The Type Of Food And Initial Bacterial Count Influence The Antibacterial Efficacy Of Cold Atmospheric-Pressure Plasma Against A Multi-Drug-Resistant Salmonella

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Introduction: Approximately 1.2 million illnesses are caused by Salmonella every year in the U.S. resulting in 380 deaths and 19,000 hospitalizations. The major implicated foods are poultry and fresh produce. We recently achieved complete inactivation (>6 log10 CFU/cm² sample surface) of a multidrug-resistant strain of Salmonella enterica serovar Heidelberg (MDR-SH) after 4 min exposure to cold atmospheric-pressure plasma (CAP) on stainless steel surface. However, only ~4 and ~3 log reductions were seen on lettuce and chicken, respectively, after 5 min exposure. We hypothesized that the difference is due to the nature of the treated samples and to the initial high bacterial count. This study aimed to test these hypotheses.

Methods: Stainless steel discs were coated with three different concentrations of bovine serum albumin solutions (1%, 5%, and 10%) followed by spiking the discs with ~6.5 Log10 CFU of MDR-SH. After drying, the samples were exposed to CAP generated by a two-dimensional air-based plasm microdischarge array setup (2D-APMA) for 1 to 10 min at 10 cm distance. The surviving bacterial cells were eluted and then counted by plating serial 10-fold dilutions of the eluate on tryptic soy agar plates. The reduction in bacterial numbers was calculated by the difference between bacterial counts with and without CAP treatment. In another experiment we compared the bactericidal efficacy of CAP against MDR-SH spiked at low and high initial counts of bacteria (~3.5 and ~6.5 log10 CFU/1 cm²) on three different sample types (stainless steel discs, lettuce leaves, and pieces of chicken breast).

Results: The anti-MDR-SH efficacy of CAP was significantly suppressed in all BSA-coated steel samples as compared to the non-coated sample. The higher the BSA concentration, the higher the suppression in the anti-MDR-SH efficacy. The initial bacterial load significantly affected the anti-MDR-SH efficacy on all tested samples. At the low and high initial counts the MDR-SH was completely killed after 30s and 3 min exposure on stainless steel, respectively. On lettuce leaves, the low counts of bacteria were completely killed after 1 min exposure while at high count only ~3.5 logs were killed after 10 min exposure. On chicken breast, neither low nor high count samples showed complete killing. Approximately, 1 log and 4 logs were surviving after 10 min exposure at low and high counts, respectively.

Significance: While plasma inactivation of other serovars of Salmonella has been assessed previously, this is the first analysis of the efficacy of plasma on the inactivation of MDR-SH on different food and food-contact surface. The results show that CAP generated by our unique 2D-AMPA setup is promising as an alternative technology for destroying MDR-pathogens on leafy vegetables, chicken flesh and food-contact surfaces.
An urgent need is to produce food in a manner that is safe, efficient, and sustainable. Dairy production is a complex system involving animal, environmental, economic, and societal health. Sustainable production can be considered as the long-run ability of dairy systems to produce safe milk from healthy cows in a way that is compatible with the systems' dependence and impact on social, economic, and environmental resource stores. Sustainability is an ideal that forces consideration of the consequences of a decision relative to how it will impact resources required to achieve a long-term goal. It is difficult to define and quantify but important to keep sight of, as a sustainability lens often leads to a different decision than a more immediate view would suggest. Therefore, it is critical to be guided by a conceptualization of “sustainable” that captures the complexity of the system in a way that accounts for potential tradeoffs and externalities of a given management or policy decision. The global and U.S. dairy industry, including Minnesota, is experiencing an accelerating trend of consolidation and intensification, as milk is produced by fewer herds of a larger average size. This trend reflects the greater efficiency of larger herds in converting inputs (economic, energy) into milk production; conversely it shows the difficulty of smaller herds to remain economically viable in an increasingly competitive industry. We hypothesize that a resilient and sustainable dairy sector is characterized by a diversity of herd sizes: that maintaining small herds is important for the livelihood of rural communities and for the resilience of the industry in the face of shifting cultural and environmental forces as well as other unforeseen shocks. Our objective is to identify leverage points and creative avenues to increase the economic viability and overall sustainability of small and mid-sized Minnesota herds. Systems analysis and modeling provide an approach to consider the inputs and impacts of herd diversity along with the greater question of sustainable dairy production.
Prevalence And Antibiotic Resistance Levels Of Pathogenic Bacteria Isolated From Raw Milk Collected From Selected Areas Of Nakasongola District, Central Uganda

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Background  Milk contamination with bacteria that are resistant to commonly used antibiotics can be a major risk to public health. Milk supply to Kampala a major city in Uganda mainly comes from pastoral and agro-pastoral areas, Nakasongola being one of them. This study was conducted to determine the prevalence and antibiotic resistance levels of pathogenic bacteria isolated from raw milk collected from selected areas of Nakasongola district. Methods  A cross-sectional study involving a total of 100 milk samples collected from farms and milk collecting centers were tested for pathogenic bacterial isolates and their response to commonly used antibiotics. Microbial contaminants were tested by microbiological isolation of common milk-borne bacteria and antimicrobial susceptibility of the isolates was done using a panel of 8 antibiotics by disc diffusion method following the National Committee for Clinical Laboratory Standards guidelines. Questionnaires were administered to farmers and milk vendors both on the farm and at the milk collecting centers for additional data regarding management practices that were likely to explain the outcomes. Results : The prevalence of bacterial pathogens from raw milk was at 38% (38/100). The main isolated microorganisms were Staphylococcus aureus (44.7%), Coagulase Negative Staphylococci (28.9%), Escherichia coli (13.2%), Streptococcus agalactiae (7.9%) and Salmonella spp. (5.3%). High antimicrobial multi-drug resistance (over 40%) was observed especially in Penicillin, Ampicillin and Gentamycin which were the commonly used antibiotics in animal treatment in the study area. Conclusions: It was concluded that Tetracycline and Oxacillin would be the appropriate antibiotics to use in treatment since these showed a desirable sensitivity level. There could be drug failure in the antibiotics that showed resistance, i.e. Ampicillin, Amoxicillin and Gentamycin. Recommendations: Farmers should observe and practice proper hygienic measures during milking, packaging and transportation to the collecting centers. Policy makers should enact strict measures against consumption of raw milk and indiscriminate use of antibiotics during treatment interventions in animals.
4 - Agriculture, nutrition and health (including food security, protection and safety)

Assessment Of Milk-Borne Bacterial Hazards In Milk Chain Values In Selected Sites Of Tigray Region, Ethiopia.

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Background: Foodborne diseases are an important cause of morbidity and mortality worldwide. Despite being a nutritional-balanced foodstuff, milk is well known as a medium that favours growth of several microorganisms. Up to 90% of all dairy related diseases are due to pathogenic bacteria found in milk. In Tigray region where milk pasteurization is negligible practice, the burden of milk-borne bacterial diseases is expected to be high. However, data that examine the burden of the problem and factors associated with its occurrence is scanty. Objectives: The objective of this study was to assess the prevalence of milk-borne bacterial pathogens, isolate the common pathogenic bacteria and assess the factors associated with presence of pathogenic bacteria in milk chain values in selected sites of Tigray region. Materials and Method: A cross-sectional study design was used. The study population was all dairy farmers, milk vendors/shops, cafeterias and restaurants owners who sell milk in different forms in the selected seven Kebelles in Mekelle, Wukro and Adigrat cities during the study period. Three hundred fifteen respondents were interviewed using structured and pre-tested questionnaire and 315 milk samples were obtained for testing. Cluster sampling strategy was used for sampling. Laboratory analyses were carried out in the Bacteriology Laboratory of the College of Veterinary Medicine, Mekelle University. First, enumeration of microorganisms was done using colony counting methods to establish the microbial load in milk and then detection of microorganisms was done using enrichment methods and performing various biochemical tests with pure cultures obtained from presumptive colonies by following standard procedure. The bacteriological tests considered for determination of the bacterial load in raw milk samples were total bacterial count (TBC), staphylococcus count (SC) and coliform count (CC). Plate count agar (HiMedia, India) was used for total bacterial count while Baird-Parker Agar Base (Oxoid, UK) enriched with egg yolk Tellurite emulsion (Damstadt, Germany) for staphylococcus isolation and violet red bile agar (HiMedia, India) for coliform isolation and identification, respectively. The detail laboratory procedures used for isolation and identification of the bacteria are described elsewhere. Peptone water was used for serial ten-fold dilutions following standard procedure. The data were entered into Epidata software by an independent data clerk, exported to SPSS version 20 for windows for analysis. Descriptive statistics were depicted using simple frequencies, percentages, measures of central tendency (mean, median) as appropriate. Bivariate and multivariable logistic regressions were used to control the possible confounding effect of selected variables and to determine the independent predictors of bacterial contamination of milk. Finally results were depicted using tables, charts, graphs and COR and AOR and their corresponding 95% confidence interval. Results: From the 315 milk samples examined in the laboratory, the prevalence of bacterial milk contamination was found to be 50%. Staphylococcus aureus, Escherchia coli, Klebsella pneumonia, Klebsella oxytoca and Citrobacter freundii were the main bacterial species isolated and identified from the milk samples. Among the variables examined using bivariate logistic regression for association and independence, the type of business was statistically associated with high burden of bacterial pathogen. Milk vendors, cafeterias and restaurants were nearly 3 times at higher risk of exposing to bacterial pathogen (AOR=2.72, 95% CI= 1.60-4.61) when compared with dairy producers. Conclusion: This study has documented high prevalence of bacterial pathogens in milk and milk by-products and the contamination level of milk has increased significantly along the milk chain value in the study area. Significance: The health risks associated with milk is assessed. This study has shown that dairy farmers need introduce best farm management practices and health mangers and policy makers are informed to enhance their regulatory function and educate all actors along the milk chain value to improve their awareness on general milk handling practices to ensure the safety of milk sold for different consumers.
Evidence is accumulating that neonicotinoids, the most widely used class of insecticides, can cause lethal and sub-lethal effects in vertebrates. Birds may be exposed to neonicotinoids by ingesting treated seeds, or via other means such as contact with contaminated soil or water. This study evaluated the effects of oral imidacloprid (IMI) exposure on immune function in 6-12 week old white leghorn chickens (Gallus gallus domesticus). Five doses of IMI were evaluated, as well as a vehicle control group. IMI doses included 0.04%, 0.33%, 3.3%, 10% and 15% of the reported LD50 in domestic chickens (104.1 mg/kg). Birds were exposed to imidacloprid via gavage once daily for seven consecutive days. The following immune function assays were performed over the 21-day study: phytohemagglutinin-A (PHA) response test, sheep red blood cell (SRBC) antibody agglutination and hemolysis titers, and a delayed type hypersensitivity test. The results indicate that IMI did not cause significant immune suppression. Temporary neurologic signs were observed in a dose dependent manner. Neurologic signs ranged from mild depression to a complete lack of response to external stimulation in the most severe cases. The estimated median effective dose (ED50) was ~10.86 mg/kg, which is equivalent to a 1 kg bird ingesting as few as 8 treated seeds and exhibiting moderate clinical signs. Moderate clinical signs included moderate sedation, increased respiratory effort, ataxia and whole-body tremors. The neurologic signs noted in this study may affect a bird's ability to survive in the wild. This study provides evidence that field realistic doses of IMI may impair avian survival due to neurologic signs, but may not be immunotoxic.
Foot and mouth disease virus (FMD) is a disease that affects cattle, pigs, and other ruminants that can lead to huge economic losses if introduced to a country free from the disease. In the past two decades, many of the most widespread and significant viral lineages have emerged from the south Asia region, especially India. Therefore, understanding the FMD situation in India is critical not only for its own progress towards reducing the impact of the disease, but also for global progress. As an endemic country, the most common serotypes are O, A and Asia 1. The first phase of FMD control program (FMD-CP1) commenced in 2003 and was implemented in 54 districts of 10 states. Mass vaccination of all cattle and buffalo was carried out twice a year with the locally produced trivalent vaccine. Our objective here is to assess the epidemiological outcome of FMD-CP1 (2003-2010) based on data collected by the Project Directorate on Foot and Mouth Disease. For each of 20 rounds of vaccination, serum antibody titers of randomly selected cattle and buffalo were measured pre- and post-vaccination from the districts involved in FMD-CP1, yielding a sample size of 997893. Antibody status was determined by the Liquid Phase Blocking Elisa (LPBE). We describe temporal trends in the percent of the population in each district that was vaccine-protected from FMD pre and post-vaccination. We demonstrate an overall increase over 8 years in the proportion protected, though even after 10th round of biannual vaccination, in some districts the average protected antibody titers dropped as low as 53% prior to the subsequent round of vaccination. We also show that the number of outbreaks per year, controlling for population size; was lower in districts participating in the control program compared to those that were not. In 2011, India expanded their control program to include 167 remaining districts of the country. Spatial and temporal analysis of the dynamics of FMD in vaccinated districts is essential for meeting this goal.
Alternatives to Antibiotics in Animal Agriculture

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Background: The use of antibiotics in any setting contributes to the growing global threat of antibiotic resistance, so it is important to minimize the use of these drugs by eliminating unnecessary uses and finding other ways to prevent infections. In animal agriculture, non-antibiotic alternative products such as vaccines or probiotics play a crucial role in allowing farmers and veterinarians to reduce the use of antibiotics.

Methods: A comprehensive literature review was conducted to summarize the options available to reduce the need for antibiotics in animal agriculture through the use of non-antibiotic alternative products. Academic veterinarians and food-animal experts with species-specific experience in clinical and extension work were consulted to provide feedback on the use of alternative products in the commercial setting and to confirm the findings from the literature search. Results: There is a body of scientific studies available that found promising results on the efficacy of some alternatives as growth promoters and, to a more limited extent, for use in disease prevention. Vaccines are among the most promising and widely used of these alternatives, but pre- and probiotics and other innovative products are also in use or currently being investigated. Many of these have been shown to simultaneously prevent infection and improve animal performance. To date, there are fewer options available for treatment. The effectiveness of alternative products can vary considerably by species and purpose of use. More research is needed to understand exactly why efficacy is so variable and to ensure optimized use. Alternative products also differ in how their use has to be timed to ensure effectiveness. A variety of other alternatives for growth promotion and/or disease prevention show positive early results, but more data under realistic conditions are urgently needed, as are data on potential interactions among alternatives. Conclusion: Overall, alternatives have the potential to replace antibiotics in many situations. Focused research and development will help bring promising technologies to the veterinary market and guide their use. That, in turn, will help reduce antibiotic use in animal agriculture without endangering animal health, productivity, and welfare.
Campylobacteriosis caused by Campylobacter jejuni (C. jejuni) is a serious, yet common foodborne disease in the U.S. The prevalence of fluoroquinolone-resistant (FQ-R) Campylobacter from poultry has increased substantially since the ban of fluoroquinolone use in the poultry industry in 2005. To date no clear selective pressures that explain this effect have been documented. We investigated two factors, limited bioavailability of iron in poultry and activity of microcin B17 released from commensal Escherichia coli (E. coli) in poultry as indirect selective pressures conferring fitness advantages in FQ-R C. jejuni compared to its susceptible wild-type counterpart. Five FQ-susceptible (FQ-S) C. jejuni isolates were selected from litter collected from broiler chicken farms. Using antibiotic selection, five FQ-R strains were created. Application of cell lysates containing active microcin B17 indicated that microcin B17 inhibits growth of Campylobacter regardless of the fluoroquinolone resistance phenotype. To compare the relative expression of genes involved in iron acquisition and regulation, two-step reverse transcription quantitative PCR (RT-qPCR) is being performed on six target genes using rpoA as a reference gene. To induce iron-depleting conditions similar to that of the poultry gut, 2,2'-dipyridyl was added at 0 and 100μM to Mueller-Hinton broth containing FQ-R or FQ-S C. jejuni grown to mid-log phase. RNA was extracted at 0, 3, 5, 10, 30 and 60 minutes using TRIzol reagent. The detailed results of the RT-qPCR will be discussed in a poster. This project aims to link genetics with eco-epidemiology to untangle the complex situation of FQ-R C. jejuni ecology and further our understanding to develop effective mitigation strategies to specifically target FQ-R Campylobacter in broiler chickens.
Understanding movement patterns between farms is an essential component in developing effective surveillance and control programs in livestock populations. This is particularly important in the commercial swine industry, where large numbers of pigs are moved between farms frequently. Here, we describe the annual movement patterns between swine farms in three production systems in the United States and identify farms which may be targeted to increase the efficacy of infectious disease control strategies. Our results revealed a high amount of variability in movement patterns across production systems, indicating that quantities captured from one production system and applied to another may lead to invalid estimations of disease spread. Furthermore, we showed that targeting farms based on their mean infection potential, a metric that captured the temporal sequence of movements, substantially reduced the potential for transmission of an infectious pathogen in the contact network, and performed consistently well across production systems. Our results demonstrate the importance of fine-scale temporal movement data and the need for in-depth understanding of the contact structure in developing more efficient disease surveillance and response strategies in swine production systems.
Last-resort antibiotic resistant E. coli in food producing animals in Pakistan with zoonotic potential

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Colistin is currently considered the last-ditch antibiotic for the treatment of infections caused by multidrug-resistant bacteria worldwide in human. Colistin is frequently used in poultry and live stocks in Pakistan. In this study, we report on the detection and molecular characterization through whole genome sequencing (WGS) of colistin resistant mcr-1 carrying E. coli from poultry in Pakistan. Colistin resistant E. coli from fecal samples of broilers were identified using cultivation on MacConkey agar supplemented with 2 mg/L colistin. For genetic characterization, WGS was carried out on Illumina MiSeq (Illumina, USA). In-silico analysis was performed on web service of the Center for Genomic Epidemiology. Single nucleotide polymorphism-based phylogeny was determined by the software package Harvest Suite and phylogenetic tree was prepared using iTol. Differences in number of SNPs were calculated using MEGA 7 pairwise analysis of core genomes. Of 200 broilers screened 22 (11%) carried colistin-resistant E. coli isolates with MIC ranging from 2-8 mg/L. Ten different sequence types were detected of which ST10 and ST58 were most common complexes. All isolates carried mcr-1 genes whereas mcr-2 and other variants were not detected. Most of the isolates also carried the beta-lactam gene blaCTX-M-15 or blaCTX-M-14 genes. Other resistances include aminoglycosides strA and strB (16/22), tetracycline (tetB) (22/30) and 5/22 qnrS1. Colistin resistance was associated with IncX4, IncI2 and IncY replicon plasmids. Phylogenetic analysis showed a very high genetic similarity among six E. coli isolates with low numbers of SNPs. Presence of certain clinically relevant phylogenetic clones and plasmids underlines the zoonotic potential of these multi-resistant bacteria.
Nutritional recovery and its Determinants among children Aged 6-59 months admitted with Severe Acute Malnutrition at Mwanamugimu Nutrition Unit, Mulago Hospital

