Canadian Association of Veterinary Epidemiology and Preventive Medicine Conference

Program and Schedule

Thinking outside the Epidemiological Tool Box

May 16 -17, 2016

University of Guelph
Thank you to our sponsors!

- Ontario Veterinary College - Deans’ Office
- Population Medicine Department, OVC, University of Guelph
- University of Guelph - Office of Graduate Studies
- Centre for Public Health and Zoonoses

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We are pleased to offer the following short course after the CAVEPM Conference:

**Introductory Network Analysis**  
**Instructors: Drs. Olaf Berke & Zvonimir Poljak**

Network analysis is an increasingly important methodology used in animal and public health for various purposes. The past two decades have seen the rise of spatial or geographical epidemiology. Geographical location could in many cases be just an indicator for contact between individuals where close proximity is increasing the likelihood of contacts and the chances of passing infectious diseases. If the contact networks are known a more direct analysis is possible. This course will introduce the basic terminology and concepts of network analysis. The topics discussed will include methods to process network data, visualize networks, and provide and interpret statistics at different levels.

Hardware and software: Participants are welcome to bring their own laptop with the freeware programs R/igraph and UCINET installed.

**May 18-20  9am - 4:30pm  Room 1810 PAHL**

At the end of the course students should be able to:
- Import, and manage the data using network analysis software
- Describe and characterize a contact network, and
- Understand the basic methods of network analysis
**Welcome Reception & Registration**

Join us Sunday, May 15th at the Bullring Pub for light fare and good conversation. [www.uoguelph.ca/campus/map/bullring/](http://www.uoguelph.ca/campus/map/bullring/)

The Bullring is the only building on campus with one continuous wall that supports the roof. The Bullring was built in 1901 and was originally used as a pavilion for the study and judging of horses, cattle, sheep and swine. Since then, the Bullring has been a popular bar/dance club and is now a coffeehouse.

**Scientific Presentations**

Scientific oral presentations and registration

[www.uoguelph.ca/campus/map/ahl/](http://www.uoguelph.ca/campus/map/ahl/)

The Pathobiology/Animal Health Lab Building is easily recognizable by its large glass sections. Room 1800, on the main floor will be where registration and speaking activities will occur on Monday and Tuesday of the CAVEPM conference. This building also hosts a Second Cup coffee shop.

**Poster Viewing, Breaks & Lunch**

Lunch, poster viewing, and wellness breaks

[www.uoguelph.ca/campus/map/ovc/](http://www.uoguelph.ca/campus/map/ovc/)

The OVC Learning Commons, formerly the OVC Library, is a bright and open, newly renovated area in the main OVC building. Accessible by the grand staircase that faces Gordon street, the learning commons is on the second floor. Wheelchair and elevator access doors are provided at the entrance facing College Ave.
## Program

### Monday, May 16

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<tr>
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<th>Location</th>
<th>Session</th>
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<tr>
<td>7:00am - 8:00am</td>
<td>Learning Commons (OVC Library)</td>
<td>Poster Set-up</td>
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<tr>
<td>8:00am - 12:00pm</td>
<td>Registration</td>
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<tr>
<td>8:30am - 8:45am</td>
<td>PAHL 1800</td>
<td>Welcoming Remarks</td>
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<tr>
<td>8:45am - 9:30am</td>
<td>PAHL 1800</td>
<td>Plenary Speaker: Dr. Lea Berrang-Ford McGill University</td>
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<tr>
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<td></td>
<td><em>Epidemiologic paradigms and grand challenges in global environmental health</em></td>
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<tr>
<td>9:30am - 10:30am</td>
<td>PAHL 1800</td>
<td><strong>FOODBORNE PATHOGENS AND ZOONOSES AT THE FARM LEVEL</strong></td>
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<tr>
<td></td>
<td></td>
<td>Margaret Ainslie A longitudinal study of <em>Salmonella</em> in pigs</td>
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<td>Laura Falzon From the lab to the field and back to the desk: Experiences evaluating a ruminant brucellosis test in Côte D'Ivoire</td>
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<td>Juliana Ferreira Dynamics of Influenza virus transmission in a swine herd and analysis of risk factors for recurrent infections</td>
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<td>Saranya Nair Time course of <em>Salmonella</em> shedding in naturally-infected grower-finisher pigs</td>
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<tr>
<td>10:30am - 11:00am</td>
<td>Learning Commons</td>
<td>Wellness Break and Poster Viewing</td>
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<tr>
<td>11:00am - 12:00pm</td>
<td>PAHL 1800</td>
<td><strong>FOODBORNE PATHOGENS AND ZOONOSES AT THE FARM LEVEL</strong></td>
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<tr>
<td></td>
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<td>Katrina Ponich Antimicrobial resistance of bovine <em>Salmonella</em> isolates obtained by Alberta Agriculture and Forestry (2006 - 2014).</td>
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<td>Victoriya Volkova Impact of antimicrobial drug use on resistance in foodborne pathogens: Estimation of the exposure and effect</td>
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<td><strong>FOOD SAFETY, INSPECTION, EDUCATION AND SURVEILLANCE</strong></td>
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<td>Ana Pascual-Linaza Efficiency of and risk factors associated with post-mortem surveillance for Bovine Tuberculosis in cattle in Northern Ireland</td>
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<td>Agricola Odoi Are beef tapeworm identification rates in South Africa influenced by the provider of inspection services?</td>
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**Lunch and Poster Viewing**
## Monday, May 16th - afternoon session

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<tr>
<td>1:30pm - 2:15pm</td>
<td>PAHL 1800</td>
<td>Plenary Speaker:</td>
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<td><strong>Dr. Kamran Kahn</strong></td>
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<td><strong>St. Michael's Hospital; University of Toronto</strong></td>
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<td><em>When academia met industry: A modern-day story in global health</em></td>
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<td>2:15pm - 3:15pm</td>
<td>PAHL 1800</td>
<td><strong>Food Safety, Inspection, Education and Surveillance</strong></td>
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<td><strong>André Ravel</strong></td>
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<td>Combining exposure assessment, Bayesian model, and molecular data to quantify the sources of human campylobacteriosis</td>
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<td><strong>Shannon Majowicz</strong></td>
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<td>Food safety in a sample of Ontario high school students: knowledge, attitudes, and practices</td>
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<td><strong>Cheryl Waldner</strong></td>
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<td>Exploring new technologies to support investigation of foodborne disease</td>
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<td><strong>Barbara Wilhelm</strong></td>
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<td>Risk profile and quantitative human exposure assessment of Hepatitis E Virus from pigs or pork in Canada</td>
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<tr>
<td>3:15pm - 3:45pm</td>
<td>Learning Commons</td>
<td>Wellness Break and Poster Viewing</td>
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<tr>
<td>3:45pm - 4:45pm</td>
<td>PAHL 1800</td>
<td><strong>Planning and Prioritizing Public and Animal Health Decisions</strong></td>
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<td><strong>Catherine Bouchard</strong></td>
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<td>Integration of social and environmental vulnerabilities to prioritize and adapt local response against Lyme disease in Canada</td>
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<td><strong>Marion Ripoche</strong></td>
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<td>Spatial heterogeneity in <em>Ixodes scapularis</em> distribution within the Lyme disease emergence zone in southern Canada</td>
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<td><strong>Melissa McLaws</strong></td>
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<td>Which vaccines are most important? A decision support tool for foot and mouth disease vaccine bank managers</td>
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<td><strong>Courtney Primeau</strong></td>
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<td>Using integrated assessment modeling to investigate factors affecting the recovery of antimicrobial resistant bacteria along the food chain: A pilot study</td>
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<td>4:45pm - 5:00pm</td>
<td>PAHL 1800</td>
<td><strong>Closing Remarks</strong></td>
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### CAVEPM 2016 Banquet Location

6 - 10 PM  
Art Gallery of Guelph

Located on University campus - join us at the CAVEPM 2016 Banquet for a trendy evening of station-style dining featuring a special menu of delicious food along with great conversation and viewing of contemporary art. Formerly known as the Macdonald Stewart Art Centre: 358 Gordon St. Guelph
## Program

**Tuesday, May 17th - morning session**

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<tr>
<td>8:00am - 9:30am</td>
<td>PAHL 1800</td>
<td><strong>Issues in Veterinary Epidemiological Teaching and Research</strong></td>
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<td>Cathy Bauman</td>
<td>The first Canadian national dairy study: Myelinating new pathways</td>
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<td>Brandy Burgess</td>
<td>Epidemiology education in the veterinary curricula - The current state of affairs</td>
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<td>Jan Sargeant</td>
<td>Development of the STROBE-Vet Statement: Strengthening the reporting of observational studies in epidemiology - Veterinary extension</td>
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<td>Charlotte Winder</td>
<td>Utility of an online learning module for teaching disbudding in dairy calves, including cornual nerve block application</td>
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<tr>
<td>9:30am - 10:00am</td>
<td>Learning Commons</td>
<td>Wellness Break and Poster Viewing</td>
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<tr>
<td>10:00am - 11:30am</td>
<td>PAHL 1800</td>
<td><strong>Epidemiology of Production in Agricultural Systems</strong></td>
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<td>Suppada Kananub</td>
<td>Descriptive analyses of bulk tank milk composition, and factors associated with somatic cell counts and milk urea nitrogen in central Thailand</td>
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<td>Chunu Mainali</td>
<td>Epidemiological characterization of small poultry flocks in Alberta</td>
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<td>Omid Nekouei</td>
<td>Lifetime effects of infection with Bovine Leukemia Virus on longevity and milk production of Canadian dairy cows</td>
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<td>Melissa Moggy</td>
<td>A mixed methods study of management practices associated with cattle pain and stress in western Canada cow-calf operations</td>
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<tr>
<td>11:30am - 1:00pm</td>
<td>Learning Commons and PAHL 1800</td>
<td><strong>Epidemiology of Infectious Diseases in Agricultural Species</strong></td>
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<tr>
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<td>Emily Arndt</td>
<td>Prevalence of <em>Streptococcus suis</em> in clinical cases and healthy-carrier pigs</td>
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<td>Danielle Hopkins</td>
<td>An investigation of the factors contributing to mortality during an outbreak of <em>Streptococcus suis</em> infection in nursery pigs and vaccine efficacy</td>
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<tbody>
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<td>1:00pm - 2:30pm</td>
<td>PAHL 1800</td>
<td><strong>Epidemiology of Infectious Diseases in Agricultural Species</strong></td>
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<td>Chika Okafor: Prevalence of <em>Tritrichomonas foetus</em> in Tennessee beef bulls</td>
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<td>Niorn Ratanapob: Causes of death in young lambs submitted for post-mortem examination to the Atlantic Veterinary College diagnostic services (2005-2014)</td>
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<td>Kelsey Spence: Describing the Ontario equine movement network to understand the risk of disease introduction and spread</td>
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<td>Trisha Westers: Evaluation of treatment criteria for use in targeted selective treatment programs to control Type II Haemonchosis in periparturient ewes in Ontario</td>
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<tr>
<td>2:30pm - 3:00pm</td>
<td>Learning Commons</td>
<td>Wellness Break</td>
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<tr>
<td>3:00pm - 4:30pm</td>
<td>PAHL 1800</td>
<td><strong>Epidemiology in Small Animal Populations</strong></td>
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<td>Natasha Janke: Recent trends in cat admissions and the effect of the capacity for care program at the Guelph Humane Society, 2011 - 2015</td>
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<td>Aileigh Kay: Factors influencing time to adoption for dogs in the British Columbia SPCA shelter system</td>
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<tr>
<td>4:30pm</td>
<td>PAHL 1800</td>
<td><strong>Epidemiology and Connections in Networks, Space, and Time</strong></td>
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<td>Rob Deardon: Infectious disease transmission models with uncertain underlying contact network information</td>
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<td>Amy Greer: Using the Incidence Decay and Exponential Adjustment (IDEA) model to understand the early dynamics of the 2014 Porcine Epidemic Virus (PEDV) outbreak in Ontario</td>
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<td>Tatiana Petukhova: Comparison of time series models for prediction of Influenza A Virus frequency in Ontario swine</td>
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<td><strong>Closing Remarks and Awards</strong></td>
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A LONGITUDINAL STUDY OF SALMONELLA IN PIGS

Margaret Ainslie¹, Vahab Farzan², Robert Friendship³, Cornelis de Lange¹, Brandon N Lillie¹

¹Department of Pathobiology, ²Department of Population Medicine, ³Department of Animal Bioscience; University of Guelph

The objective of this study is to investigate Salmonella shedding and colonization in pigs from birth to slaughter. Eight farms were included in the study. On each farm a winter and summer cohort were monitored. For each cohort sixty piglets were selected from eight to ten sows within 24-96 hours after farrowing. During the nursery stage, pigs received either a high complexity (HC) or low complexity diet (LC; containing reduced animal protein). Fecal samples or rectal swabs were collected within 24-96 hours after birth (only in cohort 2), at weaning, end of nursery, end of grower, and before marketing. Tissue samples were collected at slaughter. All samples were cultured for Salmonella. A multi-level mixed-effects modelling method was used to analyze Salmonella shedding at different stages of production as well as among pigs in two different nursery diet groups. Spearman’s rank correlation was used to determine the association between Salmonella shedding and presence of Salmonella in tissue samples. Salmonella was detected in 4.9% (20/409) of piglets within 24-96 hours after birth, 10.9% (80/735) at weaning, 14.1% (92/651) at end of nursery, 8.4% (40/487) at end of grower, and 25.7% (93/362) of pigs at end of finisher. Salmonella was cultured from 22.4% (70/312) of tonsils and 31.6% (60/190) of lymph nodes but presence of Salmonella in tissue samples was not correlated with fecal shedding (P>0.05). Multilevel mixed-effects analysis of data collected to date indicates an increase in prevalence of Salmonella shedding from early life to the finisher period (P<0.05) with no effect of dietary treatment on Salmonella shedding and colonization (P>0.05). These results suggest that Salmonella shedding peaks near the end of the finishing period and remains high at slaughter. However, detection of Salmonella shedding in finisher pigs may not be a good indicator for presence of Salmonella at slaughter.

