24th Annual Meeting of the Canadian Animal Health Laboratorians Network (CAHLN)

May 24-27, 2026

University of Guelph, Guelph, Ontario

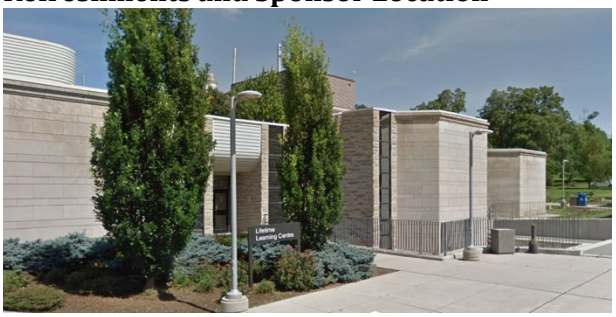
Conference Locations and Parking

Conference Location

OVC Enhanced Clinical Learning Centre
25 McGilvray St, Guelph, ON
ROOM ECLA 1720

To view this location on the campus map, please click here: https://www.uoguelph.ca/maps/?uid=077

Refreshments and Sponsor Location



OVC Lifetime Learning Centre
25 McGilvray St, Guelph
LLC 1707 B and C

For directions, please click here:
https://www.uoguelph.ca/eaccess/services/ovc-enhanced-clinical-learning-centre

Opening Reception Location

University Club, University of Guelph
5th Floor, University Centre
Reynolds Walk, Guelph, ON

To view this location on the campus map, please click here: https://www.uoguelph.ca/maps/?uid=158

Banquet Location

Summerlee Science Complex Waasamowin
570 Gordon St #474

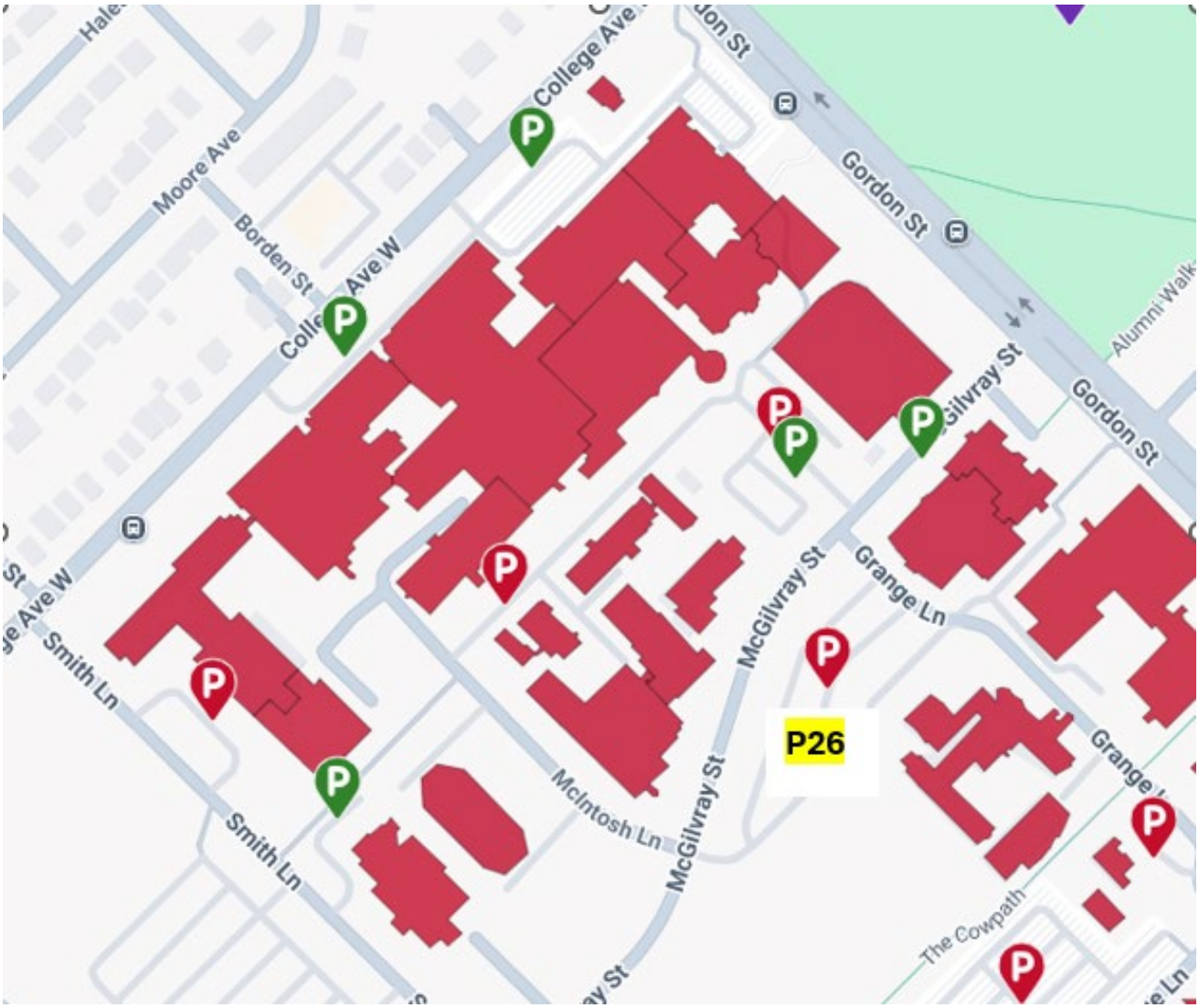
To view this location on the campus map, please click here: https://www.uoguelph.ca/maps/?uid=140

Parking

Parking passes can be purchased from University of Guelph parking services here: https://www.parking.uoguelph.ca/find-parking/visitor-parking

The closest parking for the conference is in lot P26 (red zone) and at the visitor parking locations pictured below.

To use the green visitor parking spots, you will need to download the PayByPhone App.



2026 CAHLN Conference Wi-Fi details

Network: uog-guest
Username: **uogevents2026**
Password: **6512**

If you're not able to access the login page, please visit: https://neverssl.com

24th Annual Meeting of the Canadian Animal Health Laboratorians Network

(CAHLN)

Innovation and Action: From Sequencing to Surveillance

University of Guelph

May 24-27, 2026

CAHLN 2026 ORGANIZING COMMITTEE:

Durda Slavic, Bacteriologist, Animal Health Laboratory, University of Guelph (Chair)
Maria Spinato, Director, Animal Health Laboratory, University of Guelph
Emily Brouwer, Veterinary Pathologist, Animal Health Laboratory, University of Guelph
Michael Deane, Communications Manager, Animal Health Laboratory, University of Guelph
Helen Oliver, Executive Assistant, Animal Health Laboratory, University of Guelph
Sofija Jelacic, Office Administrative Assistant, Animal Health Laboratory, University of Guelph
Tim Pasma, Client Services Veterinarian, Animal Health Laboratory, University of Guelph
Tanya Rossi, Data Manager / OAHN Coordinator, Animal Health Laboratory, University of Guelph

CAHLN EXECUTIVE COMMITTEE (2024-2026)

President:	Clarice Lulai-Angi, Nepean, Ontario
Past President:	Yanyun Huang, Saskatoon, Saskatchewan
President Elect:	Durda Slavic, Guelph, Ontario
Vice President:	Olivia Labrecque, Saint-Hyacinthe, Quebec
Secretary-Treasurer:	TBD

24th Annual Meeting of the Canadian Animal Health Laboratorians Network (CAHLN)

May 24-27, 2026

University of Guelph

Guelph, ON

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, molecular biology and epidemiology.

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)
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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)
2018 – Winnipeg (University of Manitoba)
2019 – St Hyacinthe (Université de Montréal Faculté de médecine vétérinaire)
2021 – Calgary (Virtually held by University of Calgary's Faculty of Veterinary Medicine)
2022 – Whistler (Fairmont Chateau Whistler)
2023 – Saskatoon (University of Saskatchewan)
2024 – Ottawa (Infinity Conference Centre)
2025 – Calgary (Calgary TELUS Convention Centre)
2026 – Guelph (Animal Health Laboratory/Ontario Veterinary College)

24ème réunion annuelle du Réseau canadien de travailleur en santé animale

(RCTLSA)

Du 24 au 27 mai 2026

Animal Health Laboratory (AHL)

University of Guelph

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)
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2004 – Guelph (Animal Health Laboratory/Ontario Veterinary College)
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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, NBDFA, Fredericton, NB
2016 - Alfonso Lopez, AVC (retired), UPEI, Charlottetown, PEI
2017 - Doug Campbell, U of Guelph, ON
2018 – Yanyun Huang, PDS, Saskatoon
2019 – Carl A. Gagnon, FMV, St. Hyacinthe, QC
2021 – Murray Hazlett, AHL, Guelph, ON
2022 – Hélène Philibert – WCVM, Saskatoon, SK
2022 – Moira Kerr – WCVM, Saskatoon, SK
2023 - Carmencita Yason - Atlantic Veterinary College, NS
2024 - Durda Slavic - U of Guelph, ON
2025 - Yohannes Berhane, CFIA, Winnipeg, MB

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: Jamie Rothenburger Guelph, ON and Ellie Milnes Toronto Zoo, ON
Poster: Corrine Schut Guelph, ON
2018 – Oral: Maodong Zhang, Saskatoon / Poster : Samira Yousefi, OVC, Guelph, ON
2019 – Oral: Christian Lalonde, FMV, St. Hyacinthe, QC
Poster: Passoret Vounba, FMV, St. Hyacinthe,QC
2021 – Oral: Summer Hunter, UCVM, Calgary, AB Poster: Mike Zabroski, WCVM, Saskatoon, SK
2022 – Oral: Lisa Lee – WCVM, Oral First: Darcy Sutherland – UBC, Vancouver, BC, Oral Second: Dr. Ellen Boyd – UBC, Vancouver, BC, Oral Third: Dr. Laurence Daigle – CDVUM, Saint-Hyacinthe, QC
2023 -
2024 –
2025 - Oral: Bradley DeWolf, Department of Pathobiology, OVC, University of Guelph
Poster: Ethan Kenmuir, Department of Pathology and Laboratory Medicine, University of British Columbia

CAHLN 2026 Sponsors

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Stago CANADA

Conference Schedule

CAHLN / RCTLSA WELCOME RECEPTION
Sunday, May 24, 2026

University Club, 5th Floor, University Centre, 50 Stone Road E.

5:30 pm – 7:30 pm | Reception for all conference participants. Appetizers and refreshments. Official welcome.

CAHLN / RCTLSA 24th Annual Meeting
Monday, May 25, 2026

Theme: Technological innovation

ECLA 1720, OVC Enhanced Clinical Learning Centre, University of Guelph

8:00 am | Registration
Outside room ECLA 1720, OVC building

8:15 am | Dr. Rebecca Hallett (Associate VP Research, University of Guelph) – Welcome Message

8:25 | Dr. Clarice Lulai-Angi (CFIA; President CAHLN) – Welcome Message

8:30 am – 9:15 am | Dr. Geoffrey A. Wood (University of Guelph)
MicroRNAs for Diagnosis and Prognosis of Canine Cancers

9:15 am – 10:00 am | Dr. Emmeline Tan (IDEXX)
Digital Pathology: A Diagnostic Clinical Pathologist's Perspective

10:00 am – 10:30 am | Refreshments and sponsor display
LLC 1707 B&C

10:30 am – 11:15 am | Dr. Nicole Ricker (University of Guelph)
Translating Data into Decisions: Advances in Sequencing Technologies for Rapid Diagnostics and Metagenomic Surveillance

11:15 am – 12:00 pm | Dr. Oliver Lung (CFIA/ACIA)
Genomic Detection of Pathogens at CFIA's High-containment lab: One Health Observations in Airborne, Aquatic, and Terrestrial Animals

12:00 pm – 1:30 pm | Lunch and sponsor displays (LLC 1707 B&C)

1:30 pm – 1:50 pm | Dr. Vincent Baby (CDVUM)
Whole Genome Classification System for Porcine Reproductive and Respiratory Syndrome Virus Type 2 (Betaarterivirus americense) Strains Combining ORF5, nsp3-4-5 and Indels

1:50 pm – 2:10 pm | Daniël Kos (University of Regina)
Hybridisation Probe Capture for Disease Surveillance in the Beef Industry.

