16th Annual meeting of the
Canadian Animal Health Laboratorians Network
(CAHLN)

16ème réunion annuelle du
Réseau canadien de travailleur en santé animale
(CAHLN)

June 4-7, 2017
4 au 7 juin, 2017

Laboratory based disease intelligence in 2017:
new and practical approaches

L'intelligence des maladies à base de
laboratoire en 2017: Approches nouvelles
et pratiques

Hosted by:
Animal Health Laboratory, Laboratory Services Division
University of Guelph, Guelph, ON
16th Annual Meeting of the Canadian Animal Health Laboratorians Network (CAHLN)

Animal Health Laboratory (AHL)
University of Guelph
June 4-7, 2017

CAHLN 2017 ORGANIZING COMMITTEE:
Melanie Barham, OAHN Coordinator, Animal Health Laboratory, University of Guelph (Chair)
Grant Maxie, Director, Animal Health Laboratory, University of Guelph
Michael Deane, Communications Administrator, Animal Health Laboratory, University of Guelph
Helen Oliver, Executive Assistant, Animal Health Laboratory, University of Guelph
April Nejedly, Office Assistant, Animal Health Laboratory, University of Guelph

CAHLN EXECUTIVE COMMITTEE (2016-2017):
President: Jim Goltz, Fredericton, New Brunswick
Past President: Catherine Brisson, Nepean, Ontario (agreed to extended term)
President Elect: Melanie Barham, Guelph, Ontario
Vice President: To be determined – representative of 2018 host site
Secretary-Treasurer: Dale Godson, Saskatoon, Saskatchewan

The CAHLN 2017 Organizing Committee would like to recognize the following for their invaluable support in organizing the CAHLN 2017 Annual Meeting at the Animal Health Laboratory, University of Guelph:

1. Drs. Marg Stalker and Marina Brash
2. Josie Given and Rina Pigozzo
3. Session moderators
4. All Sponsors, Other Supporters and Exhibitors for CAHLN 2017
5. All invited Speakers
6. All participants who are presenting scientific talks or posters
7. U of G Conference Services, OVC Deans Office, the University Bookstore, OVC Pet Trust, Alumni Affairs, OVC Pet Trust, and Parking Services
8. Laboratory Services Division Financial Supervisor – Karen Nakatsu
9. Executive Committee members – Jim Goltz, Catherine Brisson, Melanie Barham, Dale Godson
The CAHLN was established in 2002 to facilitate exchange of information on animal health diagnostic trends, techniques and research, to provide a venue for networking, to identify common issues of concern, and to improve linkages among organizations and scientific staff involved in animal health diagnostic work in Canada.

The CAHLN is comprised of individuals across the wide spectrum of laboratory disciplines, including bacteriology, pathology, immunology, virology, parasitology, toxicology and molecular biology.

Previous annual meetings:

2002 – Ottawa (CFIA – Ontario Laboratory Fallowfield)
2003 – Ottawa (CFIA - Ontario Laboratory Fallowfield)
2004 – Guelph (Animal Health Laboratory/Ontario Veterinary College)
2005 – St-Hyacinthe (Faculté de Médecine Vétérinaire)
2006 – Ottawa (CFIA - Ontario Laboratory Fallowfield)
2007 – Saskatoon (Western College of Veterinary Medicine/Prairie Diagnostic Services)
2008 – Ottawa (CFIA - Ontario Laboratory Fallowfield)
2009 - Charlottetown (Atlantic Veterinary College)
2010 - Calgary (College of Veterinary Medicine, University of Calgary)
2011 - Guelph (Animal Health Laboratory/Ontario Veterinary College)
2012 – Winnipeg (CFIA – National Center for Foreign Animal Disease)
2013 – St-Hyacinthe (Faculté de Médecine Vétérinaire)
2014 – Ottawa (CFIA – Ontario Laboratory Fallowfield)
2015 – Saskatoon, SK (Western College of Veterinary Medicine/Prairie Diagnostic Services), in conjunction with the World Association of Veterinary Laboratory Diagnosticians meeting
2016 – Charlottetown (Atlantic Veterinary College - University of Prince Edward Island)
2017 – Guelph (Animal Health Laboratory/Ontario Veterinary College)
16ème réunion annuelle du Réseau canadien de travailleur en santé animale
(RCTLSA)
Du 4 au 7 juin 2017

Animal Health Laboratory (AHL)
University of Guelph
Building 89
419 Gordon Street
Guelph, ON
N1G 2W1

Le RCTLSA a été créé en 2002 dans le but de favoriser l'échange d'information sur les tendances, les techniques et la recherche en matière de diagnostic en santé animale; de fournir une occasion de réseautage afin de dégager des sujets de préoccupation communs dans ce domaine; et de faciliter les relations entre les organisations et le personnel scientifique dont le travail touche le diagnostic en santé animale au Canada.

Le RCTLSA comprend des personnes provenant de toutes les spécialités de diagnostic en laboratoire, incluant des spécialistes en bactériologie, en pathologie, en immunologie, en virologie, en parasitologie, en toxicologie et en biologie moléculaire.

Les congrès annuels précédents:

2002 – Ottawa (CFIA – Ontario Laboratory Fallowfield)
2003 – Ottawa (CFIA - Ontario Laboratory Fallowfield)
2004 – Guelph (Animal Health Laboratory/Ontario Veterinary College)
2005 – St-Hyacinthe (Faculté de Médecine Vétérinaire)
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2017 – Guelph (Animal Health Laboratory/Ontario Veterinary College)
CAHLN / RCTLSA AWARDS

1. CAHLN Laboratorian of the Year - Prix du Diagnosticien du RCTLSA

The Canadian Animal Health Laboratorians Network (CAHLN) awards a plaque annually to a laboratorian based on his or her noteworthy contributions to veterinary laboratory medicine in Canada. A nominee might be an outstanding diagnostician, educator, researcher, mentor of future laboratorians, or other contributor to the field. The award is presented at the CAHLN Annual meeting.

Le Réseau canadien des travailleurs des laboratoires de santé animale (RCTLSA) décerner chaque année une plaque à un des siens, pour sa ou ses contributions à la médecine vétérinaire de laboratoire au Canada. Le comité des récompenses accueillera les noms qui seront proposés par tout travailleur canadien de laboratoire. Le candidat peut être un diagnosticien, un éducateur, un chercheur, un mentor de la relève ou n'importe qui du domaine, dont l'apport est remarquable. La récompense est décernée à la réunion annuelle du Réseau.

Past winners:
2003 - Lloyd Spencer, CFIA, Nepean, ON
2004 - Ian Barker, OVC, Guelph, ON
2005 - Marcelo Gottschalk, FMV, St. Hyacinthe, QC
2006 - John Robinson, MAL, Abbotsford, BC
2007 - John Fairbrother, FMV, St. Hyacinthe, QC
2008 – W.D.G (Bill) Yates, CFIA, Lethbridge, AB
2009 – Gerald R. Johnson, AVC, Charlottetown, PEI
2010 – Ted Clark, Calgary, AB
2011 – Josepha DeLay, AHL, U of Guelph, Guelph, ON
2012 – Mark Swendrowski, MAFRI, Winnipeg, MB
2013 – Grant Maxie, AHL, U of Guelph, Guelph, ON
2014 – John Pasick, NCFAD, CFIA, Winnipeg, MB
2015 – James P. Goltz, NBDFAD, Fredericton, NB
2016 - Alfonso Lopez, AVC (retired), UPEI, Charlottetown, PEI
2017 -

2017 -
2. CAHLN Graduate Student Presentation Award

A plaque is awarded annually to a graduate student based on the quality of their presentation at the CAHLN annual meeting. Presentations are judged on the originality of the subject, contribution of the presentation to our knowledge base, the student's understanding and delivery of the topic, and their ability to deal with questions. The award is presented at the CAHLN Annual meeting.

Chaque année, une plaque est remise au finissant qui a présenté le meilleur exposé dans le cadre de l’assemblée annuelle du Réseau canadien des travailleurs des laboratoires de santé animale (RCTLSA). Les exposés sont jugés selon l’originalité du sujet, la contribution de l’exposé à notre base de connaissances, la compréhension et la présentation de la matière, ainsi que la capacité des finissants de répondre aux questions. La récompense est décernée à la réunion annuelle du Réseau.

Past winners of the CAHLN Graduate Student Presentation Award:
2003 – Sherry Andrews, WCVM, Saskatoon, SK
2004 – Noel Harrington, OVC/CFIA, ON
2005 – Guillaume Bruant, FMV, St. Hyacinthe, QC
2006 – Yuanmu Fang, WCVM, Saskatoon, SK
2007 – Kathi Ellis, WCVM, Saskatoon, SK
2008 – Angela Catford, OVC, Guelph, ON
2009 – Raphael Vanderstichel, AVC, Charlottetown, PEI
2010 – Guilherme Gomes Verocai, UCVM, Calgary, AB
2011 – Olivier Côté, OVC, Guelph, ON
2012 – Jason Struthers, WCVM, Saskatoon, SK
2013 – Janet Sunohara-Neilson, OVC, Guelph, ON
2014 – Cathy Bauman, OVC, Guelph, ON
2015 – Oral: Arinjay Banerjee, Dept. of Veterinary Microbiology, Univ of Sask
Poster: Thushari Gunawardana, Dept. of Veterinary Pathology, Univ of Sask
2016 – Oral: Christina Solis Worsfold, UCVM, Calgary, AB
Poster: Iman Mehdizadh Gohari, OVC, Guelph, ON
2017 - Oral:
Poster:
A very special thanks is extended to all of our sponsors for your contributions to the CAHLN/RCTLSA 2017 Annual Meeting
## CAHLN / RCTLSA WELCOME RECEPTION

Sunday, June 4, 2017

Lifetime Learning Centre, Building 77, University of Guelph

<table>
<thead>
<tr>
<th>17:30-19:00</th>
<th><strong>Registration and Reception</strong> for all conference participants. Tours of the C.A.V. Barker Museum.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Rooms 1707 B and C</td>
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<tr>
<td>19:00-19:15</td>
<td><strong>Official Welcome</strong></td>
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<tr>
<td></td>
<td>Room 1714</td>
</tr>
<tr>
<td>19:15-20:00</td>
<td><strong>Presentation</strong></td>
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<tr>
<td></td>
<td>Andrew McEwen: “Maintaining the Mobility of the Corps:” Horses, Mules, and the Canadian Army Veterinary Corps in the Great War.</td>
</tr>
<tr>
<td></td>
<td>Room 1714</td>
</tr>
<tr>
<td>20:00-21:00</td>
<td><strong>Networking</strong></td>
</tr>
</tbody>
</table>
### CAHLN / RCTLSA 16th Annual Meeting

**Monday, June 5, 2017**  
**08:30 – 17:00**

**Building 89 PAHL, Room 1800**

**Overall Theme:** Practical approaches to disease intelligence

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Presenter</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:45</td>
<td>Registration – outside Room 1800</td>
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<tr>
<td>8:05</td>
<td>Official Opening and Welcome</td>
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<tr>
<td><strong>8:45 – 12:00</strong></td>
<td><strong>Plenary Session 1</strong></td>
<td><strong>Moderator:</strong> Grant Maxie</td>
</tr>
<tr>
<td>8:45</td>
<td>Bovine Tuberculosis in Canada</td>
<td>Debbie Barr, Director, Animal Health, Welfare and Biosecurity Division, Canadian Food Inspection Agency</td>
</tr>
<tr>
<td>9:15</td>
<td>Bovine tuberculosis investigation in western Canada: a case study of the role of an animal health diagnostic laboratory</td>
<td>Carl Johnson, Chief Executive Officer, Prairie Diagnostic Services</td>
</tr>
<tr>
<td>9:30</td>
<td>Emergence of <em>Echinococcus multilocularis</em> in dogs in Ontario: implications for public and wildlife health?</td>
<td>Andrew Peregrine, Associate Professor, Ontario Veterinary College</td>
</tr>
<tr>
<td>10:00-10:30</td>
<td><strong>HEALTH BREAK, POSTER, TRADE SHOW AND NETWORKING</strong></td>
<td></td>
</tr>
<tr>
<td>10:30</td>
<td>Using laboratory techniques to answer wildlife disease questions</td>
<td>Doug Campbell, Veterinarian, Canadian Wildlife Health Cooperative, Ontario Veterinary College</td>
</tr>
<tr>
<td>11:00</td>
<td>One Health in action: the critical role of laboratory-based animal disease intelligence to public health</td>
<td>Catherine Filejski, Public Health Veterinarian, Infectious Diseases Policy and Programs Unit (Health and Long-Term Care)</td>
</tr>
<tr>
<td>11:30</td>
<td>Incorporating lab data into dairy herd management: a vision</td>
<td>Dave Kelton, Dairy Farmers of Ontario Chair in Dairy Cattle Health, Professor, Ontario Veterinary College</td>
</tr>
<tr>
<td><strong>12:00-13:30</strong></td>
<td><strong>Lunch, CAHLN business meeting, OVC tours</strong></td>
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<tr>
<td><strong>Companion Animals, all species</strong> – concurrent session</td>
<td><strong>Moderator:</strong> Andrew Vince</td>
<td></td>
</tr>
<tr>
<td>13:30</td>
<td>Diagnosis and genetic variation of an invasive microsporidium <em>(Nosema ceranae)</em> in honey bees <em>(Apis mellifera)</em></td>
<td>Mollah Md. Hamiduzzaman, Ernesto Guzman-Novoa, Paul H. Goodwin</td>
</tr>
</tbody>
</table>
Different approaches for the diagnosis and classification of canine lymphoma
[Graduate student presentation]
Nariman Deravi, Veronica Parsons, Dorothee Bienzle

Determining average cat weights through the use of big data
[Graduate student presentation]
Adam Campigotto, Theresa Bernardo, Zvonimir Poljak, Elizabeth Stone, Deborah Stacey

Prevalence of potentially zoonotic and non-zoonotic parasites in domestic dogs in rural, urban and First Nations communities across Ontario, Canada
[Graduate student presentation]
Rachel Imai, John R. Barta

Canine pulmonary hyalinosis
Gwendolyn Conant, Margaret Stalker, Jeff L Caswell

HEALTH BREAK, TRADE SHOW, POSTER VIEWING AND NETWORKING

An introduction to high-throughput immunohistochemistry
[Graduate student presentation]
Courtney R. Schott, Geoffrey A. Wood

Equine
Moderator: Peter Physick-Sheard

An electronic solution for equine infectious anemia (EIA) submissions
Joanna Sawicki, Jim Fairles

Canadian Pari-Mutuel Agency Equine Drug Control Program: diagnostic testing in a forensic regulatory environment
Lydia Brooks

Racehorse mortality in Ontario: postmortem procedures and results
Josepha DeLay, Bruce Duncan, Adam Chambers

Analysis of the Ontario Racing Registry, 2003-2011
Peter Physick-Sheard

Seroprevalence of Borrelia burgdorferi and Anaplasma phagocytophilum in horses in Ontario
Megan Neely, Scott Weese, Alison Moore, Murray Hazlett, Luis Arroyo

Analytical validation of cardiac troponin I assays for use in the horse
Tanya M. Rossi, David L. Pearl, W. Glen Pyle, M. Grant Maxie, Peter A. Kavsak, Peter W. Physick-Sheard
### Ruminants – concurrent session

**Moderator:** Andrew Brooks

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Presenter(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>13:30</td>
<td>Cull cows at auction and provincial slaughter plants in Ontario</td>
<td>Todd Duffield</td>
</tr>
<tr>
<td>13:45</td>
<td>Postmortem evaluation in cases of suspected humane transport violation</td>
<td>Andrew Brooks, Jan Shapiro</td>
</tr>
<tr>
<td>14:00</td>
<td>Overview of a milk bacteriology QA program for veterinary clinics</td>
<td>Jim Fairles, Josie Given</td>
</tr>
<tr>
<td>14:15</td>
<td>Detection of bovine viral diarrhea (BVD) virus in ear skin tissue samples: evaluation of a combination of QIAGEN MagAttract 96 cador pathogen extraction and virotype BVDV RT-PCR-based amplification</td>
<td>Roger Maes, Patrick Bronson-Doherty, Mike Chumbley, Annabel Wise, Suzanne Kull-Mason, Vittoria Miller, Daland C. Herrmann, Carsten Schroeder</td>
</tr>
<tr>
<td>14:30</td>
<td><em>Streptococcus gallolyticus</em> subsp. <em>pasteurianus</em> meningoencephalitis and septicemia in goats</td>
<td>Murray Hazlett, Emily Brouwer, Josepha DeLay, Amanda Mansz, Durda Slavic</td>
</tr>
</tbody>
</table>

**14:45-15:15 HEALTH BREAK, TRADE SHOW, POSTER VIEWING AND NETWORKING**

**15:15** Unravelling the genetics of infectious disease susceptibility in livestock with the use of high throughput technology.  
[Graduate student presentation]  

### Swine

**Moderator:** Jim Fairles

<table>
<thead>
<tr>
<th>Time</th>
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<th>Presenter(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>15:30</td>
<td>Analytical verification and use of a multiplex real time RT-PCR to identify porcine epidemic diarrhea virus, transmissible gastroenteritis virus, and porcine deltacoronavirus</td>
<td>Sarah Gresch, Benjamin Miller1, Nitipong Homwong, Douglas G. Marthaler</td>
</tr>
</tbody>
</table>
15:45  Measuring incidence and prevalence of PRRS in Ontario sow herds.  [Graduate student presentation]  
**Juliana Bonin Ferreira**, Zvonimir Poljak

16:00  Near real-time processing, analysis, and reporting of incidence and prevalence of porcine epidemic diarrhea virus and porcine deltacoronavirus in Ontario swine herds  [Graduate student presentation]  
**Toluwalope Ajayi**, Zvonimir Poljak, Rozita A. Dara

16:15  Development of a multiplex molecular detection assay for swine enteric viruses using fluidic bead-based technology  
**Dante Mateo**, Tokinori Iwamoto, Richard Green, Dan Hurnik, Elizabeth Dobbin, Carmencita Yason

**Cross-species**  
Moderator: **Nicole Nemeth**

16:30  Pathology of wild urban rats  
**Jamie L. Rothenburger**, Chelsea G. Himsworth, Nicole M. Nemeth, Piper M. Treuting, Claire M. Jardine

16:45  Improving production of high titer lentiviral vectors for in vivo gene therapy applications  [Graduate student presentation]  
**María C. Rosales Gerpe**, Sarah K. Wootton

17:00  *Mycobacterium* epizootic in a zoo population of Chinese gliding frogs (*Rhacophorus dennysi*): investigation, management, and public health response  [Graduate student presentation]  
**Ellie Milnes**, Pauline Delnatte, Kevin May, Jennifer Ma, Frances B Jamieson, Durda Slavic, Dale Smith
CAHLN / RCTLSA 16th Annual Meeting
Tuesday, June 6, 2017
8:30-17:00

Building 89 PAHL, Room 1800

Plenary Session 2
Theme: Making best use of laboratory data
Moderator: Jim Goltz

8:30
Technological trends: transforming health data into intelligence.
Theresa Bernardo, IDEXX Chair in Emerging Technologies and Bond-Centered Animal Healthcare, Ontario Veterinary College

9:00
From data to intelligence- AgConnect laboratory data in decision support
Matt Cochran, Program Director, Institute for Infectious Animal Diseases, Texas A&M University

9:30
Asymmetric informatics - lessons from a decade of NAHLN messaging
Michael Martin, Epidemiologist, Office of the State Veterinarian, Clemson University

10:00-10:30 HEALTH BREAK, POSTER, TRADE SHOW AND NETWORKING

10:30
Use of laboratory data for near-real time disease reporting, prediction, and understanding complex problems
Zvonimir Poljak, Associate Professor, Ontario Veterinary College

11:00
Veterinary forensic science: new approaches to an old problem
Beverly McEwen, Veterinary Pathologist, Animal Health Laboratory

11:30
From mammals and birds to bees: Adapting veterinary testing protocols for honey bee diagnostics
Paul Kozak, Pat Bell-Rogers, Ontario Ministry of Agriculture, Food, and Rural Affairs (Kozak), Animal Health Laboratory (Bell-Rogers)

12:00-13:15 Lunch
TSE meeting (by invitation, Room TBD)

Health management of laboratorians
Moderator: Melanie Barham

13:30
Navigating and leading change in a professional environment
Evelina Rog

14:30
Intake of laboratory submissions during a disease outbreak – the trials and tribulations and the need to upgrade our “new” facility
Jim Fairles
14:45-15:15  **HEALTH BREAK, TRADE SHOW, POSTER VIEWING AND NETWORKING**

15:15  Veterinary mental health  
**Colleen Best**

15:45  Mental health in the workplace: practical tools to recognize issues and help colleagues  
**Dianna Chinnery**

16:15  Injury prevention and return to work post-injury for desk- and lab-based work  
**Andrew Stolfi**

16:45  Ergonomics  
**Stacey Speagle**

18:00-21:00  **CAHLN Gala: Gourmet Dinner with Ceili and live entertainment.**  
Location: **Creelman Hall**  
The Laboratorian of the Year and Grad Student Award will also be presented at the Gala.
### Poultry

