacteria.

In Canada, the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) tests for specific pathogenic and commensal bacteria for AMR along the food chain (farm to retail). Limited non-pathogenic bacteria that harbor AMR genes would be detected through these testing efforts. This means that an important transmission pathway of AMR
through the food chain is currently under characterized in non-pathogenic bacteria. There is a need to close this gap in our surveillance to help ensure that AMR is not being transmitted through these sources.

METHODS: This project uses the Canadian Food Inspection Agency's (CFIA) food monitoring programs that sample and test eggs, meat, fish, dairy, fresh fruits, fresh vegetables, raw ground beef, raw beeftrim, and processed foods for pathogenic and non-pathogenic bacteria. These sampling programs target both domestic and imported foods. The samples are processed as per CFIA's standard analytical methodologies for regulatory testing; however, an aliquot of sample homogenate was taken for direct plating on non-selective media in addition to the regulatory
tests.

A subset of these plates, approximately 800 to 900, will have one or two colonies isolated for DNA extraction. These colonies are subjected to whole genome sequencing and analysed for identity and for the presence of AMR markers through various bioinformatics pipelines. Furthermore, all isolates are frozen for future characterization.

RESULTS:
Through the use of bioinformatics databases, several AMR markers have been identified including resistance to those antibiotics that are of critical importance to human health based on a preliminary data set of 70 isolates. Some bacteria exhibit multidrug resistance while others have single marker for resistance to a class of antibiotics such as beta-lactams. The project is ongoing and additional results are expected through to the end of 2018.

CONCLUSIONS: The current limited sequencing data shows the potential presence of AMR genetic markers in the microbiome of food in Canada. This type of study can be expanded to be used to benchmark and to identify trends as actions are taken to combat the spread of AMR and increase the prudent use of antibiotics. We plan to test the validity of the genetic data using phenotypic AMR testing in follow-up studies and identify strains that are truly resistant to the antibiotics they may carry genes for.

PREVALENCE AND SURVEILLANCE OF RESISTANCE

P205 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

Epidemiology of Multidrug-resistance Tuberculosis in Bhutan: understanding the increasing burden, quality care and associated risk factors

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BACKGROUND: Multidrug-resistant Tuberculosis (MDR-TB) is a major growing public health problem that threatens progress made in TB care and control worldwide, including Bhutan. This is the first ever study attempted in Bhutan to describe MDR-TB epidemiology in terms of spatial, temporal and person distribution. We also assessed disease burden, associated risk factors and the level of quality care to understand areas of improvement in patient treatment and care.

METHODS: We conducted a descriptive study of the MDR-TB cohort patients by recruiting all the cases (census) undergoing treatment (March-June 2016). 83 MDR-TB patients were interviewed face-to-face using a standard questionnaire by the investigators. Findings are expressed in percentages, rates, ratios, relative risks and presented in graphs, charts, tables and figures.

RESULTS: Since 2005 to 2016, 306 cases of MDR-TB were reported in Bhutan. Females were affected 66.27% (55/83) about two times more than males 33.73% (28/83). The southern districts of Samdrupjongkhar (16.87%) and Samtse (14.46%) had the highest MDR-TB cases followed by Trashigang (12.05%) in the east. Gidakom, JDW National Referral and Phuntsholing hospitals had catered to maximum number of these patients. Dependents (50.62%), no education (24.10%), students (29.63%) and housewives (25.93%), joint family (68.29%) and married (56.63%) were predominantly affected by MDR-TB. Poor ventilation at home (RR=1.5, 95% CI: 1.16-2.20) was the only associated relative risk among others. Majority (91.57%) has suffered from pulmonary TB prior to MDR-TB with alarmingly high rate of treatment failure (65.85%).

CONCLUSION: In the last one decade, MDR-TB is increasingly reported in Bhutan. We recommend both targeted programmatic intervention and individualized patient treatment and care program for a successful treatment outcomes. Future, inter-disciplinary study design using the One Health approach to investigate pathogen behavior in a different milieu of humans and animals in response to anti-tubercular agent may contribute to currently pressing issue of antimicrobial resistance.

P206 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

Zoonotic E. coli as a Potential Driver of Antimicrobial Resistance in Pastoralist Communities of rural Western Uganda

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INTRODUCTION: Careless use of antimicrobials in animal husbandry is thought to be a driver for selection and transfer of drug resistant pathogens from animals to humans trough the food chain. We aimed at determining the potential of Zoonotic *E. coli* as route of transfer of antimicrobial resistance from animals to humans.

METHODOLOGY: A cross-sectional study was done and *E. coli* isolate from the guts of 180 individuals from pastoralist communities of Kasese Western, Uganda. Culture and isolation was done by conventional methods, while serotyping and PCR were done to characterize the isolates. *E. coli* isolates were screened for resistance mechanisms including Extended Spectrum β-lactamase, Carbapenemase and AmpC production using disc diffusion based methods.

RESULTS: The prevalence of Enterohemorrhagic *E.coli* (EHEC) was 16% (28/180). Of the EHEC, 94% (26/28) belonged to phylogroup B1, 3% (1/28) to A, and 3% (1/28) to B2. The most prevalent virulence gene in the EHEC was *Stx1* (100%, 28/28) followed by *Stx2e* (94%, 26/28), while none was *Stx2* positive. The highest resistance was observed in Cotrimoxazole (89%, 25/28), Tetracycline (71%,20/28), Ampicillin (65%,18/28) and Nitrofurantoin (28%,8/28). At least 17%, (5/28) of the EHEC were ESBL positive, of these only one was a Carbapenemase producer.

CONCLUSION: The study suggests that zoonotic bacteria are potential drivers of antimicrobial resistance to humans in this community. We recommend a one health approach to establish drivers for the spread MDR bacteria in pastoralist communities.

P207 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

Multidrug Resistance among Escherichia coli and Klebsiella Pneumoniae Isolated from Out-Patients in Pastoralist Communities of Kasese District, Uganda

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BACKGROUND: Antimicrobial resistance is a global public health crisis that requires urgent attention. We aimed at establishing the magnitude of antimicrobial resistance among *Escherichia coli* and *Klebsiella pneumoniae* isolated from out patients from pastoralist communities of rural Western Uganda and the prevalence of zoonotic E. coli.

METHODS: This was a descriptive cross-sectional study carried out among pastoralists that live in and around the Queen Elizabeth Protected Area (QEPA) ecosystem. Blood and stool samples were collated from individuals from pastoralist communities who presented to the health facilities with fever and/diarrhea without malaria and delivered to the microbiology laboratory of Makerere University College of Health Sciences for culture and sensitivity.

RESULTS: A total of 300 participants presenting with fever and/or diarrhea without malaria were recruited into the study, with 204 yielding organisms of interest from stool. Out of 204 stool samples that were positive, 181 (89%) grew *E. coli*, 22 (11 %) were *K. pneumoniae* whereas 1 (1%) were *K. oxytoca* and 5 (2.4%) were Shigella spp. Generally, high antibiotic resistance patterns were detected among *E. coli* and *K. pneumoniae* isolates. High resistance against cotrimoxazole 74%, ampicillin 67%, cefazolin 41%, amoxicillin/clavulanate 37 %, tetracycline 35% and ciprofloxacin 31 % was noted among the *E.coli* whereas among *K. pneumoniae* ampicillin 100%, cotrimoxazole 68%, nitrofurantoin 64%, tetracycline 50%, amoxicillin/clavulanate 46%, cefazolin 46% and cefuroxime were the most resisted. Multidrug resistance was noted in 57% and 82% of the *E. coli* and *K. pneumoniae* respectively. None of the *K. pneumoniae* was resistant to erteapenem and only 0.6% of the *E. coli* was resistant to erteapenem. Also, low resistance to imipenem was noted. Isolates producing extended spectrum β-lactamase-(ESBL) comprised 12 and 23 % of *E. coli* and *K. pneumoniae* respectively. The prevalence of Enterohemorrhagic E.coli (EHEC) was 16% (28/180). These EHEC isolates belonged to phylogroups; B1 (94%, 26/28), B2 (3%, 1/28) and A (3%, 1/28). The most prevalent virulence gene was *Stx1* (100%, 28/28) followed by *Stx2e* (94%, 26/28); none of the isolates was *Stx2* positive

CONCLUSION: We demonstrated high antimicrobial resistance, including multidrug resistance, among *E. coli* and *K. pneumoniae* isolates from the participants. We recommend a One Health approach to establish the sources and drivers of this problem to inform public health.

P208 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

Spread of Escherichia coli carrying blaCTX-M and blaCMY-2 in Senegalese chicken farms through clones and plasmids

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Emergence of enterobacteria producing extended-spectrum beta-lactamases (ESBL/AmpC) due to antimicrobial use in animal production is a great concern for both human and animal medicine. In Senegal, antimicrobial use is not regulated and poultry production units can be located in inhabited houses. In this context, the risk that pathogenic or antimicrobial-resistant *Escherichia coli* may be transmitted from chickens to humans cannot be excluded. We hypothesized that *E. coli* from chicken sources in Senegal are ESBL/AmpC-producers and thus, dangerous for humans. The aim of this study was determine whether healthy chicken farms are a source of ESBL/AmpC-producing *E. coli*.

E. coli were isolated from 32 farms in the region of Dakar, Senegal. Generic isolates and specific isolates selected on medium enriched with ceftriaxone 1mg/L were characterized with respect to antimicrobial resistance (AMR), clonal relationship, and plasmids carrying ESBL/AmpC-genes.
Presumptive ESBL/AmpC-isolates were recovered from 17 (53.1%) farms. In the generic collection, 1.5% of isolates were classified presumptive ESBL-producers and 5.7% as presumptive AmpC-producers; prevalence in the enriched collection was 17.0% and 43.1%, respectively. Presumptive ESBL/AmpC-isolates from the specific collection (63 isolates originating from the 17 farms) and randomly selected from the generic collection (128 isolates originating from the 32 farms) were examined by PCR for bla_{CTX-M} gene encoding resistance to ceftriaxone and bla_{CMY-2} gene encoding resistance to ceftiofur. These isolates were also examined for the four phylogenetic groups A, B1, B2 and D. bla_{CTX-M}/bla_{CMY-2}-producing isolates were identified in 10 farms. In the generic collection, 1.0% and 3.0% of isolates, all belonging to phylogroupe A, were positive for bla_{CTX-M} and bla_{CMY-2}, respectively. In the specific collection, 35% and 19% were bla_{CMY-2} and bla_{CTX-M} respectively. Bla_{CMY-2}-producing isolates were distributed among the four phylogroups whereas bla_{CTX-M}-isolates belonged to phylogenetic group A, B1 or D. The bla_{CTX-M}/bla_{CMY-2} isolates showed high genetic diversity as demonstrated by Pulsed-Field Gel Electrophoresis (PFGE). The bla_{CTX-M} gene was carried by incompatibility plasmid incI1 or incK, whereas bla_{CMY-2} was located on incI1, incK or incB/O; these plasmids also co-transfer resistance against other antimicrobials such as tetracycline or sulfamides.

Although the use of third generation cephalosporins in poultry production in Senegal has not been reported, our results demonstrated that *E. coli* recovered from healthy chickens may produce ESBL/AmpC. The presence of these ESBL/AmpC-producers may be due to co-resistance following the extensive use of other antimicrobials the resistance genes for which co-exist on the same resistance plasmids as cephalosporins. This study underlines the importance of monitoring *E. coli* in healthy chickens in Senegal and of regulating antimicrobial use in poultry. Moreover, it is important to raise awareness of poultry farmers in regard to biosecurity measures, as these *E. coli* carrying ESBL/AmpC genes could be transmitted to humans via contaminated carcasses or through direct contact.

P209 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

Antimicrobial Resistance of Shigatoxigenic E.coli to commonly prescribed antibiotics in diarrhoea patients from Kitale County Referral Hospital, Kenya

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INTRODUCTION: Shiga toxin-producing *Escherichia coli* (STEC) are among the *E.coli* pathotypes which cause food-borne illnesses ranging from mild diarrhea to more severe condition that may progress to hemorrhagic colitis (HC) and hemolytic uremic syndrome (HUS) that can be fatal. STEC is transmitted through various multiple reservoirs including; food products; healthy and diarrhoeagenic cattle; camels, small ruminants. Antimicrobial resistance (AMR) its evolution and mechanisms of resistant genes and molecular epidemiology of foodborne pathogens is a global threat that necessitated immediate attention for proper management of patients with diarrheal diseases. The burden of STEC and its AMR in patients with diarrheal illness in Kitale County Referral Hospital Trans-Nzoia County which is a cross-border site adjacent to Uganda has not been established. Therefore this study sought to determine the prevalence of STEC, its virulence genes associated with disease and antimicrobial resistance among patients seeking treatment for diarrheal illness at Kitale County Referral Hospital

METHODS: Stool samples from patients seeking treatment for diarrheal illness and had consented to participate in the study were collected cultured for enteric bacteria and identified using conventional biochemical methods. Suspect *E.coli* isolates were further characterized using Conventional multiplex PCR. Antimicrobial susceptibility testing was done for all pathogenic isolates using Kirby Bauer disc diffusion method.

RESULTS: A total of 295 participants were enrolled; median age 120 months (IQR: 36-312). Children aged <5years were the majority of whom 54% (160) were females. Antimicrobial resistance to commonly prescribed antibiotics were observed for all pathogenic isolates. Trimethoprim / Sulphurmethoxazole) was the drug which exhibited the highest resistance at (94%, 95% CI 70 to 99%).

CONCLUSION AND RECOMMENDATION: Highest resistance to commonly prescribed antibiotics as well as emerging resistance to new drugs is a subject of concern not only in Kenya but globally. This may require change of policy in increased AMR surveillance as well as management of patients with diarrhoeal diseases.

P210 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

Near-equilibrium prevalence of antimicrobial resistance in an informal urban community

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BACKGROUND: Efforts to preserve the utility of existing antibiotics have focused predominantly on improving prescription guidelines and compliance to reduce unnecessary antibiotic use. Nevertheless, the relationship between antibiotic use and antibiotic resistance remains poorly understood where socio-economic and environmental determinants impact both use and resistance. We examined this relationship in Kibera, a slum in Nairobi, characterized by high population density, high burden of disease and poor sanitation.

METHODS: Two-hundred households were enrolled in a 5-month longitudinal study with one adult (≥18 years) and one child (≤5 years) participating per household. Fortnightly interviews (n=1,516) were conducted and 6,674 samples collected (2,341 stool, 2,843 hand swabs and 1,490 water samples). *E. coli* (n=34,042) were isolated and tested for susceptibility to nine antibiotics.

RESULTS: Eighty percent of *E. coli* were resistant to ≥3 antibiotic classes. Stool isolates were resistant to trimethoprim (mean: 81%), sulfamethoxazole (80%), ampicillin (68%), streptomycin (60%) and tetracycline (55%). Multivariable linear mixed-effects models identified children eating soil (0·27-0·80 $\log_{10}$) and informal hand-washing stations shared by multiple households (β = 0·22 to 0·51 $\log_{10}$) as the key risk-factors for increased individual and household antimicrobial resistance (AMR) levels. Rainy conditions were associated with reduced AMR load (1·19 to 3·26 log).

CONCLUSIONS: In this community 87% of respondents reported using an antibiotic in the past 12 months and yet antibiotic use, *per se*, provides little explanatory power for the prevalence of antibiotic resistance. This suggests that this community is experiencing a “saturated” level of AMR where incremental changes in antibiotic use have little measurable effect on AMR prevalence. We surmise that poor sanitation drives disease burden, antibiotic demand, and subsequent transmission of resistant bacteria within and between households. In such communities, sanitation, hygiene and disease transmission will be the limiting factors for controlling AMR.

P211 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

A comparison of antibiotic resistance trends of E. coli among bovine and human isolates in Washington State.

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Antibiotic resistant genes and bacteria pass readily between animals, humans, and their shared environments, and therefore represent a classic zoonotic disease threat. There is a need for improved stewardship of antibiotics in human medicine, animal medicine, as well as agriculture and aquaculture. Despite this, our traditional methods of tracking the emergence of antibiotic resistant strains of bacteria have been fragmented between human and animal sectors, and generally non-existent in the environmental realm. We report on the efforts of the Washington State One Health Steering Committee to assemble an ongoing database of antibiotic resistance in humans, animals and the environment. The Washington Integrated Surveillance for Antibiotic Resistance (WISAR) database includes human and animal data from hospitals, laboratories, and clinics in Washington State, as well as human and animal data from the US National Antibiotic Resistance Monitoring System. Looking at multiple year trend data from the WISAR database creates an opportunity for a collaborative effort to discuss the next stages for local efforts in antimicrobial stewardship across human, animal and environmental sectors. We used the WISAR database to study the patterns of resistance to five classes of antibiotic of *E. coli* from bovine and human isolates in Washington State from 2002 – 2017. This comparative analysis allows for an understanding of: 1) what conclusions can be made between data sets? 2) how valid are these conclusions 3) what data is needed to make this type of comparison in resistance across sectors?

P212 - AMR 04 - PREVALENCE AND SURVEILLANCE OF RESISTANCE

Antimicrobial resistance prevalence in Harbour seal (Phoca vitulina) pups and weaners stranded in the Netherlands and antibiotic treatment effect in their gut microbiome during rehabilitation

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BACKGROUND: The Sealcentre Pieterburen rehabilitates seals stranded in the Netherlands. Every year orphan harbour seal (*Phoca vitulina*) pups and sick weaners with critical health status are admitted. Seals can be considered as sentinels for the marine environment they live in.

