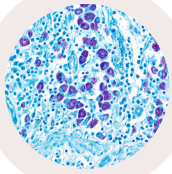
Canadian Animal Health Laboratorians Network
Réseau Canadien des Travailleurs des Laboratoires de Santé Animale






2021 Proceedings

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The Program

Monday June 7, 2021 via Zoom

09:00 - 09:15	Welcome and Opening Remarks Registration | Robert McCorkell, UCVM Interim Dean
09:15 - 10:15	Changes I've seen in 50 years of Veterinary Pathology | Grant Maxie
10:15 - 10:40	Bronchopneumonia with interstitial pneumonia in beef feedlot cattle | Luke Haydock
10:40 - 11:05	Clostridial hepatitis caused by Clostridia novyi-group bacteria in 4 mature equids in southern Alberta | Jennifer Davies & Ashley Whitehead
11:05 - 11:15	Break
11:15 - 11:40	Velogenic Newcastle disease in feral pigeons and the value of citizen science | Dayna Goldsmith
11:40 - 12:15	Veterinary Forensic Postmortem Standards | Beverly McEwen
12:15 - 13:00	Lunch | Come have lunch with us: Networking Opportunity
13:00 - 14:00	Selected Emergig Swine Diseases in China – Through the Lens of a Chinese in Canada | Yanyun Huang
14:00 - 14:15	Septicemic pasteurellosis causing peracute death and necrotizing myositis in a beef heifer (Bos taurus) in Alberta Canada | Douglas Doyle-Baker
14:15 - 14:30	Pathology of free-ranging urban Leporidae in Calgary, Alberta | Summer Hunter
14:30 - 15:15	Meeting | Provincial Diagnostic Laboratory Reports
15:15 - 16:00	Meeting | Canadian Association of Veterinary Pathologists (CAVP) Annual Business Meeting

Tuesday June 8, 2021 via Zoom

9:00 - 10:00	From Mink to Ministries: Lessons Learned from BC LOGI2C – the BC Laboratory for the One Health Genomics Innovation and Implementation Community | Chelsea Himsworth & Natalie Prystajecky
10:00 - 10:25	The Western Canadian Animal Health Network: collaboration and crowdsourcing data | Barbara Wilhelm
10:25 - 10:50	Animal Health Informatics: Integrating Animal Health Information in Canada | Theresa Burns
10:50 - 11:00	Break
11:00 - 12:00	Poster: Sarcocystis species protozoal encephalitis in a wild black bear (Ursus americanus) | Madison Anderson
	Poster: Using whole-genome sequencing to examine the relatedness and antimicrobial resistance elements of E. coli isolates within a One Health continuum | Alyssa Butters
	Poster: Lesions of Mycobacterium avium spp. hominissuis infection in a wild mule deer (Odocoileus hemionus) resemble Mycobacterium bovis | Brock Chappell
	Poster: Improving methods of control of American foulbrood in honey bees in Saskatchewan | Michael Zabrodski
	Poster: Duck atadenovirus A 2019 and 2020 outbreaks in ducklings including whole genome sequence of the viruses | Marika Köszegi
	Poster: Bovine Astrovirus and its Potential Role in Bovine Lymphocytic Encephalitis | Dominique Comeau
12:00 - 13:00	Lunch | CAHLN Annual General Meeting – Everyone Welcome
13:00 - 14:00	A One Health Approach to Understanding Resistance | Sylvia Checkley
14:00 - 14:25	Neonatal calf diarrhea diagnostics at Prairie Diagnostic Services: lessons learned over the last two-decade | Musangu Ngeleka
14:25 - 14:40	Rapid Salmonella serotyping by sequencing on nanopore platform | Anatoliy Trokhymchuk
15:00 - 16:00	Awards | Laboratorian of the Year and Student Awards, Networking, and Sponsor Breakout Rooms

Program continues the next day

Wednesday June 9, 2021 via Zoom

9:00 - 10:00	Effect of restriction in the use of antibiotics in food animals on antibiotic resistance in food animals and humans | Herman Barkema
10:00 - 10:25	Current trends in knowledge transfer | Melanie Barham
10:25 - 10:50	Operational and quality management challenges during the early days of the SARS-CoV-2 pandemic: One veterinary diagnostic laboratory's experiences | Maria Spinato
10:50 - 11:05	Break
11:05 - 11:30	Oral fluid as an aggregate sample for early detection of African Swine Fever virus: evidence from four independent pen-based experiments| Kalhari Bandara Goonewardene
11:30 - 11:55	Assessment of Metagenomic Sequencing and qPCR for Detection of Influenza D virus in Bovine Respiratory Tract Samples | Maodong Zhang
11:55 - 12:20	First whole genome sequences of equine influenzavirus A (H3N8) in Canada | Chantale Provost
12:20 - 12:45	Torque teno equus virus 2 (TTEqV2), a novel Anellovirus species and the first complete Mutorquevirus genome | Oliver Lung
12:45 - 13:00	Closing Remarks
13:15 - 14:15	Meeting | CAHLN Bacteriology/AST Working Group

SPEAKERS'

Presentations

Changes I've seen in 50 years of Vet Pathology

Author: Dr. Grant Maxie, DVM, PhD, Diplomate ACVP

University of Guelph (retired)

Technology has advanced tremendously in the 50 years since my graduation from the DVM program at WCVM in 1969 – from typewritten to cloud-based records, from individual bench-top tests to automated testing of bar-coded samples, from Kodachromes to digital pathology, new pathogens have emerged, and, none too soon, biosafety had improved greatly in postmortem suites. The demand for forensic autopsies has increased, not without its own perils, such as vicarious trauma. The explosion in molecular-based testing has supported the diagnostic process and also driven the need for bioinformatics. Surveillance outcomes have been enhanced by the wealth of information generated from diagnostic cases. Still, case coordination by pathologists remains central to the rendering of accurate diagnoses. Documentation within quality programs, not the least of which with respect to the ongoing competence of pathologists, has become paramount. Despite the impressive progress made in pathology and related disciplines, eternal truths remain – "more is missed by not looking than not knowing"; competence must be not only maintained but documented; agent ≠ infection ≠ disease; and test standardization and validation is essential. Accurate diagnoses still depend on relevant histories, astute observations, appropriate sample selection, valid testing, and careful integration of results.

Selected Emerging Swine Diseases In China - Through The Lens Of A Chinese In Canada

Author: Dr. Yanyun Huang

CEO and Anatomic Pathologist, Prairie Diagnostic Services Inc.

Seeking to be trained as a diagnostic veterinary anatomic pathologist, I moved from China to Canada in 2005. With a strong interest in pigs and the emotional connection to my homeland, I kept an eye on swine health events in China. Several major emerging and re-emerging swine diseases occurred in the past 16 years in mainland China. At least one of these diseases travelled to North America.