2:10 pm – 2:45 pm | Dr. Yanyun Huang (Prairie Diagnostic Services)
Bovine Abortion Investigation Using a Reproductive Pathogen Sequencing Panel (BovReproSeq) as a Diagnostic Tool

2:45 pm – 3:15 pm | Refreshments and sponsor displays
LLC 1707 B&C

3:15 pm – 3:30 pm | Dr. Ruwani Karunarathna (Prairie Diagnostic Services)
Improved Molecular Detection of Salmonella Enteritidis in Poultry Fluff via Real-Time PCR assay

3:30 pm – 3:45 pm | Dr. Lowia J. Al-Hussinee (University of Guelph)
Validation of a real-time polymerase chain reaction (qPCR) assay for detection of Flavobacterium branchiophilum in gill disease of salmonids

3:45 pm – 4:00 pm | Lisa Ledger (University of Guelph)
20 Years of Barcode Scanning: Identifying difficult-to-culture pathogens with universal PCR sequencing primers.

4:00 pm – 4:45 pm | Laboratory Reports

6:00 pm – 10:00 pm | Banquet
Science Complex Waasamowin Atrium, University of Guelph

CAHLN / RCTLSA 24th Annual Meeting
Tuesday, May 26, 2026

Theme: One health lens: Communication and collaboration

ECLA 1720, OVC Enhanced Clinical Learning Centre, University of Guelph

8:00 am | Registration
Outside room ECLA 1720, OVC building

8:30 am – 9:15 am | Dr. Andrew Papadopoulos (University of Guelph)
Combatting Online Misinformation

9:15 am – 10:00 am | Dr. Heather McClinchey (Ontario Ministry of Health)
Diphtheria in a Donkey … The Opportunities and Hurdles in Adopting a One Health Approach

10:00 am – 10:30 am | Refreshments and sponsor display
LLC 1707 B&C

10:30 am – 11:15 am | Dr. Scott Weese (University of Guelph)
Pitfalls, challenges and opportunities; lived experiences with scientific communications

11:15 am – 11:40 am | Dr. Maureen Anderson (OMAFA)
Rabies Response & Surveillance in Ontario: A One Health Team Effort

11:40 am – 12:00 pm | Dr. Brian Stevens (University of Guelph)
The Role of Wildlife Disease Surveillance in Advancing One Health

12:00 pm – 1:30 pm | Lunch and sponsor displays
LLC 1707 B&C

1:30 pm – 2:15 pm | Dr. Josip Rudar (CFIA)
Biosecurity at the Edge: Using Efficient Deep Learning to Identify Important Animal Health Pathogens and Disease Vectors

2:15 pm – 2 :30 pm | Dr. Vanessa Morton (PHAC)
From Poultry to People: The Value of a One Health Approach to Salmonella Enteritidis Outbreak Investigations

2:30 pm – 2:45 pm | Dr. Chao Chun Liu (Simon Fraser University)
SamnSero: Integrating Nextflow and ONT to Assess Salmonella Risk in Real-Time

2:45 pm – 3:15 pm | Refreshments and sponsor displays
LLC 1707 B&C

3:15 pm – 3:30 pm | Dr. Rasaq A. Ojasanya (University of Guelph) * Student Presentation
Risk Factors for Antimicrobial Resistance in Urinary Escherichia coli from Dogs in the United States (2018–2024)

3:30 pm – 3:45 pm | Dr. Wallis Rudnick (PHAC)
Results of an AMRNet-Vet Survey of Challenges, Lab Practices, and Prioritization of Harmonized Guidelines for Antimicrobial Susceptibility Testing among 9 Public Veterinary Laboratories in Canada

3:45 pm – 4:00 pm | Parichay Subedi (University of Saskatchewan) * Student Presentation
Antimicrobial Susceptibility of Trueperella pyogenes isolates from British Columbia, Canada

4:00 pm – 4:15 pm | Dr. Cassandra Reedman (PHAC)
Evaluating Associations between Antimicrobial Use and Antimicrobial Susceptibility Testing Results in Clostridium perfringens in Canadian Broilers, Turkeys, and Layers (2018-2023)

4:15 pm – 4:30 pm | Dr. Hugh Cai (University of Guelph)
Theileriosis in Dairy Cows from Eastern Ontario

4:30 pm – 4:45 pm | Dr. Alexandra Reid (OMAFA)
Piscine Lactococcosis Surveillance in Rainbow Trout in Ontario, Canada 2023-2025

4:45 pm – 5:00 pm | Dr. Bradley DeWolf (University of Guelph)
Association between Salivary Anti-CarLA IgA Concentrations in Ontario Pastured Sheep and Offspring Performance

6:00 pm – 8:00 pm | BBQ and Arboretum Tour
Guelph Arboretum
University of Guelph

CAHLN / RCTLSA 24th Annual Meeting
Wednesday, May 27, 2026

Theme: Disease surveillance and preparedness

ECLA 1720, OVC Enhanced Clinical Learning Centre, University of Guelph

8:30 am – 9:15 am | Dr. Zvonimir Poljak (University of Guelph)
Beyond Positives to Signals: What Submissions, Negatives, and Metadata can (and can't) Reveal about Disease Trends

9:15 am – 10:00am | Dr. Amy Greer (Trent University)
Preparedness Prior to Possible Incursion: Using Models to Assess the Risk of H5N1 Influenza Introduction and Spread in Ontario Dairy Cows

10:00 am – 10:30 am | Refreshments
ECLA 1720

10:30 am – 11:15 am | Dr. Tanya Rossi (University of Guelph)
The Ontario Animal Health Network's Contributions to Knowledge Transfer and Acquisition

11:15 am – 11:30 am | Dr. Andrew Brooks (University of Guelph)
Foreign Animal Disease Emergency Exercises – 15 Years of Continuous Improvement

11:30 am – 11:45 am | Ashley Lacey (University of Guelph)
Proficiency Testing in an Animal Health Laboratory

11:45 am – 12:00 pm | Dr. Angela Riveroll (University of Prince Edward Island)
Development of a Proficiency Testing Program for Swine Enteric Viruses for Veterinary Laboratories in Canada

12:00 pm – 12:15 pm | Student award and closing remarks

12:15 pm | Boxed Lunch and Departure

Poster Presentations

Room 1707 B&C Bldg. 77, Lifetime Learning Centre
Monday May 25th morning, to Tuesday May 26th after PM coffee

Poster No.	Authors	Title	Presenter
1	Grace Couper, Zvonimir Poljak	Natural Language Processing and Machine-Learning Models in Veterinary Free-Text Clinical Records: A Scoping Review	Grace Couper
2	Jonathan Morton, Janel Wessel, Vanessa Cowan	Investigating The Effect of Endurance Racing on Cardiac Troponin I Release in Saskatchewan Horses	Jonathan Morton
3	Brittany M. Naeckel, R. Darren Wood, James A. Mori	Successful long-term control of feline primary erythrocytosis with chlorambucil monotherapy	Brittany M. Naeckel
4	Victoria Allicock, Doug Hodgins, Cathy Bauman, Andrew Peregrine, Emma Borkowski	Evaluation of antibodies to a carbohydrate larval antigen(CarLA) in Ontario lambs of different ages experimentallyinfected with Haemonchus contortus across a simulated grazing season	Victoria Allicock
5	Kelsey Holland, Mikaela Jahncke, Lisanework Ayalew, Shivani Ojha	Investigation of the fecal microbiome of raccoons (*Procyon lotor*) in a captive environment	Shivani Ojha
6	Nadia Dsouza, Alan Chicoine, Joe Rubin	Antimicrobial Resistance and Prevalence of Canine Uropathogens in Saskatchewan (2023–2026)	Nadia Dsouza
7	Cassandra Reedman, Agnes Agunos, Richard J. Reid-Smith, Amrita Bharat, Justin Carr, Dale Douma, Ruwani Karunarathna, Beverly Morrison, Matt E. Saab, Durda Slavic, Wallis Rudnick	A descriptive analysis of diagnostic poultry antimicrobial resistance data from the Canadian AMRNet-Vet program	Cassandra Reedman
8	Lilani Munasinghe	Leukemia in a Corn Snake (*Pantherophis guttatus*) Initially Suspected as Severe Leukocytosis Associated with Infection	Lilani Munasinghe

The presenters will be available in the poster room on Tuesday from 1:00 to 1:30PM.

MicroRNAs for Diagnosis and Prognosis of Canine Cancers

Geoffrey A. Wood

Ontario Veterinary College, Department of Pathobiology, University of Guelph

Biography

Dr. Wood's overall research goal is to improve cancer diagnostics and treatment in veterinary species as well as humans by employing a One Health approach. He is particularly interested in using plasma microRNAs a biomarkers of cancer, and has established tissue microarrays of various cancer types to look for novel prognostic proteins and/or therapeutic targets.

He co-leads the Dog Osteosarcoma Group: Biomarkers Of Neoplasia (DOGBONe), and with his collaborators, he uses cross-species cancer genetics to look for mutations that are common or disparate across multiple species including humans.

Digital Pathology: A Diagnostic Clinical Pathologist's Perspective

Emmeline Tan

IDEXX

Biography

Dr. Tan received her DVM from the Ontario Veterinary College in 2000 and was in companion animal/emergency practice for 5 years in the Pacific Northwest before returning to complete a DVSc in clinical pathology in the Department of Pathobiology, OVC . She became a Diplomate of the ACVP (clinical pathology) in 2009. From 2009-2013, Dr. Tan worked in the Department of Pathobiology, teaching clinical pathology to veterinary students, mentoring pathology graduate students, and performing diagnostic work for OVC Health Sciences Centre cases. Dr. Tan joined IDEXX in 2013.

Translating Data into Decisions: Advances in Sequencing Technologies for Rapid Diagnostics and Metagenomic Surveillance

Nicole Ricker

Ontario Veterinary College, Department of Pathobiology, University of Guelph

Biography

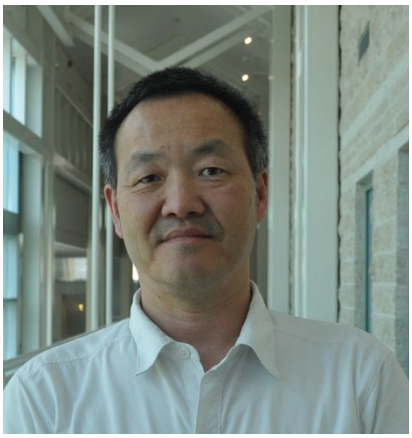
Dr. Ricker is an Associate Professor with the Department of Pathobiology and a recently appointed Tier 2 Canada Research Chair in Systems Approaches to Reducing Antimicrobial Resistance. She completed her undergraduate degree in microbiology at the University of Guelph and her graduate degrees in environmental science at the University of Toronto, focused on genomics of environmental bacteria. For her post-doctoral work, she was cross-appointed at the USDA National Animal Disease Center and Iowa State University, using bioinformatic tools to investigate antimicrobial resistance in swine. She re-joined the University of Guelph as faculty at the Ontario Veterinary College in 2018 with research interests ranging from microbiology and molecular biology to computational biology and bioinformatics. Dr. Ricker's current research is focused on developing management strategies for antimicrobial resistance in livestock in a One Health context, including developing surveillance tools and evaluating alternatives to antibiotics in the swine and poultry industries.

Genomic Detection of Pathogens at CFIA's High-containment lab: One Health Observations in Airborne, Aquatic, and Terrestrial Animals

Oliver Lung

CFIA/ACIA

Biography



Dr. Oliver Lung's research interests include identification, transmission and evolution of novel and unexpected pathogens in terrestrial and aquatic animals. He obtained his Ph.D. in Molecular Biology and Genetics from Cornell University in 2000. He joined the Canadian Food Inspection Agency's Animal Disease Research Institute as a Research Scientist and led the microarray facility until 2015. In 2015, he established and led the Genomics Unit at the Canadian Food Inspection Agency's high-containment laboratory at the National Centre for Foreign Animal Disease (NCFAD) in Winnipeg. His lab operates a unique containment level (CL) 3 high-throughput sequencing (HTS) facility as well as a CL2 HTS lab that conducts whole-genome sequencing and metagenomics sequencing, genomics data analysis, and reporting of approximately 4000 samples a year containing various known, novel, and unexpected pathogens. His lab has discovered several new viruses.

