The International Conference on Diseases in Nature Communicable to Man

University of Guelph

August 7 - 9, 2016

Program & Schedule
Sunday, August 7th

7:00 - 9:00pm
Meet and greet at the Brass Taps Campus Pub
Registration available
University Centre,
University of Guelph

Brass Taps entrance inside the University Centre
University Centre entrance

The 71st International Conference on Diseases in Nature Communicable to Man is co-hosted by:

www.ovc.uoguelph.ca/cphaz
www.cwhc-rcsf.ca
Monday, August 8th

Please note: All events will take place in Rozanski Hall, University of Guelph, unless otherwise stated. Registration, lunch, and breaks will be in the main foyer and all sessions will be in room 103. Posters will be set up on Monday before 8:30am and displayed in the foyer for the duration of the event.

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<th>Time</th>
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<tr>
<td>7:45 - 8:30 am</td>
<td>Arrival, registration and poster set up</td>
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<tr>
<td>8:30 - 8:45 am</td>
<td>Opening remarks</td>
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<tr>
<td></td>
<td>Dr. John Livernois, Associate Vice-President (Research Services), University of Guelph</td>
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<td>Dr. Jeffrey Wichtel, Dean - Ontario Veterinary College</td>
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<td>Dr. Muhammad Morshed, INCDNCM President</td>
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<td>8:45 - 9:30 am</td>
<td>R.R. Parker Memorial Lecture: Emerging zoonoses: causes, consequences and how we can respond</td>
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<td>Dr. Nicholas Ogden, Public Health Agency of Canada</td>
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<td>Drivers of emerging and re-emerging infectious diseases in Canada and globally</td>
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<td>Preparing for emerging infectious diseases through prediction and willingness to control</td>
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<td>A WALK ON THE WILD SIDE: ZOONOSES IN OUR WILDLIFE POPULATION</td>
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<tr>
<td>9:30 - 10:10 am</td>
<td>Nicole Nemeth The red fox (<em>Vulpes vulpes</em>) as a potential sentinel for <em>Blastomyces dermatitidis</em> in Ontario, Canada</td>
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<td>Jane Parmley Avian influenza in wild birds - 2015 surveillance results from Ontario</td>
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<td>10:10 - 10:40 am</td>
<td>Break</td>
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<tr>
<td>10:40 - 12:00 pm</td>
<td>Ying Bai Molecular survey of bacterial infections in bats from Georgia (Caucasus)</td>
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<td>Arinjay Banerjee Activation of the toll-like receptor-3 (TLR3) pathway in Big brown bat (<em>Eptesicus fuscus</em>) cells does not activate pro-inflammatory genes: A reason for the lack of overt virus-induced pathology in bats?</td>
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<td>Rajnish Sharma Exposure to <em>Toxoplasma gondii</em> in wolverines from Yukon, Canada</td>
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<td>Andrea Thomas-Bachli Sociodemographic factors associated with citizen reports of dead corvids during the introduction of West Nile virus in Ontario; applications for spatial scan statistics</td>
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<tr>
<td>12:00 - 1:20 pm</td>
<td>Lunch/Poster session (students participating in poster competition, please be at your posters from 12:50 - 1:20pm)</td>
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<td>Time</td>
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<td>1:20 - 2:00 pm</td>
<td>The changing status of plague in the modern world</td>
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<td>Dr. Kenneth Gage, Centers for Disease Control and Prevention</td>
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<td>- Current status of plague in the world</td>
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<td>- Potential emerging risk factors of plague in the developing and developed world</td>
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**Beware the bite: Emerging vector-borne zoonoses**

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<th>Speaker/Topic</th>
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<td>2:00 - 3:20 pm</td>
<td>Kevin Fonseca - Testing for Zika virus - An Alberta perspective</td>
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<td>Michael Kosoy - Bartonella of domestic sheep and sheep keds: cultures, genetic characterization, and ecological connections</td>
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<td>Mark Nelder - Human pathogens associated with <em>Ixodes scapularis</em>: The never-ending story...</td>
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<td>Mariola Mascarenhas - A scoping review of research investigating Chikungunya virus (CHIKV) and its competent vectors</td>
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<td>3:20 - 3:50 pm</td>
<td>Break</td>
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<td>3:50 - 4:30 pm</td>
<td>A review of the 2015-16 Zika virus outbreak</td>
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<td>Dr. David Safronetz, Public Health Agency of Canada (Presentation given by Robbin Lindsay)</td>
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<td>- Current status of zika virus as an emerging pathogen with pandemic potential</td>
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<td>- Current difficulties and issues with the interpretation of zika virus serologic results</td>
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<td>4:30 pm</td>
<td>End of Day 1 Scientific Sessions</td>
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**INCDNCM Social Dinner**

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<td>6:00 - 10:00pm</td>
<td>Diseases in nature attributable to man</td>
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<td>Guest Speaker: Dr. Doug Campbell</td>
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<td>Canadian Wildlife Health Cooperative</td>
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<td>Atrium, Summerlee Science Complex</td>
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<td>Display and special presentation by Dr. Lisa Cox, curator of the OVC C.A.V. Barker Museum of Canadian Veterinary History</td>
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Tuesday, August 9th

Please note: All events will take place in Rozanski Hall, University of Guelph, unless otherwise stated. Registration, lunch, and breaks will be in the main foyer and all sessions will be in room 103.

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<th>Time</th>
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<tr>
<td>8:00 - 8:45 am</td>
<td>Business Meeting/Poster viewing</td>
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<td>8:45 - 8:50 am</td>
<td>Opening remarks</td>
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| 8:50 - 9:30 am | Trust and research in Canada’s arctic: Foodborne and waterborne disease  
  Dr. Sherilee Harper, University of Guelph & Dr. Victoria Edge, Public Health Agency of Canada  
  - Unique aspects of public health based on research and Indigenous communities  
  - Impacts of climate change on the health and wellness of Indigenous populations in remote areas |
| 9:30 - 10:30 am | From forest to farm to fork: The role of wildlife in foodborne diseases  
  Nadine Vogt  
  Mythri Viswanathan  
  Genet Medhanie  
  Mythri Viswanathan: Cluster analysis of Campylobacter isolates obtained from beef cattle, dairy cattle, and mammalian wildlife on Southern Ontario farms (2010)  
  Genet Medhanie: On-farm starling populations and other environmental and management factors associated with the presence of cefotaxime and ciprofloxacin resistant E. coli among dairy cattle in Ohio |
| 10:30 - 11:00 am | Break                                                                |
| 11:00 - 12:00 pm | On the lookout: Surveillance approaches and applications          
  Frank Pollari  
  Muhammad Morshed  
  Marion Ripoche  
  Frank Pollari: FoodNet Canada: Canadian integrated enteric disease surveillance system  
  Muhammad Morshed: An update on Lyme disease in British Columbia: Tick surveillance study  
  Marion Ripoche: Passive tick surveillance as an early warning system for emerging Lyme disease risk: mapping tick establishment and early human cases in a Lyme disease emergence zone in southern Canada |
| 12:00 - 1:20 pm | Lunch/Poster session (students participating in poster competition, please be at your posters from 12:50 - 1:20pm) |
The International Conference on Diseases in Nature Communicable to Man