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Introduction: The prevalence of Acute Malnutrition in Uganda is 4% among children and of these 1% has got Severe Acute Malnutrition (SAM). Previous studies show that only 66.9% children admitted in hospital for SAM recover. In Uganda, factors that determine recovery and its duration are not known. Characterizing these factors would improve management of SAM and ultimately its treatment outcomes. Objective: To assess nutritional recovery and its determinants among children with SAM at Mwanamugimu Nutrition Unit (MNU), Mulago Hospital Uganda. Methods: We conducted a hospital-based retrospective cohort study including 400 children aged 6-59 months with SAM admitted from March 2014 to June 2015. The primary study was titled “role of probiotics in the recovery of children with severe acute malnutrition (ProbiSAM)”. Data on socio-demographic, anthropometric, clinical and caregiver characteristics were analyzed using STATA 13.0. Time to recovery was described using Median and Kaplan Meier curves. Bivariate and multivariate cox regression models were fitted to identify predictors of nutritional recovery. Adjusted hazard ratios (AHR) with their 95% CI were reported and p-values less than 0.05 considered as significant. Results: Recovery rate was 1.84 per 100-person years observation. The proportion of the children who recovered was 69% (CI: 64.0, 73.3), with a median time to recovery of 35 days (IQR: 25-56). The independent predictors of poor recovery were HIV (Adjusted Hazard Ratio (AHR): 0.4 95% CI: 0.19, 0.91), severe wasting with a MUAC ≤ 115mm (AHR: 0.2 95% CI: 0.15, 0.32) and dermatosis (AHR: 0.6 95% CI: 0.39, 0.89). Conclusion: The recovery rate was below the acceptable national standards. Nevertheless, median time to recovery was within acceptable minimum range of 54 days by the Ugandan national nutritional guidelines. This study recommends targeted interventions to address management of SAM-Edematous children with HIV and or dermatosis. Further studies on the effect of HIV, dermatosis on edematous malnutrition are highly recommended to guide better management of these children.
Nutritional Recovery And Its Determinants Among Children Aged 6-59 Months Admitted With Severe Acute Malnutrition At Mwanamugimu Nutrition Unit, Mulago Hospital

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The prevalence of Acute Malnutrition in Uganda is 4% among children and of these 1% has got Severe Acute Malnutrition (SAM). Previous studies show that only 66.9% children admitted in hospital for SAM recover. In Uganda, factors that determine recovery and its duration are not known. Characterizing these factors would improve management of SAM and ultimately its treatment outcomes. To assess nutritional recovery and its determinants among children with SAM at Mwanamugimu Nutrition Unit (MNU), Mulago Hospital Uganda. We conducted a hospital-based retrospective cohort study including 400 children aged 6-59 months with SAM admitted from March 2014 to June 2015. The primary study was titled "role of probiotics in the recovery of children with severe acute malnutrition (ProbiSAM)". Data on socio-demographic, anthropometric, clinical and caregiver characteristics were analyzed using STATA 13.0. Time to recovery was described using Median and Kaplan Meier curves. Bivariate and multivariate cox regression models were fitted to identify predictors of nutritional recovery. Adjusted hazard ratios (AHR) with their 95% CI were reported and p-values less than 0.05 considered as significant. Recovery rate was 1.84 per 100-person years observation. The proportion of the children who recovered was 69% (CI: 64.0, 73.3), with a median time to recovery of 35 days (IQR: 25-56). The independent predictors of poor recovery were HIV (Adjusted Hazard Ratio (AHR): 0.4 95% CI: 0.19, 0.91), severe wasting with a MUAC < 115mm (AHR: 0.2 95% CI: 0.15, 0.32) and dermatosis (AHR: 0.6 95% CI: 0.39, 0.89). The recovery rate was below the acceptable national standards. Nevertheless, median time to recovery was within acceptable minimum range of 54 days by the Ugandan national nutritional guidelines. This study recommends targeted interventions to address management of SAM-Eedematous children with HIV and or dermatosis. Further studies on the effect of HIV, dermatosis on edematous malnutrition are highly recommended to guide better management of these children. The prevalence of Acute Malnutrition (AM) in Uganda is 4% among children and only 66.9% of these AM children admitted in hospital are able to achieve recovery. In addition, Uganda still records high death rates of up to 20% among children hospitalized with SAM (Nyeko, 2016; UNICEF, 2016). These recovery rates are arguably lower than those prescribed by the Ugandan Ministry of Health guidelines on integrated management of severe acute malnutrition that require recovery rates to be greater than 75%. The gaps in the achieved levels of recovery rates point to suboptimal management and inevitable need to enhance conditions that improve and accelerate SAM recovery (Lenters et al., 2013; Desyibelew et al., 2017) However, factors that determine SAM recovery and its duration are not known. Characterizing these factors would improve the management of SAM and ultimately its treatment outcomes. The findings of this study will inform the guideline on determinants of nutritional recovery among children admitted with SAM. Knowledge of the predictors of time to recovery is critical to design interventions to minimize associated morbidity and mortality and therefore increase recovery rate.
Characterization of Staphylococcus aureus at the Swine-Human Interface

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Swine industry workers are at elevated risk of harboring S. aureus in their noses due to exposure to animals harboring livestock-adapted S. aureus. To assess the biological nature and health implications of nasal colonization with livestock isolates, we conducted a longitudinal study of 66 swine veterinarians, together with a concurrent study characterizing S. aureus populations in 38 US swine herds. Veterinarians submitted nasal swabs monthly for 18 months, together with information on animal exposure and relevant health events. Veterinarians had an elevated prevalence of S. aureus (65%) and MRSA (9%) relative to the general US population, and predominantly (>85%) harbored isolates of three genotypes (ST398, ST9, ST5) that comprised >99% of isolates from pigs. Persistent colonization with a single genetic variant (spa type) occurred in 21% of veterinarians, but without reports of significant health events. Whole genome sequencing of isolates was used to compare virulence determinants and antibiotic resistance genes among isolates. No differences were observed between the isolates from pigs and veterinarians. However, both virulence genes and antibiotic resistance genes clustered by sequence type (ST398, ST9, ST5). These three predominant S. aureus lineages in swine in the USA appear to have evolved independently, suggesting a limited effect of horizontal gene transfer among sequence types. All three lineages are capable of long-term colonization of humans, but lacked major human virulence genes, including enterotoxins, Panton-Valentine leukocidin or toxic shock syndrome toxin genes. Although occupationally derived S. aureus colonization is common in swine workers, current knowledge suggests minimal health concerns in otherwise healthy individuals. A 5-year study is now in progress to assess this in more detail.
The accurate identification of eosinophils in the gastrointestinal (GI) tract of dogs with eosinophilic GI disease (EGID), including inflammatory bowel disease (IBD), by histological evaluation has been problematic. While the currently used H&E staining method detects intact eosinophils, it does not detect degranulated (activated) eosinophils, thus under representing disease state. Our aim was to develop a more accurate method for eosinophil identification and quantification to diagnose canine EGID on the basis of eosinophilic inflammation, including degranulation. Endoscopically obtained paraffin-embedded intestinal tissue (gastric, duodenal and colon) from dogs with IBD was used. The study groups were dogs with lymphocytic-plasmacytic enteritis (LPE, n=10), eosinophilic enteritis (EE) (n=11), and controls (n=11). Consecutive tissue sections were immunostained with monoclonal antibodies (mAb) against the granule protein eosinophil peroxidase (EPX) and H&E. Eosinophils were manually quantified (400× magnification). Degranulated eosinophils were identified based on free cytoplasmic granules and/or extracellular matrix deposition of eosinophil secondary granule proteins. Eosinophils were classified as intact or degranulated. The number of gastric, duodenal and colonic eosinophils was significantly higher in EPX mAb-stained sections compared to H&E stained sections independent of localization (p < 0.0001). The number of intact and degranulated eosinophils was significantly lower in both the bottom and upper regions of duodenal lamina propria of the control group compared with the number of intact and degranulated eosinophils for EE and LPE (p < 0.001). EPX-mAb allows for the unique assessment of eosinophil degranulation. Immunohistochemical detection of EPX provides a more reliable method to detect tissue infiltrating eosinophils in the GI tract compared with H&E staining and demonstrates its feasibility as an alternative diagnostic strategy for pathologists/clinicians to yield expedient assessments of dogs with EGID accurately. Further studies evaluating the diagnostic value of EPX and understanding the functional role of eosinophils in canine IBD will serve as a useful comparative model for human IBD.
The Impact of Host Cellular Cholesterol Levels on Influenza A Viral Infection in Primary Avian Tracheal Epithelial Cell Culture Systems

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Influenza A viruses (IAV) infect many avian species including domestic turkeys, chickens, ducks, and wild birds. Although it is known that this RNA virus undergoes mutations and/or genetic re-assortment that is the basis for adaptation to new hosts and interspecies transmission, the host factors that contribute to susceptibility are not well elucidated. One possible host factor is the cholesterol level within the plasma membrane of a host cell. In these studies, we used Madin-Darby Canine Kidney (MDCK) cells and primary avian tracheal epithelial cells to evaluate the impact of host cellular cholesterol levels on IAV swine-origin H1N1 viral infection. First, we used MDCKs as a model cell line by manipulating the cholesterol levels using cholesterol-depleting agent methyl-beta cyclodextrin and evaluating the differences in viral replication as a result of the varied cholesterol levels. Our results showed that cellular cholesterol levels of MDCK cells are strongly correlated to number of vRNA copies produced as a result of IAV infection. Additionally, we observed that differences in cellular cholesterol between the treated and untreated groups remained statistically significant over time by comparing the means of cholesterol levels from 0 - 96 hours post-treatment. After establishing MDCKs as a model cell line, we began using primary avian epithelial cells in our experiments. Similar to the MDCK cells, we treated the primary cells with methyl-beta cyclodextrin at various concentrations followed by IAV infection. Here, we report our results of the present study and compare them to the previous results found in our MDCK model for the relationship between host cellular cholesterol and IAV infection.
Influenza A viruses (IAVs) subtype H1 have been reported in broad species. IAV-H1 can infect and causes mild to severe respiratory diseases in poultry, swine as well as human. In Thailand, IAV-H1N3 was first isolated from Thai free-grazing duck. The virus has a genomic signature resemble to human influenza. This study aimed to determine virulence and transmission of IAV-H1N3 virus in experimental chickens. The experiment included 3 groups of 4-week chickens: inoculated group (n=8), contacted group (n=4) and control group (n=3). Chickens of inoculated group were infected with 0.1 ml of 106.5 EID50 of IAV-H1N3 virus via intranasal route. Two days after inoculation, four chickens were added in infected chickens cage as contacted chickens. Oropharyngeal and cloacal swabs were collected for IAV detection by qRT-PCR. Our result showed that all chickens did not show any clinical sign during experimental period (14 days). Oropharyngeal swabs from inoculated group were positive for IAV at D1-D10. In inoculated group, viral shedding was highest at D3. While the virus could not be detected in contacted group. In summary, chickens can infect with IAV-H1N3 without any clinical signs. Infected chickens can shed the virus though oral route. The IAV-H1N3 was evaluated as low virulence with poor transmission among chickens. Our future study, the virulence of this virus will be evaluated in other animal models.
The Wild Primate Microbiome Partially Protects Against Obesity

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The gastrointestinal tract hosts trillions of bacteria that together form the gut microbiome. Metabolic diseases such as obesity and diabetes are correlated with shifts in microbiome composition and have been on the rise in Westernized countries. At the same time, Westernized diets low in dietary fiber have been shown to cause loss of gut microbial diversity. However, the link between microbiome composition, loss of dietary fiber, and obesity has not been shown. We used nonhuman primates (NHPs) to study the effects of lifestyle disruption on gut microbiome composition. Captive NHPs are typically exposed to low-fiber diets and tend to have human-associated microbiota. In order to explore interactions between the gut microbiota and dietary fiber, we transplanted captive and wild primate gut microbiota into germ-free mice and then exposed them to either a high- or low-fiber diet. We found that the group receiving captive primate microbiota became obese, regardless of diet, and had higher levels of circulating inflammatory cytokines, while mice receiving a high-fiber diet and wild primate microbiota remained healthy. Using 16s rRNA gene sequencing we identified key bacterial taxa in each group, specifically a high abundance of Bacteroidetes in captive donor mice and a higher abundance of Firmicutes in the wild donor mice. These results suggest that wild NHP microbiota could serve as a reservoir for potentially protective therapeutic microbes effective in cross-species transplants.
Eighteen male kids were divided into three equal groups in a completely randomized design and allotted to three dietary treatments. The kids of the control group (K0) were fed a concentrate mixture (CM) containing soybean meal (SBM) and groundnut cake (GNC) as the main source of protein, maize grain and wheat bran as other ingredients in CM, while in the treatment groups the SBM and GNC protein of the control CM was replaced by Ksheerabal thailam residue (KTR) protein either at 20 (K20) or 40 (K40) percent in the test CM. Finger millet straw was offered as sole roughage. The kids were fed for 150 days. The KTR contained 27.2 % CP, 11.3% EE, 5.3% crude fibre and saponins (11.4%) and essentials oils [caryophyline (26.69%), 7-methyl-Z-tetradcen-1-ol-acetate (24.58%) and eugenol (22.34%)]. The live weight, ADG and nutrient intake were similar whereas ether extract digestibility was higher (p<0.05) in K40 than K0. There was no effect on rumen fluid pH, individual and total volatile fatty acids concentration, while NH3-N concentration was decreased by 10.1 and 23.8%, respectively in K20 and K40 at 4hr. The rumen bacterial community profile was analyzed by Next Generation Sequencing based amplicon sequencing of 16S rRNA gene (V3-V4 region) under Illumina MiSeq Platform (2×300 bp chemistry). The bioinformatics analysis of the metadata using the QIIME pipeline identified 1,982, 2,010, and 1,825 OTUs from K0, K20 and K40 groups, respectively. The bacterial profile analysis at family level revealed the predominance of Prevotellaceae representing 54.1%, 55.4% and 61.4% of total bacterial populations in K0, K20 and K40 respectively. It is therefore, concluded that protein from SBM and GNC can be replaced by KTR up to 40% in the concentrate mixture for feeding to goat.
Foot-and-mouth disease virus (FMDV) causes a disease that affects domestic livestock and numerous wildlife species. FMD can lead to huge economic losses if introduced to a country free from the disease, but causes sustained and chronic impact in endemic regions through trade restrictions and food insecurity. In the past two decades, many of the most widespread and important viral lineages have emerged from the Indian sub-continent. Therefore, understanding the FMD situation in India is critical for both Indias and global progress towards reducing the impact of the disease. The first phase of Indias FMD control program (FMD-CP1) commenced in 2003 and was implemented in 54 districts of 10 states. Mass vaccination of all cattle and buffalo was carried out twice a year with the locally produced trivalent vaccine. Our objective herein was to assess epidemiological outcomes of FMD-CP1 (2003-2010) based on data collected by the Directorate on Foot and Mouth Disease. For each of 20 rounds of vaccination, serum antibody titers of randomly selected cattle and buffalo were measured pre- and post-vaccination from the districts involved in FMD-CP1, with a total of 997,893 animals tested. Antibody status was determined by the Liquid Phase Blocking Elisa (LPBE). We describe temporal trends in the percent of the population in each district that were inferred to be protected from FMD pre and post-vaccination. We demonstrate an overall increase over 8 years in the percent protected. However, even after the 10th round of biannual vaccination, in some districts the average protected antibody titers dropped as low as 53% prior to the subsequent round of vaccination. We also show that the number of outbreaks per year, controlling for population size, was lower in districts participating in the control program compared to those that were not. In 2011, India expanded their control program to include the 167 remaining districts of the country, with the ultimate goal of creating FMD-free zones. Spatial and temporal analysis of the dynamics of FMD in vaccinated districts is essential for meeting this goal.
Mycobacterium bovis, the causative agent of zoonotic tuberculosis (TB), is naturally resistant to the frontline TB drug pyrazinamide. Currently, applied TB diagnostic tools do not make this distinction between M. bovis and Mycobacterium tuberculosis – information that would be useful to the physician for drug choices as well as epidemiologists to choose appropriate mitigation strategies. Sputum samples from 34 suspected tuberculosis patients submitted at Mbarara Hospital in Uganda were analyzed. GeneXpert and sputum smear microscopy was done on the samples. Out of 34 suspected patients, 24 were GeneXpert MTB positive and 1 of them showed rifampicin resistance by GeneXpert-RIF. To evaluate if there were any M. bovis strains in this set of samples, pncA, which carries the C169G mutation that is found in almost all M. bovis strains, was targeted. This allows the differentiation between M. tuberculosis and M. bovis. To enhance sensitivity, nested PCR was performed to account for the varying and low DNA concentrations in the samples and amplicons were sequenced. pncA sequences were aligned against both M. bovis AF2122/97 and M. tuberculosis H37Rv to identify mutations. Of the 34 samples, 33 were pncA gene positive with no mutations. This suggested three things: a) that all samples were likely M. tuberculosis; b) all 33 samples were susceptible to pyrazinamide which is a first line tuberculosis treatment drug, including sample #85 that had rifampicin resistance reported by GeneXpert analysis. Detection of rifampicin resistance is used as a surrogate marker for multi-drug resistance, which is questionable in this case; c) twenty-four samples tested positive for M. tuberculosis complex by GeneXpert, but the pncA analysis suggested that 9 more samples were positive for pncA, suggesting that the GeneXpert identified these samples as false negatives. Out of the 24 GeneXpert positive samples for M. tuberculosis complex, conventional IS6110 PCR detected 18 positives. This suggested that 6 GeneXpert positive samples were likely false-positives. Among the 10 GeneXpert negatives, 3 samples were confirmed as positive by IS6110 PCR, suggesting that these were misclassified as false negatives by GeneXpert. This study highlights that interpretation of the GeneXpert results which must be done carefully taking into consideration the prevalence of the disease in the area. Furthermore, none of the human pulmonary TB cases were caused by M. bovis. Future studies should target high risk groups with intimate animal contact in pastoral settings of Uganda to help identify extent of interspecies transmission of M. bovis. Additionally, targeting extrapulmonary cases may be beneficial in identifying zoonotic events.
The world's first large-scale population-wide study of human-animal health interactions, HUNT One Health, commenced in Norway in the late autumn of 2017. The objective of the project is to provide access to research material to obtain new knowledge on associations between microorganisms, antimicrobial resistance and human and animal health. HUNT One Health is an expansion of HUNT (the Nord-Trøndelag Health Study; https://www.ntnu.edu/hunt), a large human population-wide health project that has been ongoing since the mid 1980-ies. In the initial phase of HUNT One Health, coordinated efforts will focus on collection of fecal samples in addition to health information. Dry fecal samples suitable for studies of microbiota on DNA-level will be collected from cattle, pigs, sheep, dogs and horses, while HUNT simultaneously will collect various types of samples, including stools, from humans. Routines for retrieval, analysis and quality assurance need to be established. A common identification system will enable linking data retrieved from the animals with data from their respective owners. In the successive phases, the biobank will be expanded to include animal cohorts and various sample types also from animals. The availability of biological research material and associated metadata from animals and the people in contact with the animals is expected to open for a broad range of interesting and high-impact studies in the coming years. The ability to link human and animal microbiotas and other health parameters on a large scale makes this project unique. The research material will be (conditionally) available also to the broad international scientific community.
Antimicrobial resistance has been recognized as one of the world's most pressing public health problem. The extensive use of antibiotics has led to the development and selection of resistant bacteria in different settings. Beyond the use of drugs for therapeutic purposes in the human and animals, antibiotics are also used as prophylactic agents and as animal growth promoters in agriculture. Animals may act as reservoirs of resistant bacteria that can be transmitted to humans, or vice versa via the food chain. The consequences of antimicrobial resistance represent a growing threat. This study seeks to understand the prevalence of resistance, extended-spectrum β-lactamase (ESBL) production in Escherichia coli isolated from dairy cattle and farm workers and study the inter-farm differences influence on resistance emergence. For the purpose, a total of 567 (523 from dairy cattle and 44 from dairy workers) confirmed E. coli strains were subjected to in vitro antibiotic susceptibility (including ESBL) testing by disc diffusion method. The E. coli isolates were tested against 19 different antibiotics. Antimicrobial usage at different farms was recorded. There was wide spread multidrug resistance among the E. coli isolates, 90% of E. coli isolates were resistant against 3 or more antibiotics. Among the cattle isolates, highest resistance was observed against erythromycin (90.1%), followed by ceftazidime (87.2%), cefotaxime (78.5%), carbenicillin (71.9%), sulphadiazine (67.5%), nitrofurantoin (65.9%), ampicillin (64.9%) and others. Resistance against gentamicin, amakacin, and enrofloxacin was lowest (<20%). These antibiotics could be used for the treatment, if required. A very high percentage (89.06%) of the isolates were found to be ESBL positive as determined by phenotypic method. All the isolates were also subjected to determination of ESBL resistance genes. Emergence of antimicrobial resistant E. coli in human and animals is a matter of concern and requires continuous monitoring.
Genome Characterization Of Turkey Rotavirus G Strains From the United States Identifies Potential Recombination Events With Human Rotavirus B Strains