**Moderator:** Marina Brash

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Authors/Contact</th>
<th>Page</th>
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</thead>
<tbody>
<tr>
<td>13:15</td>
<td>Potential pathogens detected in wild turkeys (<em>Meleagris gallopavo</em>) in Ontario</td>
<td>Amanda MacDonald, Claire Jardine, Jeff Bowman, Evelin Rejman, John Barta, Hugh Cai, <strong>Nicole Nemeth</strong></td>
<td>79</td>
</tr>
<tr>
<td>13:30</td>
<td><em>Mycoplasma synoviae</em> in domestic meat-type geese</td>
<td><strong>Alexandra Reid</strong></td>
<td>80</td>
</tr>
<tr>
<td>13:45</td>
<td>Using phylogenetic analysis to examine the changing strains of infectious bronchitis virus infections in Ontario over time</td>
<td><strong>Emily Martin</strong>, Marina Brash, Margaret Stalker, Davor Ojkic</td>
<td>81</td>
</tr>
<tr>
<td>14:00</td>
<td>Mapping of the Ontario IBV outbreak</td>
<td><strong>Alexander Heim</strong></td>
<td>81</td>
</tr>
<tr>
<td>14:15</td>
<td>Infectious bronchitis virus: practical experience from broiler breeders in Ontario</td>
<td><strong>Rachel Ouckama</strong>, <strong>Fernando Salgado-Beirman</strong></td>
<td>82</td>
</tr>
<tr>
<td>14:30</td>
<td>Ontario small poultry flock disease surveillance: year one</td>
<td><strong>Leonardo Susta</strong>, Nancy Brochu, Marina Brash, Csaba Varga, Michele Guerin</td>
<td>83</td>
</tr>
<tr>
<td>14:45-15:15</td>
<td>HEALTH BREAK, TRADE SHOW, POSTER VIEWING AND NETWORKING</td>
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<tr>
<td>15:15</td>
<td>Evaluating virulence genes and antimicrobial susceptibility of avian pathogenic <em>Escherichia coli</em> from Ontario broiler and broiler-breeder flocks</td>
<td><strong>Csaba Varga</strong>, Marina Brash, Emily Martin, Rachel Ouckama, Mike Petrik, Cynthia Philippe, Alex Weisz, Elizabeth Black, Shahbaz Ul Haq, Mike Joyce, Kathleen Long, Joanne Rafuse, Lloyd Weber, Melanie Barham, Durda Slavic, Tim Pasma, Patrick Boerlin, Michele Guerin</td>
<td>84</td>
</tr>
<tr>
<td>15:30</td>
<td>Antimicrobial resistance to extended-spectrum cephalosporins in <em>Enterobacteriaceae</em> from chickens and pigs in Canada [Graduate student presentation]</td>
<td><strong>Pauline Zhang</strong>, Richard J. Reid-Smith, Durda Slavic, Anne E. Deckert, Patrick Boerlin</td>
<td>85</td>
</tr>
<tr>
<td>15:45</td>
<td>CgFARAD: knowledge transfer database update</td>
<td><strong>Ron Johnson</strong></td>
<td>86</td>
</tr>
</tbody>
</table>
16:00  
CgFARAD: knowledge transfer research update  
**Ron Johnson**  

16:15  
Use of hock flexion resistance as a means of identifying dead-on-arrivals (DOAs) at shackling in an end-of-lay hen slaughter line gas stunning system - shackle line worker evaluation  
**Rachel Ouckama**, Fernando Salgado-Bierman, Michele Guerin, Marina Brash

16:30  
Nutritional strategies for enhancing gut function in broiler chickens challenged with coccidiosis  
**Elijah Kiarie**, Emily Kim, Haley Leung, John Barta

16:45  
Oral administration of PLGA-encapsulated CpG ODN and *Campylobacter jejuni* lysate reduces cecal colonization by *C. jejuni* in chickens  
**Khaled Taha-abdelaziz**, Douglas Hodgins, Tamiru Alkie, Wanderely Quinteiro-Filho, Alex Yitbarek, Jake Astill, Shayan Sharif

18:00-21:00  
**CAHLN Gala: Gourmet Dinner with Ceili and live entertainment.**  
Location: **Creelman Hall**  
The Laboratorian of the Year and Grad Student Award will also be presented at the Gala.
National surveillance update, AMR, cross-species
Moderator: Dale Godson

8:30 Development of innovative surveillance methods with the community for emerging and zoonotic diseases
Andrea Osborn, Harry Gardiner, Zana Dukadzinac, Archie Stewart, Ruth Tecl-Mariam

8:45 The Canadian Animal Health Surveillance System achievements and opportunities
Andrea Osborn, Cheryl James, Keith Murch, Francois Bedard

9:00 Routine antimicrobial susceptibility testing data generated by a public animal health diagnostic laboratory: challenges and opportunities to antimicrobial resistance surveillance
Anatoliy Trokhymchuk, Musangu Ngeleka

9:15 Passive tick surveillance in New Brunswick: translating data into information and intelligence
James P. Goltz, L. Robbin Lindsay

9:30 Evaluation of real-time PCR reagents for the identification of influenza virus RNA
Kristen Mesires

9:45 Overview of the Ontario Animal Health Network swine surveillance network to improve disease emergency preparedness and its linkage to the Canadian Swine Health Information Network
Christa Arsenault, Grant Maxie, Paul Innes, George Charbonneau, Chris Byra

10:00 HEALTH BREAK, POSTER, TRADE SHOW AND NETWORKING

Fish
Moderator: Hugh Cai

10:30 Antimicrobial resistance in Ontario aquaculture
Marcia Chiasson, Véronique LePage, Steve Naylor

10:45 Laboratory detection approaches to fish pathogen surveillance in Ontario
Roz Stevenson, Melinda Raymond, Steve Lord, Lucy Mutharia
Cross-species

11:00 Qualitative LC-MS/MS method for the detection of desmethylbromethalin in adipose tissue
Felipe Reggeti, Nick Schrier

11:15 Choosing and interpreting laboratory testing in an environment of increasing technology
Wendy Witbeck

11:30 CAHLN 2018 & Closing Remarks – Melanie Barham

12:00 Boxed Lunch – to be picked up outside Room 1800
### Poster Presentations

**Room 1707 B&C**

Bldg. 77, Lifetime Learning Centre

Monday June 5th morning, to Tuesday June 6th after PM coffee

<table>
<thead>
<tr>
<th>Poster No.</th>
<th>Authors</th>
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</tr>
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<tbody>
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<td>1</td>
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The presenters will be available in the poster area during Health Breaks on Monday and Tuesday.
**CAHLN / RCTLSA WELCOME RECEPTION**

Sunday, June 4, 2017

Lifetime Learning Centre, Building 77, University of Guelph

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<td>17:30-19:00</td>
<td><strong>Reception</strong> for all conference participants. Tours of the C.A.V. Barker Museum.</td>
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<td>19:15-20:00</td>
<td><strong>Presentation</strong>&lt;br&gt;<strong>Andrew McEwen:</strong> “Maintaining the Mobility of the Corps:” Horses, Mules, and the Canadian Army Veterinary Corps in the Great War Room 1714</td>
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<td>20:00-21:00</td>
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“Maintaining the Mobility of the Corps:”
Horses, Mules, and the Canadian Army Veterinary Corps in the Great War

Andrew McEwen
Veterinary historian

Abstract

Animal transportation played a crucial role in the Canadian Expeditionary Force (CEF) during the Great War. Horses and mules provided the overwhelming bulk of draught power in the combat zone by hauling artillery, supplies, and ambulances, packing ammunition, serving as officers’ riding mounts, and chargers for cavalrymen. By the Armistice of 11 November 1918, the CEF alone utilized 24,134 horses and mules in France and Belgium.

The task of overseeing their health and working efficiency fell to just a few officers and enlisted personnel of the Canadian Army Veterinary Corps (CAVC). Only 73 college-educated Veterinary Officers, and 780 Other Ranks, presided over this truly living and breathing transportation system. They treated diseases, wounds, exhaustion, malnourishment, and exposure to the elements. They saved what animals they could, and humanely destroyed those they could not. They were, in the words of Canadian Corps commander Lieutenant-General Sir Arthur Currie, essential for “maintaining the mobility of the Corps.”

This presentation will show that Canada’s horses and mules, and the veterinary efforts to keep them healthy, exerted a clear impact on combat operations in the Great War. It explores their foundations in pre-war Canadian society to understand how both became key facets of the Dominion’s war effort. It explores the broader British Imperial context both served within and on the battlefield, where these animals, and their veterinary caretakers, played an indispensable role in the course of the war on the Western Front from 1915 to 1918. Utilizing a broad array of unexamined historical material from multiple Canadian and British archives, this presentation ultimately imparts the enormous influence horses, mules, and veterinarians exerted upon the Canadian Great War experience.
Overall Theme: Practical approaches to disease intelligence

7:45 – 10:00  Registration – outside Room 1800
10:00 – 17:00 Exhibitors Hall Open – 1707, B and C, Lifetime Learning Centre, Building 77

8:05 – 8:30  Official Opening and Welcome

8:45 – 12:00  Plenary Session

8:45  Bovine tuberculosis in Canada
Debbie Barr, Director, Animal Health, Welfare and Biosecurity Division, Canadian Food Inspection Agency

9:15  Bovine tuberculosis investigation in western Canada: a case study of the role of an animal health diagnostic laboratory
Carl Johnson, Chief Executive Officer at Prairie Diagnostic Services

9:30  Emergence of Echinococcus multilocularis in dogs in Ontario: implications for public and wildlife health?
Andrew Peregrine, Associate Professor, Ontario Veterinary College

10:00-10:30  HEALTH BREAK, POSTER, TRADE SHOW AND NETWORKING

10:30  Using laboratory techniques to answer wildlife disease questions
Doug Campbell, Veterinarian, Canadian Wildlife Health Cooperative, Ontario Veterinary College

11:00  One Health in action: the critical role of laboratory-based animal disease intelligence to public health
Catherine Filejski, Public Health Veterinarian, Infectious Diseases Policy and Programs Unit (Health and Long-Term Care)

11:30  Incorporating lab data into dairy herd management: a vision
Dave Kelton, Dairy Farmers of Ontario Chair in Dairy Cattle Health, Professor, Ontario Veterinary College

12:00-13:30  Lunch, CAHLN business meeting, OVC tours
Bovine tuberculosis in Canada

Debbie Barr

Animal Health, Welfare and Biosecurity Division, Canadian Food Inspection Agency, Ottawa

Abstract

In late September 2016, the Canadian Food Inspection Agency (CFIA) received notification from the United States of America (US), confirming that a cow originating from Alberta and slaughtered in the US, was positive for bovine tuberculosis (bTB). Subsequently, the CFIA initiated and continues to undertake complex epidemiology assessments which have informed the completion of an extensive trace-out, resulting in placement of quarantines, and the completion of intensive and at times challenging on-farm and laboratory testing.

The CFIA has utilized a series of testing approaches tailored to the associated risk of a location or animal which include: caudal-fold tuberculin test (CFT), serology, histology, PCR, and tissue culture, as well as the application of comparative cervical tuberculin (CCT) and specialized serological tests for specific situations. The use of these diagnostic tools has enabled the CFIA to complete the diagnostic testing and remove controls on animal movement and quarantines as quickly as feasible.

This presentation will provide an overview of the bTB investigation, including challenges and successes associated with the response.
Bovine tuberculosis investigation in Western Canada: a case study of the role of an animal health diagnostic laboratory

Carl K. Johnson, Brian Chelack, Anatoliy Trokhymchuk

Prairie Diagnostic Services, Saskatoon, Saskatchewan

Abstract

Earned by hard work and at great expense, maintaining a tuberculosis-free status is a strategic imperative for both Canada’s national herd and for access to world markets for Canada’s beef industry. Ever increasing cross-border movement of people and animals and the endemic presence of the pathogen in wildlife, impose a constant threat of bovine tuberculosis re-introduction into commercial herds. The recent outbreak of bovine TB in beef herds on the southern Alberta–Saskatchewan border has been an unprecedented investigational challenge and learning experience with regard to management of a reportable disease in mature beef cattle in a remote part of the Canadian prairie. The use of a modern and publicly funded animal health diagnostic laboratory to assist in such an investigation presented both a creative opportunity to help solve a mounting backlog of cases, and a logistical nightmare of planning, execution, and expense.

In December 2016, CFIA approached Prairie Diagnostic Services (PDS) seeking additional resources to help address the overwhelming backlog of diagnostic work required. PDS is a veterinary diagnostic laboratory (VDL) located at the Western College of Veterinary Medicine (WCVM) and provides diagnostic, teaching, and research services as part of its mandate of support for the provincial Ministry of Agriculture and the WCVM. PDS also provides fee-for-service diagnostics for the veterinary profession and animal health and agricultural industries of western Canada. Although PDS is able to manage potentially zoonotic infectious agents, the facility is not designed for high volume tissue harvest from heavy animals. Similarly, the PDS and WCVM staff and volunteers would need to perform this work on top of the regular diagnostic, teaching, and research commitments.

PDS processed 140 head of cattle requiring confirmatory testing with the help of core PDS technical staff, WCVM faculty, clinicians, and graduate students, CFIA veterinarians and staff, and supporting animal handling personnel and carcass disposal services. Between December 2016 and February 2017, PDS planned 4 intensive postmortem examination / tissue harvest campaigns, helping to reduce the backlog to a level best managed again by CFIA in local abattoirs. Personnel, facility, and scheduling challenges aside, this exercise has validated the merit of using a VDL necropsy facility to assist in a government agency’s response plan.
Emergence of *Echinococcus multilocularis* in dogs in Ontario: implications for public and wildlife health?

Andrew S. Peregrine, Jonathon Kotwa, Claire Jardine, Benoît Cuq, Nicola Mercer, Bruno Gottstein

Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario (Peregrine, Kotwa, Jardine, Cuq); Wellington-Dufferin-Guelph Public Health, Guelph, Ontario (Mercer); and Universitat Bern, Bern, Switzerland (Gottstein).

Abstract

*Echinococcus multilocularis* is a zoonotic tapeworm with a high case-fatality rate in patients when left untreated. Historically, the parasite was known to occur in wildlife in 13 US states and 3 contiguous Canadian provinces (Alberta, Saskatchewan, Manitoba); adult tapeworms reside in the small intestine of wild canids, and the intermediate "larval" stage (alveolar hydatid cysts) occurs in the liver of wild rodents. Dogs, and to a lesser extent cats, can also be definitive hosts for *E. multilocularis* if infected rodents are ingested. However, strangely, outside Alaska, no dog in either the US or Canada has been reported with an intestinal infection.

Prior to 2012, *E. multilocularis* had never been identified in Ontario. However, in that year, hepatic alveolar echinococcosis (disease caused by the presence of alveolar hydatid cysts) was diagnosed in a 2-yr-old dog that had lived permanently in southern Ontario. Histology of the liver revealed multi-vesiculated coalescing cystic structures surrounded by fibrosis; lining individual cysts was a hyaline membrane ("laminated layer") that stained with periodic acid-Schiff. Sequence data for the mitochondrial 12S rRNA gene, and restriction fragment length polymorphism analysis of the mitochondrial NADH dehydrogenase 1 and 12S rRNA genes, confirmed the diagnosis. Between 2013 and 2016, 4 additional cases were similarly diagnosed in southern Ontario. None of the 5 dogs were related; 4 of the dogs had never travelled outside southern Ontario; the fifth dog had visited Alberta. In 2016, hepatic alveolar echinococcosis was diagnosed for the first time in a rodent in southern Ontario, in a chipmunk. Furthermore, *E. multilocularis* was shown to be present in wild canids across southern Ontario. As a result, the parasite now appears to be endemic in this region.

We will review the diagnosis of alveolar echinococcosis, why the disease is thought to occur in dogs, the prognosis for such cases, and the public health concerns associated with such infections. Reasons for the emergence of alveolar echinococcosis in dogs in Ontario and the likely impact of *E. multilocularis* on the health of both people and wildlife populations will be discussed. As well, strategies to minimize the risk of human infection will be reviewed.
Using laboratory techniques to answer wildlife disease questions

Doug Campbell
Ontario Veterinary College

Abstract

Free-ranging wildlife in Ontario has been exposed to many new and often serious diseases over the past 30 years, due to changing environmental circumstances and the inadvertent movement of pathogens by people. Detection and surveillance of these diseases has typically progressed through a discovery phase, based upon passive surveillance, into more active surveillance, in which molecular laboratory methods play a central role. The talk will examine some of the challenges in providing surveillance for wildlife disease and the critical interplay between field observations, pathology, and more specialized laboratory support in understanding and monitoring these diseases.

One Health in action: the critical role of laboratory-based animal disease intelligence to public health

Catherine Filejski
Infectious Diseases Policy and Programs Unit (Health and Long-Term Care)

Abstract

The concept of One Health is based upon the observation that the increasing convergence of people, animals, and the environment is creating an escalating dynamic in which the health of each group is more and more inextricably connected in real time. One of the best examples of the importance of One Health approaches to successful prevention, control, and management of disease is the field of infectious diseases. 75% of new emerging infectious diseases (EIDs) since 1975 have been zoonotic in origin, and EIDs are having an increasing effect on human health. A One Health approach is essential to managing infectious disease risks, and this presentation will provide an overview of Ontario’s experience with public health management of zoonotic and vector-borne diseases, and how laboratory-based animal disease intelligence is critical to ensuring successful public health responses to emerging disease risks, covering both previous success stories and ongoing challenges.
Incorporating lab data into dairy herd management: a vision

Dave Kelton
Ontario Veterinary College

Abstract

Veterinarians actively involved in delivering dairy health management programs for progressive dairy producers rely on data that is accurate and timely to deliver their programs. These data come from many sources, including farm systems, practice based programs, and a number of laboratories. The challenge for the advising veterinarian is to combine these data to generate information that has value for the dairy producer and generates billable hours for the veterinarian. Diagnostic laboratories generally have the best equipment and the most capable experts, which allows them to generate very valuable diagnostic data for individual animals on individual farms. The value proposition comes when these data are combined with available denominators (numbers for animals at risk), with clinical / sub-clinical disease data (attack rates), with treatment data (which products and which protocols), and with outcome data (prudent antibiotic use). The challenge in this data-sharing model is the linking of data from multiple sources. The technology exists to make this process fast and simple, but only if the foundational elements are in place. These foundational elements include unique farm and animal identifiers that are used by all data providers. If we can sort out the unique identifier issue across the sector, the value will accrue to all stakeholders, the producers, the veterinarians and the data providers. In addition, if the unique farm identifiers are geo-located, additional benefits will accrue to the industry as a whole by making passive surveillance accurate and affordable.
### Companion Animals, all species

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<td>Diagnosis and genetic variation of an invasive microsporidium (<em>Nosema ceranae</em>) in honey bees (<em>Apis mellifera</em>)</td>
<td>Mollah Md. Hamiduzzaman, Ernesto Guzman-Novoa, Paul H. Goodwin</td>
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<td>Different approaches for the diagnosis and classification of canine lymphoma</td>
<td>Nariman Deravi, Veronica Parsons, Dorothee Bienzle</td>
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<td>14:00</td>
<td>Determining average cat weights through the use of big data</td>
<td>Adam Campigotto, Theresa Bernardo, Zvonimir Poljak, Elizabeth Stone, Deborah Stacey</td>
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<td>Prevalence of potentially zoonotic and non-zoonotic parasites in domestic dogs in rural, urban and First Nations communities across Ontario, Canada</td>
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<td>14:30</td>
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<td>15:15</td>
<td>An introduction to high-throughput immunohistochemistry</td>
<td>Courtney R. Schott, Geoffrey A. Wood</td>
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Diagnosis and genetic variation of an invasive microsporidian (*Nosema ceranae*) in honey bees (*Apis mellifera*)

Mollah Md. Hamiduzzaman, Ernesto Guzman-Novoa, Paul H. Goodwin

School of Environmental Sciences, Ontario Agricultural College, University of Guelph, Guelph, Ontario

Abstract

Nosemosis caused by the obligate intracellular microsporidian fungi, *Nosema ceranae* and/or *Nosema apis*, is a gut disease that is very detrimental to honey bees (*Apis mellifera*). *N. apis* was thought to be the common parasite in the midgut of western honey bees, but recently the involvement of *N. ceranae* has been reported by many groups. Traditionally, light microscopy, single and duplex PCR methods have been used to identify the spores of *Nosema* spp.