Dr. Lung is also an Adjunct Professor at the University of Manitoba. He is an Editor for Scientific Reports and Discovery Viruses and a reviewer for various scientific journals.

Whole Genome Classification System for Porcine Reproductive and Respiratory Syndrome Virus Type 2 (Betaarterivirus americense) Strains Combining ORF5, nsp3-4-5 and Indels

Vincent Baby, Marika Koszegi, Onyekachukwu Henry Osemeke, Chantale Provost, Carl A Gagnon

Centre de diagnostic vétérinaire de l'Université de Montréal (Baby, Koszegi, Provost, Gagnon)
Swine and Poultry Infectious Diseases Research Centre, Faculté de médecine vétérinaire (Osemeke, Gagnon)

Abstract

Porcine Reproductive and Respiratory Syndrome (PRRS) disease was first observed in 1987 in the United States of America. This disease is responsible for the loss of billions of dollars worldwide in the pig industry and since the discovery of its etiological agent, the virus denomination and classification method has often changed. The current PRRS virus classification system is based on the ORF5 viral gene phylogeny which represents only 4% of the viral genome. However, veterinarian practitioners are confronted with cases of unexpected severity while viral isolates are classified as vaccinal strains. As this virus evolves at high speed by combining an error prone RNA polymerase and a high recombination rate, the ONI classification system (ONI standing for ORF5, nsp3-4-5 and indel) is hereby proposed to better discriminate vaccinal strains from viral recombinants while remaining simple to use. This system was made using a dataset of 1809 publicly available complete genome sequences from 14 countries including 130 newly deposited Canadian sequences. This system combines the current ORF5 classification with a phylogeny of the nsp3, nsp4 and nsp5 segments of ORF1a viral gene as well as groups based on insertions and deletions (indels) at the whole genome scale. For example, the reference strain ATCC VR-2332 would be classified as 5A-n67-IDVR-2332 in this proposed system. Clusters of nsp3-4-5 sequences were determined using sequence identities, revealing 77 clusters distributed around the world. Most clusters were shown to be specific to a single country while 2 clusters associated with vaccinal, and highly pathogenic strains were shown to be widely distributed. Indel groups were made using hierarchical clustering based on the presence of events. Each sequence had an average of 3.68 indel events with most events observed in the nsp2 viral gene. However, some countries shown more an enrichment in indel events in other genes. For example, Canadian strains had a greater number of indel events in the nsp7 gene than any other country. The ONI system was also used to reclassify seemingly vaccinal strains based on their ORF5 lineage alone. For example, of 50 Canadian PRRS virus strains sharing the same ORF5 lineage as the Ingelvac MLV PRRS vaccinal strain, 22 (44%) were identified as different using the ONI classification, with 4 (8%) strains being viral genome recombinants. Bioinformatic tools will be presented and made available for anyone who would like to analyze their own sequences in the form of a Nextstrain community dataset and the IDindel suite of python scripts.

Bovine Abortion Investigation Using a Reproductive Pathogen Sequencing Panel (BovReproSeq) as a Diagnostic Tool

Yanyun Huang, Dhinesh Periyasamy

Prairie Diagnostic Services

Abstract

Prairie Diagnostic Services (PDS) developed and validated a Bovine Reproductive Pathogen Sequencing Panel (BovReproSeq) for the simultaneous detection and partial characterization of 17 pathogens associated with bovine reproductive loss. The assay integrates multiplex PCR with high throughput sequencing to enable parallel analysis of bacterial, protozoal, and viral agents. Target organisms include *Coxiella burnetii, Chlamydia abortus, Ureaplasma diversum, Campylobacter fetus* subsp. *fetus* and *venerealis*, *Campylobacter jejuni, Leptospira* spp., *Listeria monocytogenes, Bacillus licheniformis, Mycoplasma bovis, Trueperella pyogenes, Tritrichomonas fetus, Neospora caninum, Toxoplasma gondii, Sarcocystis* spp., bovine alphaherpesvirus 1 (BoHV-1), and bovine viral diarrhea virus (BVDV). Assay development and validation have been previously published (Periyasamy, 2024).

In spring 2025, BovReproSeq was incorporated into a comprehensive diagnostic investigation of 86 beef cattle abortion cases. Additional diagnostic workups included necropsy, histopathology, bacterial culture, trace mineral analysis, and vitamin A and E testing. An etiological diagnosis was achieved in 77% of cases. Infectious etiologies accounted for 47% of abortions, followed by nutritional deficiencies (22%) and congenital anomalies (8%); 23% of cases remained undiagnosed. Among infectious causes, bacterial pathogens predominated, with *Trueperella pyogenes* (n=5) and *Bacillus licheniformis* (n=4) most frequently identified. Viral etiologies were uncommon, with BoHV-1 identified as the cause of abortion in five cases. Notably, *Mannheimia haemolytica* and *Mycoplasma bovis* were each identified as the etiologic agent in a single case. Although these organisms are common bovine pathogens, they are not typically associated with abortion and may have been missed without a comprehensive diagnostic approach.
The integration of BovReproSeq into routine diagnostic workflows enhanced pathogen detection and contributed to a high diagnostic yield. These findings support the utility of BovReproSeq in bovine abortion investigations and highlight the importance of a comprehensive, multi-modal diagnostic approach.

Reference

Periyasamy, Dhinesh, Yanyun Huang, and Janet E. Hill. "Targeted syndromic next-generation sequencing panel for simultaneous detection of pathogens associated with bovine reproductive failure." *Journal of Clinical Microbiology* 63.1 (2025): e01433-24.

Hybridisation Probe Capture for Disease Surveillance in the Beef Industry.

Daniël Kos, Ashlyn Kirk, Murray Jelinski, Antonio Ruzzini, Andrew D.S. Cameron.

Institute for Microbial Systems and Society, Faculty of Science, University of Regina

Abstract

Infectious diseases cost the Canadian beef industry millions annually through reduced performance and death loss. Bovine respiratory disease complex and its sequelae (*e.g.* septic arthritis, myocarditis) is the leading concern. We previously showed that targeted hybridisation probe capture outperforms shotgun metagenomics in the detection of cattle pathogens. Herein we apply capture to disease surveillance in the beef industry of western Canada. We designed a custom probe panel to include (i) 30 antibiotic resistance genes (ARGs) frequently found in the feedlot environment, plus (ii) a wide variety of bacterial pathogens (19 unique species, 2 broad genera) that infect ruminants. In the first study we conducted pathogen and ARG surveillance across Saskatchewan by swabbing feedlot water bowls (n=19) and collecting water in bottles (n=23). A subsequent study used deep nasopharyngeal swabs (DNS) to test cattle (n=47) at arrival, 1st pull and 2nd pull. In water samples PubMLST strain type was established in 48% for *Pasteurella multocida* (11 x ST1, 2 x ST7, 2 mixed), 46% for *Mannheimia haemolytica* (7 x ST1, 6 mixed), 42% for *Histophilus somni* (2 x ST3, 9 mixed), and 33% for *Mycoplasmopsis bovis* (2 x ST300, 6 mixed). In DNS samples strain type was established in 49% for *P. multocida* (13 x ST1, 3 x ST3), 38% for *M. haemolytica* (12 x ST1), 48% for *H. somni* (1 x ST1, 6 x ST3, 5 x ST4, 1 x ST5, 2 mixed), and 55% for *M. bovis* (1 x ST45, 12 x ST295, 3 mixed). Detection of the above species by hybridisation probe capture outperformed 16S rDNA amplification. Furthermore, the panel allowed for sensitive detection of lesser studied pathogens including *Ureaplasma diversum, Mycoplasmopsis bovirhinis*, *Metamycoplasma alkelescens*, *Bibersteinia trehalosi,* and *Trueperella pyogenes*. The flexibility in probe binding allowed for detection of untargeted microbes such as *Mannheimia pernigra*, which was prominent in both water and DNS. ARG detection in both water and DNS followed previously established trends of strong detection of *estT, mphE, msrE, sul2, tet(H), tet(W/N/W)*, alongside a wide variety of other ARGs. There were more ARGs in 1st pull samples than on arrival. Whether bottle or gauze was more effective in detection efforts was feedlot dependent. This work revitalises strain typing schemes in an age of increasingly accessible sequencing and takes advantage of the existing groundwork to greatly increase sensitivity and subsequent interpretive power over both random sequencing and amplification based microbial community analysis techniques.

20 Years of Barcode Scanning: Identifying difficult-to-culture pathogens with universal PCR sequencing primers.

Lisa Ledger, Nathan Bennoit, Tanya Brock, Calvin Kellendonk, Qiumei You, Lowia Al-Hussinee, Patricia Bell-Rogers, Jacob Avula, Hugh Cai

Animal Health Laboratory, Laboratory Services Division, University of Guelph

Abstract

For the past 20 years, the Animal Health Laboratory at the University of Guelph has used a selection of universal DNA barcoding primer sets for molecular identification of parasites, bacterial and fungi. While the ideal matrix for molecular identification is a pure isolate or unmixed tissue sample, of 852 samples submitted for molecular identification 317 (37.21%) were from non-isolates. The fraction of non-isolate submissions varies by the identification requested: only 23.62% (n=206) of testing requests for 16S rRNA bacterial identification are from non-isolates, compared to 80.83% (n = 156) for fungal or parasite ID using 18srRNA and ITS primer sets.

For non-isolate or mixed tissue samples, the primary challenge lies in overcoming the presence of environmental contaminants or host DNA. For FFPE tissues, the effects of formalin fixation on DNA limit the selection of primer sets, as a working size limit of 500 bp or less falls below the product size amplified by our 18S rRNA or 16s rRNA primer sets. When a sample can be successfully sequenced, there may be additional challenges in providing species-level identification in species-rich genera, or for species where a lack of sequence information exists in public databases.
We review a selection of historical submissions to illustrate different techniques used to overcome challenges to identification by sequence analysis, including recent forays into next-generation sequencing approaches such as targeted metagenomics. These submissions include 16s rRNA bacterial identification of *Nocardia* from FFPE tissues, fungal ITS identification of *Aspergillus* from an enucleated equine eye, 18S rRNA identification of *Babesia odocoeilei* and *Theileria orientalis* from blood samples, COI identification of tissue-embedded avian mites and copepod parasites of fish, a multi-primer approach to speciating *Aspergillus oryzae* from chicken lung nodules, and a combination of Sanger and 18s rRNA metagenomic sequencing to identify *Opisthorchiidae* oocytes in a canine liver sample.

Overall, using Sanger sequencing we have been able to identify organisms in 46.69% (n = 148) of non-isolate submissions, compared to 96.63% (n = 517) of isolates or pure tissues submitted. Wider inclusion of metagenomic approaches is expected to increase the success rate for non-isolate species identification in the future.

Improved Molecular Detection of Salmonella Enteritidis in Poultry Fluff via Real-Time PCR assay

Ruwani Karunarathn, Dhinesh Periyasamy, Chao Chun Liu, Musangu Ngeleka

Prairie Diagnostic Services (Karunarathna**,** Periyasamy, Ngeleka); Department of Molecular Biology and Biochemistry, Simon Fraser University (Liu)

Abstract

Salmonella Enteritidis (SE) remains a leading cause of human foodborne illness and is frequently associated with contaminated poultry products. Importantly, SE is the only non-typhoidal *Salmonella,* for which eradication measures are implemented currently upon detection in poultry farms in Canada. The high stakes associated with SE detection thus necessitate rapid and accurate diagnostic methods to ensure food safety and protect industry integrity. Conventional identification in veterinary diagnostic laboratories relies on bacterial culture followed by serotyping and whole genome sequencing (WGS). However, centralized serotpying and the high cost and turnaround time of WGS can delay reporting by several weeks. To address these limitations, we adapted the iQ-Check Bio-Rad SE PCR assay for direct detection of SE from poultry fluff samples, enabling SE detection within 48 hours of sample collection.

A total of 230 samples were collected from Saskatchewan and British Columbia and pre-enriched in buffered peptone water (1:10, 1% BPW). DNA extracted from pre-enriched samples was screened using the adapted PCR assay. In parallel, samples underwent secondary enrichment in Rappaport–Vassiliadis medium and were analyzed using a validated metagenomic sequencing (MGS) workflow. Traditional culture on selective media followed by serogrouping (Group D detection) and WGS was performed for comparison.