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Rotavirus G (RVG) strains have been detected in a variety of avian species, but RVG genomes have been published from only a single pigeon and two chicken strains. Two turkey RVG strains were identified and characterized, one in a hatchery with no reported health issues and the other in a hatchery with high embryo/poult mortality. The two turkey RVG strains shared only an 85.3% nucleotide sequence identity in the VP7 gene while the other genes possessed high nucleotide identity among them (96.3-99.9%). Low nucleotide percentage identities (31.6-87.3%) occurred among the pigeon and chicken RVG strains. Interestingly, potential recombination events were detected between our RVG strains and a human RVB strain, in the VP6 and NSP3 segments. The epidemiology of RVG in avian flocks and the pathogenicity of the two different RVG strains should be further investigated to understand the ecology and impact of RVG in commercial poultry flocks.
Foot-and-mouth disease virus (FMDV) is a highly contagious animal disease of significant economic importance. East Africa has one of the most complicated FMDV situations in the world, with diverse management practices including pastoralism and a high density of FMDV-susceptible livestock and wildlife. The control of FMDV in Uganda could result in improved animal health and increased economic security for many Ugandans. This study aims to describe the epidemiology of FMDV in Uganda in order to inform control strategies in Uganda and similar FMDV-endemic areas. The specific aims were to 1) estimate the sub-regional prevalences and geographic distribution of the various FMDV serotypes, 2) elucidate the phylogeographic history of the serotypes circulating in the country, and 3) investigate risk factors which may play a role in the maintenance and circulation of FMDV within Uganda. Here, we report the results of analyses of a three-year cross-sectional survey of over 14,000 cattle, including data on ELISA for FMDV antibodies, genetic sequencing, and numerous herd-level and spatial factors. Preliminary results suggest FMDV prevalence varies greatly across different regions in Uganda, with spatial analyses demonstrating a heightened risk of exposure in the Eastern and Northern regions. Further, the different serotypes were spatially clustered, with serotype O primarily clustered in the Northern, Central, and Eastern regions, and serotypes SAT 1 and SAT 2 primarily clustered in Central and Western regions. Risk factor analysis revealed that factors such as proximity to a national park or wildlife reserve and management practices play a role in the maintenance of the disease. As there is no one-size-fits-all approach to FMDV control, these results will help inform which control strategies will be best suitable for various landscapes and management styles in East Africa and beyond.
Surge in Canine cardiomegaly: A retrospective study of signalment, presentation and clinical findings in 231 cases

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OBJECTIVE: To review the clinical and diagnostic findings of cardiomegaly from a population of dogs presented to the Veterinary College hospital, Bangalore, India. METHODS: A retrospective study of the case records of dogs with cardiomegaly collected between December 2016 and January 2018. RESULTS: There were 231 dogs with cardiomegaly of which 66.67 per cent were male, with a majority of dogs aged between 5 to 8 years (35.49%; 82/231). Labrador Retrievers were the most affected (24.67%; 57/231) followed by the Indian non-descript dogs (13.85%; 32/231), Pomeranians (11.25%; 26/231) and Golden Retrievers (10.82%; 25/231). Over 73.68 per cent of the Labradors affected were male (42/55). The most common signs were dyspnoea (61.03%), anorexia (54.97%) and coughing (42.43%). The majority of dogs (58%) had a tall QRS complex followed by tachycardia (30.73%), increased P wave amplitude (20.34%) and ST depression (18.61%) at presentation. Over 63 per cent had radiographic signs of generalised cardiomegaly, 15.58 per cent showed signs of right heart enlargement and 29.87 per cent of dogs had pneumonic changes or lung consolidation. Dogs were subjected to echocardiography for further investigation. CLINICAL SIGNIFICANCE: The recent past has seen a surge in the number of cases affected with cardiomegaly which occurs primarily in medium to large breed dogs, with males being more affected than females. The duration of clinical signs before referral is often short and the survival times are poor. Greater awareness of the susceptible breeds, clinical signs and diagnostic findings may help in early recognition of this disease which often has a short clinical phase.
Pastoralists are people whose livelihoods depend on animals for food, transport and income, and due to the close contact with their animals and various risk factors, they are at higher risk of zoonotic diseases including brucellosis. A study was conducted to estimate the sero-prevalence of brucellosis in camels, to identify the risk factors that could be associated with the prevalence and to assess the potential risk factors for its zoonotic transmission in Fafen Zone, Somali Regional State, Ethiopia. Camels were selected by systematic random sampling, serum collected, while Rose Bengal Plate Test and Complement Fixation Technique were used to screen and confirm the reactors. Information on risk factors like sex, age, herd size, parity and abortive history of each sampled camel was recorded while camel owners were interviewed about their awareness of the disease and its transmission modes. The overall prevalence of camel brucellosis was 1.53%. Higher prevalence was observed in female and adult camels with a prevalence of 2.5% and 2.34%. Higher prevalence of Brucella (25%) was also recorded in adult female camels with a history of abortion, from adult female camels with no history of abortion. These findings show that brucellosis is an important and established disease in the study area and is a potential public health hazard in the pastoralist community.
OBJECTIVE: To review the clinical, diagnostic and therapeutic protocols of canine babesiosis from a population of dogs presented to the Veterinary College hospital, Bangalore, India. METHODS: The number of dogs with babesiosis is reported by counts extracted from the records of the hospital from December 2016 to January 2018 (retrospective study-14 months). RESULTS: There were 102 cases of dogs diagnosed with canine babesiosis of which 92 (90.19%) were affected with Babesia gibsoni and 10 (9.80%) with Babesia canis by peripheral blood smear examination. Major clinical manifestations were anorexia (90.19%; 92/102), pyrexia (58.82%; 60/102), mucous membrane pallor (52.94%; 54/102), vomiting and/or diarrhoea (50.98%; 52/102). Labrador retrievers were the most affected breed (23.52%; 24/102) followed by Indian non-descript dogs (11.76%; 12/102). Leukocytosis (56.86%), anaemia (81.37%) and thrombocytopaenia (77.45%) were the consistent haemogram findings with 34.31 per cent showing normal leukocyte values. Samples with low parasitaemia were subjected to PCR for speciation. Majority of dogs diagnosed with B.gibsoni were subjected to a triple drug therapy of doxycycline, clindamycin and metronidazole (30.39%) of which 96.77 per cent recovered uneventfully. Dogs with B.canis were treated with a combination of imidocarb dipropionate and doxycycline (9.80%) with good clinical response and those in critical condition were treated with diminazine aceturate along with doxycycline (4.70%) of which 80% recovered. CLINICAL SIGNIFICANCE: The spectrum of Babesia pathogens that infect dogs should gradually be elucidated with the aid of meticulous clinical investigation and molecular techniques. This study highlights the need for accurate detection and species recognition for the selection of the correct therapy and prognosis.
Sports Fishing in the North Rupununi, Guyana: One Health Approach from a Conservation Perspective

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The northern Rupununi is one of the few areas in the world where the Arapaima, a very large species of a freshwater fish, is found. Investment from the private sector, government and international agencies supported research that showed the Arapaima were worth more to the community if used in a catch and release sport fishery than a yearly harvest quota (or taken through poaching). The rich biodiversity of the region was used to create jobs in a way that is sustainable and which keeps families together. Ecotourism is a fast-growing alternative to mining and forestry for local jobs. The Guyanese government provided special permits to test whether the Arapaima, a protected species, could be safely handled using catch and release fly-fishing techniques. Three eco-lodges worked together to develop standards of practice that would sustain the fishery. Training in hospitality services, as well as in medical care, was given to community members to prepare them to provide excellent service to workers and guests. The project employed local Amerindian communities, especially providing new opportunities for female residents. Positive environmental impacts came through investment in solar energy and planting new fruit and vegetable crops for guests. The new capacity being built through this expanding eco-tourism opportunity is being used as a foundation to attract new resources to monitor the health of fish, domestic animals, wildlife, people and ecosystems around the eco-lodges. Northern Rupununi is under pressure from logging, gold mining, oil prospecting, bauxite mining, wildlife trade, burning, grazing for agriculture, and expansion of towns and villages. Understanding how these activities are affecting human, animal and ecosystem health will inform development policies that ensure safe, sustainable and healthy use of natural resources.
Does Aquaculture Increase Antibiotic Resistance in the Environment?

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Point sources such as wastewater treatment plants, terrestrial agriculture, and aquaculture, release antibiotic residues, antibiotic resistant bacteria, and antibiotic resistance genes (ARG) to the aquatic ecosystem. However, results from a systematic literature review conducted by our team showed that increases of ARG in the natural environment associated with specific point sources have not been quantified. The goal of this study was to evaluate the potential impact of trout farms on the increase and dissemination of ARG in adjacent rivers. We collected river sediment samples upstream and downstream from five different freshwater trout farms over time in southern Chile. After DNA extraction, we used a microfluidic qPCR approach to quantify 48 different ARG covering different mechanisms of resistance. We also conducted surveys to obtain information about management practices including antibiotic use. A total of 97 samples were collected. The most frequently detected ARG were tetC, sul1, int1, and tetA. Surveys revealed that florfenicol and oxytetracycline were the antibiotics of choice, and their amounts varied among the farms. Preliminary results showed a general trend of higher ARG levels at downstream sites compared to upstream sites. Data are being further analyzed to quantify the impact of these farms on increases of ARG in the downstream watershed. It is critical to design epidemiological studies, which, combined with molecular methods, can help in evaluating the potential impact of point sources such as trout farms in the dissemination of ARG in the natural environment that can ultimately affect human, animal, and ecosystem health.
Evolutionary Conservation of Methylation in CpG Sites within Ultraconserved Non-Coding Elements

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Epigenetic biomarkers are valuable tools to assess both current and historic environmental exposures. However, current biomarkers suffer from several drawbacks. DNA methylation can be assessed using pyrosequencing assays with great sensitivity, but assays must be designed in a species-specific manner. Also, most inter-species epigenetic comparisons of exposure are assessing different target regions by necessity, limiting the strength of inferences. Here we present the use of ultraconserved non-coding elements (UCNEs) as cross-species, conserved target elements harboring interindividual epigenetic variation. UCNEs are defined as having >95% sequence identity between human, mouse, and chicken genomes. Despite the extreme sequence conservation, we show that both inter-species and interindividual variation in DNA methylation is present. We assessed 5 UCNEs via pyrosequencing in a panel of 96 humans. The mean DNA methylation ranged from 4% to 91% with standard deviations ranging from 2 to 15. We also assessed 13 UCNEs in a panel of 56 different vertebrate species. The p-values from Pagel's lambda provides evidence of clade specific methylation at certain UCNE locations. We propose the use of UCNEs as target loci for use as epigenetic biomarkers where the identical assay can be used for any vertebrate species in an affected region.
Practices Of Using Pesticides Among Sprayers In A Rural Commune In Vietnam

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Pesticides are used commonly in agricultural activities as a method to contribute considerably to agricultural outcomes. However, the inappropriate application of pesticides can have negative impacts on the environment and human health. This study aimed to evaluate the practice of using pesticide among 215 applicators experiencing at least one-time spraying pesticide in the open field in the past three months in Namphong commune in Namdinh province of Vietnam. This cross-sectional study was conducted from September 2015 to December 2015. Face to face interviews using a constructed questionnaire were carried out to assess the previous practices of all participants. The result revealed that most of the applicators (85.1%) were men, and only 14.9% of them were women. 87.9% of pesticide sprayers aged 21 to 59; 97.2% of the participants left the pesticide waste and containers in the fields straight after spraying. There was only 6.5% of applicators frequently wearing all necessary kinds of personal protective equipment The proportion of sprayers who had appropriate practices was about 46%, and 54% of them had inappropriate practices. This study indicated that sprayers were at risk of being exposed pesticides due to their poor practices. A strategy to improve users' practices related to spraying pesticides is necessary to reduce the risk of pesticide exposure for farmers.
Ixodids Ticks from Three Agroecosystems in Uganda: An Insight into Tick Borne Coxiella spp. from Rural Uganda

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Background: Hard ticks are among the most important vectors for several pathogens transmitted to animals and humans. Ticks have high endosymbiont richness with commensal, mutualistic and parasitic interactions. One group of endosymbionts are the Coxiella-like bacteria, which are fundamental for the reproductive fitness of some tick species. The pathogenic potential of Coxiella endosymbionts is unknown, but recent studies suggest that Coxiella burnetii, the zoonotic agent of Q fever, evolved from a Coxiella-like progenitor hosted by ticks. The goal of this study was to survey the bacterial diversity in ticks and characterize infection with Coxiella-like bacteria for each tick. Method: Ticks were collected in Uganda from 3 rural areas: Hoima, Karamoja and Kasese. A total of 1,087 ticks were collected from cattle and goats, of which 527 were identified to a genus level, and 560 to a species level. Subsequently bacterial 16S rRNA gene was extracted and amplified using the V4 hypervariable region. Amplicons were sequenced on an Illumina MiSeq in 2 × 250 paired-end mode. Results: The most abundant species in Hoima were Rhipicephalus appendiculatus, R. evertsi, R. microplus and R. decoloratus; in Karamoja were Amblyomma variegatum, R. evertsi, R. pravus, R. appendiculatus; in Kasese were R. appendiculatus, A. variegatum, R. decoloratus, R. evertsi. Microbiome analysis is currently underway to assess important tick vectors of Coxiella burnetii and shall be presented. Significance: The results from this study will serve to advance our knowledge on Coxiella species, its presence and role in Uganda tick populations. Data generated will serve as a baseline for long term ecological studies assessing tick borne diseases and inform management policies at the local level.
Ecosystem/Environmental health and sustainability

Understanding the Role of Anthropogenic Landscapes in Wildlife Antimicrobial Resistance: Merging Metagenomics and Spatial Epidemiology