In this study, firstly, we aimed to investigate the prevalence of antimicrobial resistance (AMR) in bacteria isolated from the rectum of harbor seals admitted at the Sealcentre. Secondly, we analyzed the gut microbiome composition of the seals before and during rehabilitation to investigate the influence of antibiotic (AB) therapy and the rehabilitation process on their commensal gut flora.

METHODS: During summer 2015 and winter 2015-2016, rectal swabs were collected from 200 harbour seals at admission, during rehabilitation and before release. If the seal received AB treatment, samples were taken before and after treatment. The swabs collected at admission were streaked onto different selective media to screen for clinically relevant AMR bacteria. Whole genome sequencing (WGS) was performed on positive cultures to determine the antibiotic resistance genes and for comparison with human isolates by a core genome multi-locus sequence typing (cgMLST) approach.

From all swabs collected, DNA was isolated and amplicon sequencing was performed using Illumina Miseq 2x300bp on 450 bp of the 16S V3–V4 region. Reads were analyzed using Mothur. α- and β-diversity were determined using Shannon and Unifrac, respectively. Statistical analyses were performed using Wilcoxon signed rank tests. *Random Forest* analysis was performed using the Bioconductor *randomForest* package 4.6-10.

RESULTS: At admission, ESBL-producing *E. coli* were isolated from 4 harbour seal pups (2%) and MRSA was isolated from 1 weaner (0.5 %). The ESBL- producing E. coli carried CTX-M-15 and CTX-M-27 and differed only in 40 of 2764 analyzed genes from human *E. coli* isolates. MRSA belonged to clonal complex 9 and had spa-type t1430, it did not contain the virulence factor PVL. Furthermore, 16S amplicon analysis indicates that AB treatment has a severe but short-lived effect on the seal microbiome which returns to normal within approximately four days.

CONCLUSION: We observed a low prevalence of ESBL-producing *E. coli* and MRSA in stranded harbor seal pups and weaners. The isolated bacterial strains are closely related to those found in humans and livestock and contain the same resistance genes. The effect of AB treatment on the seal gut microbiome is extensive, however it is transient. Analysis of the complete resistome will be undertaken using shotgun metagenomics and qPCR.

NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS

P213 - AMR 05 - NOVEL STRATEGIES FOR AMR INTERVENTIONS / PREPAREDNESS

The impact of national policies & programmes targeting antimicrobial resistance: A systematic review

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BACKGROUND: The spread of antimicrobial resistance (AMR) is recognized as an imminent threat to global health that requires concerted national and international action. As countries begin implementation of their national action plans to curb antimicrobial resistance, assessing the impact of different strategies is crucial. However, evidence for the impact of different policy options is limited, making it difficult to prioritise interventions and assess their sustainability and effectiveness. In this systematic review, we assess evidence for the impact of national policies and programmes targeting antimicrobial resistance.

METHODS: We searched seven databases up to May 2017 and examined reference lists of retrieved articles. We included articles that described the outcomes national policy or programme implementations with specific aims to target antimicrobial resistance in human health. Two reviewers independently screened and extracted data from articles, and these studies were appraised for quality and risk of bias. We classified interventions into those aimed at curbing excessive antibiotic use and those aimed at reducing antibiotic demand. Where possible, we standardized antibiotic use outcomes into defined daily doses (DDD).

RESULTS: We identified 32 relevant studies from upper middle- or high-income. Policies to curb the unnecessary supply of antibiotics included the institution of stricter antibiotic guidelines (10 studies), the restriction of antibiotic usage without prescriptions (16 studies), the restriction on antibiotics available for reimbursement (3 studies) and the separation of drug prescribing from dispensing (2 studies). To reduce antibiotic demand, interventions included funding more research (1 study), infection prevention and control measures (5 studies), and educational campaigns for healthcare professionals (4 studies) and the general public (11 studies). Additionally, 12 studies described country-wide surveillance systems that were used to evaluate the progress of interventions in terms of resistance rates, illnesses, and overall antibiotic usage. A wide range of outcome measures were used to evaluate the effectiveness of interventions, including defined daily doses (DDD), antibiotic prescription rates, patient antibiotic consumption proportions, and volume and value of antibiotic sales. Of 11 studies that provided DDD measurements, 10 studies showed a decrease in overall DDDs of antibiotic consumption with an average decrease of 24.3% post intervention.

CONCLUSION: We found evidence of impact from a modest number of national AMR policies and programmes. However, evidence from low- and middle-income countries is lacking, and wide variation in outcome measures hinders comparison of experiences across countries. To monitor implementation of national action plans and global progress in curbing AMR, guidance on harmonized surveillance systems and standardized outcomes will be critical for identifying and prioritizing effective interventions. Future research should focus on the formation of subsequent, sustainable initiatives in addressing the problem of AMR in lower and lower-middle income countries.

ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS

P214 - AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS

Barriers to, and enablers of, implementing antimicrobial stewardship programs in veterinary practices.

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BACKGROUND: Antimicrobial stewardship programs are yet to be widely implemented in veterinary practice and medical programs are unlikely to be directly applicable to veterinary settings.
Objective
To gain an in-depth understanding of the factors that influence effective antimicrobial stewardship in veterinary practices in Australia.

METHODS: A concurrent explanatory mixed methods design was used. The quantitative phase of the study comprised an online questionnaire to assess veterinarians' attitudes to antimicrobial resistance and antimicrobial use in animals, and the extent to which antimicrobial stewardship is currently implemented (knowingly or unknowingly). The qualitative phase used semi-structured interviews to gain an understanding of the barriers to and enablers of antimicrobial stewardship in veterinary practices. Data were collected and entered into NVivo v.11, openly coded and analysed according to mixed methods data analysis principles.

RESULTS: Veterinary practices rarely had antimicrobial prescribing policies. The key barriers were a lack of antimicrobial stewardship governance structures, client expectations and competition between practices, the cost of microbiological testing, and a lack of access to education, training and antimicrobial stewardship resources. The enablers were concern for the role of veterinary antimicrobial use in development of antimicrobial resistance in humans, a sense of pride in the service provided, and preparedness to change prescribing practices.

CONCLUSION: This study can guide the development and establishment of antimicrobial stewardship programs in veterinary practices, by defining the major issues that influence the prescribing behaviour of veterinarians.

P215 - AMR 06 - ALTERNATIVE APPROACHES TO TACKLING RESISTANT INFECTIONS

Non-antibiotic approaches at drying-off for treating and preventing intramammary Infections in dairy cows: a systematic review and meta-analysis.

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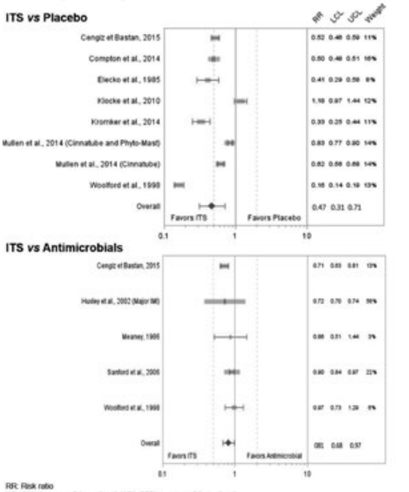
BACKGROUND: Quarters of all cows are generally infused with an antibiotic (AB) at dry off which is a very important cause of AB use in dairy production. The objective of this study was to identify therapies other than ABs for treatment and prevention of intramammary infections (IMI) at dry off in dairy cows.

METHODS: Eligible studies were selected by 3 reviewers from CAB Abstract, Pubmed and Web of Science from January 1970 to May 2016. Risks of bias were evaluated using the Cochrane Collaboration's tool. Outcomes of interest were IMI prevalence post-calving, IMI incidence rate over the dry period and clinical mastitis incidence at beginning of following lactation. A meta-analysis was conducted when possible.

RESULTS: A total of 2,816 manuscripts were first identified to finally reach 27 manuscripts corresponding to 32 studies. Except for 4 experimental bacterial challenges, all study were clinical trials on natural IMI. The non-AB treatments evaluated were: internal teat sealant (ITS) (bismuth subnitrate 65%, n=13; bismuth subnitrate 65% and chlorhexidine, n=2; botanical ITS, n=2; experimental ITS, n=1), biologics (n=3), vitamin E with or without selenium (n=3), homeopathy (n=1), botanics (n=1), and different others products (n=3). On the 27 manuscripts, only 2 (7.5%) had no source of bias. Selective outcome reporting (44%) and inadequate generation of randomised sequence (26%) were the most frequent bias noted.
We were able to perform a meta-analysis for the evaluation of ITS administration without ABs. Results showed a significant benefit on IMI incidence (Figure 1), but not on IMI prevalence at calving or clinical mastitis incidence when compared to a placebo treatment. Compared to an AB treatment, a lower IMI incidence was again observed for bismuth subnitrate-based ITS (Figure 1). Botanical ITS, however, were significantly less effective than antimicrobials. Only 4 studies compared the effectiveness of ITS without AB to AB treatment on IMI prevalence at calving. Important heterogeneity between studies was, however, observed and a meta-analysis was therefore not performed. Since only 2 studies compared CM incidence between ITS and antibiotic treatment, no meta-analysis was performed for that effect either. No other alternative approaches demonstrated consistent effectiveness for the treatment and prevention of IMI at dry off.

Figure 1. Impact of Internal Teat Sealant (ITS) on dry period IMI incidence when compared to a placebo or an antibiotic treatment.



RR: Risk ratio
LCL 95% lower confidence level; UCL: 95% upper confidence level

CONCLUSIONS: ITS use without AB administration appeared as an interesting alternative to blanket dry cow therapy for the prevention of IMI at dry off. No alternative therapies had consistently demonstrated effectiveness for the treatment of IMI at dry off in clinical trials.

SCIENCE POLICY INTERFACE

SPI

P216 - SCIENCE POLICY INTERFACE

Fostering One Health research and education in Pakistan

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The Global Health Security Agenda (GHSA) is a partnership of about 50 nations launched to advance a “world [that is] safe and secure from global health threats posed by infectious diseases” (https://www.ghsagenda.org/about). To succeed in this mission GHSA “depends upon collaboration among the health, security, environment and agriculture sectors” locally, regionally and internationally. Moreover, according to a recent commentary, scientific collaborations beyond a country's own borders are increasing for countries at the forefront of research [Nature 2017 (550):32, October 5, 2017].

To nurture these connections among countries and build inter-disciplinary cadres of skilled and trained individuals, the US National Academy of Sciences, Engineering and Medicine (NASEM), in partnership with the Pakistan Academy of Sciences, is supporting a fellowship program to build capacity of early to mid-career Pakistani scientists whose research projects follow the One-Health approach. This program, adaptable to different country settings, creates a model for fostering enduring international and national research collaborations and cooperation in preparedness and response to zoonotic diseases and other shared environmental health risks.

For the pilot phase of this 12-month fellowship, five Pakistani researchers mentored by international One-Health experts, participated in 2 NAS-sponsored scientific symposia, and spent up to 5 months at host research laboratories in Kenya, Thailand and Singapore. The fellows were integrated in the hosts’ research teams and participated in on-going studies, while also receiving training relevant to their own Pakistan-relevant One Health research. All fellows’ findings were presented at international research conferences.

The unique elements of this program are designed to assist a country in which human, animal, and environmental health scientists and professionals work together in advance of a public health threat, to become resilient in the face of an actual outbreak. The program also highlights the mutual benefits and ease for researchers from diverse countries to work toward a common goal. Through this project, Pakistani scientists are exposed to examples of One Health efforts in other countries, but also have the opportunity to establish collaborations across the academic, research and policy/governmental sectors of their own country to counter naturally occurring, accidental or man-made health threats. This presentation will focus on the strengths of the fellowship, describe the goals, success stories and outcomes of the pilot and the current second rounds, and provide a concept for global inter-connectedness through education and training in One-Health pillars.

CONCLUSIONS: In Pakistan, the One-Health Research Fellowships a) enabled capacity building opportunities through the initiation of One-Health curricular initiatives in institutions of higher education; b) fostered the emergence of a One-Health research network; and c) produced widespread anticipation for the 2nd round of applications (open now).

P217 - SCIENCE POLICY INTERFACE

Incorporating Sand Dynamics into Beach Water Quality Science and Policy

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Dr. Ricardo Jorge, Portugal

Water quality monitoring and science at nearshore/beach areas is largely limited to microbial/bacterial contamination of water. However, recent research has found that the sand at beaches can be more contaminated than the water itself. Given that most beachgoers spend more time in the sand than the water, they are potentially exposing themselves to higher concentrations of microbes than previously thought.

Dynamic exchange of microbes between water and sand has been observed in marine and freshwater systems across the world. Microbes are often deposited from the water, into the sand at the beach during intermediate wave events. When wave energy is high enough, these accumulated microbes can be washed out of the sand and back into the water in a process deemed resuspension. This is in addition to the microbes in the sand that come from humans, wildlife, and waste materials. Within the sand, microbes can move around via spaces between sand grains and may also form biofilms attached to sand grains.

When beachgoers play in the sand or the water, they expose themselves to the bacteria contained in it. This may lead to compromised health conditions, including respiratory, gastroenteric, and ear infections. By focusing monitoring and research efforts on water quality at the expense of sand conditions, we may be unintentionally putting beachgoers in danger with our existing protocols.

The good news is, researchers are beginning to understand how sand and water interact to form the microbial community at beaches. Collaborative field and numerical modeling studies have characterized the impacts of sand on beach health, and there has been a shift in scientific focus to the entire beach system, or “beachscape”, rather than just the water. The political realm is also beginning to get involved, with discussions of including sand impacts and dynamics in recreational water guidelines currently underway.

The issue of recreational water quality is the epitome of a one health challenge – microbial communities are impacted by human and environmental factors, wildlife usage, and even meteorological conditions. These microbial communities can then feed back to the human system by infecting beachgoers from both the water and the sand. In terms of human health, the paramount goal is to minimize the chance of infection in beachgoers, which will lead to increased visitation at beaches as well as social and economic gains for nearshore areas via tourism. By broadening research foci to the entire beachscape, we can better understand what may make the system dangerous to beachgoers, and we can improve beach management for human, economic, and environmental health.

A recurring issue in natural resources is the disconnect between research and policy outcomes. The prospective inclusion of sand as a source of microbial contamination at beaches in future beach health guidelines is a concerted and encouraging attempt to bridge that disconnect. Though policy discussions are ongoing, there is promise that research into sand-water interactions will influence human health, environmental health, and policy outcomes as they relate to marine and nearshore systems.

CONCLUSIONS: Beach monitoring for health only involves water quality sampling, but research indicates that sand is a contamination source to beaches, possibly causing illness in beachgoers.

This is an opportunity to connect environmental research to health policy outcomes at beaches, and sand may indeed be included in future beach/human health policy.

P218 - SCIENCE POLICY INTERFACE

Attacking the Hydra: Antimicrobial Stewardship in Primary Health Care

Jason R. Vanstone

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Antimicrobial stewardship is now a required organizational practice for every acute care centre in Canada. However, it is important to note that the majority of antibiotics are prescribed not in acute care centres, but in primary health care clinics. Thus, in addition to providing education and interventions in the acute care setting, the Regina Area Antimicrobial Stewardship Program has made it a priority to engage with community-based prescribers in their primary care clinics. We have undertaken an audit and feedback program to inform community prescribers of their practice and promote behavioural changes towards optimal antimicrobial use. While prescribers are actively engaged in the process, there are barriers within the health system structure and policy which make progress difficult (e.g., fee-for-service health care, contract employees, limited support for antimicrobial stewardship programs). Addressing these barriers may lead to more productive interventions in primary health care.

CONCLUSIONS: Antimicrobial stewardship programs need to engage with primary health care clinics if we are ever to truly begin tackling the problem of antimicrobial resistance. Policy changes may help to enhance this engagement.

P219 - SCIENCE POLICY INTERFACE

Tuberculosis among captive elephants and mahouts: Implications to health policy

Dr. David Abraham

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BACKGROUND: Humans are the only reservoir hosts of Mycobacterium tuberculosis, a unique multi-host pathogen, which is known to cause spillover infection in many other mammalian species. We gathered empirical data and examined the epidemiology and public health significance of tuberculosis transmission from mahouts to cohabiting captive Asian elephants (Elephas maximus). With the help of evidence based results, we intend to formulate specific policy guidelines to help mitigate the risk of cross-species infection.

METHODS: During the different components and phases of the collaborative research project, which spanned almost a decade, we screened nearly a thousand captive elephants and almost an equal number of mahouts in the southern Indian states of Kerala, Karnataka and Tamil Nadu. By isolating M. tuberculosis by sputum culture and also by undertaking a one-to-one questionnaire survey, we identified nearly 30 mahouts with either current or history of active pulmonary tuberculosis. By isolating M. tuberculosis from lung nodules obtained during post-mortem examinations, we identified nearly 50 elephants with active disease. A systematic identification and testing of the traceable mahout and elephant contacts of each of the diseased mahout and elephant were also done.

RESULTS: Two of the mahouts with pulmonary tuberculosis were identified to have cared for two of the diseased elephants. Almost all of the diseased mahouts had familial history of tuberculosis. In many such cases, the families' history superseded the mahouts' contact with diseased elephants. Cutaneous tuberculosis was identified in two mahouts associated with two diseased elephants. Prevalence of positive tuberculin skin test results were almost the same in mahouts who attended diseased elephants and in those who did not. Very few live elephants in contact with the diseased elephants tested positive for tuberculosis infection.