FROM THE LAB TO THE FIELD AND BACK TO THE DESK: EXPERIENCES EVALUATING A RUMINANT BRUCELLOSIS TEST IN CÔTE D’IVOIRE

Laura C. Falzon¹, Sylvain Traoré², Bassirou Bonfoh², Jean-Baptiste Assamoï², Vessaly Kallo³, Gertraud Schüpbach¹, Esther Schelling⁴

¹Veterinary Public Health Institute, University of Bern, Switzerland, ²Centre Suisse de Recherches Scientifiques, Abidjan, Côte d’Ivoire, ³Sécrétaire General du Conseil de l’Ordre National des Vétérinaires de Côte d’Ivoire, Côte d’Ivoire, ⁴Swiss Tropical and Public Health Institute, Basel, Switzerland

Brucellosis is an economically important zoonosis. While most diagnostic tests for brucellosis can only be performed in the laboratory, the Fluorescence Polarization Assay (FPA) was developed as a field test. The objective of this pilot project was to evaluate the feasibility of using the FPA for rapid diagnosis of ruminant brucellosis at an abattoir in Abidjan, Côte d’Ivoire. Due to lack of approval, blood samples could initially only be collected from small ruminants at a live animal market. These samples were processed and tested with the FPA in a laboratory. When approval was granted, blood samples were collected from ruminants at the abattoir. These samples were processed immediately and the FPA was performed on site. To assess the FPA intra-test agreement, some of the serum samples tested at the abattoir were re-tested with the FPA in a laboratory. To assess inter-test agreement, all serum samples were then tested with the Rose Bengal Test (RBT). A total of 236 serum samples were tested with the FPA; 106 and 130 from the animal market and abattoir, respectively. Of these, 31 were positive and 31 were suspicious for brucellosis. The FPA was repeated on 37 of the 130 samples collected at the abattoir, and comparison of results indicated poor intra-test agreement (Kappa = 0.16 to 0.27). The RBT was performed on 231 samples, and of these 10 were positive. A comparison of FPA and RBT results indicated poor inter-test agreement (Kappa = -0.08 to 0.14). The FPA did not perform well in tropical field conditions and this will be discussed with the manufacturing company. Additionally, several challenges were encountered while working on the field, including lack of handling facilities at the abattoir and no animal identification system. These findings highlight the importance of conducting pilot projects before embarking on larger epidemiological field studies.
DYNAMICS OF INFLUENZA VIRUS TRANSMISSION IN A SWINE HERD AND ANALYSIS OF RISK FACTORS FOR RECURRENT INFECTIONS

Juliana B Ferreira1, Helena Grgić1, Robert Friendship1, Greg Wideman2, Eva Nagy3, Zvonimir Poljak1.

1Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada; 2South-West Veterinary Services, Stratford, Ontario; 3Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada.

Influenza A virus (IAV) is a pathogen endemically present in most swine-producing regions. The changing nature of commercial swine production and emergence of different variants could result in different dynamics of IAV infection, and the resulting clinical disease. Therefore, the objectives of this study were to describe patterns of IAV infection in pigs after weaning in multi-source nursery herds, and to determine factors that contribute to such patterns. An all-in/all-out nursery barn, with piglets from 5 different sow sources, was included in the study. Within 2 hours of arrival, 400 pigs were selected for the initial virological testing. Nasal swabs were collected weekly for virus isolation from 81 and 75 pigs, for two trials, respectively. Eight hemagglutination inhibition assays were used for antibody titers. Risk factor analysis for virological positivity and likelihood of recurrent infection was conducted using logistic regression and survival analysis.

In Study 1, at ~30 days post-weaning, 100% of pigs were positive and shedding viruses, with 35 (43.2%) pigs being positive recurrently. In Study 2, 48% pigs were positive only once and 10.7% pigs were positive recurrently. Results indicated that IAV can circulate during the nursery phase in a cyclical pattern and the likelihood of recurrent infections was higher for pigs with higher levels of heterologous (within-subtype) maternal immunity (p<0.05), but only for the H3N2 strain, which could explain ongoing issues in the nursery. However, the presence of high heterologous immunity is not likely the full explanation for all recurrent infections because some pigs with low heterologous infections were also noticed to be recurrently infected. A high degree of within-pen clustering was also observed, suggesting that transmission within a pen played an important role. Thus, the study of prolonged or recurrent IAV infections could be important when trying to control IAV infection in nursery barns.

TIME COURSE OF SALMONELLA SHEDDING IN NATURALLY-INFECTED GROWER-FINISHER PIGS

Saranya Nair, Vahab Farzan, Terri L O’Sullivan, Robert M Friendship

Department of Population Medicine, University of Guelph, Guelph Ontario, Canada

The presence of multi-drug resistant Salmonella spp. in the swine population is an important food safety concern. Understanding the patterns of Salmonella shedding from the grower stage until slaughter will help to improve prevention and control strategies. The objectives of this study was to determine how long pigs shed Salmonella if they enter a grower barn already naturally-infected and whether Salmonella can be detected from such pigs at slaughter. Nine-week-old pigs (n=45) were purchased from a farm with a history of salmonellosis and housed at the University of Guelph research facility for 10 weeks. Weekly fecal samples and tissue samples collected at slaughter were cultured for Salmonella. A multilevel mixed-effects logistic regression model was used to analyze the prevalence of Salmonella shedding at the pig level. A Kaplan-Meier survival function and a Cox proportional hazard model were used to present and evaluate Salmonella shedding over the time. Salmonella was cultured from all pigs at least once. Out of the 45 pigs, 41 pigs were positive 4 times and one pig tested positive 8 times. The highest prevalence of Salmonella shedding was at 10 weeks of age (80%) and at 13 weeks of age (91%). As pigs aged from 10 to 17 weeks of age, there was a significant decrease in Salmonella shedding (P<0.001). At slaughter, Salmonella was isolated at least once from a spleen, liver, lymph node, or tonsil, and thrice from cecal contents. Of the 7 pigs (16.3%; 7/43) harboring Salmonella at slaughter, 5 (71%) of those had not tested positive on weekly fecal checks for at least 7 weeks or longer. These findings indicate that the absence of Salmonella detection in fecal samples in pigs in the late finisher stage may not be indicative of the carcass being Salmonella-free at slaughter.
ANTIMICROBIAL RESISTANCE OF BOVINE SALMONELLA ISOLATES OBTAINED BY ALBERTA AGRICULTURE AND FORESTRY (2006-2014)

Katrina L Ponich¹, Sylvia L Checkley¹, Rashed Cassis², Carol Goertz², Delores Peters³, Simon JG Otto³

¹Department of Ecosystem and Public Health, University of Calgary, Faculty of Veterinary Medicine. ²Agri-Food Laboratories Branch, Food Safety Division, Alberta Agriculture and Forestry. ³Animal Health Branch, Animal Health and Assurance Division, Alberta Agriculture and Forestry.

Background: Antimicrobial resistance (AMR) has become a global one-health concern, negatively impacting both animal and human health. Bovine salmonellosis has grave economic implications for producers due to loss of production and calf mortality, and its zoonotic potential is a public health concern. Antimicrobial resistance can limit treatment options for bovine and human Salmonella infections. It is essential to develop a better understanding of the prevalence of AMR in bovine Salmonella to identify effective treatment options and to protect human health by improving antimicrobial stewardship.

Objective: To characterize the antimicrobial susceptibility profiles of bovine Salmonella species isolates obtained by Alberta Agriculture and Forestry (AF) and to provide AMR surveillance information.

Methods: S. Typhimurium and S. Dublin are classified as Reportable pathogens in cattle in Alberta under the Animal Health Act. From 2006-2014, AF obtained Salmonella isolates from 84 farm visits (fecal samples or environmental swabs) through the Disease Investigation and other programs under the directive of the Alberta Veterinary Surveillance Network. Antimicrobial susceptibility testing was completed using Sensititre CMV3AGNF plates. Analysis will be completed using SPSS and STATA.

Results: Preliminary results show that twelve different Salmonella serotypes were isolated from these 84 farm visits. Of these serotypes S. Typhimurium (n=54) and S. Dublin (n=14) samples predominate. Three serotypes demonstrated resistance to three or more antimicrobial classes. This work is ongoing. Final results will be available and discussed in May 2016.

Conclusion: These findings are of paramount importance to guide bovine antimicrobial stewardship for both producers and veterinarians by providing information on the extent of antimicrobial resistance in Salmonella from cattle in Alberta. This research will provide a basis for future work in Alberta by providing a piece of surveillance information that can be used alongside other AMR surveillance intelligence in Canada.
IMPACT OF ANTIMICROBIAL DRUG USE ON RESISTANCE IN FOODBORNE PATHOGENS: ESTIMATION OF THE EXPOSURE AND EFFECT

Victoriya Volkova1, Casey Cazer2, Yrjö T. Gröhn2

1Department of Diagnostic Medicine/Pathobiology, Institute of Computational Comparative Medicine, College of Veterinary Medicine, Kansas State University, USA. 2Department of Population Medicine and Diagnostic Sciences, College of Veterinary Medicine, Cornell University, USA

Antimicrobial drug use in food animals is a driver of antimicrobial resistance. Veterinary pharmacologists have studied the drugs’ pharmacokinetics and pharmacodynamics against the target pathogens. However, the exposure of non-target enteric bacteria (potential foodborne pathogens) of the treated animals to the drugs or their active metabolites is a food safety concern. The effective exposure likely occurs in the lower intestine. We developed a pharmacokinetic-modeling based framework for projecting the active concentrations of antimicrobial drugs and their metabolites in the intestines of animals treated parenterally and orally. We applied the framework to parenteral cephalosporin ceftiofur and oral chlortetracycline in beef cattle. Our studies indicate that the intestinal antimicrobial concentrations relate non-linearly to the animal-level treatment doses and schedules. The fraction of administered drug to which enteric bacteria are exposed differs sizably among antimicrobials, and for a given antimicrobial likely differs among food-animal species. It is further influenced by production practices, e.g., feeding choices. This may explain the inconsistent results of studies evaluating the impact of antimicrobial use in farm animals on resistance operating with the use estimates at the animal or farm level. Further, describing the effect of the intestinal antimicrobial concentrations requires new pharmacodynamic models reflecting the high concentrations and variable susceptibility of enteric bacteria in the anaerobic intestinal conditions. Our experimental research shows that the antimicrobial susceptibility of foodborne pathogens Escherichia coli and Salmonella enterica changes significantly in anaerobic vs. aerobic conditions. We will present our approach to estimating the antimicrobial exposure of enteric bacteria and its effect on resistance in foodborne pathogens. We hypothesize that the realistic estimation of the exposure and effect can provide the missing link for evaluating how antimicrobial use practices in food animals impact resistance.
EFFICIENCY OF AND RISK FACTORS ASSOCIATED WITH POST-MORTEM SURVEILLANCE FOR BOVINE TUBERCULOSIS IN CATTLE IN NORTHERN IRELAND

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Post-mortem examination continues to play an important surveillance role in the bovine tuberculosis (bTB) eradication programme in Northern Ireland. The proportion of new bTB herd breakdowns disclosed by the detection of bTB lesions in animals routinely slaughtered has been estimated at between 18 and 28% annually in the period 2011–2013.

The purpose of this study was to compare the performance of different slaughterhouses in Northern Ireland in detecting bTB-lesioned animals at routine slaughter (LRS), to assess the risk factors associated with disclosure, and to apply the findings to maximise the sensitivity of bTB slaughterhouse surveillance.

Univariate statistical analysis on cattle slaughtered in Northern Ireland (2011–2013) revealed that the risk of LRS disclosure varied between slaughterhouses, ranging from 0.08 to 0.54%. Furthermore, the risk of confirmation of these LRS as bTB by follow-up laboratory testing varied between slaughterhouses, ranging from 57.9 to 72.4%.

A logistic regression model showed that the risk of LRS disclosure significantly increased with age, and was higher in purchased animals, during winter months, in animals coming from high bTB incidence areas and in animals slaughtered from herds with a bTB restriction in the last two to three years (p<0.05).

Adjusting for animal and herd factors (age and sex of the animal, slaughter season, bTB incidence of the area of origin, time the herd of origin had a bTB restriction status, and whether the animal was purchased or homebred), the risk of LRS disclosure and bTB confirmation changed very little for each slaughterhouse. Therefore, these differences are highly likely to be due to factors related to the slaughterhouses, rather than to different classes of animals (or their source) killed in each of them.

Examination of procedures within these slaughterhouses is recommended to identify factors that could be improved to increase the sensitivity of their bTB surveillance.
ARE BEEF TAPEWORM IDENTIFICATION RATES IN SOUTH AFRICA INFLUENCED BY THE PROVIDER OF INSPECTION SERVICES?