In 2006, the early days of industrialization of the Chinese swine sector, a mysterious disease causing high mortality in nursery and finishing pigs occurred in many provinces and reportedly killed over 2 million pigs. The disease was referred to as Swine High Fever Disease. The outbreaks were characterized by high fever, respiratory signs, cutaneous congestion and hemorrhage. The disease was later attributed to a highly pathogenic strain of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV). At that time, entrepreneurs and farmers who were hoping for better lives just began to invest in the swine industry without much veterinary support. The disease understandably lead many into bankruptcy and unverified reports of farmers committed suicide surfaced.

Also reported to begin from 2006, Porcine Epidemic Diarrhea (PED) outbreaks were diagnosed in PEDV-vaccinated farms. The outbreaks were said to be increased remarkably in 2010. The disease caused high mortality in neonatal pigs, but severity was milder as age increased. The PEDV involved were found to be genetically different compared to the vaccine strain (CV777) at that time. The exact losses due to PED in China was not well documented. Unfortunately, in 2013, PEDV genetically related to the Chinese strains appeared in the United States, and later Canada. The impact of PED to the United States was complicated but significant. The US slaughtered 5.2 million less pigs in "the year of PED", compared to the year before, which was a 4.6% decrease. The plausible way of introduction of PEDV to the US was later suspected to be through imported feed ingredients.

Beginning from 2011, reproductive failure, neurological diseases of neonatal pigs and respiratory diseases in nursery to finishing pigs were noticed in several Chinese provinces. The mortality in neonatal pig with neurological signs reached 100%. The etiology was identified as Pseudorabies virus (Suid Herpes Virus 1), despite that the affected farms were vaccinated by traditional vaccines based on the Bartha-K61 strain. It was revealed that the culprit strain the these outbreak was a variant, which would not be completely protected by traditional vaccines.

In 2016, a novel coronavirus, referred to as swine acute diarrhea syndrome coronavirus (SADS-CoV) was identified in China. SADS-CoV was alleged to be associated with diarrhea outbreaks in a large Chinese pig system with about 40% mortality. The virus was thought to have a bat origin. SADS did not appear to spread further.

In 2018, African Swine Fever (ASF) emerged in China, possibly from Russia through smuggled pig products. Within 8 months, ASF was diagnosed in all Chinese provinces. The mortality was reported to be 100% eventually if not depopulated. In one year, there was 130 million head reduction in the Chinese pig inventory compared to the year before (40.5%). By this time, the Chinese swine industry was much more developed compared to that in 2006. There were a numbers of mega-sized pig production companies that had a lot of financial resources to combat the outbreaks. These companies developed various strategies to control and prevent ASF, including aggressive testing and removal, which significantly reduced the losses of outbreaks. Unfortunately, inadequately attenuated ASFV in illegal vaccines in China recently were shown to transmit between pigs and caused clinical signs that were not typical of ASF, which is more difficult to diagnose and posed significant challenges for eradication. A recent study mimicking trans-pacific shipping conditions found that ASFV was able to survive in some feed ingredients, posting a significant risk to the swine industry in North America.

During my quest of information on disease outbreaks in China, it became apparent that, it was as difficult for me to understand North America when I was in China, as to obtain timely and accurate information from events happening in China when I am in Canada. This highlights the importance of monitoring oversea disease outbreaks through surveillance intelligence. Diagnosticians working in Canadian provincial laboratories also need to familiarize ourselves with important foreign animal diseases and developments of the industry. Diseases on the other side of the globe can, and will probably continue to come to North America. Significant disease outbreaks also impact the mental health of producers and veterinarians. In the era of globalization, there is truly only one swine health, and one health.

References

Tian, Kegong, Xiuling Yu, Tiezhu Zhao, Youjun Feng, Zhen Cao, Chuanbin Wang, Yan Hu et al. "Emergence of fatal PRRSV variants: unparalleled outbreaks of atypical PRRS in China and molecular dissection of the unique hallmark." PloS one 2, no. 6 (2007): e526.

Chen, Jianfei, Chengbao Wang, Hongyan Shi, Huaji Qiu, Shengwang Liu, Xiaojin Chen, Zhibang Zhang, and Li Feng. "Molecular epidemiology of porcine epidemic diarrhea virus in China." Archives of virology 155, no. 9 (2010): 1471-1476.

Li, Wentao, Heng Li, Yunbo Liu, Yongfei Pan, Feng Deng, Yanhua Song, Xibiao Tang, and Qigai He. "New variants of porcine epidemic diarrhea virus, China, 2011." Emerging infectious diseases 18, no. 8 (2012): 1350.

An, Tong-Qing, Jin-Mei Peng, Zhi-Jun Tian, Hong-Yuan Zhao, Na Li, Yi-Min Liu, Jia-Zeng Chen et al. "Pseudorabies virus variant in Bartha-K61–vaccinated pigs, China, 2012." Emerging infectious diseases 19, no. 11 (2013): 1749.
Stevenson, Gregory W., Hai Hoang, Kent J. Schwartz, Eric R. Burrough, Dong Sun, Darin Madson, Vickie L. Cooper et al.

"Emergence of Porcine epidemic diarrhea virus in the United States: clinical signs, lesions, and viral genomic sequences." Journal of veterinary diagnostic investigation 25, no. 5 (2013): 649-654.
Schulz, Lee L., and Glynn T. Tonsor. "Assessment of the economic impacts of porcine epidemic diarrhea virus in the United States." Journal of animal science 93, no. 11 (2015): 5111-5118.

Dee, Scott, Casey Neill, Aaron Singrey, Travis Clement, Roger Cochrane, Cassandra Jones, Gilbert Patterson, Gordon Spronk, Jane Christopher-Hennings, and Eric Nelson. “Modeling the transboundary risk of feed ingredients contaminated with porcine epidemic diarrhea virus.” BMC veterinary research 12, no. 1 (2016): 1-12.

Zhou, Ling, Yuan Sun, Tian Lan, Ruiting Wu, Junwei Chen, Zixian Wu, Qingmei Xie, Xiangbin Zhang, and Jingyun Ma. “Retrospective detection and phylogenetic analysis of swine acute diarrhoea syndrome coronavirus in pigs in southern China.” Transboundary and emerging diseases 66, no. 2 (2019): 687-695.

Zhou, Xintao, Nan Li, Yuzi Luo, Y. E. Liu, Faming Miao, Teng Chen, Shoufeng Zhang et al. “Emergence of African swine fever in China, 2018.” Transboundary and emerging diseases 65, no. 6 (2018): 1482-1484.

Ma, Meilin, H. Holly Wang, Yizhou Hua, Fei Qin, and Jing Yang. “African swine fever in China: Impacts, responses, and policy implications.” Food Policy (2021): 102065.

Dee, Scott A., Fernando V. Bauermann, Megan C. Niederwerder, Aaron Singrey, Travis Clement, Marcelo De Lima, Craig Long et al. “Survival of viral pathogens in animal feed ingredients under transboundary shipping models.” PloS one 13, no. 3 (2018): e0194509.