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The use of antimicrobial drugs within animal-based agriculture and clinical settings continues to raise public health concerns over selection for antimicrobial resistant (AR) bacteria. Concern is further heightened by growing evidence that residual antibiotics and AR bacteria may leach from anthropogenic sources into natural ecosystems, creating novel opportunities for the evolution, maintenance, and dispersal of AR genes within bacteria populations. However, we know relatively little about the geographic distribution of AR in natural environments and how specific anthropogenic sources of AR contribute to emergence in wildlife and environmental reservoirs. Recent advances in metagenomic sequencing technology allow for characterization of the AR potential of a microbial community and linkage of specific microbial taxa to particular AR genes of interest. Here, we use metagenomics to explore spatial patterns of AR genes from two owl species—Bubo virginianus and Strix varia—that may serve as sentinels of AR in the natural environment. We collected cloacal swabs from 80 owls recovered throughout Minnesota and identified enterobacteria-associated AR genes using shotgun metagenomic sequencing. We then applied tools from spatial epidemiology to investigate how anthropogenic landscapes—both agricultural and urban—shape the distribution of AR genes. Further, we compared owl AR genes to those found in 23 samples from commercial poultry farms to evaluate the extent of AR gene sharing between agricultural and wildlife samples. Preliminary data indicate that AR gene prevalence in wild owls was relatively low compared to levels found in other studies on raptors. However, among owls that did exhibit AR, we detect genes conferring resistance to a range of antibiotic classes, including clinically relevant extended-spectrum beta-lactamases. Additionally, over 60% of AR genes found in owls are also identified in poultry samples, suggesting a possible link between agricultural AR sources and wildlife. Our results establish baselines for monitoring the distribution of AR in natural environments and provide insight into the role anthropogenic sources may play in AR gene dissemination.
A Household-based Survey of Environmental Practice on Dengue Prevention and Control with One Health Framework in the Central of Thailand

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The aim of this study was to identify the environment practice of prevent and control dengue endemic with one health framework for household level in the Central Region of Thailand. The levels of knowledge, attitudes, and preventive behavior (KAPs) and household environment survey including Breteau index (BI), Container index (CI), and House index (HI) among 422 household representatives were collected at three endemic areas (top three areas) in Central Region of Thailand. The results revealed that the majority of respondents in this study were female, had primary school education, had high level of knowledge, positive attitudes for household environmental practice toward one health framework, good preventive behavior in terms of personal preventive behavior, vector control management level, social-support level and community participation were more likely to support household environmental practices (p-value \(\lt 0.01\)). The entomologic survey on HI, CI, and BI survey indicated that three endemic areas were high risk area (urgently to prevention and control). The finding of this study suggested that the health education of vector control management, the empowerment of social-support activities from village health volunteers, public health workers such as weekly cleaning and eliminate breeding site indoor and outdoor should be promoted. Furthermore, one health framework in three dimension; animal health, environment, and human health should be proposed for implementing in community–based behavior change to sustainably dengue prevention and control.
Ecosystem/Environmental health and sustainability

Pollution reduction experiments in the mountains of Chiang Mai, Thailand

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Project: Tests the efficacy of biochar as soil decontaminant to contain pesticide runoff from upland rose farms from contaminating river feeding water supply of Chiang Mai city. Immediate benefits of demonstration of efficacy (confirmation of base hypothesis): Scientific confirmation of low-cost, easily implemented means to reduce “poor man’s pollution” from large residues of pesticide use across wide agricultural areas. Broader implications: Scientific confirmation for the demand critical to building a market of biochar, itself made from crop waste as a means to reduce open field burning, a source of eCO2, smog precursor, black carbon and PM2.5 (smoke) another form of poor man pollution. Project tests a US State Department award-winning proposition that Thailand “Kill two birds (water and air pollution) with one (biochar) stone” put forward by a retired American professor who runs the Warm Heart Foundation, a community development organization in Chiang Mai. Collaborators: Project team includes researchers from soil science, environmental water science, toxicology, economics and political sciences with collaboration of rose village farmers keenly interested to build tourism destination out of conservation farming experimental site. Methodology: Multi-plot comparison of runoff from identical rose fields (area, soil, plants, slope), control plot with plots testing three levels of biochar application. Biochar trenched between rows of plants on contour to capture runoff. Multiple sample collections at identical rainfall points (e.g., following first 100 mm) with tests run within 8 hours. Current status: Poster reports preliminary experimental results. If results confirm efficacy, poster will also explore potential for practicality widespread application low-cost biochar to reduce pesticide pollution from fields. Team will seek funding for funding to track results for four more years to test continued efficacy.
Protecting the Health of Minnesotans from Climate Change Impacts

Kristin Raab, Minnesota Department of Health

K Raab, MN Department of Health, USA; B Hoppe, MN Department of Health, USA; N Tupper, MN Department of Health, USA.

The Minnesota Department of Health’s (MDH) Climate & Health Program spearheads activities to create healthier and more resilient communities in the face of climate change. MDH's three-pronged approach involves researching the effects of climate change on health to inform interventions and policies; communicating to audiences so that they better understand the health consequences of climate change and have strategies to adapt; and developing planning resources to ensure that communities are prepared. This poster will highlight an example from each approach. Applied Research: Private well users (21% of Minnesotans) are vulnerable to well contamination from extreme precipitation. MDH created a method for ascertaining extreme precipitation projections to characterize future flood impacts on private wells and potential exposure to nitrate contamination. To do this, MDH developed a GIS-based composite index utilizing precipitation projections, well locations, land use, and demographic information to demonstrate future vulnerability in June when rainfall is heaviest and nitrate fertilizers are applied to cropland. The method is transferable to other jurisdictions. Communications: MDH facilitated a partnership with the Minnesota Pollution Control Agency and the Department of Transportation to increase awareness of the new Air Quality Index (AQI) forecasting and alert program and to communicate clearly and consistently about air quality health risks and protective actions. The communications campaign resulted in more than 70,000 social media impressions and supported a 7% increase in AQI sign-ups. Planning: MDH collaborated with U-Spatial, University of Minnesota, to develop a free, online, GIS-based tool that maps community climate vulnerabilities and assets to assist planners with targeting resources to areas and populations most vulnerable to climate change.
Research and Development at the Community Level: Case study of an Ecohealth Project at the human-domestic animal and wildlife interface in Western Uganda

Innocent Rwego, University of Minnesota and OHCEA

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Background: Ecohealth approach has been recognized as a comprehensive approach to understanding health at the human, animal and environmental interface in a social ecological context. Community capacity is impeded by persistent exposure to complex public health problems not addressed by vertical interventions, including food and water insecurity, the effects of climate change, unsustainable natural resources, and political conflict and mobile populations. The objectives of the Ecohealth project in Kasese, Rubirizi and Rukungiri Districts in Western Uganda was to understand the disease dynamics at the human-domestic animal and wildlife interface and, and together with the community, identify interventions that can be implemented to address the identified challenges. Methods: Using an Ecohealth approach communities participated in identifying, ranking and prioritizing health and environmental challenges in their population(s), as well as the variables that drive poor health in humans and animals and/or contribute to environmental degradation. Samples were collected from domestic animals, analysed and data dissiminated back to the community. Using participatory methods, the research team engaged with nine communities to identify interventions that would be implemented. Results and conclusion: An average of 5 interventions per community were initially selected. Each community zeroed on an intervention, provided strategies for implementation and feasibility for each intervention assessed. Significance: Selected interventions including training on zoonotic disease management to the health care workers and the community plus construction of community animal health infrastructures will support better management of diseases at the human-domestic animal and wildlife interface.
Defining Environmental Justice: The Indian Context

Kara Suvada, RTI International

K Suvada, RTI International, USA.

Background. India is a powerhouse nation that is rapidly growing and developing. The country is one of the foremost leaders in Asia, and has emerged as a world power. In terms of the environment, India is one of the first countries in the world to have established a “green” court specifically for addressing legal cases related to the environment, and was a leading voice in the Rio+20 United Nations Conference on Sustainable Development in 2012. India is home to 13 of the 20 most polluted cities globally, making environmental challenges a familiar concept to the nation (1). Aims. While India has informally practiced, and dealt with environmental justice for many years, this article is an argument that a formal definition is necessary. In the context of the globally recognized One Health Initiative, understanding issues in environmental health and justice is crucial to reinforcing the relationship between human health and the environment. Methods. An extensive review of scholarly and news sources from multiple perspectives regarding environmental justice and health were reviewed. Case studies were also presented to highlight examples of environmental issues in India. Results and Conclusions. After a review of more than 35 sources, a definition of environmental justice was constructed with the argument that India has many factors to contend with when dealing with environmental health and justice.

39 - Ecosystem/Environmental health and sustainability

National Institute of Environmental Health Sciences (NIEHS) Research, Translation, and Stewardship

Kimberly Thigpen Tart, National Institute of Environmental Health Sciences

K Thigpen Tart, National Institute of Environmental Health Sciences, USA.

The National Institute of Environmental Health Sciences (NIEHS) is one of 27 Institutes and Centers of the National Institutes of Health, an operating division of the U.S. Department of Health and Human Services. The mission of the NIEHS is to discover how the environment affects people, in order to promote healthier lives. The Vision of the NIEHS is to provide global leadership for innovative research that improves public health by preventing disease and disability. NIEHS works to accomplish its mission by conducting and funding research on human health effects of environmental exposures; developing the next generation of environmental health scientists; and providing critical research, knowledge, and information to citizens and policymakers to help in their efforts to prevent hazardous exposures and reduce the risk of preventable disease and disorders connected to the environment. This poster describes selected research, translation, and stewardship priorities of the NIEHS, and provides contact information for key programs.
Wildlife exposure to antimicrobial resistant (AMR) bacteria has been extensively reported, especially in human dominated landscapes. However, it is unclear whether exposure is solely driven by environmental context or whether wildlife species characteristics are also important. Disentangling these relationships is crucial for understanding how AMR bacteria are disseminated in the environment, and what the consequences might be for public and animal health. As a model for this issue, we investigated whether wildlife exposure to cefotaxime-resistant bacteria, from the family Enterobacteriaceae, was a function of spatial overlap with people and domestic dogs, or whether differences could also be explained by the type of host species sampled. Fecal samples and rectal swabs were collected from 31 raccoons, 23 opossums, and 23 coyotes, sampled from five sites (three public and two privately-owned) in north-western Chicago, USA. Cefotaxime-resistant Enterobacteriaceae were detected in 25.8% of raccoon, 21.7% of coyote, and 13% of opossum samples. While raccoons had a higher recovery prevalence, we detected no significant difference in resistance patterns by host species or by site. There was, however, a significant difference by sex, where females tended to have a higher prevalence than males, regardless of the host species sampled. The lack of difference detected between areas highly used (public sites) and areas less used by people and dogs (private sites) may, in part, be due to the fact that wild animal populations in these suburban areas are well mixed and range widely, and differences are more likely to be observed across a larger scale (e.g. urban vs. suburban sites). Bacterial species identification revealed that 46.7% of resistant bacteria were Escherichia coli, 20% Enterobacter aerogenes, 20% Citrobacter freundii, and 13.3% Hafnia alvei. This suggests that multiple cefotaxime-resistant bacterial species are disseminated in the environment, and that resistance genes may be transferred between bacterial species in wildlife.
Mission Mosquito: Building and Expanding an International Network for Innovation in Health Communication

Tanya Maslak, Battelle

Vector-borne diseases account for 17% of all infectious diseases globally, impacting 50% of the world’s population. The burden of such diseases is highest in tropical and subtropical regions, often in places where capacity for prevention or adequate response may be low. Nonetheless, many innovative health communication and public health prevention measures to protect populations against Zika and other mosquito-borne diseases have been implemented in these regions. The Mission Mosquito project, a collaboration between the U.S. Department of State and Battelle Memorial Institute, is a public diplomacy effort that seeks to build and expand an international network for innovation in health communication to increase global engagement in the discussion around vector-borne disease, especially in areas at increased risk. Twenty nominees from the Western Hemisphere, Africa, East Asia, the Pacific, and South/Central Asia – countries that either experience Zika and/or are at risk for other mosquito-borne diseases – will engage in a two-week multi-directional information sharing program (ISP) across the United States in May 2018. The ISP is focusing on topics such as disease surveillance, vector control, citizen science, public-private partnerships, and risk communication as they relate to Zika and other mosquito-borne diseases. Participants will be encouraged to apply the new knowledge, skills, tools, and networks acquired during the ISP through follow-on pilot projects or public outreach campaigns in their home countries. Lastly, the participants will continue to serve as leaders in sustaining a communication network to share best practices, lessons learned, and new research and tools in preventing the future spread of vector-borne disease. This poster will highlight our approach for multi-directional information sharing and applied learning to reduce the spread of infectious disease and promote global health diplomacy.
African countries receive substantial technical and financial support from bilateral and multilateral partners to address neglected health threats such as tropical diseases and pandemics. However, capacity to prevent, detect and respond effectively to such threats remains inadequate. In West Africa for example, the Ebola outbreak and response efforts have questioned the efficacy and impact of this support, since health systems of affected Ebola countries were so weak and collapsed. The outbreak exposed gaps in animal and human health systems leadership, governance, preparedness, prevention, detection and response capabilities in most of African countries. In fact, the majority of African countries are not yet compliant with the IHR and the PVS core capacities requirements to address potential public health events of national and international concern. From 2006-2017 a scoping was conducted in East, West and Central Africa countries. This was supplemented with results of joint external evaluation, aimed at monitoring progress in developing and maintaining core capacities. Results show that few African countries have leveraged technical and financial support provided by partners to reinforce health system. Contributing factors to low impact of foreign support include investing on emergency relief mechanisms instead of strengthening regular programs; non-alignment of partners’ to national priorities, and poor coordination of partners’ funds. In addition, beneficiaries poorly understand the different mechanisms and the timeframe used by the partners to strengthen limited national capacities. Building Public Health diplomatic skills of African Environment, animal and human health practitioners will optimize the opportunity of partner support to strengthen national health systems.
Infectious Disease Outbreaks and Biosecurity

Scenario based outbreak investigation - A One Health approach to respond the threats of Emerging Infectious Diseases

Muhammad Asaduzzaman, International Centre for Diarrheal Disease Research, Bangladesh (icddrb)

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It is important to recognize the outbreaks of infectious diseases, so that control measures can be engaged to contain the current outbreak and prevent future events. But, the disease epidemiology may be unknown with a complex pathogenesis. In order to increase national capability for responding to such diseases, a One Health scenario-based teaching strategy and resources have been developed and tested in Bangladesh, funded by the European Union. The core of the strategy is a staged description of a novel zoonotic disease outbreak, where participants from human, animal and wildlife health sectors are progressively given information about the epidemiology of the disease and associated implications for disease control and management of social and economic impacts. They are taught to use the information to develop an integrated understanding of why the various manifestations in different countries and situations have occurred, and provide guidance to policy makers on actions they should take from local to international levels. Part of the simulation exercise involves a field trip to gather information from livestock owners. A cadre of One Health professionals is now trained to deliver a scenario-based workshop as well as to conduct investigating a disease of unknown origin, using this One Health approach. Review sessions throughout the simulation help participants develop an integrated understanding of key epidemiological principles and their application. There is a clear need to build skills and relationships across human health, domestic animal health and wildlife health to apply a One Health approach to investigating unusual disease events of unknown origin.
Carbapenem resistance has become an urgent public health concern largely because carbapenem-resistant Enterobacteriaceae (CRE) resistant to all other clinically relevant antimicrobials have become globally disseminated throughout in recent times. Carbapenems are not approved for usage in livestock production system anywhere in the world; nonetheless its resistance is being reported from certain parts. Due to the constantly changing nature of resistance, monitoring of antimicrobial attributes of normal intestinal E. coli from food animals is a necessary and important measure to assess ongoing trends. The aim of this study was to investigate the carbapenem resistance in Escherichia coli strains from neonatal calves. For the purpose, a total of 603 confirmed E. coli strains from fecal samples of neonatal calves were initially subjected for the detection of carbapenem resistance. On preliminary screening 129 (21.4%) strains were found to be resistant and were further confirmed by double disc synergetic test. All the 129 carbapenem resistant strains as well as 219 non resistant E. coli strains were subjected to genotypic detection and confirmation of carbapenem resistance genes including blaNDM gene. Nine strains were found positive for the presence of blaNDM gene. None of the strains showed the presence of blaOXA, blaKPC, and blaIMP genes. NDM positive strains also produced Extended Spectrum Beta-lactamases (ESBL) and were multi drug resistant (MDR). Breed of calves, location, health status and age group had no statistical significance with occurrence of blaNDM gene positive E. coli, however sex of calf was significantly associated.
Bovine tuberculosis (bTB) is a disease with major implications for both animal and human health. Many countries invest big efforts in the control of the disease in cattle, mainly through test-and-slaughter programs. However, these efforts are impaired by problems related to the diagnosis of the infection, especially in early stages. In Spain, the eradication program is based on skin testing and parallel use of the interferon-gamma assay in infected herds. But, due to the limitations of those techniques, it is hard to determine the probability of freedom from disease. Here, a scenario tree representing every diagnostic alternative applied in bovine herds based on their bTB status in the region of Castilla y Leon (the biggest livestock producer of Spain) was designed to determine the probability of herds being bTB free after the successive application of the diagnostic tests. For this purpose, the Precision Tree7.5 (Palisade Co, USA) tool was applied. To investigate the effect of uncertainty on the efficacy of diagnostic tests and on the real prevalence of disease, distributions built with values extracted from literature and expert opinion were used, by means of @RISK7.5 (Palisade). The theoretical tree was validated using official data obtained in the region in the period 2010-2015. Our analyses demonstrate the great impact that changes in the assumed sensitivity and specificity of diagnostic tests have on the expected performance of the program and expose the possibility of persistence of infected animals even after several repetitions of the herd test, depending on the diagnostic approach applied.
Evaluation Of The Survival Of Viral Pathogens In Contaminated Feed Ingredients Using Transboundary Shipment Models