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Bovine cysticercosis is linked to human taeniasis resulting from consumption of raw or undercooked infected meat. In South Africa, hiring of meat inspectors is the responsibility of the abattoir operators potentially leading to conflict of interest. The aim of this study was to investigate cysticercosis identification rates in beef carcasses inspected in a province of South Africa and to identify predictors of variations in identification rates. Data of over 1.4 million carcasses inspected at 26 South African abattoirs from 2010 to 2013 were included in the study. Cysticercosis identification rates were computed and generalized estimating equations used to investigate predictors of cysticercosis identification rates. Overall identification rates was 0.70% (95% CI: 0.45, 0.95). Significantly (p<0.05) lower rates were reported during summer (0.55%). Some geographic areas reported higher identification rates than others. The identification rates of high throughput abattoirs was 9 times higher (RR: 9.4; 95% CI: 4.7-19.1) than those of low throughput abattoirs. Similarly, the identification rates were almost 2 times higher (RR: 1.6; 95% CI: 1.7-3.5) in carcasses of animals from feedlots than in those from non-feedlot sources. Interestingly, there was no association between the number of meat inspectors or the provider of inspection services and identification rates. The lack of association between identification rates and provider of inspection services may suggest that conflict of interest due to abattoir owners hiring and directly paying for inspection services might not significantly impact identification rates. However, this needs more investigations. Improved capture of abattoir surveillance data will need to include data on farm address to enable trace-back. Moreover, information on the type of identified cysts (alive or calcified) need to be collected to help better estimate risk to consumers. However, this study provides useful baseline data to guide future studies, surveillance data collection and control efforts.

COMBINING EXPOSURE ASSESSMENT, BAYESIAN MODEL, AND MOLECULAR DATA TO QUANTIFY THE SOURCES OF HUMAN CAMPYLOBACTERIOSIS

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Campylobacter is the leading bacterial cause of infectious enteric disease. Its zoonotic transmission is complex with several reservoirs and several pathways involved. While chicken meat is the main source of human campylobacteriosis, its quantitative importance relative to the other sources is still imprecise. Such quantification, known as source attribution, has been proven helpful to direct public health prevention and control efforts more efficiently. The study aimed at attributing human campylobacteriosis cases to several sources using Canadian data. We used a Bayesian model previously developed in Denmark. Basically the model compares the distribution of the pathogen strains observed in each source with the strains detected in clinical cases. We modified the original model in two ways. First, we used a new molecular test developed in Canada, Comparative Genotype Fingerprinting (CGF), to describe all Campylobacter strains. All isolates came from the Ontarian sentinel site of FoodNet Canada over the years 2006-2011. Second, we included into the model a parameter measuring the human exposure to Campylobacter through each source estimated at the population level. The human cases were attributed to eight sources: farm animals (cattle, chicken, swine), beef, chicken, turkey, and pork meats, and surface water.

Over the 13 exposure assessed, chicken meat and contact with farm animals ranked relatively high, beef and water moderate, and pork very low. According to the proportional similarity index, the CGF subtypes showed moderate similarity between human strains and chicken meat and cattle strains, low with live chicken and water, and very low with beef, turkey and pig/pork. The Bayesian model attributed 72% of attributable human cases to chicken meat, 23% to beef, 5% to water, and less than 1% to all other sources. Not considering exposure changed the attribution estimates, with more cases attributed to contact with live chicken and cattle.
EXPLORING NEW TECHNOLOGIES TO SUPPORT INVESTIGATION OF FOODBORNE DISEASE

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Studies tracking the source of foodborne outbreaks traditionally involve telephone interviews several days after illness onset, and can be adversely affected by participant recall. This project will evaluate new technology for gathering data on food consumption and occurrence of gastrointestinal illness using Ethica, a versatile smartphone app developed by the applicants. This pilot study provides a unique opportunity to measure the extent of participant recall bias and the resulting limitation of current investigation strategies.

University students were recruited for a project to determine the utility of the app. Students are a good target population, as most have smartphones and frequently use them for data sharing and communication. Students are also often challenging to recruit using current interview methods. Further, many are learning to cook, or eat out frequently, elevating their risk for foodborne disease.

Over a 10 week period, participants were asked to report any gastrointestinal symptoms using Ethica. During the first 10 days, participants were also asked to take photos and answer 3 times daily surveys on recent food choices. Participants reported whether they were eating in restaurants or take-out food. The Ethica app linked participant data to location. Participants also completed an online survey either 1 or 2.5 weeks after day 5 asking them to recall their food choices for days 2 to 8. By comparing the survey with the Ethica data, the extent of recall bias will be assessed. This proof of concept study will also examine the feasibility of using Ethica to support investigation of enteric illness and inform dynamic simulation models of outbreak detection. Using participants’ reported experiences with the system, the project will identify hurdles to scaling up the use of Ethica to a larger, more diverse study population and to applying this technology to other questions not sufficiently answered using traditional survey techniques.
RISK PROFILE AND QUANTITATIVE HUMAN EXPOSURE ASSESSMENT OF HEPATITIS E VIRUS FROM PIGS OR PORK IN CANADA

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The role and importance of pigs and pork as sources of zoonotic hepatitis E virus (HEV) has been debated in Canada and abroad for over 20 years. To further investigate this question, we compiled data to populate a risk profile for HEV in pigs or pork in Canada. We organized the risk profile (RP) using the headings prescribed for a foodborne microbial risk assessment, and used research synthesis methods and inputs wherever possible in populating the fields of this RP. A scoping review of potential public health risks of HEV, and two Canadian field surveys sampling finisher pigs, and retail pork chops and pork livers provided inputs to inform this RP. We calculated summary estimates of prevalence using the Comprehensive Meta-analysis 3 software, employing the method of moments.

Overall, we found the incidence of sporadic locally-acquired Hepatitis E in Canada, compiled from peer reviewed literature or from diagnosis at the National Microbiology Laboratory to be low relative to other non-endemic countries. In contrast, we found the prevalence of detection of HEV RNA in pigs and retail pork livers, to be comparable to that reported in the USA and Europe. Quantitative estimation of risk of foodborne HEV from exposure to pigs/pork was not possible due to data gaps including dose-response data. However, we drafted risk categories (high/medium/low) for acquiring clinical Hepatitis E from exposure to pigs or pork, and hypothesize that the proportion of the Canadian population at high risk from either exposure is relatively small.
INTEGRATION OF SOCIAL AND ENVIRONMENTAL VULNERABILITIES TO PRIORITIZE AND ADAPT LOCAL RESPONSE AGAINST LYME DISEASE IN CANADA

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Lyme disease exhibits spatial and temporal variability that challenges public health authorities to prioritize prevention and control strategies that are well-adapted to the local context. Not only must decision-makers understand spatial variation in the ecological risk in order to prioritize areas for interventions, but they must also understand how knowledge, attitudes and practices about Lyme disease vary in the targeted populations. Consequently, a socio-ecological approach is needed to maximize the efficacy of the public health response to Lyme disease while adapting interventions to the local context. The Montérégie region is an important area of Lyme disease emergence in Southwestern Quebec. Spatial variation in the level of knowledge about the disease, the adoption of individual preventive behaviors and risk perceptions in Montérégie were assessed using data from a websurvey conducted in 2012. Also, tick density observed in the environment through previous field surveillance (2007 to 2012) within the study area was used as a proxy variable reflecting key environmental drivers such as hosts, climate and habitat risk factors that naturally shaped tick density and distribution. The objective of this study was to integrate selected social and ecological factors important for Lyme disease prevention to create new risk maps for Montérégie: i) a vulnerability index map and ii) a prioritization index map that considered the population at risk. As expected, the socio-ecological risk was not homogeneous and significant variation was noted within the region. Furthermore, in order to validate these maps, we used available epidemiological data on the confirmed human cases of Lyme disease. We believe that such integrated socio-ecological maps are a valuable tool to prioritize and adapt communication, prevention or control interventions to the local characteristics of targeted populations in Montérégie and in other Lyme disease endemic regions.

SPATIAL HETEROGENEITY IN *IXODES SCAPULARIS* DISTRIBUTION WITHIN THE LYME DISEASE EMERGENCE ZONE IN SOUTHERN CANADA

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Since its first detection in Canada in the early 1990s, *Ixodes scapularis* continues to expand its range northward. However, the pattern of tick establishment is far from uniform in space, suggesting that ecological factors acting at patch and microhabitat scales may have an influence on invasion success for *Ixodes scapularis*. Here, we investigate the heterogeneity of nymphal tick distributions within and among woodlands in the primary Lyme disease emergence zone in southern Quebec. In 2013-2014, ticks were collected through drag sampling at 50 sites (public and private woodlands) in southern Quebec (2000 m dragged per site). Three of these sites were more intensively sampled in 2013: in each site, around 20 randomly-placed plots consisting of four 100 m transects parallel to a park trail (0, 20, 40 and 60 m from the trail) were sampled. The influence of different ecological factors on nymphal density at the site, plot and transect scale was analyzed using mixed-effects models. Spatial distribution of nymphs was very heterogeneous among sites (0 to 44 nymphs per 100m², median=1.5) and also within them (0 to 25 nymphs per plot in intensively sampled parks, median=2), with spatial clustering of ticks observed at each geographic scale. Preliminary results show that nymphal density decreased with elevation of the site (p=0.02), decreased with increasing relative humidity of the plot (p=0.01), was lower in plots near gravel vs soil trails (p=0.04), and was higher in transects far from the trail (p=0.008). Taking into account the heterogeneous distribution of nymphs at a fine spatial scale could help better target preventive messaging and other interventions in public-access woodlands such as nature parks. Further studies are needed to elucidate the ecological mechanisms underlying these differences in tick distribution, and how they are likely to change over time.
WHICH VACCINES ARE MOST IMPORTANT? A DECISION SUPPORT TOOL FOR FOOT AND MOUTH DISEASE VACCINE BANK MANAGERS

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Foot and mouth disease (FMD) significantly constrains trade in animals and animal products, and most FMD-free countries invest considerable resources to prevent and prepare for possible incursions. As part of these efforts, multinational and national vaccine banks have been established to enable rapid implementation of emergency vaccination in the event of an outbreak. FMD is caused by a virus with 7 serotypes and multiple strains within serotypes, with no cross protection between serotypes and variable protection between strains within each serotype. Therefore, to be effective, the banks should hold vaccine strains suitable for protection against the virus strains most likely to cause an incursion.

We developed a semi-quantitative spreadsheet model to assist vaccine bank managers worldwide prioritize which antigens to hold in the bank. The tool combines two distinct considerations: 1) which strains pose the greatest threat of incursion into a given area (antigen risk score) and 2) the effectiveness of available vaccines to protect against each circulating strain (coverage score). The antigen risk score is derived by combining the relative importance of possible source regions (i.e. FMD endemic areas) with the relative prevalence of circulating strains in the source regions. These values are determined by expert elicitation. The relative importance of different source regions will vary according to the location of the vaccine bank, and will be influenced by proximity, connectedness of countries (e.g. by immigration and trade) and the prevalence of FMD virus. The coverage score is calculated for each combination of vaccine and virus strain according to the percentage of virus isolates that match the vaccine in question. Finally, the coverage score and the antigen score are combined to yield a vaccine score for each vaccine strain eligible for inclusion in the bank.

The use of this tool is being piloted by vaccine bank managers.

USING INTEGRATED ASSESSMENT MODELING TO INVESTIGATE FACTORS AFFECTING THE RECOVERY OF ANTIMICROBIAL RESISTANT BACTERIA ALONG THE FOOD CHAIN: A PILOT STUDY

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There is a great volume of data about antimicrobial resistance (AMR). An integrative assessment model (IAM) is mathematical framework that can be applied to describe the epidemiology of AMR using existing data and describe the relative contributions of different food-animal production systems to the overall epidemiology. The objective of this pilot study was to build a framework for a larger IAM using three scenarios: 1) ceftiofur-resistant Salmonella Heidelberg from broiler chickens; 2) fluoroquinolone-resistant Campylobacter jejuni from broiler chickens; and 3) macrolide-resistant Campylobacter coli from pigs. Data were captured from a literature search and the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS). References with data on factors associated with AMR from any geographical population and/or AMR and AMU frequency data from a Canadian population were retained. Data were manipulated using a spreadsheet software program and then inputted into a quantitative decision modelling software. Key nodes in the quantitative model were farm, abattoir and retail and were populated with 1) frequency data from the CIPARS surveillance program and 2) data on factors from the literature search. For each scenario, the literature search only identified up to 10 references suitable for use in the model. Most factors associated with the occurrence of AMR were measured at the farm including AMU and management systems (e.g. organic). The ceftiofur-resistant S. Heidelberg in broiler chicken scenario included a factor at retail (vacuum-packaging) and the macrolide-resistant Campylobacter coli in pigs scenario included factors at abattoir (management system). Despite the volume of literature on the topic of AMR, when investing a very specific aspect of AMR in agri-food, the volume of data is very small. Despite this limitation, we were able to build quantitative models investigating factors that may impact the probability of recovery of specific AMR bacteria at points along the food-chain.
THE FIRST CANADIAN NATIONAL DAIRY STUDY: MYELINATING NEW PATHWAYS

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Large scale studies that involve collaborative research among teams with overlapping interests is a current trend in epidemiological research. This is driven by lack of available research funding, limitations of infrastructure and expertise, and the complexity of biological relationships. While there are many benefits to undertaking these large population studies, the inaugural ones face many hurdles. However, once these challenges are circumvented it eases the ability to repeat the format and expand them to other sectors. The objective of this project is to share the lessons learned from expanding dairy research from the regional to the national level as they are applicable to all sectors of veterinary and public health in Canada.