CONCLUSION: Almost all of the mahouts come from underprivileged families and along with their elephants follow nomadic lifestyles. Hence, locating the subjects for contact tracing and follow-up testing were difficult. Under the tropical climatic conditions in southern India, while the evidence is strong to suggest intra-species transmission among mahouts and inter-species transmission between mahouts and elephants in both directions, it appears weak to suggest intra-species transmission among elephants. Further study and analyses are needed to better understand the risks of anthropozoonosis and zooanthroponosis. Preliminary insights seem to suggest that the risk of cross-species pulmonary tuberculosis infection to a captive elephant from a diseased mahout outweighs the risks to a mahout or another elephant, from a diseased elephant.

Formulating as well as implementing policy guidelines for the prevention and control of cross-species tuberculosis transmission, in the existing cultural and religious contexts of captive elephant management systems in southern India is a significant challenge.

P220 - SCIENCE POLICY INTERFACE

Epidemic clones of community-acquired methicillin-resistant Staphylococcus aureus in slaughter pigs, Cuba

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The WHO, FAO and OIE, promote a global action plan under the One Health approach for a rapid containment antimicrobial resistance (AMR). In 2011 in Cuba, human infections caused by MRSA were predominantly associated with the USA300 clone, and the Latin American variant (USA300-LV) was not identified. Although these lineages are generally not associated with nasal carriage in pigs, which usually harbor the livestock-associated MRSA (LA-MRSA) lineage ST398, the presence of human epidemic clones in pigs cannot be excluded. Following the One Health recommendation, the epidemiological MRSA situation in slaughter pigs from three Cuban provinces was investigated. From May to July 2015, 22 of 285 nasal swabs taken at one central slaughterhouse from fattening pigs raised in the provinces of Mayabeque (n=67), Matanzas (n=90) and Cienfuegos (n=128) were found to carry MRSA (prevalence 7.7%). Isolates were obtained after two-step of enrichment and selective cultivation in Müller-Hinton (MH) broth. MRSA were identified by matrix-assisted laser desorption/ionisation time of-flight mass spectrometry (MALDI-TOF/MS) and by detection of the methicillin resistance gene mecA by PCR. The minimum inhibitory concentrations (MICs) were determined by microdilution in MH broth using the Sensititre susceptibility plate EUST. Antibiotic resistance and virulence genes were detected using microarrays (Alere). Isolates were characterized using pulsed field gel electrophoresis (PFGE), multilocus sequence typing (MLST), Staphylococcus protein A (spa) typing, SCCmec typing, ACME typing and mec-associated direct repeat unit (dru) typing. PFGE revealed three groups of MRSA. The MRSA isolates gathering into PFGE cluster I shared the same PFGE profile as the USA300 epidemic clone as well as the same genetic properties (ST8 except one ST173, SCCmec IVa, dru dt9g, PVL+, ACME I +). The isolates belonged to spa type t024 also contained the sek and seq enterotoxin genes. The strains were resistant to β-lactams (mecA, blaZ), macrolides [msrA, mph(C)], aminoglycosides [aph(3')-III] and fluoroquinolones [GrlA(S80-Y) and GyrA(S84-L)]. MRSA clones of PFGE cluster II were characteristic to USA300-LV (ST8, spa t008, SCCmec IVc, dru dt7j, PVL+ and ACME–). These clones were resistant only to β-lactam antibiotics (mecA, blaZ). The third PFGE cluster (cluster III) contained clones belonging to ST5, spa t010, SCCmec IVc, dru dt10a. They were all PVL– and ACME–, contained the enterotoxin genes sea(N315), seb, sel, selm, seln, selo, egc and selu, and were resistant to β-lactams (mecA, blaZ) as well as to the aminoglycosides gentamicin and kanamycin [aac(6'-Ie-aph(2')-Ia]. These findings demonstrate that pigs from Cuba carry MRSA belonging to the same clonal lineages than those found in humans causing infection in the community. It is therefore of major veterinary and public health importance to take specific preventive measures and
antimicrobial stewardship in both human and animal settings to limit the spread of MRSA.

CONCLUSIONS: The pig husbandry of Cuba act as an unsuspected reservoir of epidemic MRSA strains including those of the USA300 lineage. Even if USA300-LV has not so far been reported in humans in Cuba, its introduction into pig husbandry is not likely to be directly associated with trade of animals, since no pigs are known to have been imported from Latin America. The presence of successful epidemic clones may represent a major public health importance to take adequate measures to limit the spread of the life-threatening bacteria both in the pig and human populations.

P221 - SCIENCE POLICY INTERFACE

One Health -Easy to Say & Hard to Do – Using Progressive Project Management and Social Innovation to Implement One Health

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One Health is an approach to understanding and improving human, animal and ecosystem health at a time when all are at rapidly increasing risk. One Health practitioners work with challenges that are complex; characterised by unpredictability, urgency and conflict over values (whose opinion counts). However, practitioners also generally implement projects; time-bound initiatives that involve a measurable, desired change in response to prescribed actions. This creates at least two significant barriers to successful implementation.

First, although One Health projects secure impressive technical content expertise, they often do not include concomitant process expertise in the form of an appropriately skilled, experienced and resourced project management team. Second, even when a project management team is in place, there is a fundamental mismatch between the fluid, unpredictable nature of One Health challenges and implementation environments and the incremental and often rigid structure of conventional project management and reporting, which is the principle tool used to address them.

The first barrier can be addressed by engaging a project team that is familiar and experienced with both conventional project management and more progressive project management approaches that are applicable in conditions of partial information and ambiguity. The second can be addressed by drawing on tools and skills from disciplines that explicitly innovate in complex systems, such as systemic design and social innovation.

We maintain that a deliberate merging of progressive and mission-oriented project management with systemic design in an adequately resourced project implementation team can significantly reduce these barriers and dramatically increase the probability of success of complex One Health initiatives. In this view, the project team deliberately and progressively manages and designs both process and content as the nature of the initiative and challenge emerges throughout implementation. The team must have adequate expertise in the disciplinary details of One Health and the technical requirements of conventional project management. It must also have expertise with skills and techniques from progressive project management and systemic design, such as design and systems thinking, emotional intelligence, facilitated collaboration, conflict resolution, developmental evaluation and cross-sectoral communication.

We illustrate these points using our recent experience implementing the successfully, concluded 3-year Caribbean-wide project, One Health One Caribbean One Love. It was implemented by the University of the West Indies and its project partners. Project results included sustained, cross sectoral collaboration to achieve a regional One Health framework, 29 Caribbean professionals trained in Leadership and One Health, a regional One Health network across 12 Caribbean countries, 12 national small-scale One Health projects that demonstrated the value of a One Health approach and 500 One Health “First Responders”, trained in recognition and response to priority animal and zoonotic diseases.

In practice, the project involved equal parts developing and delivering technical content, facilitating collaboration and collective action, and managing project details such as logistics, monitoring, evaluation and reporting.

CONCLUSIONS: Implementing One Health involves steps that may seem simple, but that in practice speak to other disciplines such as systemic design and project management. Fully embracing these perspectives can significantly increase the likelihood of success. One Health is a collaborative approach. It is important to collaborate with the right people.

P222 - SCIENCE POLICY INTERFACE

AFTOSA: From Foot-and-Mouth Disease to One Health

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This is to share the evolution of the Pan American Foot-and-Mouth Disease Center (known as PANAFTOSA) since its establishment 66 years ago. Over time, from a Foot-and-Mouth Disease (FMD) scientific center PANAFTOSA incorporated the other Veterinary Public Health (VPH) functions of the Pan American Health Organization (PAHO) and is now providing technical cooperation with the One Health approach.

PANAFTOSA was established in 1951 in Rio de Janeiro, Brazil as part of the PAHO's VPH Program though an agreement with the Ministry of Agriculture, Livestock and Food Supply of Brazil. Beside PANAFTOSA, the PAHO's VPH Program included the Pan American Institute for Food Protection and Zoonoses, Buenos Aires, Argentina, along with several VPH technical advisors based on the PAHO Country' Offices. Early in the 90's, PAHO started consolidating its VPH technical cooperation portfolio at PANAFTOSA. Today, the Center's technical cooperation includes: (a) emerging and neglected zoonotic diseases; (b) food safety, food borne diseases and Antimicrobial Resistance in the food of animal origin value chain; and (c) Hemispheric Program for the Eradication of for Foot-and-mouth Disease (PHEFA).

PANAFTOSA is unique within the United Nations and Inter-American Systems for fostering health-agriculture alliances to promote public health and wellbeing. Its technical cooperation, positioned on health promotion and diseases prevention, requires interacting with a wide range of stakeholders, including public health, animal health and production partners, from government administrations, academia and scientific institutions, philanthropic, non-governmental and other international and regional organizations, and the private sector. Delivering such technical cooperation, with the contribution of different disciplines and programs, requires leadership and coordination to implement system approaches, such as "farm-to-fork" for food safety and "One Health" for risks analysis at the human-animal-environment interface.

PANAFTOSA technical cooperation drives changes in countries policies through a threefold approach by: i) defining regional strategies and technical guidelines; ii) mobilizing high level support through advisory mechanisms , , , , which also ensure the ongoing strategic alignment of its technical cooperation with the needs of the countries, and iii) delivering technical cooperation to countries, including providing training of staff; mobilizing resources (such as scientific expertise, financial, political resources); disseminating information; promoting research; developing norms, plans and policies; along with providing direct technical consultancy.

Besides the above-mentioned, PANAFTOSA also integrates important laboratory capacities. It manages a OIE/FAO Reference Laboratory (BSL4, OIE standard), along with the production capacities for developing and providing diagnostic tools for disease surveillance to the countries; which inform on disease risks along with financially sustain some of PANAFTOSA´s technical cooperation.

While it is difficult to quantify the effectiveness of PANAFTOSA technical cooperation, its regional work on FMD eradication and canine rabies elimination provide a proxy to such measurement. On such regional experiences the Global FMD Control Strategy and the Global Framework to Eliminate Rabies are based. The very same approaches are now used to address new health challenges such as Antimicrobial Resistance in the food of animal origin value chain.

CONCLUSIONS: PANAFTOSA has endured because of the continuing alignment of its technical cooperation with the needs of the countries and technical mandates of the Pan American Health Organization, and the sustained support of the Ministry of Agriculture, Livestock and Food Supply of Brazil, which firmly recognizes PANAFTOSA as a fully independent international entity hosted by Brazil. PANAFTOSA is on a journey to consolidate its regional influence on One Health; revamping its strategic approach, portfolio, workforce and culture – while preserving its historical heritage of working with the animal health and production, and public health sectors, exploring new partnerships such as wildlife and environment, for the promotion of public health and welfare of the Americas.

P223 - SCIENCE POLICY INTERFACE

Establishment of a sustainable emerging disease surveillance program at a human/wildlife interface.

Robert J. Fischer

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The majority of emerging infectious disease threats are zoonotic, often have a high mortality rate when transmitted to the human population and occur in areas lacking the technical expertise to identify these threats. To truly be effective in communicating the importance of the potential threat posed by these emerging pathogens the communities at these interfaces must be involved. It is particularly important to educate and enable the people that inhabit the human/wildlife interface to actively participate in methods used to mitigate these threats. The U.S. National Institutes of Health, Laboratory of Virology has several projects, particularly in Africa, involving the training of host country nationals at many levels. One such project is a collaboration between the Virus Ecology Unit and the Wildlife Conservation Society (WCS) in the Republic of Congo (RoC) to sample animal carcasses for the presence of high consequence pathogens.

There have been seven documented spillover events of Ebola virus (Zaire) (EBOV) in the RoC since 1976. EBOV can cause fatal disease in several wildlife species including gorillas, chimpanzees, duikers and forest hogs. In five of the seven outbreaks in RoC a gorilla or chimpanzee carcass was implicated as the potential spill-over source. A putty nosed monkey (Cercopithecus nictitans) was suspected in one of the remaining outbreaks and the other was an unknown source. Traditionally an animal found dead in good condition might be harvested for food. Rapid diagnosis of carcass samples is critical to determine what the final disposition of the carcass should be. An infected carcass will need to be buried and or burned to prevent contact with people and scavenging by forest animals.

WCS hires many local people in various capacities throughout the RoC. They employ local trackers and researchers as well as support anti-poaching efforts. As these professionals work in the forest they occasionally encounter carcasses where the cause of death may not be readily evident. We have teamed up with WCS to devise a carcass sampling SOP and trained select teams to safely collect samples for further laboratory testing to determine if the cause of death was Ebola virus disease (EVD). The SOP and training includes procedures for proper donning and doffing of PPE, safe techniques for collecting samples, and effective methods of sample inactivation.

We are currently expanding the protocol to include point of encounter (PoE) analysis of the collected sample. qRT-PCR was the primary diagnostic tool used in diagnostic laboratories during the West African outbreak. Recent technological developments have resulted in nucleic acid extraction protocols and qRT-PCR instruments that can readily be deployed to the field. We have coupled our laboratory verified inactivation protocol with an easy to use commercial field extraction protocol to produce RNA for use in a qRT-PCR. We are assessing the sensitivity and ease of use field of portable qRT-PCR instruments.

Training local teams to identify and eliminate these potential outbreak sources allows a rapid response to a potentially deadly threat. Additionally, their knowledge and perspectives regarding deadly diseases will disseminate throughout the village and region.

CONCLUSIONS: Training local teams to identify and eliminate these potential outbreak sources allows a rapid response to a potentially deadly threat. Additionally, their knowledge and perspectives regarding deadly diseases will disseminate throughout the village and region.

P224 - SCIENCE POLICY INTERFACE

A Case Study on One Health Approach in Addressing Antimicrobial Resistance in Cambodia

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BACKGROUND: Cambodia is witnessing the raising threat of Antimicrobial Resistance (AMR), brought about by the overuse and misuse of antimicrobials in human and agriculture (including terrestrial/aquatic animals and plants), with serious negative impacts on food safety/security and environment. As a middle lower-income country with a great burden of infectious disease and limited resources, Cambodia is significantly affected by AMR. This issue cannot be solved by one sector alone, but require a true One Health (OH) approach at all levels, primarily at national level.

In Cambodia, some of the recent achievements to address AMR include the National Policy to Combat Antimicrobial Resistance (2014) and National Strategy to Combat Antimicrobial Resistance (2015-2017). Between 2017 and 2018, a Multi-Sectoral Action Plan (MSAP) on AMR is developed to guide Cambodia's continuing work on AMR by engaging the Ministry of Health (MOH), Ministry of Agriculture Forestry and Fisheries (MAFF) and Ministry of Environment (MOE).

A case study was conducted alongside the process of the MSAP development to describe challenges, successes and lessons learned during the application of a multi-sectoral approach in Cambodia, specifically in relation to the efforts made towards the development of One Health mechanisms driving the development and implementation of the MSAP on AMR.

METHODOLOGY: Identified key stakeholders for the development of the case study were those involved in the process leading the drafting of the MSAP on AMR. Government institutions and partners of relevant sectors (human/animal health and agriculture) were identified and targeted to respond to a written questionnaire followed by a face-to-face meeting to validate the answers and capture perceptions of respondents.

RESULTS : Preliminary results indicate that a majority of the respondents perceive that the country is applying, to some extent, a multi-sectoral OH approach to define the MSAP on AMR. An important contributing factor was the establishment of a Technical Working Group (TWG) on AMR that includes technical staff from the key Ministries and development partners.

IDENTIFIED CHALLENGES: The respondents identified lack of communication and coordination between stakeholders to be one of the major challenges with different Ministries being primarily focused on different mandates. Additionally, inadequate resources and capacity including human resource and facilities to support the implementation of identified joint activities was also highlighted, as well as resources to generate evidence in support of control measures. Gaps in legislation and law enforcement was another mentioned challenge. Finally, public awareness was recognized to still be limited.

SOLUTIONS: to improve multi-sectoral collaboration, the country needs to identify a leading agency and gain support from external partners in bringing stakeholders together and facilitate the coordination mechanism. Furthermore, is the MSAP considered as an important tool to define responsibilities and mandates, and clarify the route of communication, collaboration and coordination across sectors. Enhancing high-level participation in the TWG on AMR is essential in gaining political and financial support.

Cambodia is adopting a progressive approach in addressing AMR. The MSAP is a fundamental step, allowing the definition of roles and responsibilities of key national stakeholders and effective implementation of action. Nonetheless, full acceptance and recognition from the general public will ease the effort driven to effectively implement control measures.

P225 - SCIENCE POLICY INTERFACE

Exploring agropastoral health seeking behaviour and attitudes towards animal vaccination in Arri, Northern Tanzania.

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AIM: The proposed presentation will detail emergent results from an 8 month PhD fieldwork period in Babati district of Northern Tanzania. The aim of the research was to explore how those living in an agropastoral community engage in health seeking behaviours in response to febrile illness with a view to identifying barriers to effective treatment and where possible health interventions can be made.