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The goal of this study was to evaluate survival of important viral pathogens of livestock in animal feed ingredients imported daily into the United States under simulated transboundary conditions. Eleven viruses were selected based on global significance and impact to the livestock industry, including Foot and Mouth Disease Virus (FMDV), Classical Swine Fever Virus (CSFV), African Swine Fever Virus (ASFV), Influenza A Virus of Swine (IAV-S), Pseudorabies virus (PRV), Nipah Virus (NiV), Porcine Reproductive and Respiratory Syndrome Virus (PRRSV), Swine Vesicular Disease Virus (SVDV), Vesicular Stomatitis Virus (VSV), Porcine Circovirus Type 2 (PCV2) and Vesicular Exanthema of Swine Virus (VESV). Surrogate viruses with similar genetic and physical properties were used for 6 viruses. Surrogates belonged to the same virus families as target pathogens, and included Senecavirus A (SVA) for FMDV, Bovine Viral Diarrhea Virus (BVDV) for CSFV, Bovine Herpesvirus Type 1 (BHV-1) for PRV, Canine Distemper Virus (CDV) for NiV, Porcine Sapelovirus (PSV) for SVDV and Feline Calicivirus (FCV) for VESV. For the remaining target viruses, actual pathogens were used. Virus survival was evaluated using Trans-Pacific or Trans-Atlantic transboundary models involving representative feed ingredients, transport times and environmental conditions, with samples tested by PCR, VI and/or swine bioassay. SVA (representing FMDV), FCV (representing VESV), BHV-1 (representing PRV), PRRSV, PSV (representing SVDV), ASFV and PCV2 maintained infectivity during transport, while BVDV (representing CSFV), VSV, CDV (representing NiV) and IAV-S did not. Notably, more viruses survived in conventional soybean meal, lysine hydrochloride, choline chloride, vitamin D and pork sausage casings. These results support published data on transboundary risk of PEDV in feed, demonstrate survival of certain viruses in specific feed ingredients (“high-risk combinations”) under conditions simulating transport between continents and provide further evidence that contaminated feed ingredients may represent a risk for transport of pathogens at domestic and global levels.
Owning backyard poultry has become increasingly popular in recent years as interest in locally produced food, including eggs, has grown. As more people live in close association with poultry there is a concern regarding the seriousness of a potential zoonotic influenza epidemic. This concern was revisited during the 2014-2015 outbreak of H5 highly pathogenic avian influenza (HPAI) in the United States, which infected 104 Minnesota poultry flocks. During the outbreak, targeted poultry sampling was conducted in control areas surrounding positive premises (radius of 10 km), which included 1,400 backyard flocks. Despite extensive surveillance, only one positive backyard flock was identified among the 104 HPAI infected flocks, indicating a need for understanding avian influenza exposure among poultry. The current study focused on establishing seroprevalence of avian influenza among backyard poultry flocks identified during the 2014-2015 HPAI control area surveillance. Blood samples (n=498) were collected via venipuncture from 33 flocks. Serum was tested for avian influenza antibodies using an enzyme-linked immunosorbent assay (ELISA) followed by agar gel immunodiffusion at the Minnesota Board of Animal Health Poultry Testing Laboratory. Test results did not indicate the presence of antibodies for avian influenza despite proximity to HPAI infected flocks. These results may suggest differences in exposure or host defense mechanisms between backyard and commercial flocks. Further research is needed to better understand the exposure and transmission of avian influenza in backyard poultry and the potential risks that backyard poultry pose to their owners.
In recent years, a worldwide dissemination of CTX-M betalactamase-type in Escherichia coli strains isolates from community-acquired urinary tract infections (CA-UTI) has been observed. However little is known on the prevalence and risk factors of this global threat in developing countries. The aim of this study was to study the prevalence and risk factors for CA-UTI in Yaoundz, Cameroon. Eighty six patients with urinary E.coli infection were recruited from 10 health structures in the city of Yaounde, Cameroon. After taking the first urine, feces were collected from the patients for the study of the intestinal flora. The sample collection of feces was done on a selected gel of enterobacteria resistant to third-generation cephalosporin. The molecular typing of extended-spectrum ?-lactamase (ESBL) was carried out. Eighty-six strains of E. coli from 86 patients were included in the study. It was found that 39 (45.3%) strains produced an ESBL. Among the risk factors, previous use of antibiotic and the dry season were associated with the presence of an ESBL-producing strain in the urine. All ESBL were identified as CTX-M and the production of CTX-M was found to be significantly associated with resistance to fluoroquinolones, aminoglycosides and to the association of trimethoprim-sulfamethazole. The prevalence of CTX-M ESBL in Yaounde Cameroon, provides new evidence on the global dissemination of CTX-M and the extent of this phenomenon in developing countries.
Classical Swine Fever (CSF) is a devastating disease of swine that can have a major economic impact on affected regions and countries. The State of Mato Grosso in Brazil is part of a CSF-free zone that has been officially recognized by World Animal Health Organization (OIE). However, the status to CSF is uncertain in some nearby located States and countries, which may result in risk for introduction of the disease into Mato Grosso. Here, we used a qualitative risk assessment to qualify the risk of CSF introduction into the State of Mato Grosso through live introduction of pigs with the ultimate objective of supporting prevention and early detection activities in the region. Results suggest that the risk of introduction through movement of live animals is extremely low. Results are explained, at least in part, because pigs are typically shipped into commercial farms, which have higher biosecurity levels compared to backyard pigs. Although the risk was extremely low, outputs were sensitive to changes in the status of farms at the origin, and depended on maintaining high biosecurity standards at the farms of destination. In conclusion, results demonstrate the importance of maintaining effective surveillance and biosafety programs to prevent or detect in advance the introduction of CSF in Mato Grosso. With actions that intensify inspections to prevent illegal traffic and active surveillance actions of the Official Veterinary Service prioritizing areas that favor the illegal entry of animals or in properties that have high ingress of animals.
Non-typhoidal Salmonella enterica (NTS) is a major cause of foodborne bacterial illness worldwide. Even though NTS infections are caused by many serotypes, periodic increases in the number of infections may occur due to few emerging serotypes/strains. Recently, Salmonella enterica serotype 4,[5],12:i:-, a variant of S. Typhimurium that lacks the 2nd phase flagellar antigen, has emerged globally in both human and livestock animals, but the exact mechanisms that have led to its emergence and potential persistence in animal reservoirs are not clear. Previous comparative genomic studies performed by our group have demonstrated that most of the isolates recovered in recent years are most similar to a well-defined clone that shares certain virulence and resistance genes. Here, we analyzed the whole genome sequences (WGS) of a well characterized panel (n=90) of S. 4,[5],12:i:- isolates recovered between 1992 and 2016 from different host species using Genome Scale Metabolic Models (GEMs) to identify differential metabolic routes present in strains belonging to this emerging clone. The presence of essential reactions (required to maintain critical cellular functions) under aerobic and anaerobic conditions as well as the ability to use compounds as exclusive sources of carbon or nitrogen were predicted for the whole panel through the use of different GEMs. Overall 149 metabolic routes (out of >3,500 evaluated) were present/absent in at least one of the isolates of the panel. Multiple correspondence and random forest analyses demonstrated that some of these were distinctly associated with strains belonging to the emerging clone, particularly those involved in the metabolism of arsenate compounds, which may provide a competitive advantage to grow and persist in hosts under certain environmental conditions.
Farm Biosecurity At Backyard Poultry Of Bangladesh And Its Role In Spread Of Avian Influenza

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Objectives: The farm biosecurity at backyard poultry that might have contributed to the spread of avian influenza in Bangladesh, specially rural areas is very poorly studied. Therefore, this study is aimed to characterize biosecurity practices of rural backyard poultry for rapid detection and effective risk management of incursion of avian influenza viruses. Materials & Methods: This cross sectional survey was carried out using pretested questionnaire in backyard Poultry holdings of Kalkini Upazila of Madaripur district in Dhaka division which has a relatively low proportion of commercial poultry farms and high proportion of backyard poultry holdings. Results: The study revealed that about 70% backyard farm owners do not maintain the standard biosecurity measures whereas one third (30%) of the study included farms rear multiple poultry species which are fed in same container and kept in same shed. No poultry workers found to use any personal protective equipments (PPEs) while cleaning the litter/mats. More than 80% farms allow free roaming of birds in the house and more than 60% farms do not separate sick birds from healthy ones. Not only that, sick birds are kept in living room in 18% farms. All these play an important role in spillover of avian pathogen to human. Conclusion: The findings from this study will support the development of risk-based surveillance and contingency policies as well as to minimize the spread between poultry units and also from poultry to people for avian influenza viruses in Bangladesh.
The purpose of this study was to estimate the prevalence of failure of passive transfer of immunity (FTP) into calves and to identify putative risk factors. A cross-sectional study was conducted between June 2013 and February 2017. Data from 4,263 calves from 5 dairy herds of Buenos Aires province, Argentina, were recorded. Calf management practices were similar in the 5 dairy herds, with consumption of colostrum by natural suckling and the supply of 4 liters of additional colostrum (bottle or esophageal tube). Serum samples were collected from 4,263 healthy heifer calves. The concentration of total serum proteins (TSP) was quantified by refractometry between 2 and 7 days of life. A TSP value ≤ 5.2 g/dL was the FTP indicator. The association of FTP with three factors, dystocia, twins and sex, was evaluated through logistic regression. The estimated prevalence of FTP was 21% (898/4,263). FTP was not associated with dystocia (OR = 1.2; 95% CI 0.8 – 1.6; p = 0.2253) neither with twins (OR = 1; 95% CI 0.6-1.5; p = 0.9460). However, the occurrence of FTP was significantly associated with male calves (OR = 1.6; 95% CI 1.3-2; p < 0.0001). This could be due to differential management of male calves about colostrum consumption due to its lower economic value. This work can guide preventive strategies that limit the occurrence of FTP.
The Dynamics Of Puma (Puma Concolor) Contact Networks And Consequences For Pathogen Transmission

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Predicting how a pathogen may transmit across a population can be greatly affected by the contact structure of that population. These contact "networks" are generally dynamic within populations, with contact rates and patterns varying over time. Such variations may be particularly difficult to characterize in wildlife populations, where individual interactions may be difficult to observe, and long-term studies may be lacking. In this preliminary study, we examine the contact structures of puma (Puma concolor), a cryptic carnivore, over time, and relate these structures to pathogen transmission. We use telemetry data from puma from southern California to calculate contact networks using several different approaches, including home range overlap according to kernel density. We then examine these contact networks longitudinally, with networks calculated repeatedly over the course of up to 10 years to examine changes in network structure over time. Future work will repeat this analysis in study areas in Colorado and Florida, resulting in network analyses performed across varying degrees of anthropogenic land-use change. The results of these network analyses can then shed light on how directly-transmitted pathogens are likely to spread or be limited in these populations. The results of this work will be especially applicable to wildlife managers by illustrating how pathogen transmission-and therefore puma population health-may be affected by temporally dynamic network structures or network variability associated with factors such as changing population density or anthropogenic land use.
Climate and environment can have major effects on the epidemiology of diseases. Anthrax, a disease caused by a spore-forming bacterium, is a perfect example because its occurrence is highly correlated with weather and environmental conditions and tends to recur years apart. The state of Minnesota USA and the country of Kazakhstan are two Anthrax endemic sites at similar latitudes in the western and eastern hemispheres. Our objectives were to compare the spatiotemporal trends of Anthrax occurrence considering the climatic and environmental determinants at the two sites using historical records. Animal Anthrax cases between 1911 to 2005 (n=255) reported by the Minnesota Board of Animal Health, and between 1933-2014 (n=3,997) reported by the Cadastral register of stationary unfavorable foci on Anthrax in the Republic of Kazakhstan, were analyzed. Preliminary analyses identified two peaks in the epidemic curve in Minnesota in 1940, and 2005, while, a long-term outbreak between 1935 and 2005 was detected in Kazakhstan, with a peak in 1970. Rose diagrams which were used to recognize the directionality in Anthrax spread suggested that relative to the index case in Minnesota in 1912, 54.1% of the subsequent cases were spread in a Northwestern direction, whereas, relative to the index case in Kazakhstan in 1933, 87.9% of the subsequent cases were spread Northward. To detect potential disease hotspots over time the spatiotemporal permutation (STP) model of the spatial scan statistic was used. The STP, set to a maximum 10%-spatial and 5%-time windows, detected 15 clusters with radiuses between 2 and 80 Km and 1 to 2 years of duration, with observed-to-expected ratios (O/E) between 4 and 63 in Minnesota, while, 17 clusters with radiuses between 18 and 309 Km, 1 to 3 years of duration, and O/E between 3 and 57 for Kazakhstan were detected (p&lt;0.05). Investigating the drivers behind the northward trend and the spatiotemporal hotspots over time would improve our knowledge and preparedness for Anthrax. Therefore, in subsequent steps, a time-series analysis will be used to evaluate the association between historic animal Anthrax and climatic-environmental determinants comparing the two distinctly different endemic sites.
55 - Infectious disease spread and health

Assessing Potential Pathways Of Zoonotic Diseases At The Human-Wildlife Interface In Communities Around Hoima District, Western Uganda.

Shamilah Namusisi, Makerere university / University of Minnesota

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There is growing recognition that human-wildlife interactions pose significant public health concerns. Unfortunately, limited information on the frequency and nature of contact between humans and wildlife at community level pose a barrier to assessing the risk of disease spillover to humans. Since the first Ebola outbreak in 2000, Uganda has suffered several outbreaks. Communities within fragmented forests of Hoima District are perceived to be of high risk due to their more frequent exposure to wildlife, such as bats and non-human primates. In this cross-sectional study, we engaged community members (N=370) to better characterize their exposure to these perceived risks, as well as to gain an understanding of their perception of this risk to human health. Results show that wild meat is still consumed and 64% of respondents reported sharing hunted meat at community level. Most hunted animals are edible rats and non-human primates (45.8% and 29.0% respectively) and 7.9% of respondents had ever fallen sick after eating wild meat. Search for animal proteins and medical / cultural use are the common reasons why communities still hunt for wild animals (55.3% and 22.7% respectively). Generally, respondents were less aware (37.0%) of diseases transmissible from wildlife to humans despite the fact that majority (88.7%) had heard of Ebola or Marburg disease. These findings will be used to inform an ongoing national effort on strengthening zoonotic disease surveillance and infectious disease risk mitigation campaign.
Coupling Climate-Based Models With Agent Based Models For Understanding And Forecasting Rift Valley Fever Epidemics In Ferlo Region (Senegal).

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Rift Valley Fever is a major public health problem in the Sahelian region. Rift Valley Fever dynamics depend on complex interactions between animal hosts, mosquito vectors, and viruses that are influenced by environmental and climatic factors. The objectives of this study were to analyze and model with an agent based formalism the relationships between climate factors, animals, water ponds, Aedes vexans and culex poicilipes vectors and Rift Valley Fever outbreaks in Ferlo region (Senegal), and build a software platform that can help to provide a warning system. We used the multi-agent platform called CORMAS for building the various software agents (hosts, mosquitoes, water ponds) with their behaviors and the climate database containing daily temperature, daily precipitation, and daily humidity. We carried out several simulations of the model and results showed that the occurrence of outbreaks in Ferlo region (Senegal) was strongly influenced by climate during each year. Sensitivity analysis was conducted to estimate the yearly risk of an outbreak as a function of the meteorological variables. Local threshold values of maximal temperature and relative humidity were identified and correlated with animal infections. The outbreak and propagation of Rift Valley Fever in Ferlo were essentially driven by climate factors like daily temperatures and daily precipitation during each year. A software platform that we have developed will enable health authorities to predict the outbreak risk of Rift Valley Fever. The open code source of the model could be used to improve vector-borne disease management in other world regions.
Infectious disease spread and health

Association Between Results On Diagnostic Tests For Bovine Tuberculosis And Johne's Disease In Cattle In Spain

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Bovine Tuberculosis (BTb) is a chronic disease broadly distributed worldwide caused mainly by Mycobacterium bovis. BTb has a large impact in animal health and can pose a threat to human health due to its zoonotic nature. In spite of efforts devoted to improve diagnostic performance, the accuracy of bTB diagnostic tests is still impaired by several factors including cross-reactivity with other mycobacterial infections. Among them Mycobacterium avium subsp paratuberculosis (MAP), the etiological agent of Johne's disease (JD), that is present in the majority of countries with animal production, has been identified as a source of cross-reaction in both the simple-intradermal-test (SIT) or the interferon-gamma assay (IFNγ). However, the effect of the continuous use of these tests over time on the prevalence of MAP infection has not been elucidated yet. The aim of this study was to characterize the effect of the repeated use of bTB diagnostic tests in JD serological status in cattle to evaluate the potential diagnostic interference under field conditions. A total of 93 bTB-JD infected herds located in the Castilla-y-León region in Spain were selected on the basis of history of bTB infection and one or more JD-seropositive animals as determined by a JD ELISA (Biodyr ®). A Bayesian mixed-effects regression model was run to assess the effect of being subjected to routine bTB diagnostic tests on the JD serological result while accounting for other potential risk factors. Results showed a significant association (P<0.01) between bTB history and JD within-herd prevalence. Preliminary results indicate that animals with (a) most recent skin tests, (b) with a greater number of skin tests implemented the previous year, and (c) with positive results to the last SIT, were associated with positive serological result to JD. This association could be due to an increase in the sensitivity of JD ELISA resulting of an anamnestic effect after the tuberculin inoculation, or a potential reduction on the specificity of the test due to cross reactivity between the two pathogens. Further analysis adjusting for herd-level factors (management, biosecurity, JD herd status in the previous years) should be conducted in order to fully evaluate the relationship between the application of bTB diagnostic tests on the results observed in the JD tests under field conditions.
Are Movements Important In The Transmission Of Bovine Tuberculosis In Castilla y Leon, Spain?