From Mink to Ministries: Lessons Learned from BC LOGI2C – the BC Laboratory for the One Health Genomics Innovation and Implementation Community

Authors:

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  - Co-Program Head, Molecular and Microbial Genomics, BCCDC Public Health Laboratory
  - Clinical Assistant Professor, Pathology and Laboratory Medicine, University of British Columbia.
- Dr. Chelsea Himsworth, DVM, PhD
  - Diagnostic Pathologist and the Leader for Veterinary Science and Diagnostics at the Animal Health Centre, BC Ministry of Agriculture.
  - BC Regional Director for the Canadian Wildlife Health Cooperative and an Assistant Professor in the School of Population and Public Health, University of British Columbia.

In December 2020, an outbreak of SARS CoV-2 occurred in farmed mink in British Columbia (BC). Immediately, a One Health laboratory team (composed of members of the BC Centre for Disease Control’s Public Health Laboratory and the Animal Health Centre, BC Ministry of Agriculture, Food, and Fisheries) was mobilized to support the outbreak response. Specifically, the team: compared methods of sample collection and diagnostic assays for the detection of SARS CoV-2 in mink; used genomics to assess the degree of viral evolution in mink and to infer transmission patters among mink and between mink and humans; performed surveillance of wildlife to detect viral spillover; and investigated the use of environmental samples for surveillance of SARS CoV-2 in mink farms. This integrated response highlighted the value of and opportunities for intergovernmental laboratory collaborations, but also critical barriers and capacity gaps, particularly regarding genomics for One Health and animal health. This presentation will share results of the mink program, as well as lessons learned from the journey of the BC LOGI2C team.

A One Health Approach to Understanding Antibiotic Resistance

Author: Dr. Sylvia Checkley DVM, Ph.D., University of Calgary, Faculty of Veterinary Medicine, Department of Ecosystem and Public Health, Antimicrobial Resistance – One Health Consortium

COLLABORATIONS: Public Health Agency of Canada (CIPARS and FoodNet Canada), Agriculture Agri-Food Canada, Alberta Agriculture and Forestry, Alberta Health Services, Alberta Precision Laboratories, University of Alberta, University of Saskatchewan

Antibiotic resistance is undeniably one of the most pressing and complex issues faced by our generation - a critical issue with a broad range of stakeholders in agriculture and the agri-food sector, medicine (both human and veterinary), as well as many stakeholders across the environmental domain. Activities to detect, measure and mitigate antibiotic resistance require a One Health approach with the inclusion of these broad stakeholders to ensure representative and robust research and surveillance with respect to study design, data collection, laboratory analysis, statistical analysis and interpretation. Antibiotic use is associated with antibiotic resistance, but other drivers of resistance exist. Key knowledge gaps exist concerning environmental transmission pathways and environmental drivers of antibiotic resistance. Together, we need to work to respond to this challenge effectively.

Effect of restriction in the use of antibiotics in food animals on antibiotic resistance in food animals and humans

Author: Dr. Herman Barkema, DVM, Ph.D., University of Calgary, Faculty of Veterinary Medicine, Department of Production Animal Health– One Health Consortium

Antimicrobial resistance (AMR) is considered one of the greatest threats to global and public health today. The World Health Organization has called for urgent action. Antimicrobial use (AMU) in human medicine, veterinary medicine, and agriculture has been linked to the rise of AMR globally.

In a systematic review of 181 studies, interventions that restrict AMU in food-producing animals were associated with a reduction in the presence of antimicrobial-resistant bacteria in these animals. The pooled absolute risk reduction of the prevalence of AMR in animals with interventions that restricted AMU commonly ranged between 10 and 15%, depending on the antimicrobial class, sample type, and bacteria under assessment. Similarly, in the human studies, the pooled prevalence of AMR reported was 24% lower in the intervention groups compared with control groups, with a stronger association seen for humans with direct contact with food-producing animals.

In a sub-analysis, we analyzed whether different types of restriction are associated with differential effectiveness in reducing resistance. We created a classification scheme of different approaches to antimicrobial restriction: 1) Complete restriction; 2) Single antimicrobial-class restriction; 3) Single antimicrobial restriction; 4) All non-therapeutic use restriction; 5) Growth promoter and prophylaxis restriction; 6) Growth promoter restriction; and 7) Other/Undetermined. A total of 114 studies were included. The most frequently studied intervention type was complete restriction (n=43), followed by restriction of non-therapeutic (n=29) and growth promoter (n=17) indications. None examined growth promoter and prophylaxis restrictions together. Though complete restrictions were associated with a 17% reduction in AMR, less prohibitive approaches also demonstrated reduction in AMR of 9 to 29%. Broad interventions that restricted global AMU appeared to be more effective in reducing AMR compared to restrictions that narrowly target one specific antimicrobial or antimicrobial class. Importantly, interventions that allowed for therapeutic AMU appeared similarly effective compared to those that restricted all uses of antimicrobials, suggesting that complete bans are not necessary.

What remains unknown, however, are whether (and what) unintended consequences may arise from such interventions. We therefore undertook a sub-analysis of the original review to address this research question. A total of 47 studies described potential consequences of antimicrobial restrictions. There were no consistent trends to suggest clear harm. There may be increased bacterial contamination of food products, the clinical significance of which remains unclear. There is a need for rigorous evaluation of the unintended consequences of antimicrobial restrictions in human health, food availability, and economics, given their possible widespread implications. These findings directly inform the creation of specific policies to restrict AMU in food-producing animals.

Finally, we summarized effects of interventions reducing AMU in food-producing animals on the prevalence of AMR genes (ARGs) in bacteria from animals and humans. A positive effect of intervention (reduction in prevalence or number of ARGs in group(s) with restricted antimicrobial use) was reported from 29 studies for at least 1 ARG. We detected significant associations between a ban on avoparcin and diminished presence of the vanA gene in samples from animals and humans, whereas for the mecA gene, studies agreed on a positive effect of intervention in samples only from animals. Comparisons involving mcr-1, blaCTX-M, aadA2, vat(E), sul2, dfrA5, dfrA13, tet(E) and tet(P) indicated a reduced prevalence of genes in intervention groups. Conversely, no effects were detected for beta-lactamases other than blaCTX-M and remaining tet genes. In conclusion, the available body of scientific evidence supported that restricted AMU in food animals was associated with an either lower or equal presence of ARGs in bacteria, with effects dependent on ARG, host species and restricted drug.

