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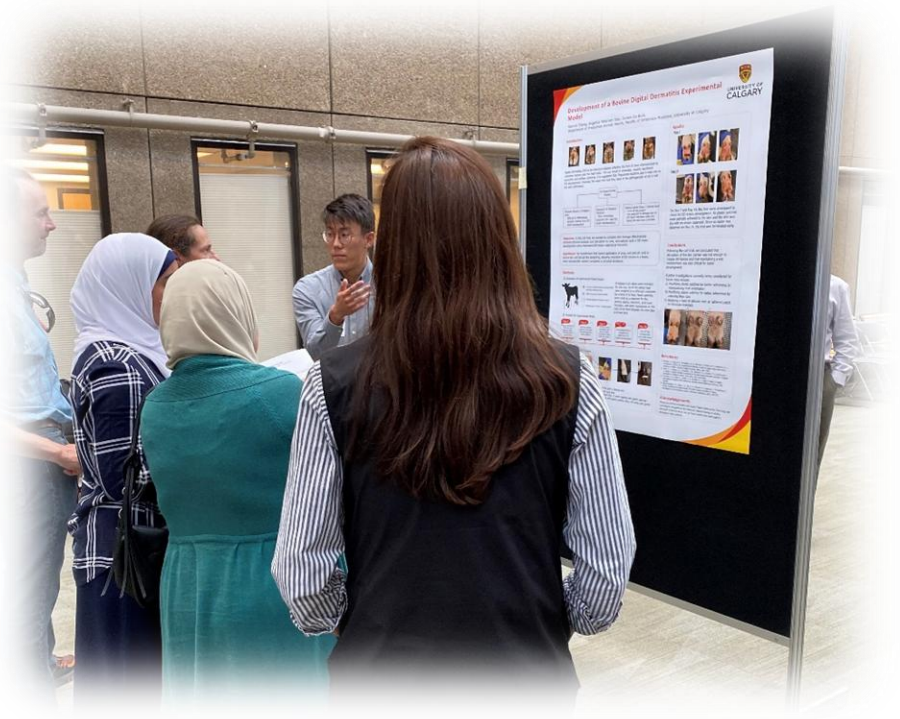
FACULTY OF VETERINARY MEDICINE



UCVM SURE Research Day 2026

August 14, 2026

8:25 a.m. – 4:00 p.m.

Health Sciences Centre (HSC) Theatre 3 and Feasby Mall

PROGRAM and ABSTRACT BOOKLET

Message from Dr. James Wasmuth, Associate Dean, Emerging Scholars

Welcome to the 2026 UCVM SURE Research Day! This year 65 students registered in the SURE (Summer Undergraduate Research Experience) program. Funding to support students and the program has come from PURE, NSERC, Alberta Innovates, The McCaig Institute, O'Brien studentship awards, RDAR, the UCVM Office for Emerging Scholars, and supervisors' grants. Eight of our SURE students are in the DVM program; others joined us from Biomedical Engineering, Health Sciences and Medicine, Kinesiology, and Arts. We also welcomed two students from other universities: USaskatchewan and UToronto.

Education, training and research are central to the mission of the Faculty of Veterinary Medicine. Today's program features 16 oral presentations and 33 poster presentations spanning a diverse range of veterinary medical research. We are also delighted to have Dr. Samia Hannaoui deliver the keynote lecture. Dr. Hannaoui is an emerging leader in prion disease research, investigating the transmission dynamics of Chronic Wasting Disease in cervids and its potential risks to livestock and human health. Her work on cross-species transmission and gut–brain pathways is reshaping our understanding of CWD spread.

We invite you to engage fully with all presentations: ask questions, offer feedback.

Above all, today celebrates what our students have achieved this summer. You planned and executed experiments, learned new methods, built datasets and tools, analysed results, and, as we will soon see, translated findings into engaging presentations. Many of you contributed to ongoing lab projects, improved protocols, and strengthened collaborations. Your work advances the research mission of the Faculty of Veterinary Medicine, while building your own skills in inquiry, communication, and teamwork. I hope that this experience fuels your curiosity and confidence to carry an interest in research into the next stages of your education and careers. I hope many of you consider coming back to VetMed. Thank you to our postdoctoral fellows and graduate students for contributing to the success of the SURE program.