Conducting a country-wide priorities assessment prior to the undertaking of the study stimulated stakeholder awareness, allowed future participants to give input to the issues of focus and built momentum for future participation. As we moved beyond provincial borders the inclusion of impartial organizations, such as printing companies, helped build trust and improve participation, when sharing confidential information. The development of standardized templates for data submission, assessment protocols for students, and labels for all sample submissions ensured less time was spent merging data, ensured high quality data were collected and minimized loss of samples due to mislabeling. The incorporation of social media, on-line questionnaire software and tablets were new resources that yielded higher than expected response rates and reduced time and errors in data transfer. However, these devices also brought new challenges with respect to internet access and data coding.

The lessons learned from conducting the first national dairy study will ensure that the next version of this study will occur with greater ease and minimize the time delays incurred. Sharing the benefits and challenges associated with this experience assists other researchers in planning future studies.

EPIDEMIOLOGY EDUCATION IN THE VETERINARY CURRICULA – THE CURRENT STATE OF AFFAIRS

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While general consensus is that epidemiology is important to the practice of veterinary medicine, veterinary students tend to under appreciate the relevance of epidemiology to their life-long learning and future practice. As a result, student engagement and content delivery can be a challenge for educators. The objective of this study was to characterize core epidemiologic content, delivery, and learning strategies employed by educators in the veterinary curricula. An on-line survey was conducted in the Fall of 2015 of epidemiology educators responsible for delivery of core epidemiological content in the professional veterinary medical curricula at colleges in North America and abroad. The Associate Dean for Academic Affairs, or their equivalent, at each institution was contacted to identify educators responsible for delivery of this content at their respective institutions, both past and present. Subsequently, each identified educator received a personal invitation to participate in the survey. Additionally, epidemiology educators were invited to participate through postings on professional membership listservs and an epidemiology educators’ forum was conducted to develop a deeper understanding of the issues. In total, 51 educators participated representing 36 colleges (23 North American; 13 International). Among survey participants, 78.4% were currently teaching and 66.7% had been teaching for greater than 5 years. The majority of educators delivered epidemiology content in a stand-alone course (66.7%) and facilitated learning through lectures and activities (72.5%). This study provides a consensus on core content that we should strive to incorporate into the veterinary curricula and a pathway for the future of veterinary epidemiology education.
UTILITY OF AN ONLINE LEARNING MODULE FOR TEACHING DISBUDDING IN DAIRY CALVES, INCLUDING CORNUAL NERVE BLOCK APPLICATION

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Although disbudding/dehorning (DD) dairy heifers is necessary for the safety of humans and other cattle, it has been identified as a key animal welfare issue when done without appropriate analgesia. Reported use of pain control for DD by North American producers ranges from 15-60%. Cautery disbudding is the most commonly used method; best practices include local anesthetic given as a cornual nerve block (CNB) and administration of a non-steroidal anti-inflammatory drug (NSAID). While NSAID administration is uncomplicated, CNB administration requires technical training. Typically producers learn this technique in-person from their veterinarian, although other teaching methods including online videos exist. To the authors’ knowledge, no DD training methods have been studied for efficacy. Our objective was to determine if an online, interactive module could teach naïve participants cautery DD technique, including CNB, as compared to hands-on learning. Thirty-four student volunteer participants were recruited. Hands-on training was done with live animals, in small groups, by a registered veterinary technician (RV T) following an established protocol, while online training was self-directed and used an interactive training module. Assessments of competency were performed by a blinded evaluator who examined knowledge, handling, CNB technique, disbudding technique, time taken, and confidence scoring (both pre- and post- evaluation). Success of CNB was based on lack of pain-related behaviours from an established DD ethogram during the first five seconds of disbudding iron application. The hands-on training group had no CNB failures. Online training was numerically less effective (25% CNB failures) but not statistically (p=0.126). Online learners were significantly more knowledgeable (p=0.040), but significantly less confident (p=0.001), had poorer handling skills (p=0.023), and took more time to perform all tasks (p=0.010). Although online learning was surprisingly effective, best practices for teaching disbudding techniques should clearly involve hands-on training. Online learning alone may be appropriate for hard to reach populations.
MARGINAL STRUCTURAL COX MODEL TO DETERMINE CLINICAL MASTITIS EFFECT ON QUÉBEC DAIRY COW CULLING RISK

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At the cow level, clinical mastitis is a known risk factor for culling in dairy cattle especially when considering the culling risk as time dependent in survival analyses. In such context, culling decision can be based either on current disease status (clinical mastitis) or on milk yield. But high producing cows have greater risk of experiencing mastitis, and mastitis can have an indirect effect on culling risk through decreased milk production. Milk yield confounds clinical mastitis, and hence must be adjusted for, however, it is also on the causal pathway between exposure and outcome and hence cannot be adjusted for. Adjusting for time-varying confounders that are affected by prior exposure may adjust away part of the exposure effect and induce confounding and selection bias. Therefore, the study objective was to estimate the causal association between clinical mastitis and culling, in the presence of a time-varying confounder, milk yield, using Marginal Structural Models (MSMs)

A retrospective cohort study was conducted using data from Québec dairy herds using a preventive medicine software. Data were extracted for all lactations starting in 2010 (9454 cows; 191 herds). MSMs were used to estimate hazard ratios (HR) in heifers and cows separately. Censoring was accounted for in MSMs by including inverse probability of censoring weights. The crude HR for clinical mastitis was 1.69 [95% CI: 1.29, 2.22] and 2.06 [1.77, 2.4] in heifers and cows, respectively. Using MSMs to control for time-varying milk yield, HR were 1.55 [1.15, 2.08] and 1.57 [1.32, 1.86] for heifers and cows, respectively. Pregnancy was the strongest predictor to remain in the herd for either heifers or cows. In conclusion, when exposure and confounders vary during follow-up, conditioning on time-dependent confounders could induce substantial bias. Statistical techniques to assess causal effect like MSMs have to be used to address this issue.
DESCRIPTIVE ANALYSES OF BULK TANK MILK COMPOSITION, AND FACTORS ASSOCIATED WITH SOMATIC CELL COUNTS AND MILK UREA NITROGEN IN CENTRAL THAILAND

Suppada Kananub1, John Vanleeuwen2, Pipat Arunvapas1

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Bulk tank data related to milk composition, somatic cell counts (SCC), and milk urea nitrogen (MUN) are routinely collected on Thai dairy farms; however, the use of these data are limited to the purpose of milk price estimate, and have not been applied to their maximum extent, such as to evaluate farm management and predict the effect of milk quality on marketability. This preliminary study describes the situation of bulk tank milk composition in Central Thailand, as well as factors associated with SCC and MUN. In total, 59,011 monthly bulk tank milk records from 2,415 farms collected by Nong Pho Milk Collecting Center from September 2014 to August 2015 were analyzed. More than 50% of observations were from farms having fewer than 10 cows.

Mean percentages (95%CI) of fat, protein, lactose, and total solids were 3.86 (3.85-3.86), 3.21 (3.20-3.21), 4.62 (4.61-4.62), and 12.39 (12.38-12.39), respectively. Mean (95%CI) MUN and SCC were 13.19 (13.16-13.21 mg/dl) and 693 x103 cells/ml (687-700), respectively. Minimum and maximum SCC were 14x103 and 23,690x103 cells/ml, and 2.0 and 33.7 mg/dl for MUN, respectively.

Using univariable analyses, slightly higher mean logSCC was seen in the rainy season (mid-May to mid-October) than in winter (mid-October to mid-February) and summer (mid-February to mid-May). Higher MUN was manifested in winter, followed by the rainy and summer seasons, corresponding to the variation in feed amounts and quality by season. MUN and logSCC tended to vary with farm size, with high variation demonstrated in farms having more than 30 milking cows, whereas the smaller farms showed low variation. Multivariable regression analyses will be used for further investigation to analyze factors to predict SCC and MUN, while controlling for confounders and other significant variables. This information would develop milk quality awareness on farms that could then lead to improved farm management.

Epidemiological Characterization of Small Poultry Flocks in Alberta

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Very limited information regarding distribution, composition and management characteristics of small poultry flocks is available in Alberta which has important implications in the spread of avian diseases and zoonoses of public health concern. Therefore, a survey was conducted to gain initial epidemiological insight into Alberta’s growing small poultry flock populations and potential areas of risk. Information on flock demographics and bird health, as well as production and biosecurity practices were gathered and analyzed from 206 surveys representing respondents from 43 counties. The results showed variation in flock size and composition indicating a diverse population of both small flock owners and flocks. Laying hens were the most commonly reported type of bird (93.4%), followed by ducks and geese (35.3%), turkeys (33.8%) and broiler chickens (33.1%). In addition, 58.1% reported having more than one type of bird in their flock. Personal consumption (81.8%) and sale of eggs (48.2%) were the most commonly reported purposes for owning a flock. Birds were predominantly purchased from breeders (59.6%) followed by multiple sources (55.3%) and hatcheries (44.1%). Our findings suggest that producers in Alberta are largely new to production; most (73.1%) reported having poultry for less than five years and 25.6% for less than one year. Flock health management revealed inconsistent use of medical interventions such as vaccinations, treatments and veterinary consultation. There is potential for contact to occur directly and indirectly between flocks and humans based on information gathered regarding housing and movement of birds as well as movement of people and visitors.

The results revealed a huge variation in both basic husbandry and biosecurity practices, identifying important gaps for educational interventions and opportunities to improve the health of Alberta’s flocks and mitigate risks to public health.
LIFETIME EFFECTS OF INFECTION WITH BOVINE LEUKEMIA VIRUS ON LONGEVITY AND MILK PRODUCTION OF CANADIAN DAIRY COWS

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Enzootic bovine leukosis is an economically important disease of dairy cattle caused by bovine leukemia virus (BLV). The economic impacts of the infection have been debated in the literature. The present study was conducted to determine the lifetime effects of BLV infection on longevity and milk production of dairy cows in Canada.

The data were aggregated from a combination of two data sets: 1) BLV serum-ELISA test results from Canada-wide surveys of production limiting diseases, which took place between 1998 and 2003 in 8 provinces, and 2) longitudinal production data for all cows in the former study, extracted from the Canadian DHI database. All participant cows had been culled/died by the onset of this study. A historical cohort study was designed, including cows which tested positive to BLV-antibodies in their first lactation (n = 1858) and cows which tested negative in their second or later lactations (n = 2194). To assess the impacts of infection with BLV on longevity, a discrete-time survival analysis was carried out. The effect of BLV on the lifetime milk production was evaluated using a multilevel linear regression model.

Overall, 4052 cows from 348 herds were enrolled in the study. In the longevity model, cows which were positive to BLV had consistently greater probabilities of being culled (or dying) than the negative cows. In the milk production model, infected cows with 2 and 3 lactations showed significantly lower lifetime milk productions [-2554 kg (-3609 to -1500) and -1171 kg (-2051 to -292), respectively] compared with their negative counterparts. As the cows lived longer (> 3 lactations), the differences in lifetime milk production between the two cohorts were no longer significant. With the high prevalence of BLV in Canadian dairy cows and its detrimental economic impacts, pursuing a broad-based control program in Canada is necessary.
A MIXED METHODS STUDY OF MANAGEMENT PRACTICES ASSOCIATED WITH CATTLE PAIN AND STRESS IN WESTERN CANADIAN COW-CALF OPERATIONS.

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Public concern for the welfare of production animals is driving changes within the agricultural industry. In response, the “Code of practice for the care and handling of beef cattle” was recently revised. Implementation of the Code is dependent on its feasibility and perceived importance to producers. However, there is a lack of information regarding current management practices within the Canadian beef industry. The objective of this mixed method study was to describe pain and stress-associated practices implemented on farm and producer perceptions towards mitigation strategies. For the quantitative aspect of this study, a questionnaire about calving management, calf processing, weaning, and euthanasia was delivered to 109 cow-calf producers in Western Canada. For the qualitative aspect, 15 respondents were purposively sampled based on questionnaire responses for semi-structured individual interviews. The prevalence of pain mitigation strategies for dystocia and caesarean section by respondents were 54.8% and 100%, respectively. The majority of operations (96.6%) reported castrating calves prior to 3 months of age. Dehorning was practiced by 58.8% of respondents, 96.0% of which reported dehorning calves prior to 3 months of age. However, the majority of operations did not utilize pain mitigation strategies for castration and dehorning (88.2% and 94.2%, respectively). Branding was practiced by 56.7% of respondents, 3.9% of which utilized pain mitigation. Thematic content analysis revealed that producer perception of pain was influenced by animal age, common sense, relatability to cattle, and visual evidence of pain. Additionally, factors that influenced participant rationale behind the implementation of pain and stress mitigation practices included: access to information and resources, age of the animal, benefit to operation, cost and logistics, market demands, and personal conscience. The results of this study benefit the Canadian beef industry by benchmarking current practices and producer perceptions, which may provide direction for future policy-making, research, and extension efforts.
PREVALENCE OF STREPTOCOCCUS SUIS IN CLINICAL CASES AND HEALTHY-CARRIER PIGS

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The objective of this study was to investigate the serotype distribution of *Streptococcus suis* isolates recovered from clinical and healthy-carrier pigs, and to compare culturing and PCR methods for *S. suis* detection. Nasal, tonsilar, and vaginal swabs were collected from healthy pigs and tonsilar and meningeal swabs as well as tissue from tonsil and lymph nodes from clinically-ill pigs were gathered from pigs on 17 farms. Duplicate swabs were collected: one used for culturing and serotyping, and another tested by PCR for the presence of the *gdh* gene. A logistic regression method with farm as a random effect was used to compare the presence of *S. suis* and its serotypes in diseased and healthy pigs, and among pigs at different stages of production. Of 405 samples, 310 were collected from healthy and 95 from sick pigs. There was no significant difference between recovering the bacteria from suckling versus nursery pigs (P =0.7), or from sows versus finishers (P =0.9). However, *S. suis* was more likely to be recovered from suckling and nursery piglets than from sows and finishers (P <0.001). *Streptococcus suis* was also more commonly recovered from healthy pigs as opposed to sick pigs (P <0.001). However, it is possible that some sick pigs might have been treated with antibiotics before sample collection. Seventeen serotypes were identified, with type 6 being the most common serotype. However, this type was only isolated from healthy pigs. Nineteen percent and 52% of isolates were autoagglutinated and untypable, respectively but untypable isolates were more likely to be recovered from healthy pigs (P <0.01). There was no agreement between the culturing and PCR methods for *S. suis* detection. More clinical cases are needed to draw conclusions regarding the serotype distributions in sick pigs.