ORAL

Presentations

First whole genome sequences of equine influenzavirus A (H3N8) in Canada

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Equine influenzavirus is one of the most economically important contagious respiratory diseases of horses. The disease is characterized by rapidly spreading clinical signs that include pyrexia, depression, anorexia, harsh dry cough, nasal discharge, and secondary bacterial respiratory infections. Outbreaks of equine influenza virus (EIV) have been reported worldwide. Influenza is endemic in the horse populations of Europe and North America, and several outbreaks have been reported throughout Canada. During summer 2020, an EIV outbreak occurred in the veterinary teaching hospital of the Faculty of Veterinary Medicine of the Université de Montréal. Cases were first confirmed by RT-qPCR and sequenced by high-throughout sequencing using a MiSeq (Illumina) to obtain their complete genome in order to compare them and confirm their relationship. Moreover, to the authors' knowledge, no complete genome of a Canadian EIV are available within the public nucleotide databases. Tweeny-one H3N8 samples were completely sequenced and compared. For the H3 gene segment, 19 samples are clustered within the Florida clade 1 sub-lineage and are closely related to A/Equus ferus caballus/USA/176576/2019 strain, and 2 samples are closely related to vaccine strain Kentucky/1/91. The two horses had indeed been vaccinated with a commercial vaccine containing this strain a few days before. For the N8 gene segment, 19 samples are clustered within the Florida clade 1 sub-lineage and are closely related to A/Equus ferus caballus/USA/220792/2018 strain. All other segments were also compared to references strains to generate phylogenetic trees. H3 antigenic sites of all samples were compared to the one of vaccinal strains. A four amino acids difference within antigenic sites C, D, and E was observed between the 19 Florida clade 1 sub-lineage isolates. No difference in H3 amino acids compared to the vaccinal strains were observed within the antigenic sites for the two samples related to the vaccinal strain. The results suggests that 19 samples were all related to the same EIV outbreak and that two samples were related to the vaccinal strains following vaccination and had no relation with the EIV outbreak. In conclusion, complete genome sequencing tools are useful in hospital settings to provide epidemiological information, and may assist veterinary hospitals in improving biosecurity rules.

Assessment of Metagenomic Sequencing and qPCR for Detection of Influenza D Virus in Bovine Respiratory Tract Samples

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High throughput sequencing is currently revolutionizing the genomics field and providing new approaches to the detection and characterization of microorganisms. The objective of this study was to assess the detection of influenza D virus (IDV) in bovine respiratory tract samples using two sequencing platforms (MiSeq and Nanopore (GridION)), and species-specific qPCR. An IDV-specific qPCR was performed on 232 samples (116 nasal swabs and 116 tracheal washes) that had been previously subject to virome sequencing using MiSeq. Nanopore sequencing was performed on 19 samples positive for IDV by either MiSeq or qPCR. Nanopore sequence data was analyzed by two bioinformatics methods: What's In My Pot (WIMP, on the EPI2ME platform), and an in-house developed analysis pipeline. The agreement of IDV detection between qPCR and MiSeq was 82.3%, between qPCR and Nanopore was 57.9% (in-house) and 84.2% (WIMP), and between MiSeq and Nanopore was 89.5% (in-house) and 73.7% (WIMP). IDV was detected by MiSeq in 14 of 17 IDV qPCR-positive samples with Cq (cycle quantification) values below 31, despite multiplexing 50 samples for sequencing. When qPCR was regarded as the gold standard, the sensitivity and specificity of MiSeq sequence detection were 28.3% and 98.9%, respectively. We conclude that both MiSeq and Nanopore sequencing are capable of detecting IDV in clinical specimens with a range of Cq values. Sensitivity may be further improved by optimizing sequence data analysis, improving virus enrichment, or reducing the degree of multiplexing.

Veterinary Forensic Postmortem Standards

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At the 2019 Internal Veterinary Forensic Sciences business meeting, a motion was passed to establish standards for veterinary forensic postmortems. An ad hoc committee of 7 board-certified veterinary pathologists was struck to develop these minimum standards. The primary objective was to provide a process framework to veterinarians for the postmortem examination of non-human animal remains, and to provide a reference for legal or law enforcement professionals.

Methods: A survey series of itemized activities and processes of the veterinary forensic postmortem based on published human forensic autopsy standards and the veterinary forensic necropsy was completed by the pathologists. Teleconference discussions followed, and items that were agreed upon by consensus were included in the proposed standards.

Results: The veterinary forensic postmortem standards document provides minimum standards for veterinarians who perform forensic postmortem examinations. Included standards cover preliminary procedures, evidence documentation, external and internal postmortem examination and documentation, lesion and injury descriptions, ancillary tests, and the postmortem examination report.

Discussion: Opinions and interpretations of a forensic case made by a veterinarian must be formulated after consideration of all available information; this document lists all the information the veterinarian should consider. Most veterinarians and veterinary pathologists will exceed these minimum performance standards and are encouraged to do so.

Current trends in knowledge transfer

Author(s) name(s) / Affiliation(s):

Barham M., Deane M. | Animal Health Laboratory, University of Guelph

Knowledge transfer remains a rapidly evolving world, particularly with pressures from the COVID-19 pandemic, which exponentially increased rates of online learning and screen time1. Social networks have also increased in use throughout the pandemic2. Simultaneously, attention spans, whereby we can meaningfully concentrate on materials, have decreased to eight seconds or less3, alongside our collective ability to focus on a cause or issue4.

However, the outlook for knowledge transfer is not entirely bleak. The move to provide different and virtual materials and conferences has also presented positive accessibility options in an accelerated manner5. New opportunities are emerging in how we consume information, how we transfer information to clients and producers, and how we learn collectively as a group.

This presentation will take a global look at what is working in 2021 in the arena of knowledge transfer and will cover trends and tactics in sharing information, as well as ideas for efficiently adapting current materials to meet new needs without overwhelming audiences as we face the evolving pandemic and post pandemic world.

Velogenic Newcastle disease in feral pigeons and the value of citizen science

Author(s) name(s) / Affiliation(s):

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- Victoria Bowes, Animal Health Centre

Avian paramyxovirus 1 (PMV-1), the causative agent of Newcastle disease, was the cause of death in two feral pigeons (Columba livia) submitted to the diagnostic services unit (DSU) this winter. The animals were found by a good Samaritan who had noticed an increased occurrence of dead and dying pigeons on her daily dog walks. She noted that the dead birds appeared in good body condition and were not scavenged. Both submitted pigeons had lesions suggestive of an avian paramyxovirus infection including lymphoplasmacytic interstitial nephritis with tubular necrosis. One of the birds also had a marked lymphocytic pancreatitis with single cell necrosis and lymphoid depletion of the spleen. Infection with avian paramyxovirus 1 was confirmed through PCR testing and both isolated viral strains were positive for the APMV-1 Fusion gene. Concurrently, two clusters of pigeon mortality in the Vancouver area were reported by the public to the BC Wild Bird Mortality Reporting line and both were confirmed to be caused by an identical velogenic PMV-1.

Similar outbreaks of velogenic Newcastle disease have now recently been reported in feral and domestic pigeons in Alberta, British Columbia and Ontario.