Finally, thank you to Erin Fraser (Office of Emerging Scholars) for exceptional coordination and communication support for today's event.

Enjoy SURE 2026!

Sincerely,

James Wasmuth

Associate Dean, Emerging Scholars, UCVM

Agenda

8:25	**Welcome and Introductions – Theatre 3:** James Wasmuth
Oral Presentation Session #1 – Theatre 3 Chair: James Wasmuth	
8:30	**Gabrielle Ting (Anderson Lab)** *Documenting variation within the diplocaulid nectridean Diceratosaurus brevirostris from Linton and Five Points, Ohio*
	Julia Rawleigh (Pajor Lab) *Identification of the Sexually Active Group in Beef Heifers Using Automated Monitoring Devices*
	Ember Wilson (Schaetzl Lab) *Investigating A Reliable Oral Dosage For Complete Attack Rate In Prion Challenged Wild-type Mice*
	Sraddha Uppili (Cobo Lab) *Investigating the Role of Proteases in the Host-Immune Response during Swine Dysentery*
9:30	**Mini-Break**
Oral Presentation Session #2 – Theatre 3 Chair: James Wasmuth	
9:35	**Jordan Chen (Biernaskie Lab)** *Mapping the Role of Revascularization and Reinnervation in Regenerative Versus Fibrotic Wound Healing*
	Elliott Brien (van der Meer Lab) *BCoV Molecular Epidemiology in Western Canada: Enteric vs Respiratory Isolates*
	Gabriel Ciupa (Gilch Lab) *Engineering peptide aptamers to improve their anti-prion activity*
	Kenda Swanson (Hordle Lab) *Canine Nausea: A Scoping Review*
10:35	**Coffee Break**
Oral Presentation Session #3 – Theatre 3 Chair: James Wasmuth	
11:00	**Gabrielle Schroeder (Rosa Lab)** *Feral Horse Parasite Abundance in Relation to Their Plant Communities*
	Abigail Dean (Gilleard Lab) *Nemabiome ITS2 metabarcoding validation of a semiquantitative diagnostic qPCR panel to be used in clinical diagnostics and herd health management of ovine gastrointestinal nematodes*
	Madalyn Arsenault (Remnant Lab) *Identifying Priority Learning Outcomes for Clinical Educators in Distributed Veterinary Clinical Education: A Modified Delphi Study*
	Anysia Normand (De Buck Lab) *Improving Phage-Based Prevention of Johne's Disease Using CRISPR Genome Editing*
12:00	**Lunch and Poster Session - HRMB Atrium & Feasby Mall** ***Lunch will be available for registrants only***
Oral Presentation Session #4 – Theatre 3 Chair: James Wasmuth	

14:00	**Kathan Pathak (Alfajaro Lab)** *RNA Virus Surveillance in Wild American Martens Across Canada*
	Bondie Phan (Niu Lab) *Evaluating the Efficacy of Various Phage Cocktails against Multidrug-Resistant Escherichia coli ST131*
	Manar Bairq (Ungrin Lab) *Development and Validation of a High Throughput UV Plate-Reader Workflow for Rapid Microbial Contamination Detection in Mammalian Cell Culture*
	Saniru Kularatne (Soghigian Lab) *Prevalence of West Nile Virus in Mosquitoes Around the Calgary Area*
15:00	**Keynote Speaker – Theatre 3**
	Dr. Samia Hannaoui "The Protein That Breaks the Rules *Prions and Prion Diseases"*
15:45	**Prizes and Closing Remarks:** James Wasmuth and Erin Fraser

ABSTRACTS

Listed alphabetically by first name of presenting author

Contents

Crosstalk Between Autophagy and Hsp110 Homologues in Prion Disease

Aarushi Vasal[1-4], Matteo Mosca[1-4], Mariam Ansari[1-4], Basant Abdulrahman[1-4],Hermann Schaetzl[1-4]

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Keywords: *Prion diseases, Autophagy, Hsp110 homologues*