AN INVESTIGATION OF THE FACTORS CONTRIBUTING TO MORTALITY DURING AN OUTBREAK OF STREPTOCOCCUS SUIS INFECTION IN NURSERY PIGS AND VACCINE EFFICACY

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*Streptococcus suis* has 35 serotypes that are present as commensal bacteria or opportunistic pathogens in the nasal cavity and tonsils of the majority of pigs. The occurrence of *S. suis* clinical infections in swine herds is usually characterized by a low incidence of clinical cases that show signs consistent with septicemia, and neurological involvement. Prognosis is often poor, even when treated promptly. Occasionally, *S. suis* causes major outbreaks involving a large proportion of pigs, but factors contributing to development of clinical cases are poorly understood. In this study the production records from a 300-sow farrow to-finish herd that experienced an outbreak of *S. suis*-related mortality were examined. The objectives of the study were 1) to investigate sow- and litter-level factors that were associated with the hazard of dying during the nursery phase; 2) to evaluate the direct efficacy of an autogeneous *S. suis* vaccine. The farm-level data used in the study were: sow parity, litter size at birth and weaning, and date of weaning and mortality. To evaluate the vaccine efficacy, 4 weaning cohorts were included in the trial with 25% and 75% of piglets within a litter randomly allocated to the non-vaccinated and vaccinated group, respectively. A Cox’s proportional hazard model was used to evaluate both risk factors and direct vaccine efficacy. Preliminary analysis indicates that the mortality within litters was > 20% for each weaning cohort during the 3rd or 4th week in the nursery. The results of this study may help to determine litter-level risk factors for *S. suis* clinical disease and may provide information to help veterinarians design more effective *S. suis* control strategies.
CAUSES OF DEATH IN YOUNG LAMBS SUBMITTED FOR POST-MORTEM EXAMINATION TO THE ATLANTIC VETERINARY COLLEGE DIAGNOSTIC SERVICES (2005-2014)

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The objective of this retrospective study was to identify causes of mortality in PEI-sourced live-born lambs less than 90 days of age, submitted for post-mortem examination to AVC Diagnostic Services, 2005-2014. Abnormal findings from 367 submissions were categorized by body system using gross and histopathological results. Results from further diagnostic tests were also examined. The primary cause of death was classified into one of eight categories: infection, trauma, congenital defects, dystocia, milk aspiration, starvation (including hypothermia/hypoglycemia), nutritionally-related diseases and others. Lesions in the respiratory system were present in almost 70% of the submissions but the gastrointestinal system was the most common system associated with death, responsible for death in 25% of submissions. The most frequent primary cause of death was infection (41%). The most common infected body systems were the gastrointestinal (39%) and respiratory (24%) systems. Bacteria and protozoa were responsible for 62% and 20% of lambs that died due to infection, respectively. The next most frequent cause of death was the category of nutritionally-related diseases, such as intestinal torsion and ruminal acidosis (8%). Cause of death could not be identified in 28% of the submissions. The likelihood of infection being identified as the primary cause of death increased with age. Almost all deaths due to nutritionally-related disorders occurred in lambs over 2 days old, whereas, trauma was more common in the first week compared to later in life. This study presents the first data on cause of lamb mortality in PEI flocks, and provides valuable initial information to guide further prospective investigations.

The predominance of infectious diseases in the older lamb submissions suggests future studies should focus on risk of pathogen challenge and resistance to infection in the early growing period.

PREVALENCE OF TRITRICHOMONAS FOETUS IN TENNESSEE BEEF BULLS

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The objective of this study was to estimate the prevalence of Tritrichomonas foetus infections in Tennessee (TN) beef bulls through active surveillance and diagnostic laboratory data. T. foetus is a venereal transmitted protozoan of cattle causing bovine Trichomoniasis. Diseased bulls tend to be asymptomatic carriers, while infections in cows and heifers may result in embryonic and fetal loss, vaginitis, or pyometra. This disease potentially cost the U.S. beef industry over $650 million annually. While the reported individual bull prevalence rates of Trichomoniasis in the U.S. are estimated at 0 to 7.8%, the prevalence in TN beef bulls are unknown. Beef bulls were actively sampled from March 2014 through June 2015 at 2 cattle abattoirs and 2 stockyards that serve most beef bulls in TN. Preputial smegma was collected from 458 TN bulls and cultured for T. foetus as well as evaluated microscopically every other day for seven days for any growth resembling T. foetus. An aliquot of the culture media from each sample was used for DNA extraction and subsequent real-time PCR testing. Additional data from 2 state diagnostic laboratories included 947 T. foetus tests (culture and/or real-time PCR) performed at the TN Department of Agriculture Kord Animal Health Diagnostic Laboratory in Nashville, TN and the University of TN College of Veterinary Medicine Biomedical and Diagnostic Sciences in Knoxville, TN between October 2013 and May 2015. This study would help estimate the prevalence of bovine Trichomoniasis for TN beef bulls and could influence possible control measures in the industry.

Key Words: Bovine trichomoniasis, beef bulls, Tennessee
Horses travel frequently to participate in sporting events, putting them at higher risk for transmitting or acquiring an infectious disease. As horses travel, they form a distinctive contact structure that must be considered when estimating the potential for disease introduction and transmission within the population. In Ontario, limited data exists to describe this network, limiting the ability to understand the effect of these travel patterns on the potential risk of disease. The objectives of this research were to describe the number and nature of contacts between Ontario horses as they travel, and to determine how this distinct contact structure influences the risk of disease introduction and spread. Horse owners and trainers were enrolled in a 7-month longitudinal study and were asked to document their travel patterns over a competition season. From May to November 2015, participants received a monthly questionnaire that asked about details of their travel patterns during that month. Directed networks were constructed to represent travel patterns in 1-month time periods, where the nodes represented facilities and the edges represented movements of one or more horses between facilities. A total of 223 participants were enrolled in the study and provided information on 571 horses. Response rates between May and November varied, but were greater than 60% every month.

Network measures are currently being calculated to explore the characteristics of horses and premises that may be at higher risk of transmitting or acquiring disease. Future research will focus on incorporating the contact data into computer simulation models to determine how a disease could potentially spread between horses in the network. The outcomes of this research will support targeted disease surveillance programs to reduce the emotional and economic consequences of equine infectious disease.
EVALUATION OF TREATMENT CRITERIA FOR USE IN TARGETED SELECTIVE TREATMENT PROGRAMS TO CONTROL TYPE II HAEMONCHOSIS IN PERIPARTURIENT EWES IN ONTARIO

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Type II haemonchosis is often associated with late gestation and parturition in ewes in Canada. Due to widespread concerns about development of anthelmintic resistance (AR), targeted selective treatment (TST) is a possible strategy to control clinical signs of haemonchosis while still maintaining parasite refugia. However, conducting fecal egg counts (FEC) on individual animals is often cost-prohibitive, so clinical indicators that identify ewes with high FEC are essential for TST programs. The study objectives were to evaluate the ability of four TST indicators to identify periparturient ewes with high *Haemonchus* sp. FEC, and to determine appropriate cutpoints for the most effective indicators. A field study was conducted during two lambing seasons on three farms in Ontario with documented AR and problems with type II haemonchosis. Periparturient ewes were selected for treatment with closantel, a novel anthelmintic to Canada, if they met at least one of four criteria: a) grazed pasture for only one year; b) body condition score (BCS) ≤2; c) Faffa Malan Chart (FAMACHA©)score ≥4; and/or d) ≥3 nursing lambs. Fecal samples were collected on the treatment day from each of 20 randomly selected treated and untreated ewes on each farm. Mean *Haemonchus* sp. FECs were significantly higher in treated ewes (n=136) than in untreated ewes (n=103) on the day of treatment, over both years of the study (p=0.001). A linear mixed model was fit with logarithmic-transformed FEC as the outcome variable, the four indicators and year as fixed effects, and farm as a random effect. FAMACHA© score was the sole indicator to remain significantly associated with *Haemonchus* sp. FEC (p=0.002). A receiver-operator characteristic curve determined that test sensitivity was maximized (92.4%) with FAMACHA© score ≥3. FAMACHA© score should therefore be included in TST programs to identify individual ewes requiring treatment at lambing due to *Haemonchus* sp.
Recent Trends in Cat Admissions and the Effect of the Capacity for Care Program at the Guelph Humane Society, 2011-2015

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In recent years, there has been a growing concern regarding homeless cat populations and how they can be successfully and humanely reduced. Shelters are constantly overwhelmed by the influx of unowned cats. In 2014, the Guelph Humane Society implemented the Capacity for Care (C4C) program at its shelter. The purpose of this program is to improve the movement of cats through the shelter and control for overcrowding by scheduling intakes, decreasing length of stay and increasing adoption rates, while simultaneously decreasing euthanasia rates. Currently, there are no long term studies that assess the effectiveness of the Capacity for Care program. This study is investigating the time trends in admission rates of cats to the Guelph Humane Society, and the effectiveness of the C4C program adjusted for long term trends and seasonality using a modern time series method for count data. Between January 2011 and December 2015, a total of 3295 live cats were admitted to the Guelph Humane Society. The average monthly intake of cats to the shelter decreased from 52 to 37, when the C4C program was implemented. This decrease, however, is not significant after taking into account a secular decreasing trend in the cat intake numbers. The results also display a strong seasonal peak in admissions over the summer months. In conclusion, the lack of effect of the C4C program on cat intake could signify that there remains a demand for shelter space, especially in peak season, despite decreased cat admission rates. Further investigation into the causes of the long term decrease in admissions is required, as there could be several contributing factors.

Factors Influencing Time to Adoption for Dogs in the British Columbia SPCA Shelter System

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Companion animal overpopulation is a growing issue in many countries throughout the world that results in millions of animals being relinquished to shelters each year. For each animal submitted to a shelter, three main categories of characteristics influence the time until the animal is adopted: characteristics of the individual animal (e.g., breed, age, sex), the animals prior history (e.g., reproductive status, source), and characteristics of the shelter system holding the animal (geographic location, holding capacity). Identifying which of these categories has the greatest effect on the time to adoption is important because only some of these factors (e.g., shelter management) are under the direct control of the shelter, while others may be addressed via outreach (e.g., reproductive status), changes in legislation (e.g., animal source), or education (e.g., preference for certain pet characteristics). This is the first study exploring this topic in Canada. Using a Cox proportional hazards frailty model, we are exploring these issues using data from 31 shelters that are part of the BC SPCA shelter system. Results have indicated that surrender reason, age, where the animal was obtained, coat colour, breed, human population density of shelter location and the year the animal entered the shelter are significantly associated with time to adoption. Information gained from this research will identify the characteristics of animals that make them less likely to be adopted quickly. Given limited resources, this would inform shelters how best to allocate their resources particularly around targeting interventions to improve adoption rates in their shelters.
DOMESTIC DOG POPULATION DYNAMICS IN VILLA DE TEZONTEPEC, HIDALGO, MEXICO: TOWARDS IMPROVED CANINE POPULATION AND RABIES CONTROL.

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The surplus of free-roaming dogs in developing countries poses risk to the safety and health of people via potential transmission of zoonotic diseases, including canine-mediated rabies, as well as via physical attacks and intimidation associated with these animals. An understanding of the ecology and demography of a domestic dog population, as well as dog ownership practices, is essential for the design of effective dog population control programs. The objective of this study was to characterize the owned dog ecology and demography in Villa de Tezontepec, Hidalgo, Mexico. The study was conducted in four neighborhoods in Villa de Tezontepec, Hidalgo. Face-to-face surveys were administered over a two-week period to 329 randomly selected households using a stratified two-stage cluster sampling design. Within each household, adults were asked to answer questions related to their dogs and their care. Approximately 75% (214/278) of participating households owned dogs, producing a human: owned dog ratio of 3.2:1. One-quarter of owned dogs were spayed or neutered, with the majority (78.4%) having been done under the subsidized government spay/neuter program. In addition, 87% (352/405) of owned dogs were reported by their owners to have been vaccinated against rabies during the 2015 government vaccine campaign. Less than half (45%) of dog-owning households kept their dogs confined at all times. At least once a week, 34% of all households surveyed provided food to free-roaming dogs, and 44% reported having free-roaming dogs visit their property on a daily basis. This study provides in-depth understanding of the dog ecology and demography in this population. These results will inform the development of an agent-based mathematical model to evaluate the effects of different dog population control strategies on dog ecology and demography in small semi-urban communities.