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Between-farm transmission of bovine tuberculosis (bTB) occurs, mostly, through fence-to-fence contact between neighboring farms or movement of infected animals. Unfortunately, bTB detection is frequently delayed and identification of the source of introduction is often difficult, particularly in endemic regions. Here, we characterized the cattle movement network of Castilla y Leon, a high bTB-prevalence (1.9% at the farm-level in 2015) region in Spain, over six years and analyzed distribution of bTB to ultimately assess the likelihood of spatial and movement-mediated transmission. We analyzed movement and bTB data from 27,633 units located in the region, of which 87% were involved in ~1.4 million movements of ~8.8 million animals. Network-level connectivity was low, although a few highly connected units were identified. Up to 15% of the herds became bTB-positive at some point during the study, with the highest percentage found in bullfighting and beef herds. Although bTB-positive herds had a significantly higher degree and moved more cattle than negative herds, results of the k-test, a permutation-based procedure, suggested that positive farms were not significantly clustered in the movement network. Location was a likely risk factor as bTB-positive farms tended to be located within 5 km from each other. Results suggested that movements may be a source of bTB in cattle in Spain, although contact network did not influence bTB spread. The description of the movement network in Castilla y Leon may be valuable for bTB surveillance in Spain. Moreover, results may be used to assess the risk associated with movements for multiple diseases.
Our research addresses the current challenge in epidemiological processes modeling of applying data-driven models in data-scarce regions. A network framework upon which to model disease spread was created using fine-grained urban built-up areas derived from satellite imagery and high-resolution population data. Using the resulting geospatial network and the population attributes of its nodes, we estimated the commuting rates between road-connected urban areas. As a result, we obtained a directed and edge-weighted network of the mobility patterns between urban areas. 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 also determined the effects of various vaccination scenarios on outbreak spread and impact. Simulation results were comparable to data collected during an actual outbreak of pandemic influenza in Rwanda between 2009-10 with respect to outbreak length and geospatial spread. The probability of outbreak occurrence reduced when vaccinating the area of infection origin, whereas outbreak impact was lower when larger urban areas were vaccinated. In conclusion, our modeling approach can be valuable for planning and control purposes in real outbreak scenarios where traditionally required modeling data is unavailable. Additionally, while we simulated influenza, it is possible to model other infectious diseases like Ebola in West Africa, where high population mobility lead to immense outbreak propagation.
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Infectious Diseases Associated With Agricultural Land-Uses In South East Asia

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Agriculture has been implicated as a potential driver of varying human infectious diseases. However, the generality of disease-agriculture relationships has not been systematically assessed, hindering efforts to incorporate human health into land-use policy. We conducted a systematic review and meta-analysis to test and quantify the associations between agricultural land-use and human infectious disease, focussing on the highly diverse yet tractable model system of South-East Asia. Pooled results from 37 eligible studies yielding 34 effect sizes show that people who live, work in or near agricultural land are on average 1.5 times more likely to be infected with a pathogen than controls (OR 1.54, CI 1.30 – 1.83, p < 0.0001). This effect rose to a 2-4 fold increase in the odds observed for some land-use types (palm oil OR 3.25, CI 2.29 – 4.61; rubber OR 2.19, CI 1.76 – 2.73) and was most pronounced for hookworm (OR 2.42, CI 1.56 – 3.75), malaria (OR 1.80, CI 1.38 – 2.34), Scrub typhus (OR 2.37, CI 1.41 – 3.96) and Spotted fever group (OR 3.91, CI 2.61 – 5.85) subgroups. In other land use and disease subgroups, no change in odds was detected (e.g., rice, vegetable and fruit farming; leptospirosis, schistosomiasis). No evidence of significant publication or measured or unmeasured confounder bias was detected. Current evidence suggests that agricultural land uses consistently exacerbate human infectious diseases in SE Asia. Although responses clearly vary by land-use and disease types, generalizable results from this and further studies could help identify co-management opportunities for health and the environment.
The Metabolic Differences Of Pseudomonas Aeruginosa In Commonly Used Growth Media

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Cystic Fibrosis (CF) is a congenital disease that leads to many symptoms including increased mucus production and decreased mucociliary clearance in the lung which provides a platform for microbial infection. Pseudomonas aeruginosa is the most prevalent and persistent pathogen present in patients with CF and has been shown to form biofilms at sub-inhibitory concentrations of antibiotics. The aminoglycoside family of antibiotics are commonly used to treat P. aeruginosa infections in clinical settings, but are often given at sub-inhibitory doses. Sub-inhibitory concentrations of antibiotics induce changes in secondary metabolism in P. aeruginosa that could be used to influence bacterial growth.

There are currently four main types of media used to grow P. aeruginosa; their effect on growth and metabolism is poorly characterized. Leuria broth (LB) is commonly used in laboratory settings; ISP2 broth is a nutrient deficient media; Mueller-Hinton is commonly used in clinical laboratory settings; and Artificial Sputum Media has been used to mimic the growth conditions of the CF lung, however its effect on metabolism has yet to be characterized. In this study, we determined the effect of media and sub-inhibitory concentrations of aminoglycosides on P. aeruginosa secondary metabolism. First, sub-inhibitory concentrations of aminoglycoside antibiotics were determined for P. aeruginosa, growing the microbe as biofilms in each media with various levels of antibiotics. The samples were measured for overall growth (measuring both biofilm and planktonic growth) and liquid chromatography tandem mass spectrometry (LC-MS/MS) was used to measure the production of secondary metabolite differences between conditions. We found differences in planktonic and biofilm growth, as well as the secondary metabolite production across media, even at the same concentration of antibiotic, demonstrating that misleading conclusions could be drawn from inaccurate representations of microbial growth. This work illuminates a shortcoming in determinations of P. aeruginosa pathogenesis in both clinical and laboratory settings and will inform how to better study pathogen virulence in CF.
Influenza A virus (IAV) is a global, endemic infection that causes significant morbidity and productivity losses in swine and poses a substantial threat to public health. The objective of this study was to test additional intervention strategies aimed at reducing the incidence of IAV in piglets and in breeding herds overall. We developed a stochastic Susceptible-Exposed-Infectious-Recovered-Vaccinated (SEIRV) model of IAV dynamics in a swine breeding that reflects the spatial organization of a standard breeding herd and accounts for the different production and immune classes of pigs therein. The tested interventions included fifteen different vaccine and biosecurity strategies. In concert, mass vaccination, early weaning of piglets (removal 0-7 days after birth), gilt isolation, gilt vaccination, and longer periods between introductions of gilts (6 months) were the most effective at reducing prevalence: endemic prevalence overall was reduced by 51% relative to the null case, endemic prevalence in piglets was reduced by 74%, and IAV was eliminated completely from the herd in 23% of all cases. Based on the global sensitivity analyses, the incubation period, infectious period, duration of immunity, and transmission rate for piglets with maternal immunity are parameters that warrant increased attention for obtaining empirical estimates. Our findings support other modeling and empirical studies that suggest that piglets play a key role in maintaining IAV in breeding herds. We recommend a combination of biosecurity measures in combination with targeted homologous vaccination or vaccines that provide wider cross-protective immunity to prevent incursions of virus to the farm and subsequent establishment of an infected piglet reservoir.
Infectious disease spread and health

A Community-Based One Health Education Program On Infectious Diseases Among Post-Flood Victim

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Flood is associated with increased risks of infectious diseases through water and food contamination. Flood victims may be exposed to higher risks of infectious diseases such as cholera, leptospirosis, hepatitis A, typhoid fever, diarrhea and skin infections. Kelantan is one of the state in north-east Malaysia was badly affected by flood in 2014 and largest recorded flood in the history for a decade. The project was carried out to prepare the special made education materials on infectious disease and to develop skill in communication among undergraduate students in One Health concept to educate the post-flood victim villagers. There were two phases of the activity: Phase 1 involved the workshop which provides participants on One Health concept and the important aspect for community education and was conducted by several method of teaching such as interactive talk, play role, simulation activity and group discussion. Participants were divided into 10 groups and had assigned to prepared education materials such as poster, pamphlet and booklet targeted to village people. Topic given was based on local health issues of infectious diseases. Phase 2 involved the fieldtrip which a platform to all participants to deliver their leadership and communication skills. A total of 92 undergraduate Health Sciences students from various universities were involved in this program. The villagers have opportunity to gain the knowledge by health talk, health screening and health exhibition, as well as teaching material (posters, brochures and booklet). All students were handed over to 40 identified foster families and were stayed overnight in which they carried out the promotion of health education using their teaching material provided. Fourteen education material were successfully produced; 6 posters and brochures on Dengue, Parasite, E. coli, Typhoid, Leptospirosis, Nematode and 4 booklets (up to 10 pages) on Vector, Water borne diseases, Zoonosis diseases, Nematode. Each of them are in Malay language, the contents and examples were closely related to the local scenario. This program not only exposed students to a worthy experience but also provided the opportunity for the students to give back and reach out to the community. The education materials produced are very valuable as it can be used for other post-flood victims with local scenarios and easy to understand.
Building on over three decades of collaboration, NIEHS was designated as a World Health Organization (WHO) Collaborating Centre for Environmental Health Sciences in September 2013. The Collaborating Centre provides a focal point and resource for the Institute to fulfill its strategic goals in global environmental health. This formal partnership with WHO provides NIEHS with new opportunities for translating research findings into effective public health interventions to improve health around the world. NIEHS efforts in the first designation period (2013-2017) focused on Children's environmental health, electronic waste, developmental origins of health and disease (DOHaD), climate change and cookstoves and indoor air pollution. NIEHS sponsored and attended numerous groundbreaking events, collaborated with researchers and professionals around the world to author publications and supported global environmental health training and capacity building efforts in the U.S. and globally. A network of researchers focused in e-waste was established as was a formal network of WHOCC's working in children's environmental health. NIEHS was redesignated as a WHOCC in 2017 and will focus new activities around children's environmental health, environmental factors and non-communicable diseases, health consequences of weather and climate extremes and supporting the WHO Chemical Risk Assessment Network. Under these areas, NIEHS will continue work on existing projects focused on e-waste, indoor air pollution, and DOHaD. The Institute also plans to expand work into new and emerging areas, such as chronic kidney disease of unknown origin (CKDu).

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Rotavirus belongs to the family Reoviridae, genus rotavirus and can be classified into genotype as GxPx; G (1-27), P (1-37). Rotaviruses, strains G3P[3] and G3P[9], play an importance role as zoonotic pathogens. The virus has been reported worldwide in various host species such as human, pig, cattle, bat and dog. In dog, canine rotavirus (CRV) causes subclinical or mild gastroenteritis disease. It has been documented that CRV G3P[3] is a predominant strain circulating in dog population and may cause severe gastroenteritis in human. The objective of this study was to survey CRV in dogs in Thailand during 2016 – 2018. In this study, 315 rectal swab samples were collected from 107 healthy dogs and 208 sick dogs with gastroenteritis (diarrhea, vomit). The samples were collected from dogs with various age, breed and genders. Identification of CRV was performed by using VP6 gene specific primers with RT-PCR assay. Then, genotype of CRV was identified by direct VP7 and VP4 genes sequencing. Our results revealed that the occurrence of CRV was 3.7% (4/107) in healthy dogs and 0.5% (1/208) gastroenteritis dogs. 80% (4/5) of positive CRV were young age of dogs (lower than 4 months). Preliminary result of genetic characterization of a CRV was genotype G3P[3]. To this point, CRV G3P[3] genotyping in dogs is in-process to evaluate the risk of canine-human interface in Thailand.
Mitigating the Risk of Emerging Contaminants through Surveillance and Education

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The presence of pharmaceuticals and other commercial and industrial chemicals in the aquatic environment is well documented by hundreds of reconnaissance studies over the past two decades. These contaminants are surprisingly widespread in surface water, often appearing in lake water without an apparent source. Many of these contaminants are toxic or endocrine active, adversely affecting fish and wildlife at part per trillion concentrations. In addition, trace levels of antibiotics in surface water are suspected of promoting bacterial antibiotic resistance. In the absence of environmental regulatory standards for these chemicals, the challenge is to combine the measurements of contaminants in the environment with an understanding of their effects on ecosystems and with efforts aimed at preventing their release to the environment. Predicated on the earlier monitoring results of chemicals of emerging concern in surface water by government agencies, we are analyzing these chemicals in surface water, sediment, and fish tissue on the Grand Portage Indian Reservation and surrounding region, with the goal of understanding whether these chemicals are exerting adverse effects on fish species and, subsequently, on the traditional subsistence hunting and fishing that is of cultural importance to the Grand Portage Band of Chippewa. Initial study reveals that several of these contaminants are present in samples of water, sediment, and fish tissue, including the x-ray contrast agent iopamidol, the antidepressants sertraline and amitriptyline, triclocarban, and naproxen. Recognizing the importance of preventing the release of pharmaceuticals to surface water, the Univ. of Minnesota College of Veterinary Medicine and the Minnesota Pollution Control Agency have formed a unique partnership to promote research, education, and communication on the ecological risks posed by pharmaceuticals and the importance of pharmaceutical stewardship to prevent their unintended release to the environment.
Emerging Of Brucellosis And Q-Fever In Kosovo: Public Health Puzzles

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The uncoordinated control of Brucellosis in the post war time in Kosovo has contributed for many animal outbreaks and a persistent human incidence. Q-fever in Kosovo became recognized only after large outbreaks of foreign military contingents based in Kosovo. Among several outbreaks in the last years, in 2011, an outbreak of Brucellosis in a sheep herd with 293 sheep and goats was registered with high abortion rate and infection of a family member from the household, despite prior vaccination of the herd. The analysis of blood and milk samples using Brucella Lader PCR revealed a Brucella field strain being the Biovar 3. In 2017 in middle Kosovo, an outbreak with high abortion rate in a goat herd was registered with abortions rate of 70 % with a suspicion of Brucellosis. The laboratory analysis using RBT revealed 4 Brucella positive sheep and after analysis for Q fever, by employing qPCR, 80 animals resulted positive out of total 123 animals. Human outbreaks of Q-fever have not been registered as the disease mainly develops as pneumonia and seems to be misinterpreted by physicians with the flue. The data show that the epidemiology of Brucellosis in Kosovo is not well understood and requires both the veterinary and public health authorities to establish better common policy on its control and eradication. Q-fever in Kosovo shows to have emerged and a better collaboration of veterinary and public health research and government institutions has to be established, although limited resources make it difficult.
The global Definition of One Health is “the collaborative effort of multiple disciplines - working locally, nationally, and globally - to attain optimal health for people, animals, and environment”. Implementation of a One Health approach requires a team effort that brings together professionals who come from a variety of disciplines, including human medicine, veterinary medicine, ecosystem health, and agriculture. Because of the different situations and contexts within the EU there is no single optimal policy instrument for the EU as a whole. To develop policy instruments, on the base of standards it is necessary to collect, integrate and discuss knowledge in relation to current practices by government and industries and work in a collaborative manner to pool their knowledge, develop trust and gain motivation to implement measures for implementation of One Health. The principles of good monitoring require that all regulatory functions should be transparent, accountable, proportionate, consistent, and targeted only at cases in which action is needed. The EU COST funded Action TD1404 “Network for Evaluation of One Health” (NEOH) aims to enable evaluations of One Health activities by developing and applying an evaluation framework and protocol. Developed handbook for evaluation as major outcome of NEOH sets out protocol for the evaluation of One Health and a series of methods adding greater certainty on the when, where and how to evaluate one health initiatives. Evaluation provide a system that allows capturing and documenting costs and benefits across sectors to demonstrate overall costs, benefits, trade-offs and their distribution also recognise differences and variation in the level of knowledge of One Health, differences in implementation and differences in the perception of One Health. Evaluation should assess the degree to which One Health is anchored in the legislation as factor which facilitating One Health approaches. In other words, if legislation does not demand integrated approaches from stakeholders, these will only be implemented in rudimentary forms. Outcome of evaluation will realise with embedding evaluation report firmly in the policy cycle. Qualitative evaluation of One Health approach is critical to avoid missing hazards and using resources inefficiently. It is important to realise that each evaluation adds information that will enable future progress. Clear conclusions about One Health features and criteria that could be used for benchmarking which will lead towards links between animal health, human health and environmental health and promote effective communication between sectors. For better implementation, complementary policy/tools are needed, such as implementation of standard procedure for evaluation of impact and achievements of One Health initiatives. Such instruments should attempt to foster One Health Implementation.
Addressing Community Health Challenges Using One Health Approach In Bwera Demo Site, Kasese District Uganda

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Background: The One Health concept represents a collaborative, multi-disciplinary approach used to achieve optimal health among humans, animals and the environment. The one health approach recognizes that the health of domestic animals, wildlife and people are inextricably linked to one another and the environment. It aims at preventing and providing solutions to the complex health challenges like diseases, poverty and food insecurity through collaboration, cooperation and partnerships. The multi-disciplinary approach under one-health creates a conducive environment for in-depth assessment of the factors contributing to ill-health and thus averting the complex health challenges. This is achieved by providing holistic and multi-faceted solutions.

Methods: During the one month field attachment in Bwera, students from different academic disciplines used integrated tools that is focus group discussions (FGDs), Key informant interviews, direct observations, questionnaires and face to face interviews to assess, diagnose and prioritize the key health challenges in Bwera - Mpondwe community. It is through this, that transformative knowledge on mitigating and risk preventative measures for health problems were provided to the community. Also key health challenges were identified during Bwera attachment using the above tools which was followed by developing sustainable interventions through community engagement.

Results: Assessment it was revealed that a high prevalence of bilharzia of 40% was observed. In Nyakatonzi challenges like; brucellosis, hepatitis B prevalence at 10.8 % (Kagando Hospital January, 2016-June, 2017 kabatoro, they are faced with shortage of safe water for drinking, lack of protective equipment during salt mining activities, air pollution by ammonia, and shortage of food due their location in the middle of the park and lack of latrines in close proximity around the mining areathey are faced with; shortage of safe water for domestic consumption, water pollution, poor sanitation. Recommendations: Continuous sensitization programmes about sanitation and hygiene should be put in place for sustainability of the project. Use of personal protective equipment should be enforced for the people involved in slaughtering and collection of animal products such as blood. There should be formulation of vendors' committees in the different market departments to oversee sanitation in those sections. Mobile testing services for bilharzia should be put in place before medication administration. Community members should be encouraged to screen and vaccinate against Hepatitis B and for those who took the first dose should endeavor to go for the following doses in time. There is need for more sensitization of the public on the practices that lead to and the dangers of AMR.