Prion diseases are fatal neurodegenerative disorders caused by the accumulation of misfolded proteins (prions), which affect both animals and humans and can possess zoonotic potential. The accumulation of prions disrupts proteostasis which contributes to neuronal dysfunction. Cells rely on proteostatic mechanisms, such as autophagy and mammalian heat shock proteins, to maintain cellular protein quality control. Emerging evidence suggests that autophagy and molecular chaperones may function cooperatively rather than independently; however, the molecular relationship between the two has not been well characterized. Evaluating the relationship between Hsp110 homologues and autophagy in neuronal cell lines may provide insight into how they cooperate to maintain proteostasis during prion pathogenesis. This project aims to determine whether the loss of Atg5-mediated autophagy alters the expression of Hsp110 homologues in both prion-infected and uninfected mouse neuroblastoma cells. Wild-type (WT) and Atg5-knockout (KO) mouse neuroblastoma (N2a) cell lines were used in which the expression of Hsp110 homologues, Apg-1, Apg-2, and Hsp105, was examined. Protein expression was assessed through Western blotting, and quantification was then conducted through densitometric analysis of Western blot bands normalized to β-actin. Western blot analysis revealed differential expression of Hsp110 homologues in the Atg5 KO cell line, relative to the WT. The findings suggest that autophagy influences Hsp110 homologue regulation, supporting the potential crosstalk between the proteostasis pathways. In conclusion, our findings support a role for Atg5-mediated autophagy in modulating Hsp110 homologues expression and suggest coordinated regulation of proteostasis pathways in neuronal cells.

Nemabiome ITS2 metabarcoding validation of a semiquantitative diagnostic qPCR panel to be used in clinical diagnostics and herd health management of ovine gastrointestinal nematodes

Abigail Dean[1], Elizabeth Redman[1], Christian Savard[2], John Gilleard[1]

[1]Faculty of Veterinary Medicine, University of Calgary, [2]Biovet,- a division of Antech

Keywords: *Nematodes, qPCR, Metabarcoding*

Anthelmintic resistance in ovine gastrointestinal nematodes is driving the need for diagnosis-led control. Genera-specific TaqMan quantitative PCR (qPCR) assays have been developed for Haemonchus, Teladorsagia, Cooperia, Trichostrongylus, and Nematodirus. We used internal transcribed spacer 2 (ITS2) nemabiome metabarcoding to test their accuracy in determining genus-level composition in ovine fecal samples. We compared genus composition determined by qPCR and ITS2 metabarcoding on the same fecal samples. Agreement per genus was quantified using Lin's concordance correlation coefficient (CCC) with 95% confidence intervals. We first applied the assays to DNA from 500-1000 L1 and L3 larvae extracted by coproculture from 4 countries with differing parasite communities (Canada, Northern Ireland, Greece, and Argentina; n = 33). Concordance between assays was moderate to strong across four sheep genera (Lin's CCC 0.70-0.80: Haemonchus, Teladorsagia, Trichostrongylus, and Cooperia). We next applied the assays in triplicate to DNA from three fecal aliquots from ovine samples across a range of fecal egg counts. We found good agreement between assays and technical replicates, but some variance between fecal aliquots of the same sample. Concordance (Lin's CCC) was highest for Haemonchus (0.92) and lowest for Teladorsagia (0.54). Overall, there was good agreement between ITS2 metabarcoding and qPCR, but future work will reduce variance between fecal aliquots to improve panel accuracy in clinical samples. These findings support the integration of the qPCR panel into routine veterinary diagnostics for ovine gastrointestinal nematodes.

Asporin as a potential driver of the acquisition of fetal-like regenerative competency

Anna Zhu, Eren Kutluberk, Ross Fitzsimmons, Dragana Ponjevic, Jeff Biernaskie

Faculty of Veterinary Medicine, University of Calgary; Alberta Children's Hospital Research Institute

Keywords: *Antlerogenesis, Regeneration, Asporin*

The annual regrowth of reindeer antlers is one of the few instances of complete mammalian organ regeneration. Antler skin, or ‘velvet’, is also remarkable in its ability to regenerate scarlessly following injury, unlike the skin of other mammals or reindeer back [Sinha et al., Cell, 2022]. This regenerative ability depends on resident fibroblasts that are transcriptionally distinct from other dermal fibroblasts typically prone to fibrosis. This study seeks to understand how and from where velvet fibroblasts arise as antlerogenesis begins.