CAN NORTH AMERICAN ANIMAL POISON CONTROL CALL CENTRE DATA PROVIDE EARLY WARNING OF OUTBREAKS ASSOCIATED WITH CONTAMINATED PET FOOD: USING THE 2007 MELAMINE POISONING OUTBREAK IN COMPANION ANIMALS AS A CASE STUDY

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In 2007 the largest pet food recall in North America due to a chemical contaminant occurred as a result of adulteration of pet food with an industrial chemical, melamine. This pet food contamination affected over 100 pet food brands and caused acute renal failure in thousands of pet dogs and cats across North America. The American Society for Prevention of Cruelty to Animals (ASPCA) operates a poison control hotline that records data on companion animal exposure to potential toxic or poisonous substances. This hotline could be used to develop a quantitative syndromic surveillance system to identify poisoning outbreaks more quickly than traditional methods. The objective of our study was to use call centre data from the ASPCA poison control hotline to assess if various statistical approaches (e.g. temporal scan statistic) could identify the 2007 melamine pet food contamination outbreak by using calls which included syndromes related to renal failure. We used data from this hotline from January 1, 2005 to December 31, 2014 inclusive, to construct a Poisson regression model, controlling for month, to predict the expected number of calls concerning a renal syndrome for each month over the study period. These expected numbers of calls were subsequently used as the “offset” for temporal scan statistics, based on a Poisson model, to identify temporal clusters of excess calls concerning the urinary system, compared to the expected call numbers. Using this approach we were able to retrospectively identify a temporal cluster of calls concerning the urinary system 22 days before the first voluntary recall of contaminated products. These results suggest that these data coupled with scan statistics may be a useful for quantitative syndromic surveillance of large scale poisoning events.
INFECTIONOUS DISEASE TRANSMISSION MODELS WITH UNCERTAIN UNDERLYING CONTACT NETWORK INFORMATION

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Contact networks are of key importance when considering the spread of infectious diseases. These contact networks may represent trading relationships, supplier routes, social relationships or spatial relationships. Thus, when fitting infectious disease transmission models in order to understand underlying disease dynamics, it is often vital to account for contact information. Unfortunately, often reliable, complete data on such contacts are difficult to obtain. The information may be expensive to collect, or there may be privacy/confidentiality/commercial issues that make it difficult to obtain complete, error-free contact data. The Bayesian statistical framework is ideal for fitting models when data have some degree of uncertainty associated with them (e.g., measurement error, incomplete data, etc.). Unfortunately, fitting models within such a framework usually requires computationally intensive techniques such as Markov chain Monte Carlo (MCMC) that can take can long time to carry out. Here, we examine the use of disease models fitted within a Bayesian statistical framework that account for uncertainty in the underlying contact network. We show that accounting for this uncertainty can very much help in achieving accurate parameter estimation, and thus, say, prediction of the future course of an epidemic. We also quantify the computation run-time associated with such analyses for different population sizes, and compare MCMC-based analyses with those carried out using newly developed approximate Bayesian computation (ABC) simulation-based techniques. We show that ABC-based analyses can produce excellent model fitting results in a much shorter time span than the equivalent MCMC based analyses. Results are shown on simulated data, as well as data from real agricultural systems (e.g., the UK 2001 foot-and-mouth disease epidemic).

USING THE INCIDENCE DECAY AND EXPONENTIAL ADJUSTMENT (IDEA) MODEL TO UNDERSTAND THE EARLY DYNAMICS OF THE 2014 PORCINE EPIDEMIC DIARRHEA VIRUS (PEDV) OUTBREAK IN ONTARIO.

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The United States swine industry was first confronted with porcine epidemic diarrhea virus (PEDV) in 2013. In young pigs, the virus is highly pathogenic and the associated morbidity and mortality has a significant negative impact on the swine industry. We have applied the IDEA model to better understand the 2014 PEDV outbreak in Ontario. Using our simple, 2-parameter IDEA model, we have evaluated the early epidemic dynamics of PEDV on Ontario swine farms. We estimated the best-fit $R_0$ and control parameter ($d$) for the farm-to-farm transmission component of the outbreak by fitting the model to publicly available cumulative incidence data. We used maximum likelihood to compare model fit estimates for different combinations of the $R_0$ and $d$ parameters. Using our initial findings from the iterative fitting procedure, we projected the time course of the epidemic using only a subset of the early epidemic data. The IDEA model projections showed excellent agreement with the observed data based on a 7-day generation time estimate. The best-fit estimate for $R_0$ was 1.87 (95% CI: 1.52 – 2.34) and for the control parameter ($d$) was 0.059 (95% CI: 0.022 – 0.117). Using data from the first three generations of the outbreak, our iterative fitting procedure suggests that $R_0$ and $d$ had stabilized sufficiently to project the time course of the outbreak with reasonable accuracy. The emergence and spread of PEDV represents an important agricultural emergency. The virus presents a significant ongoing threat to the Canadian swine industry. Developing an understanding of the important epidemiological characteristics and disease transmission dynamics of a novel pathogen such as PEDV is critical for helping to guide the implementation of effective, efficient, and economically feasible disease control and prevention strategies that are able to help decrease the impact of an outbreak.
COMPARISON OF TIME SERIES MODELS FOR PREDICTION OF INFLUENZA A VIRUS FREQUENCY IN ONTARIO SWINE

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Pigs are susceptible to infection with variants of swine, human and avian influenza viruses and may, therefore, play an important role in the evolution of influenza A virus. Over the last decade, the dynamics of influenza A virus in swine (IAV-S) have been characterized by detection of numerous influenza variants that create opportunities for emergence of further novel recombinants. This could result in increased incidence of infection with IAV-S and warrants surveillance activities using different approaches. One of the approaches is to use diagnostic data for surveillance including the evaluation of long term trend, assessment of seasonality, detection of outbreaks, and short term prediction of disease events. As for prediction, the availability of modelling techniques allows to compare different models for their predictive power. The objective of this study is to compare forecasting methods among existing time series models with the use of the diagnostic IAV-S data. Diagnostic data were obtained from AHL and aggregated into monthly and weekly time series. We then apply ARIMA, Random Forest, and GLARMA models and compare their predictive accuracy for prospective surveillance using the root square mean error (RMSE). We also examine the effects of humidity and temperature on the outcomes. Preliminary statistical results for the number of positive virological submissions at monthly level suggest that temperature and humidity have an insignificant effect (p > 0.05) when added to models individually and together. Random Forest model has a slightly smaller prospective RMSE compared to ARIMA and GLARMA models (2.5; 2.66, 3.0, respectively).


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West Nile virus (WNv) first appeared in Ontario in dead birds in 2001, and humans in 2002. By 2002, surveillance efforts focused on testing of corvids found dead and reported by citizens across Ontario, in addition to testing of trapped mosquitoes and human case reports. The objective of this study was to examine the spatial and temporal trends in the citizen sightings to provide insight into their utility for timely identification of areas where West Nile virus appeared, relative to WNv-positive corvids, mosquitoes and humans. Sightings by public health units (PHUs) were examined descriptively and using scan statistics. There were 12,295 sightings of dead corvids reported by residents in 35 of 37 Ontario PHUs. Of these, 958 were tested for WNv and 278 tested positive. The southern PHUs showed the highest density of sightings, but some northern PHUs also demonstrated high sightings per capita. In the majority of PHUs, the first WNv-positive bird and the highest proportion of positive tests occurred earlier than the rise in citizen sighting reports, and provided early warning of WNv before human cases occurred. Scan statistics identified a significant temporal cluster of WNv-positive corvids which started earlier than a significant temporal cluster of citizen sightings. Spatial clusters of dead corvid sightings were similar to spatial clusters of WNv-positive corvids. The space-time clusters of sightings and WNv-positive birds showed some similarities in space and time, however there was a cluster of sightings reported in the northern PHUs which preceded a cluster of WNv-positive corvids in the same region. From this study it appears that engaging citizens to report found dead corvids was useful for collecting data on WNv. However, in most PHUs the first WNv-positive dead corvid tests provided more rapid detection of areas where WNv was present compared to measures based on sightings alone.
A PHYLODYNAMIC EXTENSION TO INDIVIDUAL LEVEL MODELS

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Phylo dynamics is an emergent field that explores the joint dynamics of disease spread and evolution. Phylo dynamic models utilize traditional epidemic surveillance data in addition to pathogen genetic sequence data. When epidemic and evolutionary processes occur on similar time scales, phylo dynamic models can be used to improve our understanding of disease dynamics. Specifically, with phylo dynamic models the routes of disease transmission can be inferred more accurately and disease model parameter estimation can be improved. A phylo dynamic extension to the individual level models of infectious disease transmission of Deardon et al. (2010) is presented. Simulation methods are described, which have value as scenario analysis tools. These methods are used in a simulation study, highlighting the particular strengths of phylo dynamic individual level models. Finally, computational methods for Bayesian inference, enabling the fitting of phylo dynamic individual level models to current or past disease outbreaks are discussed. There are opportunities to better inform infectious disease control strategies in production animal systems through the use of these models, when, as is increasingly common, pathogen genetic sequence data are available.

MULTI-CRITERIA DECISION ANALYSIS AS A PARTICIPATIVE AND TRANSDISCIPLINARY TOOL TO EVALUATE LYME DISEASE PREVENTIVE INTERVENTIONS

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Background: The recent emergence of Lyme disease in Quebec, Canada, is a good example of a complex health issue. Preventive interventions can have environmental, social and economic impacts and decision-making requires a system approach allowing the integration of multiple aspects of interventions.

Objectives: This study had a two-fold objective: first, to realize a multicriteria decision analysis (MCDA) for evaluating and comparing Lyme disease preventive interventions in Quebec, Canada and secondly, to evaluate the MCDA model elaborated in Quebec in a different epidemiological context, in Switzerland, where Lyme disease has been endemic for more than 30 years.

Methods: MCDA models were developed using a participatory approach with key stakeholders in both studied regions. Decision criteria and rankings of the interventions were computed and compared.

Results: Decision criteria included considerations in the fields of public health, animal and environmental health, social, economic and operational impacts. All criteria from the Quebec model were considered relevant in Switzerland. Interventions targeting humans outranked tick control interventions in both models.

Conclusions: MCDA was used to structure key decision criteria and capture the complexity of Lyme disease management. MCDA represents an interesting systematic approach for public health planning and zoonoses management with a “One Health” perspective. This study demonstrated that MCDA enables a clear identification of complementary interventions that could be used to improve the relevance and acceptability of zoonoses prevention and control strategies proposed by public health decision-makers.
A PROVINCIAL OBSERVATORY IN MOTION: COPING WITH CLIMATE CHANGE AND ZOONOSES

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Reviewed by the Collaborateurs de l’Observatoire

Zoonoses represent up to 75% of new or emerging infectious diseases and generate about a billion sick people each year worldwide (Jones, Patel et al. 2008, Karesh, Dobson et al. 2012). In the province of Quebec, zoonoses such as Lyme disease, campylobacteriosis or West Nile virus are responsible for hundreds of reported human cases yearly (in 2015, respectively: 153, 2,481 and 45) (personal communication, MSSS, January 28th 2016). The dynamics of these infections is complex, often involving multiple reservoirs, vectors or transmission modes that can be influenced by climate change, which require a multidisciplinary approach in order to respond adequately to the public health challenges they represent. Approaches like « One Health » and « Ecohealth » have (re-)surfaced recently and recognize the intimate connection between human, animal and ecosystem health. A new public health network structure has emerged in Quebec in November 2015 to address specifically climate change and zoonoses: the Observatoire multipartite québécois sur les zoonoses et l’adaptation aux changements climatiques. The coordination of this Observatory is shared between the Institut national de santé publique du Québec (INSPQ) and the Faculty of veterinary medicine of the Université de Montréal (UdeM). The objective of the network is to facilitate research collaborations and information access in public health at the human-animal-environment interface; with a main goal of strengthening cooperation between academia and policy-makers. The provincial observatory mandate is accomplished by providing interdisciplinary and intersectorial expertise and leadership in research, knowledge transfer and provincial networking activities. This innovative Observatory will facilitate integrated and economically efficient actions against zoonoses in the context of climate change adaptations.

NATIONAL DAIRY STUDY – A FOCUS ON UDDER HEALTH AND MILKING MANAGEMENT ON CANADIAN FARMS

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Guidelines for proper milk harvest and mastitis prevention have been widely studied and publicized in the dairy industry, yet a portion of the producer population is still not following or adopting the best practice. This project was part of the first National Dairy Study (NDS) conducted in Canada, and funded by Dairy Farmers of Canada through the Dairy Research Cluster 2 program. The objective of this part of the study was to describe the current adoption of recommended milking practices on dairy farms across all of Canada’s 10 provinces.