BACKGROUND: The burden of endemic zoonoses disproportionately affects those in underprivileged communities and has significant impacts on rural livelihoods. The problem is further exacerbated by lack of appropriate health care and entrenched structural barriers, inhibiting individuals from pursuing effective remedial actions in response to animal and human febrile illnesses (many of which are zoonotic). My research is concerned with how agropastoralists in Northern Tanzania engage with and negotiate different health seeking strategies in order to pursue optimal health outcomes for themselves, their families and their livestock. Included in this is an evaluation of knowledge, attitudes and acceptance of animal vaccination as a means to safeguarding animal and human wellbeing.

METHODS: All fieldwork was undertaken in the Babati district of Northern Tanzania, over a period of 8 months. A mixed method approach was adopted, whereby I conducted 100 health seeking behaviour surveys across two sub-villages, asking people to detail all the remedial actions they took in response to their most recent episode of febrile illness. Subsequently, I conducted further interviews with 50 of these respondents to assess their knowledge, attitudes and acceptance of animal vaccination. Throughout the fieldwork period I also conducted 20 key informant interviews with animal and human health professionals at various health facilities, as well as focus groups to attain general information relating to the main challenges and issues people face in accessing appropriate health care. This mixed method approach allowed me to triangulate my results whereby I could asses concurrence or divergence of responses.

RESULTS: Emerging results reveal the long-term and reiterative nature in which people experience and contend with animal and human febrile illness. Barriers at health service providers impede ability to pursue effective remedial actions that can keep illness at bay. As such, people are often left to negotiate between lesser effective remedies at the community level until the illness returns. This lack of agency also extends to vaccination, where people acknowledge its importance but are not in the habit of administering it to their animals themselves, believing it to be the responsibility of the government to do so. However, willingness to use vaccination is high if certain conditions are met such as; knowledge shared beforehand and administered by ‘experts’ i.e. official vaccinators.

CONCLUSIONS: Wider systemic and structural barriers in the Tanzanian health system constrain individual agency when pursuing remedial actions in response to febrile illness. As such, there is opportunity for animal vaccination to play an important role in safeguarding animal and human wellbeing. However, attention to local attitudes and perceptions towards vaccination must be taken into consideration for any future interventions to be effective.

LATE BREAKERS

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P226 - LATE BREAKERS

Influenza at a wildlife - livestock interface: surveillance and transmission dynamics in traditional Mexican swine farms

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Characterization of wildlife-livestock interface represents a key element to understand epidemiological dynamics. Almost 77% of livestock pathogens infect multiple host species, including wildlife. In addition, wild birds in proximity to farms, backyard productive systems with low biosecurity measures and close contact among several animal species are considered risk factors for the emergence and spread of influenza A virus (IAV). In Mexico, backyard farms represent an important percentage of the national animal production and play an essential role in the rural household economy. Nevertheless, some gaps remain in our knowledge of infectious disease at the swine-wildlife interface. We hypothesized, first, that the spatial and temporal convergence of backyard pig farms and the migration of waterfowl enhance the diversification of influenza A viruses. Secondly, pig trade is an important driver for the spread of influenza among farms. Therefore, two approaches were performed to examine these hyphotheses. The primary aim of this study was to evaluate the molecular prevalence of influenza virus in backyard pigs from the wildlife-livestock interface. Backyard farms near to Lerma swamp, a natural protected area and bird conservation zone with legal waterfowl hunting, were selected as a relevant surveillance area for influenza virus. During the 2016-2017 winter season, 175 pigs from seven backyard farms located within a radius of 5 km from the marsh boundaries were sampled and tested by highly sensitive qRT-PCR. Although all farms were characterized by lack of vaccination, low farm biosecurity, close contact between poultry and swine, animal sharing among farms, close proximity to other farms and short distance to roads, all pig nasal swabs tested negative for molecular detection of IAV. The secondary aim of this study was to analyze the impact of swine trade network in the transmission of influenza among backyard farms using a susceptible-infected-recovered (SIR) modeling framework. Three different scenarios of connectivity among farms (low, medium and high) were simulated and compared. Our results suggest that half of the pig population would be infected within five days in the high connectivity scenario and the number of infected farms would be approximately 15-fold higher compared to the low connected one. The consequence of these connectivity modifications may directly influence both time and duration of influenza virus transmission. In conclusion, a better understanding on the dynamics of influenza viruses among wild birds, poultry and pigs are crucial for tailoring optimal surveillance and control strategies. Moreover, the complexity of the system involving human, animal and environment interactions enhances the necessity to further evaluate the interface interdisciplinarity with a ‘One Health’ approach to explain a holistic phenomenon that affects both animal and human health.

P227 - LATE BREAKERS

Influenza A virus surveillance based on a socio-ecosystem approach in a wild bird–backyard poultry interface in Mexico

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The dynamics of influenza A virus infection is determined generally by viral features, ecological factors, and anthropogenic influences. A socio-ecosystem approach is determinant in the study of avian influenza virus dynamics. Our study site is characterized by social factors such as rural production with limited financial resources, low biosecurity systems, hunting activities, and informal animal trade; and environmental aspects such as natural habitats of migratory waterfowl in contact with backyard poultry farms, where the virus could be transmitted. This study aims to identify the circulation of avian influenza viruses in migratory waterfowl and domestic poultry that coexist in a wildlife-domestic interface, characterized by no animal health surveillance. We hypothesized that in a wetland located within the Pacific Flyway, several factors such as temporal and spatial coincidence of migratory waterfowl with backyard poultry near the swamp, as well as human factors, facilitate avian influenza virus interspecies transmission. The study was performed in a Protected Natural Area of Mexico where regulated duck hunting activities developed each winter season. Surrounding this region, there is a rural area with several backyard poultry systems that hosts different animal species, and where unregulated trade of domestic animals is practiced. Sampling was conducted on the 2016-2017 winter season. Real-Time RT-PCR assays were performed to 598 cloacal swab samples corresponding to 10 wild duck species, and 103 oral and cloacal swab samples from five domestic avian species. Biosecurity surveys were applied to farm poultry owners. Geographical Information Systems were applied to characterize the region based on official data. Twenty-two samples were positive to influenza A virus, twenty-one of these correspond to three migratory ducks: *Anas crecca, Anas discors, Anas clypeata*, and one to a resident duck, *Anas platyrhynchos diazi*, a species not reported before as positive to avian influenza virus. All domestic bird samples were negative to PCR test. Virus isolation was performed to positive duck samples, nine of them were submitted to nucleic acid sequencing for virus typing for further analyses. The biosecurity surveys demonstrated low biosecurity and minimal health measures. Despite the virus detection in the wild birds, there was no evidence of interspecies transmission according to the molecular diagnosis. Additional substantial tools such as ecological, environmental and modelling analyses are been incorporated to better understand the dynamics of the interspecies transmission of avian influenza virus in Mexico focused on the wildlife-backyard poultry interface.

P228 - LATE BREAKERS

Mitigation and monitoring of risk of plague reemerging by development of new mapping method for natural FOCI

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Y. pestis is the causative agent of Plague that is categorized as a reemerging bacterial zoonotic disease. 46 strains of *Y. pestis* isolated from various vectors and reservoirs are maintained in the National Repository of Bacteria and Viruses (NRB&V) of National Center for Disease Control and Public Health (NCDC)/Lugar center in Georgia. The purpose of this study was to create new maps of natural foci sites of Plague in Georgia and other Countries of Caucasus region (sites for *Y. pestis* isolates) based on Historical and Geographical data maintained in the NRB&V data system. Using Spatial Analyst and Geostatistical Analyst Extensions as tools to monitor Plague vectors distribution will help to control Plague reemerging risks.

All procedures related to maintenance of Y. pestis culture collection are done in Biosafety Level3(BSL3) laboratory according to the relevant BS&S and requested ISO standards.

Y. pestis strains were isolated from the rodents and fleas collected in the different mountainous and plains/foothill foci of Georgia during 1968-1997. Beside Georgia several strains of *Y. pestis* were isolated from foci in Azerbaijan, Armenia, Kabardino Balkaria (Russia) and Dagestan (Russia) in 1975-1976 years.

The Geographical Information System (GIS) were used for mapping the sites of *Y. pestis* Isolates in the Caucasus Region. The ArcMap application of ArcGIS 10.3 was used for transferring existing data to UTM WGS1984 Coordinate System.

The passports (Data Sheets) of the corresponding strains were studied to analyze the historical and geographical data for sites of *Y. pestis* isolates throughout the Caucasus region.

Maps were created on the base of Spatial Data and Former Soviet Military maps (1: 200 000 and 1:500 000 scale).

The points created on the ArcMap completely matched with spatial distribution of *Y. pestis* vectors and reservoirs in Georgia, particularly: *M. arvalis, C. caspius, C. teres* in the mountainous focus and *M. cibicus (erythrourus)*, *X. conformis, C. leviceps* in the plains/foothill focus.

The results obtained in this study would be used for further investigation (using Spatial Analyst and Geostatistical Analyst Extensions) of spatial distribution of vectors and reservoirs of Especially Dangerous Pathogens (EDP)/ Infections that is very important to control and mitigate reemerging of Plagues and other EDPs over the Caucasus region.

P229 - LATE BREAKERS

Enabling better surveillance and early detection of zoonotic diseases through online clinical decision support

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BACKGROUND: Emerging zoonotic infectious diseases present a growing threat to the healthcare of populations around the world. Over the past fifteen years there has been an increasing number of zoonotic infectious diseases that constitute a major threat to global health. Healthcare professionals need resources that support surveillance and early detection, and that will help them to care for patients effectively. However traditional methods of education and support will struggle to build the capacity in healthcare and education that is needed, as they cannot be scaled up sufficiently to support all relevant healthcare professionals in a short period of time.

BMJ Best Practice is the online clinical decision support tool of the BMJ. It provides evidence based, continually updated and practical resources to help healthcare professionals improve the care that they provide. We conducted an analysis of infectious disease resources on BMJ Best Practice to evaluate if they were a feasible means of educating and supporting healthcare professionals in this clinical area.

METHODS: We conducted an analysis of usage by healthcare professionals of clinical decision support resources on BMJ Best Practice related to zoonotic infectious diseases.

We conducted a quantitative analysis of the data on the BMJ Best Practice topics that relate to infectious diseases: we analysed the clinical categories that were most used as well as the actual topics that were most used. We conducted an in-depth analysis of the sections of the resources that were most used (for example the sections on diagnosis or management), and the search terms that were most frequently entered into the site.

RESULTS: Analysis of the usage data revealed significant usage of clinical decision support resources on zoonotic infectious diseases by healthcare professionals. The most frequently used zoonotic diseases included those on Anthrax, Yersinia, Ebola and Tularaemia. Other infectious diseases such as pulmonary tuberculosis and hepatitis C were also well used. The most used sections within resources included those on diagnosis, differential diagnosis and investigations. The most frequently used search terms included those on zoonotic diseases, other general infectious diseases and non-infectious diseases.

CONCLUSIONS: Online clinical decision support resources are a feasible means of supporting and educating healthcare professionals in zoonotic infectious diseases. Healthcare professionals will use online resources on these diseases, and their pattern of use suggests that they are most interested in learning real-world skills in diagnosis that will help them in their day-to-day clinical practice.

P230 - LATE BREAKERS

A novel spotted fever group (SFG) Rickettsia species detected in Argasid ticks collected from toads in Brazil; cause for concern or simply symbiosis?

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BACKGROUND: The association between ticks and wildlife is a major area of modern acarological research, driven primarily by studies of the ecology of tick-borne pathogens of man and domestic animals. Before 2004, *Rickettsia rickettsii* (the eitological agent of Brazilian spotted fever; BSF), was the only tick-associated *Rickettsia* documented in Brazil. Currently, 10 tick-borne rickettsial agents, have been detected in that country using molecular surveillance techniques. The pathogenicity of most agents is undetermined, but serological data demonstrated the capacity for some to infect wild and domestic animals, raising the possibility for infection of humans. The value of conducting field studies, as a component of a One-Health strategy for the surveillance of emerging rickettsial diseases, should not be underestimated. The detection and characterization of novel rickettsial agents and their tick hosts, provides a platform to develop strategies for the prevention of outbreaks through the identification of potential interactions resulting from human encroachment into environments inhabited by ticks in consequence of activities including deforestation, uncontrolled urbanization and the practice of eco-tourism. Most surveys have focused on warm-blooded animals, with limited attention given to associations between ticks and cold-blooded species. Similarly, few studies have evaluated soft-bodied argasid ticks as sources of *Rickettsia*. This study reports the molecular characterization of a novel Rickettsia species detected in the soft tick *Ornothodoros faccinii*, parasitizing the toad *Thoropa miliaris* in south-eastern Brazil.

METHODS: Molecular analyses, PCR and sequencing of amplicons, were performed using the *16S rDNA, htrA, gltA, ompB, sca1* and *scaD* genes as markers. The Maximum likelihood method was used for phylogenetic inference. Monophyletic clades with 2% evolutionary divergence between clades were considered distinct groups of Rickettsial organisms.

RESULTS: The bacterium detected in this study pertains to the genus *Rickettsia* based on the nucleotide similarity values recorded for all the markers examined. However, it exhibited levels of similarity of less than 98% for all the targets, except *16S rDNA*, indicating that it is a new *Rickettsia* species. The novel Rickettsia formed a unique cluster, sandwiched between the “massiliae group” and the “helvetica group” for the markers (*htrA, gltA, sca1 and scaD*). The same close relationship was also verified by the low evolutionary divergence between the novel Rickettsia and the “massiliae” and “helvetica” groups.

CONCLUSION: The association between a soft tick and a SFG *Rickettsia* was unprecedented in Brazil, as was the presence of a SFG *Rickettsia* in ticks infesting a cold- blooded host. The pathogenicity of this rickettsial agent was not determined, thus it is not clear if our findings represent a cause for concern or simply symbiosis.

P231 - LATE BREAKERS

Effects of land use practices on mosquito community abundance and diversity in Eastern Ontario

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BACKGROUND: Widespread land use changes related to agricultural cropland expansion and urbanization in eastern Canada, have impacted the habitat, biodiversity and abundance of a vast array of organisms. Habitat change can affect breeding sites and reservoirs of disease vectors, such as mosquitos. Mosquitos can spread diseases such asWest Nile Virus and Eastern Equine Encephalitis. Thus the ecology of mosquitos can determine mosquito-borne disease epidemiology, but the factors shaping the variation of local vectors remain unknown. We suggest that landscape transformation due to human activities produces substantial impacts on vector-borne pathogen transmission, affecting the environmental conditions necessary for the survival of disease carrying mosquitoes. In the present work, we explore the mosquito abundance and biodiversity in association with land-use characteristics.

METHODS: Mosquitos were trapped at 56 sites along urban-agricultural gradients between May and August 2017 in eastern Ontario using CDC light traps and BG-Sentinel traps. Additional data from mosquito surveillance in the city of Ottawa are obtained to account for the urban gradient where mosquitos were trapped weekly from June to October 2017 using CDC light traps. Then we explore relationships between these variations and environmental determinants such as climatic variables (temperature and precipitation) and land use characteristics (land use type, forest density, water presence, vegetation type, etc.) using regression models.

RESULTS: The preliminary results obtained from the data of 2017 show that mosquito abundance and biodiversity vary across the agricultural-semi-urban-urban gradients and seasonally from spring through fall. Our results also show that urbanization and forest density are important to consider when studying mosquito abundance and biodiversity variation.

CONCLUSION: This study shows the relevance of considering the land use factor in modeling mosquito communities in response to climate change. The abundance and biodiversity of mosquito was related to land use characteristics. Urbanization can increase the risk of exposure to MBD by favoring loss of mosquito biodiversity and increasing the number of mosquito species like Culex pipiens-restuans that are primary MDB vectors in eastern North America.

P232 - LATE BREAKERS

Estimation of key Taenia solium transmission parameters across different epidemiological settings: implications for transmission modelling

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BACKGROUND: Taeniasis and cysticercosis caused by the cestode, *Taenia solium* is a zoonotic neglected tropical disease (NTD) responsible for a significant global public health and economic burden. The 2012 World Health Organization (WHO) roadmap on NTDs had proposed that, by 2015, a validated strategy should be available for the control and elimination of *T. solium* taeniasis/cysticercosis and that, by 2020, appropriate control and elimination interventions should be scaled up in selected countries. With 2020 on the horizon, mathematical models of *T. solium* transmission are urgently needed to inform and optimize the design of potential intervention strategies, but firstly need to parameterized for the human and porcine host in a variety of transmission settings in order to maximize the accuracy of subsequent projections.

METHODS: The aim of this research was to estimate the force of infection (indicative of the intensity of underlying transmission) in the porcine host from a variety of epidemiological and geographic settings. A systematic search of the literature was conducted to collate serological age-prevalence data from pigs based on porcine cysticercosis antibody diagnostics. Catalytic models were fitted within a Bayesian framework to the collated observed and adjusted prevalence data.

RESULTS: Force of infection with respect to exposure of pigs to *T. solium* eggs in the environment varied between settings (n = 8 datasets from South and Central America and n =2 datasets from South-East Asia) and by endemicity (seroprevalence of the entire dataset). Model selection further indicated that a model including seroreversion was preferential to the model only allowing for seroconversion in the porcine host.

CONCLUSIONS: We discuss the findings in the context of supporting further development of *T. solium* transmissions models that consider infection dynamics in both pig and human hosts. Ultimately, we show how this framework will facilitate bespoke location-specific model parameterizations which will be used to project more accurately the effectiveness of different intervention strategies, facilitating progress towards the WHO's control and elimination goals. We furthermore outline future work directed at estimating the rate at which pigs develop viable larval infections, and the obstacles associated with conducting this work including the limitations inherent to antigen-based survey data.