To assess transcriptional changes in fibroblasts during antlerogenesis, single-cell RNA sequencing (scRNA-seq) was conducted on skin adjacent to the velvet-free antler in autumn, healing skin of the shed antler wound site in winter, and skin of the early growing antler in spring.

Transcriptomics identified genes uniquely upregulated at the healing skin stage. One of these was Aspn (encoding the extracellular matrix protein Asporin), which was enriched in dermal fibroblasts at the onset of pedicle growth as scalp skin was becoming velvet-like. Interestingly, a transient burst of Asporin is essential for fetal-like reversion in intestinal cells following injury [Iqbal et al., 2025, Cell Stem Cell]. Immunofluorescence staining revealed that Asporin was highly expressed in the upper dermis of scalp skin adjacent to the future antler.

These results suggest that Asporin may be contributing to the transition towards velvet in these fibroblasts, mirroring repair of the intestinal crypt. Future work will determine whether treating cultured scalp fibroblasts with Asporin converts them to a more velvet-like state, thereby assessing the protein function.

Exposure and Host Risk Factors Associated with Alveolar Echinococcosis in Animals and Humans Globally: A Scoping Review

Annalise D. Tremblay[1],*Nakeesha S. Sadiq[1],*, Heather Ganshorn[2], Kinga Kowalewska-Grochowska[3], Stephen D. Vaughan[4], Jamie L. Rothenburger[1,5]

[1]University of Calgary, Faculty of Veterinary Medicine, Calgary, AB, [2]University of Calgary, Libraries and Cultural Resources, Calgary, AB, [3]Department of Laboratory Medicine and Pathology, Faculty of Medicine and Dentistry, University of Alberta, Edmonton, AB, [4]Cumming School of Medicine, University of Calgary, Calgary, AB, [5]Canadian Wildlife Health Cooperative (Alberta Region), Calgary, AB

*These authors contributed equally to this work

Keywords: *Alveolar Echinococcosis, Echinococcus multilocularis, risk factor*

Introduction: Alveolar Echinococcosis is a fatal zoonotic disease, caused by the larval stage of the tapeworm Echinococcus multilocularis, that infects the liver of animals and humans. Currently, this disease is emerging rapidly in parts of the Northern Hemisphere, but there is a knowledge gap regarding how atypical hosts acquire this infection. To address this gap, our objective was to systematically identify and synthesize the global scientific evidence on risk factors for Alveolar Echinococcosis in humans and animals.

Methods: This scoping review follows the guidelines of JBI Manual for Evidence Synthesis. Methodology reporting followed the PRISMA scoping review extension (PRISMA-ScR) guideline. Five online databases were searched using keyword combinations of “Echinococcus multilocularis*” and “Alveolar Echinococcosis*” to identify peer-reviewed and grey scientific literature. Literature published in English between January 1, 2000, and May 25, 2026, was assessed. We screened articles using an independent, 2-stage process with pre-defined inclusion/exclusion criteria in Covidence software and extracted data for structured synthesis.

Results: We screened 7264 titles and abstracts, and approximately 1200 full-text sources, for an estimated 250 studies to be included in the final review. Preliminary results suggest that human exposure and host risk factors would be occupation and immunosuppression, respectively. For animals, important exposure and host risk factors are coprophagy and pregnancy, respectively.

Discussion/Conclusion: We expect to provide a comprehensive summary of Alveolar Echinococcosis risk factors for humans and animals that can aid in disease prevention. The results will be used to develop risk factor questionnaires for future case-control epidemiological studies of Alveolar Echinococcosis.

Climate-Based Prediction of Seasonal Mosquito Vector Dynamics in Calgary, Alberta