Among 89 culture-positive samples, 38 were identified as Group D, of which 37 were PCR-positive for SE. However, the single Group D isolate that was PCR-negative was reclassified based on sequencing results, as both WGS and MGS identified it as *S.* Kentucky (Group C3). Among the 51 Group D-negative isolates, 49 were PCR-negative, demonstrating high specificity. This robust specificity is further supported by the observation that 139 of 141 (98.5%) culture-negative samples were also PCR-negative. Overall, the PCR results demonstrated 100% concordance with WGS for SE detection, highlighting its potential to replace conventional approaches. The discrepancy between serogrouping and molecular methods further highlights the potential for misclassification when relying on agglutination-based methods.

This adapted PCR-based workflow enables SE detection within 48 hours, significantly reducing turnaround time compared to conventional approaches. Implementation of this method offers a rapid, cost-effective alternative for routine surveillance, benefiting both diagnostic laboratories and poultry producers through timely decision-making and reduced operational costs.

Validation of a real-time polymerase chain reaction (qPCR) assay for detection of *Flavobacterium branchiophilum* in gill disease of salmonids

Lowia J. Al-Hussinee, Heindrich N. Snyman, Lisa Ann Ledger, Patricia Bell-Rogers, & Hugh Y. Cai

Animal Health Laboratory, Laboratory Services Division, University of Guelph

Abstract

Flavobacterium branchiophilum (F. branchiophilum) is a psychrophilic bacterium that colonizes gill tissues forming filamentous structures that attach to the epithelial cells leading to epithelial hyperplasia, necrosis, and impaired respiratory function. This condition, known as bacterial gill disease (BGD), is confined to the gill tissues. It affects salmonid species worldwide and poses a particular health concern with especially significant economic impact in intensive aquaculture systems. Predisposing environmental factors such as overcrowding, suboptimal water quality, elevated ammonia concentrations, low dissolved oxygen levels, and excess suspended organic matter can increase susceptibility to infection.

Conventional diagnosis of BGD typically relies on wet mount microscopic examination of gill biopsies, histopathological assessment, and bacterial culture. Wet mount examination provides rapid results but may lack sensitivity, while histopathology requires additional processing time. Isolation of *F. branchiophilum* in bacterial culture can be challenging due to the organism's fastidious growth characteristics and prolonged incubation period. Therefore, the Animal Health Laboratory (AHL) developed and validated a probe-based real-time polymerase chain reaction (qPCR) assay as a more rapid alternative diagnostic method, improving detection sensitivity and specificity for confirming suspected BGD cases.

Primer and probe sequences were derived from the 16S rRNA gene sequence of a clinical isolate (AHL 23-013476) which demonstrated 99.8% identity to *F. branchiophilum.* DNA from 21 common fish pathogens, including closely related *Flavobacterium species*, demonstrated no cross-reactivity. Analytical sensitivity was evaluated using ten-fold serial dilutions in BGD-negative fish tissue homogenate, both of genomic DNA from *F. branchiophilum* isolate 23-013476 and of synthetic DNA (gBlock). The limit of detection (LoD) was determined to be 1.37×10^1 copies per 2 µl DNA extract, or approximately 3.245 x 10^3 copies per 25 mg of gill tissue, demonstrating high analytical sensitivity.

Diagnostic performance of the assay was further evaluated using field cases submitted for suspected BGD based on gill biopsy and histopathological findings. The qPCR assay successfully detected *F. branchiophilum* in samples exhibiting filamentous bacteria consistent with BGD lesions. The assay demonstrated superior sensitivity compared to wet mount examination and high specificity with no false-positive amplification observed among other tested fish pathogens. Implementation of this assay supports improved diagnostic confidence and timely management of bacterial gill disease in salmonid aquaculture systems.

Combatting Online Misinformation

Andrew Papadopoulos

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

Biography

Andrew Papadopoulos is the Coordinator of the Master of Public Health Program at the University of Guelph. He is the current chair of the National Collaborating Centre for Methods and Tools, Canada, served as chair of the National Collaborating Centre for Environmental Health for seven years and as chair of the Canadian Network of Schools and Programs of Population and Public Health for three years. Additionally, he was past-chair of the Natural, Physical, and Engineering Science Research Ethics Board and the Board of Graduate Studies at the University of Guelph.

Diphtheria in a Donkey … The Opportunities and Hurdles in Adopting a One Health Approach

Heather McClinchey

Ontario Ministry of Health

Biography

Dr. Heather McClinchey, DVM, is proud to be a veterinarian, farmer, wife, mother, and One Health champion. She graduated from the Ontario Veterinary College and went into mixed animal practice for several years before pivoting to small animal practice ownership. In 2018, she returned to OVC to complete a Master of Public Health degree. She has the coolest job in the world now, working as the veterinary consultant in the Office of the Chief Medical Officer of Health, a position that she's held since 2021.

Pitfalls, challenges and opportunities; lived experiences with scientific communications

Scott Weese

Department of Pathobiology, Ontario Veterinary College, University of Guelph

Biography

Scott Weese is a veterinary internal medicine specialist and the chief of infection control at U of G's Ontario Veterinary College. He is an expert in infectious and parasitic animal disease, including rabies, tick-borne diseases, antimicrobial resistance and emerging diseases. He is the former Canada Research Chair in Zoonotic Diseases.

Weese focuses on a range of infectious disease issues of animals and humans, including antimicrobial resistance, antimicrobial stewardship, emerging infectious diseases and infection control. He also writes and speaks extensively about infectious (and often zoonotic) diseases, particularly on Worms and Germs Blog.

Rabies Response & Surveillance in Ontario: A One Health Team Effort

Maureen Anderson

Ontario Ministry of Agriculture, Food and Agribusiness (OMAFA)

Biography

Dr. Maureen Anderson, DVM, is a graduate of the Ontario Veterinary College and is ACVIM board-certified in large animal internal medicine. Her graduate and post-graduate work had a strong focus on infectious disease control and zoonotic diseases in particular.
She is currently Lead Veterinarian - Animal Health and Welfare at the Ontario Ministry of Agriculture, Food and Agribusiness, where she continues to work in areas bridging animal and public health, including rabies and antimicrobial stewardship, and co-leads the companion animal Ontario Animal Health Network (OAHN).

The Role of Wildlife Disease Surveillance in Advancing One Health

Brian Stevens

Canadian Wildlife Health Cooperative

Abstract

Wildlife disease surveillance plays a critical role in advancing One Health by providing early detection of zoonotic pathogens. Selected diseases covered show how wildlife monitoring supports early detection of emerging health risks.

Biosecurity at the Edge: Using Efficient Deep Learning to Identify Important Animal Health Pathogens and Disease Vectors

Josip Rudar

Canadian Food Inspection Agency (CFIA)

Biography

Josip Rudar earned his BA in Microbiology at the University of Guelph in 2008 and completed a Bachelor of Education from the Western University in 2010. He completed an Masters in Bioinfomatics at the University of Guelph in 2017. His research interests include the genomics of SARS Cov-2 and use of deep learning models to predict influenza A virus subtypes and host source. Since 2021 he has held the position of Science Laboratory Evaluator at the Canadian Food Inspection Agency, Genomic Unit

From Poultry to People: The Value of a One Health Approach to Salmonella Enteritidis Outbreak Investigations

Vanessa Morton

Public Health Agency of Canada (PHAC)

Abstract

Introduction: In Canada, *Salmonella* Enteritidis (SE) is the most commonly reported *Salmonella* serotype in human cases. All human *Salmonella* isolates undergo whole genome sequencing (WGS). The sequencing data are compiled in the PulseNet Canada database at the National Microbiology Laboratory. Sequence data from *Salmonella* isolated from animal, environmental, and food samples are also integrated into this national database. The integration provides opportunities to identify transmission pathways and identify sources of illness in outbreak investigations. From October 2024 to December 2025 a national outbreak investigation was conducted into the largest Canadian *Salmonella* WGS cluster. Domestic poultry consumption was identified as a risk factor but additional analysis using a subcluster approach was needed to understand how this contributed to illnesses.

Methods: All *Salmonella* isolates from human, animal, environmental and food sources were entered into the PulseNet Canada database. WGS was used to identify isolates that belonged to this cluster. Human SE cases in this cluster were interviewed to collect epidemiological data (food consumption, travel, and animal contact) in the 7 days prior to illness onset. Metadata for non-human isolates (sample source, collection date, and location) was obtained from national surveillance programs (the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) and FoodNet Canada) and from passive animal health surveillance. Cases were further classified into subclusters of highly related isolates (<= 3 allele differences). Subclusters were analyzed using a One Health approach, combining human exposure data, and non-human isolate metadata to identify likely transmission routes.
Findings: Between October 2024-December 2025, 1806 human isolates were associated with this WGS SE cluster. In addition, 285 isolates from non-human sources were associated with this cluster; 94% were either from poultry or their environment. Metadata was available for approximately 60% of the non-human isolates. Integration of human and non-human samples enabled the identification of two specific strains that were circulating in broiler chicken production in specific areas of the country and helped track the transmission through the production chain. Through subcluster analysis methods it was determined that 37% (663/1806) of human cases in the cluster were likely associated with domestic poultry exposure.

Conclusions: This investigation demonstrated how integration of human, food and animal surveillance data can support outbreak investigations. Genomic and epidemiologic evidence indicate that SE transmission occurs across multiple stages of broiler production and ultimately reaches consumers. These findings highlight the value of a One Health surveillance approach for enteric disease in Canada.

SamnSero: Integrating Nextflow and ONT to Assess Salmonella Risk in Real-Time

Chao Chun Liu, Ruwani Karunarathna , Dhinesh Periyasamy, Musangu Ngeleka

Department of Molecular Biology and Biochemistry, Simon Fraser University (Liu); Prairie Diagnostic Services (Karunarathna, Periyasamy, Ngeleka,)

Abstract

Timely detection and reporting of emerging diseases and risk factors in the environment is critical to the control and prevention of infectious disease transmissions. While the rapid evolution of sequencing technologies in recent years has enabled the characterization of the full complement of genetic materials from clinical or environmental samples within one working day, diagnostic turnaround times remain suboptimal. In 2015, a sequence analysis workflow, called “What’s in my Pot” was published, demonstrating the possibility of classifying sequencing data in parallel with sequencing, i.e. in real-time by exploiting the live basecalling feature of Oxford Nanopore Technologies (ONT). Coupling data analysis with data generation is a highly promising strategy to reduce the time costs of routine diagnostics and enable faster responses to health emergencies. To extend beyond species identification, we present SamnSero, an open-source EPI2ME-compatible Nextflow pipeline designed to analyze nanopore data from bacterial isolates or metagenomic samples in real-time to monitor the risk of *Salmonella enterica* in agricultural settings. The software consumes streaming data from ONT sequencers and continuously updates the diagnostic results (e.g. taxonomic profile, risk gene annotation, typing), as new sequences become available. By iteratively assembling *Salmonella* genomes during sequencing, we demonstrated the feasibility of accurately serotyping *Salmonella* isolates within less than an hour of sequencing–a process that typically takes several hours by conventional workflows. Future work will focus on large-scale validation and integration of SamnSero into routine diagnostic workflows at Prairie Diagnostic Services. This implementation will accelerate the reporting of high-risk *Salmonella* in poultry and egg production systems, supporting more rapid interventions to protect public health and agricultural biosecurity. Racehorse mortality in Ontario: postmortem procedures and results

Risk Factors for Antimicrobial Resistance in Urinary Escherichia coli from Dogs in the United States (2018–2024) * Student Presentation

Rasaq A. Ojasanya, J. Scott Weese, Kurtis E. Sobkowich, Anne Deckert, Donald Szlosek, Andy Plum, Theresa M. Bernardo, and Zvonimir Poljak

Department of Population Medicine, Ontario Veterinary College, University of Guelph (Ojasanya, Sobkowich, Deckert, Bernardo, Poljak); Department of Pathobiology, Ontario Veterinary College, University of Guelph (Weese); Centre for Public Health and Zoonoses, Ontario Veterinary College, University of Guelph (Weese); IDEXX Laboratories Inc. (Plum, Szlosek)

Abstract:

Background: Bacterial cystitis, most commonly caused by *Escherichia coli*, is a leading indication for antimicrobial use in dogs and contributes to antimicrobial resistance (AMR), a growing One Health concern. This study evaluated patient-, socioeconomic-, and geographic-level factors associated with resistance in urinary *E. coli* isolates from dogs across the United States.