P233 - LATE BREAKERS

A comparison of goat breeds and routes of infection as a challenge model for Rift Valley Fever Virus

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BACKGROUD: Rift Valley Fever virus (RVFV) is a zoonotic mosquito-borne RNA virus of the *Phenuiviridae* family. Infection causes abortions in pregnant animals, high mortality in neonate animals and mild to severe symptoms in people. There is currently an ongoing effort to produce safe and efficacious veterinary vaccines against RVFV in livestock to protect against both primary infection in animals and zoonotic ourbreaks. To test the efficacy of these vaccines it is essential to have a reliable challenge model in relevant target species, such as sheep and goats.

METHODS: We have evaluated a variety of infection conditions including three breeds of goats (Boer, Nubian and LaMancha), three different routes of inoculation (intranasal, mosquito-primed subcutaneous and subcutaneous) using an infectious dose of 107 pfu/ml, two strains of RVFV (ZH-501 and CFIA-Kenya-UAP) and compared the effect of using virus stocks produced in either mammalian or mosquito cells.

RESULTS: Our results demonstrated that viremia occurred most consistently with the mosquito cell-derived virus, and reached the highest peak titer in the Nubian goats, particularly when infected intranasally (10^3-10^5 pfu/ml). All groups achieved a robust neutralizing antibody response with similar kinetics. The Nubian breed was unique in that we detected nasal and oral shedding of viral RNA (1.5x101 – 8x106 genome copies/swab) and infection of different tissues.

CONCLUSIONS: Overall, we have identified that the Nubian goat breed is useful for RVFV vaccine efficacy testing and have demonstrated that a needle-free intranasal inoculation method produces robust viremia in goats. Both of these factors could be utilized in future vaccine and challenge studies.

P234 - LATE BREAKERS

Human seroprevalence to eleven zoonotic pathogens in the US Arctic, Alaska

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BACKGROUND: Due to their close relationship with the environment, Alaskans, particularly Alaska Native people, are at risk for zoonotic diseases. One way to assess disease burden in a population is to determine the antibody seroprevalence using infectious agent-specific antigens. The objective of this study was to determine the seroprevalence of 11 zoonotic pathogens in people living in Alaska.

METHODS: In a 2007 avian influenza exposure study, we recruited persons with varying wild bird exposures. Using sera from this study, we tested for antibodies to *Brucella* spp., *Cryptospordium* spp., *Echinococcus* spp., *Giardia intestinalis*, *Toxoplasma gondii*, *Trichinella* spp., *Coxiella burnetii*, *Francisella tularensis*, California serogroup bunyaviruses, and Hepatitis E.

RESULTS: Eight hundred eighty-seven persons had sera tested including 454 subsistence bird hunters and family members, 160 sport bird hunters, 77 avian wildlife biologists, and 196 persons with no wild bird exposure. A subset (n=481) of sera was tested for California serogroup bunyaviruses. We detected antibodies to 10/11 pathogens. Age and gender adjusted seropositivity to Cryptosporidium spp. (29%), California serotype bunyaviruses (27%), and *G. intestinalis* (19%) were the most common; 63% (301/481) of sera had antibodies to at least one pathogen. Females were more likely to be seropositive to *Cryptosporidium* spp. (35.7% vs. 25.0%; p=0.01); males were more likely to be seropositive to *G. intestinalis* (21.8% vs. 15.5%; p=0.02). Alaska Native persons were more likely than non-Native persons to be seropositive to *C. burnetii* (11.7% vs. 3.8%; p=0.005) and less likely to be seropositive to Hepatitis E (0.4% vs. 4.1%; p=0.01). Seropositivity to *Cryptosporidium* spp., *C. burnetti*, Hepatitis E, and *E. granulosus* was associated with increasing age ($p \leq 0.01$ for all) as was seropositivity to ≥1 pathogen ($p<0.0001$).

CONCLUSION: Seropositivity to zoonotic pathogens is common among Alaskans with the highest seroprevalence to *Cryptosporidium* spp., California serogroup bunyaviruses, and *G. intestinalis*. This study provides a baseline for use in assessing seroprevalence changes over time.

P235 - LATE BREAKERS

Development of pre-pandemic influenza vaccine against highly pathogenic H5 strains

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The emergence of highly pathogenic avian influenza A viruses (HPAI) and their spillover into human population poses substantial economic burden and public health threats. Among HPAI, H5 viruses are of particular concern given their global spread and pandemic potential. In this study, we aimed at developing a novel pre-pandemic H5 influenza vaccine that is of potential importance in improving pandemic preparedness. The first North American HPAI H5N1 strain (A/Alberta/01/2014) was selected for recombinant H5 hemagglutinin (HA) design.

Recombinant H5 HA is expressed in both the mammalian and the bacterial system for comparison of H5 antigenicity from distinct expression hosts. Before examining the antigenicity of the two antigens in mice, we established the mouse diseases model for the HPAI H5N1 virus (A/Alberta/01/2014) with 3 different doses. Rapid body weight loss and severe mortality were observed in mice challenged with all 3 doses. Viral replication could be detected by $TCID_{50}$ in lung tissues of mice from all 3 doses group and in spleen tissues of mice from 10^5 PFU challenged group by $TCID_{50}$. Innate immune gene upregulation in mouse lung and brain tissues were quantified by qPCR. Immunogenicity and protective efficacy of H5 immunogens will later be determined by vaccination and challenge studies *in vivo*.

P236 - LATE BREAKERS

Diversity of mcr-4 harbouring Escherichia coli isolates from food and livestock in Germany

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BACKGROUND: Colistin is considered as highest priority critically important antibiotic commonly used only to treat severe human infections caused by multidrug- and/or carbapenem-resistant Gram-negative bacteria. In 2017, Carattoli et al. reported on the identification of a novel mobilizable colistin resistance-gene, *mcr-4*, in *Salmonella enterica* serovar Typhimurium (4,5,12:i:-). In this study, colistin-resistant *Escherichia coli* isolates from the German national monitoring programme for antimicrobial resistance in zoonotic agents from the food chain were investigated for the presence of *mcr-4* and further genetically characterized.

METHODS: Antimicrobial resistance in *E. coli* was determined as recommended by 2013/652/EU with the broth microdilution method according to CLSI guidelines and EUCAST epidemiological cut-off values. Isolates with an MIC ≥4 mg/l were subjected to PCR, S1-PFGE, Illumina MiSeq-sequencing and bioinformatical analyses were per formed to identify and characterize *mcr-4* harbouring isolates in detail. The transferability of *mcr-4* harbouring plasmids was investigated by *in vitro* filter mating experiments.

RESULTS: Up to now, in 13 *E. coli* isolates, recovered between 2010 and 2017. Sanger sequencing of PCR products revealed that two novel variants of the *mcr-4* gene (*mcr-4.2* and *mcr-4.3*) are prevalent in the German *E. coli* isolates. Genome determination and bioinformatical analysis revealed that the isolates differ in their MLST-, sero- and fim-type. However, all of them belong to a highly conserved ColE-plasmid prototype but the plasmids differ substantially in size and genetic composition. Further genetic features of the isolates and plasmids will be presented in detail.

CONCLUSION: Our findings indicate that *mcr-4* is after *mcr-1* the most prevalent *mcr*-like colistin resistance determinant in German *E. coli* isolates from food and livestock. Further information on the stability of *mcr-4* harbouring genetic elements, their transmission routes as well as their distribution in livestock, food products and humans are needed to assess the potential impact of this resistance determinant on public health.

P237 - LATE BREAKERS

Klebsiella plasmids and their relevance for the transfer of antimicrobial resistance determinants

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BACKGROUND: *Klebsiella* spp. are Gram-negative opportunistic pathogens prevalent on plants, in water and soil but also colonizing a wide range of livestock/wildlife animals. Klebsiellae were recognized as an important threat to global public health due to their high level of antimicrobial resistance, mainly associated with the presence of mobile genetic elements. In this study, resistance-plasmids of *Klebsiella* spp. isolates from livestock/wildlife were investigated to elucidate their potential for the spread of antimicrobial resistance.

METHODS: Antimicrobial susceptibility testing of *Klebsiella* spp. isolates was performed using broth microdilution following CLSI guidelines and EUCAST epidemiological cut-off values. S1-PFGE, whole genome sequencing and bioinformatics were performed to reveal the genetic basis of the observed resistance and the composition of the plasmids. The transferability of the plasmids was characterized by filter-mating studies.

RESULTS: Molecular analysis of two multidrug-resistant *Klebsiella pneumoniae* strains revealed that the individual isolates carry one and four plasmids, respectively. These can be efficiently transferred from *Klebsiella pneumoniae* to *E. coli* and other genera of the Enterobacteriaceae by filter-mating studies. The plasmids differ significantly in size and genomic composition. The genetic background of the isolates, the antimicrobial resistances and the transfer regions on the plasmids will be presented in detail.

CONCLUSION: Our study underlines the high mobility and transferability of resistance genes from animal derived *Klebsiella pneumoniae*, pointing at the potential transfer of these genes to human pathogens.

P238 - LATE BREAKERS

Identification of Aedes albopictus (Skuse, 1894) in Kinshasa/RDCongo.

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INTRODUCTION: *Aedes albopictus* is an invasive mosquito native to Asia and widely distributed in the temperate regions of Europe and tropical America and Africa during the last three decades. It transmits Zika, Dengue, Chikungunya, and Yellow Fever.

MATERIAL AND METHODS: An entomological survey aimed at identifying species of Aedes was conducted in the Kinshasa City-Province in the Democratic Republic in March 2017.
The larval survey was carried out at the end of the Yellow Fever epidemic in all 24 Communes of the city of Kinshasa. The larvae and nymphs harvested from Aedes were raised at the insectarium at the Medical Entomology Service of the National Institute of Biomedical Research (INRB) and the species identified morphologically with a stereoscopic binocular magnifying glass using a key dichotomous identification (Gillies and Coetzee, 1987).

RESULTS: Of 1299 identified Aedes, n = 917 (71%) were females and 337 (25.9% were males) *Aedes aegypti* was more abundant n = 973(74.9%) than *Aedes albopictus* n = 281(21.63%). Of the 281 Aedes albopictus identified in 10 communes out of the 24 surveyed, 208 (74%) were females and 73 (26%) were males.

CONCLUSION: Presence of *Aedes albopictus* in Kinshasa with occupation of nearly half of the Communes of the city-province of Kinshasa. *Aedes albopictus* has been predominant on *Aedes aegypti* since 2016 in some Communes of Kinshasa.

P239 - LATE BREAKERS

Operationalizing One Health approach in Uganda: challenges and opportunities

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BACKGROUND: About seventy five per cent of emerging infectious diseases are of animal origin. A One Health approach (OH) that integrates the health of humans, animals and the environment holds promise in mitigating these public health threats. Uganda is described as one of the 'hot spots' for emerging zoonotic disease outbreaks. This paper highlights the state of OH implementation, challenges faced and opportunities for operationalization of OH in Uganda.

METHODS: Review of the activities and milestones achieved in implementing OH. In addition, a review of challenges facing OH implementation from records review such as; JEE report, workforce assessment report and through sharing in OH meetings.

RESULTS: The country has embraced OH approach, though still infancy stages. In 2016, the four sectors (Ministry of Health (MOH), Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), Uganda Wild Life (UWA) and Ministry of Water and Environment (MWE) formed a collaboration -The National One Health Platform to foster OH implementation. The platform has a Framework, a legal document that legalizes their formal collaboration and guides their operations. A list of seven priority zoonotic diseases in the country was developed, for better focus and guide the use of limited resources optimally. A National OH Strategic Plan was launched recently and it lays emphasis on priority zoonotic disease and anti-microbial resistance. In addition, some efforts in academia through One Health Central and Eastern Uganda have tried to introduce OH in academia such as revising curriculum to incorporate OH competencies, OH Institute, a virtue insititte that orients students in OH competencies, involving students in disease outbreak investigation, etc. However, their challenges facing the operationalization of OH in the country. These include; i) lack of coordination, collaboration and information across the key sectors. Beyond meetings, there is no effort in doing joint planning and budgeting for OH activities. For example, at the moment response to outbreaks still happens in silos. iii) Lack of government by in and committing funds for OH. Most of what has been achieved in implementation OH is donor driven. iv) Lack of awareness about the approach and its rationale. Not much sensitization has been conducted from national to community level to garner support for OH. iii) Lack of OH policy to guide the budgeting for OH activities.

CONCLUSION: Moving forward, there in need to do the following; i) lobby for government commitment, ii) key sectors to move away from only meetings to joint planning, budgeting and develop joint programs and projects ii) conduct intense advocacy for one health across all levels, and iii) training the future OH workforce capable of collaborating and available them job opportunities. This will lead to better disease prevention, detection and response including influenza.

P240 - LATE BREAKERS

What is the cost of snakebite envenoming? A One Health approach to the economic impact assessment of snakebite based on primary data collection and multi-method analysis

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BACKGROUND: Evidence on the economic impact of diseases is needed to effectively allocate resources to mitigation activities. Quantitative information on economic impact can also be key in raising awareness and in shaping policy-making, particularly in the case of neglected tropical diseases such as snakebite envenoming.
A two-fold impact associated to One Health threats can occur, with impacts on the human health dimension further amplified by livestock losses and the resulting impact on livelihoods. Whilst there is a need for a One Health view of economic impact that can capture the multiple dimensions of impact in these cases, the majority of studies tend to focus on only one of these components, including for snakebite where a possible dual socio-economic impact has not been assessed to date. Importantly, studies that have addressed the dual disease impact of other One Health issues have highlighted important data gaps in the economic models and the need for a stronger data foundation. We present a study designed to assess the economic impact of snakebite in Nepal and Cameroon that incorporates One Health economics thinking and tools, from a primary data collection stage to a multi-method analysis phase.

METHODS: As part of a wider project (Snake-Byte), the economic impact of snakebite will be assessed using a One Health perspective, to capture the dual impact on health and livelihoods in affected communities for the first time. Primary data on human and animal mortality and morbidity, health care costs, livestock production, and market data will be provided by a national household survey, covering the human and the animal health dimensions jointly. This data will be used to populate the burden of disease assessment model, estimate health care costs, and assess losses in animal production and animal health expenditure and the associated livelihood impact. In addition, animal loss equivalents will be estimated and combined with human health burden using the zDALY metric recently proposed by Torgerson *et al*. (2018).

RESULTS: Results generated will allow a better understanding of the One Health economic impact of snakebite and fill evidence gaps on both the topic and on the application of economics to One Health challenges. Through discussion on the methodological design, including data collection and needs for the multi-method approach, lessons can be draw about how One Health approaches to economic impact assessments can be considered within study designs.

CONCLUSIONS: The study presented provides an example of how a One Health economics approach can be used at different stages of a study design to determine the dual impact at the human-animal interface of snakebite envenoming. Through the establishment of a solid foundation on primary data and interdisciplinarity, the value of economic evidence for policy-making on prevention and control can be improved.

P241 - LATE BREAKERS

Comparison of the Effectiveness of Colistin Monotherapy and Colistin-meropenem Combination Therapy in the Treatment of Nosocomial pneumonia Caused by Carbapenem resistant Acinetobacter baumannii

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BACKGROUND: *Acinetobacter baumannii* has emerged as an important nosocomial pathogen worldwide. In Thailand the incidence and mortality rate of carbapenem-resistant *A. baumannii* (CRAB) has been increased. This organism is the common pathogen that can caused HAP and VAP. CRAB tends to susceptible only colistin so that colistin would be the last line treatment of HAP or VAP caused by CRAB. The recent data from in-vitro studies found that colistin and meropenem combination therapy could exert synergistic effect. However, some in-vivo studies showed that no significant differences between colistin monotherapy and colistin–meropenem. In addition, the data in recent clinical studies to compare synergistic effect were still limited. The objective of this study is to determine the clinical outcome, microbiological response and mortality rate between colistin monotherapy and colistin-meropenem in HAP or VAP caused by CRAB.

PATIENTS AND METHODS: A retrospective analytical cohort study between 1 January 2013 to 31 August 2017 in Chiang Mai University Hospital was performed. A total of 193 patients who received colistin monotherapy and colistin-meropenem combination therapy were meeting the inclusion criteria of the study.

RESULTS: The good clinical outcome were not significantly different between patients who received colistin monotherapy and colistin-meropenem combination therapy (OR =1.27 [95% CI= 0.67-2.42], p= 0.456) and mortality rate at the end of

treatment were not significantly different between patients who received colistin monotherapy compare with colistin-meropenem (OR=1.29 [95% CI=0.62-2.65], p=0.497). At 28 days after the end of treatment showed that survival patients in colistin monotherapy are 1.15 times to patients who received colistin-meropenem (95% CI= 0.63-2.12, p=0.648). In addition, microbiological response defined as the eradication of pretreatment isolated pathogens in post-treatment cultures showed that patients who received colistin monotherapy can eradicate pathogen 1.21 times to colistin-meropenem (95% CI=0.63-2.29, p=0.560), although there were no significant difference in clinical outcome, mortality rate and microbiological response between colistin monotherapy and colistin-meropenem.

CONCLUSION: No significant difference in effectiveness of colistin monotherapy and colistin-meropenem in HAP or VAP caused by CRAB. So that colistin monotherapy was treatment option for the management of HAP or VAP caused by CRAB.