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<td>1:20 - 2:00 pm</td>
<td><strong>Re-emergence of raccoon rabies in Ontario</strong></td>
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<td><em>Mr. Tore Buchanan, Ontario Ministry of Natural Resources and Forestry</em></td>
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<td>- Targeting rabies in wildlife through immunization programs</td>
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<td>- Factors contributing towards the re-emergence of rabies in raccoons</td>
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<td>2:00 - 3:20 pm</td>
<td><strong>Vector-borne zoonoses special topic: Lyme disease</strong></td>
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<tr>
<td>Katie Clow</td>
<td>The effect of abiotic and biotic factors on the establishment of <em>Ixodes scapularis</em> populations in Ontario, Canada</td>
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<td>Christine James</td>
<td>Epidemiology of <em>Ixodes scapularis</em> on pet dogs in an emerging Lyme disease area in Ontario</td>
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<tr>
<td>Lisa Waddell</td>
<td>Systematic review and meta-analysis of the accuracy of diagnostic tests for North American Lyme disease in humans</td>
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<td>Kevin Stinson</td>
<td>Teaching tick identification to frontline medical personnel in the Canadian Forces Medical Services</td>
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<td>3:20 - 3:40 pm</td>
<td><strong>Break</strong></td>
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<td>3:40 - 4:40 pm</td>
<td><strong>Moving beyond: Policy and programming for zoonoses in nature</strong></td>
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<td>Curtis Russell</td>
<td>Public Health Ontario’s new interactive West Nile virus weekly report</td>
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<td>Lorne Jordan</td>
<td>National farm-level biosecurity standards in Canada: Implications for zoonotic disease management</td>
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<td>Jan Sargeant</td>
<td>A quantitative approach to the prioritization of zoonoses in North America</td>
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<tr>
<td>4:40 - 5:00 pm</td>
<td><strong>Awards and closing remarks</strong></td>
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<td>A longitudinal study of <em>Salmonella</em> shedding in pigs</td>
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<td>Gitanjali Arya</td>
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<td>Trends in non-typhoidal <em>Salmonella</em> from non-human sources: a Canadian Reference Laboratory Perspective</td>
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<td>Wolfgang Beyer</td>
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<td>Recombinant peptides and FIS tested as vaccine candidates for immunogenicity and protectiveness in farm goats</td>
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<td>Kristin Bondo</td>
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<td>Epidemiology of <em>Salmonella</em> in raccoons and the environment on swine farms and conservation areas</td>
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<td>Alexandra Brower</td>
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<td>Epidemiological investigation of <em>Brucella canis</em> in Arizona; Preliminary report</td>
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<td>Aleksandra Cetera</td>
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<td>Tick-borne pathogens detected in ticks removed from companion and wild animals in southern Ontario</td>
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<td>Elizabeth Hartnett</td>
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<td>Risk factors associated with <em>Baylisascaris procyonis</em> infection in raccoons (<em>Procyon lotor</em>)</td>
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<td>Stefanie Kadykalo</td>
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<td>Antimicrobial resistance patterns in clinical isolates of <em>Salmonella</em> and <em>E. coli</em> from cattle, poultry and swine in Ontario, 2007-2015</td>
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<td>Luz Kisiel</td>
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<td>Domestic dog ecology in Villa de Tezontepex, Hidalgo, Mexico, and implications for canine rabies transmission</td>
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<td>Melissa Mackinnon</td>
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<td>Annual variation in susceptibility of <em>Campylobacter jejuni</em> isolates to tetracycline from retail chicken surveillance</td>
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<td>Jordan Minigan</td>
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<td>Effects of climate change on American dog tick (<em>Dermacentor variabilis</em>) distribution will influence bovine anaplasmosis risk in North America</td>
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<tr>
<td>Jane Parmley</td>
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<td>2014 highlights from the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS)</td>
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<td>Marion Ripoche</td>
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<td>Spatial heterogeneity in <em>Ixodes scapularis</em> distribution within the Lyme disease emergence zone in southern Québec (Canada)</td>
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<td>Kathryn Smith</td>
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<td>Prevalence of Powassan virus in southwestern Ontario, with a focus on vector and host dynamics</td>
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<td>Sonu Subudhi</td>
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<td>Interactions of a Coronavirus with its natural host: the Canadian little brown bat (<em>Myotis lucifugus</em>) – Impact of “stress” on virus-host interplay</td>
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<tr>
<td>Scott Weese</td>
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<tr>
<td>Prevalence and characteristics of <em>Clostridium difficile</em> from polar bears</td>
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Please note: Posters will be displayed from 8:30am Monday, August 8th until 4:45pm Tuesday, August 9th. If you are displaying a poster, please take it with you at the end of the conference.

Thank you for participating in the 2016 International Conference on Diseases in Nature Communicable to Man.
71st International Conference on Diseases in Nature Communicable to Man

August 7-9, 2016

University of Guelph
Guelph, Ontario, Canada

R. R. Parker Memorial Speaker:

Dr. Nicholas Ogden
National Microbiology Laboratory
Public Health Agency of Canada

“Emerging Zoonoses: Causes, Consequences and How We Respond”

Registration closes July 22, 2016

More information at:
https://sites.google.com/site/incdncm
A walk on the wild side: Zoonoses in our wildlife population

The red fox (*Vulpes vulpes*) as a potential sentinel for *Blastomyces dermatitidis* in Ontario, Canada

Nicole Nemeth1,2, Doug Campbell1, Lenny Shirose1, Paul Oesterle1,2, Beverly McEwen3, and Claire Jardine1,2

1Canadian Wildlife Health Cooperative, 419 Gordon Street, Guelph, Ontario, Canada; 2University of Guelph, Pathobiology Department, Guelph, Ontario, Canada; 3Animal Health Laboratory, Guelph, Ontario, Canada.

*Blastomyces dermatitidis* is a fungal pathogen that can lead to fatal infections in humans and other animals. Infection usually occurs via inhalation of fungal spores from an environmental reservoir, often soil. Infection rates and associated disease (blastomycosis) are most commonly reported in humans and dogs along the Great Lakes and other major waterways in the U.S. and Canada. However, the geographic distribution of *B. dermatitidis* is difficult to determine because the fungus is not readily recoverable or uniformly distributed within the environment. Widely distributed and common wild canid species, such as the red fox (*Vulpes vulpes*), are susceptible to infection with *B. dermatitidis*, have relatively small and well-defined home ranges, and live in close contact with the soil. The objective of the present study was to assess companion animal and wildlife cases of blastomycosis in Ontario from 1991-2014 for taxonomic, temporal or geographic patterns in comparison with previously reported human cases in the region. Data from the Canadian Wildlife Health Cooperative and Animal Health Laboratory at the University of Guelph in Ontario, Canada were included. Although dogs were much more commonly diagnosed with blastomycosis (n=222, comprising 88.8% of companion animals), the timing (i.e., November-March) and geographic distribution (i.e., northern region) of blastomycosis detections in red foxes (n=11, comprising 78.6% of wildlife cases) were more closely aligned with human cases. The susceptibility, distribution and biology of red foxes suggest that this species could serve as a potential sentinel for environmental risks of *B. dermatitidis* that threaten public and animal health.

Avian influenza in wild birds - 2015 surveillance results from Ontario

Jane Parmley1, Paul Oesterle2, Davor Ojkic3, Tore Buchanan4, Matt Purvis4, Lenny Shirose1, David Cristo1, Doug Campbell1, and Claire Jardine1,2

1Canadian Wildlife Health Cooperative, University of Guelph; 2University of Guelph, Department of Pathobiology, Guelph, Ontario, Canada; 3Animal Health Laboratory, Guelph, Ontario, Canada; 4Ontario Ministry of Natural Resources and Forestry

Rationale: In 2015, three Ontario farms were infected with highly pathogenic avian influenza (AI) virus resulting in the death of nearly 80,000 birds and serious economic losses for industry. Wild waterfowl play an important role in the ecology of AI. Because of the threat that AI poses to the health of domestic poultry, Canada has a national program to test wild birds for the virus.

Objectives: To present AI surveillance results from wild birds tested in Ontario in 2015.

Methods: Live wild ducks were captured at 34 locations across Ontario. Oropharyngeal and cloacal swabs were collected from each bird and screened for the presence of AI. Positive samples underwent further screening specifically for subtypes H5 and H7. Wild birds found dead that were submitted to the Canadian Wildlife Health Cooperative for cause of death assessment were also screened for AI.

Results: In total, 1681 live wild waterfowl were sampled and tested for AI. Of these, 455 tested positive; 29 also tested positive for the H5 subtype and 1 bird also tested positive for the H7 subtype. Among birds found dead, 2/335 tested positive for AI. No highly pathogenic AI viruses were detected in any wild bird tested in 2015.

Conclusion: Surveillance of wild birds provides important information about which AI subtypes are circulating in a region. A better understanding of how AI viruses move from wild birds into poultry barns is needed to increase the value of surveillance data and better inform on-farm biosecurity practices.
Molecular survey of bacterial infections in bats from Georgia (Caucasus)

Ying Bai1, Lela Urushadze2,3, Lynn Osikowicz1, Clifton McKee1, Andrei Kandaurov1, Ivan Kuzmin1, Ketevan Sidamonidze2, Davit Putkaradze2, Paata Imnadze2, Michael Kosoy1

1Division of Vector-Borne Disease, Centers for Disease Control and Prevention, Fort Collins, Colorado 80521, USA, 2National Center for Disease Control and Public Health, Tbilisi 0177, Republic of Georgia, 3Institute of Zoology, Ilia State University, Tbilisi 0162, Republic of Georgia 4Department of Pathology, University of Texas Medical Branch, Galveston, TX, 77555, USA

Rationale: Bats are important reservoirs to many zoonotic pathogens. The status of bacterial infections in bats in the country of Georgia is unknown.

Objectives: To understand occurrence and distribution of bacterial infections in the bats.

Methods: Using molecular approach, 218 bats belonging to eight species collected from four regions of Georgia were examined for Bartonella, Brucella, Leptospira, and Yersinia.

Results: Bartonella was detected in 77 (35%) bats of eight species from all four regions. The prevalence ranged 6% - 50% among bat species. The Bartonella represented 24 variants and were clustered into 20 phylogroups. Brucella was detected in two Miniopterus schreibersii bats and two Myotis blythii bats, all of which were captured in one region. Leptospira was detected in 25 (13%) bats that included four M. schreibersii bats and 21 My. blythii bats and were distributed within two regions. The Leptospira represented five variants with four of them being close to the zoonotic pathogen L. interrogans (1.4% distance). No Yersinia was detected.

Mixed infections were observed in some bats. Two bats (one My. blythii bat and one M. schreibersii bat) were infected with Bartonella, Brucella, and Leptospira; two bats (one My. blythii bat and one M. schreibersii bat) were infected with Bartonella and Brucella; and eighteen bats (15 My. blythii bats and three M. schreibersii bats) were infected with Bartonella and Leptospira.

Conclusion: Bats from Georgia are exposed to multiple bacterial infections. Further studies are needed to evaluate whether these agents may cause infections in the bats and human.