Methods: From 2018 to 2024, a total of 393,972 clinical urinary *E. coli* isolates, obtained from 339,977 dogs at a national commercial diagnostic laboratory, met the inclusion criteria for analysis after excluding isolates from the first six months of the study period, although these excluded data were retained to ascertain the number of prior positive cultures within the preceding six months. Multilevel logistic regression models were used to examine the relationships between selected exposures of interest and AMR, accounting for clustering at the patient, county, and state levels.

Results: Resistance was highest to amoxicillin (27.39%; 95% CI: 27.25–27.53). Across antimicrobials, the largest proportion of variation occurred at the patient level (range: 22.2–46.1%). The odds of detecting resistance increased linearly with the number of prior positive cultures in the preceding six months. After adjustment for other variables, each 1% increase in the annual county-level percentage of dogs receiving culture and susceptibility testing was associated with a 1–2% decrease in the odds of detecting resistance (OR: 0.98–0.99; $p<0.001$). States with 1,500–1,999 housing units per veterinarian had higher odds of marbofloxacin resistance (OR: 1.85, 95% CI: 1.20–2.84, adjusted $p = 0.027$) than states with 500–999 units, a pattern consistent across other antimicrobials.

Conclusions: Patient-level factors, particularly recent repeated positive cultures, were strongly associated with AMR in canine urinary *E. coli*, likely reflecting cumulative antimicrobial exposure and/or persistent resistant infections. In contrast, the odds of detecting AMR were lower in counties with more frequent microbiological testing and greater veterinarian density, underscoring the role of diagnostic stewardship and equitable access to veterinary care as key components of One Health strategies to mitigate AMR in companion animals.

Results of an AMRNet-Vet Survey of Challenges, Lab Practices, and Prioritization of Harmonized Guidelines for Antimicrobial Susceptibility Testing among 9 Public Veterinary Laboratories in Canada.

Wallis Rudnick, Violetta Zaitseva, Justin Carr, Carolee Carson, Julie-Hélène Fairbrother, Ruwani Karunarathna, Beverly Morrison, Sarah Pike, Neil Pople, Matthew E. Saab. Durda Slavic

Public Health Agency of Canada (Rudnick, Zaitseva, Carson); Provincial Veterinary Lab, Fredericton (Carr); Université de Montréal and Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec (MAPAQ) (Fairbrother); Prairie Diagnostic Services (Karunarathna); Diagnostic Services Unit, University of Calgary (Morrison); Animal Health Division, Department of Fisheries, Forestry & Agriculture (Pike); Veterinary Diagnostic Services, Manitoba Agriculture (Pople); University of Prince Edward Island (Saab); Animal Health Laboratory, Guelph (Slavic)

Abstract

AMRNet is a lab-based antimicrobial resistance surveillance program led by the National Microbiology Laboratory of the Public Health Agency of Canada, active since 2021.

Methods
In October 2025, AMRNet-Vet, the veterinary component of AMRNet, sent out a survey to 10 public veterinary laboratories (one in each province) to gather information about challenges associated with antimicrobial susceptibility testing (AST), current testing and interpretation practices, and importance of guideline harmonization for certain animal species and bacterial-animal combinations for veterinary laboratories in Canada.

Results
A total of 11 valid responses were received from nine laboratories; most commonly microbiologists/bacteriologists (5/11) and laboratory technologists (3/11). The lack of available animal-species-specific veterinary breakpoints from the Clinical and Laboratory Standards Institute (CLSI) was identified as an important challenge by respondents. Specific issues highlighted included challenges communicating with clients or providing clients with information on antimicrobials of interest. Challenges associated with absence of harmonized standards for composition of antimicrobial panels for veterinary use were less of a concern, but respondents highlighted that the lack of harmonization makes it challenging to compare susceptibility results across laboratories or to literature.

Antimicrobial susceptibility testing methods varied between labs. Interpretation practices also varied between labs, although VET01S approved breakpoints where animal-species-specific breakpoints exist and human breakpoint recommendations from VET01S were most commonly used. Practices for reporting interpretation sources to clients also differed between labs with an equal split between always reporting interpretation sources for AST results and reporting them only by request, when the information was available to them.

When asked about which animal species it would be most helpful to have new harmonized breakpoint interpretation guidelines, respondents prioritized dogs, cats, and cattle and placed the least importance on aquatic species. The same species were prioritized for bacterial-animal combinations for which it would be helpful to have harmonized guidelines for breakpoint interpretations.

Conclusion
In summary, the lack of available breakpoints is a challenge for Canadian veterinary laboratories. Susceptibility testing and interpretation practices vary among veterinary labs. Results emphasized the

need for updated and more harmonized guidelines for breakpoint interpretation in animals, with priority given to dogs, cats and cattle.

Antimicrobial Susceptibility of Trueperella pyogenes isolates from British Columbia, Canada

Parichay Raj Subedi, Kazal Krishna Ghosh, Florence Huby, Joseph Elliot Rubin

Department of Veterinary Microbiology, University of Saskatchewan (Subedi, Ghosh, Huby, Rubin); Animal Health Centre, Government of British Columbia (Ghosh)

Abstract

Trueperella pyogenes is a Gram-positive bacterium that colonizes the skin and mucus membranes of the upper respiratory, gastrointestinal, and urogenital tracts of agricultural and wild animals. As an opportunistic pathogen, this organism is associated with purulent infections of the respiratory, digestive, and reproductive systems. These infections result in economic losses due to decreased milk production and quality, reproductive failures, and partial or total carcass condemnation during slaughter. Despite its clinical importance and frequent isolation from clinical specimens, there is limited information on its antimicrobial resistance patterns. Furthermore, very limited interpretive criteria are available for categorizing antimicrobial susceptibility test results. The Clinical and Laboratory Standards Institute (CLSI) currently only publishes susceptible breakpoints for penicillin, ampicillin, erythromycin, and trimethoprim-sulfamethoxazole. In the present study, 120 *T. pyogenes* isolates grown from diagnostic submissions to the Animal Health Centre in British Columbia (2023-2025) were characterized. Minimum inhibitory concentrations (MICs) to a broad panel of 19 drugs were determined by the agar dilution method according to the CLSI guidelines. Most isolates were categorized as susceptible to penicillin (97.5%) while only a small minority were susceptible to ampicillin (4.2%). The MIC distribution for both drugs was unimodal, indicating a homogeneous response across the population. Similarly, 81.6% of isolates were susceptible to trimethoprim-sulfamethoxazole with a unimodal distribution. The MIC distribution of the lincosamide and macrolide antibiotics tested was heterogeneous, suggesting the presence of both wild-type organisms and those with acquired resistance mechanisms. 66.6% of isolates were susceptible to erythromycin. The difference in the frequency of penicillin and ampicillin susceptibility was surprising and may reflect limitations in the current interpretive breakpoints. As both drugs are similar β-lactams, this may indicate the need for the CLSI breakpoints to be revised. For other drugs, the MIC distribution patterns observed suggest the presence of resistant subpopulations of *T. pyogenes,* highlighting the potential impact of resistance and **emphasizing the importance of antimicrobial stewardship.** The present study provides the first regional data on antimicrobial susceptibility of **T. pyogenes** in British Columbia and highlights gaps in the existing interpretive guidelines. Overall, our results will form the basis for future investigations to understand the mechanism of resistance in *T. pyogenes* and help establish evidence-based breakpoints.

Evaluating associations between antimicrobial use and antimicrobial susceptibility testing results in *Clostridium perfringens* in Canadian broilers, turkeys, and layers (2018-2023)

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Center for Foodborne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada (Reedman, Hill, Reid-Smith, Agunos); National Microbiology Laboratory, Public Health Agency of Canada (Charlebois); Department of Population Medicine, Ontario Veterinary College, University of Guelph (Hill, Reid-Smith); Animal Health Laboratory, University of Guelph (Slavic)

Abstract

Necrotic enteritis, caused by *Clostridium perfringens*, is an important enteric disease that impacts various performance metrics in poultry including feed conversion ratio and mortality rate. In Canada, the majority of antimicrobials administered through feed on broiler and turkey farms are intended or used for necrotic enteritis control. A strong association between higher antimicrobial use (AMU) in poultry production and increased antimicrobial resistance levels has commonly been reported, particularly involving antimicrobials commonly used for treating necrotic enteritis. The objective of this study was to characterize the antimicrobial susceptibility testing (AST) results of *Clostridium perfringens* isolates recovered from healthy broiler, turkey, and layer flocks in Canada, and to evaluate potential associations between AST results and reported AMU.

Methods
AMU data from questionnaires, and fecal samples for AST, were collected by 17 poultry veterinarians across Canada. Data from 210 broiler, 91 turkey, and 66 layer flocks from 2017 to 2018 (broilers only), 2021, and 2023 were included in the analysis. Minimum inhibitory concentration (MIC) results for tested antimicrobials were categorized as high or low based on available clinical breakpoints and determined cut-off values based on the available data. Dependent on levels of AMU and distributions of MIC data, mixed-effect logistic regression models examined the relationship between bacitracin use and high MICs in broilers and turkeys.

Results
Bacitracin was the most commonly reported antimicrobial used across all three commodities. Significant differences in MIC distributions for bacitracin were observed among the three commodities, with broilers demonstrating the highest percentage of isolates in the highest measurable MIC range for the majority of tested antimicrobials. Logistic regression analysis revealed a statistically significant relationship (*P*-value ≤0.05) between bacitracin use and MIC values for both broilers and turkeys. For every 1 mg/kg increase in bacitracin use the odds of detecting a high MIC value increased by 4.5 % in broilers (OR = 1.045) and 9.6 % in turkeys (OR = 1.096).

Conclusion
These findings suggest that elevated AMU, particularly bacitracin, is associated with reduced susceptibility (higher MICs) in *C. perfringens* isolates from poultry, highlighting the need for prudent use of antimicrobials to preserve antimicrobial efficacy.

Theileriosis in Dairy Cows from Eastern Ontario

Hugh Cai, Kristiina Ruotsalo, Tim Pasma, Lisa Ledger, Patricia Bell-Rogers, Cynthia Miltenburg, Oliver Lung, Vladislav Lobanov, Jeff Gross, Elias Taylor, Maria Spinato

Animal Health Laboratory, University of Guelph (Cai, Ruotsalo, Pasma, Ledger, Bell-Rogers, Spinato); Ontario Ministry of Agriculture, Food and Agribusiness (Miltenburg); Canadian Food Inspection Agency National Centre for Foreign Animal Disease (Lung); Centre for Food-borne and Animal Parasitology (Lobanov); AAC Genomics Facility, University of Guelph (Gross, Taylor)

Abstract

A 5-year-old Holstein cow imported from the United States in July 2025, presented with pale mucous membranes, decreased appetite, and reduced milk production after attending a local livestock show in Ontario, Canada. Hematologic evaluation revealed marked regenerative anemia (hematocrit 0.15 L/L; hemoglobin 43 g/L), mild neutropenia, and mild to moderate lymphocytosis, with marginal hyperbilirubinemia on serum biochemistry. Peripheral blood smear examination demonstrated frequent polychromasia, basophilic stippling, and intraerythrocytic oval to linear and signet-ring–shaped piroplasms consistent with *Theileria* spp. PCR targeting the 18S rRNA gene confirmed infection with the *Theileria orientalis* complex. Genotyping by major piroplasm surface protein (MPSP) gene PCR and sequencing, as well as Oxford Nanopore Technologies metagenomics performed at CFIA National Centre for Foreign Animal Disease (CFIA, NCFAD) and the University of Guelph AAC Genomics Facility (AACGF), identified *T. orientalis* genotype Ikeda.

Following identification of the index case, 46 herd mates were tested. After clinical recovery, the index cow remained PCR-positive with an increased Ct value compared to the initial sample. One additional subclinical cow was identified as PCR-positive and confirmed as *T. orientalis* Ikeda. No organisms were observed on blood smears from other herd mates.