We have developed a semi-quantitative triplex PCR assay to detect and quantify *Nosema* infections, which is simple, economical, and will be useful in laboratories where real-time PCR is not available. A rapid DNA extraction method, and a spore quantification method were developed using multiplex PCR to co-amplify the *N. apis* and *N. ceranae* 16S rRNA gene with the ribosomal protein gene, *RpS5*, from honey bees. It has been reported that *N. ceranae* originated in east Asia as a parasite of *Apis ceranae*, and spread worldwide infecting *A. mellifera*. To investigate the genetic variation of *N. ceranae* samples from different locations, novel genetic markers, simple sequence repeat (SSR) length polymorphisms, were used. Single nucleotide polymorphisms (SNPs) in the aligned sequences that reveal genetic variation among and within the populations will be discussed. In addition to evaluating genetic diversity, those tools could be useful to compare between invasive species versus native ranges.
Different approaches for the diagnosis and classification of canine lymphoma

Nariman Deravi, Veronica Parsons, Dorothee Bienzle

Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

Lymphoma in domestic animals is a heterogeneous disease with variable prognoses. In humans, lymphoproliferative diseases are classified by World Health Organization (WHO) criteria that imply specific response to therapy and prognosis. This classification involves cytomorphology, histopathology, immunophenotyping, and molecular analysis. Similar techniques are available for animals, although to a more limited extent. Because canine lymphoma is most often a diffuse and homogeneous neoplasm, cytology samples are usually sufficient for diagnosis. Histopathology is valuable for categorizing lymphoma according to tissue architecture, cell type, cell size, nuclear morphology, and mitotic index, but requires anesthesia to obtain suitable samples. The immunophenotype of lymphoma can be determined by flow cytometry, whereby the full range of ~25 antibodies that react with fresh cells can be utilized, and quantitative information about each type of lymphocyte antigen is obtained. On the other hand, immunohistochemistry (IHC) involves application of antibodies to sections of formalin-fixed tissue. The advantage of IHC is concurrent assessment of tissue histomorphology and antigen expression, and the main disadvantage is limited antibody reactivity with formalin-fixed epitopes. Alternatively, tissue samples may be prepared as frozen sections, which allows the full range of antibodies to be applied but requires substantial technical skill. Molecular analysis is increasingly feasible with technologies such as whole exome sequencing, and will likely gain in popularity once bioinformatic analytical skills are more commonplace.

Canine T-cell lymphoma includes subtypes with biologic behaviour ranging from indolent to rapidly progressive. Correlation between different diagnostic approaches is unknown. We have attempted to integrate cytologic, histopathologic, formalin-fixed and frozen-section IHC, and flow cytometric findings for canine T-cell lymphoma. Results indicate that cytologic and histomorphologic appearance is highly suggestive of certain immunotypes, and that flow cytometric and frozen-section IHC phenotypes are correlated. These results expand knowledge of the biology of canine T cell lymphomas, and can be translated to prognosis and chemotherapeutic approaches.
Determining average cat weights through the use of big data

Adam Campigotto, Theresa Bernardo, Zvonimir Poljak, Elizabeth Stone, Deborah Stacey

Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

Electronic medical records from over 19 million feline patients were used to determine the average body weight (BW) of different breed and sexes of cats. Knowing the body weight (BW) development for cats provide important health information for owners and veterinarians to help guide discussions on what to expect from weight loss and obesity resulting from aging. However, such information is not easily available, particularly for uncommon breeds. Using electronic medical records to examine clinical data from animals over several decades allows for uncommon occurrences to be observed sufficiently. Processing and analyzing large amounts of already existing data from medical records can help to fill the gap in this fundamental knowledge. Thus, our objective was to determine the impact of breed and sex on the BW at each year of age in cats.

A retrospective cohort study was performed using BW data gathered from domestic cats from 3,972 unique veterinary clinics in the United States and Canada from 1981 to 2016 through electronic management records (Avimark, Cornerstone, Impromed, or Intravet) made available for analysis from a veterinary diagnostic company (IDEXX Laboratories, Inc.). Initially, BW from all cats recorded in the electronic medical records (n = 19,416,753) were included in the study population and examined using descriptive statistics. Linear regression was used to assess association between BW and age, breed, sex, decade of measurement, and their interactions. Accuracy of predictions was evaluated on a validation dataset. Descriptive statistics and linear regression models and predictions were created using Python.

Our study is the first using such big data approaches to provide important information on the average body weight of cats over a lifetime and for different breeds. Our study demonstrates that the use of big data could help in addressing questions that were previously not feasible in the area of companion animal health.
Prevalence of potentially zoonotic and non-zoonotic parasites in domestic dogs in rural, urban, and First Nations communities across Ontario, Canada

Rachel Imai, John R. Barta

Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

A wide range of parasitic infections are prevalent in Canadian domestic dogs. However, no study to date has examined the prevalence of potentially zoonotic parasites in dogs in various communities across Ontario. Access to permanent veterinary services is limited in some areas of Ontario and veterinary clinics are not usually found on First Nations reserves. Human exposure to zoonotic parasites may be elevated where free-roaming dogs have access to contaminated water and infected raw meat through scavenging. Wild or domestic dogs may serve as bridges for such zoonoses. There is also concern regarding transmission of parasitic infections from infected to healthy dogs within these communities.

Our goal was to determine the prevalence of potentially zoonotic and non-zoonotic parasitic infections in domestic dogs that may impact the health of humans and domestic dogs in these Ontario communities. Fecal samples \( n = 127 \) from dogs in rural, urban, or First Nations communities were collected to determine the prevalence of parasites identified in each community; parasites with potential zoonotic risk to humans were of particular interest. Samples were processed using the Cornell Wisconsin centrifugal flotation method employing sucrose flotation medium (SG of 1.27-1.33).

Preliminary results showed that the overall prevalence (at least 1 parasite identified) of intestinal parasites in the canine fecal samples was 20% \( n = 26 \); only 2 dogs were infected with more than 1 parasite. Protistan parasites detected included *Giardia* sp. and *Cystoisospora* sp., and helminths detected included hookworms (*Ancylostoma*/*Uncinaria* sp.), ascarids (*Toxocara*/*Toxascaris* sp.), and whipworms (*Trichuris* sp.). Of the 28 parasite infections identified, 18% (5 of 28) were potentially zoonotic and 82% (23 of 28) were non-zoonotic.

This study serves as a preliminary assessment of the prevalence of dog parasites in select Ontario communities; potentially zoonotic parasitic infections were found that may warrant more active surveillance and, potentially, more active control.
Canine pulmonary hyalinosis

Gwendolyn Conant, Margaret Stalker, Jeff L Caswell

Department of Pathobiology, Ontario Veterinary College (Conant, Caswell), Animal Health Laboratory, Laboratory Services Division (Stalker), University of Guelph, Guelph, Ontario

Abstract

Canine pulmonary hyalinosis is a rare alveolar filling disorder. This disease is of unknown pathogenesis and etiology. Pulmonary hyalinosis is characterized by the accumulation of unknown amorphous material within the alveoli of the lungs. This disease has been identified both as a cause of death and as an incidental finding during necropsy. Pulmonary hyalinosis is histologically consistent, characterized by: (i) abnormal multifocal accumulations of amorphous material within the alveoli; and (ii) a variable macrophage and multinucleate giant cell response. The material is birefringent in polarized light and stains strongly periodic acid-Schiff (PAS) positive.

While possible pathogeneses of this disease include (i) excess endogenous protein production, (ii) impaired removal of endogenous protein, and (iii) the ineffective clearance of exogenous material; we hypothesized that this insoluble material may be caused by excess endogenous protein production and/or impaired removal of an endogenous surfactant protein. We extracted from lung tissue samples from a healthy dog and one with pulmonary hyalinosis. The samples were assessed with SDS-PAGE, mass spectrometry, and a microarray was created from 9 cases for immunohistochemistry. Two unambiguous proteins were uniquely identified in the pulmonary hyalinosis sample: (1) pulmonary surfactant-associated protein A, and (2) an uncharacterized protein.

These data were partially consistent with the hypothesis of an abnormal accumulation of an endogenous surfactant protein. Identification of the accumulated material is essential for understanding the pathogenesis and whether all cases represent a single disease process.
An introduction to high-throughput immunohistochemistry

Courtney R. Schott, Geoffrey A. Wood

Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

The search for predictive biomarkers using genomics and proteomics is a crucial part of modern biomedical research and requires the evaluation of multiple molecular targets in large cohorts of patients. Most high-throughput array technologies are limited by the necessity for unfixed tissue samples, thus eliminating the option of using valuable archives of routinely collected formalin-fixed paraffin-embedded (FFPE) tissue. Tissue microarray (TMA) technology is a laboratory tool that allows investigators to compile large numbers of tissue samples into an array while taking advantage of archived FFPE tissue. The use of TMA technology for immunohistochemistry (IHC) allows for accelerated, highly consistent slide processing.

Like many high-throughput techniques, management and analysis of the large volume of data generated from a TMA is considerably more challenging than the construction, sectioning, and immunohistochemical processing. Automated image analysis can reduce the time required for the pathologist to interpret the immunolabeling and in certain scenarios, where commercial algorithms exist (in human oncology), it can even minimize the pathologist’s role. However, the development of reliable algorithms requires pathology expertise.

An overview of TMA planning, design, and construction will be provided. The basics of automated image analysis and algorithm design on the Leica platform will be introduced and some veterinary specific challenges will be addressed.
Ruminants

13:30  Cull cows at auction and provincial slaughter plants in Ontario  
      Todd Duffield  

13:45  Postmortem evaluation in cases of suspected humane transport violation  
      Andrew Brooks, Jan Shapiro  

14:00  Overview of a milk bacteriology QA program for veterinary clinics  
      Jim Fairles, Josie Given  

14:15  Detection of bovine viral diarrhea (BVD) virus in ear skin tissue samples: evaluation of a combination of QIAGEN MagAttract 96 cador pathogen extraction and virotipe BVDV RT-PCR-based amplification  
      Roger Maes, Patrick Bronson-Doherty, Mike Chumbley, Annabel Wise, Suzanne Kull- Mason, Vittoria Miller, Daland C. Herrmann, Carsten Schroeder  

14:30  *Streptococcus gallolyticus* subsp. *pasteurianus* meningoencephalitis and septicemia in goats  
      Murray Hazlett, Emily Brouwer, Josepha DeLay, Amanda Mansz, Durda Slavic  

14:45-15:15  HEALTH BREAK, TRADE SHOW, POSTER VIEWING AND NETWORKING  

15:15  Unravelling the genetics of infectious disease susceptibility in livestock with the use of high throughput technology.  
      [Graduate student presentation]  
Cull cows at auction and provincial slaughter plants in Ontario

Todd Duffield

Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

In Ontario, through the Livestock Community Sales Act (LCSA), animals arriving at salesyards are screened by lay inspectors, who work for the salesyard, but are trained by OMAFRA. LCSA trained veterinarians inspect all animals at the salesyard and conduct thorough examinations on segregated animals that were either screened by the lay inspectors or identified by themselves as being abnormal. Decisions on the fate of these animals can be euthanasia, direct to slaughter, ring announcement, return to consignor, or treatment at the salesyard.

Cull beef and dairy cattle euthanized at Ontario slaughter facilities range from 0.2-0.6% of total cull cattle offered for sale. Approximately one-third of animals euthanized are lame, one third are recumbent, and one third are sick.

Approximately 1-1.5% of cull cows offered for sale are sent direct to slaughter by veterinary inspectors. Provincial data indicates that 5-8% of whole carcasses of cull cows are condemned. The 5 most common reasons for condemnation are endocarditis, peritonitis, septicemia, mucoid degeneration, and lymphosarcoma. Currently, there are no condemnation data specific for the cull cows from auctions that are sent direct to slaughter. This information would be extremely useful for aiding decision making at salesyards.

Postmortem evaluation in cases of suspected humane transport violation

Andrew Brooks, Jan Shapiro

Animal Health Laboratory, Laboratory Services Division, University of Guelph, Kemptville, Ontario

Abstract

The Animal Health Laboratory at Kemptville has performed postmortem examinations on several animals submitted by OMAFRA where non-compliance to federal and provincial regulations that govern the movement of fallen or unfit animals was suspected. These humane transport cases, which may proceed to legal action, pose several challenges that differ from our routine diagnostic work.

A series of cases will be presented to illustrate our approach to these legal postmortems including documentation, lesion recording, and interpretation of lesion age and significance.
Overview of a milk bacteriology QA program for veterinary clinics

Jim Fairles, Josie Given

Client Services Veterinarian (Fairles), Client Outreach Technician (Given), Animal Health Laboratory, Laboratory Services Division, University of Guelph, Guelph, Ontario

Abstract

Diagnostic laboratories have as a priority the provision of timely and accurate results to their clients. The laboratory quality program underpins this work. Quality becomes part of the “culture” at a diagnostic lab. With the increased use of point-of-care testing by veterinarians, their clients also want timely and accurate results.

One such area of testing at a food animal veterinary clinic is bovine milk culture for mastitis. Veterinarians are being asked to be “prudent” with the use of antibiotics, and a program that can reduce the need is testing prior to treatment. Many of the bovine-oriented veterinary clinics in Ontario now have “in-house” milk bacteriology labs. Providing an answer on whether to treat or not to treat a cow within 24 hours certainly aids in the prudent use of antibiotics. Reference veterinary diagnostic labs have difficulty in providing this turnaround simply due to location, distance, and transportation.

Since May 2016, The Animal Health Laboratory with the aid of funds from the Disease Surveillance Project (http://www.uoguelph.ca/omafra_partnership/en/partnershipprograms/DiseaseSurveillancePlanDSP.asp) has offered a milk bacteriology in-clinic laboratory proficiency program. The purpose of the Milk Bacteriology In-Clinic Laboratory Proficiency Program (https://www.uoguelph.ca/ahl/content/ahl-labnote-47-ahl-milk-bacteriology-clinic-laboratory-proficiency-program) is to provide an external quality assurance program for assessing and monitoring laboratory methods in veterinary practice laboratories for the diagnosis of bovine intramammary infections. This program provides education and self-assessment for in-clinic staff. Improved laboratory quality assurance will ensure accurate and appropriate bovine mastitis diagnoses and improve client confidence.

This concept can also be applied to other areas for veterinary in-clinic laboratory practice including clinical pathology and parasitology. Results to date have been mixed with some clinics wanting more training. This program with funding from DSP will conclude April 2018.
Detection of bovine viral diarrhea (BVD) virus in ear skin tissue samples: evaluation of a combination of QIAGEN MagAttract 96 cador pathogen extraction and virotype BVDV RT-PCR-based amplification

Roger Maes, Patrick Bronson-Doherty, Mike Chumbley, Annabel Wise, Suzanne Kull-Mason, Vittoria Miller, Daland C. Herrmann, Carsten Schroeder

Diagnostic Center for Population and Animal Health, Michigan State University, Lansing, Michigan, USA (Maes, Chumbley, Wise, Kull-Mason, Miller); and QIAGEN Leipzig GmbH, Leipzig, Germany (Bronson-Doherty, Herrmann, Schroeder).

Abstract

BVD is one of the most important viral diseases of cattle. A key element in its control is the detection of persistently infected (PI) animals. Different sampling strategies and assay formats are currently available for this purpose.

An in-house duplex real-time RT-PCR assay detecting a BVDV conserved target sequence within the 5'UTR and an in vitro transcribed RNA internal control (IC) to monitor PCR inhibition has thus far been used. The PCR template consists of RNA extracted from an aliquot of the supernatant from 10 pooled ear skin pieces that are mechanically disrupted in lysis buffer.

This established method was compared to a method referred to as the QIAGEN workflow. Ear skin samples were individually soaked in PBS for 1-2 h. Pools were created by combining aliquots from 10 individual samples. RNA was extracted from an aliquot of the pooled fluids using the QIAGEN MagAttract 96 cador Pathogen Kit. Extracted RNA was tested for the presence of BVDV using the QIAGEN virotype BVDV RT-PCR reagent.

Comparison of the 2 workflows was done on 9 BVDV-positive samples, 14 negative samples, and 3 pooled samples. Each sample was extracted in triplicate and each RNA extract tested for BVDV in triplicate.

The results indicate that the sensitivity of the QIAGEN workflow was higher than for the in-house duplex assay, evidenced by a signal threshold that was on average 3 Ct values lower than for the in-lab assay. Furthermore, the IC of the virotype BVDV RT-PCR reagent performed better than the IC of the in-house duplex real-time RT-PCR assay, and the standard deviation of the Ct value for each positive sample (extracted and tested in triplicate) was lower when using the QIAGEN workflow. In addition, the QIAGEN workflow was more cost-efficient.
**Streptococcus gallolyticus subsp. pasteurianus meningoencephalitis and septicemia in goats**

Murray Hazlett, Emily Brouwer, Josepha DeLay, Amanda Mansz, Durda Slavic

Animal Health Laboratory, Laboratory Services Division (Hazlett, Brouwer, DeLay, Slavic), and Department of Pathobiology, Ontario Veterinary College (Mansz), University of Guelph, Guelph, Ontario

**Abstract**

Formerly belonging to *Streptococcus bovis* biotype II/2 complex, *Streptococcus gallolyticus* subsp. *pasteurianus* is associated with septicemia, meningitis, and endocarditis in humans. It is commonly found in the alimentary tract of ruminants and has been isolated from cases of septicemia in goslings, ducklings, and turkey poults. We have recently seen 4 cases of acute suppurative meningoencephalitis and septicemia associated with this organism in young goats.

Case 1 was a 2-mo-old goat that was presented from a farm having several kids with neurologic signs (opisthotonos, ataxia). Postmortem revealed severe neutrophilic meningitis and ventriculitis. *S. gallolyticus* subsp. *pasteurianus* was isolated in large numbers and almost pure culture from brain swabs.

Case 2 involved two 1-mo-old goats, 2 of which were presented with stiff joints and weak hind or front ends. About 10% of kids were affected. The major findings in the first kid were severe suppurative arthritis and severe suppurative meningoencephalitis with occasional microabscesses in the perivascular neuropil. The second kid had only arthritis. *S. gallolyticus* subsp. *pasteurianus* (3+) was isolated from meninges of kid A as well as in pure culture (lower numbers) in 2 of the affected joints.

Case 3 involved two 4-wk-old meat goats. The kids would go off feed, with some seeming neurologic and star-gazing. An autopsy was performed on the farm on 2 of the goats, and fixed tissues submitted for histology. Histologically, both goats had severe neutrophilic meningitis and evidence of septicemia. Although treated, *S. gallolyticus* subsp. *pasteurianus* was among the bacteria isolated from the submitted brain sample in one goat with *Staphylococcus aureus* and *Streptococcus pluranimalium*.

Case 4 involved a 32-d-old goat kid displaying neurologic signs and was reported as a “herd health problem”. At autopsy, there was severe suppurative meningoencephalitis - *S. gallolyticus* subsp. *pasteurianus* was isolated (3+) with occasional *Pseudomonas aeruginosa*.

Although cases of septicemic listeriosis can look similar, these are rare. We strongly suspect involvement of *S. gallolyticus* subsp. *pasteurianus* as the cause of septicemia and meningoencephalitis, sometimes with arthritis, in all 4 of these herds.
Unravelling the genetics of infectious disease susceptibility in livestock with the use of high-throughput technology


Department of Pathobiology (Fraser, Hammermueller, Lumsden, Hayes, Lillie), Department of Clinical Studies (Arroyo), Ontario Veterinary College, University of Guelph, Guelph, Ontario; Animal Health Centre, BC Ministry of Agriculture, Abbotsford, British Columbia (Snyman); and Ontario Institute for Cancer Research, Toronto, Ontario (Meyer).

Abstract

Mutations in genes of the innate immune system are associated with increased susceptibility to infectious disease. Modern technologies, such as next-generation sequencing (NGS), offer powerful, large-scale approaches to investigating the genetic basis of infectious disease susceptibility in livestock.

Using NGS, we aimed to identify functionally significant mutations in innate immune genes, such as collagenous lectins, associated with infectious disease susceptibility in horses, cattle, and pigs. To identify genetic mutations, genomic DNA was obtained from liver collected at postmortem (horses, cattle) or slaughter (pigs). For horses and cattle, animals were classified based on the presence of infectious disease as “normal” or “diseased”. Members of each species were grouped (3-5/group) based on dominant disease process and equimolar amounts of DNA were pooled. By contrast, all pigs were considered “normal” and sequenced individually. Using probe-based enrichment, candidate innate immune genes and surrounding regulatory DNA were targeted for sequencing. To investigate the relationship between mutations and gene expression in pigs, hepatic RNA was extracted and gene expression analyzed using a microarray. In horses, 5,145 single nucleotide variants (SNVs) were found (35 missense mutations); 47 SNVs were differentially distributed between “normal” and “diseased” populations. In cattle, 6,525 SNVs were identified (54 missense mutations); a separate 54 of which were unevenly distributed between the 2 populations. In pigs, 41,894 SNVs were identified, 369 of which significantly affected gene expression.

High-throughput sequencing offers an effective and economical approach towards understanding the pathogenomics of infectious disease susceptibility in livestock.
### Equine

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An electronic solution for equine infectious anemia (EIA) submissions

Joanna Sawicki, Jim Fairles

Virology Technical Supervisor (Sawicki), Client Services Veterinarian (Fairles), Animal Health Laboratory, Laboratory Services Division, University of Guelph, Guelph Ontario

Abstract

GlobalVetLink (GVL) (https://www.globalvetlink.com/products/equuslink/) offers web-based applications to animal health practitioners, owners, and laboratories to simplify the submission process and offer time-saving solutions. The EquusLink specifically, allows electronic health certificate generation for equine infectious anemia (EIA). The service has been successful in the United States since 2001 and, after CFIA approval, became available at the Animal Health Laboratory in 2016 after a successful pilot test run with 3 clinics. Since then, the Animal Health Lab has processed close to 300 submissions with great results.

Quicker communication is one the biggest advantages of this system, given that accredited veterinarians and the CFIA can access results from anywhere at any time enhancing turnaround time for clients. After a test certificate is digitally created containing all required information, the lab can automatically view and anticipate the submission. Accuracy is enhanced as information can be updated up to the point of approval making it simpler to address submission errors. In the event that an error occurs after test approval, the veterinarian can void the submission. The ability to include colored photos of the horse on the certificate allows better identification. The reporting of final results into the online platform decreases data entry time from 5 min to 1 min while still improving accuracy due to embedded checks by the system.