P242 - LATE BREAKERS

Effect of antibiotic de-escalation for treatment gram negative bacterial infections with extended-spectrum-β-lactamase-producing organism at Maharaj Nakorn Chiang Mai Hospital

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BACKGROUND: Antibiotic de-escalation for treatment gram negative bacterial infections after documented sensitivity reported is a potential strategy to reduced bacterial resistance in hospital. This study aim to evaluate effects of antibiotic de-escalation for treatment gram negative bacterial infections with extended-spectrum-β-lactamase (ESBL)-producing organism in patients admitted in Maharaj Nakorn Chiang Mai Hospital

METHODS: A retrospective chart review in patients reported gram negative bacterial infections with extended-spectrum-β-lactamase-producing (ESBL) organism between 1 January 2014-31 December 2014. Antibiotic de-escalation was define as change antibiotics from broad spectrum antibiotic to narrow spectrum antibiotic.

RESULTS: The patients with gram negative bacterial infections with ESBL 301 patients were evaluated; 153 were de-escalated and 148 were not de-escalated antibiotics. Means age of each group was 60.61 ± 21.69 and 65.41 ± 17.43years in de-escalate and not de-escalate group, respectively. The majority of patients in both group were admitted in inpatients ward (84.3% vs 86.5%; de-escalate group and not de-escalate group,respectively). Urinary tract infection was the most common in this study. In clinical outcome, patients in de-escalate group was clinical cure higher than not de-escalate group(64.7% vs 35.6%, $p<0.001$, respectively) as the microbiological outcome, patients in de-escalate group was microbiological successful higher than not de-escalate group (86.9% vs 50%, $p<0.00$, respectively). The survival at hospital discharge in de-escalate group also higher than not de-escalate group(92.8% vs 55.5%, $p<0.001$ respectively).
In consequence, recurrent rate at 30 days after discharge from hospital, duration of antibiotics use and lengh of hospitalization were not difference in both group.

CONCLUSIONS: Antibiotic de-escalation for treatment gram negative bacterial infections after documented sensitivity to narrow spectrum antibiotic was effective and safe in patients with gram negative bacterial infections with ESBL producing organism

P243 - LATE BREAKERS

A new global medical concept - one health - Romania

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BACKGROUND: The credits of the first approaches on the various components of One-Health, their gathering into one concept, and also their dissemination in the common practice, are assigned to the United States in 2003, especially with the contribution of two structures, respectively: One Health Commission and One-Health Initiative. In May 2014 all the original Romanian approaches and ideas related to these issues were reunited within the new global medical concept One Health. In this regard, the greatest achievement of Romania was the setting up in May 2015, of the One Health – New Medical Concept Association, as an independent and a legal structure. This paper aims to review the evolution of the One-Health concept in our country and the Romanian contributions in this field.

METHODS: The study followed the history of *One-Health* concept in our country and the joint implication of the institutions involved. There were highlighted the contributions of our country, as well as the implications of applying the concept in Romania.

RESULTS: *One-Health* concept had a long history in our country, with some precursor elements. The new global medical *One-Health* concept - the final outcome of the Romanian contributions to the *One Health* concept (2014), comprises of 6 areas of influences (all connected and intertwined), respectively: comparative medicine (human medicine and veterinary medicine); zoonosis; comparative oncology; environmental medicine; occupational medicine; food and nutrition medicine.

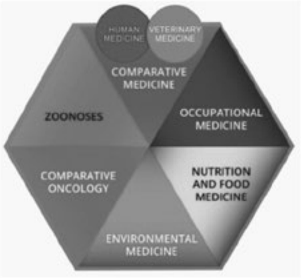

Fig. 1 - Logo: One-Health – New Medical Concept Organization

The 6 areas of influences are well-depicted in the logo of our national organization: One-Health – New Medical Concept Organization. This structure had major achievements in the field: organizing (within the Romanian Academy of Sciences) the National Center of Excellency One Health; organizing scientific meetings on this subject both at national level or abroad (in 2018 the Second European Interregional One Health Conference will be organized in Romania); participation of our specialists in different international conferences; editing a professional Journal: the International Journal of One Health – published in English, with 3 issues in 2017; organizing regional branches and units; signing of many agreements with research and development institutions for the implementation of the new concept – in Romania or abroad; drawing up and organizing training and curricula for postgraduate courses in Romania etc.

CONCLUSIONS: Following the study, can be concluded that Romania was significantly involved in *One Health* concept evolution and appliance and nevertheless it will have more to say in the future.

P244 - LATE BREAKERS

Sero-prevalence of Brucellosis and risk factors associated with past infection in the General Rural Population of Punjab, India

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BACKGROUND: Brucellosis is a neglected zoonotic disease of global health importance. Brucellosis is endemic in Punjab, India, a state that is home to over 7-million cattle and buffalo, many of which are kept in rural households as a long-standing intervention to support food security and rural incomes. Although there are documented cases of acute febrile brucellosis requiring hospital care, the burden of disease and main routes of transmission to humans are not known. Seroprevalence estimates of brucellosis in this region of rural Punjab, and an identification of the main modes of transmission in this population, can support new policies to effectively control this vaccine preventable zoonosis.

METHODS: Between December 2015 and July 2017, we conducted a cross-sectional survey in 60 villages in Ludhiana district, Punjab (India) using a multi-stage random sampling strategy with probability proportional to size. In each village 20 households were randomly selected, and from each household up to two eligible individuals were selected stratified by age and sex. Information regarding demographics and brucellosis risk factors were collected using structured questionnaires. A 4mL blood sample was also obtained from each participant, and sera were tested using the Rose Bengal Test (RBT) as well as by commercially available ELISA kits. Brucellosis seropositivity was defined as testing positive by RBT and/or IgG ELISA. The estimated population prevalence of brucellosis is presented standardized for differences in the age and sex distribution of the survey population and the 2011 Indian census for the state of Punjab. Associations between risk factors and human brucellosis seropositivity were evaluated using multivariable logistic regression models with village-level random effects to identify the main modes of transmission.

RESULTS: A total of 1927 individuals were contacted, of which 1801 individuals (93.5%) from 1084 households were successfully enrolled. The overall prevalence of brucellosis was 2.24% (95% CI: 1.61-3.11), with age-specific seroprevalence increasing in young adulthood, peaking in middle age and then declining slightly. Assisting with calving/abortions of large ruminants (aOR= 2.18, 95% CI: 0.96-4.95, p=0.07) and consumption of goat/sheep milk (aOR= 4.26, 95% CI: 1.33-13.6, p=0.03) were both independently associated with increased odds of infection, after controlling for age, sex, wealth and household head occupation. Consumption of large ruminant milk was not found to be statistically important.

CONCLUSIONS: Serological evidence for human brucellosis in rural Punjab indicates zoonotic risk from household livestock ownership. A novel finding in this study is the strong association of brucellosis with goat/sheep milk consumption. Strategies to reduce risk in this region should include exploring reasons for consumption of unpasteurized goat/sheep milk, targeted advice on boiling all milk before consumption, and importantly the use of protective equipment when assisting large ruminants with parturition. Cattle vaccination programmes in Punjab should also include household herds.

P245 - LATE BREAKERS

Proprotein convertase subtilisin/kexin type 9 interacts with hepatitis C virus NS5A protein and inhibits viral replication

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BACKGROUND: Proprotein convertase subtilisin/kexin type 9 (PCSK9) is a serine protease that plays an important role in lipid homeostasis through facilitating the degradation of low-density lipoprotein receptor (LDLR). Hepatitis C virus (HCV) is a positive-sense single-stranded RNA virus that can result in chronic hepatitis. No HCV vaccine has been developed and the current antiviral treatments have some limitations. Although PCSK9 has been shown to inhibit HCV replication, the underlying mechanism has not been thoroughly characterized.

METHODS: We measured the replication of an HCV genome with luciferase reporter by luciferase assay and reverse transcription quantitative real-time PCR in HCV genomic replicon cells. Co-immunoprecipitation assay was used to identify the interaction between PCSK9 and NS5A. NS5A dimerization was studied by split-luciferase complementation assay. NS5A and HCV RNA binding was examined by RNA and protein immunoprecipitation assay.

RESULTS: We first confirmed the inhibitory effect of PCSK9 on HCV replication. Then we demonstrated that PCSK9-induced LDLR degradation was not involved in HCV replication regulation using gain-of-function (D374Y) or loss-of-function (Δaa. 31-52) PCSK9 mutants for LDLR degradation. Moreover, the auto-cleavage of PCSK9 played a role in HCV replication since only uncleaved proPCSK9 suppressed HCV replication and cleaved PCSK9 did not have effect on HCV replication. Next, we found that PCSK9 could interact with several HCV proteins including NS5A. The PCSK9 interacting region of NS5A was aa. 95-215 in Domain I. The interaction between PCSK9 and NS5A inhibited NS5A dimerization and HCV RNA binding to NS5A.

CONCLUSIONS: Considering that NS5A dimerization, RNA binding activity of NS5A is required for HCV replication, the interaction between PCSK9 and NS5A could be a mechanism of how PCSK9 inhibits HCV replication. This study may improve the understanding of the antiviral effect of PCSK9 on HCV and help optimize anti-HCV regimens.

P246 - LATE BREAKERS

A qualitative inquiry to understand the drivers affecting uptake of health promotion intervention to reduce zoonotic infections and non-prescribed veterinary antibiotics use in peri-urban small holder dairy farms in India

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BACKGROUND: India is one of the largest producers of milk and peri-urban areas are the main contributor to meet the rising demand of the cities. Per-urban areas do not fall under the jurisdiction of either rural or urban municipal and civic bodies. Lack of stringent policy and legislative provisions have contributed to adoption of questionable farming practices that not only adversely affect the outputs and profits, but also place farmers, their animals and consumers at risk of health hazard. In light of limited evidence on the burden of the zoonotic infection and non-prudent use of veterinary antibiotics in India, a study was conducted across three sites to understand the potential risky practices and factors contributing to the burden. To address the same, an intervention package was developed and implemented for one year. Farmers were trained on disease transmission, hygiene practices, biosecurity and rational use of antimicrobials etc. Significant changes were observed in knowledge and attitude, but no changes were observed in practices. Study aims to understand the drivers affecting uptake of health promotion intervention package.

METHODS: All the intervention farms were considered as the sampling universe to capture the data addressing the central research question. Thematic guides were developed using the intervention package. Barriers and facilitators to the uptake of practices related to infection control as well as prudent use of antimicrobials were documented across each theme. Sampling was stopped once the saturation of data reached across all themes under inquiry. Data was analyzed using Atlast ti.v7.

RESULTS: A total of 19 interviews were conducted across the three sites. These included 6 farmers each at Guwahati and Ludhiana site and 7 at Bangalore site. Financial stress was found to be a major barriers in the intervention related to infection control as well as prudent use of antimicrobials. Perceived risk of disease, unavailability of trained veterinarian and lack of infrastructure in the peri-urban settings were others reasons for the non-compliance, majority in Guwahati and Ludhiana site. However, Bangalore study site emerged as positive deviance model. Subsidized feed, concentrate and easy availability of veterinarian, and incentivized system were found to facilitators of the intervention uptake. This could be attributed to the presence of strong cooperative support.

CONCLUSION: Increased level of knowledge and improved attitude towards the prescribed practices could only translate behavioural change through support from health system and policy level efforts. Strengthening extension services through better penetration in the community like cooperative movement etc. and establishment of new veterinary colleges and other institutions to bridge the human resources gap can contribute to relatively more prudent use of antibiotics.

P247 - LATE BREAKERS

Understanding the Role of Porcine Reproductive and Respiratory Syndrome Virus Minor Glycoproteins in Porcine Immune Response

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Porcine reproductive and respiratory syndrome virus (PRRSV) is one of the most important pathogens in the pork-producing industry worldwide. PRRSV causes a respiratory disease complex which affects swine of all ages. It also results in reproductive failure in sows. PRRSV is positive-strand RNA virus. The virus contains seven glycoproteins, of which four are envelope glycoproteins named GP2a (ORF2a), GP3 (ORF3), GP4 (ORF4), and GP5 (ORF5). To date, little is known about structural requirements for PRRSV infection and virion formation. The results from sparse studies point to an essential role for GP2a/GP4 and GP3 in PRRSV assembly and antigenic regions, however, nothing is yet known about the function of the minor structural proteins. We hypothesize that the three-dimensional structure of PRRSV envelope glycoproteins GP2a, GP3 and GP4 is critical for the induction of neutralizing antibodies against PRRSV.

We have tested two particular methods for the expression and purification of GP4 ectodomain in order to study its structure. First, GP4 was expressed with a hexahistidine tag, and purified by Ni- NTA chromatography, following solubilization from the inclusion bodies. Analysis of the purified protein by ^{1}H, ^{15}N HSQC NMR indicated that the protein was unfolded. Second, we expressed GP4 ectodomain as a fusion with a chitin-binding domain and a self-cleaving intein. Although the fusion protein was expressed in the cell, we were unable to recover any GP4 upon cleaving the fusion protein, implying that GP4 was insoluble. We conclude that isolated GP4 is misfolded and may require interaction with the other virion proteins or chaperones for proper folding. This in turn could reveal antigenic regions, to better generate neutralizing antibodies thus resulting in vaccination strategy improvement.

P248 - LATE BREAKERS

Exploring effective therapeutic options against Extensively Drug Resistant (XDR) S. Typhi infections

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BACKGROUND: In November 2016, an outbreak of ceftriaxone resistant *Salmonella enterica* serovar Typhi was detected in children from Hyderabad, Pakistan, by the Microbiology laboratory in Aga Khan University, Karachi. Subsequent molecular analysis of the isolates at the Sanger Institute, U.K., revealed that the *S*. Typhi H58 haplotype had acquired an Inc Y plasmid encoding resistance against third-generation cephalosporins such as ceftriaxone, commonly prescribed against multi-drug resistant (MDR) *S*. Typhi. Although, vaccination against S. Typhi is the ideal strategy of effectively dealing with XDR and limiting its spread in the community, especially children, accessibility of the available conjugate vaccine will be limited by economic factors and social misapprehensions in low-middle income countries. Therefore, it is imperative that therapeutic options for effectively treating extensively drug resistant (XDR) *S*. Typhi cases be determined. The study herein aims to explore antimicrobials that can be used as effective therapeutic options to manage XDR *S*. Typhi infections.

METHODS: Phenotypic resistance profile of 208 XDR *S*. Typhi isolates from the Hyderabad outbreak were determined by retrospectively analysing Minimum Inhibitory Concentrations (MICs; µg/mL), obtained from VITEK laboratory records. MICs against the following antibacterials were obtained: ampicillin, ceftazidime, cefepime, ciprofloxacin, levofloxacin, meropenem, ertapenem, and trimethoprim sulfamethoxazole. Additionally, susceptibility against imipenem was determined using disc diffusion test. Of these 208 XDR isolates, 48 were isolates that had been characterized by whole genome sequencing. Azithromycin MICs were determined for 40 isolates by Etest (bioMereiux).

RESULTS: Consistent with susceptibility profile of MDR S. Typhi, the XDR isolates also showed complete resistance against ampicillin (MIC_{90} >=32 µg/mL) , ceftazidime (MIC_{90} >=64 µg/mL), cefepime (MIC_{90} >=64 µg/mL) and trimethoprim sulfamethoxazole (>=16/304µg/mL). All isolates were resistant to ciprofloxacin and levofloxacin, with MIC_{50} 2 µg/mL & MIC_{90} 4 µg/mLfor both antibiotics. All isolates were susceptible to ertapenem (n=205, MIC_{50} and MIC_{90} of <0.5 µg/mL, meropenem (n=206, MIC_{50} and MIC_{90} 0.3 µg/mL). Azithromycin and imipenem disc susceptibility testing was performed on all 206 isolates with 100% susceptibility. Etest for azithromycin showed MIC_{50} and MIC_{90} of 4 µg/mL (n=40).

CONCLUSION: Azithromycin, ertapenem, meropenem and imipenem are effective therapeutic options on the basis of in vitro testing. Ongoing surveillance and monitoring of MDR and XDR *S*.Typhi strains against these antibiotics is essential to identify emerging resistance and to guide future strategies in drug development for treatment of enteric fever.

P249 - LATE BREAKERS

Estimation of the incidence of human brucellosis infection in Punjab, India, using a reversible catalytic mathematical model fitted to sero-prevalence data

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BACKGROUND: There is few data on the incidence of human brucellosis – an important but neglected zoonotic disease – in many developing countries, including in India. The absence of robust surveillance systems and diagnostic challenges hinder the establishment of evidence-based control strategies. Mathematical models can provide a useful platform to combine snapshot prevalence data and the current knowledge of human brucellosis' natural history, to improve our understanding of its transmission and epidemiology in a setting. We combined literature information and data from a large seroprevalence survey of human brucellosis within a mathematical model framework, to estimate the incidence of human infection in rural India where household herds are common.

METHODS: We built an SIS reversible catalytic mathematical model to estimate the seroconversion rate (SCR – rate at which populations become seropositive for Brucella, incident infections) and sero-reversion rate (SRR - rate at which populations revert to seronegative, then converted to duration of infection) in Ludhiana district, Punjab (India). The parameters were estimated using maximum likelihood by fitting the model to Brucella age-specific seroprevalence data from a population-based cross-sectional survey of 1900 individuals aged ≥5 years old, randomly sampled across 60 villages. We defined a brucellosis seropositive subject as one testing positive to either of RBT or a validated commercial IgG ELISA. Two alternative models were explored, with different assumptions on the age at first infection, and uncertainty around estimates was quantified by bootstrapping assuming a binomial distribution of seropositivity. Model fits were compared using likelihood ratio tests and Akaike Information Criterion (AIC).