This report documents the first known detection of *T. orientalis* genotype Ikeda in Ontario and in Canada. Given the pathogenic potential of the Ikeda genotype and its association with significant economic losses internationally, heightened awareness and prompt diagnostic evaluation of regenerative anemia in cattle are warranted. Early recognition through blood smear examination and confirmatory PCR testing is critical for disease detection, surveillance, and regulatory response.

Piscine Lactococcosis Surveillance in Rainbow Trout in Ontario, Canada 2023-2025.

Alexandra Reid, Marcia Chiasson, Kerry Hobden, Peter Addison, Hugh Cai, Patricia Bell-Rogers, and Calvin Kellendonk.

OMAFA

Abstract

Piscine lactococcosis (PL), a disease with high mortality in rainbow trout and an emerging zoonotic disease, is caused by a trio of bacteria: *Lactococcus garvieae*, *L. petauri*, and *L. formonensis*. First detected across Canada and the United States in 2020, the disease was devastating with mortality of over 90% reported and complete depopulation in some facilities. Evidence after California's large outbreak showed that wild freshwater fish could be asymptomatic hosts, and PL could also be detected in the environment. As a re-emerging pathogen, we have little information about the presence, host state and environmental reservoirs. For two consecutive years, every month, we tested 10 and then 14 rainbow trout premises for both fish and environmental samples. The first year, the Ministry of Natural Resources tested their fish monthly at culture stations and the environment, and then for logistical reasons sampling was moved to the laboratory instead of *in situ*. Overall compliance with sampling was high. As well, part of this project was to validate a specific media for PL, which showed superior sensitivity over standard fish culture media, including detecting *P. garvieae* which had not been detected before in Ontario. Moreover, this methodology detected a small PL outbreak in 2024 that was not detected by producers based on mortality, rates being lower than 2020. Wild fish were not positive, but briefly two samples from culture station environs were not-consecutively positive during the outbreak in farmed fish. Environmental persistence did not occur after detection. Most strains were unrelated to each other, showing the difficulty of creating autogenous vaccines for these pathogens. This validates the usefulness of specific media and surveillance as a tool to understand patterns and persistence in a re-emerging zoonotic pathogen, and as an educational tool.

Association between Salivary Anti-CarLA IgA Concentrations in Ontario Pastured Sheep and Offspring Performance

Bradley D. DeWolf, Cathy A. Bauman, Paula I. Menzies, Emma A. Borkowski, Richard J. Shaw, Andrew S. Peregrine

Department of Pathobiology, Ontario Veterinary College, University of Guelph (DeWolf, Borkowski, Peregrine); Department of Population Medicine, Ontario Veterinary College, University of Guelph (Bauman, Menzies); AgResearch Limited, Grasslands Research Centre, New Zealand (Shaw)

Abstract

Immunity to gastrointestinal nematodes (GIN) develops in lambs following exposure to parasites on pasture. Previous data have demonstrated that the concentration of salivary immunoglobulin A (IgA) against carbohydrate larval antigen (CarLA), found on the surface of all infective GINs, is an indicator of GIN immunity in sheep in Ontario. Considered a moderately heritable trait, the relationship between salivary anti-CarLA IgA in ewes and their offspring has not been investigated in Canada. As such, this study measured the salivary anti-CarLA IgA responses of Canadian ewes and their progeny, and examined associations with the performance of pastured lambs. In 2022, 98 replacement ewe lambs were randomly selected from 10 farms in Ontario, following their first grazing season. At selection, saliva samples were collected for anti-CarLA IgA testing, and fecal egg count (FEC), weight, body condition, fecal consistency, hematocrit, and anthelmintic treatment history were recorded. The ewes were re-sampled 4 weeks after returning to pasture in 2023; their offspring (n=107) were sampled 60 days after turnout. At sampling, 22.4% (24/107) of offspring lambs had detectable salivary anti-CarLA IgA, with a mean FEC of 1120 eggs per gram. Linear mixed modeling revealed that 2022 salivary anti-CarLA IgA concentration in dams was positively associated with offspring weight after 60 days of grazing pasture, when age and sex were controlled (β=0.834; p=0.008). These data suggest that acquired immunity to GIN starts developing in Canadian lambs within 60 days of turnout, and that the salivary anti-CarLA IgA response of the dam appears to predict lamb performance.

Beyond Positives to Signals: What Submissions, Negatives, and Metadata can (and can't) Reveal about Disease Trends

Zvonimir Poljak

Department of Population Medicine, Ontario Veterinary College
University of Guelph

Biography

Zvonimir Poljak graduated from the University of Zagreb with a Doctor of Veterinary Medicine (DVM) degree, followed by an MSc and PhD in Epidemiology from the University of Guelph. Currently an Associate Professor at the Ontario Veterinary College, Poljak's research specializes in epidemiology and animal health, with a focus on infectious disease surveillance, emerging pathogens, and the application of data science in veterinary medicine and public health.

Preparedness Prior to Possible Incursion: Using Models to Assess the Risk of H5N1 Influenza Introduction and Spread in Ontario Dairy Cows

Amy Greer

Trent University

Biography

Dr. Amy Greer is an Associate Professor in the Department of Biology at Trent University. She was inducted into the Royal Society of Canada, College of New Scholars in 2023. Dr. Greer previously (2014-2024) held a Canada Research Chair in Population Disease Modeling and was an Associate Professor in the Department of Population Medicine, Ontario Veterinary College at the University of Guelph. Dr. Greer was also the (2022 - 2023) Graduate Program Coordinator for the Department of Population Medicine.

Dr. Greer has previously held scientific positions in the Centre for Communicable Diseases and Infection Control at the Public Health Agency of Canada and the Dalla Lana School of Public Health at the University of Toronto.

She completed her postdoctoral training at the Hospital for Sick Children in Toronto. Dr. Greer's research program explores the introduction, spread, dynamics, and control of infectious diseases in populations. She integrates empirical data with mathematical models to test the mechanisms leading to the epidemic spread of pathogens and identify optimal intervention and control strategies. Her research aims to examine the effectiveness and cost-effectiveness of both public health and veterinary health interventions in order to make informed decisions regarding public health policy.

The Ontario Animal Health Network's Contributions to Knowledge Transfer and Acquisition

Tanya Rossi

Animal Health Laboratory, University of Guelph

Biography

Tanya Rossi is a veterinary epidemiologist focusing on health surveillance systems and data management. She earned her DVM degree from the Ontario Veterinary College in 2009 and a PhD in epidemiology in 2017. She has previously worked in large animal practice, public health, and animal and human health surveillance. She currently acts as the Ontario Animal Health Network coordinator and the Animal Health lab's epidemiologist and data manager.

Foreign Animal Disease Emergency Exercises – 15 Years of Continuous Improvement

Andrew Brooks, Hein Snyman, Emily Martin, Maria Spinato

Animal Health Laboratory, University of Guelph

Abstract

Over the past 15 years, the Animal Health Laboratory (AHL) has conducted annual emergency preparedness exercises to test and refine standard operating procedures for managing suspected reportable (foreign) animal disease (FAD) postmortem submissions. These exercises provide an essential mechanism for ensuring the AHL can respond effectively to FAD suspects, for maintaining staff readiness, and for verifying communication and notification pathways among the AHL, the Department of Pathobiology (OVC), the University of Guelph, the Canadian Food Inspection Agency (CFIA), and the Ontario Ministry of Agriculture, Food and Agribusiness (OMAFA). This presentation will outline how these exercises are planned and executed, and will highlight how evaluator feedback from CFIA and OMAFA participants has driven continuous improvement in AHL emergency procedures.

Proficiency Testing in an Animal Health Laboratory

Ashley Lacey

Lab Services, University of Guelph

Abstract

In an animal health laboratory, participation in proficiency testing is an important aspect of a quality management system and a valuable activity to participate in. As an introduction to proficiency testing, this presentation will look at what proficiency testing is, including an overview of the participation process, why a laboratory might participate in proficiency testing, and the importance and benefits of proficiency testing in an animal health laboratory, touching on real world examples seen in our laboratory.

Development of a Proficiency Testing Program for Swine Enteric Viruses for Veterinary Laboratories in Canada

Angela Riveroll

University of Prince Edward Island

Abstract

Proficiency testing (PT) is a critical component of quality management for veterinary testing laboratories. Currently PT modules for swine enteric viruses (SEVs) are not available in Canada, although, many veterinary laboratories offer diagnostic testing for SEVs. The development of a SEV PT module was initiated to enable veterinary laboratories in Canada to assess and demonstrate the accuracy of their test results in comparison to other participating laboratories with respect to specificity, sensitivity, and inclusivity. This PT program will also enable veterinary laboratories to assess the performance of new assays in development for SEV detection. The SEV pilot PT program will be offered through the International Veterinary Proficiency Testing Center (IVetPTC) at the Atlantic Veterinary College (AVC) in Prince Edward Island, Canada.

The development of a proficiency testing program for SEVs involved 4 key steps (1) Sending a questionnaire to participating laboratories to identify needs, (2) Preparing relevant proficiency testing materials, (3) Designing quarterly PT schemes (4) Developing an electronic PT module for data entry, analysis, reporting and feedback.

Animal health laboratories across Canada were contacted two years ago to determine their interest in participating in a pilot SEV proficiency testing scheme; four laboratories responded to the survey and provided information regarding technologies currently used for SEV detection, assay design and gene targets for molecular assay detection. This information was used to design PT materials, which consist of inactivated, whole, reference viruses or gene-specific armored RNA constructs, which were spiked into a specific-pathogen-free (SPF) fecal matrix. Reference materials in development were assessed by RT-qPCR to ensure target stability for specific pathogen detection. Three distinct SEV PT panels were designed, including: two quantitative panels (porcine coronaviruses [TGEV, PEDV and PDCoV]) and (porcine rotaviruses [PRVA, PRVB and PRVC]) with high, medium and low viral loads to assess assay sensitivity; and one qualitative panel (random SEVs including pan-Canadian viral variants) to assess assay specificity and inclusivity.

An electronic SEV module was designed to capture participant and assay information and to facilitate data entry, data analysis and electronic reporting. Data analysis options include quantitative analysis (Z-scores and a Kernel Density Plot) for test groups that use similar technologies and qualitative analysis (presence/absence) for new tests and unique technologies. Cost-free pilot SEV PT schemes will be offered quarterly, and reports will be forwarded to participating laboratories. Feedback will be requested from participating labs and will be used to improve the PT program.

Poster 1: Natural Language Processing and Machine-Learning Models in Veterinary Free-Text Clinical Records: A Scoping Review

Grace Couper, Zvonimir Poljak

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

Abstract

Veterinary records are typically written as open text fields, making it difficult to assign a diagnostic code or estimate the prevalence of an illness without reading a full record. However, natural language processing can be trained to detect the presence of a specific illness or categorize a record to a diagnosis class. This review aims to summarize the existing literature on the use of natural language processing to extract data from veterinary electronic health records. It will highlight which existing models show the most promise and describe the limitations of previous models.

A scoping review is being conducted, including studies with animal clinical, laboratory, or surveillance text data that utilize natural language processing. Databases searched include IEEE Xplore, CABI Digital Library, Web of Science, Compendex, and Medline. Search terms used were related to machine learning or natural language processing, veterinary medicine, and the types of data and records.

The search resulted in 477 articles after duplicates were removed, and 71 articles were included in the full-text screening. Forty-five articles used natural language processing and were included in the scoping review. One key difference between studies was the use of pre-existing large language models, such as BERT or ChatGPT. Studies that built off existing models did not necessarily have improved accuracy, particularly when models were not trained on veterinary health records.

Additionally, some studies trained models to identify one condition, where each record did or did not contain information on that condition, while other studies trained models to match a diagnosis code or theme to a record. Studies assessing the presence or absence of one symptom, diagnosis, or treatment had better outcomes, including sensitivity, specificity, and F-1 scores, compared to models matching records to a list of numerous codes. One challenge seen in many studies is the decreased accuracy when a model is applied to new data from a different source, highlighting the variability in free-text records, particularly across organizations.

Studies that detected the presence or absence of an illness had better accuracy than models that categorized records into diagnostic themes. Additionally, studies that built off existing models tended to have improved accuracy.