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Surveillance Of Potential Zoonotic Pathogens In Bat-Human Interface Areas, Thailand

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Bat is well-known as a reservoir of viral pathogens of public health importance such as SARS, MERS, Ebola, Nipha, Hendra, etc. Potential zoonotic viruses are increasingly discovered since next generation sequencing (NGS) was applied. This study aimed to identify zoonotic viruses including Coronavirus (CoV), Niphavirus (NiV) and Influenza A virus (IAV) in bats in Thailand. Sample collection was conducted in high risk bat-human interface areas in 9 provinces of Thailand during September to December 2017. Rectal swabs (n= 361), oral swabs (n= 361) and urine samples (n= 51) were collected from 361 bats. The samples were subjected for viral identification by using RT-PCR with specific primers for CoV (RdRp gene), NiV (N gene) and IAV (M gene). Preliminary results showed that out of 348 samples, 1.4% (5/348) was positive for CoV of wrinkled-lipped bat (Chaerephon plicatus), while no evidence of NiV and IAV were observed. Characterization of 5 Thai-CoVs by partial RdRp gene sequencing showed that the viruses were classified into alphacoronavirus. Further comprehensive characterization of Thai-CoVs by using Illumina (Miseq) is in-process. Moreover, serological testing of human in high risk bat-human interface areas in 9 provinces will be included in the study.
Operationalizing One Health Principles in Kasese District

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Globally, addressing complex community challenges in terms of emerging and re-emerging zoonotic and non-infectious diseases, food insecurity, poverty, poor education and climate change has not been so easy. The invention of collaborative, multidisciplinary approach by One Health partners through student attachments is creating an impact in addressing complex challenges of the communities following the Kasese one health field attachment. The 2017 One Health cohort after their theoretical training at Makerere university, travelled to Kasese and designed a general objective of using their multidisciplinary competences to promote human, Animal and environmental health through sensitization and training, and working with community members in Hima, Karusandara and Kasese municipality in Kasese district.

Students interacted with communities with the aid of the field supervisors to put theory into practice and the activities commenced with introduction of the team to relevant authorities and community entry in the first week of the attachment to conduct needs assessment, week two was to prioritize the needs and starting the intervention for achieving short term objectives such as creation of awareness about zoonoses, health talks in schools and in public places like markets and others. In week three and four, the team still continued with more interventions for achieving intermediate outcomes which included secondary and primary school outreach, training briquette making to Mwolem women market group and the communities around Hima town council. This followed with report writing and conduction of feedback meeting to Hima town council, Karusandara Sub-county and Kasese District technical and political leadership.

Findings were poor solid waste disposing techniques, inadequate hand washing facilities in both schools and households, diseases for humans, crops and Animals (zoonotic and non-zoonotic), low uptake of antenatal care and inadequate vaccination for HPV, prolonged drought, to mention but a few. The One Health field attachment-2017 concluded that there is need to incorporate a multidisciplinary approach while addressing community health problems.
Antimicrobial resistance (AMR) is a major global threat of increasing concern to human and animal health. AMR development is accelerated, in part, when there is inappropriate or excessive use of antimicrobials, which play a critical role in the treatment of terrestrial and aquatic food producing animals and plants, helping to assure food safety and quality, animal health and welfare and farmer livelihoods. Unfortunately, the transmission chain and epidemiology of AMR are still lacking, which is critical in most Latin-American countries to promote scientifically sound policies and implementations. Here, we designed and applied a three-step One Health participatory approach to identify key risk factors and propose a ranking at national level for implementations to tackle the potential transmission of AMR to humans. These three-steps included 1) a country-level systematic review of the scientific literature to identify key individuals and characterize research and collaboration networks, 2) a number of personal interviews to capture risk perceptions and current knowledge on implementations, and 3) a One-Health participatory workshop to prioritize national implementations based on their potential impact (reduction of AMR transmission) and feasibility to be implemented in a short, medium or long terms. Overall, the overconsumption of antimicrobials in humans and food production animals, the suboptimal use of antimicrobials in humans, and the intra-hospital transmission of infections were among the most critical risk factors. In terms of the implementations, education and training to human health and veterinary practitioners were among the most needed due to the high impact in reducing the risk and the feasibility in the short term. Also, implementations in biosecurity or enhancing biosecurity among health centers for both human and veterinary medicines were identified as crucial. There were also at least seven implementations that can be considered of high impact to be implemented in a relative short term (less than 3 years). This work provides a participatory framework to capture most dimension’s perspectives under a "One Health" context to rank the most important risk factors and prioritize key implementations aimed to promote health and reducing the risk of AMR transmission to humans.
Sea Lice Veterinary Treatment: A Challenge for the Salmon Industry and Environment in Southern Chile.

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The sea lice Caligus rogercresseyi is the most important parasite for the salmon industry in southern Chile, the second largest industry worldwide. Sea lice pose no direct threat to humans who consume the fish. Each year, thousands of dollars are spent in the treatment against this infestation, affecting growth performance, increasing the feed conversion rate as well as increasing costs associated with delousing of the carcasses during processing. Most of the medicines that are being used are not novel, and historically most have been applied as pesticides in agriculture. However, the use of all these compounds is not without complications. For example, there is the possibility for sea lice to develop resistance to these products. This resistance results in the need for more aggressive treatment routines to be employed. Parallel to the increase for salmon derived, there is an increase in the reports of infestation. The foregoing presumes a density-dependent dynamics in the epidemiology of the sea lice and the expansion of the problem in the dimensions of 'One Health'. This makes it necessary to explore the patterns of the density-dependent relationship between the amount of salmon in production, the infestation of the parasite, and the quantities of drugs necessary to reduce parasitic load. We will present the results of using an extensive dataset from all farms growing salmonids along the Chilean coast. We will evaluate if densities of farmed salmonids surrounding individual farms have a strong effect on farm levels of parasitic sea lice.
Strategies For Writing A Grant Application

Susana Mendez, National Institutes of Allergy and Infectious Diseases

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The poster describes tips and strategies that may be useful to increase the applicant's success while writing a grant application. This includes what to do before the writing starts, how to facilitate the review of the application by the reviewers, and what to do after review. The relevance of the Overall Impact Score, Review Criteria Score and Additional Review Criteria are discussed. Common problems of unsuccessful applications are presented. Recent policy updates are included.
The University of Rwanda Student One Health Student Club (SOHIC) invites students from varied disciplines to join the club and participate in extracurricular practical and experiential learning activities that focus on collaborative prevention of and response to infectious zoonotic disease threats, such as Ebola, Anthrax, and Brucellosis. Since 2012, thousands of students of joined the club, and in 2017-2018, there are approximately 600 active students. SOHIC leaders have implemented activities with, and without, funding support. Examples of funded activities include student-focused development (e.g., the Global Health Case Competitions, infectious diseases management trainings), and community-focused outreach (e.g., the One Health Akagera field attachment, hygiene and sanitation community health education campaign). The SOHIC also initiated and continues to sustain unfunded activities including an active social media network and information sharing strategy (i.e., What's app, Facebook, Twitter), and an informal student debate program to build skills and knowledge related to One Health concepts and challenges. Students also implemented an Ebola awareness campaign in response to the Spring 2017 Ebola outbreak in neighboring Democratic Republic of Congo (DRC) with four confirmed deaths. The students sought to increase community member awareness of and factual knowledge about Ebola through this health education campaign in Karongi district, the western province of Rwanda bordering DRC. SOHIC members have disseminated their club model, and successes, in international and regional conferences, and have served as mentors to students seeking to start clubs at their respective universities. Importantly, the SOHIC has demonstrated leadership succession and club sustainability since 2012. While the club benefits from funding that facilitates robust extracurricular activities (such as 2-week field experiential learning projects), the club also leads numerous unfunded internally and externally focused activities. In this way, the University of Rwanda SOHIC is a sustainable success and significant contributor to advancing the skills, knowledge, and leadership of our future One Health Workforce.
One Health Pre-service Education and Training as a Long-term Solution to Building a One Health Workforce

Irene Naigaga, One Health Central and Eastern Africa (OHCEA)

One Health Central and Eastern Africa (OHCEA) is an international university network of 24 Schools of Public Health and Veterinary Medicine in 16 universities in 8 countries of East, Central and Western Africa. OHCEA is using a regional approach to capacity building in One Health to produce a workforce with skills to prevent and mitigate complex health challenges at the human-animal-ecosystem interface. OHCEA’s One Health educational and training programs target pre-service, in-service and faculty. The pre-service education integrates the principles and practices of One Health into university curricula of veterinary, public health, environment and nursing through class- and field-based experiential learning at One Health demonstration sites. Other disciplines like social sciences and mass communication are also being incorporated in these experiential learning programs. This paper highlights the long-term advantages and benefits of pre-service One Health education generated from OHCEA’s eight-year experience in conducting One Health experiential learning programs. The advantages and benefits include 1) a common understanding and respect for the contribution of graduates from different disciplines in managing complex health challenges in communities, 2) improved cross-sectoral networking and One Health leadership skills demonstrated through the different OH interventions by multi-disciplinary teams of students 3) cost-effectiveness where One Health training is integrated within basic university curricula compared to high costs incurred during residential in-service trainings 4) opportunity to leverage on numbers, as it is easier to pool a large number of multi-disciplinary professionals at pre-service level than when they are already into service. The paper further discusses key drivers for pre-service One Health education and training at OHCEA institutions such as, institutionalization of One Health education and training; and support by governments at policy and action levels.
In Uganda, many software applications have been created for example the UHIN: It is a mobile health solution which started in 2003. It uses existing GSM/GPRS/ WiFi links with PDAs to support (community) health workers creating a regional eHealth network. (Mimbi & Bankole, 2015) On top of the existing methods, the 2017 OHCEA field attachment team decided to try a new method with the use of electronic display devices to disseminate information to the communities they visited. The devices used included laptop computers, tablets and smart phones. While at the demo site, the students visited various communities including hospitals, markets, fishing villages, pastoralist communities and schools. Here they interacted with the community, assessed their health challenges and used their multi-disciplinary abilities to come up with suitable interventions that would benefit the communities. They worked with the purpose of assessing the effect of the use of electronic display technology in the dissemination of health information. And the objectives of assessing the change in the number of people attending the sessions in 2017 compared to those from 2014. To assess the number of people who stayed for the full sensitization session. To ascertain the percentage of information that the people can pass on after a session. Various methods were used for example registration, head count of the sessions, post session evaluations and skit acting and screening. All of which were compared to those of the year 2014. The results showed a significant increase by over 60% in the number of people who attended the sensitizations in 2017 compared to those of the 2014 session. This was due to the attraction of the electronic display devices. 80% of the people that attended the session stayed till the end. This is because they could relate to the information that was being disseminated as the students created it customary for these communities and over 57% of the people could relay the key points of the message. It was concluded that the use of the electronic display devices as a method for disseminating health information has a significant effect on the attendance and retention of the information by the people.
ProgRESSVet (Programa Regional de Educación Sistemática de Servicios Veterinarios): Systematic Education to Promote Capacity and Development

Mary Katherine O’Brien, University of Minnesota-Twin Cities

M K O’Brien, University of Minnesota-Twin Cities, USA; E Leon, Centro Buenos Aires para la Capacitación de los Servicios Veterinarios, Argentina; A Perez, University of Minnesota-Twin Cities, USA.

Capacity building and workforce development for Veterinary Services is challenging for a number of reasons, including barriers related to language, financial resources, and time constraints. The capacity building process has traditionally been limited to efforts that lack of the known attributes for sustainable development, such as continuity and systematic coordination of the learning process in a timely and affordable manner. ProgRESSVet (Programa Regional de Educación Sistemática de Servicios Veterinarios) is an innovative educational initiative that aims to increase the capacity of Veterinary Services in Spanish-speaking countries of the Americas. Collaboratively developed and is offered through partnership between the Center for Animal Health and Food Safety (CAHFS) at the University of Minnesota and Centro Buenos Aires para la Capacitación de los Servicios Veterinarios (CEBASEV), with the technical collaboration of many professionals from different countries of the Americas, ProgRESSVet courses are delivered on-line, employing the best known and innovative practices for distance, technology-supported education. Individual courses based on OIE Advanced Competencies include learning activities and assessments aligned with content-specific learning goals, with focus on the application, integration, and sharing of new knowledge and skills. Based upon the OIE’s Advanced Competencies for Veterinary Service professionals, the program seeks to enhance both the knowledge and skills necessary for advanced practice in Veterinary Services. Beyond individual and group training, ProgRESSVet is aligned with the OIE’s conceptualization of the Veterinary Services as a Global Public Good, encouraging participants to see their work as an active part of the One Health paradigm of broader national, regional, and international systems. The poster describes the educational model of ProgRESSVet and includes results from the inaugural 2017 cohort of participants.
Does Climate Matter To Human Rabies Lethality? Multilevel Ecological Study In Vietnam

Juhwan Oh, Seoul National University College of Medicine

*J Oh, Seoul National University College of Medicine, Department of Medicine, South Korea.*

Climate influence including potential influence in some viral diseases such as Zica and Dengue Fever call attention. Air temperature and humidity influence in Rabies infection were known in animal experiment. However, climate influence on Human Rabies infection, which is one of preventable zoonotic disease death in low- and middle income countries, were rarely known yet. Number of Human Rabies death cases per month per province for last 20 years (from 1997 to 2016) were utilized as outcome variable from 6 provinces in Viet Nam. Monthly average measures of four climate variables (temperature, humidity, sunshine duration, raining) of 6 provinces from diverse ecological region from 1997 to 2016 were used for the empirical analysis. Total cases of Human Rabies suspicious cases due to animal bites were used as co-variates. After removing the monthly data with missing information, Poisson regression was applied for statistical analysis using 954 place (province)-time (specific year-month) ecological measurements. Human Rabies deaths with no post exposure prophylaxis were also investigated with similar analysis. Climate influenced the lethality of Human Rabies. Of Human Rabies suspicious cases with Post-exposure prophylaxis treatment due to animal bite, higher air temperature, measured by monthly average, reduced the number of deaths in a month while higher absolute humidity (monthly average) increased the number of death among the treated cases per each months, after controlling for the total prophylactically treated Human Rabies. One degree Celsius (C) higher temperature in monthly average decreased 0.60 cases of prophylactic treatment patients (p=0.004). On the other hand, one mb higher absolute humidity in monthly average increased 0.66 cases of Human Rabies death of the prophylactic treatment patients (p<0.001). These climate factors similarly influenced monthly Human Rabies deaths without post-exposure prophylaxis vaccination treatment. Further investigation to understand climate impact on Human Rabies treatment effectiveness in the death cases even after standardized post-exposure prophylactic treatment for Human Rabies Treatment as well as natural consequences of Human Rabies after animal bites need to begin.
Over 50 nations and UN agencies worldwide have come together since 2014 to coordinate and collaborate to strengthen prevention, detection and response to infectious disease threats and antimicrobial resistance using a One Health approach under the Global Health Security Agenda (GHSA). A One Health approach promotes multisectoral, transdisciplinary collaboration with the goal of achieving optimal health outcomes for people and animals and a safer environment. University of Minnesota (UMN) One Health faculty are on the front lines of implementing GHSA programs in or with 22 countries in Africa, Asia, Europe and North America. Through the USAID One Health Workforce project, UMN supports 79 universities in 14 countries to build new and innovative programs to meet workforce needs in their countries. UMN in collaboration with the US Department of Agriculture has also developed new tools and approaches for supporting multi-sectoral collaboration and coordination including the One Health Systems Mapping and Analysis Resource Toolkit (OH-SMART), used in or with 19 countries to strengthen systems for climate change resilience, antibiotic resistance, National Action Planning and infectious disease prevention, detection and response. Partners in this work include country governments, industry partners, US State Agencies, US government agencies, the UN Food and Agriculture Organization and the World Health Organization. Outcomes of the work to be presented include multi-sectoral zoonotic disease action plans in the US, Africa and Pakistan, updated National Antimicrobial Resistance Action Plans in Southeast Asia and programs and approaches to strengthening a One Health Workforce globally.
The Development Of A One Health Curriculum For Universities In Vietnam

Phuc Pham-Duc, Vietnam One Health University Network

P Pham-Duc, Vietnam One Health University Network (VOHUN) / Hanoi University of Public Health, Vietnam; Nguyen-Thu-Bich, Vietnam One Health University Network (VOHUN), Vietnam; T Le-Thu-Huyen, Vietnam One Health University Network (VOHUN), Vietnam; S G Fenwick, Tufts University, USA.

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.
A Model For Equitable Global Health Research: Uganda Research Training Collaborative

Lawrence Mugisha, Makerere University

J Rhein, University of Minnesota, USA; D Meya, Makerere University, Uganda; L Mugisha, Makerere University, Uganda; M McCoy, University of Minnesota, USA.

The Uganda Research Training Collaborative (URTC) model was piloted in 2016 with the aims of 1) creating a novel model of research training that benefits students from Ugandan partner institutions and from the University of Minnesota Academic Health Center; 2) developing mentorship skills among faculty and building a community of global health mentors; and 3) providing global health research capacity- and skill-building opportunities for students in Uganda and the University of Minnesota (UMN). The model recruited 15 students from across health science disciplines at Makerere University, Mbarara University of Science and Technology, and the University of Minnesota and formed four multidisciplinary teams. Each team was assigned one mentor per trainee to provide oversight and guidance on the development of the team research project. Teams worked together to develop student-initiated research projects. Over the 18-month program period, students were mentored through the stages of research planning, research ethics approval processes, and conducting research. Through surveys and focus groups, Center for Global Health and Social Responsibility staff and affiliated faculty mentors have assessed the effectiveness and adaptability of the model for broader implementation at other international partner locations. Initial evidence demonstrates a high level of engagement from faculty mentors and trainees, increased awareness of collaboration between UMN and partner institutions in Uganda, and successful progression by student teams to implement research plans. Additional interventions will be required to achieve program goals around mentor engagement and skill building. Program challenges include financial and logistical sustainability due to limited inputs such as funding, staffing, and mentor experts. The URTC model's significance is to demonstrate the potential and adaptability of a model for research training that is built on equitable principles for learners and mentors from each institution.
MAN-IMAL: An Experimental One Health Degree Program Around The Triad Animal-Man-Food

N Ruvoen, Oniris, MAN-IMAL program; France.