The GVL support line is always available for troubleshooting any system problems that may occur, and the response from both lab personnel and referring veterinarians has been positive.
Canadian Pari-Mutuel Agency Equine Drug Control Program: diagnostic testing in a forensic regulatory environment

Lydia Brooks

Canadian Pari-Mutuel Agency, Ottawa, Ontario

Abstract

The Canadian Pari-Mutuel Agency (CPMA) is a federal organization that reports to the Minister of Agriculture and whose mandate is to protect the horse-racing betting public. To meet its mandate, the CPMA manages an Equine Drug Control Program (EDCP) to detect prohibited drugs that can affect the outcome of a race. The EDCP encompasses the collection and testing of urine and blood samples obtained from horses participating in races where there is pari-mutuel betting. Testing of samples obtained from racehorses outside of the pari-mutuel race environment (e.g., non-wagering races, out of competition testing) is under the authority of provincial regulators.

Collection and analytical services are contracted out and performed using CPMA-approved procedures for proper sample collection, handling, and transport, which must be adhered to so that chain-of-custody rules are followed and proper samples are obtained for toxicologic analysis. The diagnostic laboratory, which is designated as an `official laboratory' and is ISO/IEC 17025 accredited, processes the samples following strict procedures to maintain the chain-of-custody in the laboratory and to ensure that the results can withstand quasi-judicial scrutiny. Samples are analyzed using cost-effective methods and state of the art technology. Each sample is screened for more than 250 prohibited drugs in a single test using high-performance liquid-chromatography-mass-spectrometry. A random subset of samples is selected for additional testing for drugs that cannot be included in the regular screen. When a prohibited drug is confirmed in a sample, a Certificate of Positive Analysis is issued. The certificate is forwarded to the corresponding provincial regulatory body for adjudication based on their rules of racing.

This presentation will focus on the challenges the CPMA faces when regulating prohibited substances present in the horse at the time of the race. These include commonly prescribed veterinary medications, human medications, illegal substances, environmental contaminants, and endogenous substances, as well as the legal challenges associated with proving that a given concentration of drug does or does not affect the horse’s performance and thus the outcome of the race.
Racehorse mortality in Ontario: postmortem procedures and results

Josepha DeLay, Bruce Duncan, Adam Chambers

Animal Health Laboratory, Laboratory Services Division, University of Guelph, Guelph, Ontario (DeLay); and Alcohol and Gaming Commission of Ontario, Toronto, Ontario (Duncan, Chambers)

Abstract

Formal investigation of racehorse mortality is routinely conducted in an increasing number of racing jurisdictions in an effort to improve the health, welfare, and safety of these animals. In 2003, the Alcohol and Gaming Commission of Ontario (AGCO; formerly the Ontario Racing Commission) established a Death Registry for mandatory reporting of racehorse deaths in the province. Since that time, postmortem examination has been carried out at the Animal Health Laboratory, University of Guelph on 1,013 Ontario horses submitted through the Death Registry program. Postmortem results provide information on individual animal deaths, as well as material and data for research on catastrophic injuries and sudden death among racehorses.

The causes and prevention of fracture of axial or appendicular skeleton, and exercise-associated sudden death, are of special concern to the horseracing industry worldwide. Approximately 50% of Death Registry postmortem cases involved limb fracture. Since 2015, computed tomography (CT) has been carried out on the majority of these cases to identify pre-existing lesions potentially contributing to fracture. The cause of exercise-associated sudden death is often obscure. In this population, 163 of 1,013 (16%) cases had a history of sudden death.

Standardization within and among institutions of examination protocols for racehorse deaths allows direct comparison of results between racing jurisdictions and expands research opportunities. The presentation will include a description of racehorse postmortem protocols used at the Animal Health Laboratory, and will expand on results of Death Registry postmortems.
Analysis of the Ontario Racing Registry, 2003-2011

Peter Physick-Sheard

Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

This study analyzed the Ontario Racing Commission Death Registry (DR) for 2003-11. The database contains all cases of mortality occurring in Ontario racehorses within 60 days of a horse racing or being entered to race, and covers Thoroughbred (Tb), Standardbred (Sb), and Quarter Horse (Qh) racing. It includes circumstances of loss, presumed cause, and demographic features, and also final diagnosis for cases submitted for postmortem (59%).

All-cause mortality was 2.973 (Tb), 0.566 (Sb) and 1.729 (Qh) deaths/1000 starts. Mean annual individual horse risk was 0.911%, 0.196% and 0.613%, respectively. Overall, the most common complaints were musculoskeletal injury (48%), sudden death (15%), colic (11%), medical complaints (9%), and iatrogenic problems (7%). Proportions varied widely by breed. Greatest hazard for all breeds was maximal exercise, whether race, qualifying, or training. Mortality was variously influenced by age, sex, and race conditions for all breeds, with wide variation by industry. Finishing position was a strong and consistent indicator of mortality risk. Maximum effort influenced the timing of both exercise-associated and non-exercise-associated mortality in a manner suggesting significant impact of management strategies.

The data cover mortality only, but provide insight into probable causes of morbidity. Associations suggest strategies by which mortality and morbidity might be reduced on an industry-specific basis.
Seroprevalence of *Borrelia burgdorferi* and *Anaplasma phagocytophilum* in horses in Ontario

**Megan Neely**, Scott Weese, Alison Moore, Murray Hazlett, Luis Arroyo

Departments of Pathobiology (Neely, Weese) and Clinical Studies (Arroyo), Ontario Veterinary College, and Animal Health Laboratory, Laboratory Services Division (Hazlett), University of Guelph; and Ministry of Agriculture, Food and Rural Affairs (Moore), Guelph, Ontario

**Abstract**

Lyme disease - a multi-systemic tick-borne disease, caused by the bacterium *Borrelia burgdorferi* - is of growing concern in Ontario. A reportable disease in humans, Lyme disease also notably affects dogs and horses; however, very little is known about Lyme disease in horses. Another tick-borne bacterial pathogen of concern is *Anaplasma phagocytophilum*, the cause of equine granulocytic anaplasmosis. Given predictions of expanding tick populations, it is imperative to develop an understanding of these equine diseases.

Our objectives in this study were to 1) to identify the prevalence of *B. burgdorferi* and *A. phagocytophilum* seropositivity in Ontario horses; 2) identify geographic risk factors; and 3) compare a SNAP test to a Lyme multiplex assay. Veterinary clinics (*n* = 80) from across Ontario enrolled to participate in the study. Serum samples from 564 horses were submitted along with a questionnaire that evaluated demographics, clinical history, and farm management for each horse in the study. Sera were examined with an IDEXX SNAP 4Dx test, and by an equine Lyme multiplex assay at Cornell University.

The overall prevalence of *B. burgdorferi* exposure was 14.7% (83 of 564), with pronounced regional variability. On the SNAP test, ~5% (27 of 564) of the samples were positive for *B. burgdorferi*, and 1% (6 of 564) were positive for *A. phagocytophilum*, of which 3 horses were co-infected. OspF was the most frequently found antibody on the multiplex assay as 8% (45 of 564) were positive; the overall prevalence with the multiplex assay was ~12% (65 of 564).

Knowing the distribution and risk factors for *B. burgdorferi* and *A. phagocytophilum* exposure will aid in the continued monitoring and prevention of the associated diseases.
Analytical validation of cardiac troponin I assays for use in the horse

Tanya M. Rossi, David L. Pearl, W. Glen Pyle, M. Grant Maxie, Peter A. Kavsak, Peter W. Physick-Sheard

Department of Population Medicine (Rossi, Physick-Sheard, Pearl), Department of Biomedical Sciences (Pyle), Ontario Veterinary College, and Animal Health Laboratory, Laboratory Services Division (Maxie), University of Guelph, Guelph, Ontario; and Department of Pathology and Molecular Medicine, McMaster University, Hamilton, Ontario (Kavsack)

Abstract

Human cardiac troponin I (cTnI) assays have been used in equine medicine, often without prior analytical validation for equine use. In the absence of appropriate validation, the clinical significance of assay results is uncertain and can lead to misdiagnosis. Our study followed the American Society for Veterinary Clinical Pathology guidelines and investigated linearity, precision, limit of quantification (LoQ), and comparative recovery for several commercial cTnI assays.

Clinically acceptable linearity was observed in assays A-D, whereas assay E did not detect equine cTnI in any sample. Comparative recovery revealed 1-3 fold differences between assay results, and low analyte recoveries (2.2-3.4%) were observed in assay F. Precision was investigated in assays A and B, and found to be within acceptable limits. LoQ was 1.53 ng/L for assay A, and 0.031 µg/L for assay B. Assays A and B performed within clinically acceptable limits and were deemed suitable for use in equine medicine. Assays C and D did not undergo full validation but had acceptable linearity, which indicates potential as equine laboratory tests. Assays E and F are unsuitable for use in horses given issues with detection of equine cTnI.

The variability in results between assays indicates that reference intervals and cut-offs for diagnostic decision making are assay-specific and should be established prior to adoption by diagnostic laboratories.
CAHLN / RCTLSA 16th Annual Meeting  
Swine Session  
Monday, June 5, 2017  
15:30-16:30  

PAHL Building 89, Room 1810  

Moderator: Jim Fairles

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Sarah Gresch, Benjamin Miller1, Nitipong Homwong, Douglas G. Marthaler | 59   |
| 15:45  | Measuring incidence and prevalence of PRRS in Ontario sow herds.  
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| 16:00  | Near real-time processing, analysis, and reporting of incidence and prevalence of porcine epidemic diarrhea virus and porcine deltacoronavirus in Ontario swine herds  
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| 16:15  | Development of a multiplex molecular detection assay for swine enteric viruses using fluidic bead-based technology  
Dante Mateo, Tokinori Iwamoto, Richard Green, Dan Hurnik, Elizabeth Dobbin, Carmencita Yason | 62   |
Analytical verification and use of a multiplex real time RT-PCR to identify porcine epidemic diarrhea virus, transmissible gastroenteritis virus, and porcine deltacoronavirus

Sarah Gresch, Benjamin Miller1, Nitipong Homwong, Douglas G. Marthaler

University of Minnesota Veterinary Diagnostic Laboratory, St. Paul, MN (Gresch, Marthaler), Department of Animal Science, Kasetsart University, Kamphaeng Saen Campus, Kamphaeng Saen, Nakhon Pathom, Thailand (Homwung)

Abstract

Enteric coronaviruses cause significant economic losses for swine farmers. Three coronaviruses that are prevalent in North America are porcine epidemic diarrhea virus (PEDV), transmissible gastroenteritis virus (TGEV), and porcine deltacoronavirus (PDCoV). To maintain and monitor herd health, swine veterinarians routinely request screening for PEDV, TGEV, and PDCoV by real time RT-PCR (rRT-PCR). Performing multiple rRT-PCRs for these pathogens is time-consuming and labor-intensive. The University of Minnesota (UMN) needed a fast, rRT-PCR to identify and differentiate the 3 pathogens within a single multiplex RT-PCR.

A comparison was performed between QIAGEN’s virotype PEDV/TGEV/PDCoV Reagents with virotype mix 1 + IC, and the UMN’s in-house TGEV and duplex PEDV/ PDCoV rRT-PCR methods. QIAGEN’s new triplex rRT-PCR simultaneously generates results for the 3 different pathogens, reducing the amount of labor associated with PCR preparation compared to an individual rRT-PCR for TGEV and a duplex rRT-PCR for PEDV/PDCoV. The included internal control verifies that each individual PCR reaction is performed appropriately, and the triplex results are available within an hour compared to an hour and half with the in-house rRT-PCR assays, reducing turnaround-time.

Porcine feces/fecal swabs (n = 127), intestines (n = 99), oral fluids (n = 92), and environmental samples (n = 42), totaling 360 samples, were tested in the comparison study. The reproducible limit of detection using the new virotype reagents was 0.32 TCID\(_{50}\) for PEDV, 5.6 \times 10^{-3} TCID\(_{50}\) for TGEV, and 0.50 TCID\(_{50}\) for PDCoV. The amplification efficiency for PEDV, TGEV, and PDCoV targets were 0.9965, 1.0017, and 0.9825, respectively. The diagnostic sensitivity and specificity was 100% for TGEV, but was slightly lower for PDCoV, 91.5% and 98.1%, respectively. PEDV had a diagnostic specificity of 98.6% but had the lowest diagnostic sensitivity of 86.7% due to disagreements of results with oral fluid samples.

Overall, the new multiplex rRT-PCR method provided by QIAGEN proved to be an efficient, convenient, and valid tool for simultaneous PEDV, TGEV, and PDCoV surveillance.
Measuring incidence and prevalence of PRRS in Ontario sow herds

Juliana Bonin Ferreira, Zvonimir Poljak

Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

Porcine reproductive and respiratory syndrome (PRRS) is characterized by severe reproductive losses, increased mortality, respiratory disease, and decreased growth rate. In addition, it is currently the most costly disease for the swine industry and within Canada alone is estimated to cost the industry $130 million per year. Surveillance for PRRSV is complicated because of continuous emergence and transmission of novel field strains, widespread use of attenuated vaccines, and the large number of herds that are under continuous infection control measures. Therefore, the use of molecular tools for PRRSV surveillance is necessary, and the results should be accompanied by relevant clinical and epidemiologic information. Our objective is to set up a low-cost surveillance system that would have broad surveillance coverage, and would allow near real-time data collection and analysis, and dissemination of results.

Baseline data will be collected from 2 major sources: the Ontario PRRS area regional control and elimination (ARC&E) database and farms that are not part of the program. The baseline data will consist of information about participating sites including type of production (farrow-to-finish, farrow-to-wean, farrow-to-grow, herd size, county) and information about current status with respect to PRRS classification. After baseline data collection, weekly reports about new cases and other status changes will be collected. Clinical impact during new outbreaks will be investigated immediately upon notification and 2 months after the start of the outbreak. Selected cases with no clear source of infection will be thoroughly investigated.

Ultimately, weekly incidence of new clinical cases and new infection cases will be produced. Prevalence plots will be produced, and the genetics of the virus and herd demographics will be used to investigate its relative importance for severity of PRRS outbreaks.
Near real-time processing, analysis, and reporting of incidence and prevalence of porcine epidemic diarrhea virus and porcine deltacoronavirus in Ontario swine herds

Toluwalope Ajayi, Zvonimir Poljak, Rozita A. Dara

Department of Population Medicine, Ontario Veterinary College (Ajayi, Poljak), and School of Computer Science (Dara), University of Guelph, Guelph, Ontario

Abstract

Porcine epidemic diarrhea virus (PEDV) and porcine deltacoronavirus (PDCoV) emerged in Canada in early 2014 with most cases detected in Ontario. Since then, provincial veterinary authorities and health organizations have successfully identified the source of the outbreak, reduced incidence, and subsequently started working on PEDV and PDCoV elimination from individual herds and production systems. However, these 2 pathogens remain among the most important viral pathogens in Ontario, and monitoring progress in controlling them at the provincial level is of interest to multiple stakeholders. In addition, given the success of PEDV and PDCoV elimination programs at the herd-level, there is also interest in their complete elimination from the Ontario swine industry. Regardless of the future goal of current disease control programs (DCP), monitoring incidence and prevalence of these 2 pathogens is of high importance for the swine industry. In particular, emphasis is on providing data analysis and information to relevant stakeholders in near-real-time.

Therefore, the objective of this study was to design approaches that allow for efficient calculation of incidence and prevalence of PEDV and PDCoV-infected sites from currently existing sources in near-real-time. The Ontario Swine Health Advisory Board (OSHAB) database was used as the source of data. Database linkage was established through ODBC connectivity, with data processing conducted in R, and final reports indicating weekly number of new cases, as well as the number and proportion of sites in a specific PEDV or PDCoV infection status in a given week. Line and area plots were used to display the disease frequency information through a time-series reporting interface. The reports are run on a weekly basis and allow interactive exploration of disease dynamics.

In brief, incidence and prevalence have been decreasing in each of the 3 subsequent years reaching herd-level prevalence of 1.3% (0.8-2.2%) and 0.2% (0.0-0.6%) in the last week of 2016 for PEDV and PDCoV, respectively. Furthermore, such numbers support the planning of elimination efforts for the 2 pathogens.
Development of a multiplex molecular detection assay for swine enteric viruses using fluidic bead-based technology

Dante Mateo, Tokinori Iwamoto, Richard Green, Dan Hurnik, Elizabeth Dobbin, Carmencita Yason

Regional Diagnostic Virology Services and AVC Diagnostic Services, (Mateo, Iwamoto, Green, Dobbin, Yason), and Department of Health Management, Atlantic Veterinary College, University of Prince Edward Island (Hurnik)

Abstract

Several enteric viral pathogens are known to cause devastating loses in farmed pigs. Rapid and high-throughput detection tools are essential for efficient diagnosis and mitigation of infectious disease outbreaks.

During the CAHLN conference last year, we introduced the use of fluidic-bead based technology (Luminex) for the detection of salmonid pathogens. This technology had been shown to be effective for simultaneous detection of human pathogens in clinical samples. Using the same technology, we have developed a multiplex detection assay capable of detecting 6 swine enteric viruses: porcine epidemic diarrhea virus (PEDV), transmissible gastroenteritis virus (TGEV), porcine deltacoronavirus (PDCoV), porcine rotavirus A (PRVA), porcine rotavirus B (PRVB) and porcine rotavirus C (PRVC).

This assay consists of target specific primer extension (TSPE) on PCR amplified products, followed by hybridization of biotinylated TSPE products to different fluorescent microspheres specifically assigned to each targeted virus. The presence or absence the 6 viruses targeted by the assay is evaluated using MagPix equipment and specialized software (Luminex).

Swine enteric virus isolates and homogenates from different parts of Canada and some isolates from USA were used in the development of the assay. The conserved regions of genes commonly used for molecular testing by veterinary diagnostic laboratories were selected in multiplex assay design. Plasmids containing specific viral inserts were used as positive controls. The assay demonstrated high analytical sensitivity and specificity. The assay detected only targeted pathogens and did not detect unrelated pathogens or blank samples. The diagnostic sensitivity and specificity of the assay is underway.

The assay can be used as low- or high-throughput with potential application to pathogen surveillance in addition to diagnosis. Moreover, there is potential to increase the number of targets to cover genotypes and other enteric pathogens of swine.
Cross-species session
Monday, June 5, 2017
16:30-17:15
PAHL Building 89, Room 1810
Moderator: Nicole Nemeth

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<td>Improving production of high titer lentiviral vectors for in vivo gene therapy applications</td>
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<td><em>Mycobacterium</em> epizootic in a zoo population of Chinese gliding frogs (<em>Rhacophorus dennysi</em>): investigation, management, and public health response</td>
<td>Ellie Milnes, Pauline Delnatte, Kevin May, Jennifer Ma, Frances B Jamieson, Durda Slavic, Dale Smith</td>
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Pathology of wild urban rats

Jamie L. Rothenburger, Chelsea G. Himsworth, Nicole M. Nemeth, Piper M. Treuting, Claire M. Jardine

Department of Pathobiology (Rothenburger, Nemeth, Jardine), Canadian Wildlife Health Cooperative Ontario-Nunavut Region (Rothenburger, Nemeth, Jardine), Ontario Veterinary College, University of Guelph, Guelph, Ontario; School of Population and Public Health, University of British Columbia, Vancouver, British Columbia (Himsworth); Animal Health Centre, British Columbia Ministry of Agriculture, Abbotsford, British Columbia (Himsworth); Canadian Wildlife Health Cooperative British Columbia, Abbotsford, British Columbia (Himsworth); School of Medicine, University of Washington, Seattle, Washington, USA (Treuting).

Abstract

Norway and black rats (*Rattus norvegicus* and *R. rattus*) are considered among the most successful of invasive species, inhabiting cities worldwide. Despite their significant role in zoonotic pathogen transmission, agriculture damage, and as urban pests, remarkably little is known about naturally occurring diseases in urban rats.

The purpose of our study was to describe the gross and microscopic pathology in a population of 725 live-caught urban rats from Vancouver Canada. Gross lesions were present in 111 of 725 (15.3%) of rats. The most frequent histologic lesions included cardiomyopathy, respiratory tract inflammation, esophageal and stomach *Eucoleus* sp. (nematode) infection associated with proliferative and hyperkeratotic gastritis, hepatitis associated with *Capillaria hepatica* infection, and *Trichosomoides crassicauda* infection of the urinary bladder.

Given the severity of microscopic lesions and the frequency of parasitic infection, natural disease may be an important factor contributing to urban rat mortality. There is also the potential that these co-infections/co-morbidities could influence the ecology of zoonotic pathogens carried by rats, which is an area of future investigation.
Improving production of high titer lentiviral vectors for in vivo gene therapy applications

Maria C. Rosales Gerpe, Sarah K. Wootton

Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

Lentiviral vectors (LVs), which are comprised of a self-inactivating genomic backbone, a desired transgene gene, and an envelope (Env) glycoprotein (GP) for pseudotyping, remain attractive tools for in vivo gene delivery given their ability to integrate into the host genome and promote stable transgene expression. A widely used approach is to produce and test vectors in HEK 293T cells using the vesicular stomatitis virus Env (VSV-G), as these pseudotyped virions can enter a wide range of cell types. We have found that this cell line is indeed optimal in the production of LVs, but not necessarily the best tool for evaluating transduction efficiencies of different pseudotyped vectors. In addition, despite being highly efficacious in vitro, VSV-G pseudotyped LVs perform poorly in vivo, particularly in the lungs, because of the absence or low numbers of VSV-G receptors on the apical membrane of the airway epithelium. In contrast, Env GP from viruses such as jaagsiekte sheep retrovirus (JSRV) and enzootic nasal tumor virus (ENTV), which naturally target the apical membrane of the respiratory epithelium, can be used to pseudotype LVs and mediate entry into a variety of mammalian cell lines including OA3T.s and A549s, as well as sheep lung organotypic cultures. Finally, a common method for concentrating LVs after production is ultracentrifugation, but this results in significant loss of infectious virus.