Activation of the toll-like receptor-3 (TLR3) pathway in Big brown bat (Eptesicus fuscus) cells does not activate pro-inflammatory genes: A reason for the lack of overt virus-induced pathology in bats?

Arinjay Banerjee1, Noreen Rapin1 and Vikram Misra1

1Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan.

In recent years, viruses that cause no overt disease in bats have spilled over to humans and other species causing serious and often fatal disease. These include coronaviruses that cause SARS (Severe Acute Respiratory Syndrome), MERS (Middle-East Respiratory Syndrome) and PED (Porcine Epidemic Diarrhea). Since pathology in these diseases is largely attributed to an over-active inflammatory response, we are exploring the hypothesis that bat cells respond to TLR3 activation with a strong antiviral response, but unlike in human cells, the inflammatory response is not activated.

Here we present data comparing the response of human and bat cells to activator of the toll-like receptor-3 (TLR3) pathway, poly(I:C). The transcripts for several inflammatory, interferon and interferon response genes were then measured using quantitative real-time PCR. We have identified that although bat cells significantly upregulate interferon beta transcripts in response to poly(I:C), transcripts of pro-inflammatory genes (eg.TNF) are significantly less upregulated compared to human cells. To determine if this lack of expression of TNF in respond to poly(I:C) was due to unresponsiveness of the TNF promoter, we examined promoters for both bat and human genes. We found bat cells did not overtly upregulate pro-inflammatory cytokines, possibly due to repression of the promoter by the proto-oncogene c-Rel. c-Rel has been hypothesized to be under positive selection in bats due to its role in the DNA repair pathway. In conclusion, c-Rel could be repressing the inflammatory gene promoters, allowing bats to mount a strong antiviral response to coronaviruses but not an overt inflammatory response.
EXPOSURE TO *Toxoplasma gondii* IN WOLVERINES FROM YUKON, CANADA

**Rajnish Sharma**1,2, J Harms2, T Jung2, P Kukka2, J Singh3, A Gajadhar4 and E Jenkins1

1Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, 52 Campus Drive, Saskatoon, Saskatchewan, Canada, S7N 5B4; 2Environment Yukon, 10 Burns Road, Whitehorse, Yukon, Canada, Y1A 4Y9; 3Department of Veterinary Biomedical Sciences, Western College of Veterinary Medicine, University of Saskatchewan, 52 Campus Drive, Saskatoon, Saskatchewan, Canada, S7N 5B4; 4Parasitix Lab Services, 326-111 Research Dr, Saskatoon, SK S7N3R2, Canada.

Rationale: *Toxoplasma gondii* is an important zoonotic parasite infecting a wide range of mammals in northern Canada, and risk factors identified for exposure of humans include consumption of game meat, handling and skinning animals. Wolverines (*Gulo gulo*) are an economically important species in northern Canada because of their valuable fur, and therefore postmortem samples are available for testing from harvested animals. Due to their predatory and scavenging lifestyle, this carnivorous species can act as a good indicator for monitoring of *T. gondii* transmission in northern ecosystems.

Objectives and Methods: To determine sero-prevalence of *T. gondii* in wolverines from Yukon, Canada, we used a modified agglutination test (cut-off value 1:25) to test thoracic cavity fluids (n=99).

Results: Antibodies to *T. gondii* were detected in 17.2 % of 99 animals (titers of 1:25 in 1 wolverine, 1:50 in 3, 1:100 in 1 and 1:200 in 12). Significantly higher prevalence was observed in adult (28.6%, 10/35) than juvenile (10%, 6/60) wolverines (p= 0.02, chi square test), suggesting that risk of food and water -borne exposure increases with age. Prevalence rates did not differ between female (17.9%, 7/39) and male (16.7%, 10/60) wolverines (p=0.87). Wolverines from five out of 11 ecoregions were positive with prevalence between 12 and 50%.

Conclusion: This is the first report of *T. gondii* in wolverines from Yukon and our results suggest a widespread exposure among wolverines from different ecoregions. Molecular characterization of *T. gondii* from tissue samples is in progress in order to provide further information about sources and transmission of *T. gondii* in terrestrial ecosystems of north western Canada.

SOCIODEMOGRAPHIC FACTORS ASSOCIATED WITH CITIZEN REPORTS OF DEAD CORVIDS DURING THE INTRODUCTION OF WEST NILE VIRUS IN ONTARIO; APPLICATIONS FOR SPATIAL SCAN STATISTICS.

**Andrea Thomas-Bachli**1, David L. Pearl1, Olaf Berke1, E. Jane Parmley2, Ian Barker2

1University of Guelph, Department of Population Medicine; 2University of Guelph, Department of Pathobiology; Guelph, Ontario, Canada.

Rationale: West Nile virus (WNv) was identified in most regions of Ontario by the end of 2002. Surveillance of WNv at the time included testing of corvids found dead and reported by citizens across Ontario.

Objective: The objective of this study was to examine associations between the rate of dead corvid sightings and sociodemographic factors.

Methods: Weekly citizen sightings within forward sortation areas (FSA) were linked to census data. We evaluated the associations between the rate of sightings and sociodemographic factors using multilevel negative binomial models with a random effect for FSA.

Results: There were 12,295 sightings of dead corvids reported by citizens in 83.3% of Ontario FSAs. The number of sightings by FSA ranged from 0-407, with a mean of 20.7. Factors associated with the weekly rate of sightings included the proportion of seniors in the population, the proportion of citizens with no knowledge of either official language, the proportion of households with children, the proportion of the population with a Bachelor's degree or higher education level, and the latitude of the FSA. There was a higher rate of sightings in FSAs with greater proportions of households with children, and higher proportions of the population with Bachelor's degrees. FSAs with higher proportions of the population having no knowledge of either official language were associated with lower rates of sightings. This effect was potentiated by higher proportions of seniors in the population, and increasing latitude.

Conclusion: These findings will be used to inform spatial scan statistics, to reduce confounding and improve space-time cluster detection.
**Testing for Zika virus - An Alberta perspective**

*Kevin Fonseca¹, Kanti Pabbaraju¹, Sallene Wong¹, Raymond Tellier¹*

¹Provincial Laboratory for Public Health, 3030 Hospital Drive NW, Calgary, AB.

Rationale: Zika virus (ZIKV) has emerged in South America and the Caribbean, favored travel destinations for Canadians, resulting in a significant volume of a new and rapidly evolving area of laboratory testing and interpretations.

Objectives: To compare results of serological and molecular testing for ZIKV and travel-related arboviruses in conjunction with physician ordering practices

Methods: ProvLab Alberta data on ZIKV testing for a six month period (December to June, 2016) will be analyzed for the numbers of samples tested, together with the distribution of the numbers of positive travel related arbovirus cases.

Results: Preliminary data suggests that although ZIKV is the top ordering request for returning travellers from South America and the Caribbean, other arboviruses are equally important. The pitfalls of cross-reactivity between the flavivirus group will be explored and lessons learned will be illustrated.

Conclusion: Although ZIKV is the most frequently ordered test, Dengue virus is also a significant cause of travel-related illness.

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**Bartonella of domestic sheep and sheep keds: cultures, genetic characterization, and ecological connections**

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Cultures of *Bartonella melophagi* were isolated from blood of domestic sheep and from sheep keds (*Melophagus ovinus*) from the southwestern United States. All cultures were confirmed as positive by amplification of the fragment of the gltA gene and the reference strains were subjected to the characterization by additional five genetic markers, electronic microscopy, and biochemical properties. The sequence analyses of a reference strain performed by six molecular markers consistently demonstrated that *B. melophagi* relates, but differ from other Bartonella species isolated from domestic and wild ruminants. The analysis of genome composition and gene profile for *B. melophagi* was conducted using the complete genome sequence of the strain. Presence of 183 genes specific for *B. melophagi*, being absent in genomes of other Bartonella species associated with ruminants has also demonstrated a separation of this bacterial species. Bartonella DNA was found in all investigated sheep keds; however, culturing of these bacteria from sheep blood rejects a speculation that *B. melophagi* is an obligatory endosymbiont. Instead, the results support the hypothesis that the domestic sheep is a natural host reservoir for *B. melophagi* and the sheep ked is the likely vector for this Bartonella species. This bacterium was not found in blood of bighorn sheep and domestic goats belonging to the same subfamily *Caprinae*. A potential role of sheep-derived Bartonella as human pathogens will be discussed.
**human pathogens associated with ixodes scapularis: the never-ending story...**

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Rationale and Objectives: The blacklegged tick has been present in Ontario for over 40 years, but in the last ten years has been expanding its range in southern Ontario, an area where exposure to blacklegged tick bites and tick-borne pathogens is increasing. We performed a systematic review to evaluate the public health risks posed by expanding blacklegged tick populations and their associated pathogens.

Methods: We followed PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines for conducting our systematic review. We searched Ovid MEDLINE, Embase, BIOSIS, Scopus and Environment Complete databases for studies published from 2000 through 2015.