During the spring of 2015 every licensed dairy producer in Canada was invited to complete a comprehensive questionnaire that addressed a range of health and management issues. The questionnaire was available in both English and French, could be accessed electronically, by paper copy, or could be completed by phone interview. The questions addressing udder health were adapted from a bilingual questionnaire previously validated by Dufour et al. (2010). Of nearly 12,000 Canadian dairy producers 1,342 completed the survey. The adoption of recommended milking practices varies across farms and provinces, with markedly different adoption rates for different practices. Some of the practices, most notably the use of a post milking teat disinfectant, were reported to be widely adopted. Other practices, including cleaning gloves with disinfectant between cows and use of a pre milking teat disinfectant are much less widely in use. What remains to be explained are the reasons behind choices producers make, and why certain practices are used more widely than others. A qualitative study using a focus group approach will investigate barriers to uniform adoption of recommended best practices and determine the reasons behind producer decisions and perceptions of appropriate milking management.
CHARACTERISTICS OF INFECTION CONTROL PRACTICES AT NORTH AMERICAN VETERINARY TEACHING HOSPITALS – PROMOTING A SAFETY CULTURE IN VETERINARY MEDICINE

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Infection control is crucial to the operation of veterinary hospitals to not only protect the patients and hospital, but to protect personnel. Veterinary personnel have an increased lifetime risk for developing a zoonotic infection. In fact, in a study conducted in 2006, the majority of Veterinary Teaching Hospitals (VTHs) surveyed reported significant health problems due to zoonotic infections among hospital personnel. Cryptosporidium parvum infections accounted for 68% of these infections. The objective of this study was to characterize current infection control practices in place for the prevention of healthcare-associated infections, including zoonotic infections, in North American VTHs. All VTHs located in North America that had been operational for at least one year (n=35) were eligible to participate in this study. A phone survey was conducted from July-December 2015 of biosecurity experts which addressed policies for hygiene, surveillance, patient contact, education, awareness, and enteric infectious disease control. Among participating VTHs, greater than half (20/35) reported significant outbreaks of disease among hospitalized patients in the previous 5 years; most commonly due to Salmonella enterica or equine herpesvirus-1. Additionally, 50% reported significant health problems in personnel, in the previous 2 years that most likely resulted from zoonotic infection. Of these, Cryptosporidium was identified as the most common agent. The majority of VTHs surveyed had a committee that oversaw biosecurity program activities as well as written biosecurity policy documents, however, only half conducted mandatory training on the biosecurity program. The results of this study will help to improve strategies for preventing healthcare-associated infections, including zoonotic infections, among patients and veterinary personnel; and allow for targeted educational tools to promote a safety culture in veterinary medicine.
INVESTIGATION OF THE DETERMINANTS OF ANTIMICROBIAL USE IN LIVESTOCK AND COMPANION ANIMALS AMONG VETERINARY CLINICIANS AT THE UNIVERSITY OF TENNESSEE VETERINARY MEDICAL CENTER

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In veterinary medical practice, antimicrobials are used to maintain health and productivity. Approximately 80% of the annual antimicrobial consumption in U.S is attributed to antimicrobial use in food producing animals. It is still unclear what influences clinicians to delay or start the use of antimicrobials and the class of antimicrobials to use. The objective of this study is to understand how and why clinicians make a judgment call on antimicrobials. The University of Tennessee Institutional Review Board will approve the survey and methods to be used in the study for the Protection of Human Subjects in Research. An online questionnaire will be administered to 123 clinicians at the University of Tennessee Veterinary Teaching hospital. Epidemiologists, social scientists and anthropologists will validate the questionnaire. The survey will be administered in July 2016 and remain open for access for 4 weeks. Reminder e-mails will be sent to participants weekly during the survey period. Participants will be required to make single online submissions to avoid multiple entries. No personal information will be attached to survey responses. The survey will include demographic information, education experiences, years of experience in clinical practice, prescribing practices, extra-label use practices, and views related to antimicrobial use, antimicrobial resistance and antimicrobial stewardship, adherence to U.S Food and Drug Administration and American Veterinary Medical Association policies on judicious use of antimicrobials, views related to training of veterinary students on rational use of antimicrobials. The results of this study could be helpful in improving educational practices on judicious use of antimicrobials.
A SCOPING REVIEW OF PUBLISHED RESEARCH ON LYME DISEASE

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Endemic regions for Lyme disease (LD) in Canada exist due to established populations of tick vectors and animal reservoirs for Borrelia sp. associated with human disease. Climate change could expand tick vector ranges increasing the public health impact from LD and other tick-borne diseases. A scoping review of published research was conducted to identify and characterize the scientific evidence concerning key aspects of LD to support public health efforts addressing this emerging issue. An expert advisory group provided insight on priority topics and review scope. A search strategy implemented in eight databases captured published primary research literature investigating LD: a) surveillance and monitoring in North America; b) evaluation of diagnostic tests; c) risk factors; d) interventions; e) North American public attitudes/perceptions; and f) the economic burden or cost-benefit of interventions. Analysis identified topic areas with solid evidence and knowledge gaps. Of 16,516 records screened, 1839 relevant articles were identified and analysed. Results included: surveillance and monitoring in North America (n=704), evaluation of diagnostic tests (n=660), risk factors (n=449), intervention strategies (n=161), public knowledge/attitudes/risk perceptions in North America (n=172), and the economic burden of LD or cost-benefit of interventions (n=27). Most primary research investigated: Borrelia burgdorferi (n=1507), humans (n=1003), and Ixodes scapularis (n=392). Limited research was identified for other Borrelia sp. The main surveillance techniques reported were targeted sampling (n=448) and use of sentinel animals (n=100). Intervention studies focused on vaccination (68), chemical control (40), personal protection (23) and public education (11). This scoping review summarizes the chronology, distribution and characteristics of primary research underpinning the LD issue. Sufficient data was identified for systematic reviews of the accuracy of diagnostic tests, risk factors for human illness, efficacy of intervention strategies, and the prevalence and/or incidence of LD in humans or Borrelia sp. in animal reservoirs or ticks in North America.

INVESTIGATION OF THE POTENTIAL RELATIONSHIP BETWEEN INFLUENZA A VIRUS (IAV) AND STREPTOCOCCUS SUIS INFECTIONS IN WEANLING PIGS

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Streptococcus suis is present on all swine farms with sporadic outbreaks of disease occurring most often in weanling pigs. Factors that influence transition from tonsillar colonization to clinical disease are poorly understood. It has been shown that adherence and virulence of S. suis increases when swine epithelial cells were pre-infected with classical H1N1 influenza virus. Influenza A virus (IAV) is also a common post-weaning pathogen. The objectives of this study are to determine if infection with IAV predisposes piglets to develop clinical signs of S. suis infection, and to determine if pigs that develop clinical S. suis disease have defective innate immunity. This study will look at naturally infected piglets to determine if an in-vivo relationship between IAV and S. suis exists. The interaction will be analyzed using a case-control study design. Cases will be selected if they are demonstrating clinical signs for acute meningitis caused by S. suis infection and controls will be healthy age-matched pen mates. Post-mortem examinations will be conducted on the cases. Nasal swabs, blood samples and tonsil swabs will be taken from both cases and controls. Bacterial swabs will be cultured for S. suis and the isolates will be serotyped. Blood samples will be tested for the presence of different classes of antibody (IgA and IgM) against IAV to determine the recent and/or historical IAV infection. A tail tissue will be collected from cases and controls and DNA will be extracted and used to identify the genetic markers associated with innate immunity to S. suis and IAV. The cases and controls will be compared to determine if recent infection with IAV is associated with systemic infection with S. suis, which could elucidate pathogenesis of S. suis infection, and contribute to the design of control strategies.
A SCOPING REVIEW OF PUBLISHED RESEARCH ON THE POPULATION DYNAMICS AND CONTROL PRACTICES OF COMPANION ANIMALS

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Companion animal overpopulation is a growing concern affecting countries all over the world. In Canada, according to the Canadian Federation of Humane Societies, 60% of both cats and dogs that entered a shelter in 2012 were stray. Overpopulation is a very diverse issue and it can affect society in multiple ways, including impacts on public health, environmental destruction and shelter management. Due to this diversity there are many different control practices which have been implemented to try to manage companion animal overpopulation to varying successes. The purpose of this scoping review was to use structured and transparent methods to identify all globally published research investigating companion animal population dynamics and current companion animal population control practices. To date, a comprehensive search strategy has been implemented in 5 online databases (PubMed, CAB Direct, Agricola, PsycINFO, and Scopus) which has resulted in the identification of 7,855 unique citations. The identified citations have been screened for relevance by two independent reviewers. Of these, 1,400 were deemed relevant. Full articles were procured and 813 articles were confirmed relevant. A grey literature search was conducted through relevant websites resulting in the identification of 83 unique citations. Of these, 67 citations were deemed relevant through relevance screening. Full articles were procured and 55 articles were confirmed relevant. Pertinent information from these articles including population type, theme, outcomes and effectiveness of control practices has been extracted and summarized. Final results will be presented, including a summary of the quantity, distribution, and characteristics of research in this area. The results from this study will inform the direction of future research on companion animal population dynamics and control as a result of mapping out and evaluating the current research gaps, needs and opportunities in this area.
MANAGING VETERINARY EUTHANASIA AND CLIENT GRIEF SUPPORT

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For many pet owners, companion animals are regarded as integral members of the family. So, when a pet dies it is commonplace for pet owners to grieve their loss as they would a family member. Research has shown that the grief reaction to pet loss (i.e. death or euthanasia of a pet) is similar, if not identical to the grief reaction of losing a significant other. However, unlike human loss, pet loss is not widely acknowledged as a legitimate source of grief. In some cases, pet owners experience an increased grief reaction because the normal process of grieving is prolonged and complicated. Past research has shown that the circumstances surrounding the pet’s death and how well the veterinary team manages the actual euthanasia process can either alleviate or aggravate client grief. Current research into the most effective way to euthanize a companion animal and support clients through their grief process is very limited. A better understanding of what is currently being practiced in veterinary clinics in terms of euthanasia and the support offered to clients may inform effective protocols or guidelines to meet these needs. Existing research suggests that pet cremation and memorialization are also important factors that may help reduce grief due to pet loss, however a better understanding of the role and value of pet cremation and memorialization services is also needed. At this stage of this project, focus group and/or individual interviews are being organized with Guelph-area veterinary clinics. The interview data will be used to investigate current euthanasia practices before, during and after euthanasia as well as client grief support methods. It is anticipated that the collection of qualitative data will be used to inform a quantitative questionnaire design, results from which will aid in developing protocols for veterinary clinics to guide the management of euthanasia protocols and meet the emotional needs of clients.
USE OF NOVEL PROXIMITY LOGGING TECHNOLOGY TO QUANTIFY EQUINE CONTACT PATTERNS IN ONTARIO EQUINE FACILITIES

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Equine social contact patterns are complex and can demonstrate marked variability within and between facilities. However, such contact pattern data within an equine facility has yet to be explicitly characterized. The characterization of such contact data is essential to the understanding and accurate description of equine contact networks. This research will apply novel proximity logging technology to collect the data necessary for the quantification of equine contact networks.

The objective of this study is to describe and quantify the contact patterns of horses within equine training facilities. Ontario equine riding facilities of various disciplines (pleasure riding, racing and sport/competition) and sizes will be recruited to participate. Questionnaires will be administered to facility managers/owners to obtain horse-level information such as signalment and routine daily activities. A sample of horses from each participating facility will be fit with a small, non-invasive proximity logger onto their tack/equipment. These Internet of Things (IoT) based loggers will record each time individual horses come within 2m of one another, the duration of the contact, and which tags (horses) were in contact. Data will be collected at each facility for one week between April and July, and another week between August and November to account for seasonal differences in the facility’s schedule. The contact data will be used to describe the contact network of horses within the facility. This data will subsequently be used to compare equine contact patterns between facilities and disciplines.

The empirical network data compiled will be used to inform dynamic disease transmission models. These models use computer simulations to evaluate the way different equine pathogens may behave if they were introduced to different types and sizes of facilities, as well as to assess the impact of prevention and control strategies. Accurate equine contact pattern data is needed to properly inform these dynamic models.

FOOT-AND-MOUTH DISEASE VIRUS SURVIVAL IN U.S. SOIL OVER TIME

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Foot-and-Mouth Disease (FMD) is considered to be one of the most economically significant global livestock diseases. In the U.S., economic optimization models have demonstrated that the highest mean epidemic impact of a potential FMD outbreak would occur in livestock-dense regions, resulting in national agriculture losses of $2.3 to $69.0 billion dollars. In the case that an FMD outbreak were to occur in the U.S., mass depopulation, carcass disposal and disinfection protocols for infected premises have been designed to prevent further viral spread. Due to the fact that the FMD virus (FMDV) is spread mechanically via the environment, characteristics of viral environmental stability are important. Temperature and adsorption to soil particles have been determined to be the most important factors affecting general virus survival; however, the role of these factors in FMDV survival has not previously been tested. We examined soil environments typical of U.S. regions containing the highest cattle population densities: Tennessee, Georgia, Nebraska, California, Pennsylvania, Kentucky, and Iowa. We determined the effect of these soil types on FMDV infectivity over seven distinct time points between 0 hours and 12 days at incubation temperatures of 25°C and 37°C. FMDV infectivity was quantified via virus titrations and subsequent tissue-culture infectious dose (TCID50) calculations. Positive and negative control samples were also tested. As expected, incubation temperatures had more of an impact on infectious viral retention in soil than pH differences between soil types. Iowa soils retained infectious virus at the 5 day time point, when virus in most other soil types was undetectable. Consequently, areas with high ambient temperatures may require less disinfection effort and may have lower between-farm transmission rates. Additional investigations into FMDV survival in clay soils, such as those in Iowa, may aid in developing better disinfection protocols.
CHARACTERIZING THE RELATIONSHIP BETWEEN LIVESTOCK ANTIMICROBIAL USE AND ANTIMICROBIAL RESISTANCE IN PEOPLE IN ONTARIO: AN INTEGRATED ASSESSMENT MODEL

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Antimicrobial resistance (AMR) is a complex health issue with multiple determinants, exposures and outcomes. Although antimicrobial use (AMU) and AMR data have been collected for years, our understanding of how animal AMU affects AMR in people is limited. Integrated assessment models (IAM) are mathematical frameworks that process existing data from complex systems into interpretable information. Our goal with this project is to use an IAM to translate existing agricultural AMU and AMR data into relative estimates of risk to human health from AMR E. coli, Salmonella enterica and Campylobacter species with an Ontario focus. Completed key elements and outputs include: 1) a conceptual model (expanding upon existing AMU/AMR models) that more fully describes where (animals, humans, crops) and how (e.g. prophylaxis) antimicrobials are used, where resistant bacteria occur, their movement along the food chain and ecosystems, and factors that are known or hypothesised to be associated with AMR or AMU; and 2) retrieval, assessment and organization of existing data and development of data management and manipulation tools to use these data in a quantitative decision modelling software. Ongoing and next steps include: 1) completion of pilot quantitative decision models and assessment of the model framework for expansion into other aspects of AMR; 2) knowledge translation including peer-reviewed publication(s), plan language summaries, presentations, and qualitative models that simply explain the outputs of quantitative models and highlight data gaps and research needs; and 3) consultations with stakeholders and experts to assist in data and model interpretation and validation. By the end of this project, we expect to have a better understanding, yet still incomplete, of the relationship of animal AMU and human AMR. Our intention is to create a framework that will transparently integrate available data, quantify current knowledge, identify research gaps, and that can be updated as more information becomes available.