With the aim of optimizing and standardizing production of LVs, we produced LVs pseudotyped with Env GPs from JSRV, ENTV, Zaire Ebola virus, which has been previously shown to be more efficient than VSV-G, and VSV and evaluated 3 methods of concentration: ultracentrifugation, polyethylene glycol (PEG) precipitation, and tangential flow filtration (TFF). In addition, we compared 3 quantification techniques: a reverse transcriptase (RT) activity assay, p24 ELISA, and a transducing units (TU) assay.

In vitro transduction in HEK 293T cells may not accurately reflect the transduction efficiency of a particular pseudotype, and the use of tissue slices, which maintain architecture and polarity, represent a better tool for more accurately evaluating transduction competency of LVs.
**Mycobacterium epizootic in a zoo population of Chinese gliding frogs (Rhacophorus dennysi): investigation, management, and public health response**

Ellie Milnes, Pauline Delnatte, Kevin May, Jennifer Ma, Frances B Jamieson, Durda Slavic, Dale Smith

Toronto Zoo, Scarborough, Ontario (Milnes, Delnatte); Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario (Milnes, Smith); Public Health Ontario, Toronto, Ontario (May, Ma, Jamieson); Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Ontario (Jamieson); Animal Health Laboratory, University of Guelph, Guelph, Ontario (Slavic)

**Abstract**

Mycobacteriosis is a significant cause of morbidity and mortality in captive amphibians. Thus far, only non-tuberculous mycobacteria (NTM) have been identified in amphibians. The most common NTM isolates are *Mycobacterium marinum*, *M. fortuitum*, and *M. xenopi*.

The diagnosis of mycobacteriosis in living amphibians is difficult. Endoscopic examination of the coelomic cavity for gross lesions with collection of biopsy samples is recommended, but may be unrewarding until lesions are advanced enough to be seen grossly, and is technically challenging in many species. The gold standard for diagnosis is a combination of histopathology and culture, with species identification by molecular techniques.

We describe laboratory testing and clinical management of a mycobacterial epizootic in Chinese gliding frogs (*Rhacophorus dennysi*) at the Toronto Zoo. The Public Health Ontario Laboratory found that the mycobacterial isolate from the frogs was identified initially by a commercial line-probe assay as *M. tuberculosis* complex, provoking biosecurity measures and human health concerns. Further molecular testing and 16S sequencing confirmed the species identity as *M. marinum*.

A retrospective review of Toronto Zoo pathology reports for Chinese gliding frogs found that mycobacteria are highly pathogenic in this species, resulting in severe, chronic, multisystemic gross and histologic lesions. Treatment of mycobacteriosis in amphibians is not recommended. Antibiotic therapy carries an unacceptable risk of antibiotic resistance given the lack of established treatment protocols for amphibians, and there is a health risk to animal care staff because of the zoonotic potential of *M. marinum*. 
# Overall Theme: Making best use of laboratory data

## Plenary Session 2

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Technological trends: transforming health data into intelligence

Theresa Bernardo

Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

Emerging technologies have disrupted many sectors (communication, publishing, music, transportation, retail, recruiting, etc.), but have not yet had a profound effect on the health of individuals and populations. We will examine technological trends and their impact on epidemiology, particularly data, research and surveillance, as well as the importance of networks. Data can now be collected or accessed from multiple sources (sensors, social media, images, sound, etc.) that can be combined in unique and unusual ways. Many innovative applications have arisen from disasters (natural or man-made) that have particular relevance for surveillance and response to disease outbreaks. Other combinations of technological advances and delivery models will have implications for laboratorians, such as point-of-care testing. Insights from real-time monitoring and advances in data analytics will support the current shift from disease prevention to wellness promotion for all.

From data to intelligence- AgConnect laboratory data in decision support

Matt Cochran

Institute for Infectious Animal Diseases, Texas A&M University, College Station, TX

Abstract

AgConnect is a concept of technology-enhanced information sharing, data integration, visualization, and decision support for animal agriculture and animal health officials. The concept has been implemented to date through a series of applied research projects and the resultant development of a prototype system. Whether supporting syndromic surveillance, business continuity, or emergency response, laboratory data is a consistently critical element in decision support. The utility of laboratory data is predicated upon fundamental organization and standardization, with laboratories leading the way. These building blocks can then begin transformation into intelligence with application of appropriate context or metadata. The means to this transformation requires application of interfaces that allow data access to both internal and external customers.

The AgConnect prototype has succeeded as a neutral aggregation and integration platform for use by veterinarians, production animal health staff, and animal health regulatory officials. However, success continues to be redefined, and we live in an era of accelerated disease emergence. Disease intelligence today relies heavily on inference made available through correlations and conclusions drawn by trained professionals who have the right data. Disease intelligence tomorrow will likely include pattern recognition and enhanced data packaging, performed by a trained machine.
Asymmetric informatics - lessons from a decade of NAHLN messaging

Michael Martin

Office of the State Veterinarian, Clemson University, South Carolina

Abstract

Laboratory test results are normally communicated to submitting veterinarians, animal health regulators, etc. one case at a time in human-readable reports. Sometimes they are grouped into spreadsheets or other aggregate data packages. But in major animal disease events such as PED in swine and HPAI in poultry, these methods overwhelm the system's capacity for data entry, conversion, and collation. The National Animal Health Laboratory Network’s (NAHLN) laboratory result messaging standard was designed to address that situation.

At the root of the issue is that different laboratories use different names for tests, specimens, etc. and different data formats for their storage and export. Medical (and veterinary) informatics standards have been carefully developed over decades to ensure that disparate systems can "speak a common language." The NAHLN carefully selected leading informatics standards to serve as the core of its messaging protocol. This standard profile has successfully encoded all of the various data types and tests that have been presented over its 13 years in operation.

But the problem with this standardization approach is that very few veterinarians are well versed in the underlying informatics. Early NAHLN efforts at education were met with, at best, mixed success. Even with understanding of the standards, many labs lack the technically skilled staff necessary to implement the transformations and logic necessary to convert local formats into the standards. (Even fewer would be in a position to receive the standardized data from any sender and convert to local terminology.) The NAHLN has struggled with this problem for most of its existence.

The challenge becomes how to benefit from the universal meaning and flexibility of established informatics standards without having to stock every lab with sufficient specialized expertise. The solution takes different forms. These share a common theme of concentrating the informatics expertise in a center of excellence that serves all participants in the data exchange. This can be described as "asymmetric informatics." Some networks concentrate the expertise in the receiving system and accept data in each sender’s native format; converting the data centrally on receipt. Others, including the NAHLN, work out the details for each messaging scenario and provide documentation, training, and support on a scenario-by-scenario, test-by-test basis, thus simplifying the problem for the senders. This requires more technical and content sophistication in the laboratories than the fully centralized model but much less than the symmetric model.

The NAHLN’s experience shows that medical informatics standards can be useful in veterinary laboratory integration. However, it is essential to account for the asymmetry in informatics expertise.
Use of laboratory data for near-real-time disease reporting, prediction, and understanding complex problems

Zvonimir Poljak

Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

Results of laboratory testing are fundamental for making health decisions about individual animals, specific herds, or entire production systems. The fundamental requirement for such data is to be based on an accurate test with good reproducibility. The results of testing based on such assays are fully utilized in the hands of veterinary practitioners who can interpret the data in the context of specific disease and demographic situations, and then make recommendations. This additional information may or may not be a part of laboratory submissions. When aggregated to a suitable level, laboratory data could be utilized further to inform broader audiences and provide additional insight into disease trends, or to improve understanding of disease epidemiology. This data utilization depends on the goal of the analysis, but most critically on the availability and quality of associated epidemiologic information.

The objective herein is to provide an overview of approaches that have been used in our research group to establish near-real-time analysis and disease reporting, disease prediction, and understanding of complex problems using laboratory data. In this overview, approaches to reporting of laboratory submissions; and incidence and prevalence of major endemic swine diseases will be presented. In addition, use of data to address specific questions about disease transmission within and between herds will be discussed, together with assessment of control options.
Veterinary forensic science: new approaches to an old problem

Beverly McEwen

Animal Health Laboratory, Laboratory Services Division, University of Guelph, Guelph, Ontario

Abstract

Animals may be victims, evidence, or perpetrators of a crime. When discovered at scenes of serious crimes against people, animals are often both victim and evidence. Internationally, submissions of animals to veterinary diagnostic laboratories from law enforcement agencies have dramatically increased over the past 15 years. Reasons for this are speculative but factors likely include changes in legislation and mandatory reporting of suspected animal abuse by veterinarians. Yet, animal abuse rarely occurs in isolation - when animals are abused, people are at risk and when people are abused, animals are at risk. Animals may be sentinels for domestic abuse, and cruelty to a pet is a recognized mechanism of psychological control over a partner: no species of animal is immune to these crimes. The link between animal abuse and concurrent or predicted interpersonal violence is well established. But are veterinary diagnosticians ready and capable to address the fundamental assumption for forensic cases that their duty is to the court?

Cases must not only be scientifically credible, but legally credible. Fortunately in the past 10 years, the scientific literature, presentations, conferences, undergraduate and graduate training, and online graduate programs have expanded to meet the growing needs of this subspecialty. Veterinary pathologists in this emerging discipline are in the fortunate position of learning from examples of systemic failings in medical forensic pathology, such as inadequate oversight, training, and certification. They can also benefit from the recent advances in several jurisdictions that have rectified these issues.

Cases submitted to the Animal Health Laboratory by law enforcement agencies for postmortem will be used to illustrate examples of animal cruelty and the context in which they arise.
From mammals and birds to bees: adapting veterinary testing protocols for honey bee testing

Paul Kozak, Patricia Bell-Rogers

Ontario Ministry of Agriculture, Food and Rural Affairs (Kozak), and Animal Health Laboratory, Laboratory Services Division, University of Guelph (Bell-Rogers), Guelph, Ontario

Abstract

The western honey bee (*Apis mellifera*) is a major contributor to the agri-food sector as part of the diverse industry of beekeeping in Ontario. The importance of honey bee health has recently been underscored by well-documented health issues in honey bee populations in North America. The detection of pests and diseases of honey bees has typically been addressed through provincial Apiary Inspectors (Ontario Ministry of Agriculture, Food and Rural Affairs) and the detection and confirmation of symptoms in the field. This approach works relatively well in that there are methods developed for identifying diagnostic symptoms and bioassays to accurately detect levels of pests and diseases in honey bee colonies. In the past, laboratory methods were required to identify pest prevalence and intensity for surveillance and response to honey bee pests and diseases (e.g., tracheal mites). More recently, there is a growing move to detecting pests and diseases using molecular analysis. This has allowed apiculture to leverage the resources and services already available to other sectors of agriculture, while using new tools and approaches to defining the pest and disease status of beekeeping in Ontario.

The University of Guelph, Animal Health Laboratory (AHL) has offered laboratory testing for livestock, pets, and poultry for many years, but recently began offering tests for other food-producing animals. This required that our veterinary testing methodology be adapted for a less traditional specimen type: live honey bees. The AHL collaborated with government (OMAFRA), the Ontario Beekeepers’ Association Technology Transfer Program, and honey bee researchers to design methods and procedures to sample live bees in the field and then developed protocols to process bees for automated nucleic acid extraction.

Currently the AHL has 16 different (7 viruses, 2 fungal pathogens, 3 species of parasitic mites, bacteria, protozoans, and markers for honey bee fitness) molecular-based assays for honeybee pathogens/pests for the detection of the presence or absence and quantifying the levels. The types of testing, applications of the tests, and methods to adapt the process for sampling vertebrates to sampling a species of insect that live in colony units of tens of thousands of individuals will be discussed.
Poultry

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Potential pathogens detected in wild turkeys (Meleagris gallopavo) in Ontario

Amanda MacDonald, Claire Jardine, Jeff Bowman, Evelin Rejman, John Barta, Hugh Cai, Nicole Nemeth

Department of Pathobiology, Ontario Veterinary College (MacDonald, Jardine, Rejman, Barta, Nemeth); Canadian Wildlife Health Cooperative (Jardine); Trent University, Peterborough, Ontario (Bowman); and Animal Health Laboratory, Laboratory Services Division, University of Guelph, Guelph, Ontario (Cai)

Abstract

Wild and domestic turkeys (Meleagris gallopavo) are susceptible to the same pathogens and commonly overlap geographically. In some instances, the 2 groups may have direct contact or access to shared, contaminated substrates. In Ontario, wild turkey populations have re-established following reintroduction in 1984. We sought to determine the prevalence of potential poultry pathogens in wild turkeys in Ontario and determine the distribution of potential disease “hotspots.”

Hunter-harvested wild turkeys (n = 152) from across southern Ontario underwent gross postmortem examination and sampling. Swabs and tissues were tested by pathogen-appropriate tests (e.g., bacterial culture, fecal floats, and PCR). Samples from the majority of wild turkeys tested positive for Mycoplasma spp. (150 of 152; 98.7%), Eimeria spp. (99 of 131; 75.6%), and lymphoproliferative disease virus (LPDV; 101 of 152; 66.4%). Six Mycoplasma spp. were cultured, most commonly M. gallopavonis (147 of 152; 96.7%) and M. gallinaceum (36 of 152; 23.7%) and rarely M. meleagridis (3 of 152; 2.0%), and M. iowae and M. synoviae (each with 1 of 152; 0.7%); 56 turkeys (36.8%) had multi-species Mycoplasma spp. infections. Four Eimeria spp. were detected in a subset of turkeys and fecal oocyst loads were generally low. The most common species was E. meleagris (10 of 11; 82%), followed by E. adenoeides (6 of 11; 54%), E. dispersa (3 of 11; 27%), and E. innocua (1 of 11; 9%); with multi-species infections in over half (6 of 11; 54%). No LPDV-positive turkeys had microscopically-evident lymphoid proliferation in liver, spleen, or bone marrow. Two (1.3%) turkeys had poxviral-associated skin lesions. All turkeys tested negative for avian influenza viruses and Salmonella spp.

Wild turkeys that tested positive for potential poultry pathogens were widely scattered across southern Ontario. Apparently healthy wild turkeys commonly shed various potential poultry pathogens. Sources of infection in wild turkeys are unknown, but could be from contact with contaminated substrates in the environment (e.g., bedding, carcasses). Disease transmission from wild to domestic turkeys may be less likely given low parasite burdens (e.g., Eimeria spp.) or non-pathogenic species (e.g., Mycoplasma spp.). Continued vigilance for morbidity and mortality in wild turkeys, as well as consideration of strategies to reduce contact between poultry and wild turkeys as well as potentially contaminated substrates in the environment, is needed.
Mycoplasma synoviae in domestic meat-type geese

Marina Brash, Alexandra Reid

Animal Health Laboratory, Laboratory Services Division, University of Guelph (Brash); and Veterinary Inspection and Audit Unit, Food Inspection Branch, Ontario Ministry of Agriculture, Food and Rural Affairs (Reid), Guelph, Ontario

Abstract

Approximately 2,000 12-wk-old geese were presented for slaughter at an Ontario abattoir July 14 2016, and there were elevated condemnations for extensive airsacculitis, purple discoloration of carcasses, and inadequate bleed-out, but bodies were generally in good body condition. Birds did not display clinical signs on antemortem inspection. Aspergillosis was suspected with a history of being raised on straw and some partially processed frozen carcasses were submitted to the Animal Health Laboratory for diagnosis July 19. Submitted geese had tracheal exudate, moderate pulmonary congestion and edema, and mild airsacculitis. Geese were tested for avian paramyxovirus and avian influenza virus by PCR, and tissues submitted for mycoplasma and fungal culture, as well as histopathology.

Lesions in submitted geese were judged to be less severe than photographs from the abattoir as well as most airsacs were removed. More typical intact carcasses were submitted in a subsequent lot on July 22 and again had tracheitis, bronchopneumonia, and marked chronic serofibrinous airsacculitis, and samples were collected for repeat testing. Subsequent shipments from this same flock continued to have elevated condemnations with similar postmortem findings throughout July and August.

Geese owned by this producer were housed in several multi-age barns on one premises, and cohorts were sent to slaughter 2 days a week over 2 weeks. A private veterinarian was contacted and treatment with antibiotics was initiated. Given high condemnations again after the medication withdrawal period was met, a third submission was made from a different cohort on August 17. Affected geese again had chronic serofibrinous airsacculitis. Meanwhile, mycoplasma culture results from the pooled tracheas from the first submission had been reported and were positive for Mycoplasma synoviae. Airsac swabs and lung from all 3 lots were then retested for M. synoviae by PCR, and all samples from all lots were PCR-positive. M. synoviae is an unusual finding in geese not raised on mixed-species poultry premises.
Using phylogenetic analysis to examine the changing strains of infectious bronchitis virus infections in Ontario over time

Emily Martin, Marina Brash, Margaret Stalker, Davor Ojkic

Animal Health Laboratory, Laboratory Services Division, University of Guelph, Guelph, Ontario

Abstract

Historically, Ontario poultry flocks have experienced sporadic outbreaks of infectious bronchitis virus (IBV) infections characterized by both respiratory and renal disease outbreaks in broilers, and egg production issues in egg-laying flocks. Prior to 2002, a few of the strains were genotyped and were found to be related to IBVs circulating in the USA.

In 2012 and 2013, increasing numbers of IBV cases, involving broilers, layers, and broiler breeders, were reported, and clinical presentations included similar signs of respiratory and renal disease, spikes in mortality, and drops in egg production. We conducted a more comprehensive analysis of the IBV isolates submitted to the Animal Health Laboratory. In addition to the continued presence of the US variant-like IBV strains, strain 4/91 was identified. This strain was previously only identified in Europe, Asia, and South America, and emerged as the predominant strain in Ontario affecting all of the commercial commodity groups. In 2014, the number of AHL submissions decreased, only to start to climb again in 2015 and 2016.

We genotyped the IBV samples from 2014 to the present in order to identify the predominant IBV strains, to compare these genotypes with the previous genotyping data to determine if there is continued shifting of the predominant strains over time, and to determine if there is an association between particular IBV strains and disease processes in the various chicken production groups.

Mapping of the Ontario IBV outbreak

Alexander Heim

Ontario Ministry of Food, Agriculture, and Rural Affairs

Abstract

A pilot project was conducted to highlight the benefit of the Animal Health Lab's collection of premises identification (PID) numbers on lab submissions. Six veterinarians opted to participate in providing data on positive lab submissions. Positive samples that were associated with PIDs and were mapped according to lower-tier municipality level, facilitated analysis of disease progression while maintaining client anonymity.
Infectious bronchitis virus: practical experience from broiler breeders in Ontario

Rachel Ouckama, Fernando Salgado-Beirman

Maple Lodge Hatcheries Ltd., Port Hope, Ontario

Abstract

Among broiler-breeder producers, infectious bronchitis virus is a genuine and current concern. Effects have ranged from “textbook” signs, to devastating production drops, to frustrating continuous low-grade mortality. Recently, IBV-positive cases have been associated with fertility issues, and low-grade spikes in mortality. Theoretically, with good biosecurity this virus should be easily eliminated from a premises. However, this is not always the case. Although often considered a fragile virus, IBV can persist on farms, especially on farms with multiple flocks.

This talk will focus on 3 important practical aspects of dealing with IBV in the field; IBV survival in the barn, best management practices relevant to IBV biosecurity, and lastly case studies so that we can learn from our mistakes.
Ontario small poultry flock disease surveillance: year one

Leonardo Susta, Nancy Brochu, Marina Brash, Csaba Varga, Michele Guerin

Department of Pathobiology (Susta, Brochu), and Department of Population Medicine (Guerin), Ontario Veterinary College, and Animal Health Laboratory, Laboratory Services Division, University of Guelph (Brash); and Ontario Ministry of Agriculture, Food and Rural Affairs (Varga), Guelph, Ontario

Abstract

Although the number of small poultry flocks has markedly increased over the past few years in Ontario, few data are available regarding disease prevalence in these flocks. Because of limited biosecurity and contact with wild birds, these flocks may act as potential reservoirs of avian and zoonotic pathogens.

To assess the health status and the prevalence of infectious agents in small flocks throughout Ontario, a prospective surveillance study was established for small flock postmortem submissions to the Animal Health Laboratory (AHL), over a 2-year period (October 1, 2015 – September 30, 2017). To participate, flocks must reside in Ontario and meet the criteria for a non-commercial, non-quota flock (<300 broilers, <100 layers, <50 turkeys, <300 waterfowl or game birds). Upon the owner’s consent and completion of a standardized questionnaire concerning husbandry and biosecurity, a full postmortem examination, as well as a pre-set array of tests for infectious agents, is conducted at a discounted fee.