Results: Seventy-eight studies were included in the final review, 64 (82 %) studies met ≥75 % of the quality assessment criteria. Blacklegged ticks harbored 91 distinct taxa, 16 of these are tick-transmitted human pathogens, including species of *Anaplasma*, *Babesia*, *Bartonella*, *Borrelia*, *Ehrlichia*, *Rickettsia*, *Theileria* and *Flavivirus*. Organism richness was highest in the Northeast (Connecticut, New York) and Upper Midwest US (Wisconsin); however, organism richness was dependent on sampling effort. The primary tick-borne pathogens of public health concern in Ontario, due to the geographic proximity or historical detection in Ontario, are *Anaplasma phagocytophilum*, *Babesia microti*, *B. burgdorferi*, *Borrelia miyamotoi*, deer tick virus and *Ehrlichia muris*-like sp.

Conclusions: Our review is the first systematic assessment of the literature on the human pathogens associated with the blacklegged tick. As Lyme disease awareness continues to increase, it is an opportune time to document the full spectrum of human pathogens transmittable by blacklegged ticks.

**a scoping review of research investigating chikungunya virus (CHIKV) and its competent vectors**

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Rationale: Chikungunya (CHIK) infections are caused by the chikungunya virus (CHIKV), an alphavirus transmitted to humans by two predominant species of mosquitoes; *Aedes aegypti* and *Aedes albopictus*. Although CHIKV infection does not contribute largely to mortality, it causes acute and chronic morbidity. There is a risk that CHIKV will affect new areas over time.

Objectives: Results from this scoping review can identify critical knowledge gaps and support evidence-informed decision-making on public health risks associated with Chikungunya infections.

Methods: A search strategy was developed and implemented in seven databases (Scopus, Pubmed, CINAHL, CAB Abstracts, LILACS, Agricola and Cochrane) and grey literature to identify relevant articles, followed by comprehensive search verification. Relevance screening and data characterization levels were conducted by two independent reviewers. The body of research was descriptively analyzed for several population, outcome and exposure combinations to highlight main knowledge gaps and areas with significant evidence.

Results: We captured 12,420 unique abstracts, of which 1,818 (14.6%) were relevant to our study. Pathogenesis (23.4%) and epidemiology (20.5%) were commonly studied. Fewer studies focused on diagnostic tests (5.6%), treatment (3.5%) and mitigation strategies (8.7%). The majority of articles studied humans (36.9%) and were conducted in Asia (33.8%). Vector competence, phylogeny and behavioural results will also be presented.

Conclusion: This scoping review provides insight into the overall burden of CHIKV infections in humans, factors that may determine the magnitude and long term outcomes of CHIKV outbreaks, inputs for risk modelling, effective mitigation strategies and other considerations important for decision-making and public health planning.
WATERFOWL AND THE INTRODUCTION OF FOODBORNE PATHOGENS TO AGRICULTURAL ENVIRONMENTS IN SOUTHERN ONTARIO (2013-2015)

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Rationale: Canada geese (Branta canadensis) are one of the most common waterfowl species in Canada. There are concerns that geese, being highly mobile, transmit pathogens between agricultural and recreational areas.

Objectives: To determine whether geese pose a biosecurity threat to farms in Southern Ontario, a cross-sectional study was performed to measure the carriage of Salmonella, Campylobacter, and antimicrobial-resistant E. coli isolates obtained from goose fecal samples.

Methods: A total of 416 samples were obtained from three sources: hunter-caught birds, diagnostic specimens submitted to the Canadian Wildlife Health Cooperative, and fresh fecal samples. Escherichia coli isolates were tested for susceptibility to 15 antimicrobials using the Canadian Integrated Program for Antimicrobial Resistance Surveillance panel. The following factors association with the prevalence of Salmonella, Campylobacter, and antimicrobial-resistant E. coli were examined using exact logistic regression: season & source-type.

Results: The prevalence of Campylobacter, Salmonella, and E. coli were 11.8%, 0%, and 71.4%, respectively. Among the E. coli isolates, 8.0% had reduced susceptibility to one or more antimicrobials, and 5.7% were multi-drug resistant. Nineteen unique E. coli resistance patterns were identified with some including resistance to antimicrobials of highest importance in human medicine. Multidrug-resistance was significantly higher in the spring compared to fall and summer. Escherichia coli carriage varied significantly by season and source-type, but the remaining outcomes did not.

Conclusion: Isolating Campylobacter and antimicrobial-resistant E. coli from Canada geese suggests that these birds may play a role in disseminating these pathogens within the environment, and pose a threat to animal and public health.

CLUSTER ANALYSIS OF CAMPYLOBACTER ISOLATES OBTAINED FROM BEEF CATTLE, DAIRY CATTLE, AND MAMMALIAN WILDLIFE ON SOUTHERN ONTARIO FARMS (2010)

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Rationale: It has been shown that common foodborne pathogens can be exchanged at the wildlife-livestock interface.

Objectives: The objectives of this study were to identify the potential sharing of Campylobacter subtypes between livestock and wildlife using molecular subtyping data and to assess if mammalian wildlife and livestock carry host-adapted subtypes of Campylobacter jejuni.

Methods: Using data collected from a cross-sectional study of twenty-five farms, we assessed clustering of molecular subtypes of C. jejuni based on a Campylobacter-specific 40 gene comparative genomic fingerprinting assay (CGF40), using UPGMA analysis, multiple correspondence analysis, and exact logistic regression to determine if and what genes distinguish wildlife and livestock subtypes in our study population.

Results: A total of 33 livestock and 26 wildlife C. jejuni isolates were subtyped using CGF40; only one subtype was seen in both wildlife and livestock isolates. Dendrogram analysis, based on UPGMA, revealed a single cluster containing all but 2 wildlife subtypes, while the remaining branches contained the majority of livestock subtypes. The results of multiple correspondence analysis agreed with dendrogram analysis by showing clear differentiation between livestock and wildlife subtypes. Exact logistic regression, conducted gene-by-gene, revealed 11 genes that were predictive of whether an isolate’s CGF40 subtype was of wildlife or livestock origin. For most of these genes, their presence was predictive of an isolate being of livestock origin.

Conclusions: We concluded from dendrogram analysis, multiple correspondence analysis, and exact logistic regression that mammalian wildlife typically carry subtypes of C. jejuni that are different from those carried by livestock.
On-farm starling populations and other environmental and management factors associated with the presence of cefotaxime and ciprofloxacin resistant E. coli among dairy cattle in Ohio

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Rationale: European starlings (Sturnus vulgaris) have been implicated as vectors of zoonotic pathogens and antimicrobial resistant organisms. Although antimicrobial resistant E. coli, Salmonella and Campylobacter jejuni have been isolated from European starlings, their role in the dissemination of antimicrobial resistant organisms in livestock facilities needs further investigation.

Objective: To determine whether on-farm starling density and other environmental and management factors were associated with the presence of ciprofloxacin and cefotaxime resistant E. coli among dairy cattle farms in Ohio.

Methods: Bovine fecal pats from 150 farms were tested for the presence of cefotaxime and ciprofloxacin resistant E. coli. Each farm was visited twice during the summer and fall of 2007-2009. Multilevel logistic regression models with a random intercept to account for clustered data were used to assess the associations between antimicrobial resistance and various factors related to starling density and movement, and farm characteristics and management.

Results: The odds of detecting cefotaxime and ciprofloxacin resistant E. coli in the fecal pats were significantly higher in 2007 compared to 2008 and 2009, and in fall compared to summer. The odds of detecting resistant E. coli to each antimicrobial was significantly higher in bovine samples from farms closer than 60 km to starling night roost sites. The presence of calves on a farm reduced the odds of detecting cefotaxime and ciprofloxacin resistant E. coli.

Conclusion: European starlings, through their movements between nights roost and daily feeding sites, appear to play a role in the dissemination of antimicrobial resistant organisms among livestock facilities.

FoodNet Canada: Canadian Integrated Enteric Disease Surveillance System

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Rationale - Integrated surveillance and source attribution have been advocated in Canada and abroad to facilitate reduction of the burden of enteric diseases. FoodNet Canada (FNC), of the Public Health Agency of Canada, is an integrated, sentinel site surveillance initiative designed to help answer these complex questions.

Objectives – FNC determines significant risk factors for enteric illness, and the relative contribution of foods and other sources to illness, to inform food and water safety policy in Canada.

Methods - FNC collects data from sentinel communities to detect trends in human enteric illness and exposures from food, animal, and water sources; It is currently active in three sentinel sites, in the Fraser Valley, BC, Calgary and Central Zones, Alberta, and Middlesex-London, Ontario. Active monitoring of enteric pathogens on farms (dairy, beef, swine, broilers, layers), retail food (raw chicken breasts, pork chops, and ground beef) (produce - soft berries, fresh cut fruits, leafy greens (episodic)), and untreated surface water is conducted. In parallel, enhanced epidemiological and microbiological data are collected for the human cases, based on a strong collaboration with the local public health unit and both private and public health diagnostic laboratories. Source attribution estimations are generated by combining comparative exposure assessment into Bayesian models with molecular subtypes.

Results - The presentation will highlight results from FNC’s integrated analysis with a focus on Campylobacter source attribution and science to inform prevention.