ESTABLISHMENT OF THE NEAR REAL-TIME REPORTING MECHANISM FOR SURVEILLANCE OF INFLUENZA A VIRUS IN SWINE

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Influenza A virus (IAV) regularly causes outbreaks of respiratory disease in pigs worldwide. The virus can circulate among swine herds throughout the year causing different level of respiratory disease. Our research is focused on processing and summarizing the laboratory swine influenza data in a user-friendly report minutes after the data become available. This is a necessary condition for near real-time disease surveillance and disease investigation. With the use of descriptive statistics, ARIMA time series techniques and the Farrington method, we detect unusual weeks and months with respect to the number of samples submitted to a laboratory as well as the number of positive records. The long term trends in laboratory disease submissions can be visualized after accounting for the seasonality effect. Short terms forecasting at weekly and monthly levels are incorporated in the analyses. All obtained results are highlighted in our reporting mechanism. The results of this research represent real-time, semi-automated, efficient ongoing processing and analysis of data, interpretation of results, and the communication of findings to producers, swine veterinarians, and regulatory experts.
A HAPLOTYPE IDENTIFICATION SYSTEM FOR ANTIMICROBIAL RESISTANCE GENES IN SHOTGUN METAGENOMIC DATA

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Antimicrobial resistance genes (ARGs) represent <0.1% of DNA in a typical metagenomic sample; attaining sufficient sequencing coverage to confidently identify ARG SNPs within such data is cost-prohibitive. Bait capture (e.g., Agilent’s SureSelect system) can selectively enrich for target genes within metagenomic DNA, but this method has yet to be applied to ARGs. The overall goal of this project was to design an ARG bait capture system and validate its use in metagenomic fecal samples collected from poultry, swine, and beef production and human wastewater treatment plants (WWTP).

We developed an optimized bait design to target >4,000 known ARGs. We tested the efficiency of these baits on 16 fecal samples that were shotgun sequenced both before and after enrichment with the designed baits. Abundance of ARGs increased from an average of 0.21% (range 0.002% to 0.41%) of all DNA sequences in the non-enriched samples to an average of 37% (range 5% to 64%) in the enriched samples. All ARGs, classes and mechanisms of resistance identified in the nonenriched samples were also identified in the enriched samples, indicating that the baits likely captured all available targets. In addition, more ARGs, classes and mechanisms of resistance were identified in the enriched samples, suggesting that bait enrichment affords increased sensitivity compared to the nonenrichment approach. ARG composition was similar between enriched and nonenriched samples, with a majority of ARG-assigned DNA classified into tetracycline, macrolide-lincosamide-streptogramin (MLS), betalactam and aminoglycoside resistance classes. In both the enriched and nonenriched sample sets, ARG composition differed significantly between the beef, poultry, beef and WWTP samples, suggesting that the resistance ecology within each system is unique. Finally, distinct haplotypes were identified in the enriched samples, suggesting that bait-enriched metagenomic sequencing could provide SNP profiles that could potentially be used to track antimicrobial resistance genes through time and space.

A REGRESSION-BASED ALARM FOR EARLY DETECTION OF EPIDEMICS OVER NETWORKS

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Forecasting the beginning of outbreaks of infectious diseases is well studied for the case of simple disease generating models. However, epidemics over real-world, heterogeneous networks tend to exhibit a more complex behavior. We propose a regression-based monitoring system suitable for non-homogeneous populations, and derive its statistical properties over simulated networks. We then illustrate its use on observed rates of influenza-like illness from the French Sentinelle network. The aim of this research is to show that this alarm can detect the start of the influenza season faster than other traditionally used statistical alarms, for the same levels of sensitivity and specificity.
UNDERSTANDING MAJOR CAUSES OF MORTALITY IN ONTARIO RAPTORS USING A PASSIVE SURVEILLANCE PROGRAM

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Raptors are susceptible to anthropogenic causes of mortality, and as top predators, are also vulnerable to dynamic environmental conditions that may affect habitat and prey availability. We retrospectively evaluated postmortem diagnostic data from raptors submitted to the Ontario/Nunavut node of the Canadian Wildlife Health Cooperative from 1991 to 2014 (n = 1,449). Submissions encompassed 29 species, the most common of which were the red-tailed hawk (Buteo jamaicensis; 21.3%; n = 308) and great horned owl (Bubo virginianus; 16.4%; n = 237). Trauma (49.4%; n = 716), followed by emaciation (16.6%; n = 241), accounted for the majority of deaths among all raptor species and was most commonly attributed to collisions (47.3%; n = 339). Using multivariable exact logistic regressions, we assessed the impact of West Nile virus (WNV) on the proportion of submissions related to infectious diseases and whether submissions related to WNV varied by sex or age (mature vs. immature). The odds of a submission being related to an infectious cause in all raptors and red-tailed hawks were significantly greater after the arrival of WNV to Ontario (2001) compared to the period before its arrival (all raptors: OR = 1.47, p = 0.0179, 95% CI= 1.07-2.04; red-tailed hawks: OR = 2.54, p = 0.0049, 95% CI = 1.30-5.18). Age and sex were not significantly associated with the odds of a submission being infected with WNV. These results suggest that human-associated deaths (e.g., due to trauma) and emaciation are relatively common among Ontario raptor carcasses submitted for diagnostic evaluation. In addition, the introduction of WNV into Ontario has significantly increased the proportional mortality of submissions related to infectious causes. Although limited by the biases of human observation and submission of cases, this research demonstrates the potential utility of this program in identifying major causes and trends in Ontario raptor mortalities.

AN AGENT-BASED MODELING APPROACH TO DETERMINE THE IMPACT OF CONTROL STRATEGIES ON A FACILITY-LEVEL EQUINE INFLUENZA OUTBREAK

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Equine influenza (EI) is a highly contagious viral infection causing outbreaks of respiratory disease in equine populations worldwide. While vaccination may offer individual horses short-term protection against infection, variability in duration and level of immunity can affect population-level infection dynamics. Minimizing horse-to-horse contact may be an effective strategy to reduce the attack rate of EI within a facility. The objectives of this study were to evaluate the effect of: (1) increasing population-level vaccination coverage prior to EI introduction, and (2) decreasing the contact rate following EI introduction on the attack rate of infection in a simulated equine population. An agent-based model was constructed to represent a facility of 100 racehorses over 180 days, where the population was vaccinated for EI at the beginning of the simulation. One infected horse was introduced in scenarios at one, three, and five months after the start of the simulation to determine the impact of waning immunity on the results of implemented interventions. Two interventions were evaluated: (1) vaccination coverage was increased in 5% increments, and (2) contact rate was reduced at various time-points following EI introduction. The results indicate that high vaccination coverage may be sufficient to minimize the attack rate in a well-vaccinated population if EI introduction occurs within 3 months of vaccination. Additionally, reducing the contact rate by 50% or greater after EI introduction is effective in substantially reducing the attack rate if the population has been vaccinated within 3 months. There were no differences in the projected attack rate when the contact rate was reduced at different time-points following EI introduction, suggesting that the act of reducing contact between horses is more important than the time at which contact is reduced. This study highlights the benefits of incorporating multiple disease prevention and control strategies during a facility-level EI outbreak.
When estimating the burden of illness due to giardiasis, international travel cases are considered to be distinct from domestically acquired cases; however, there is no distinction made between domestic travel related cases (DTRCs) and endemic cases (ECs). This represents a considerable knowledge gap, as risk factors for contracting giardiasis via domestic travel may be different from those associated with endemic giardiasis or international travel. Therefore, the objective of our study was to identify if there were significant differences in exposure to risk factors for giardiasis among international travel related cases (ITRCS), DTRCs and ECs. Public health inspectors gathered exposure and demographic data for giardiasis cases reported in the Region of Waterloo from 2006 to 2012, inclusive. Multinomial regression models were subsequently fit to assess the differences in risk profiles between the ITRCs, DTRCs and ECs. Over the six year study period, 472 giardiasis cases were reported to the Region of Waterloo, 40% of cases were ITRCs, 6% of cases were DTRCs and 54% of cases were ECs. We found significant differences in exposures to various risk factors for giardiasis among the various case groups. Both ITRCs and DTRCs were more likely to go camping or kayaking, and consume untreated water compared to ECs. Domestic travel-related cases were more likely to visit a petting zoo or farm, and swim in freshwater compared to ECs. The findings of our study demonstrate that travel-related (domestic and international) cases and ECs have differing levels of exposure to risk factors for giardiasis. Therefore, we suggest that in future studies, DTRCs and ECs should not be included together as this may result in missing important associations or risk factors. Of greater significance, our findings are important for creating effective and targeted health promotion campaigns to prevent giardiasis in this region, by targeting specific risk activities.
Lyme disease (LD) is the most common tick-borne infection in Canada and much of the United States. The incidence of LD has been increasing since first identified in the United States in 1975. This corresponds to an increase in the Ixodes tick vector’s range across the northern states and into Canada, which may partially be due to climate change. Many imperfect diagnostic tests for LD are available and there is concern and on-going discussion that the LD tests are over used. A positive test result in a patient who does not meet the clinical criteria is likely to be a false positive result, thus requiring careful evaluation by a physician to avoid employing LD diagnostic assays inappropriately.

The objective of this systematic review is to summarize the North American evidence on the accuracy of diagnostic tests and test regimes at various stages of LD and to address the question of whether there is evidence of superior, equivalent or poor performance by the commercial (approved by the Food and Drug Administration (FDA) and/or Health Canada (HC)) and in house laboratory tests captured in this review.

Included in the review are 49 studies on diagnostic tests used in North America published since 1995 when CDC released its recommendation for 2-tier testing. Thirteen studies (78 lines of results) examined a two-tier protocol vs. clinical symptoms, 24 studies (119 lines) examined single assays vs. clinical symptoms, 9 studies (37 lines) examined single immunoblot vs. clinical symptoms, 7 studies (15 lines) compared culture or PCR direct detection methods with clinical symptoms, 22 studies (57 lines) compared two or more tests with each other and 8 studies (10 lines) compared a two-tiered protocol to another test.

The results and implications of the review findings will be discussed. The literature shows there is a dramatic increase in the sensitivity of serological tests with progression of Borrelia burgdorferi sensu lato infection from early to late LD. Thus, early LD patients run a high risk of testing negative so physician evaluation of clinical symptoms is very important. Diagnostic assays based on next generations antigens (e.g. Immunetics® C6 ELISA) and the two tiered approach have demonstrated superior specificity compared to proposed replacements and the CDC recommended western blot algorithm has equivalent or superior specificity over other proposed test positive algorithms. Direct detection methods, culture and PCR of tissue samples do not currently offer sensitive or timely diagnosis. A number of commercial and in house tests used in North America have not been evaluated in the primary literature so their performance is missing from this analysis.
A systematic review of the effectiveness of interventions to control non-typhoidal Salmonella spp. prevalence or concentration in pork was undertaken; this presentation describes the findings pertaining to interventions applied at transport and lairage. A broad search was conducted in two electronic databases. Level 1 relevance screening excluded irrelevant citations; level 2 confirmed relevance and categorized. Data were extracted, and intervention categories were descriptively summarized. Meta-analysis was performed to provide a summary estimate of treatment effect where two or more studies investigated the same intervention. We used the Grading of Recommendation, Assessment, Development and Evaluation (GRADE) approach to assess the confidence in the estimated measures of intervention. Using data from the control groups of challenge trials captured by the search, mixed logistic regression models for odds of Salmonella infection, and discrete time survival models were fitted.

The only intervention captured which was significantly associated with reduced odds of Salmonella was elimination of lairage. Using mixed logistic regression, the following were significantly (P < 0.05) associated with increased odds of fecal Salmonella shedding: oral challenge, log increase of challenge dose, and assay within the first 24 hours after challenge. Clustering by trial suggested additional unknown potential covariates. The following were positively associated with increased odds of Salmonella infection in lymph nodes, using exact logistic regression: younger animals vs. older animals; intra-nasal vs. oral challenge route; and animals sampled within the first 7 days post-challenge relative to those sampled at 14 or 21 days. Variation in one or more of these parameters across the controlled trials captured could explain the inconsistent treatment effects reported for interventions such as hygiene and disinfection.

Further research into interventions at lairage, particularly those without the potential to aerosolize Salmonella, capturing potential predictors of infection such as prevalence and load of Salmonella shedding in seeder animals, is suggested.
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