During the first year, 65 submissions, totaling 97 birds, were presented to the AHL. Chickens were most common (85% of submissions, of which layers and broilers represented 40 and 22%), followed by turkeys (6%), game birds (6%), and ducks (3%). The most common etiology for illness and/or death was bacterial (26% of birds), viral (19%, including Marek’s disease [10%]), neoplastic (12%), parasitic (11%), and idiopathic inflammatory (11%). Pre-set microbiologic tests (conducted on all submissions) showed that Campylobacter spp., Brachyspira spp., Mycoplasma synoviae, Mycoplasma gallisepticum, and Salmonella spp. were isolated in 41, 32, 25, 18, and 2% of birds. Infectious bronchitis virus, fowl adenovirus, and infectious laryngotracheitis virus were detected in 31, 31, and 12% of birds. Newcastle disease virus (vaccine strain) was isolated from 2 chickens, and avian influenza virus from one turkey (H10N8, LPAIV).

Results of this study will be used to establish a baseline for the prevalence of infectious diseases of Ontario small poultry flocks. Through the questionnaires, we aim to link specific management practices to disease prevalence. Ultimately, the findings from this study will aid in the prevention, control, and surveillance of relevant diseases among Ontario’s small poultry flocks.
Evaluating virulence genes and antimicrobial susceptibility of avian pathogenic *Escherichia coli* from Ontario broiler and broiler-breeder flocks

**Csaba Varga,** Marina Brash, Emily Martin, Rachel Ouckama, Mike Petrik, Cynthia Philippe, Alex Weisz, Elizabeth Black, Shahbaz Ul Haq, Mike Joyce, Kathleen Long, Joanne Rafuse, Lloyd Weber, Melanie Barham, Durda Slavic, Tim Pasma, Patrick Boerlin, Michele Guerin

Ontario Ministry of Agriculture, Food and Rural Affairs (Varga); Animal Health Laboratory, Laboratory Services Division, University of Guelph (Brash, Martin, Barham); Maple Lodge Hatcheries, Port Hope, Ontario (Ouckama); McKinley Hatchery, St. Mary's, Ontario (Petrik); Hendrix Genetics, Kitchener, Ontario (Philippe); Smith and Weisz Poultry Veterinary Services, Guelph, Ontario (Weisz); Elfrida Poultry Diagnostic Services, Caledonia, Ontario (Black); Lakeside Poultry Veterinary Services, Stratford, Ontario (Ul Haq); Joyce Veterinary Services, Hillsburgh, Ontario, (Joyce); Maple Leaf Foods, New Hamburg, Ontario (Long); Zorra Veterinary Services, Thamesford, Ontario (Rafuse); Guelph Poultry Veterinary Services, Guelph, Ontario (Weber); Department of Pathobiology (Boerlin) and Department of Population Medicine (Guerin), Ontario Veterinary College, University of Guelph, Guelph, Ontario.

**Abstract**

Avian pathogenic *Escherichia coli* (APEC), a subgroup of extra-intestinal pathogenic *E. coli*, cause diseases in poultry collectively named 'colibacillosis'. In broiler chickens, the most common lesions observed on gross postmortem include airsacculitis, pericarditis, perihepatitis, and cellulitis. Colibacillosis causes high morbidity and mortality in broiler chicken flocks, leading to extensive economic losses.

In Ontario, the Ontario Animal Health Network (Poultry) reports, based on practitioner clinical impressions, note that early systemic bacterial infection in chickens <14 days of age is very common; *E. coli* is the predominant bacterium isolated, with flock mortality ranging from 1.0% (normal) to as high as 15%. Similarly, in broiler chickens >14 days of age, late systemic bacterial infection caused by *E. coli* is the most common diagnosis. Previous research studies have identified correlations between antimicrobial resistance patterns and virulence genes.

There have been no studies conducted in Ontario evaluating the virulence genes and antimicrobial resistance patterns of avian pathogenic *E. coli* (APEC) strains in broiler and broiler-breeder flocks. In total, 331 clinical cases of broiler and broiler-breeder chickens with a high suspicion of colibacillosis were submitted by 8 Ontario poultry veterinarians to the Animal Health Laboratory between January 1 and December 31, 2016. Preliminary antimicrobial susceptibility testing shows that 56.8% were resistant to tetracycline, 50.2% were resistant to gentamicin, 45.6% were resistant to spectinomycin, and 44.4% were resistant to ampicillin. The top 4 virulence genes identified were: *sitA*, *iss*, *iroN*, and *iutA*.

Our study provides a benchmark from which to measure changes in the antimicrobial susceptibility and virulence gene patterns, and will offer critical information for treatment or prevention of colibacillosis in broilers and broiler breeders.
Antimicrobial resistance to extended-spectrum cephalosporins in *Enterobacteriaceae* from chickens and pigs in Canada

Pauline Zhang, Richard J. Reid-Smith, Durda Slavic, Anne E. Deckert, Patrick Boerlin

Department of Pathobiology (Zhang, Reid-Smith, Boerlin) and Department of Population Medicine (Reid-Smith, Deckert), Ontario Veterinary College; Animal Health Laboratory, Laboratory Services Division (Slavic), University of Guelph, Guelph, Ontario; and Centre for Food-borne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada, Guelph, Ontario (Reid-Smith, Deckert).

Abstract

Resistance to the critically important extended-spectrum cephalosporins (ESCs) in *Enterobacteriaceae* from animals needs to be further investigated. Antimicrobial resistance studies on this family have mainly focused on *Escherichia coli* and *Salmonella enterica*, but the role of other members of *Enterobacteriaceae* in ESC resistance epidemiology is almost unknown. This project aims to determine the diversity and spread of ESC resistance genes in *Enterobacteriaceae* species from broiler chickens and pigs in Southern Ontario, Canada, as well as to compare ESC resistance genes between their fecal and clinical isolates. To accomplish this, ESC-resistant *Enterobacteriaceae* were isolated from chicken and pig cecal samples using ESC-containing enrichment cultures and chromogenic selective agar. The cecal samples were collected by the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) from chickens and pigs in abattoirs in Ontario from November 2015 to November 2016. In addition, clinical isolates from chickens (*n* = 242) and pigs (*n* = 50) were collected from the Animal Health Laboratory from November 2015 to October 2016. All ESC-resistant cecal isolates from enrichment (*n* = 641) and clinical isolates (*n* = 355) were identified with MALDI-TOF mass spectrometry and ESC resistance was confirmed by Kirby-Bauer disk diffusion.

Overall, ESC-resistant *Enterobacteriaceae* was found in 98.3% (*n* = 238) of chicken cecal samples and in 74% (*n* = 37) of porcine cecal samples. Of these ESC-resistant isolates from enrichment, 90.4% (*n* = 501) of 554 chicken isolates are suspected AmpC producers and 7.6% (*n* = 42) are suspected ESBL producers. For the porcine ESC-resistant isolates, 74.3% (*n* = 65) of 87 isolates are suspected AmpC producers and 25.6% (*n* = 22) are suspected ESBL producers. In the clinical isolates, 35 of 235 (14.1%) were ESC-resistant for chickens and 6 of 120 (5.0%) were ESC-resistant for pigs.

Overall, there is a relatively low prevalence of ESC-resistance in clinical chicken and pig isolates. The results also suggest that there is frequent carriage of ESC-resistant *Enterobacteriaceae* in chickens and pigs in Ontario. In comparison to routine surveillance of ESC resistance performed by CIPARS, selective enrichment techniques are not used and it was found that there were low levels of ESC resistance. This indicates that ESC-resistant *Enterobacteriaceae* are only present in low concentrations in chickens and pigs.
CgFARAD: Knowledge transfer research update

Ron Johnson, Patricia Dowling, Saad Enouri

Ontario Veterinary College, University of Guelph, Guelph, Ontario (Johnson, Enouri); Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan (Dowling)

Abstract

The Canadian Global Food Animal Residue Avoidance Databank (CgFARAD) is a University-based clinical pharmacology internet web service that assists veterinarians with withdrawal periods when veterinary approved drugs are used extra-label in food-producing animals. CgFARAD receives over 2,500 requests per year from licensed veterinarians in Canada. The majority of requests are related to extra-label drug use in poultry and come from Ontario. However, requests are received across all major species and most minor species.

The CgFARAD continues to conduct relevant food safety research, including tissue depletion studies, pharmacokinetic studies, and metabolism research that assists stakeholders with mitigating risks of violative drug residues in the human food chain.

CgFARAD has recently benefited from a Growing Forward 2 grant that was secured by the Livestock Research Innovation Corporation (Guelph, ON) to i) re-tool and expand the capability of our internet website and database that is housed at the University of Saskatchewan, ii) and to establish a state of the art tissue culture suite in the Department of Biomedical Sciences at OVC.
Use of hock flexion resistance as a means of identifying dead-on-arrivals (DOAs) at shackling in an end-of-lay hen slaughter line gas stunning system - shackling line worker evaluation

Rachel Ouckama, Fernando Salgado-Bierman, Michele Guerin, and Marina Brash

Maple Lodge Farms Ltd., Brampton, Ontario (Ouckama, Salgado-Bierman); Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario (Guerin); Animal Health Laboratory, University of Guelph, Guelph, Ontario (Brash)

Abstract

This longitudinal laboratory study of euthanized fowl evaluated the degree of hock stiffness and wing position as parameters that could be used to reliably differentiate unconscious fowl from dead-on-arrivals immediately after controlled atmosphere stunning. Using a gram-force gauge, it was demonstrated that measurable resistance to hock flexion to the point of activation of the perch reflex develops rapidly after death and consistently increased over time, plateauing at 90 min. In addition, wing position of birds held upside down changed with increasing time post mortem; the more time elapsed from the point of death, the tighter the wings were held to the body. From this we hypothesize that dead birds can be readily distinguished from stunned birds based on hock resistance.

A second study was done to determine the minimum detection threshold of hock flexion resistance for employees on a shackle line to differentiate between DOAs and stunned birds. It was determined that a minimum detection threshold was a 300 gf for hock stiffness. Half of the birds crossed this threshold by 5 min post mortem, and all birds in the study population had crossed it by 21 min post mortem.

We conclude that the development of palpable hock joint stiffness is sufficiently rapid to be useful as a reliable means of differentiating between hens unconscious after CO2 gas stunning from hens that died during transport. Wing position can be used as a reliable secondary assessment as the bird is lifted to the shackle line.
Nutritional strategies for enhancing gut function in broiler chickens challenged with coccidiosis

Elijah Kiarie, Emily Kim, Haley Leung, John Barta

Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario

Abstract

Nutritionists perceive a dysfunctional gastrointestinal tract as a potential rate-limiting factor in the survival and productivity of poultry. This perception has been fostered by the emergence of ideas and concepts concerning the development and function of the digestive tract in light of advances in genetic improvement and restriction on the use of antibiotic growth promoters and anti-coccidial drugs. *Eimeria* species, the causative agents of coccidiosis, account for major economic losses in commercial poultry rearing as a result of increased mortality and morbidity linked to gut damage, resulting in impaired gut barrier function, nutrient digestion and absorption, and increased risk of bacterial infections, particularly necrotic enteritis.

Concerns over the development of *Eimeria* species resistant to existing anti-coccidial drugs and restrictive use of antibiotics to control secondary bacterial infections is making it imperative to explore alternative strategies for maintaining intestinal functionality. Numerous feed additives are claimed to attenuate or remedy structural and functional gut damage occasioned by coccidiosis. Our research has focused on testing efficacy of epidermal growth factor and yeast product rich in nucleotides in young broiler chickens subjected to *Eimeria* challenge. Epidermal growth factor (EGF) is a mitogenic and anti-apoptotic protein that elicits a broad range of bio-activities on the intestinal epithelium, including the stimulation of cellular proliferation, differentiation, and intestinal maturation. Nucleotides are the building blocks of DNA and RNA molecules and are involved in structural, metabolic, energetic, and regulatory functions at the cellular level. Our general hypothesis is that feeding these additives will promote gastrointestinal development in chicks and reduce the negative effects of *Eimeria* challenge on growth performance and indices of gut health and function.

We recently completed 2 independent experiments testing these additives in broilers orally challenged with *E. acervulina*, *E. maxima*, and *E. tenella* culture mixture. There was no interaction (*p > 0.05*) between yeast and *Eimeria* challenge on lesion scores, oocyte shedding, and growth performance. *Eimeria*-challenged birds had (*p < 0.05*) a high level of lesion scores, high oocyte shedding, reduced growth performance, as well as significant structural and functional intestinal damage. There was an interaction (*p < 0.05*) between EGF and *Eimeria* on indices of gut function such that EGF improved expression of genes for digestive enzymes, nutrient transporters, and tight junction proteins in *Eimeria*-challenged birds while there was no effect in non-challenged controls. Birds fed yeast showed better body weight (+7.6%, *p = 0.04*) and a trend on FCR (-15%, *p = 0.08*) independent of *Eimeria* challenge. Measurements of intestinal function in broilers fed yeast are under investigation.

From these preliminary observations, *Eimeria*-challenge reduced growth performance and impaired gut function; the lack of EGF or yeast effects on lesion scores and oocyte shedding suggests that these additives have negligible effects in attenuating *Eimeria* invasion of the intestinal tissues to complete its life cycle. However, feeding EGF showed beneficial effects on improved indices of gut function upon *Eimeria* challenge, and yeast supported growth performance irrespective of *Eimeria* challenge. Collectively suggesting these additives could complement other solutions to maintain intestinal function and bolster growth performance in broilers challenged with *Eimeria*. 


Oral administration of PLGA-encapsulated CpG ODN and Campylobacter jejuni lysate reduces cecal colonization by C. jejuni in chickens

Khaled Taha-abdelaziz, Douglas Hodgins, Tamiru Alkie, Wanderely Quinteiro-Filho, Alex Yitbarek, Jake Astill, Shayan Sharif

Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario (Taha-abdelaziz, Hodgins, Alkie, Quinteiro-Filho, Yitbarek, Astill, Sharif); and Pathology Department, Faculty of Veterinary Medicine, Beni-Suef University, Al Shamlah, Beni-Suef, Egypt (Taha-abdelaziz)

Abstract

Campylobacter jejuni (C. jejuni) is a major cause of bacterial food-borne illness in humans. It is considered a commensal organism of the chicken gut, and infected chickens serve as a reservoir and shed bacteria throughout their lifespan. Contaminated poultry products are considered to be the main source of infection in humans. Therefore, to reduce the risk of human campylobacteriosis, it is essential to reduce the bacterial load in poultry products.

Our study evaluated the protective effects of soluble and poly (D, L-lactic-co-glycolic acid) (PLGA)-encapsulated CpG ODN, an innate immune system stimulator, as well as C. jejuni lysate as a multi-antigen vaccine against colonization with C. jejuni. The results revealed that PLGA encapsulation enhances the ability of CpG ODN to reduce cecal C. jejuni colonization in both layer and broiler chickens when delivered orally. Encapsulated CpG ODN significantly reduced C. jejuni colonization by 1.89 log_{10} and 1.46 log_{10} in layer and broiler chickens, respectively. Similar patterns were observed with respect to C. jejuni lysate; oral administration of C. jejuni lysate reduced the intestinal burden of C. jejuni in layer and broiler chickens by 2.24 log_{10} and 2.14 log_{10}, respectively. Moreover, the combination of encapsulated CpG ODN and C. jejuni lysate synergistically reduced cecal C. jejuni colonization by 2.42 log_{10}.

These findings suggest that PLGA-encapsulated CpG ODN could be a promising strategy for control of C. jejuni in chickens. Furthermore, the combination of encapsulated CpG ODN and C. jejuni lysate is potentially promising as an oral vaccine to protect against C. jejuni.
CAHLN / RCTLSA 16th Annual Meeting
Health Management of Laboratorians
Tuesday, June 6, 2017
13:30-17:00

Building 89 PAHL, Room 1800

Moderator: Melanie Barham

**Health management of laboratorians**

13:30 Navigating and leading change in a professional environment  
_Evelina Rog_  

14:30 Intake of Laboratory submissions during a disease outbreak – the trials and tribulations and the need to upgrade our “new” facility  
_Jim Fairles_  

14:45-15:15 HEALTH BREAK, TRADE SHOW, POSTER VIEWING AND NETWORKING

15:15 Veterinary mental health  
_Colleen Best_  

15:45 Mental health in the workplace: practical tools to recognize issues and help colleagues  
_Dianna Chinnery_  

16:15 Injury prevention and return to work post injury for desk- and lab-based work  
_Andrew Stolfi_  

16:45 Ergonomics  
_Stacey Speagle_  

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Navigating and leading change in a professional environment

Evelina Rog

Human Resources-Learning and Development, University of Guelph

Notes

Intake of laboratory submissions during a disease outbreak – trials and tribulations and the need to upgrade our “new” facility

Jim Fairles

Animal Health Laboratory, Laboratory Services Division, University of Guelph, Guelph, Ontario

Abstract

One of the missions of a provincial diagnostic laboratory is to assist veterinarians, industry, and especially the provincial and federal governments in disease outbreak testing. To be able to do that, laboratories need to have the infrastructure and material and human resources in place.

The Animal Health Laboratory, with the assistance of industry, University of Guelph, and the provincial and federal governments, is able to provide all of these attributes for diagnostic testing http://www.uoguelph.ca/news/2008/05/_new_facility_w.html

Although the AHL participates in many disease outbreak simulations, it was not until the outbreak of porcine epidemic diarrhea in January 2014 when deficiencies in biosecurity and biocontainment were noted in the intake of PEDV-suspect samples. Clients and AHL staff where able to cross paths leading to potential breaches in biosecurity. Although interim precautions were put in place, we realized that an upgrade to the specimen reception space was necessary from both a biocontainment and sample flow aspect. This alteration restricted sample handling to one area of the lab which aided in cleaning and disinfection after handling potentially contaminated samples. A monitoring program was also put in place to assess the cleaning and disinfection process.

Besides altering the specimen reception space, an alternative entry point for outbreak samples into the containment level 2+ laboratory space at the AHL was initiated, which aided in intake of specimens in subsequent avian influenza outbreaks.

Lessons learned from these outbreak situations have allowed the tweaking of intake SOPs to further refine biosecurity and biocontainment procedures. This aids both regular submission intake as well as intake in outbreak situations.
Veterinary mental health

Colleen Best

Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON

Notes

Mental health in the workplace: practical tools to recognize issues and help colleagues

Dianna Chinnery

Counselling Services, University of Guelph

Notes

Injury prevention and return to work post injury for desk and lab-based work

Andrew Stolfi

Eramosa Physiotherapy Associates, University of Guelph

Notes

Ergonomics

Stacey Speagle

Human Resources-Occupational Health and Wellness, University of Guelph

Notes
## National surveillance update, AMR, cross-species

**Wednesday, June 7**
8:30 – 10:00

Building 89 PAHL, Room 1800

Moderator: Dale Godson

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Development of innovative surveillance methods with the Community for Emerging and Zoonotic Diseases

Andrea Osborn, Harry Gardiner, Zana Dukadzinac, Archie Stewart, Ruth Tecle-Mariam

Canadian Food Inspection Agency, Ottawa, Ontario

Abstract

The Community for Emerging and Zoonotic Diseases (CEZD) is a virtual network that integrates today's automated information-mining tools with human-based multidisciplinary analytical capability. The automated technology collects and filters disease signals and the expertise from within the community analyzes and disseminates intelligence information related to zoonotic and emerging infectious diseases from both open and traditional information sources. This virtual network was developed to support Canada's animal early warning, preparedness, and response capability needs regarding emerging and zoonotic diseases.

The CEZD project phase occurred in 2013-16 and it is currently in a 2-year implementation phase. The main objective is to produce early warning intelligence and analyses, and create linkages across the country to provide early warning of ongoing events internationally and domestically. The community membership now exceeds 100 individuals representing animal health specialists, epidemiologists, public health veterinarians, the Provincial and Federal Governments, academia, and multiple industry organizations.

The processes, challenges, successes, and lessons learned in the creation of the CEZD will be described. The goals for the second year of CEZD implementation will be presented, including potential methods to further develop the domestic and international intelligence generation capabilities of the community.
The Canadian Animal Health Surveillance System achievements and opportunities

Andrea Osborn, Cheryl James, Keith Murch, Francois Bedard

Animal Health Science Directorate, Canadian Food Inspection Agency (Osborn, James, Murch) Animal Industry Division, Agriculture and Agrifood Canada (Bedard)

Abstract

The Canadian Animal Health Surveillance System (CAHSS) is an initiative of the National Farmed Animal Health and Welfare Council (NFAHWC). It is a network of networks whose purpose is to work towards more “effective, responsive and integrated animal health surveillance in Canada”. CAHSS is a collaboration of industry, provincial and federal partners in animal and public health surveillance; it covers diseases and issues of importance to the network groups. CAHSS is intended to fill the need for strengthened animal health surveillance in Canada.

Sectors represented in CAHSS now include swine, poultry, equine, dairy cattle, emerging diseases, and an ad-hoc group on antimicrobial use. The initial stages of discussions on surveillance needs in beef cattle and wildlife are underway. New network groups are welcome, and encouraged to join to strengthen their existing networks and create inter-linkages between the various sectors. Current progress of the network, including the development of several tangible project proposals to advance surveillance, will be shared.

The CAHSS website (www.cahss.ca) has received a significant upgrade since its establishment in 2016. In addition to a compilation of surveillance activities in Canada, and private sites for network groups to exchange information, a searchable contact list now exists so that members can locate expertise and colleagues within the network. Network groups are encouraged to use the website to share information both publically and privately. An “alert” function has been added so that members can be notified when an event of interest occurs.