Neonatal calf diarrhea diagnostics at Prairie Diagnostic Services: lessons learned over the last two-decade

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Neonatal calf diarrhea (NCD) is one of the most common causes of pre-weaning calf morbidity and mortality in both beef and dairy operations. E. coli, C. perfringens, Salmonella spp., rotavirus (RV), bovine coronavirus (BCoV) and Cryptosporidium spp. are the common pathogens of NCD. Conventional methods for NCD diagnostics rely on: (i) bacterial culture for E. coli, C. perfringens and Salmonella spp.; (ii) RV and BCoV antigen detection using immunoassays such as fluorescence antibody test (FAT) or immunochromatography; (iii) detection of parasites using fecal flotation. In addition, E. coli typing for F5 fimbriae is performed using the slide agglutination test. These procedures were conducted at Prairie Diagnostic Services (PDS) until 2013. A retrospective analysis on ~1,500 NCD cases, submitted to the lab from 2000 to 2013, showed a diagnostic success rate (DSR) of ~32.7%, as defined by the detection of one of the pathogens mentioned above. Among these, E. coli F5 was detected in 4.4% of cases, Salmonella spp. (1%); RV and BCoV (22%); Cryptosporidium sp. (5.3%). In 2014, we introduced additional diagnostic approaches which included: (i) PCR for E. coli genes encoding virulence factors (STa, Stx1, Stx2, F5, Eae) and for RV and BCoV (ii) FAT for detection of Cryptosporidium spp. and Giardia spp. Subsequently, the DSR for potential NCD etiologic agents in ~250 cases tested in 2014 and 2015 increased to ~60%. E. coli STa:F5 was detected in 1.8% of cases, Salmonella spp. (1.2%), RV and BCoV (28.2%), Cryptosporidium spp. (26.2%). In a concurrent pilot study conducted from 2013 to 2016, we tested for the different diarrhea-causing pathogens on fresh intestinal tissues collected from 105 calves with diarrhea and 100 without diarrhea. In addition, histologic examination on related fixed tissues was performed to assess potential pathogen-induced intestinal morphological changes in calves with diarrhea. No intestinal morphologic changes were observed in calves without diarrhea; however, the intestinal lesions in calves with diarrhea were mainly associated with C. perfringens (11.4% of cases), Salmonella spp. (6.6%), E. coli STa:F5 (1%), RV and BCoV (52.4%), Cryptosporidium spp. (19.0%) and Eimeria spp. (1.9%). This study showed a DSR of ~77.5%. RV and BCoV were the most prevalent diarrhea-causing pathogens in calves; however, detection of these viruses in some control calves indicates that NCD diagnostics should include advanced microbiology techniques as well as histologic examination for confirmation of infection in some cases.

The Western Canadian Animal Health Network: collaboration and crowdsourcing data

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Background: The first Canadian regional animal health surveillance network, RAIZO (Québec) has been in operation since the 1970. Other networks in Ontario and Atlantic Canada have more recently come online. However, prior to 2020, there was no similar initiative in western Canada. The concept of a Western Canadian Animal Health Network (WeCAHN) was presented at CAHLN 2018 by Dr. Wayne Lees. Subsequently, the four western provinces, led by Saskatchewan, secured funding for year one of operation of WeCAHN, which began 1 April 2020.

Methods: Prairie Diagnostic Services (PDS), WeCAHN "champion", is the virtual home of WeCAHN, holding the funds, and providing administrative support. The coordinator works under the guidance of the WeCAHN steering committee, with representatives from the four western provinces and PDS. At an initial meeting of stakeholders, a structure consisting of species/sector specific networks, similar to OAHN and RAIZO, was recommended. Beef cow-calf, dairy, poultry, and laboratory networks were prioritised by this group for implementation in year one.

The coordinator conducted internet searches to identify potential stakeholders in the four western provinces, including industry and veterinary groups, provincial and federal government staff, veterinary diagnostic laboratories, and existing surveillance projects/programs. These stakeholders were then contacted to discuss their potential interest in participating in the networks. Concurrently, existing regional networks were contacted to learn more about their respective operations and standard operating procedures.

Results: In year one, WeCAHN has established beef cow-calf, dairy, and poultry networks (which have held three, one and one quarterly meetings respectively). These meetings include veterinary practitioners from each of the four western provinces, laboratory diagnosticians from the western veterinary diagnostic laboratories, veterinary college faculty, researchers, provincial veterinary epidemiologists, and representatives from other veterinary surveillance networks. All participants contribute data, including a practitioners' clinical impressions survey, and laboratory data extracted from the LIMS of the participating laboratories. Network findings are shared with veterinary practitioners, veterinary associations, industry, and the general public.

Plans for year two include expanded activities of the beef network, supported by a Beef Cattle Research Council Grant, as well as the initiation of a small ruminant network.

Torque teno equus virus 2 (TTEqV2), a novel Anellovirus species and the first complete Mutorquevirus genome

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The complete genome of a novel torque teno virus (torque teno equus virus 2 (TTEqV2)) was sequenced by high throughput sequencing (HTS) following pan-vertebrate virus targeted probe-based enrichment of nucleic acid extracted from lung tissue of a 7 year old Quarter Horse gelding that died of nonsuppurative encephalitis in southern Alberta, Canada. The 2,805 nucleotide circular genome contains a number of features characteristic of TTVs. There is an ORF1 encoding a putative 631 aa capsid protein with an arginine-rich N-terminus, several rolling circle replication associated amino acid motifs and a downstream polyadenylation signal. A smaller overlapping ORF2 contains an amino acid motif (WX7HX3CXCX5H) highly conserved in TTVs. The UTR contains GC-rich tracts and two 15 nucleotide sequences highly conserved in TTVs. Phylogenetic analysis of TTV ORF1 sequences available to date shows TTEqV2 clusters with the only other reported member of the Mutorquevirus genus, torque teno equus virus 1 (TTEqV1, KR902501). Genome-wide pairwise alignment of TTEqV2 and TTEqV1 shows the absence of several highly conserved TTV features within the UTR of TTEqV1, suggesting it is incomplete. The nucleotide identity of ORF1 between the two equine TTV sequences is 59.7%, which falls between the 44% and 65% identity cutoff values proposed by the International Committee on the Taxonomy of Viruses' for taxonomic classification of new Anelloviridae genera and species, respectively. Our results indicate TTEqV2 is a new species and the first complete genome within the genus Mutorquevirus.

STUDENT

Septicemic pasteurellosis causing peracute death and necrotizing myositis in a beef heifer (Bos taurus) in Alberta, Canada

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Septicemic pasteurellosis is an acute and fatal bacterial disease of cattle and wild ungulates caused by certain serotypes of Pasteurella multocida. The disease is prevalent and costly globally, but is rare in North America where reports are limited to wild ruminants. Here we report a single case of septicemic pasteurellosis in a 6-month-old, Red Angus heifer from a cow–calf operation in Alberta, Canada. Postmortem examination revealed necrotizing and hemorrhagic myositis, fibrinous pericarditis and multisystemic bacterial emboli. Pasteurella multocida serogroup B was isolated from muscle in pure culture, typing of the organism was done using polymerase chain reaction (PCR) and gene sequencing. To the best of our knowledge, this is the first reported case of septicemic pasteurellosis in beef cattle in Canada. Veterinary practitioners and diagnosticians should include septicemic pasteurellosis on their list of differentials when encountering similar presentations of peracute death and severe necrotizing myositis in Canadian cattle.