RESULTS: The survey found an overall population brucellosis seroprevalence of 2.24%, increasing from about 1% in children aged 5-14 years to peak at 3.3% in adults aged 25-34 years, and slightly reducing to 2.7% in those ≥55 years. The model-based estimate of the SCR was 17 per 10,000/year (95%CI 7 to 66 per 10,000), when excluding younger children (<5 years) not included in the survey and unlikely to be exposed to brucellosis. The estimate was slightly higher, at 30 per 10,000/year (95%CI 0 to 88 per 10,000), when there was no constraint to the age at 1st exposure, with the best fit model suggesting age at 1st exposure of 5.1 years. SRR corresponded to durations of seropositivity of between 9 and 17 years.

CONCLUSIONS: The models findings suggest that human brucellosis is most likely endemic in the study area, but with relatively low new infection rates of 17 to 30per 10,000/year, of which only a small proportion will likely progress to acute or chronic symptomatic illness. These estimates of both infection rates and duration of seropositivity are not inconsistent with the current literature. However, the estimates' precision is limited by the low seroprevalence.

P250 - LATE BREAKERS

Peri-urban dairy farming in emerging livestock systems and transmission potential of brucellosis to occupational risk groups and the general population in West and Central Africa: A tale of two countries

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BACKGROUND: Rapid urbanisation and increasing demands for dairy products are driving rapid and sometimes chaotic transition of livestock farming systems in developing countries' peri-urban areas. The spillover potential of related zoonoses to human populations is increased, and includes Brucellosis, a relatively neglected infection. Effective control programmes in these resources-constrained settings has to be adapted to the local context. Here, we contrasted the specificities of peri-urban dairy farming in a West and Central African countries, in relation to the risk of human brucellosis in occupational groups and the wider community.

METHODS: We conducted two parallel cross-sectional surveys in major peri-urban dairy farming areas of a West and Central African countries, Senegal (Dakar and Thies) and Cameroon (Bamenda). One survey collected data on randomly selected dairy farms, including information on the disease transmission potential within the herds, and animal husbandry habits that may be conducive to human transmission. The second survey enrolled a random selection of individuals involved in dairy-farming, and for whom information was obtained on determinants of occupational exposure.

RESULTS: Ninety-four dairy farms (19 modern farms (MF) and 75 traditional farms (TF)) were surveyed in Cameroon, and 152 (23MF and 129TF) in Senegal. MF in Cameroon are of smaller size than in Senegal (median 5 animals vs. 21 in Senegal), and more likely to include exotic breed (Holstein; 95% MFs vs. 7% TFs). MFs have higher milk yield than TF in both countries. Regular mixing with other livestock and pasture sharing with goats and sheep is more common in TFs in both countries. All farms in Cameroon report using vaccines for some livestock disease, vs. only 70% MFs and 66% TFs in Senegal. Bulk milk serology showed higher prevalence of Brucellosis in TFs systems in Cameroon (19%), but low to none in MFs, whereas this was reversed in Senegal (higher prevalence in MFs (9%), and lower in TFs (2%)). Cameroon's MFs report higher rate of abortions (26%) than TFs; in Senegal, MFs has very high rate of abortions (61%) than TFs (33%). Raw milk is more commonly sold in Senegal (>90% farms) compared to Cameroon's MFs (63%), Cameroon's TFs' milk production is mostly for personal use. In the survey of respectively 49 farm workers in Cameroon and 134 in Senegal, the involvement in cattle husbandry appear largely similar in both countries, including milking cows, assisting with parturition and abortions, and slaughtering. However, in Senegal, livestock workers also report more often close contacts with small ruminants, including milking sheep, and assisting them in parturition and abortion. Regular consumption of unboiled dairy products is more prevalent in Senegal (87%) vs. Cameroon (29%), and 24% Senegal participants report regular consumption of sheep milk.

CONCLUSIONS: Modern farms in Cameroon seem to have a low prevalence and low transmission potential for brucellosis, with human risk mostly occupational, compared to higher prevalence and higher transmission risk in Senegal. The prevalence is higher in Traditional Farms in Cameroon than Senegal, although traditional farms in Senegal appear to have more access to markets and therefore pose a higher risk for the general community.

P251 - LATE BREAKERS

Therapeutic failure as a challenge to overcome in the zoonotic transmission of sporotrichosis in Brazil

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BACKGROUND: Sporotrichosis is a mycosis of public health concern that affects both humans and animals, caused by dimorphic fungi which belongs to the current *Sporothrix schenckii* complex. The disease can be categorized as an anthropozoonosis since the transmission also occur through bites or scratches of infected cats to healthy individuals. In Brazil, there is an increasing number of human and animal sporotrichosis cases occurring by this transmission route, revealing an epidemic status in the last decades. The high susceptibility of domestic felines, along with their territorialist behavior and semi-domicile management that is often implemented by owners, make the understanding of feline sporotrichosis a key point for the control of the epidemic status currently in place. The long treatment course and the abandonment of therapy by owners are some of the critical conditions that favour the selection of resistant infectious agents, what could explain the therapeutic failures often observed in human and animal clinical practice. The present study aimed to determine the susceptibility profile of a large number of *S. brasiliensis* isolates obtained from animal sporotrichosis cases. Additionally, we classified the isolates as wild-types and non-wild-types.

METHODS: A total of 168 isolates from cats (141) and dogs (27) were evaluated. Identification was reached by morphophysiological characterization and PCR-RFLP. Antifungal susceptibility profile was determined through broth dilution (M38-A2) for amphotericin B, itraconazole, ketoconazole, terbinafine and voriconazole. The comparison with the proposed epidemiological cutoff values (ECVs) allow us to detect non-wild type strains harbouring probable acquired resistance mechanisms.

RESULTS: According to the morphological and physiological features, 164 isolates were identified as *S. brasiliensis* and four as *S. luriei*. However, all isolates proved to be *S. brasiliensis* by PCR-RFLP. Additionally, all of them were characterized as wild-type to amphotericin B, itraconazole and ketoconazole, drugs usually implemented in therapeutic protocols for human and animal sporotrichosis. Only eight (4.76%) were classified as non-wild-type to terbinafine.

CONCLUSION: The use of molecular tools to reach the precise identification of samples is fundamental for the differentiation of cryptic species, as in the *S. schenckii* complex. The high antifungal susceptibility observed in our large set of *S. brasiliensis* isolates, from animals allows us to suggest that the therapeutic failures described in the veterinary practice routine are not associated with the occurrence of resistant strains. Thus, it is necessary to perform pharmacokinetic and pharmacodynamic studies using the available therapeutic options, such as itraconazole, terbinafine, and amphotericin B to improve *in vivo* the outcome prediction. Host-pathogen interaction studies are also required for a better understanding of the immunological response of the feline to sporotrichosis infection. The development of new therapeutic protocols and more effective interventions in veterinary medicine will directly reflect on public health, helping in the control of this important zoonosis.

P252 - LATE BREAKERS

Bat cells persistently infected with Middle East respiratory syndrome (MERS) coronavirus: a molecular model to study spill over

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Middle-East respiratory syndrome coronavirus (MERS-CoV) is an emerging pathogen that causes disease in humans with a mortality of thirty-five percent. Bats are believed to be the original hosts for coronaviruses parasitizing many other mammalian species. However, little is known about how these viruses are retained in bat populations or the factors that lead to their spread. We have demonstrated that North American little brown bats are persistently infected with a coronavirus related to MERS-CoV, and that stress of secondary fungal infection suppresses innate antiviral responses potentially leading to increase in viral replication and spillover. To examine the molecular mechanisms that may regulate the coronavirus-bat relationship during viral persistence we tested the hypothesis that *big brown bat cells can be persistently infected with MERS-CoV and disrupting the antiviral pathways will lead to an increase in virus propagation in these cells*. We infected bat kidney cells with MERS-CoV at a multiplicity of infection of 0.01 and cultured the surviving cells for over three months. We characterized the persistently infected bat cells by demonstrating the presence of infectious virus by $TCID_{50}$, viral proteins by confocal microscopy and immune blots, viral RNA by in-situ hybridization and virus particles by electron microscopy. Our data suggest that bat kidney cells can be persistently infected with MERS-CoV. Future studies will explore innate antiviral pathways in these persistently infected cells to identify molecules that control virus propagation. Knock-down/out studies will allow us to dissect the molecular mechanisms that lead to virus spillover from this intriguing viral reservoir.

P253 - LATE BREAKERS

Altered Translation Regulation Promotes miR-122-independent Replication of Hepatitis C Virus Genomes.

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The liver-specific microRNA miR-122 plays an important role in positively modulating the Hepatitis C Virus (HCV) life cycle. It is known to promote viral stability, translation, and replication, however, the exact role of miR-122 in this process is not fully understood. Work from our lab demonstrates that, unlike the wild-type HCV genome, some full length RNAs with mutations in the 5' UTR and bi-cistronic HCV replicons containing an additional IRES can replicate at low rates in miR-122-deficient cells. Although there are reports of miR-122-independent replication of HCV, no mechanism for independent replication has been proposed. In this study, we hypothesize that an alteration in translation regulation affects viral propagation and, in-turn, promotes miR-122-independent replication. We observed that the presence of an extra IRES and mutations in the 5'UTR that enhance HCV genome translation efficiency also promoted miR-122-independent replication. These findings support the role of miR-122 in regulating HCV translation. In silico structural analysis of miR-122 bound 5'UTR of HCV shows that the bound 5'UTR forms an open structure in contrast to the unbound which forms a closed structure. The mutants which can replicate independent of miR-122 also forms an open structure similar to miR-122 bound 5'UTR of HCV. Thus, we speculate that the predicted structural change might be conferring an enhanced translation efficiency by altering IRES activity or by providing better stability and enabling the genome to propagate inside the cell. Finally, analysis of cells supporting miR-122-independent HCV replication by microscopy and flow cytometry revealed efficient replication (similar to miR-122-dependent replication) in a small number of cells, instead of low-level replication in all cells. These results suggest that establishment of replication in a high proportion of cells requires miR-122, but for genomes capable of miR-122-independent HCV replication, establishment of an infection is inefficient in the absence of miR-122. Also, this indicates miR-122 is not required to maintain the infection. Hence, we suggested that miR-122 promotion of virus translation functions to establish virus replication, but that miR-122 may be dispensable for ongoing replication of some HCV genomic RNAs.

P254 - LATE BREAKERS

Toxoplasma gondii exposure in free-ranging wolverine (Gulo gulo): serostatus and risk factors

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BACKGROUND: *Toxoplasma gondii,* an intracellular protozoan, is the etiological agent of toxoplasmosis. Exposure to *T. gondii* has been reported in people and animals in northern Canada, however limited information is available on prevelance in wildlife. The aim of this study was to identify the sero-prevelance of *T. gondii* wolverine (*Gulo gulo*) from Yukon, and associated risk factors. Wolverine were examined due to their high trophic level (bio-accumulators), predatory and scavenging lifestyle which could make them a suitable sentinel species for foodborne parasites such as *T. gondii*.

METHODS: Fluid obtained from hearts of 127 wolverines was assayed for antibodies to *T. gondii* using an Enzyme Linked Immuno Sorbent Assay (ELISA). We examined factors associated with sero-positivity, including age, sex, location and body condition index (BCI).

RESULTS: A sero-prevalence of 25.2% (32/127, 95%CI: 17.9-33.7) was observed. Higher sero-prevalence was observed in adult (≥2 years) (37%, 14/38) and yearling (1-2 years) wolverines (30%, 13/43) than juveniles (< 1 year) (11%, 5/46). Almost equal proportion of males and females (24% vs 27%) had antibodies to *T. gondii*. Logistic regression revealed that age was the only significant predictor of *Toxoplasma* exposure in wolverines, and suggested that chance of exposure to *T. gondii* increased with age. Sero-positive wolverines have been reported from various locations in Yukon indicating widespread geographical distribution.

CONCLUSIONS: Our results suggest that wolverines may be a useful indicator species for *T. gondii* occurrence.

P255 - LATE BREAKERS

Responsible antimicrobial usage in practice – putting the “Action” back in National Action Plans in Bangladesh

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BACKGROUND: The country of Bangladesh has the highest density of humans and livestock populations globally. With rapid urbanization and economic growth, the poultry industry is also growing at an unprecedented rate to meet increasing demand. To support high production levels in low biosecurity farms, large quantities of a wide variety of antibiotics including WHO critically important human antibiotics such as ciprofloxacin and colistin are being used regularly. Inappropriate usage of critically important antibiotics in human medicine is also contributing to the emergence of antimicrobial resistance (AMR) in Bangladesh. The National Action Plan on AMR containment has therefore identified a One Health approach to be the most effective means to address the growing risk of AMR in Bangladesh.

METHODS: A group of leading animal and human health professionals from both public and private sectors came together to form the Bangladesh AMR Response Alliance (BARA), a community of practice dedicated to practicing and promoting responsible MAU. BARA subsequently developed One Health AMU guidelines utilizing the WHO Essential Medicines List AWaRe classification and covering AMU in poultry and human medicine via a collaborative workshop supported and facilitated by technical experts from FAO and WHO. Three-day Continuing Professional Development Trainings for animal and human health practitioners were then organized by FAO for BARA leaders to train fellow practitioners in use of the AMU guidelines. Furthermore, a smartphone app version of the AMU guidelines was developed and an online social media group was formed to support responsible usage within the BARA community.

RESULTS: BARA has become an active One Health functional forum actively advocating for responsible use of antimicrobials in both human and veterinary medicine independent of their respective employers/sectors/affiliations. Thirteen participatory training modules on the principles of AMR and responsible AMU were developed, pretested and finalized. A total of 128 BARA members have been trained and equipped with the smartphone app to practice rational AMU. The BARA social media group is regularly updated and hosts discussions amongst BARA members of the challenges faced and success achieved. They also share AMR-related research articles, tripartite (FAO/OIE/WHO) publications, newsletters, promotional materials, video footages etc.

CONCLUSIONS: Empowered by concrete, evidence-based guidelines for responsible AMU, BARA members are serving as role models within their professional communities. Despite the challenges faced in translating theory into actual practice, they are now actively focusing on avoiding unnecessary use of antibiotics when antibiotics are not indicated, gaining confidence on the use of targeting narrow spectrum antibiotics against the causative organisms, and no longer prescribing ciprofloxacin or colistin on poultry farms.

P256 - LATE BREAKERS

Stressors in persistently infected bats may influence the severity of the disease and/or increase virus shedding

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In recent years, several viruses that cause no obvious disease in their natural bat hosts have spilled over to other species resulting in frequently fatal disease. These spillovers may be promoted by factors that disrupt the balanced relationship between viruses and the reservoir bat they have co-evolved with, leading to increased virus replication and shedding. We have detected and characterized corona and herpesviruses that infect two North American bat species – *Myotis lucifugus* and *Eptesicus fuscus*. Many (~30%) M. *lucifugus* are persistently infected with a coronavirus (*Myl*-CoV) and most (>70%) *E. fuscus* are latently infected with a gammaherpesvirus (*Ef*HV). In order to examine this bat-virus relationship, we are testing the hypothesis that ***stressors such as secondary infections will alter the bat-virus relationship, leading to increased Myl-CoV replication and reactivation of latent EfHV***. We show that the intestines of bats infected with *Pseudogymnoascus destructans (Pd),* a fungus that causes fatal White Nose Syndrome (WNS), contain on average 60-fold more *Myl-CoV* RNA than singly-infected bats and that the level of viral RNA correlates with the severity of WNS-related pathology. The intestines of bats with WNS also contain lower levels of transcripts for immune-modulatory genes. Our results suggest that the systemic effects of WNS down-regulate anti-viral responses in bats persistently infected with *Myl-CoV*, thereby increasing the potential for virus shedding. Further, we are artificially altering cellular stress-response pathways, namely unfolded-protein response, heat shock reponse, and hypoxia induced response to determine the molecular basis for the effect of stressors on viral replication and reactivation in-vitro.

Funding source: NSERC, U of S One health initiative, US fish and wildlife.

P257 - LATE BREAKERS

Genotypic characterization of salmonella spp. Isolated from wild animals in 3 selected wildlife holding centres in north central Nigeria

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BACKGROUND: *Salmonella* is the cause of salmonellosis which causes morbidity, mortality and economic losses. Wildlife have been reported to play important roles in the transmission of the organism worldwide. The c systematic periodic isolation and characterization of the organism in different settings humans, animals and the environment is of serious epidemiological importance. This study was designed to genotypically characterize *Salmonella* spp. isolated from wild animals at the Jos Wildlife Park, Jos Museum Zoo and the Unilorin Zoo, Nigeria.

METHODS: This was achieved by determining the virulence genes and resistance genes present in 12 *Salmonella* isolates (representing six serotypes) isolated from wildlife. S. Kalamu (6), S. Derby (2), S. Livingstone (1), S. Alachua (1), S. Ajiobo (1) and S. Ried (1). Illumina sequencing and in silico analysis of whole genomes was employed for the determination of both virulence and resistance genes present in the isolates. Polymerase chain reaction (PCR) was also used to amplify *invA* and *fimH* virulence genes in addition to bla_{TEM} and bla_{OXA} resistance genes.