MAN-IMAL experiments the 1) use of ICTE, but most importantly 2) a multidisciplinary approach by its study content conceived by Teacher-Researchers from the Medical sciences, Veterinary sciences and the Agricultural engineering as well as 3) by the composition of its students coming from diverse 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 also 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 present results from multiple aspects of the project. Firstly, on the successful multi-disciplinary cooperation between teacher-researchers from different scientific fields, secondly on the particularities of coordinating a cross-disciplinary and multicultural class of students and finally on the importance of the close cooperation between the support staff and Teacher-Researchers.
The Student One Health Innovation Club in Rwanda: A Model for Sustainable Extracurricular Activities Preparing the Future One Health Workforce

Serge Muhizi, University of Rwanda

M Serge, University of Rwanda, Rwanda; D Kalisa, University of Rwanda, Rwanda; A Ndikubwimana, University of Rwanda, Rwanda; R Kibuuka, University of Rwanda, Rwanda; C Porta, University of Minnesota, USA.

The University of Rwanda Student One Health Student Club (SOHIC) invites students from varied disciplines to participate in extracurricular, practical and experiential learning activities that focus on collaborative prevention of and response to infectious zoonotic disease threats, such as Ebola, Anthrax, and Brucellosis. Since 2012, thousands of students have joined the club, and in 2017, there were xxx active students. SOHIC leaders have implemented activities with, and without, funding support. Examples of funded activities include student-focused development (e.g., the Global Health Case Competitions, infectious diseases management trainings), and community-focused outreach (e.g., the One Health Akagera field attachment, hygiene and sanitation community health education campaign). The SOHIC also initiated unfunded activities including an informal student debate program to build skills and knowledge related to One Health concepts and challenges. Students also implemented an Ebola awareness campaign in response to the Spring 2017 Ebola outbreak in neighboring Democratic Republic of Congo (DRC) with four confirmed deaths. The students sought to increase community member awareness of and factual knowledge about Ebola through this awareness campaign in Karongi district, the western province of Rwanda bordering DRC. SOHIC members have disseminated their club model, and successes, in international and regional conferences, and have served as mentors to students seeking to start clubs at their universities. Importantly, the SOHIC has demonstrated leadership succession and club sustainability since 2012, and while the club benefits from funding that facilitates robust extracurricular activities (such as 2-week field experiential learning projects), the club also leads numerous unfunded internally and externally focused activities. In this way, the University of Rwanda SOHIC is a sustainable success and significant contributor to advancing the skills, knowledge, and leadership of our future One Health Workforce.
Difficulties to combat AMR in Indonesia involving multiple actors from several different sectors

Selma Siahaan, National Institute of Health Research and Development, Ministry of Health Republic of Indonesia

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Introduction: The antimicrobial resistance (AMR) situation in Indonesia is quite alarming. The available data and information show that the prevalence extended-spectrum b-lactamase (ESBL)-producing K. pneumoniae, and E. coli were significant increased and has reached around 50% in 2013, and many of animal products contain antimicrobial (AM) residues. This situation needs exceptional public health intervention. Objective: Study aims to analyze AMR situation for policy development and its strategy conducted by National Institution of Health Research and Development from December 2014 to May 2015. Method: The study sites were in 8 provinces from west, central and east regions of Indonesia. Firstly, researchers did literature reviews. Then, we conducted in-depth interviews to local government managers in health, livestock and fisheries sectors. Researchers also conducted two workshops with participants from central ministries and local government offices, non-government organization, universities and World Health Organization. RESULTS: The study results were in every sector has its own policy in terms of AMR control. To be implemented the policies relate to their actors. In health sector the main actors were health professionals who do irrational treatment with AM, consumers who do not aware about the risk of AMR and the government is rather weak in terms of monitoring the distribution of AM. Similarly, in livestock and fishery sectors the actors were farmers who used AM as feed additive and prophylaxis, consumers who did not know about AM residues in meat and government that focusing on food security rather than food safety. The tasks, functions and authorities for AM control in every level of technical units has not clear, either in central or in provinces or in districts offices. All of that create difficulties to tackle AMR problems. CONCLUSION Government should initiate and support intensive working group collaboration between sectors and national movement or campaign to control AMR.
Sources of Information Among Backyard Poultry Owners During a Highly Pathogenic Avian Influenza Outbreak in Minnesota

Riikka Soininen, University of Minnesota, Center for Animal Health and Food Safety

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During an animal disease outbreak, access to reliable and real-time information is paramount for farmers and animal owners. However, published literature on the sources of information during an outbreak in the U.S. is very limited. During the 2014-2015 outbreak of H5 highly pathogenic avian influenza (HPAI) in the United States, more than 1,400 backyard flocks were sampled in Control Areas in Minnesota for routine surveillance. To better understand sources of information during this outbreak, a survey was sent to 4,624 small-scale poultry owners throughout Minnesota. Data from 1,245 returned surveys show that 18.4% of the owners relied very much on information from the Minnesota Board of Animal Health. The next two sources the owners relied very much on were local or statewide newspapers (18.1%) and house visits from state or federal employers (15.2%). Preliminary analysis suggests a significant difference in sources of information between all respondents and people living in close proximity to an HPAI infected premises. This data gives valuable information for state officials in preparing for animal disease outbreaks to better deliver important information to animal owners. Even though house visits can give reliable information, it might take days before someone comes for a visit. House visits also take a lot of resources to execute. This study shows that faster information delivery routes such as newspapers are also very important in outbreak communication. State officials should deliver their messages through these media as well.
The Utility of Online Promotion to Encourage Patient Awareness of Aspirin Use to Prevent Heart Attack and Stroke

Brian Southwell, RTI International

Science communication practitioners sometimes overlook important facets of the information environment in which their intended audiences live. We present analysis that highlights both the importance of ensuring adequate information exposure and the ephemeral nature of campaign promotion effects. Objective: We sought to assess population response to online promotion of an educational tool to inform people about aspirin as a preventive aid that was developed for the Minnesota Heart Health Program’s Ask About Aspirin campaign. Materials and Methods: Building on literature that emphasizes the importance of investigating patterns of behavior over time in conjunction with information environment trends, we collected 156 weeks of time series data on audience behavior and predicted that outcome as a function of paid search engine advertising, paid social media promotion, and general search interest in aspirin. Results and Conclusions: Through ARIMA modeling of tool engagement data adjusted for outcome series autocorrelation, we found a significant effect of online promotional effort on audience behavior. Total paid search advertising positively predicted weekly total of individuals who started using the self-assessment tool, coefficient = .023, t = 3.28, p = .001. This effect did not appear to be an artifact of broader secular trends, as Google search data on the topic of aspirin use did not add explanatory power in the final model nor did controlling for general search interest eliminate the significant coefficient for paid search promotion. Results hold implications for understanding the nature of online campaign effects and future science communication initiatives.
Characterization of extended-spectrum beta-lactamase and colistin resistance mechanism in Escherichia coli isolated from pigs in Thailand

Suthathip Trongjit, Department of Veterinary Public Health, Faculty of Veterinary Science, Chulalongkorn University

S Trongjit, Department of Veterinary Public Health, Faculty of Veterinary Science, Chulalongkorn University, Thailand; P Assavacheep, Department of Veterinary Medicine, Faculty of Veterinary Science, Chulalongkorn University, Thailand; R Chuanchuen, Department of Veterinary Public Health, Faculty of Veterinary Science, Chulalongkorn University, Thailand.

Colistin resistance and spread of mcr-1 in bacteria associated with food animals has become a serious public concern worldwide. The objective of this study was to examine the presence of colistin resistance and its encoding genes, mcr-1 and mcr-2 in E. coli isolated from pig in Thailand. Four-hundred fifty four E. coli isolates from clinically healthy pigs (n=354) and clinically ill pigs with diarrhea (n=100) were obtained from commercial pig farm in Thailand during 2007-2016. All were determined for their susceptibility to colistin and ESBL production and screened for the presence of mcr-1 and mcr-2. Horizontal transfer of mcr-1 and mcr-2 was determined by using biparental mating. Fifteen colistin-resistant E. coli were randomly selected to characterize pmrAB by nucleotide sequencing. Colistin-resistant E. coli isolates were detected in healthy pigs (40%) and sick pigs (77%). No mutations were observed in pmrAB. The mcr-1 gene was identified in the E.coli isolates from 7% of clinically healthy pigs and 20% of clinically sick pigs. The mcr-2 gene was detected only in five E. coli isolates from healthy pigs. Fourteen percent of the healthy pig isolates and 46% of the sick pig isolates were confirmed to be ESBL positive. Eight E. coli isolates from sick pigs carried mcr-1 and simultaneously produced ESBL. Two out of eight isolates could cotransfer mcr-1 and blaCTX-M to Salmonella. The results highlight the wide distribution of colistin resistance and the co-localization of mcr-1 and ESBL genes on a single plasmid among the E. coli isolates in this collection.
Breaking Down Silos: The 5x5 Initiative to Bridge Human Health, Environmental, and Animal Research

Marcella Windmuller-Campione, University of Minnesota

M Windmuller-Campione, University of Minnesota, USA; T Potter, University of Minnesota, USA; P Schreiner, University of Minnesota, USA; J Sellman, University of Minnesota, USA; N Holtan, University of Minnesota, USA.

Objectives: Human health and medical science, environmental science and ecology, and animal science and veterinary science are all disciplines that have a depth of historic knowledge and cutting edge research. While researchers within each respective discipline are making strides to improve global health as components of OneHealth, these advances can be discipline specific and/or may not reach the total “interdisciplinary audience”. It can be difficult for individual researchers to span, connect, and develop interdisciplinary collaborations. The 5 x 5 Initiative in the Institute for Advanced Study at the University of Minnesota aims to bridge this hurdle by bringing together small groups of people (5 people) from differing disciplinary perspectives for a low-stakes, short-term exploration (5 meetings over several months).

Materials and Methods: One 5 x 5 Initiative brought together 5 researchers with expertise and passion for human, environment, and animal relationships. We will describe the formation of relationships, the building of our interdisciplinary community, and the “bridging” of languages. During our group meetings, we have engaged in open conversations and discussions where similarities and differences have emerged. A common point in all the discussions is the need for an interdisciplinary approach regarding research in human or planetary health.

Results and Conclusions: The results of our group interactions do not follow a traditional structured format, but rather highlight an example program for an interdisciplinary experience. The opportunity to participate in the 5 x 5 group has broadened our own knowledge and fostered new collaborations, which may or may not translate into direct research grants but contributes to the breadth of our research, teaching, and outreach.
The Uses Of GIS And Multisectoral Policy Analyses To Support Rabies Control In Thailand

A Wiratsudakul, Faculty of Veterinary Science, Mahidol University

A Wiratsudakul, Faculty of Veterinary Science, Mahidol University, Thailand; K Kanankege, College of Veterinary Medicine, University of Minnesota, USA; A Perez, College of Veterinary Medicine, University of Minnesota, USA; O Prasarnphanich, Thailand MOPH-US CDC Collaboration, Thailand; P Wongnak, Faculty of Veterinary Science, Mahidol University, Thailand; C Yoopatthanawong, Faculty of Veterinary Science, Mahidol University, Thailand; K Myhre Errecaborde, College of Veterinary Medicine, University of Minnesota, USA.

Rabies is a fatal zoonotic disease with a global impact, especially in endemic countries including Thailand. However, the disease is preventable with interdisciplinary approaches. Thailand aims to eradicate rabies within the country by 2020, which is in line with the World Health Organization initiative to end human rabies deaths worldwide by 2030. To support this very urgent and crucial purpose, our team is trying to expand the tools and methods available to support rabies control in Thailand by employing a multifaceted system based approach. We pilot the use of existing epidemiological data to build spatiotemporal maps that may indicate areas where rabies control efforts are most needed. Three epidemiological indicators for rabies are considered; number of animal or human rabies cases, number of dog attacks and number of post-exposure prophylaxis. A Poisson regression models will be developed to quantify the association of each indicator with other potential determinants including number of stray animals, number of garbage dumping sites, number of animal vaccines distributed and number of temples. A choropleth map indicating the risk will be generated. Our multidisciplinary team will work with key-stakeholders through a policy field analysis to ensure that the maps are made available to support continued rabies control efforts. To integrate our risk maps into program implementation, we planned to apply policy tools such as the multi-sectoral outbreak-mapping tool, so-called 'One Health Systems Mapping and Analysis Tool (OH-SMART)' to engage program managers working on the national rabies control programs. This policy tool has been exploited by over 19 countries globally to support operational multisectoral policies. The OH-SMART tool can support managers to integrate risk maps with program design and planning efforts.
The National Institutes of Health is interested in developing a robust biomedical research enterprise. This poster will help you: 1) Discover resources available to help you develop into a successful independent biomedical researcher. 2) Find out how research is solicited, and where funding opportunities are advertised. 3) Learn about training resources that are available for administrative staff and new investigators. 4) Establish proficiency with tools to help you identify and develop collaborations.
Select NIAID Research Priorities

A Zeituni, NIAID/NIH

A Zeituni, NIAID/NIH, USA; S Mendez, NIAID/NIH, USA; H Hornbeak, NIAID/NIH, USA.

Discover current Funding priorities at NIAID in response to congressional appropriations.
Current Practice Of Neuroimaging For Stroke At A Tertiary Teaching Hospital In Nepal, Where Do We Stand?

Jayanti Gyawali, Kirtipur Hospital, PHECT Nepal

J Gyawali, Kirtipur Hospital, PHECT Nepal, Nepal; R Gautam, Chitwan Medical College, Nepal.

CT and MRI have not been introduced so long for neuroimaging in medical diagnosis in Nepal. A retrospective study was carried out at Chitwan Medical College, Chitwan, Nepal during June- July, 2016 to evaluate the current practice of neuroimaging for stroke for suspected non-traumatic neuro-emergencies. The imaging data of 73 emergency patients presenting sudden onset of neurology symptoms with no history of recent trauma were analyzed by using IBM SPSS 20. All the 73 emergency patients were referred for CT scan including only 1 being referred for MRI after CT scan. CT was always preferred owing to much lower service cost of CT and lack of practice on MRI among clinicians. It was found that 66.66% (n=50) of the cases were within the age range of 51-80 years of which 62% (n=31) were males and 38% (n=19) were females. The occurrence of infarct was found to be more among male (25.55%) than female (13.33%) while the bleed was more among female (26.66%) than male (20.99%). The majority of infarct were found to be lobar (n=9, 60%) while the bleed was present in thalamus (n=5, 29.4%), basal ganglia (n=3, 17.6%), corona radiate (n=3, 17.6%), lobar (n=2, 11.7%) and others (n=4, 23.52%). From our study 56.16% cases remained undiagnosed which shows that we are far behind because the primary imaging modalities used was CT scan and those undiagnosed cases were not sent to DWI MRI for follow up. It requires establishing MRI as imaging modality for stroke, follow up of recent international protocols among clinicians and lower service cost of MRI for accurate diagnosis of stroke in Nepal.
One Health: Improving Public Health by Providing Care to Marginalized Clients and Companion Animals

Doris Leung, University of British Columbia, Community Veterinary Outreach

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Background: Current research demonstrates that pet ownership, especially amongst marginalized populations provides significant protective factors against depression, anxiety, and substance use. This generates strong motivators for positive change, resulting in improved health and well being. An estimated 20% of homeless individuals in Canada are pet owners. In British Columbia, over half of street-involved youth report having a pet. Community Veterinary Outreach (CVO) is a registered Canadian charitable organization with a mandate to improve the public health of vulnerable communities through provision of veterinary care to pets in need, and to connect pet owners to health and social services. In 2016, with collaboration from multidisciplinary community partners and academic partner University of British Columbia, CVO organized a pilot “One Health” clinic for marginalized clients and pets in Vancouver. One Health clinics respond to growing public health concerns in Vancouver’s downtown eastside. Recently, there is an increased prevalence of physical and mental health conditions amongst its residents. Moreover, marginalized pet owners face increased barriers and challenges to health care access, and often place the health of their pet before their own. This emphasizes the need for innovative methods to address health issues and promote health equity amongst this population. Methods: One Health clinics are conducted at community centres where clients are accepted on a walk-in or referral basis. The clinics offer a destigmatizing environment for clients to receive care with a multidisciplinary approach. Pets receive vaccinations, nutritional consults, referrals to sterilization services, and medical treatments. Clients receive referrals to community health clinics, mental health support, influenza vaccinations, Take Home Naloxone kits and wound care treatment from health care providers and students. Rates of uptake in human and veterinary health services are documented. Feedback from clients, health care professionals, and students are encouraged following the clinics. Results: One Health clinics provided health care services to over 200 clients and 100 pets in Vancouver from 2016 to 2017. Conclusions: In addition to receiving positive feedback from clients of One Health clinics, volunteer students and health care providers remarked about the invaluable experience of working alongside marginalized groups, with many expressing a desire to become champions for social and health change in the community. The unique application of the One Health concept, with collaboration from multidisciplinary health professionals demonstrates significant potential in improving public health of marginalized populations and their pets and can be extrapolated into communities outside of Vancouver.
Tuberculosis (TB) is a communicable disease for millennia and still remains as a major global health problem. Eliminating pulmonary TB will require interrupting TB transmission as well as major efforts to address latent TB infection. TB incidence rate was 18 per 100,000 population while TB mortality rate was 0.62 per 100,000 population in Turkey in 2016. This study, hence, aims to explore factors contributing to TB treatment among TB patients in Turkey. Between 2012 and 2015 a total of 53871 TB cases were reported in Turkey. Logistic regression analysis of these cases showed that the treatment success of patients living in 9th region is lower than 1st region (OR = 0.516; p = 0.013), the success ratio of tuberculosis treatment in HIV negative patients was 3.178 times (p < 0.001) higher than HIV positive patients, treatment success in female was 1.304 times more than in male patients (p=0.008), the treatment success of non-drug-resistant patients was 1.576 times higher than those of drug-resistant patients (p < 0.001), the success of the treatment of tuberculosis patients being Turkish citizens was higher than non-Turkish (OR= 0.367; p<0.001), the treatment success from previous treatment failures (OR= 0.367; p = 0.000) and relapse cases (OR=0.563; p=0.009) were lower than in the new case, treatment success of non-DOT (Directly Observed Treatment) patients (OR = 0.053; p < 0.001) and partially DOT-group (OR= 0.258; p <0.001) is lower than DOT group is. These results suggest that to increase the treatment successes of groups with low treatment success, new administrative and political strategies needs to developed for the patient groups needing to be addressed.