Bronchopneumonia with interstitial pneumonia in beef feedlot cattle

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Bronchopneumonia with interstitial pneumonia (BIP) is a unique and yet uncharacterised form of bovine respiratory disease in North American beef feedlot cattle that is described as a concurrent caudodorsal interstitial pneumonia (IP) and cranioventral bronchopneumonia (BP). Presented here is a continuation of disease characterisation utilising histologic and microbiological data with comparison to its constituent forms of BRD (i.e. IP and BP). 50 Cases were blindly diagnosed by histology as BIP (n = 14), IP (n = 13) or BP (n = 23). Sensitivity and specificity of post-mortem (gross) diagnosis of BIP was 86% and 78%, respectively (PPV = 44%, NPV = 96%; Prevalence = 17%). The prevalence of key histological lesions of respiratory disease in BIP cases is discussed; comparative frequency of these lesions did not reveal significant differences between BIP and BP or IP in cranioventral or caudodorsal lung samples, respectively. In cases of BIP, cranioventral lung lesions were more often consistent with chronic disease (86%; p = 0.003) while caudodorsal lung lesions were more often acute in nature (71%; p = 0.003). To date, there have been no significant microbiological differences detected between BIP cases and BP or IP cases, respectively. The microbiomes of BIP and BP lung samples have been analysed via next-generation sequencing and differences between groups are compared. Finally, data on 9909 mortalities occurring on 4 Canadian beef feedlots over a period of 3 years were evaluated to compare epidemiological features of BIP, IP, and BP. These data characterize the pathology, microbiology and epidemiology of this novel condition and directs further investigation into the pathogenesis of this important cause of mortality in Canadian beef feedlots. Initial hypotheses include dysregulation of 3-methylindole metabolism (the causative agent of acute interstitial pneumonia) by a primary inflammatory episode.

Operational and quality management challenges during the early days of the SARS-CoV-2 pandemic: One veterinary diagnostic laboratory's experiences

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The rapidly evolving SARS-CoV-2 pandemic produced significant challenges in maintaining operations and quality management of the Animal Health Laboratory, University of Guelph during the spring and summer of 2020. As cases of coronavirus spread across Canada and other countries, AHL managers met to perform a risk assessment and develop contingency plans that included cross-training staff, ordering sufficient personal protective equipment and laboratory supplies, and identifying options for clients in the event of closure of an entire laboratory section. When the pandemic was confirmed and the province of Ontario enacted an emergency shutdown order on March 17, 2020, the AHL was declared an essential service and continued operations.

Physical distancing directives, self-isolation protocols and fear of infection resulted in a significant reduction in staffing levels from April until August. In the initial months, an opportunity to work-from-home was implemented to allay fears and maintain staff morale. Many lab sections subsequently transitioned into a split-team approach that reduced staff contact between shifts. Return to full staffing in the fall of 2020 was facilitated by increased public health knowledge regarding route of coronavirus transmission, adjusted safety measures and the relatively low case count at that time. Attention to mental wellness became increasingly important as pandemic restrictions progressed.

Maintenance of AHL's quality system during the pandemic was critical to assuring clients that test results were accurate and reliable. By communicating changes in specimen receiving hours and delays in laboratory testing in advance, client expectations were managed and complaints were avoided. A planned deviation was created to track quality activities that were delayed or temporarily curtailed; for example, proficiency panel testing and scheduled calibration of balances. Internal audits were postponed until a method for conducting virtual audits could be devised and implemented. When in-person audits resumed, internal assessors reviewed scanned records in advance to limit contact time between themselves and auditees. Management reviews also transitioned to virtual meetings.

AHL has learned several lessons during this past year of operating during a pandemic; chiefly, that clear and frequent communication is the key strategy for business continuity.

Oral fluid as an aggregate sample for early detection of African swine fever virus: evidence from four independent pen-based experiments

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African swine fever has sustained its spread throughout much of the world making it a global animal health priority. The emphasis is currently on enhancing preparedness to prevent, detect and respond to a potential outbreak of ASF virus (ASFV). In the event of ASFV entry to the North American swine population, enhanced surveillance and diagnostic testing strategies will be critical to facilitate progressive response and eradication of the disease. Compared to individual animal sampling, pen-based oral fluid collection for active surveillance is a non-invasive alternative that is less demanding of labor, time and resources. To evaluate the feasibility of using oral fluid for early detection of ASFV, four independent animal experiments were conducted in weaned pigs. In these experiments, pigs were housed in numbers that mimic the industry settings (N=20-25), and infected with a highly-virulent ASFV Georgia 2007/1 strain and moderately-virulent ASFV Malta'78 strain. A single seeder pig was infected with a dose of 1 X 102 TCID50 ASFV Georgia 2007/1 or 2 X105 TCID50/ml ASFV Malta' 78 virus in the left thigh and released to the group. Pen-based oral fluid and individual oropharyngeal swabs were collected daily and blood samples from each animal were collected every other day. All samples were subsequently tested for ASFV by real-time PCR. ASFV genome was detected in seeder pig blood samples as early as one day post-infection and detected in oral fluids at low-to-moderate levels as early as 3-5 days post-infection while the pen prevalence was as low as 4% and before the seeder pigs were found dead. These results suggest that pen-based oral fluid samples may be used to supplement the use of traditional samples for rapid detection of ASFV during ASF surveillance.

Pathology of free-ranging urban Leporidae in Calgary, Alberta

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Rapid urbanization has created ideal habitat for certain species to thrive in suburban zones in the form of lawns, gardens and parks. Urban Leporidae (hares and rabbits) flourish in these green spaces, which introduces the potential for frequent interactions and disease transmission between these animals and people. Yet the diseases present in Leporidae in an urban context has yet to be explored. The objective of this study is to investigate the diseases present in Calgary's urban Leporidae population and determine the risk factors associated with disease. Pathology analyses (autopsy examination and histopathology) were performed to identify tissue changes consistent with disease, as well as supportive tests (e.g. bacterial culture) when needed to reach a diagnosis. We received 154 roadkill carcasses from the City of Calgary and The Rehabilitation Society of Canada. Of the 154 animals, 143 (93%) were White-tailed jackrabbits (Lepus townsendii), and 11 (7%) were feral European rabbits (Oryctolagus cuniculus). The majority of observed specimens were sexually mature individuals (120/154; 75%) and in moderate to good body condition (97/154; 63%). There were 77 males (52%) and 73 females (48%), among which 21 (29%) were pregnant. As expected, most individuals died of acute trauma; however, we identified gross lesions not attributable to acute trauma in 33% (51/154) of the carcasses. Common lesions observed include kidney (16/154; 10%) and liver (8/154; 5%) masses, and idiopathic splenomegaly (19/154; 12%). There were suspected parasitic cysts of the genus Taenia in 20 (13%) of observed specimens. Two individuals had severe malocclusions. Other significant incidental findings include an organizing hematoma, a healed rib fracture, and multiple instances of accessory splenic fragments ("spleenettes"), suggesting that several individuals survived previous instances of trauma. Unexpectedly, we also identified 4 cases of non-trauma related mortality; causes of death included dystocia and tularemia (Francisella tularensis subsp. holarctica) in one animal each, and aspiration pneumonia in two individuals. Further analyses to characterize lesions and causes of death are underway. The results from this study will provide a scientific understanding of background diseases and health status of rabbits and hares, informing future researchers of the disease risk of Leporidae in Canadian cities.