RESULTS: Important invasion-associated (iNTS) virulence and resistance genes were described in this study. 119 virulence genes were identified in the 12 isolates with varying virulence foci and locus tags; 5 of the *S*. Kalamu isolates and one S. Livingstone harboured 85 virulence genes representing the highest identified genes from the isolates while S. Alachua harboured 79 virulence genes, the mean of the genes harboured by isolates was 82 (P>0.05, r=0.5, LR+0.025). Virulence genes; *staE, steB, bcfA, fimA, lpfC, csgA, stbC, stcB, stdC, sipB, spaS, invI, pagN, orgA, pagC, msgA, tolC, sifA* and *sopB* were some of the important virulence genes identified. A total of 2166 antibiotic resistance genes were identified belonging to 18 classes of antimicrobial resistance genes,of which beta lactam resistance genes were 1601, while the fluoroquinolone resistance genes had the lowest identified resistance genes with only 2 identified genes (P>0.05, LR=1). Other important resistance genes found in this study include *blaLAT-1,* bla_{BIL-1}, $bla_{CMY-1-110}$, $dfrA_{1-33}$, $dfrB_{-1-8}$, *dfrC, dfrD, dfrG, dfrK, sul1, sul2*, and *sul3*. Ten (83.3%) of the Salmonella isolates were positive for *invA* gene while two *S*. Kalamu isolates (from spotted hyena and vulture) were negative. Two (16.7%) of the Salmonella isolates were positive for *fimH* virulence gene while all the other isolates were negative. The 12 (100%) isolates tested were positive for bla_{TEM} resistance gene while only 2 (16.7%) isolates, *S*. Alachua and *S*. Kalamu were positive for bla_{OXA} resistance gene (P>0.05, LR=0.96, LLA=0.317, r=1).

CONCLUSION: Results of the study suggest that serotypes of *Salmonella* isolated from these wildlife centres possess arrays of both virulence and resistance genes which make the organisms potential health threat. Further studies and constant surveillance should be done to better understand the epidemiology of *Salmonella*.

P258 - LATE BREAKERS

Rabies burden in developing countries: nigeria perspective

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BACKGROUND: Annually, up to 60,000-159,000 people died of Rabies globally and mostly in African and Asian continents. In those countries, rabies is transmitted mainly through dog bites, and the number of patients receiving post exposure prophylaxis against rabies has steadily increased particularly in their urban areas. It is alarming that in this part of the world, that preventing human rabies has being of great challenge due to some technical, intersectoral, organizational and financial barriers. In Nigeria, the first cases of rabies in humans and in animals were documented as far back as in the early 19th century. Further studies revealed rabies from frugivorous bats, in shrews and from terrestrial mammals in the twentieth century. Since then, less attentions are paid to the study, research and control of rabies in domesticated and in the wild animals. Hence, the increase in the incidence and prevalence of this deadly disease in Nigeria.

METHODS: This paper reviewed the burden of rabies and suggested directions for effective prevention and control borrowing from the strategies adopted by the developed countries. Published literature about rabies were used for the study.

RESULTS: Inadequacies in research and health education on rabies, partnership between stakeholders, infrastructure and capacity, quantities of safe and potent vaccines coupled with under-reporting of human rabies in endemic countries like Nigeria contributed to the disease being neglected by relevant authorities and subsequently poor assistance from international communities and donor agencies.

CONCLUSION: Human fatality due to rabies is mainly from bites of rabid dogs. Routine vaccination of dogs against rabies in Nigeria is low with high incidence of human rabies among illiterates and poor communities. It can be deduced that poor awareness on the consequences and severity of the disease in these communities account for the high incidence of rabies in such areas. There is need for systematic and sustained control programmes for rabies in Nigeria.

P259 - LATE BREAKERS

Health education strategies in enhancing rabies control and prevention in Nigeria.

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BACKGROUND:
The rate at which cases of rabies are reported in the media, veterinary clinics and human hospitals is alarming. Although rabies is highly feared by all, yet public awareness and knowledge of its risk factors are still very poor in Nigeria.

METHODS: The overall objective of this study was to evaluate the impacts of rabies campaign on the uptake of anti-rabies vaccination by pet owners. A rabies campaign was carried out in Ifelodun LGA of Kwara State from April 2016 – June 2016 using a public address system to communicate, inform and educate the youths and the adults in Schools, Churches, Mosques, Markets, Town halls and Community centers in the studied areas. Questionnaires were also administered to capture data on rabies, risk factors, and anti-rabies vaccination uptake. The result showed that awareness was higher and ant-rabies vaccination for pets increased after the intervention.

RESULTS: This study revealed that awareness creation through public educational campaigns might be a very useful approach for pet owners on the control of rabies in our society.

CONCLUSION: It is our recommendations that government should support regular rabies campaign and consider subsidy on anti-rabies vaccine for the control and total eradication of rabies in Nigeria.

P260 - LATE BREAKERS

One Health In Practice: Viet Nam’s Five Year Strategic Plan For One Health Approaches To Zoonotic Diseases

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Viet Nam has been one of the leaders in Asia in adopting One Health approaches for control of zoonotic diseases especially those with pandemic potential. Viet Nam has recognized the value of adopting One Health approaches building on work done with SARS and Influenza A(H5N1) and has broadened to include wildlife, environmental health, AMR and other issues. Viet Nam recently formed the One Health Partnership for Zoonoses. The One Health Partnership subsequently developed The One Health Strategic Plan for Zoonotic Diseases for 2016 – 2020 (OHSP) that outlines how zoonotic diseases in Viet Nam will be addressed, weaving together the various activities and programs that are in place or are expected. This plan not only emphasizes the need for on-going building of One Health capacities but also demonstrates how and why One Health approaches will be conducted for specific diseases or groups of diseases in Viet Nam and the expected gains over the next 5 years. The plan takes into account key regional and international activities and provides estimates of likely costs of activities and sources of funds. In the mean while, as being in the third year of implementation, the “Review of implementation progress 2016-2017 and implementation plan for 2018-2020” and the “Monitoring and Evaluation Plan” for the OHSP are being prepared, which will contribute to solid supervision and governance of the OHSP by the Government of Viet Nam. This will showcase on how One Health is being "operationalized" in Viet Nam and provides a model for consideration by other countries.

P261 - LATE BREAKERS

Phenotypic characterization and antibiogram of salmonella spp. Isolated from captive wildlife and humans in two zoos and a park in north central nigeria

Oludairo, Oladapo Oyedeji (1); Kwaga, Jacob K. P. (2); Kabir, Junaid (2); Abdu, Paul A. (2); Gitanjali, Arya (3); Perrets, Ann (3); Cibin, Veronica (4); Lettini, Antonia Anna (4)

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BACKGROUND: This study set out to phenotypically characterize *Salmonella* spp. from wild animals and humans in 3 wildlife holding centres in North Central Nigeria by isolating the organism, determining the prevalence and serotypes of the *Salmonella* spp including their antibiogram, resistance patterns and Minimum Inhibition Concentration (MIC). The study areas were the Jos Wildlife Park, Jos Museum Zoo and the Unilorin Zoo.

METHODS: Cross sectional study design and convenience/non probability sampling was employed for the study, a total of 365 samples (341 from wildlife and 24 from humans) were collected in the areas in 8 rounds of sampling. Freshly voided faeces were selected from cages housing the animals while samples were also collected from members of staff willing to participate in the study. Sterilized polythene bags were used. Conventional methods of isolation of *Salmonella* were employed and confirmation carried out using Microbact GNB 24E, the serotyping of confirmed isolates were subsequently carried out. Antimicrobial sensitivity testing and MIC were performed using disc diffusion technique and the broth micro-dilution sensititre methods.

RESULTS: Overall prevalence of 3.3% was recorded, 0.6%, 2.5% and 0.3% were the prevalence for Jos Wildlife Park, Jos Museum Zoo and the Unilorin Zoo respectively ($P^{<}0.05$). Prevalence in various animal species and humans were; carnivores 1.1%, herbivores 0%, primates 1.1%, aves 1.1%, reptiles 0% and humans 0 The following serotypes; S. Kalamu (6), S. Derby (2), S. Livingstone (1), S. Alachua (1), S. Ajiobo (1) and S. Ried (1) (LR=0.264) were isolated. This is the first report of these serotypes in zoo/park wildlife in Nigeria to the best of our knowledge. All the isolates were resistant to at least 4 antimicrobial agents with the expression of 2 main resistance patterns; OX-AMC-KZ-E (11 isolates) and SXT-OX-AMC-KZ-E (1 isolate) based on the disc diffusion sensitivity test which tested 12 antimicrobial agents. The 12 isolates were sensitive to all the 14 antimicrobial agents used for MIC. Results were statistically analysed using IBM SPSS statistics 19, chi square was used and Fisher's exact test when observed variables were less than 5.

CONCLUSION: The study demonstrated the presence of *Salmonella* in the 3 wildlife holding centres. With the description of six different serotypes. Including resistance to 4 and 5 antimicrobial agents by the isolated organisms. This may be of clinical and public health concern. Although isolation in humans was not established, the organisms' zoonotic ability have been well documented. Efforts should therefore be geared towards monitoring the serotypes and their prevalence from these centres including the antibiogram of the isolates so as to be a step ahead. Contact and interaction of wildlife with other animals and humans should be reduced to prevent transmission of the organism to *Salmonella*-free populations.

P262 - LATE BREAKERS

Qualitative Approach to Developing a One Health Intervention Strategy for Zoonosis Risk Mitigation in Southern China

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BACKGROUND: Emerging and re-emerging zoonotic diseases have been a contributor to morbidity and mortality in southern China, which harbors diverse and abundant wildlife. The over-exploitation of land and other natural resources due to urbanization has led to increasing human-animal interactions in this region that favor the emergence of zoonotic diseases in local communities. Lack of knowledge around human behavior, cognition, and local policy regarding humananimal-ecosystem interactions have been the main barriers to developing effective interventionstrategies to prevent zoonotic disease emergence.

This study aimed to develop intervention strategies based on previously identified high-risk behaviors of human populations exposed to wild and domestic animals. Incorporating an understanding of the social, environmental, and economic factors underlying human behavior into the interventions is expected to mitigate risks of zoonotic emergence in southern China.

METHODS: Standardized qualitative methods were employed for this study, including one-on-one semistructured ethnographic interviews, focus groups, and observations. In conjunction with key informants who have extensive local knowledge, community members with frequent exposure to wildlife and domestic animals were recruited by word of mouth or through snowball sampling in three provinces of South China: Yunnan, Guangdong, and Guangxi.

Participation in the study was completely voluntary with a strict informed consent process. All interviews and focus groups were conducted and recorded in local languages, then transcribed and translated into English for entry in to an electronic database. Collected data were analyzed with MAXQDA, a computer-assisted qualitative data analysis software, using a standardized code book with identified themes developed from continuous discussion and amendment within the research team during preliminarily analysis.

RESULTS: Human-wildlife-livestock interaction was reported by most respondents in their daily observation and commonly through slaughtering, hunting, and animal husbandry. Improved community environmental conditions in the past decades are still insufficient to protect this population from contact with rodents and bats. Very few respondents were able to identify links between animals and zoonotic diseases or used proper protection when in contact with

animals. In spite of an awareness of the national wildlife protection policy, many participants preferred wild over domestic animals for consumption and believed in the purported curative powers of the former.

CONCLUSIONS: This qualitative assessment of zoonosis risks in southern China provides evidence to support a one-health intervention to: 1) better monitor and manage bat populations and human activities in and around caves; 2) improve public knowledge and awareness of zoonotic disease spillover; 3) build community protection skills regarding contacting bats, rodents, and other wildlife; and 4) enhance policy enforcement of wildlife protection to reduce wildlife trade. Only through transdisciplinary efforts, can the risk zoonotic disease emergence in southern China be mitigated.

P263 - LATE BREAKERS

Attitudes Towards Wildlife Trade and Disease Risk in China

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BACKGROUND: Wildlife trade has been linked to a series of emerging infectious diseases. In China, the first spillover of SARS-CoV from bats to civets and humans is believed to occur in large wildlife markets in Guangdong province, leading to its pandemic emergence. Driven by the huge demand for wildlife or wildlife products in China, the increasing human-animal interaction in wildlife trade is thought to heighten the risk of zoonotic disease spillover.

By investigating the attitudes of Chinese nationals regarding the role of wildlife trade in disease emergence in China and globally, this study aimed to provide evidence that underpins a number of proposed policy and behavioural change interventions to reduce the risk of novel emerging infectious diseases events in China.

METHOD: An online survey was designed to test hypotheses about attitudes towards wildlife trade and disease emergence among Chinese nationals during one month from December 2015 to January 2016. The survey was randomly distributed via an online survey platform Sojump among 5,448 Internet users, and 2,238 responses were received with a response rate of 41.08%.

All responses were voluntary and confidential as informed to respondents at the onset, no identifiable information was collected from respondents. Collected data were statistically analysed with the software IBM SPSS 16.0 to summarize the data and conduct t-test and the Pearson Chi square with a 95% confidence level ($p = 0.05$).

RESULTS: Although results showed an increased awareness of wildlife conservation, 72% of respondents were involved in wildlife trade, which was not significantly related to their education levels, geographical regions, or the cognition of wildlife and emerging infectious diseases. The main groups of consumers of wildlife in China are people who reported higher income aged 25-39 years old.

There was limited knowledge of the health risks posed by wildlife among respondents, and most respondents believed that not only is it imperative to stop wildlife trade, but that enforcement of policy by government would be the most effective way towards this aim.

CONCLUSIONS: Increased awareness of conservation does not necessarily lead to decreased human-animal interaction in wildlife trade, meanwhile, the lack of knowledge about zoonotic disease emergence among the trade participants is a risk factor for disease spillover in the wildlife trade. In addition to traditional conservation perspective, there is an opportunity to leverage health impacts to reduce the wildlife trade, for protecting both wildlife and human health.

Specific interventions should be developed targeting the group with higher income at the age of 25-39 in China who consume wildlife as luxury food. The willingness to stop wildlife trade and the expectation of policy enforcement also illustrate effective interventions for reducing wildlife trade and disease risks by involving the public into policy advocacy.

P264 - LATE BREAKERS

Epidemiology of brucellosis in Nigeria

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BACKGROUND: Globally, brucellosis is considered to be the most widespread zoonosis. It continues to be a major public and animal health problem in many regions of the world, particularly where livestock production are expanding and as a major source of food and income. Uncontrolled movements; lack of veterinary support services and vaccines; and poor management practices favoured the spread of infection. Human cases continue to occur following international travel, traditional use of raw milk products and following close contact with infected animals.

METHOD: This review aimed at generating science-based information on the risk factors responsible for brucellosis endemicity in Nigeria. Using narrative approach relevant studies on this subject area were scoped focusing on science-based data collected through efficient surveillance systems and used to design purposeful practical and feasible control strategies used in other countries close to or completely free from brucellosis.

RESULT: Several authors pinned down uncontrolled animal movement, socio-cultural practices and traditional preferences to proper animal management systems as the main menace retaining the endemicity of the disease in Nigeria.

CONCLUSION: Our findings showed that brucellosis would require concerted efforts for control and possible complete eradication through inter-sectoral collaboration between ministries of agriculture-veterinary/health-medical and other stakeholders. It is our hope that this review would serve as a guideline for the successful control of Brucellosis in Nigeria.

P265 - LATE BREAKERS

One Health approach to the prevention and control of mycobacterial infections in Tanzania: Lessons learnt and future perspectives

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Southern African Centre for Infectious Disease Surveillance (SACIDS)

BACKGROUND: One Health (OH) is an integrative approach of multiple disciplines to attain health for humans, animals and the environment. The increasing close proximity between humans, livestock and wildlife and the role this plays in transmission dynamics of mycobacterial infections calls for a OH approach in surveillance of zoonotic diseases. The ubiquitous distribution and zoonotic importance of mycobacterial infections has been the subject of great interest, especially in this era of Human immunodefiency virus (HIV) infection. Traditionally, members of Mycobacterium tuberculosis complex are the most important species within the genus mycobacterium responsible for tuberculosis infection. However, in recent years, the non tuberculous mycobacteria (NTM), commonly known as mycobacteria other than tuberculosis (MOTT) or environmental mycobacteria, have been regarded as potential opportunistic bacteria in individuals with advanced HIV infection among other opportunistic infections. The challenge remains as human, livestock and wildlife share resources and have high interactions at the interface areas. This close proximity between humans and animals has increased the chance of cross species transmission of infectious pathogens that may include drug resistant mycobacteria.

METHODS: The search for literature materials on One Health and Mycobacterial infections in Tanzania was performed in PubMed and Google. Published articles on Mycobacterial infections from Tanzania between 1997 to 2017 were reviewed to explore information on One Health and Mycobacterial infections.

RESULTS: Studies conducted in Tanzania found diversity of Mycobacterial spp in animals and human with possibilities for cross species transmission of bovine tuberculosis among livestock wildlife and human. The diversity of *M. tuberculosis* and *M. bovis* among interactive hosts' has been associated with human and animal movements and species establishment in certain geographical areas.

CONCLUSION: Thus, a collaborative interdisciplinary approach among professionals could help to solve the public health threats posed by mycobacterial infections, particularly the spread of drug-resistant strains.