Conclusion – FNC provides Canadian data and information to inform food and water safety.
AN UPDATE ON LYME DISEASE IN BRITISH COLUMBIA: TICK SURVEILLANCE STUDY

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Lyme disease is a public health issue in British Columbia (BC). It has been established in BC that Borrelia burgdorferi, the causal agent of Lyme disease, is cycling in nature among Ixodes ticks and small rodents, predominantly Peromyscus maniculatus (deer mouse). Since 1993, the BC Centre for Disease Control (BCCDC) has been monitoring tick and rodent to determine the presence of Borrelia spirochetes and found tick positivity rate for B. burgdorferi is very low.

In response to public concerns regarding the low positivity rate, we conducted active field surveillance for two years (2013-2014) as well as analyzed passive surveillance data from 2002 to 2013. 0.6% Ixodes spp ticks were found positive by real time PCR. Passive tick surveillance data showed that tick positivity rate for B burgdorferi is also low in BC (21 (0.3%) positive from 6,897 adult Ixodes spp). Passive surveillance data also suggests that BC has different tick populations that vary with geographical location and climate. Ixodes pacificus ticks were the predominant species in the Lower Mainland and Vancouver Island, while Dermacentor andersoni ticks appeared more abundantly in the interior of BC. The data generated over the year suggests that Lyme disease is present in certain areas of BC at a low level. Health care professionals should be aware of the presence of this pathogen and that the risk of acquiring Lyme disease in BC while low, is clearly present.

PASSIVE TICK SURVEILLANCE AS AN EARLY WARNING SYSTEM FOR EMERGING LYME DISEASE RISK: MAPPING TICK ESTABLISHMENT AND EARLY HUMAN CASES IN A LYME DISEASE EMERGENCE ZONE IN SOUTHERN CANADA

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Lyme disease is an emerging public health threat in many regions of southern Canada. Historically, risk maps for Lyme disease have relied heavily on of ticks in the environment in order to identify areas of emerging risk; however, such maps tend to have incomplete geographic coverage and are slow to identify new risk areas. Passive surveillance of ticks submitted by medical practitioners for testing has the advantage of providing more complete geographic coverage and an early signal Lyme disease risk, but in order to do so tick submissions must be linked to meaningful risk thresholds for public health. Combining data on human cases, active and passive tick surveillance from 2009 to 2014 in municipalities across the province of Quebec, we used logistic regression models and ROC analysis to test the ability of the passive surveillance signal to discriminate between the presence or absence of established tick populations in a municipality based on active surveillance, and the occurrence of more than three human cases in the municipality. The number of submitted ticks, corrected for search effort (human population), performed only moderately well in predicting the early detection of ticks in the environment through field sampling (Se= 0.64; Sp=0.64), but was a very good predictor of the occurrence of early human cases in municipalities (Se=0.91; Sp=0.93). Passive surveillance is a promising tool for providing an early signal of emerging Lyme disease risk for people, and focusing preventive public health actions on identified risk areas ahead of the occurrence of human cases.
THE EFFECT OF ABIOTIC AND BIOTIC FACTORS ON THE ESTABLISHMENT OF Ixodes scapularis POPULATIONS IN ONTARIO, CANADA

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In eastern North America, the hard tick Ixodes scapularis, is the vector for the causative agent of Lyme disease, Borrelia burgdorferi. Prior to 1990, Long Point Provincial Park was the only known established population of I. scapularis in Ontario. Within the last two decades the spread of I. scapularis has accelerated northward and this spread is expected to continue, in part due to climate change. Other ecological factors also influence I. scapularis and may play a role in population establishment. The objective of this study was to understand what abiotic and biotic factors are significant for the establishment of I. scapularis in Ontario. Tick dragging was conducted at 154 sites in southern, eastern and central Ontario during the months of May to October 2014 and 2015. At each site, data was collected on site aspect, tree cover, understory density and composition, soil moisture and composition and the depth of litter layer. Climate normals for cumulative degree days above zero and precipitation were accessed through ANUSPLINE. Multi-level mixed logistic regression models were created to assess the impact of the ecological factors on the presence of I. scapularis. In total, I. scapularis was found at 28 sites across the study area. Cumulative annual degree days and annual precipitation were positively associated with the presence of I. scapularis, as well as the density of the understory, the presence of shrubs and the interaction of these two ecological factors. These findings add to our understanding of the factors contributing to I. scapularis population establishment in the province of Ontario, and can be used to enhance current predictive models and risks maps for I. scapularis.

EPIDEMIOLOGY OF Ixodes scapularis ON PET DOGS IN AN EMERGING Lyme disease AREA IN Ontario

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Rationale: In Ontario, Ixodes scapularis (blacklegged ticks) are the only known vector for Borrelia burgdorferi, the causal agent for Lyme disease. The extensive range expansion of this tick is a growing health concern.Humans and their canine companions are at risk of tick bites while enjoying outdoor activities, and both are susceptible to B. burgdorferi and Anaplasma phagocytophilum which can be transmitted by infected blacklegged ticks.

Objectives: Within an emerging area for Lyme disease in Ontario, our objectives were: i) identify the tick species carried by dogs, ii) determine the prevalence of B. burgdorferi and A. phagocytophilum in I. scapularis collected, and iii) identify risk factors for the carriage of I. scapularis by dogs.

Methods and Results: Working with 20 veterinary clinics from April through December 2015, we collected 985 ticks from 544 dogs. Seven species of ticks were identified (#ticks/#dogs): I. scapularis (695/463), Dermacentor variabilis (152/49), Ixodes cookei (28/19), Rhipicephalus sanguineus (102/3), Amblyomma americanum (4/3), Dermacentor albipictus (3/3), and Ixodes muris (1/1). Three dogs were carrying multiple tick species. Using PCR, we detected B. burgdorferi in 87 I. scapularis from 34 dogs and A. phagocytophilum in 4 I. scapularis from 2 dogs. Using logistic regression, we will examine the associations between pet demographics, travel history, location and ectoparasite control and the odds of the following: a dog carrying I. scapularis, and a removed tick being infected with B. burgdorferi or A. phagocytophilum.

Conclusion: This study will provide information on the epidemiology of tick carriage in dogs from southeastern Ontario.
SYSTEMATIC REVIEW AND META-ANALYSIS OF THE ACCURACY OF DIAGNOSTIC TESTS FOR NORTH AMERICAN LYME DISEASE IN HUMANS.

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Rationale: There has been increasing incidence of Lyme disease (LD) Canada and much of the United States corresponding to the expanding Ixodes tick vector’s range. Many imperfect diagnostic tests for LD are available and there is concern and on-going discussion that the LD tests are over used since a positive test result in a patient who does not meet the clinical criteria is likely to be a false positive result.

Objective/Methods: Conduct a systematic review and meta-analyses to summarize the North American evidence on the accuracy of diagnostic tests and test regimes at various stages of LD.

Results: 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.

Conclusions: Implications of the review findings will be discussed including the implications of early LD patients’ high risk of testing negative and the importance of physician evaluation of clinical symptoms. As well as an evaluation of the performance of next generations antigens (e.g. Immunetics® C6 ELISA) and the two tiered approach, which demonstrate good sensitivity and superior specificity compared to proposed replacements or direct detection methods (culture and PCR of tissue samples).

TEACHING TICK IDENTIFICATION TO FRONTLINE MEDICAL PERSONNEL IN THE CANADIAN FORCES MEDICAL SERVICES

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Lyme disease has been a growing concern in Southern Ontario for the past decade, because the causative bacterial agent (Borrelia burgdorferi) and its vector the deer tick (Ixodes scapularis) have migrated from the Northern USA. Lyme disease can be successfully treated during early localized infection, and disseminated infection can be prevented with a single prophylactic dose of doxycycline within 72 hours of initial infection. However, delays in early diagnosis of Lyme disease often results in disease progression with myriad of chronic health effects. Canadian Forces (CF) soldiers on domestic training exercises have a high risk for Lyme disease due to increased exposure to ticks during extended time working and living outdoors and poor in-field hygiene. A risk-assessment program was introduced in 2014 with the goal of reducing Lyme disease transmission in soldiers in the field, the cornerstone of which was education on tick identification and medical threat assessments by frontline CF medical personnel in areas of operation. The program has been implemented during CF exercises in southern and western Ontario, and Indiana. Medical personnel were highly receptive to the training, and readily integrated routine tick identification, proper tick removal technique and identification of symptoms of early localized infection into their patient assessment packages. The program effectively identified patients at high risk of infection in need prophylactic antibiotics or follow-up care, and such a program could readily be adapted for civilian healthcare programs to decrease the overall burden of Lyme disease in Ontario.
Public Health Ontario’s New Interactive West Nile Virus Weekly Report

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Rationale: Public Health Ontario (PHO) produces weekly West Nile Virus (WNV) reports during the mosquito season to relay information to local public health units on the current state of WNV activity in Ontario. Historically, these reports were static PDFs posted on the PHO WNV webpage. As of 2016, the information will be available on the WNV webpage as interactive tables, figures and maps, allowing users to easily select the information that is of most interest to them.

Objectives: To provide an overview of the PHO mosquito database and the new WNV interactive webpage, including its new dynamic functions.