Animal Health Informatics: Integrating Animal Health Information in Canada

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A robust animal health surveillance system is built on structured social networks using up-to-date information to track health, respond rapidly to events and set priorities. While Canada has made strong progress in recent years, particularly in creating structured social networks for animal health, there is a need for increased and more uniform capacity to use data to generate information. This is critically important due to increasing pressures related to emerging zoonotic diseases, antimicrobial resistance, and foreign animal disease (FAD) incursion risk. In Canada, current limitations to achieving maximum information from data include siloed data, heterogenous and inconsistent data formats, lack of resources to develop IT solutions for successful animal health information generation, and barriers associated with privacy legislations with information sharing among jurisdictions.

The Canadian Animal Health Surveillance System (CAHSS) brings together and uses data-driven information to demonstrate animal health, minimize impacts of disease, and guide planning on national animal health priorities. CAHSS is currently working with partners in conducting discovery projects in animal health informatics with a focus on applications that are relevant to disease detection and classification, disease reporting, and translating knowledge into actionable goals for disease surveillance. The objective is secure, well-structured, up to date laboratory and abattoir condemnation data that can be efficiently used by laboratorians, pathologists, and epidemiologists working in governments, animal health surveillance networks, industry organizations, and universities to easily generate the information they need. The system would generate and store structured datasets derived from Laboratory Information Management System (LIMS) systems, provincial abattoir systems, and other data sources. Examples of data elements within the structured dataset include but are not limited to unique case identifiers, submission date, species tested/ submitted, geographical location, disease classification, and final diagnoses.

The goal of the presentation is to generate awareness on the application of the data platform and to allow opportunities for laboratorians in Canada to participate, support, and advance the project.

Clostridial hepatitis caused by Clostridia novyi-group bacteria in 4 mature equids in southern Alberta

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Between 2014-2018, 4 cases of clostridial hepatitis were identified in mature equids residing in southern Alberta, including the first reported case in Canada. Clinical signs included acute onset of colic, depression, anorexia, tachycardia, tachypnea, fever, hemoglobinuria, icterus, and variable neurological signs. Serum biochemistry revealed marked increases in hepatic enzymes and normal bile acids. Pathognomonic subcapsular and parenchymal emphysema was observed in the liver on ultrasound. Necropsy findings included severe icterus, peritoneal effusion, localized fibrinous peritonitis, hemoglobinuric nephrosis and necrotizing hepatitis localized to the left lobes. Histologically, there was coagulative necrosis surrounded by a rim of inflammatory cells and gram-positive rods which in all 4 cases were positive for Clostridium novyi via immunohistochemistry. Polymerase chain reaction (PCR) was positive for flagellin genes (fliC) of Clostridium novyi type B and Clostridium haemolyticum in 2 horses tested to date, representing the first description of dual infection. Three of 4 horses demonstrated rapid deterioration and death within 24-48 hours of presentation. One animal responded to supportive therapy and aggressive, long-term antimicrobials. This horse has returned to her previous level of competition and is the first reported horse in the world to survive this invariably fatal disease. While clostridial hepatitis appears to be a rare disease, it should be considered as a differential diagnosis of acute hepatic disease especially in horses presenting with colic. Rapid recognition of the clinical features of this acute, fulminating infection is crucial to successful therapy and survival.

Rapid Salmonella serotyping by sequencing on nanopore platform

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Salmonella clinical infections and colonization remains a significant problem across multiple industries in animal agriculture. Timely and efficient Salmonella detection and characterization is of critical importance for clinical and husbandry decision making, but traditional salmonella serotyping is a complex and tedious process. Whole-genome sequencing (WGS) is becoming a widely accepted standard for detailed Salmonella characterization - including serotype prediction. Prairie Diagnostic Services in collaboration with Simon Fraser University researchers have developed and validated a workflow for rapid in-house Salmonella isolates characterization by whole-genome sequencing on nanopore platform. This workflow can be completed in one work day and utilizes the Salmonella In Silico Typing Resource (SISTR) developed and maintained by the Public Health Agency of Canada (PHAC). Based on over 150 isolates characterized up to date, the newly developed workflow has 100% agreement with the PHAC reference serotyping method. Besides the advantage of very quick turnaround time, the WGS data obtained from the newly developed workflow can be a powerful tool for genomic epidemiology investigations and husbandry decision making.

POSTER

Presentations

STUDENT

Sarcocystis species protozoal encephalitis in a wild black bear (Ursus americanus)

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The health of wild black bear populations is affected by multiple factors, including habitat loss and human-wildlife conflict. The role of disease in these challenged systems remains relatively unexplored. A juvenile male black bear was found dead in October, 2018 in a provincial recreational area in southwestern Alberta and was submitted to the Alberta Region of the Canadian Wildlife Health Cooperative at the University of Calgary for diagnostic investigation.

Lesions included suppurative cellulitis, fasciitis and myositis of the left lower hindlimb and lymphoplasmacytic encephalitis. Numerous intralesional protozoal schizonts were present in the affected muscle and brain. These were identified as Sarcocystis sp. with immunohistochemistry. Immunohistochemistry for canine distemper virus and rabies virus were negative. Bacterial culture yielded a pure culture of Streptococcus halicoeri from the leg lesions, which is probably secondary bacterial infection. Although the intermediate stage of Sarcocystis sp. is frequently observed in the muscle tissues of a variety of wildlife, it is rarely associated with disease. Sarcocystis sp. is a known cause of encephalitis in birds and fatal hepatic sarcocystosis has been described in black bears (Ursus americanus) and polar bears (U. maritimus). Its role as a fatal brain pathogen of wild bears remains undescribed, making this case highly unusual. Sarcocystis sp. and other infectious diseases may be an important and underrecognized cause of wild bear mortality.

STUDENT

Using whole-genome sequencing to examine the relatedness and antimicrobial resistance elements of E. coli isolates within a One Health continuum

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Increasingly, antimicrobial resistance (AMR) is regarded as an ecological concern, a shared resource of the global microbial community. Because of the genetic mobility provided by horizontal gene transfer, the relevant units of concern for AMR are often the antimicrobial resistance genes themselves and the mobile genetic elements (MGEs) that facilitate AMR transmission. This study will investigate the genetic basis of AMR in Escherichia coli in two facets within a One Health continuum: indirect transmission from food animals to humans through retail meats and AMR transmission between animals, humans, and the environment via water.