Anthony Deogracias, Michaela Seal, Alex Coker, John Soghigian

Faculty of Veterinary Medicine, University of Calgary, City of Calgary

Keywords: *Mosquito, Surveillance, Climate-based*

The recent finding of invasive Culex pipiens mosquito, a primary vector of West Nile Virus, in Calgary, Alberta in 2022, highlights the need for continued mosquito surveillance to better understand disease transmission dynamics under a shifting climate. Temperature and precipitation are key climatic drivers of mosquito abundance as higher temperature allows for shorter extrinsic incubation periods and increased rainfall creates more suitable breeding habitats. In this study, we aim to provide a climate-based framework to support mosquito surveillance and inform mosquito control strategies in Calgary. We coupled surveillance data collected by the City of Calgary with city-wide weather data from 2018 to 2025. Spearman's rank correlation was used to assess the correlations between mosquito abundance and eight climate variables. Generalized Linear Mixed Model (GLMM) will be performed for subsequent analyses to evaluate the combined effects of climatic variables and seasonal temporal variation on mosquito abundance. Preliminary results revealed peak mosquito counts as early as July and as late as September, with higher Culex pipiens counts in 2024 (n = 152) compared to 2022 (n = 15). Culex pipiens abundance was positively associated with 30-day lagged temperature ($\boldsymbol{\rho}$ = 0.36, p-value = 0.06) and negatively associated with diurnal temperature variation ($\boldsymbol{\rho}$ = -0.23, p-value = 0.25). We predict the cumulative effect of 14-day lagged temperature and precipitation to show a positive effect on mosquito abundance, consistent with known mosquito life cycle. These findings could help manage disease transmission dynamics of clinically important vectors through more effective timing of aerial insecticide applications.

Improving Phage-Based Prevention of Johne's Disease Using CRISPR Genome Editing

Anysia Normand, Bradley Dubrule, Jeroen De Buck

Faculty of Veterinary Medicine, University of Calgary

Keywords: *Genetic engineering, Microbiology, Phage therapy*

Johne’s Disease (JD) is a bacterial infection of the small intestine in cattle and ruminants caused by Mycobacterium avium subsp. paratuberculosis (Map). This disease is widespread in the dairy industry, causing significant economic losses that continue to rise due to lack of treatment options and ineffective diagnostic methods. Phage therapy, a non-antimicrobial approach, has emerged as a potential therapy for JD. Previous research in the De Buck lab identified multiple mycobacteriophages that lyse Map which can prevent development of the disease. However, mycobacteriophages face limitations in practical application due to their capacity to form lysogens, which can transfer resistance genes and confer immunity to future phage lysis. This study aimed to improve phage therapeutics for JD by preventing lysogeny through the deletion of integrase from mycobacteriophages via CRISPR cas-9 gene editing. To determine if integrase deletion prevented lysogen formation we conducted phage release assays. Wildtype phages demonstrated spontaneous phage release, which was absent in their integrase-deleted counterparts. To ensure that integrase deletion did not negatively impact phage lysis efficiency, we conducted one-step growth curve analysis to determine the mycobacteriophage’s latency period and burst size. Latency periods for wild-type and integrase-deleted phages ranged from 90 to 180 minutes and 60 to 180 minutes, respectively. Burst sizes for the wild-type and integrase-deleted phages ranged from 21 to 153 and 41 to 135, respectively. These results demonstrated that deletion of the integrase gene from the mycobacteriophages prevented lysogeny without negatively affecting their lysis efficiency.

Peripheral Auditory Hyperresponsiveness in a Mouse Model of Fragile X Syndrome

Assad Popal [1 2 3], Wenyue Xue [3], Jun Yan [2 3], Ning Cheng [2 4 5]

[1]Department of Biological Sciences, Faculty of Science, University of Calgary, [2]Hotchkiss Brain Institute, Cumming School of Medicine, University of Calgary, [3]Department of Physiology and Pharmacology, Cumming School of Medicine, University of Calgary, [4]Faculty of Veterinary Medicine, University of Calgary, [5]Alberta Children's Hospital Research Institute, Cumming School of Medicine, University of Calgary

Keywords: *Fragile X syndrome; Auditory hypersensitivity; Compound action potential.*

Introduction

Fragile X syndrome (FXS) causes auditory hypersensitivity, but where altered sound processing begins remains unclear. Research focuses on the brain, although sound is first processed by the inner ear and auditory nerve. Changes there may help explain auditory symptoms. We hypothesized that Fmr1 knockout (KO) mice would show stronger responses than wild-type (WT) mice.