Poster 2: Investigating The Effect of Endurance Racing on Cardiac Troponin I Release in Saskatchewan Horses

Jonathan Morton, Janel Wessel, Vanessa Cowan

Department of Veterinary Biomedical Sciences, Western College of Veterinary Medicine

Abstract

A common complaint among equestrians regarding their horses is poor athletic performance, usually stemming usually from underlying myocardial disease. Underlying myocardial disease is difficult to detect, and diagnosis relies on electrocardiograms and echocardiograms, devices requiring experienced operators. In humans, myocardial disease is diagnosed by measuring cardiac troponin I (cTnI), the gold standard biomarker for myocardial damage. Despite a high degree of homology between the human and equine cTnI proteins, at the Western College of Veterinary Medicine's Veterinary Medical Center (VMC), there are no rapid point-of-care (POC) tests currently available. The VMC is the only referral clinic in Western Canada, measurement of cTnI could provide clinicians with important insights into a horse's myocardial health in response to exercise or disease. We aim to assess the effects of distance on cTnI release during 25- and 50-mile endurance races. Additionally, we aim to validate the I-STAT1 for use at the VMC by comparing its agreement with an equine-specific cTnI ELISA kit.

Horses (n = 15) were recruited from Saskatchewan Long Riders endurance races (n = 4). Blood was collected from the jugular vein at three time points during the races (before, midway, and after). Blood was stored in lithium heparin and no-additive tubes, with samples for cTnI and electrolytes (sodium, calcium, potassium) being run in the field. Samples were centrifuged and stored at -80 for batch analysis.

Our preliminary data showed no evidence of an interaction between timepoint and race distance on cTnI concentrations (RM ANOVA, $F(2, 24) = 0.14$, $p = 0.87$). However, cTnI concentrations increased from resting (25mi: 0.002 ng/mL; 50mi: 0.004 ng/mL) by the mid-point (25mi: 0.01 ng/mL; 50mi: 0.014 ng/mL), though not significantly (pre vs mid, $p = 0.266$). End concentrations returned to rest values (25mi: 0.006 ng/mL; 50mi: 0.006 ng/mL). Potassium displayed a significant, strong positive correlation with cTnI concentrations post-race ($r = 0.542$, $p = 0.42$). A Bland-Altman plot indicated the mean bias between the equine ELISA and the I-STAT1 was less than 20%, meeting the American Society for Veterinary Clinical Pathology's standard for accuracy.

These preliminary results indicate that prolonged physical activity leads to transient myocardial injury and the release of cTnI in horses and that the I-STAT1 can reliably detect equine cTnI.

Poster 3: Successful long-term control of feline primary erythrocytosis with chlorambucil monotherapy

Brittany M. Naeckel, R. Darren Wood, James A. Mori

Department of Pathobiology, Ontario Veterinary College, University of Guelph

Abstract

Primary erythrocytosis (PE) is a rare myeloproliferative disorder characterized by autonomous erythrocyte production resulting in persistently increased hematocrit in the absence of secondary causes. In cats, therapeutic phlebotomy and hydroxyurea are the most described treatments; however, utility of hydroxyurea can be limited by its adverse effects. Information regarding alternative long-term medical management in feline PE remains limited. This report describes the successful long-term control of feline PE using chlorambucil monotherapy following intolerance to hydroxyurea. A 6-year-11-month-old male neutered domestic longhair cat was referred to the Ontario Veterinary College Health Sciences Centre (OVC-HSC) in August 2023 following acute cluster seizures and identification of marked erythrocytosis. Upon presentation, repeat hematologic assessment confirmed persistent severe erythrocytosis, with a PCV of 75% (reference interval [RI] 25–45), HCT of 0.77 L/L (RI 0.28–0.49), and RBC of 16.3 $\times 10^{12}$/L (RI 6.2–10.6). A diagnosis of PE was supported by exclusion of secondary causes through echocardiography, thoracic radiographs, abdominal ultrasound, clinicopathologic testing, and a low serum erythropoietin concentration of <3.8 mU/mL (RI 3.8–16.9). Initial treatment included two therapeutic phlebotomies and hydroxyurea. Hydroxyurea was discontinued after the patient developed methemoglobinemia and chlorambucil was initiated as an alternative myelosuppressive agent at 0.40 mg/kg PO three times weekly (1.20 mg/kg/week). Serial hematologic monitoring demonstrated progressive long-term control of erythrocytosis following initiation of chlorambucil. For the first nine months, PCV remained increased between 50–62%, necessitating one additional phlebotomy at a PCV of 62%, approximately one month after diagnosis. By May 2024, PCV declined from 48% to 37%. Following this response, in July 2024, chlorambucil dose was tapered down to twice weekly (0.80 mg/kg/week). Since July 2024, PCV remained stable and within the reference interval at 40–45%. Leukocyte and platelet concentrations remained within their respective RIs. Apart from intermittent vomiting following oral administration of chlorambucil, the patient tolerated alkylating therapy well. The patient's neurologic status normalized and remained stable. In March 2026, chlorambucil dosing was further reduced to a single weekly dose (0.40 mg/kg/week). As of April 2026, the patient has remained in sustained clinical remission for approximately two years. This case demonstrates that chlorambucil can provide effective long-term hematologic control of feline PE and may serve as a viable alternative when hydroxyurea is not tolerated. This case adds to the limited literature describing alternative long-term management options for feline PE.

Poster 4: Evaluation of antibodies to a carbohydrate larval antigen (CarLA) in Ontario lambs of different ages experimentally infected with *Haemonchus contortus* across a simulated grazing season

Victoria Allicock, Doug Hodgins, Cathy Bauman, Andrew Peregrine, Emma Borkowski

Departments of Pathobiology and Population Medicine, Ontario Veterinary College, University of Guelph

Abstract

Gastrointestinal nematodes (GINs) cause disease and death in pastured sheep flocks worldwide. GIN control is increasingly challenging due to the rising prevalence of anthelmintic resistance, particularly in highly pathogenic *Haemonchus contortus*. Therefore, complementary methods, such as selective breeding for effective immune responses to GINs, are needed to mitigate the impacts of GIN infection. Infective larvae of all major small ruminant GINs express a carbohydrate larval antigen (CarLA) on their epicuticle which functions as a target for host antibodies. Salivary anti-CarLA IgA antibody (ACA) titres are a heritable measure indicating the strength of host immune responses to GIN infection. However, little is known about how host factors, including age at first GIN exposure, impact ACA production in sheep and identification of animals with superior immunity. This study investigated ACA levels in naïve lambs experimentally infected with *H. contortus* beginning at 3 months (n = 16) or 6 months (n = 16) old. All 32 lambs were administered low-dose trickle infections of *H. contortus* larvae over a simulated Ontario grazing season: 20 weeks of 500 larvae three times weekly ('summer'), 16 weeks unexposed ('winter'), and another 12 weeks of infection ('spring'). Fecal egg counts and anemia scores were monitored weekly to direct anthelmintic treatment, preventing clinical disease or mortality. Select saliva samples (weeks 12, 20, and 39) were analyzed via an enzyme-linked immunosorbent assay (ELISA) for ACA evaluation. Week 12 samples tested using the standard assay (diluted 1/33) indicated that antibody titres were below the limit of detection. Following validation of the supporting reagents in the ELISA, equivalent results were observed from analysis of week 20 samples at the same dilution. Assay of samples from weeks 20 and 39 using 1/4 dilutions confirmed that titres were below the limit of detection. These results may indicate that weekly infection with 1500 *H. contortus* larvae was insufficient to produce detectable ACA titres following the initial 'summer' period of GIN exposure.

Poster 5: Investigation of the fecal microbiome of raccoons (*Procyon lotor*) in a captive environment

Shivani Ojha, Kelsey Holland, Mikaela Jahncke, Lisanework Ayalew

Department of Pathology and Microbiology, Atlantic Veterinary College, University of Prince Edward Island (Holland, Ayalew, Ojha); Hope for wildlife rehabilitation and education center, Seaforth (Jahncke)

Abstract

Raccoons are widely known wildlife species that interface and impact urban ecosystems; however, their gut microbiome is rarely explored. This study hypothesized that raccoons carry diverse bacteria, which affects their physiology and reasonably their fecal microbiome impacts urban ecology. The goal of this study was to explore the fecal microbiome of raccoons based on 16S rRNA metagenomic sequencing. A longitudinal study was conducted in two phases, involving 15 raccoons housed at a wildlife facility in Nova Scotia. The first phase involved unmanipulated juvenile raccoons, while the second phase consisted of 12 weeks old animals that received medication. The diet of animals included different food formulations. Naturally voided fecal samples were collected in sterile containers and stored at -80oC until further processing. Genomic DNA was extracted from 500 mg of each fecal sample. 16S rRNA gene sequence libraries were prepared using the Oxford Nanopore Rapid Sequencing DNA-16S barcoding kit as per the company's instructions. DNA libraries were sequenced using the Mk1B MinIon instrument. Sequence processing and taxonomic classification were performed using the EPI2ME bioinformatic platform. No significant differences in alpha or beta diversity were observed between samples collected from male and female raccoons ($p > 0.05$). However, beta-diversity comparisons showed significant difference in bacterial composition in animals fed Formula-bowls versus Formula diet ($p < 0.05$). The majority of animals that were fed Formula-bowls had a higher proportion of *Ligilactobacillus* and *Streptococcus* and less anaerobes. In contrast, most of the Formula-fed raccoons carried a higher proportion of *Escherichia*, *Shigella* and *Clostridium* species. The results highlight the significant impact of diet on the gut microbial composition of raccoons. The ongoing Phase 2 gut microbiome analyses will further enhance our understanding of bacterial community dynamics in raccoons within a captive environment.

Poster 6: Antimicrobial Resistance and Prevalence of Canine Uropathogens in Saskatchewan (2023–2026)

Nadia Dsouza, Alan Chicoine, Joe Rubin

University of Saskatchewan

Abstract

Urinary tract infections (UTIs) remain a common reason for antimicrobial use in dogs. Updated regional data on uropathogen prevalence and antimicrobial susceptibility are needed to guide empirical therapy and support antimicrobial stewardship. The objective of this study was to characterize the prevalence and antimicrobial susceptibility patterns of bacterial uropathogens isolated from canine urine samples recently submitted to a diagnostic laboratory in Saskatchewan.

Methods

A retrospective observational study was conducted using canine urine culture and antimicrobial susceptibility data from Prairie Diagnostic Services (Saskatchewan) between January 2023 and January 2026. Samples submitted for bacterial culture were included and analyzed at the isolate level. For culture-positive urine samples, antimicrobial susceptibility was performed using Kirby-Bauer disk diffusion. Descriptive statistics were used to summarize uropathogen prevalence and antimicrobial susceptibility patterns, and comparative analyses were performed where appropriate. Multidrug resistance was defined as resistance to ≥3 antimicrobial classes.

Findings

A total of 2035 canine urine samples were submitted for culture, of which 992 (48.7%) were culture-positive. After exclusion of fungal isolates, 986 bacterial-positive samples were included, yielding 1157 total bacterial isolates. *Escherichia coli* was the predominant uropathogen (n=540, 47% of total bacterial isolates), followed by *Proteus mirabilis* and *Staphylococcus pseudintermedius*. Gram-negative organisms accounted for approximately 72% of isolates, and 14% of positive cultures were mixed infections (multiple bacterial species cultured). Among mixed infections, *Enterococcus* spp. were most frequently identified (24.3%), followed by *Escherichia coli* (22.2%), *Staphylococcus* spp. (18.8%), and *Proteus* spp. (14.2%).

In *E. coli*, highest susceptibility was observed to nitrofurantoin (99%) and aminoglycosides (95%), with slightly lower susceptibility noted for enrofloxacin (94.2%), trimethroprim-sulfa (93.8%), amoxicillin-clavulanate (~82%), and amoxicillin (72%). 60% of *E. coli* isolates were pan-susceptible, and 65%, 17%, and 17% were resistant to one, two, and three or more antimicrobial classes, respectively. Multidrug resistance was most common in *Proteusand Enterococcus* spp., but infrequently observed in *Staphylococcus* and *Streptococcus* spp.