Previous dogma held that finding E. coli, a ubiquitous enteric commensal and a common pathogen of both humans and animals, in environmental samples must be indicative of recent fecal contamination. The more recent discovery of “naturalized” E. coli capable of long-term persistence and reproduction in the environment prompts a rethinking of this paradigm, however. The potential role of these naturalized strains in AMR transmission is not well understood. Further, although handling and consumption of meat products is often posited as a mode of AMR transfer between animals and humans, many studies lack sufficient genetic discrimination to definitively establish the movement of antimicrobial resistance genes between these populations.

For this investigation, E. coli has been isolated from routine surveillance of fecal samples from feedlot beef and broiler chicken production, retail beef and chicken meats, post-treatment wastewater, and private well water samples. All samples were collected in Alberta in 2018 and 2019. In addition to phenotypic AMR determination, short- and long-read whole-genome sequencing will be performed and combined into hybrid assemblies that will identify ARGs and MGEs. The resolution MGEs represents a level of resolution seldom possible in previous examinations of AMR.

Genotypic AMR profiles will be compared to the phenotypic expression of resistance for each isolate. Phylogenetic trees will elucidate the relatedness of E. coli from the various sources, and associations in the pattern and frequency of resistance elements will be examined in an epidemiological context through regression analysis with adjustment for clustering. The factors identified in this epidemiological analysis will help shape AMR mitigation strategies and contribute to the broader understanding of the ecology of AMR in a One Health context.

STUDENT

Lesions of Mycobacterium avium spp. hominissuis infection in a wild mule deer (Odocoileus hemionus) resemble Mycobacterium bovis

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Mycobacterium avium spp. hominissuis was identified in lung granulomas and a suppurative tracheobronchial lymph node from a mule deer (Odocoileus hemionus) from Banff, Canada. Infection was confirmed using molecular analyses. These lesions were morphologically similar to those in M. bovis infected animals, emphasizing that disease surveillance in wildlife populations is critical.

Improving methods of control of American foulbrood in honey bees in Saskatchewan

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American foulbrood (AFB) is a devastating disease of newly hatched honey bee larvae caused by the spore-forming bacterium, Paenibacillus larvae, which parallels Bacillus anthracis (anthrax) in its extreme infectivity, prolificity, and spore resiliency. Clinical disease often results in colony death by either natural disease progression or destruction by the beekeeper to limit the spread of spores to other colonies. North American beekeepers rely heavily on routine antimicrobial metaphylaxis to prevent disease, but treatment fails to eliminate infectious spores. As a result, beekeepers have developed a dependency on antimicrobials to prevent AFB. With the emergence of antibiotic-resistant strains of P. larvae, there is a need for alternative, evidence-based management tools to effectively reduce the use of antibiotics while maintaining sustainable beekeeping operations.

Province-wide surveillance of P. larvae spores in honey may be a proxy for evaluating yard-level AFB risk. Accordingly, we analyzed the spore content of pooled, extracted honey from 50 large-scale and 72 small-scale Saskatchewan beekeepers, representing over 70,000 of the province's 110,000 honey bee colonies. These results, in conjunction with data from an accompanying AFB questionnaire, will establish prognostic reference ranges for honey to identify the immediate risk of AFB outbreaks in antibiotic-dependent management systems. Overall, this will improve the ability of beekeepers to implement evidence-based antimicrobial use in the prevention of AFB. To date, spores have been detected in 47% of large-scale honey samples at either low (60.5%), medium (29.5%), or high (9.9%) concentrations. A smaller proportion (26%) of small-scale samples have detectable spores at low (95.7%), medium (3.4%), or high (0.9%) concentrations. Subsequent incidence of AFB was observed in 1/1 small-scale and 3/6 large-scale beekeepers with high spore concentrations, and 3/14 large-scale beekeepers with medium spore concentrations. Consistent with our current risk criteria, AFB has not been observed in large- or small-scale beekeepers with low spore concentrations.

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Duck atadenovirus A 2019 and 2020 outbreaks in ducklings including whole genome sequence of the viruses

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Duck atadenovirus A, also known as Duck adenovirus 1 (DAdV-1), is a member of the genus Atadenovirus. This virus is also responsible for the Egg Drop Syndrome (EDS) of laying hens, which causes a severe drop in egg production that could last for 4 to 10 week, and the laying of thin-shelled, soft-shelled, or shell-less eggs. Most infection with DAdV-1 in ducks and geese are asymptomatic and the rare reports of clinical signs always imply very young (4 to 20 days of age) ducklings and goslings. When sick, the symptoms in infected birds are gasping, dyspnea, coughing, and/or sneezing and mortality is, moderate (2% to 7%). This syndrome is listed as an immediately notifiable disease in Canada, because it is considered as an exotic disease for which there are no control or eradication programs. Although this virus has never been reported in commercial chicken production in Canada, DAdV-1 was identified in 2009 in 2 Muscovy duck farms in Ontario. In addition, antibodies to DAdV-1 have been detected in numerous wild waterfowl in North America, up to 42% in sampled ducks, suggesting it is widespread on the continent and that these birds act as reservoirs. The first clinical case of DAdV-1 in a commercial duck farm in Québec province was identified in 2019. More recently, a second case was reported in late 2020 in another duck farm also in Québec province. The whole genome sequencing (WGS) of the both cases revealed that both sequences shared a homology of 99.41%. The nucleotide (nt) sequences obtained from the 2019 and 2020 cases clustered with other DAdV-1 worldwide reference strains, with a nt homologous percentage varying between 98.23 to 98.33%, and 97.79 to 97.89%, respectively. However, these results suggest that Quebec strains may represent a different cluster of DAdV-1.

Bovine Astrovirus and its Potential Role in Bovine Lymphocytic Encephalitis

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Astroviruses are a well-known cause of gastroenteritis in humans and many domestic animal species. More recently, these emerged as a cause of encephalitis in cattle and other species. Encephalitis is an economically important disease in cattle due to death of animals and potential exclusion of carcases from the food chain. There is a zoonotic concern as many causes of encephalitis in cattle can also cause disease in humans. It is therefore essential to determine the causes of encephalitis and their relative importance in a population.

To investigate bovine astrovirus in Ontario cattle, 34 cases of idiopathic lymphocytic encephalitis were retrieved from the Animal Health Laboratory/Ontario Veterinary College archives. As controls 34 animals with non- lymphocytic encephalitis, and 42 animals with no neurologic disease or encephalitic lesions were included in the study. All animals were screened using RT-qPCR for bovine astrovirus. No animals from either control group tested positive for bovine astrovirus. Four animals with lymphocytic encephalitis are positive for bovine astrovirus; they all had lymphocytic perivascular cuffs affecting both grey and white matter of the cerebrum. All positive cases had a history of neurologic disease, and most displayed ataxia and staggering.

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