Methods: Mosquito data are acquired via local public health units who conduct mosquito trapping and send the captured mosquitoes to service providers for identification and WNV testing. These data are then provided to PHO, who upload it into their WNV mosquito database. The database is a custom application built using PHP programming language and hosted on a PHO Microsoft SQL Server. This project utilized the framework and processes developed as part of the development of a solution for creating interactive weekly WNV webpage.

Results/Conclusion: PHO has created a new WNV weekly report webpage that will allow users to interact with the data. They will be able to interact and manipulate the graphs, tables and figures; along with being able to select, and download WNV data for easier analysis and comparison.

National Farm-Level Biosecurity Standards in Canada: Implications for Zoonotic Disease Management

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Rationale and Objectives: Since 2006, the CFIA has been engaged in the development of National Farm-Level Biosecurity Standards for animal and plant agriculture, in partnership with national commodity associations and in collaboration with provincial governments, other federal departments, academia and other stakeholders. Objectives of the standards include: provision of guidelines for effective biosecurity practices; promotion of nationally consistent and integrated approach to reducing the risks of established, emerging and foreign animal diseases; enhancement of animal health, welfare and productivity; reduction in the frequency, scope and impact of disease outbreaks; increasing industry’s knowledge of disease risks; and identification of gaps in current control measures.

Methods: The standards define desirable target outcomes to mitigate the entry (bioexclusion), movement within (biomanagement), and release from the premises (biocontainment) of pathogens and pests. The standards are supported by producer guides that provide further information to assist producers in attaining the target outcomes. The biosecurity standards target all infectious diseases not specifically zoonotic diseases. However, many diseases of importance are zoonotic (e.g. avian influenza). Approaches target routes of transmission, and are arranged under themes addressing management of access, operations, animal health, facilities, and personnel. Risks posed by (and to) wildlife are considered, and knowledge of disease in wildlife (surveillance) informs risk assessment and encourages the implementation of biosecurity measures (e.g. avian influenza).

Results and Conclusion: Ten animal and four plant sector national standards have been produced, with two in development. Although voluntary, the standards are being integrated into producer-led assurance programming and provincial government programming.
A Quantitative Approach to the Prioritization of Zoonoses in North America

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Background: Zoonotic diseases have a major impact on public and animal health. As resources are limited for the control and prevention, it is necessary to prioritize diseases to direct resources. While there is general consensus amongst medical and veterinary professionals for the need to prioritize zoonoses, there is no uniformity or gold standard in methodological approaches. Further, there have been no current attempts to establish a framework for the prioritization of zoonoses in North America.

Objective: We used conjoint analysis (CA), a well-established quantitative method in market research, to identify the relative importance of 21 key characteristics of zoonotic diseases that can be used for prioritization. Relative importance weights from the CA were used to develop a point-scoring system to derive a recommended list of zoonoses for prioritization in Canada and the US, by health professionals (animal and human) and the public.

Methods: Hierarchical Bayes multinomial logit models were fitted to the survey data to derive CA-weighted scores. Scores were applied to 62 zoonotic diseases of public health importance in Canada and the US to rank diseases in order of priority.

Results: This study is the first to describe a quantitative approach to the prioritization of zoonoses in North America involving public participants. Despite more similarities in demographics and model fit between the combined public and combined professional groups, there was more uniformity across priority lists between the Canadian public and Canadian professionals and between the US public and US professionals.
A longitudinal study of Salmonella shedding in pigs

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Rationale: Salmonella is estimated to be one of the leading causes of hospitalization and death due to foodborne illness in Canada. On-farm interventions are thought to be the most effective way to reduce human salmonellosis.

Objective: The objective of this research was to investigate Salmonella shedding and colonization in pigs from birth to slaughter.

Methods: On eight farms, 832 pigs were tested multiple times for fecal Salmonella shedding from a few days after birth up to marketing, as well as for the presence of Salmonella in tissue samples at slaughter. During the nursery stage, pigs received either a high complexity or low complexity diet (containing reduced animal protein).

Results: Salmonella was detected in 4.9% (20/409) of piglets within 24-96 hours after birth, 10.5% (82/784) at weaning, 12.6% (94/747) at end of nursery, 12.3% (90/730) at end of grower, and 22.1% (148/669) of pigs at end of finisher. Multilevel mixed-effects analysis indicates an increase in prevalence of Salmonella shedding from early life until the finisher period (P<0.05). Salmonella was cultured from 23.2% (76/328) of tonsils and 29.1% (60/206) of lymph nodes but presence of Salmonella in tissue samples was not correlated with fecal shedding (P>0.05). Diet had no impact on shedding and colonization (P>0.05).

Conclusion: These results suggest that Salmonella shedding peaks towards the end of the finishing period and remains high at slaughter. However, detection of Salmonella positive pigs in the finishing period may not be a good indicator for presence of Salmonella at slaughter.

TRENDS IN NON-TYPHOIDAL SALMONELLA FROM NON-HUMAN SOURCES: A CANADIAN REFERENCE LABORATORY PERSPECTIVE

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Rationale and Objective: Salmonella is the most commonly reported bacterial cause of foodborne enteric illness in Canada. Characterization of Salmonella in foods, water, animals and the environment aids in control of salmonellosis. The OIE Salmonella Reference Laboratory (SRL) of the National Microbiology Laboratory at Guelph serotypes and phage types Canadian non-human isolates from surveillance, food and animal health diagnostic programs from federal, provincial and other sources. This study reviews the SRL data from these sources to identify trends in the frequency of Salmonella serovars over the years 1993-2015.

Methods: We examined the data on serovars of non-human Salmonella submitted to the SRL in the years 1993-2015 to determine trends in the frequency of the most prominent serovars and their possible links to human surveillance data.

Results: The SRL received 111,306 Salmonella isolates from 1993 to 2015. The most striking changes in serovar frequency in the past decade were increases in submissions of S. Heidelberg, S. Kentucky and S. Enteritidis. Whereas S. Kentucky is infrequently linked to human illness in Canada, the > 3-fold increase in S. Enteritidis submissions appears correlated with dramatic rises in human infections with this serovar.

Conclusions: These and other trends in the most prevalent Salmonella serovars from non-human sources will be examined further by comparison with human Salmonella surveillance data from Canada. Also, this central repository of well-characterized Salmonella isolates at the SRL is invaluable for development and evaluation of next generation methods for molecular characterization of Canadian Salmonella isolates for outbreak detection and source attribution.
Recombinant peptides and FIS tested as vaccine candidates for immunogenicity and protectiveness in farm goats

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While proving effective in controlling anthrax worldwide over the last 70 years, the Sterne live spore vaccine has a number of problems which, it is hoped, can be overcome with the advent of new generation acellular alternatives. Such vaccines could avoid current problems with side effects in certain animal species and would also permit simultaneous treatment and vaccination of animals, ensuring treated animals in an outbreak do not become reinfected.

Combinations of recombinant toxin (rPA) and spore antigen (rBclA) complemented with a synthetically produced lipopeptide adjuvant, with or without the amendment of formalin inactivated spores (FIS) of the Sterne strain, were tested for protective immunity in goats. Goat groups (n=10) of both genders, different races and sizes, from different farms were immunized 3 times s. c. at 3 weeks intervals and have been lethally challenged s. c. with spores of a fully virulent Bacillus anthracis field strain 5 weeks after the last immunization. Blood taken after each vaccination, challenge and survival of the challenge was analyzed in ELISA for IgG titers against rPA83, rBclA, FIS and vegetative antigen as well as neutralization activity in toxin neutralization assay (TNA). Goats immunized with the addition of FIS yielded 80% (8/10) survival and 50% (4/8) survived without FIS, though this difference is not significant. ELISA showed a moderate titer against rPA83 and high titers against FIS when given, while almost no titers were observed for rBclA. Generally titers against all reactive antigens were higher if FIS was part of the vaccine. The evaluation of the vaccine regimen showed the highest titers after the second immunization.

In total, immune responses in goats after vaccination with B. anthracis antigens differ from what is generally known from other animals, especially from mice experiments, and need further investigations.

Epidemiology of Salmonella in raccoons and the environment on swine farms and conservation areas

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Salmonella has been detected in the feces of many wildlife species, including raccoons (Procyon lotor), but little is known about the epidemiology of Salmonella in wildlife living in different habitat types. Our objective was to investigate demographic, temporal, and climatic factors associated with the carriage of Salmonella in raccoons and their environment on swine farms and conservation areas. Using a repeated cross-sectional study design, we collected fecal samples from raccoons and environmental samples (soil, manure pits, dumpsters) on 5 swine farms and 5 conservation areas in Ontario, Canada once every five weeks from May to November, 2011–2013. Salmonella was detected in 26% (279/1093) of raccoon fecal samples, 6% (88/1609) of soil samples, 30% (21/69) of manure pit samples, and 23% (7/31) of dumpster samples. Of samples testing positive for Salmonella, antimicrobial resistance was detected in 5% (14/279) of raccoon fecal, 8% (7/89) of soil, 10% (2/21) of manure pit, and 0/7 dumpster samples. Using multi-level multivariable logistic regression analyses, we found location type (swine farm or conservation area) was not a significant explanatory variable for Salmonella occurrence in raccoon feces or soil (p > 0.05). However, detection of Salmonella in raccoon feces was associated with rainfall, season, and sex with various interaction effects among these variables. We detected a variety of Salmonella serovars that infect humans and livestock in the feces of raccoons indicating that raccoons living near humans, regardless of location type, may play a role in the epidemiology of salmonellosis in livestock and humans in southwestern Ontario.
Epidemiological investigation of *Brucella canis* in Arizona; Preliminary Report

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Rationale: *Brucella canis* is an important reproductive pathogen in dogs and a human zoonosis. Little is known about the maintenance of the disease in canine populations, and its prevalence has not been reported for the Southwestern United States. The aim of this ongoing study is to determine the prevalence and distribution of *B. canis* in high risk canine populations in Arizona.