The challenges, lessons learned, and successes in the development of CAHSS will be described. Goals for 2017 include continued building of network groups, encouraging linkages among network groups, and implementation of project proposals leading to concrete benefits to stakeholders.
Routine antimicrobial susceptibility testing data generated by a public animal health diagnostic laboratory: challenges and opportunities to antimicrobial resistance surveillance

Anatoliy Trokhymchuk, Musangu Ngeleka

Disease Surveillance Veterinarian (Trokhymchuk), Veterinary Microbiologist (Ngeleka), Prairie Diagnostic Services, Saskatoon, Saskatchewan

Abstract

Prairie Diagnostic Services has established a dedicated antimicrobial susceptibility testing and antimicrobial resistance surveillance unit. We have invested in equipment and personnel to enhance our capacity of helping the key stakeholders, especially Western Canadian animal agriculture and animal health industries in making prudent decisions on antimicrobial usage. Antimicrobial susceptibility data are routinely generated on a daily basis to answer direct diagnostic questions, however, there is also great potential value in accessing this large dataset for the purposes of antimicrobial resistance surveillance.

We have introduced a practice of yearly antimicrobial susceptibility data summary compilation taking our regional human health hospital data analysis template as a base. This experience highlighted a number of challenges ranging from data quality to methods of analysis, interpretation criteria, and actual practical usefulness of the derived information.

We have also partnered with the Kansas State Veterinary Diagnostic Laboratory (KSVDL) and working directly with the KSVDL Microbial Surveillance Laboratory on development and validation of antimicrobial susceptibility testing methods better suited for both routine diagnostic work and antimicrobial resistance surveillance. Close collaboration with a trend-setting team required a steep learning curve and created some “lessons learned”.

Technological advances are fast-paced - tremendous turnaround time reduction and significant cost drop of whole genome sequencing generated specific interest of both national (Canadian Antimicrobial Resistance Surveillance System (CARSS)) and American (National Antimicrobial Resistance Monitoring System (NARMS)) federal programs in exploring these methods for the purposes of antimicrobial resistance surveillance. There might be merit in investigating practicality and opportunities for animal health diagnostic laboratories in adopting these new technologies for antimicrobial susceptibility testing as well.
Passive tick surveillance in New Brunswick: translating data into information and intelligence

James P. Goltz, L. Robbin Lindsay

New Brunswick Provincial Veterinary Laboratory, Department of Agriculture, Aquaculture and Fisheries, Fredericton, New Brunswick (Goltz); and Field Studies, Zoonotic Diseases and Special Pathogens, National Microbiology Laboratory, Winnipeg, Manitoba (Lindsay)

Abstract

The New Brunswick Provincial Veterinary Laboratory has been collaborating on passive tick surveillance and tick research with Dr. L. Robbin Lindsay at the National Microbiology Laboratory since 1998. Tick samples submitted by veterinarians, human hospital laboratories, physicians, and other sources in New Brunswick are forwarded to the National Microbiology Laboratory for identification or confirmation of the identification, and testing for relevant tick-borne pathogens. The National Microbiology Laboratory compiles the tick and pathogen data into its national database.

Compilation and analysis of the New Brunswick records from this database have helped ascertain which tick species occur in the province, where various tick species have been found and have become established, which pathogens they carry, and when and where they pose the greatest risks to susceptible human and animal hosts. For example, tick populations are likely to have become established at geographic sites where multiple ticks have been found on the same host species within a period of a few days, where tick nymphs and larvae have been found, and where ticks have been found repeatedly in subsequent years. At sites where ticks have become established, tick-borne pathogens often have a greater prevalence than elsewhere, at least initially. Peak submissions of adult blacklegged ticks (*Ixodes scapularis*) and lone star ticks (*Amblyomma americanum*) occur in a biphasic pattern, in May-June and October-November, whereas peak submissions of American dog ticks (*Dermacentor variabilis*) occur during the summer months.

Information from the national tick database continues to help steer research efforts, inform professionals and the public, and manage risks.
Evaluation of real-time PCR reagents for the identification of influenza virus RNA

Kristin Mesires, Wendy Witbeck, Lisa Gow, Felipe Navaro, Valerie Leathers, Michael Angelichio

IDEXX Laboratories, Westbrook, ME, USA

Abstract

Influenza A virus has proven to be a highly successful pathogen, able to infect a wide range of hosts from swine, avian, and canine, as well as humans. Rapid detection is usually in the form of virus isolation/detection or real-time polymerase chain reaction (PCR). While real-time PCR has offered significant advantages over end-point PCR, commercial real-time PCR assays still use a set of reagents, or “kit”, designed for testing a precise number of samples for a specific target(s). This approach often requires a separate testing protocol for each target, increasing time to results and hands-on time for laboratories.

IDEXX has developed real-time PCR reagents for the identification of influenza A viral RNA. The RealPCR Influenza A RNA Mix includes primers and probe for an RNA internal positive control (RNA-IPC) to monitor for proper nucleic acid extraction and inhibitors that may be present in the reaction. To date, 217 samples consisting of 18 different hemagglutinin / neuraminidase subtypes sourced from 3 different host species (swine, avian, and canine) have been tested.

Results from internal studies suggest the identification of influenza A viral RNA to be highly sensitive and specific when compared to a commercial reference test. The RealPCR Influenza A RNA Mix has been designed to work with the IDEXX RealPCR platform reagents, thus utilizing the same RT-qPCR protocol, a common positive control, and the same RNA master mix used by other RealPCR RNA reagents.
Overview of the Ontario Animal Health Network swine surveillance network to improve disease emergency preparedness and its linkage to the Canadian Swine Health Intelligence Network

Christa Arsenault, Grant Maxie, Paul Innes, George Charbonneau, Chris Byra

Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, Ontario, Canada (Arsenault, Innes), Animal Health Laboratory, University of Guelph, Ontario, Canada (Maxie), Canadian Swine Health Intelligence Network (Byra)

Abstract

In Ontario, a swine health surveillance network has been created forming a piece of the Ontario Animal Health Network (OAHN). The purpose of this network is to provide a communications platform to routinely discuss topics concerning swine health and welfare as well as to collect and interpret laboratory data, condemnation data, and clinical impressions data filled out by practising swine veterinarians within Ontario. The swine health surveillance network consists of veterinarians from private practice, the Ontario Ministry of Agriculture, Food and Rural Affairs (OMAFRA), the Animal Health Laboratory (AHL) in Guelph, the Ontario Veterinary College (OVC), and associated Ontario swine industry representatives. The formation of this network has allowed for building both relationships and trust, and practitioner involvement and expertise are critical to its success. Objectives are to obtain a current picture of diseases that are affecting Ontario swine herds while always being on the look-out for new and emerging disease threats, leading to a strong Ontario disease surveillance system.

In the case of a swine disease outbreak, the swine network may be called upon to help provide technical and practical advice. Quarterly network teleconferences include discussions of external disease threats to Canada to aid with preparation for new and emerging animal health issues (e.g. classical swine fever (CSF), porcine epidemic diarrhea virus (PEDV), and Senecavirus A (SVA)). The OAHN swine network was able to discuss SVA in detail when issues were being seen within many different states in the USA. The swine network authored communications to practising swine veterinarians as well as to producers and associated swine industry members stating the clinical signs that are associated with this virus as well as information of whom to contact if seen. From these network communications, the message “if you see clinical signs of SVA, please do not ship or transport these pigs, and contact your veterinarian immediately” was disseminated to all personnel dealing with swine. This is a great example of how the swine network has been instrumental in dealing with external disease preparedness.

Two main communications are generated from routine OAHN swine network meetings: a producer report and a veterinary report. The network allows veterinarians to determine collaboratively the messages that are communicated within the swine industry in both of these reports. Key messages are also communicated with the use of current tools and technology (e.g., podcasts, Twitter, and Facebook). Information discussed by the OAHN swine network is further integrated at the national level through the Canadian Swine Health Intelligence Network (CSHIN). Provincial swine surveillance networks exist in both Quebec with RAIZO and in the west with the Canada-West Swine Health Surveillance Network (CWSHIN). All networks use similar models with regards to the data that is collated and discussed. Clinical impression survey results received from veterinarians across Canada are entered into statistical process control (SPC) charts for each disease. A signal, such as a disease occurrence 3 standard deviations above the mean, denotes a likely change in the occurrence of the disease. The signals create cause for discussions and possible further investigation of why it was generated. It also provides a mechanism for the comparison of data from other surveillance networks across Canada. CSHIN also generates both a veterinary and producer report outlining the network discussions and comparisons on a quarterly basis.
CAHLN / RCTLSA 16th Annual Meeting
Fish
Wednesday, June 7
10:30-11:00

Building 89 PAHL, Room 1800

Moderator: Hugh Cai

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<td><strong>Roz Stevenson, Melinda Raymond, Steve Lord, Lucy Mutharia</strong></td>
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Antimicrobial resistance in Ontario aquaculture

Marcia Chiasson, Véronique LePage, Steve Naylor

Ontario Ministry of Agriculture, Food and Rural Affairs (Chiasson, Naylor); and Department of Pathobiology and Animal Health Laboratory, University of Guelph, Guelph, Ontario (LePage).

Abstract

Antimicrobial resistance (AMR) is a serious and growing public health threat in Canada and around the world. The Canadian government is working to prevent, limit, and control the spread of AMR and has proposed new regulations for AMR related to veterinary drugs.

There are few antimicrobials licensed for use in food fish in Canada, and data on the emergence of AMR for these products is unavailable. To better understand the degree of AMR in Ontario food fish production, we aimed to survey commercial finfish aquaculture farms and test for susceptibility to antibiotics.

In year one of the project, fish specimens submitted to the University of Guelph's Animal Health Laboratory as part of regular screening and fish health testing that were positive for bacterial pathogens, were further tested for minimum inhibitory concentrations (MICs) to monitor for resistance to antibiotics.

Of the cases that were submitted for bacterial cultures, many were positive for more than one pathogen. Results to date indicate that some pathogens such as Yersinia ruckeri and a possible emerging pathogen Flavobacterium psychrophilum are showing intermediate susceptibility to commonly used antibiotics, whereas others such as Flavobacterium columnare remain susceptible to common treatments.

With the exception of reportable and notifiable aquatic animal diseases, little information is available on trending of pathogens by region, pathogen transfer from different locations, virulence, treatment resistance, and general adaptations of pathogens over the years. The results of this work will help fill some of these gaps in disease surveillance.
Laboratory detection approaches to fish pathogen surveillance in Ontario

Roz Stevenson, Melinda Raymond, Steve Lord, Lucy Mutharia

Fish Health Laboratory, Molecular & Cellular Biology, College of Biological Science,
University of Guelph, Guelph, Ontario

Abstract

Microbial pathogens of freshwater fish can affect aquaculture and hatchery operations by causing production-limiting diseases. In addition, detection of specific pathogens in a population may pose biosecurity restrictions on where the fish may be moved. Ontario government hatcheries culture fish for rehabilitation purposes in the Great Lakes Basin and, for about 40 years, our laboratory has provided monitoring services for detection of potential pathogens in these fish and in wild-caught fish used as broodstock. The laboratory receives groups of whole fish and reproductive fluids from fish culture stations across the province and processes samples for detection of viruses, bacteria, or parasites of concern. Routine testing procedures involve tissue culture on fish cell lines for viruses, bacterial culture, and microscopic examination for parasites and some bacterial pathogens. Identification of presumptive isolates is by biochemical characterization, serology, PCR-based molecular methods and/or electron microscopy, which are available through associated research activities. A culture-based approach requires time and effort, particularly for a small laboratory. However, it gives better opportunities to detect target pathogens that may be present at low levels in apparently healthy fish, and to increase chances of recognizing novel or emerging disease agents in wild fish or hatchery stocks.

The most commonly detected restricted fish pathogens have been *Aeromonas salmonicida* and *Yersinia ruckeri*, both at low levels. *Renibacterium salmoninarum*, a slow-growing bacterium, is detected by immunofluorescent antibody staining. Although considered endemic in Ontario, the bacterium is detected at low levels and disease signs are rare. Cold-water disease (*Flavobacterium psychrophilum*) and bacterial gill disease (*Flavobacterium branchiophilum*) are common problems affecting fish in culture. In recent years, testing for viral hemorrhagic septicemia virus (VHSV) has been a major concern, related to its potential spread. However, main isolations have been an occasional aquareovirus and a recurring novel bacilliform virus in spawning fish. We sequenced this Chinook salmon batinivirus (CSBV), finding it was a previously unknown virus, of unknown pathogenicity for fish.

We will review some examples of changing approaches to fish pathogen detection, identification, and surveillance that we have encountered as laboratory techniques, regulatory requirements, and questions of interest have evolved.
CAHLN / RCTLSA 16th Annual Meeting
Cross-species
Wednesday, June 7
10:30-11:00

Building 89 PAHL, Room 1800

Moderator: Hugh Cai

Cross-species

11:00 Qualitative LC-MS/MS method for the detection of desmethylbromethalin in adipose tissue
Felipe Reggeti, Nick Schrier

11:15 Choosing and interpreting laboratory testing in an environment of increasing technology
Wendy Witbeck

11:30 CAHLN 2018 & Closing Remarks – Melanie Barham

12:00 Boxed Lunch – to be picked up outside of Room 1800
Qualitative LC-MS/MS method for the detection of desmethylbromethalin in adipose tissue

Felipe Reggeti, Nick Schrier

Animal Health Laboratory, Laboratory Services Division, University of Guelph, Guelph, Ontario

Abstract

Bromethalin is a non-anticoagulant neurotoxic rodenticide. It inhibits oxidative phosphorylation limiting ATP production, which causes cell swelling, increased lipid peroxidation, and other effects. Bromethalin is rapidly absorbed from the GI tract and metabolized in the liver to desmethylbromethalin (DMB), a more potent inhibitor of mitochondrial respiration. Metabolites cross the blood-brain barrier and are very lipophilic; therefore, they readily accumulate in the brain and spinal cord causing CNS edema. Diagnosis is based upon history of exposure, clinical signs, and determination of DMB in tissues. Bromethalin was registered in 1985, but because of increasing restrictions on the use of anticoagulant rodenticides, it has become more available in recent years. Exposure of pets and non-target wildlife has been documented.

The veterinary analytical toxicology section of the Animal Health Laboratory (AHL) has recently installed and verified a method developed by the California Animal Health and Food Safety Laboratory (CAHFS; Davis, California) for the qualitative determination of bromethalin. The method consists of a liquid chromatography–tandem mass spectrometry (LC-MS/MS) technique for detection of DMB in adipose tissue. Adipose tissue (0.5 g) is extracted with ethyl acetate using a Geno/Grinder homogenizer. The mixture is centrifuged and the supernatant is mixed with acetonitrile. Lipids are removed using an Agilent Enhanced Matrix Removal (EMR)-Lipid sorbent extraction technique. The resulting extractant is evaporated to dryness and reconstituted in methanol. The extract is analysed on an AB Sciex API 4000 LC-MS/MS system, where the multiple reaction monitoring method using precursor ion of m/z 562 and product ions of m/z 278 and 254 is performed. A limit of detection of 1 ppb was verified in our laboratory and a cut-off limit was determined, where false-negative rates for concentrations above the limit are low, based on specific probability.

This is an accurate, sensitive, and cost effective qualitative method to investigate bromethalin exposure as an aid in the diagnosis of intoxication.
Choosing and interpreting laboratory testing in an environment of increasing technology

Wendy Witbeck
Idexx Laboratories, Markham, Ontario

Abstract

Interpretation of laboratory test results is an increasingly important skill for veterinarians and animal health experts as technology advances and worldwide food production becomes more and more integrated. Understanding the basis of test design and the timeline and pathology of disease can add value and accuracy to laboratory test usage.

We will review the most commonly used types of serology and molecular diagnostic testing and how to interpret the results of each separately and in parallel. We will begin with a brief review of the introduction of antigens and subsequent antibody generation, then move on to some commonly used tests for each and their main benefits and drawbacks. Finally, we will discuss timelines of disease and common instances of interpretation of both agreeing and discrepant antibody and antigen test results.
## Poster Presentations

**Room 1707 B&C**

**Bldg. 77, Lifetime Learning Centre**

**Monday June 5th morning to Tuesday June 6th after pm coffee**

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<td>Risk assessment for the incursion and establishment of Orbiviruses in Ontario: Serosurveillance in cervids and cattle and characterization of current vector composition and distribution</td>
<td>Samantha Allen</td>
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<td>Kristina Santiago Mateo, Melissa Robdrup, Catherine Graham, Roberta Quaghebeur, Rakhi Katoch, Renee Anderson, Stefanie Czub</td>
<td>Determining the tissue distribution and the ability to detect Scrapie in young lambs</td>
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<td>Gabriel Desmarais, Ghyslaine Vanier, John M. Fairbrother</td>
<td>Virulence gene profile, O serotype and antimicrobial resistance of <em>Escherichia coli</em> isolates from clinical cases in poultry in Quebec from 2014 to 2016</td>
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<td>competitive affinity of an aggregation specific antibody to detect prions captured on a solid-state matrix</td>
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<td>prions captured on a solid-state matrix</td>
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The presenters will be available in the poster area during Health Breaks on Monday and Tuesday.
Poster 1: Risk assessment for the incursion and establishment of Orbiviruses in Ontario: Serosurveillance in cervids and cattle and characterization of current vector composition and distribution

Samantha Allen, Claire Jardine, Mark Ruder, Aruna Ambagala, Kathleen Hooper-McGrevy, Tara Furukawa-Stoffer, Nicole Nemeth

Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, ON (Allen, Jardine, Nemeth); Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA (Ruder); National Centre for Foreign Animal Diseases, Canadian Food Inspection Agency, Winnipeg, MB (Ambagala, Hooper-McGrevy); National Centres for Animal Disease, CFIA – Lethbridge Laboratory, Lethbridge, AB (Furukawa-Stoffer)

Abstract

Epizootic hemorrhagic disease virus (EHDV) and bluetongue viruses (BTV) are vector-borne Orbiviruses that represent imminent threats to Ontario's wildlife populations and livestock industry. Due to environmental factors and associated vector expansion, the distribution of these viruses appears to be spreading northward in the USA. Ontario is at a high risk for EHDV and BTV incursion and establishment, as demonstrated by confirmed outbreaks in white-tailed deer just south of the Ontario-U.S. border, the detection of bluetongue seropositive cattle in Ontario, and the presence of Culicoides sonorensis, a known vector for BTV in southern Ontario. Ruminants in Ontario are immunologically naïve to these viruses; thus, their introduction may lead to significant negative impacts on wild cervid populations and livestock (farmed cattle, sheep, and deer) through morbidity, mortality and production loss.

This research project seeks to characterize Culicoides vector biology and assess for possible ongoing transmission (i.e., serosurveillance) in wild cervids and livestock in high-risk regions of Ontario. To accomplish this, LED light traps will be placed on cattle farms and in natural areas across southwestern Ontario, and the Culicoides vectors will be taxonomically and molecularly identified. Blood from wild cervids and livestock will be collected and sera will be screened for antibodies to EHDV and BTV by ELISA, and the serotypes of any positive samples will be determined by serum neutralization assay. Data will undergo spatial analysis to reveal important regional and seasonal-temporal patterns in vector distribution, as well as statistical analyses to detect disease associations among age, sex, and seasonality. This information will supplement the data from ongoing annual bovine serologic survey conducted by the CFIA and help to better identify the threat of EHDV and BTV to wildlife and livestock in Ontario.
Poster 2: Determining the tissue distribution and the ability to detect scrapie in young lambs

Kristina Santiago Mateo, Melissa Robdrup, Catherine Graham, Roberta Quaghebeur, Rakhi Katoch, Renee Anderson, Stefanie Czub

Canadian Food Inspection Agency, CFIA Lethbridge Laboratory

Abstract

Transmissible spongiform encephalopathies (TSEs) are a group of fatal diseases in animals and humans that are believed to be caused by a misfolded form of a host-encoded protein (prion protein). Due to the known (e.g., BSE) and unknown (e.g., scrapie) zoonotic potential of some of the animal TSEs, they pose a challenge for those who regulate these diseases. Presently, the Canadian scrapie surveillance program targets mature (over 12 months) sheep and goats, both healthy slaughter and higher-risk animals (i.e., condemnations, deads, downers). Given the undetermined nature of its zoonotic potential, the goal of the project is to determine the potential infection risk of young sheep of under 12 months which are not part of the surveillance program and have not been tested for scrapie prior to human consumption.

Lambs were per orally challenged with classical and atypical scrapie. During incubation, recto-anal mucosa associated lymphoid tissue (RAMALT) biopsies were obtained every 3 months; the experiment was terminated after 1 year and an extensive postmortem was performed. Samples were analysed with rapid tests (BioRad TeSeE SAP ELISA, IDEXX EIA), histopathology (H&E), and immunohistochemistry (IHC).

The goals of this study were to
1. To determine the dissemination pattern of the scrapie agent at early time points post-infection in lambs of different genotype per oral (PO) challenged with classical and atypical scrapie;
2. To identify tissues that are accessible and harbour the scrapie agent early in the disease incubation in lambs of various genotypes;
3. To evaluate the performance of rapid tests for scrapie on different tissues and compare these results to IHC detection of scrapie;
4. To determine the risk involved in consuming young animals (≤12 months) which are not part of the surveillance program and have not been tested for scrapie.