Conclusions

As per previous data, E. coli continues to be the primary canine uropathogen in Saskatchewan. Although antimicrobial susceptibility patterns varied between bacterial species, most uropathogens were susceptible to most or all antimicrobials, including those commonly recommended for initial empiric therapy of urinary tract infections in dogs. These findings highlight the importance of region-specific AMR surveillance to guide empirical therapy and support antimicrobial stewardship.

Poster 7: A descriptive analysis of diagnostic poultry antimicrobial resistance data from the Canadian AMRNet-Vet program

Cassandra Reedman, Agnes Agunos, Richard J. Reid-Smith, Amrita Bharat, Justin Carr, Dale Douma, Ruwani Karunarathna, Beverly Morrison, Matt E. Saab, Durda Slavic, Wallis Rudnick

Centre for Foodborne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada (Reedman, Agunos, Reid-Smith, Rudnick); National Microbiology Laboratory, Public Health Agency of Canada (Bharat); Provincial Veterinary Lab, Fredericton, New Brunswick (Carr); Veterinary Diagnostic Services, Manitoba Agriculture (Douma); Prairie Diagnostic Services (Karunarathna); Diagnostic Services Unit, University of Calgary, (Morrison); University of Prince Edward Island (Saab); Animal Health Laboratory, Guelph, Ontario (Slavic)

Abstract

Antimicrobial resistance (AMR) is a global One Health concern with significant implications for animal, human, and environmental health. In Canada, national AMR trends are monitored through programs such as AMRNet-Vet, which compiles diagnostic laboratory data from veterinary and animal health laboratories nationwide. These data enable characterization of AMR patterns in key commodities, such as poultry, and support antimicrobial use (AMU) stewardship efforts.

Distinguishing poultry production types (i.e., broilers vs. layers), improves interpretation of AMR patterns given differences in lifespan, disease pressures, and AMU. Similarly, specimen type enhances the interpretation of AST results.

This analysis summarizes poultry bacterial recovery and antimicrobial susceptibility testing (AST) results reported to AMRNet-Vet from 2020–Mar 2025, and highlight the uses of these data in a One Health context while identifying opportunities to support continued data improvement through improved granularity and harmonization.

Poster 8: Leukemia in a Corn Snake (Pantherophis guttatus) Initially Suspected as Severe Leukocytosis Associated with Infection

Lilani Munasinghe

Prairie Diagnostic Services

Abstract

A 20-year-old female corn snake (*Pantherophis guttatus*) housed in a zoological exhibit was evaluated for decreased appetite and progressive swelling at the site of a previously suspected spinal fracture. The animal was later found with a ventral wound at the same location following a tree fall within the enclosure. The wound subsequently became infected and developed a 2 × 1 cm lateral bulging mass suggestive of an abscess. The snake was treated with ceftazidime and hydrotherapy. A fine-needle aspirate (FNA) of the mass and a complete blood count (CBC) with blood smear evaluation were submitted for evaluation.

Cytologic examination of the aspirate revealed moderate cellularity with poor cellular preservation and abundant bacterial organisms, including numerous short and long rods, spore-forming rods, filamentous bacteria, and occasional cocci, consistent with a mixed bacterial infection. The inflammatory component could not be reliably assessed due to cellular degeneration.

The CBC demonstrated marked leukocytosis. Blood smear evaluation showed a predominance of round cells with oval, indented, or kidney-shaped nuclei, sometimes prominent nucleoli, and basophilic cytoplasm often containing pink granulation and occasional vacuolation. Rare binucleated cells and occasional mitotic figures were present. Small numbers of heterophils, lymphocytes, and eosinophils were also observed. Additionally, occasional oval, thin-walled yeast organisms with rare budding yeast were identified in the peripheral blood. The marked leukocytosis raised suspicion for leukemia, either granulocytic or lymphoid in origin; however, severe infectious leukocytosis could not be excluded at that time given the infected wound and evidence of circulating yeast.

Due to clinical deterioration, the snake was euthanized and a full necropsy with histopathology was performed. Histologically, multiple organs including skin, liver, kidney, spleen, gastrointestinal tract, lung, heart, and reproductive tract were infiltrated by dense sheets of monotonous round to polygonal neoplastic cells with scant cytoplasm, coarsely stippled chromatin, and frequent mitotic figures. The spleen was completely effaced by neoplastic cells, and intravascular neoplastic cells were observed in multiple tissues.

These findings supported a diagnosis of leukemia/lymphoma with extensive visceral and cutaneous involvement. This case highlights the diagnostic challenge of distinguishing neoplastic leukocytosis from severe inflammatory leukocytosis in reptiles and emphasizes the importance of blood smear evaluation and histopathology in establishing a definitive diagnosis.

Industry Partners Directory

https://www.uoguelph.ca/ahl/

The AHL is a full-service veterinary diagnostic lab that boasts an extensive cadre of laboratorians with post-graduate training and specialty board certification. The expertise of AHL laboratorians and other University of Guelph personnel is linked to provide a single source of laboratory services in the field of animal health, encompassing both food-producing and companion animals.

https://www.bruker.com/

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Prairie Diagnostic Services (PDS) is a full-service veterinary diagnostic laboratory based in Saskatoon, Saskatchewan, serving clients across Canada. Proudly Canadian-owned and operated, we provide accurate, timely, and trusted diagnostic testing that supports animal health, food safety, and veterinary care nationwide.

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We are a Canadian company respected as a leader in the development of Quality Management Software solution (QMS) for the healthcare market.

https://www.roche.com/

Roche is a healthcare company uniquely placed to prevent, stop and cure diseases by uniting leading science and technology across diagnostics, medicines and digital solutions. The company was founded in Basel, Switzerland in 1896 and today is a leading provider of transformative medicines and diagnostics for millions of people in over 100 countries around the world. It is dedicated to tackling healthcare challenges that place the greatest strain on patients, families, communities and healthcare systems. Across its Diagnostics and Pharmaceutical divisions, Roche focused on areas including oncology, neurology, cardiovascular and metabolic diseases, ophthalmology, infectious diseases and immunology with the aim of providing real and positive change for patients, the people they love and the professionals who care for them.

https://www.sysmex.com/

Sysmex Canada, Inc. in Ontario serves as the Canadian headquarters for Sysmex Corporation Kobe, Japan. Established in January 2008, Sysmex Canada sells and supports Sysmex hematology and urinalysis automated analyzers, reagents, and information technology products and services to healthcare facilities within the country's 10 provinces and three territories.

https://www.bio-rad.com/

At Bio-Rad, we support researchers and clinicians working to improve lives through science. From life science research to clinical diagnostics, our tools help move science and healthcare forward with confidence and precision. For more than 70 years, we've delivered trusted solutions and meaningful advances that help turn possibilities into progress—every day, everywhere.

https://www.ceva.com/

Ceva Animal Health is a global veterinary health company focused on the research, development, production and marketing of pharmaceutical products and vaccines for pets, livestock, swine and poultry.

https://www.tracefirst.com/

With an exemplary track record, Trace First can help you optimize your Animal Health Information Systems. Our principal product, *CoreOne*, provides an off-the-shelf solution that is fully customizable to your specific needs.

https://www.fishersci.com/

As the premier scientific marketplace, the Fisher Scientific channel has defined choice and convenience for over a century. We keep science moving forward by offering over 2.5 million products and extensive support services to the research, production, healthcare, and science education markets around the world.

Count on us for all the elements you need to accelerate innovation, enhance productivity, and increase speed to market.

https://galenvs.com/

At Galenvs, we specialize in applying multidisciplinary technologies, leveraging data-driven methodologies, and utilizing process-driven strategies to help our healthcare and industrial customers CLEAN, MODIFY, and TARGET to achieve their biotech goals. Whether it's engineering specialized enzymes for directed evolution and carbon capture or developing custom oligo monomers for therapeutics, we offer a comprehensive suite of services tailored to meet specific client needs.

https://www.gentian.com/

Gentian is a Norwegian IVD company that specialises in developing and manufacturing turbidimetric assays that enable clinical lab professionals to achieve greater operational efficiency, thus providing faster patient results to clinicians. The current portfolio and pipeline of diagnostic reagents span areas of kidney disease, cardiac disease, inflammation, infection and veterinary medicine.

https://www.hurontechnologies.com/

Huron delivers interoperable, end-to-end digital pathology solutions that pair award-winning whole slide scanners with AI-driven analysis tools, and seamless image management. Designed for both clinical and research environments, our scalable platform accelerates diagnosis, streamlines workflows, and supports advanced disease research, all with the reliability, precision, and integration trusted by world-leading laboratories and institutions.

https://www.merck-animal-health.ca/

Merck Animal Health is a research-driven company that develops, manufactures and markets a broad range of veterinary medicines and services. We offer one of the industry's most innovative portfolios, spanning products for the prevention, treatment and control of disease in all major farm and companion animal species.

https://www.neb.com/

Created "by scientists for scientists", NEB is renowned for consistently providing exceptional product quality and unsurpassed technical support. For over four decades, NEB has been shaping the landscape of bioscience research by discovering, developing and supporting superior research reagents. From our founding principles – placing the advancement of science and the stewardship of the environment as our highest priorities – to our unique corporate culture, NEB's philosophy can be distilled down to three core values: passion, humility and being genuine.

https://norgenbiotek.com/

At Norgen Biotek Corp., our mission is to pioneer tailored research experiences for our clients by offering innovative solutions that ignite groundbreaking discoveries. We ensure the utmost quality across our range of offerings, encompassing sample collection, preservation, extraction, and detection. Our team of experts coupled with strategic global collaborators stand ready to assist you, step-by-step, throughout your scientific exploration.

https://www.vmrd.com/

VMRD was founded in 1981 by D. Scott Adams, DVM, PhD. From its site in Pullman, WA VMRD develops and manufactures diagnostic test kits and related reagents for distribution in more than 55 countries. It's mission is to provide high quality products, services and support for customers. VMRD has a strong market reputation for delivering best in class products with a uniquely personal touch.

https://ir.waters.com/

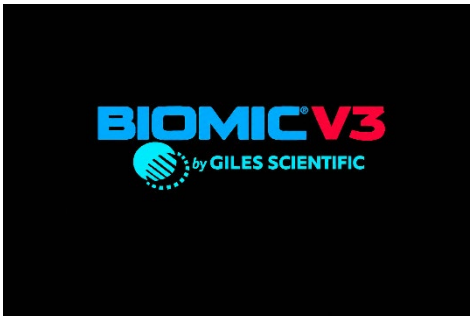
Waters is a global leader in life sciences and diagnostics, dedicated to accelerating the benefits of pioneering science through analytical technologies, informatics, and service. With a focus on regulated, high-volume testing environments, our innovative portfolio harnesses deep scientific expertise across chemistry, physics, and biology. We collaborate with customers around the world to advance the release of effective, high-quality medicines, ensure the safety of food and water, and drive better patient outcomes by detecting diseases earlier, managing routine infections, and combating antibiotic resistance. Through a shared culture of relentless innovation, our passionate team of ~16,000 colleagues turn scientific challenges into breakthroughs that improve lives worldwide.

https://www.zoetisus.com/

Zoetis is the world's leading animal health company. Our name comes from "Zoe," the Greek word for life—a reminder that sustaining and improving life through the use of science is at the foundation of everything we do.

https://www.novamed1.com/

Established in 1991, Novamed Inc. is an A2LA Accredited ISO/IEC 17025 laboratory, headquartered in Skokie, IL with operations across USA and Canada. As a national market leader in Pipette Calibration & Repair, Novamed provides both On-Site and Mail-In services. Novamed is housed in a 7000 sq.ft facility with an environmentally controlled laboratory and state of the art technology. Being an accredited laboratory, Novamed strictly adheres to all aspects of Quality Management System and ISO 17025 standards.



https://www.biomic.com/

BIOMIC V3 is an open clinical microbiology system for automating the reading and CLSI or EUCAST interpretation of antibiotic susceptibility and organism identification tests from various manufacturers. BIOMIC V3 specializes in monitoring global antimicrobial resistance (AMR) trends.

https://www.stago.com/

Stago was a pharmaceutical laboratory, founded in 1945, which now operates in the In Vitro Diagnosis (IVD) industry, wholly dedicated to the exploration of hemostasis and thrombosis.

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