Objective: Sample and test high risk Arizona canine populations for brucellosis.

Methods: To date, 196 blood samples from five counties in Arizona have been tested for *B. canis*. Study sites include humane societies, animal control facilities, reservations, and private breeding facilities. Samples were tested for *B. canis* using four testing methods: Bench top Canine Brucellosis Rapid Slide Agglutination (RSAT), Cornell Diagnostic Laboratory Slide Agglutination and Agar Gel Immunodiffusion (AGID), and Blood Culture.

Results: Across the four tests 15 dogs out of the 196 sampled (7.7%) had some type of positive result. The RSAT bench test produced the highest number of positive results: 13/196 tested positive (6.6%), and of these the follow-up RSAT+2-ME card test yielded 3 positive results. The AGID II test yielded 1 positive result (0.5%), and 3 samples (1.5%) were positive with the M-cell agglutination test. Blood culture yielded 1 positive result (0.5%).

Conclusion: Based on our preliminary data, *B. canis* prevalence appears to be lower in Arizona than that reported in other parts of the U.S. Thus far the overall prevalence rate of canine brucellosis among high risk canine populations in Arizona is: .5-7.7%.

Tick-borne pathogens detected in ticks removed from companion and wild animals in southern Ontario

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Ixodid ticks are vectors of numerous zoonotic pathogens. Global climate change has made northern latitudes (e.g., southern Ontario) more conducive to the incursion and establishment of some tick species and the pathogens they carry. Due to the risk of tick-borne pathogen transmission to humans, a better understanding of the current tick distribution and pathogen prevalence is warranted. Our objective is to determine the prevalence and geographic locations of tick-borne pathogens, including *Anaplasma phagocytophilum*, *Babesia microti*, *Borrelia burgdorferi*, *B. miyamotoi* and *Ehrlichia chaffeensis* in southern Ontario. Ixodid ticks were collected from wildlife and companion animals and by tick dragging in southern Ontario during 2015-16. Ticks were identified and tested by RT-PCR for the tick species-specific pathogens listed above. Ongoing test results reveal that 10% (3/30) of *Ixodes scapularis* tested positive for *B. burgdorferi* (the causative agent of Lyme disease), and 3.3% (1/30) for *Anaplasma phagocytophilum* (the causative agent of human granulocytic anaplasmosis). All *I. scapularis* ticks tested negative for *B. miyamotoi* and *Babesia microti* and one *Amblyomma americanum* tested negative for *E. chaffeensis*. All *Borrelia burgdorferi*-positive ticks were removed from dogs in Guelph and Lyndhurst; however, we were unable to assess dog travel history. The *Anaplasma phagocytophilum*-positive tick was removed from a red fox (*Vulpes vulpes*) in Marysville. These results suggest that zoonotic tick-borne pathogens circulate in southern Ontario; however, continued research is needed to delineate the geographic distribution and prevalence of these pathogens among ticks removed from companion and wild animals, as well as the risk they pose to humans.
**Risk factors associated with Baylisascaris procyonis infection in raccoons (Procyon lotor)**

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The raccoon (Procyon lotor) is the definitive host of Baylisascaris procyonis (raccoon roundworm), an important zoonotic parasite that can cause visceral, ocular, and neural larval migrans in humans and intermediate hosts. Previous studies on risk factors for B. procyonis infection in raccoons show mixed results, and little research has been done on the role of co-infection with other pathogens. We examined the prevalence of B. procyonis infection in southern Ontario raccoons, and assessed the role of risk factors including including age, sex, land use, fat stores, and co-infection with the Canine Distemper Virus (CDV). We conducted postmortem sampling of raccoon carcasses submitted to the Canadian Wildlife Health Cooperative (CWHC) from January 1 – July 18, 2016 (n=300), examining gastrointestinal tracts for the presence of ascarid worms and swabbing the conjunctiva of a sub-sample of raccoons to test for CDV using RT-PCR (n=156). Overall B. procyonis prevalence was 21.3% (95% CI=16.83 - 26.41; range=1-95 worms/host, median =2.5). CDV prevalence was 69.9% (95% CI=62.0 - 76.9). In univariable logistic regression models, male raccoons were 2.1 times more likely to be infected with B. procyonis than females (95% CI=1.16-3.89; p<0.05), and raccoons with excellent fat stores were 11.4 times more likely to be infected than those with poor fat stores (95% CI=4.22-31.0, p<0.05). No significant associations were found for other variables, including CDV status. This study provides insight into the prevalence of B. procyonis and associated risk factors; however, multivariable analysis would be useful to understand the interaction effects of multiple risk factors.

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**Antimicrobial resistance patterns in clinical isolates of Salmonella and E. coli from cattle, poultry and swine in Ontario, 2007-2015.**

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Rationale: Antimicrobial resistance among zoonotic pathogens is becoming a major public health concern. Exploration of pre-existing data sets from clinical veterinary laboratory submissions may provide cost-effective information on emerging resistance patterns in key species.

Objectives: The purpose of this study was to (1) describe antimicrobial resistance patterns in select clinical pathogens over time; (2) evaluate the utility of data from clinical isolates as a surveillance tool.

Methods: Antimicrobial susceptibility test results from a major veterinary diagnostic laboratory were analyzed for Salmonella and E.coli isolates from chickens, swine and cattle between 2007 and 2015. Resistance patterns over time were described graphically. Lab methodology and temporal changes in susceptibility were also compared to the results of the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) for certain antimicrobials.

Results: Salmonella resistance to ampicillin and ceftiofur in chickens dropped by almost 20% between 2013 and 2015. However, resistance in Salmonella to sulfonamides, spectinomycin and tetracycline demonstrated a slight rise (10-15%) since 2010. Results of the analysis for E.coli, as well as cattle and swine isolates are pending. There were some significant discrepancies in susceptibility test results based on the methodology (disk diffusion versus broth dilution) and interpretation used between the clinical laboratory and research program. Conclusion: Analysis of clinical isolates within the province may provide for an effective surveillance tool for updating veterinarians on emerging patterns of antimicrobial resistance in food animals. However, it is important to clearly communicate the limitations of such a dataset for predicting overall trends and guiding empirical treatment decisions.
**Domestic dog ecology in Villa de Tezontepec, Hidalgo, Mexico, and implications for canine rabies transmission**

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The overpopulation of free-roaming dogs in developing countries poses grave risk to public health and safety. Dogs remain the main reservoir and vector of rabies to humans worldwide. In Mexico, 12 cases of canine rabies were confirmed during 2012, indicating a remaining threat for transmission to humans. The objective of this study was to characterize the ecology and demography of owned dogs, and to estimate the density of the free-roaming dog population in Villa de Tezontepec, Hidalgo, Mexico. Face-to-face surveys were administered to 328 randomly selected households using stratified two-stage cluster sampling. Within each household, adults were asked to answer questions related to their dogs and their care, as well as their experiences with dog bites. Street surveys were used to visually count free-roaming dogs in randomly selected routes. Every dog observed was recorded, categorized by sex, and body condition scored. Approximately 65.2% (214/328) of households owned dogs, producing a human: owned dog ratio of 3.4:1. The majority of owned dogs (84.4%) were reportedly vaccinated against rabies in 2015. Less than half (45%) of the dog-owning households kept their dogs confined at all times. One-tenth (10.3%) of households reported that a dog had bitten a household member in the past 12 months. An average of six free-roaming dogs were observed per km of street surveyed. This study provides in-depth understanding of the domestic dog ecology and demography in this population; its data will inform agent-based mathematical simulation models to assess the impacts of dog population and rabies control programs.

**Annual variation in susceptibility of Campylobacter jejuni isolates to tetracycline from retail chicken surveillance**

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Rationale: Minimum inhibitory concentration (MIC) antimicrobial susceptibility results are discrete, interval-censored and ordinal, which can make analysis challenging. MIC data are often reported as resistant (R) or susceptible (S) using established breakpoints, but this may mask subtle temporal changes in MICs.

Objectives: To compare regression models using MIC and breakpoint susceptibility data for analysis of annual variation in susceptibility of Campylobacter jejuni to tetracycline from retail chicken.

Methods: Antimicrobial susceptibility data were obtained from the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS). Annual variation in susceptibility was evaluated using univariable linear, tobit, logistic and multinomial logistic regression. MIC, censored MIC, R/S (R ≥ 16 μg/mL) and tri-categorized (low ≤0.06-0.12, medium 0.25-8, resistant 16->64 μg/mL) data were used as outcome variables for the appropriate statistical models. Sampling year was modeled as a categorical predictor variable.