PrPSc - the marker of prion disease - was not detected in any of the RAMALT biopsies, however it was present in animals of various genotypes challenged with classical scrapie, with some correlation between IHC and rapid test results. Not unexpectedly, PrPsc was detected to a limited degree in animals challenged with atypical scrapie.
Poster 3: Virulence gene profile, O serotype and antimicrobial resistance of Escherichia coli isolates from clinical cases in poultry in Quebec from 2014 to 2016

Gabriel Desmarais, Ghyslaine Vanier, John M. Fairbrother

OIE Reference Laboratory for Escherichia coli (EcL), Centre de recherche en infectiologie porcine et aviaire (CRIPA), Faculté de médecine vétérinaire, Université de Montréal, St-Hyacinthe, QC, Canada

Abstract

Avian pathogenic Escherichia coli (APEC) causes colibacillosis, which results in morbidity, mortality and significant economic losses to the poultry industry. Characterization of clinical isolates by O-serotyping, virulence gene profile, and the definition of the antimicrobial resistance profile can lead to better knowledge of the most prevalent APEC strains among flocks. In this study, 152 E. coli isolates from broiler chickens demonstrating clinical signs associated with colibacillosis received between 2014 and 2016, were examined using multiplex polymerase chain reactions (PCRs) targeting 15 of the most important APEC/ExPEC virulence genes (iroN, hlyF, iss, iucD, ompT, kpsII, tsh, papC, cnf, hra, sitA, fyuA, ireA, cvaC, east-1). Additionally, serotyping by agglutination was done for 88 different O-serotypes and antimicrobial resistance was examined by the disk diffusion method for the following antimicrobials: gentamicin, neomycin, ceftiofur, enrofloxacin, sulfisoxazole, trimethoprim-sulfamethoxazole, ampicillin, and tetracycline.

Characterization of APEC/ExPEC clinical isolates will permit the surveillance of the different serovirotype profiles present in the poultry farms of Quebec and facilitate the tracking of pathogenic E. coli isolates between production sites and the identification of candidate strains for production of autogenous vaccines as an aid to control of this disease.
Poster 4: First case report of a fowl poxvirus infection in a wild snow bunting in Quebec

Chantale Provost, Émilie L. Couture, Stephane Lair, Carl A. Gagnon

Centre de recherche en Infectiologie Porcine et Avicole (CRIPA); Laboratoire de diagnostic virologique vétérinaire et de diagnostic moléculaire; Faculté de médecine vétérinaire, Université de Montréal (Provost, Gagnon); Centre québécois sur la santé des animaux sauvages; Réseau canadien pour la santé de la faune, Faculté de médecine vétérinaire, Université de Montréal (Couture, Lair)

Abstract

Fowl poxvirus (FPV) infections have been reported in many bird species such as turkeys, chickens, pigeons, and canaries, as well as a wide variety of wild birds. FPV belongs to the genus of Avipoxvirus and to the family of Poxviridae. FPV is present all around the globe and is of considerable economic importance, especially when affecting its natural host, the chicken. FPV cause important cutaneous lesions with proliferative growths on the unfeathered parts of the skin and/or diphtheritic lesions generally associated with necrosis in the upper respiratory and digestive tracts. FPV is a large enveloped virus and possesses a dsDNA genome that replicate entirely in the cytoplasm of the host cells.

In this study, a new FPV have been identified on a snow bunting (Plectrophenax nivalis) housed in an outdoor aviary in the region of Rimouski, Quebec. The bird was showing typical proliferative pox-like lesions on the feet and beak. The presence of the FPV was confirmed by a specific PCR assay which amplified a segment of the gene encoding for the fowlpox 4b core protein (Lee & Lee, 1997). A 576 bp sequence was obtained and sequenced. The analyses revealed 99% homology to other previously described Avipoxvirus. Electron microscopy imaging of ultrathin sectioning of the histologic lesions confirmed the presence of the poxvirus. To our knowledge, it is the first confirmed description of a case of FPV reported in a snow bunting.
Poster 5: Prevalence of NetF toxigenic Clostridium perfringens type A in foals in Kentucky and Ontario


Department of Pathobiology, University of Guelph, Guelph, Ontario (Gohari, Finley, Parreira, Boerlin, Prescott); Gluck Equine Research Center, Department of Veterinary Science, University of Kentucky, Lexington, KY, USA (Timoney); Hagyard Equine Veterinary Science, 4250 Iron Works Pike, Lexington, KY, USA (Fallon, Slovis); Department of Clinical Studies, University of Guelph, Guelph, Ontario (Abrahams, Staempfli)

Abstract

A role for C. perfringens type A in enterocolitis and necrotizing enteritis in young foals has long been suspected but not well understood, since this bacterium is also commonly present in the intestinal tract of healthy foals. However, the recent discovery of a novel beta-pore-forming toxin, NetF, which is strongly associated with foal necrotizing enterocolitis, should improve understanding of the role that C. perfringens type A plays in enteric disease in neonatal foals.

The main purpose of this study was to determine the prevalence of netF-positive C. perfringens in clinically healthy foals in southwestern Ontario and in neonatal foals with severe enteritis in Kentucky. Fecal samples (n = 137) from 88 foals at different ages (median age 2 to 4 weeks) were collected from 8 different farms on 1 or 2 occasions in Ontario. These samples were examined by culture for the presence of C. perfringens. Five C. perfringens isolates per positive sample from Ontario foals as well as single C. perfringens isolates recovered in Kentucky between 2000 and 2011 from 23 1-14-day-old foals with severe enteritis were screened by multiplex PCR for presence of the cpa, netF and cpe toxin genes.

All isolates were cpa positive, confirming their identity as C. perfringens. None of the isolates from healthy foals in Ontario was positive for netF and only 2 isolates possessed the cpe gene. Six of 23 isolates obtained from foals with severe enteritis in Kentucky were positive for both netF and cpe. This study confirms for the first time the presence of netF-positive C. perfringens in foals with necrotizing enteritis in Kentucky. Furthermore, we can conclude that NetF-toxigenic C. perfringens occur only rarely in young foals in Ontario. Further research is required to understand the epidemiology of netF C. perfringens in foals.
Poster 6: Diagnosing lymphoma when standard methods fail

Stefan M. Keller, Mei-Hua Hwang

Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada

Abstract

Clonality testing is a molecular method to diagnose lymphoma. It can be utilized if clinical and pathological assessment is equivocal. Clonality testing relies on the unique feature of lymphocytes to rearrange their antigen receptor genes. This process creates a unique gene sequence in every lymphocyte clone, much like a molecular fingerprint. Based on the size diversity of lymphocyte antigen receptor (LAR) genes within a given sample, inferences can be made as to whether lymphocytes are clonal or polyclonal, supporting neoplastic or reactive/inflammatory processes, respectively. The laboratory workflow of clonality testing comprises DNA extraction, PCR amplification of LAR genes and size separation of amplicons by capillary electrophoresis. Finally, electrophoresis profiles are interpreted in conjunction with the clinical, morphological, and immunophenotypical data. Clonality testing can be done on formalin-fixed and paraffin-embedded tissues, stained cytology specimens, flow cytometry samples or frozen materials. Clonality testing is currently done for B- and T-cell proliferations in dogs and cats. As with any other test, false-positive and false-negative results occur and the integration of histopathological and cytological findings is crucial to minimize misdiagnoses. Advances in high-throughput sequencing are currently revolutionizing the field and will soon result in more sensitive and accurate testing.
Poster 7: Comparison of deep amplicon nembiome sequencing with morphological identification to quantify species proportions of gastrointestinal larvae isolated from small ruminant feces

Emma Borkowski, Andrew Peregrine, John Gillear, Elizabeth Redman, Russell Avramenko, Rebecca Chant, Jacob Avula, Niel Karrow, Paula Menzies, Brandon Lillie

Department of Pathobiology, Ontario Veterinary College, University of Guelph (Borkowski, Chant, Avula, Lillie, Peregrine); Department of Comparative Biology and Experimental Medicine, Faculty of Veterinary Medicine, University of Calgary (Redman, Avramenko, Gillear); Department of Animal Biosciences, Ontario Agricultural College, University of Guelph (Karrow); Department of Population Medicine, Ontario Veterinary College, University of Guelph (Menzies)

Abstract

Gastrointestinal nematode parasitism has a significant impact on the health and productivity of sheep and goats worldwide. Fecal trichostrongylid-type egg counts are widely used for monitoring both infection levels and anthelmintic resistance within a flock; however, the eggs of many nematode species, including the most commonly identified species in Ontario (Haemonchus contortus, Teladorsagia circumcincta, and Trichostrongylus spp.), are identical in morphology. This necessitates larval culture to determine the species involved. The most common method involves morphologic speciation of third stage (L3) larvae cultured from feces following incubation for 7 days. However, morphologic differences are often subtle and results are consequently prone to error. In addition, culture for this duration can bias the species composition. A new approach to quantify the relative proportions of parasitic nematode larvae isolated from fecal samples, called nemabiome sequencing or metabarcoding, has been recently described for cattle gastrointestinal nematodes. This is based on deep amplicon next generation sequencing of the ITS-2 rDNA locus and is equivalent to 16S rDNA sequencing of bacterial communities commonly used in microbiome studies. We have applied this approach to populations of first stage (L1) larvae cultured for 48 hours following isolation of eggs from small ruminant feces. This study compared the species composition of pooled small ruminant fecal samples determined using traditional morphologic identification of L3 larvae with the results of this new L1 deep amplicon sequencing approach.
Poster 8: Development of a blood test for scrapie using streptavidin and the competitive affinity of an aggregation specific antibody to detect prions captured on a solid-state matrix

Andrei Soutyrine, Hongsheng Huang, Olga Andrievskaia, Ines Walther, Gordon Mitchell

Ottawa Laboratory (Fallowfield), Canadian Food Inspection Agency, Ottawa, Ontario,

Abstract

Scrapie is a fatal neurodegenerative disorder affecting sheep and goats, originating from exposure to disease-associated prions (PrPSc). An ante-mortem screening test that can detect native PrPSc in body fluids remains unavailable. Previous studies revealed insufficient sensitivity of the 15B3 antibody when used in our prion-aggregate detection-based approach. To overcome this limitation, we adopted an alternative approach to detect PrPSc in whole blood without proteinase or denaturation treatments, based on the competitive affinity of an aggregation-specific monoclonal antibody and streptavidin to PrPSc.

First, we demonstrated the ability of native PrPSc to bind to streptavidin and the inhibition of this interaction by 15B3 antibody ($p < 0.05$). This led to a new 2-step assay that involved capturing native prions from infected blood on a solid-state matrix and detection of PrPSc aggregates by evaluating the conjugate catalytic activity ratio in samples against a pre-determined threshold.

This test showed capacity for detecting scrapie prions in 500 µL of sheep whole blood spiked with scrapie brain homogenate containing ~ 5 ng of total brain protein, and estimated to have 500 fg of PrPSc, a sensitivity more than 2 orders of magnitude higher than that of a previously reported aggregation-specific ELISA. The test also allowed detection of scrapie prions in whole blood from experimentally infected sheep ($n = 3$) collected at the clinical stage of disease, and from naturally infected goats ($n = 7$) with confirmed scrapie. The specificity was estimated as 100% by testing blood of sheep ($n = 10$) from a scrapie-free flock.

Collectively, with the proposed high-throughput sample-processing platform, these initial studies allow the development of a large-scale screening test for the routine diagnosis of scrapie.
Poster 9: An investigation into distribution of serotypes and antimicrobial resistance patterns of *Streptococcus suis* isolates from clinical cases and healthy carrier pigs

Emily R. Arndt, Vahab Farzan, Janet I. Macllnnes, Robert M. Friendship

Department of Population Medicine (Arndt, Farzan, Friendship), Department of Pathobiology (Macllnnes), University of Guelph, Guelph, ON

Abstract

The objectives of this study were to investigate the serotype distribution of *Streptococcus suis* isolates recovered from healthy and diseased pigs using a multiplex PCR method and to determine antimicrobial resistance patterns. Nasal, tonsillar, and vaginal swabs were collected from healthy pigs and tonsillar and meningeal swabs as well as tissue from tonsil and lymph nodes were obtained from clinically ill pigs on 31 farms located in Ontario. A 2-step multiplex PCR test was used to serotype the isolates. Antimicrobial resistance against ampicillin, ceftiofur, florfenicol, tetracycline, tiamulin, spectinomycin, and trimethoprim/sulfa was tested using a disc diffusion method. In total, 450 samples (324 from healthy and 126 from sick pigs) were collected from 364 (285 healthy and 79 sick) pigs. *S. suis* was recovered from 293 (65%) of these samples; 219 (68%) samples from healthy and 74 (59%) from sick pigs. In total, 567 isolates (429 from healthy and 138 from sick pigs) were obtained from the 293 positive samples. Twenty-two different serotypes were identified, with serotype 31 being the most common serotype isolated - mostly from healthy pigs. Serotypes 4, 8, and 9 were the most common serotypes isolated from sick pigs. A low prevalence of resistance was seen against ampicillin, ceftiofur, and florfenicol (<1.0%), while a high prevalence of resistance against tetracycline (84.2%), tiamulin (65.2%), and spectinomycin (40.4%), and an intermediate level of resistance to trimethoprim/sulfa (13.2%) was identified. These findings indicate which serotypes are most problematic in causing *S. suis* disease as well as which serotypes may be less virulent and only found in healthy pigs. They also indicate which antimicrobial agents *S. suis* is the most resistant to. This can be used to develop more effective treatment strategies to prevent *S. suis* infection outbreaks in pigs and to design appropriate management changes.
Poster 10: Prevalence of Salmonella in nursery pigs using bacteriological and serological detection methods

Saranya Nair, Vahab Farzan, Zvonimir Poljak, Robert Friendship

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

Abstract

The prevalence of Salmonella shedding has been reported to be the highest in the nursery stage and may potentially have an impact on the growth performance of nursery pigs. It is difficult to identify asymptomatic carrier pigs because they may not shed Salmonella at the sampling time. However, serological testing methods, to assess for antibody response to Salmonella infection, may be more effective in capturing the population of intermittent shedders than traditional bacteriological methods. The objectives of this study were i) to determine the prevalence of Salmonella spp. in Ontario nursery pigs using bacteriological and serological testing methods, ii) to examine the development of antibody levels in relation to the Salmonella shedding pattern and iii) to investigate whether Salmonella status was associated with growth rate and mortality in nursery pigs.

Twenty nursery pigs between 6 and 8 weeks of age were selected from each of the thirty Ontario nursery pig barns enrolled in the study. Fecal and blood samples were collected from pigs at entry and at the end of the nursery stage. Fecal samples were cultured for Salmonella and blood samples tested by ELISA for presence of antibodies against Salmonella. Information about housing, management, feeding programs, medication, pig density, mortality, vaccination, disease history, growth performance, and feed efficiency were also collected. A multilevel regression method will be used to analyze the association of growth performance with the presence of Salmonella while taking into account potential confounders. In addition, a multilevel regression model will be used to determine the association between Salmonella seropositivity and shedding. Preliminary results have revealed that 56% (132/235) of nursery pigs were Salmonella seropositive at entry while this number was found to decline to 32% (74/233) by the end of the nursery stage. Salmonella seropositivity decreased during the nursery phase on most farms indicating the disappearance of passive immunity, but on one farm seropositivity increased indicating active infection. The results from this research will provide a better understanding of the epidemiology of Salmonella and associated laboratory testing methods within in the nursery stage.

Acknowledgements: University of Guelph-OMAFRA research partnership
Poster 11: Leukemia in horses: a case series

Carina Cooper, Stefan Keller, Luis Arroyo, Joanne Hewson, Daniel Kenney, Dorothy Bienzle

Department of Clinical Studies (Cooper, Arroyo, Hewson, Kenney); Department of Pathobiology, University of Guelph, Guelph, ON, Canada (Keller, Bienzle).

Abstract

Leukemia, a neoplasm of hematopoietic cells, is divided in lymphoid and myeloid type with acute and chronic forms based on duration of illness, severity of cytopenia, and cell composition. The objectives of this study were to describe clinical, hematological, morphological, and immunohistochemical properties of leukemia in horses. Review of medical and laboratory records over 17 years identified 16 horses diagnosed with leukemia. Horses included 9 males and 7 females ranging from 0.2 to 25.9 years (median 6.5) in age. All horses with acute lymphocytic leukemia (ALL) were < 4 years, and all horses with myelodysplastic syndrome (MDS) were > 13 years of age. Fifteen horses (93%) had thrombocytopenia (7-68 x10^9/L), eleven (69%) had anemia (hematocrit 0.08-0.27 L/L), and all had atypical leukocytes on blood films. Six cases were classified as ALL based on immunohistochemical detection of CD3, CD20, and/or CD79a antigens; 6 as acute myeloid leukemia (AML; 4 myelomonocytic, 1 basophilic, 1 eosinophilic) by >20% blast cells with expression of lab antigen and partial leukocyte differentiation; and 4 cases as MDS with refractory thrombocytopenia (n=3) or neutropenia (n=1) with excess blasts based on ineffective hematopoiesis and dysplasia. Postmortem examination identified leukemia involving lymph nodes (n=8), liver (n=8), lung (n=4), gastrointestinal tract (n=4) and kidney (n=3) in addition to hematopoietic tissue. Horses with ALL or AML survived <42 days while 2 horses with MDS had historical cytopenia exceeding 1 year, and 2 are alive 342 and 80 days after diagnosis. These findings indicate variable features and prognosis of leukemia in horses.
Poster 12: *Salmonella* shedding and antibody response to *Salmonella* in pigs from weaning to marketing

Corinne H. Schut, Vahab Farzan, Robert M. Friendship, Brandon N. Lillie

Department of Pathobiology (Schut, Lillie); Department of Population Medicine (Farzan, Friendship), University of Guelph, Guelph, Ontario

Abstract

*Salmonella* is a significant food safety concern worldwide. The majority of human salmonellosis cases are attributed to food products of animal origin, including pork, and produce contaminated by *Salmonella* shed in manure. *Salmonella* is prevalent on swine farms, highlighting the need for appropriate intervention strategies at the farm level. Isolation of *Salmonella* shed in the feces and detection of *Salmonella* antibodies are 2 approaches to determining *Salmonella* status at the pig and/or farm level. The objective of this study was to investigate the association between *Salmonella* shedding and antibody response in pigs from weaning up to marketing age. Fourteen cohorts of pigs from 8 farms were followed from birth up to slaughter. For each cohort, 60 piglets were selected from 8-10 sows (total = 832 piglets). Feces or rectal swabs and blood samples were taken at weaning and at the end of the nursery, grower, and finisher stages. Fecal samples were cultured for *Salmonella* and sera were analyzed for the presence of *Salmonella* antibodies by ELISA. Over the production period, *Salmonella* was recovered from 13% (433/3,339) of fecal samples while *Salmonella* antibodies could be detected in 18% (473/2,627) of serum samples. *Salmonella* was isolated from 11% (82/784), 13% (94/747), 12% (90/730) and 20% (135/669) of pigs at weaning, and the end of the nursery, grower and finisher stages respectively, while the percentages of pigs that tested seropositive (in the same order) were 20% (143/703), 6% (41/712), 16% (106/665) and 37% (196/525). The higher *Salmonella* seropositivity observed at weaning compared to *Salmonella* isolation may be due, in part, to the presence of maternal antibodies absorbed from the sow’s colostrum. Antibody responses in asymptomatic carriers not actively shedding at the sampling time, or from previous exposure to *Salmonella* may account for the higher *Salmonella* seropositivity at the finisher stage. These preliminary findings indicate that serology may be a useful approach to screening pig farms for *Salmonella*. 
Poster 13: Bovine mucosal gamma-delta cells in host immunity and defense

Latasha Ludwig, Rebecca Egan, Monica Baquero, Kevin Stinson, Brandon L. Plattner
Department of Population Medicine, University of Guelph, Guelph, Ontario

Abstract

Mucosal surfaces are the frontlines of host defense against many pathogens. It is at these surfaces where success or failure of host defense is thought to influence establishment of infectious disease in the host. Our laboratory is working to understand innate lymphocytes, especially gamma-delta (γδ) T cells, during early host-pathogen interactions, and how they contribute to host defense. Our hypothesis is that γδ T cells are differentially distributed along the gastrointestinal (GI) mucosal surface, where they play an important role during early intestinal infections. We tested this by first characterizing γδ T cell distribution at GI mucosal surfaces of healthy calves using spectral microscopy. Approximately 40-60% of T cells in GI mucosa are γδ T cells, but the ileum has significantly more γδ T cells compared to other GI segments. Intestinal γδ T cells are present in the lamina propria and epithelium, but are primarily WC1-, in contrast to peripheral blood.

We then used spectral microscopy and flow cytometry to show that γδ T cells are significantly recruited into the bovine ileum after intestinal Mycobacterium avium subspecies paratuberculosis (Map) infection. The majority of γδ T cells recruited into the ileal mucosa are WC1-, although a significant number of WC1+ γδ T cells are also recruited into the epithelium. These data support our hypothesis that WC1+ γδ T-cells are uniquely positioned along GI mucosa for host defense, and that WC1- and WC1+ γδ T cells play a critical role in early recognition and response to intestinal Map infection in calves.
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