Results: From 2006-2014, 50.76% of 719 Campylobacter jejuni isolates were resistant to tetracycline (95% CI 47.04-54.48). Only multinomial logistic regression identified annual variation in susceptibility. Compared to 2006, there were significantly increased odds of an isolate from 2007, 2009, 2010, 2011, 2012 and 2013 being in the medium MIC group compared to the low MIC group. There were significantly increased odds of an isolate being in the resistant group compared to the low MIC group in 2010 and 2011 compared to 2006.

Conclusion: Identification of annual variation in susceptibility of Campylobacter jejuni to tetracycline varied with model type. Only multinomial logistic regression identified the presence of changes in MIC over time.
Effects of climate change on American dog tick (*Dermacentor variabilis*) distribution will influence bovine anaplasmosis risk in North America

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Rationale: In eastern North America, the American dog tick (*Dermacentor variabilis*) is the primary vector for *Anaplasma marginale*, the causative agent of bovine anaplasmosis. Bovine anaplasmosis is currently absent from Canada, but enzootic in the USA, where it affects animal health and producer livelihoods.

Objectives: The purpose of this work was to determine the effects of climate change on *D. variabilis* distribution, and how potential changes in distribution could affect where *A. marginale* is transmitted by *D. variabilis* under climate change.

Methods: A species distribution model was developed for *D. variabilis* using Maxent software for current and future climate. Climate projections were based on four Representative Concentration Pathways for years 2050 and 2070 from the IPCC. Climate projections were combined with cattle data for the USA and Canada to determine where risk of bovine anaplasmosis will change.

Results: The area of suitable climate for *D. variabilis* is expected to increase, especially in Canada. In the southern USA, risk of bovine anaplasmosis is expected to decrease because of decreasing climate suitability for the tick, and risk will increase in Canada, especially in the Great Lakes region. The number of counties in North America that will exhibit optimal climate for *D. variabilis* will also increase, increasing risk of pathogen transmission.

Conclusions: Increasing numbers of counties and states/provinces at risk suggest that monitoring and testing efforts will need to be directed to affected areas in the future to prevent/reduce *A. marginale* transmission by *D. variabilis*.

2014 highlights from the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS)

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Rationale: Antimicrobial resistance (AMR) is a growing and global issue that threatens the health of humans and animals. Antimicrobial use (AMU) is considered to be the major risk factor contributing to the emergence and spread of resistant bacteria.

Objectives: To present key findings from the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) in 2014 with a focus on AMU and AMR data from chickens and chicken meat.

Methods: Participating broiler chicken flocks complete AMU and farm demographic questionnaires. Samples are collected on the farm (feces), at slaughter (cecal contents) and from the grocery store (fresh meat); all samples are submitted for bacterial isolation (*Campylobacter, Salmonella* and *Escherichia coli*). Antimicrobial susceptibility is performed on all isolates by broth microdilution.

Results: Ninety percent of participating poultry flocks (n=143) reported using antimicrobials in 2014; most antimicrobials were administered through feed (91%). Use of and resistance to critically important antimicrobials decreased in 2014. Specifically, resistance to 3rd generation cephalosporins decreased among *Salmonella* isolates: 13% were resistant on farm, 12% at slaughter and 21% at retail. Similar resistance trends were observed for *E. coli* from chicken. Among *Campylobacter* isolates from chicken, resistance to ciprofloxacin was 9% on farm, 11% at slaughter and 11% at retail.

Conclusions: Integrated surveillance programs can help advance our understanding of complex health issues like AMR. CIPARS findings for 2014 indicate early evidence that communication of surveillance findings to industry stakeholders and government departments can reduce AMU and AMR.
**Spatial heterogeneity in *Ixodes scapularis* distribution within the Lyme disease emergence zone in Southern Québec (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 Québec. In 2013-2014, ticks were collected through drag sampling at 50 sites in southern Québec (2000 m dragged per site). Three of these sites were more intensively sampled in 2013 with 63 randomly-placed plots consisting of four 100 m transects parallel to a park trail (0, 20, 40 and 60 m from the trail). 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 1000m2, median=1.5) and also within them (0 to 25 nymphs per plot, median=2), with spatial clustering of ticks observed at each geographic scale. Regression models showed 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). Understanding the heterogeneous distribution of ticks at a fine scale could help better target prevention and surveillance strategies in public-access woodlands.

**Prevalence of Powassan Virus in Southwestern Ontario, with a focus on Vector and Host Dynamics**

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Powassan virus (POWV) is a tick-borne flavivirus that was first isolated in 1958 from a fatal human infection in Powassan, Ontario. POWV has two distinct genetic lineages: Powassan prototype (POWV-p), which is maintained between *Ixodes cookei* ticks and groundhogs (*Marmota monax*), striped skunks (*Mephitis mephitis*) and other mammals, and deer tick virus (DTV), which is maintained between *I. scapularis* ticks and white-footed mice (*Peromyscus leucopus*). The prevalence of POWV in Ontario and involvement of wildlife in virus maintenance and transmission are poorly understood. The objective of this study is to determine the prevalence of POWV in targeted regions of Ontario and better understand wildlife host-vector ecology. We predict that striped skunks and groundhogs will have higher POWV seroprevalence than other mammals tested (e.g., raccoons [*Procyon lotor*], eastern gray squirrels [*Sciurus carolinensis*] and red squirrels [*Tamiasciurus hudsonicus*]). In summers 2015-16, tissues from 400 wildlife carcasses were collected (primarily raccoons, striped skunks, eastern gray squirrels, red squirrels, and groundhogs). Ticks are collected from carcasses and by tick dragging and burrow sampling. Homogenized tissues and ticks are being tested for POWV antigen by RT-PCR, and sera will be tested for anti-POWV antibodies by hemagglutinin inhibition and virus neutralization. Results will help determine current POWV activity in wildlife and ticks in southwestern Ontario, identify likely reservoir hosts for more targeted studies, as well as aid in assessing the potential risks of POWV infection to humans.
INTERACTIONS OF A CORONAVIRUS WITH ITS NATURAL HOST: THE CANADIAN LITTLE BROWN BAT (Myotis lucifugus) – IMPACT OF “STRESS” ON VIRUS-HOST INTERPLAY

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In recent years, coronaviruses like SARS-CoV (Severe Acute Respiratory Syndrome-coronavirus), MERS-CoV (Middle East Respiratory Syndrome-CoV) and PED-CoV (Porcine Epidemic Diarrhea-CoV) are believed to have spilled over from bats to other species, causing severe disease and mortality. The factors leading to such spillovers are largely unknown. Although bats are resilient to these deadly viruses, infection with a fungus, Pseudogymnoascus destructans, has led to catastrophic mortality in several North American hibernating bat species.

Our lab has detected a Brown Bat Coronavirus (BB-CoV) in the two main North American bat species - the big (E.fuscus) and little (M.lucifugus) brown bat. Our studies suggest that bats harbor the BB-CoV as low-level persistent infections in the gut and co-infection with P. destructans greatly increases virus RNA. We are exploring the hypothesis that secondary fungal infections, changes the coronavirus-bat dynamics leading to increased virus replication which might be attributed to altered innate immune response. We have produced BB-CoV protein specific antibodies in rabbits which would be used to detect virus infected cells in gut tissues. We have also done total RNA sequencing of gut tissue RNA from bats experimentally infected and not infected with P. destructans which contain the BB-CoV. This would help us to quantitate viral genes and bat innate response genes in presence and absence of P. destructans fungus (analysis of which is in progress).

The information from this study will be extremely helpful in understanding the reason behind increase in virus replication which might be leading to spillovers of viruses from bats to other species.

PREVALENCE AND CHARACTERISTICS OF Clostridium difficile FROM POLAR BEARS

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Rationale: Clostridium difficile has been identified in humans and a wide range of animal species, but there has been little study of remote animal populations with limited human contact. The objective of this study was to determine the prevalence and types of C. difficile in wild and captive polar bears.

Objective: To determine the prevalence of C. difficile shedding by wild and captive polar bears and characterize recovered isolates.

Methods: Fecal samples were collected from wild polar bears in the M’Clintock Channel and Hudson Strait (Nunavut, Canada), as well as a facility (PBJ) in Churchill, Manitoba that temporarily houses nuisance polar bears and captive bears in a zoological park. Enrichment culture was performed and isolates were ribotyped and toxinotyped.

Results: Clostridium difficile was isolated from 24/143 (16.8%) of samples; 18/120 (15%) wild bear samples, 4/7 (57%) from the PBJ and 2/16 (13%) samples from 2/3 (67%) zoo bears. The prevalence of C. difficile was significantly higher in bears from the PBJ vs wild bears (P=0.0042), with no difference between wild bears populations (P=0.50). Fourteen/24 (58%) of isolates were toxigenic. Four toxigenic ribotypes were identified, with one that possessed tcdA, tcdB and cdtA predominating. There was no overlap in toxigenic ribotypes between the different populations.

Conclusions: Clostridium difficile was not uncommon, with differences in type distribution amongst the different regions. The presence of strains that have not been identified in humans or domestic animals suggests that polar bears may be a natural reservoir of unique strains of this important bacterium.
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