Methods

Compound action potentials (CAPs) were recorded from adult female WT mice (n = 11) and Fmr1 KO mice (n = 9) under anaesthesia. Tones at 5, 7, 10, 14, and 20 kHz were presented across sound levels using a silver-wire electrode positioned near the cochlea. Response thresholds, amplitudes, latencies, and durations were measured. Data were analyzed using two-way ANOVA followed by Šídák's multiple comparisons test.

Results

Preliminary analyses showed that Fmr1 KO mice had significantly larger CAP amplitudes than WT mice overall (genotype effect, $p < 0.0001$; genotype-by-frequency interaction, $p = 0.0204$), with the largest differences at 10 and 14 kHz. KO mice additionally showed lower response thresholds ($p = 0.0032$) and shorter latencies ($p = 0.0071$), although group differences were significant only at some frequencies. Response duration did not clearly differ between groups.

Discussion and Significance

These findings suggest that auditory hypersensitivity in FXS may involve altered processing in the auditory periphery before signals reach the brain. Larger auditory nerve responses provide the strongest evidence for this change and support a peripheral contribution to auditory dysfunction in FXS. These results provide a basis for future studies examining how peripheral auditory changes contribute to sensory symptoms.

Evaluating the Efficacy of Various Phage Cocktails against Multidrug-Resistant Escherichia coli ST131

Bondie Phan[1], Mawra Gohar[1], Sidra Moqaddes[1], Dongyan Niu[1]

[1]Faculty of Veterinary Medicine, University of Calgary

Keywords: *Bacteriophages, Phage Therapy, Extra-intestinal Pathogenic Escherichia Coli ST131*

Background:

Escherichia coli ST131 is a multidrug-resistant (MDR) bacteria responsible for urinary tract infections in humans. Rising antimicrobial resistance has renewed interest in bacteriophage therapy.

Objective:

This study aimed to evaluate the efficacy of individual phages and phage cocktails against MDR E. coli ST131 and assess genetic determinants for anti-phage resistance.

Methodology:

Mosigivirus (186B), Lederbergvirus (186P), Kayfunavirus (204B), and Vectrevirus (261P and 266F) phages were formulated into two-, three-, four-, and five-phage cocktails (PCs). The multidrug-resistant ST131 reference strain CFT073 and clinical isolate EC16-425 were evaluated using a time-kill assay at multiplicities of infection (MOIs) of 1, 10, and 100. Bacterial growth was monitored hourly by measuring OD_{600}, and the area under the growth curve (AUC) was compared using one-way ANOVA in GraphPad Prism (v11.0.2). Phage-resistant mutants recovered from treated cultures were whole-genome sequenced, assembled using SPAdes (v3.13.1) and analyzed for SNPs using breseq (v0.35.7).

Results:

Against EC16-425, 186B and 5PC produced significantly lower AUCs(0~3.54, 0.080~0.20 respectively), indicating greater bacterial growth inhibition compared with individual phages across all MOIs ($p<0.05$). Similarly, the 2PC(186B+204B) and 3PC(186B+204B+186P) demonstrated significantly greater antibacterial activity and lower AUCs(0.123, 0.10, respectively) than individual phages at MOI 1000 ($p<0.05$). Against CFT073, 2PC exhibited significantly lower AUC(0.087~0.13) than both 2PC(266F+261P) and the individual phages across all MOIs ($p<0.05$). Genomic characterization of phage-resistant mutants is ongoing.

Conclusion

These findings suggest phage efficacy may depend on bacterial growth characteristics. We conclude that the phage cocktails demonstrate superior efficacy, being promising candidates for further evaluation in artificial urine and bladder epithelial cell culture models.

The Refinement and Validation of a Field-Based eDNA Detection Method for Wild Pigs in Alberta

Brooke McCallum-Bont[1]; Charles Xu[1,2]; Oshin Ley Garcia[1]; Mathieu Pruvot[1,2]; Soroosh Torabi[3]

[1]University of Calgary, Faculty of Veterinary Medicine, [2]Wildlife Conservation Society, Health Program, Bronx, New York, USA, [3]University of Kentucky, USA.

Keywords: *Pigs, eDNA, LAMP*

The expansion of invasive wild pigs (Sus scrofa) across Alberta poses substantial ecological and agricultural challenges. Current monitoring and tracking systems rely on costly, labour-intensive methods with low detection probabilities. This study compared the loop-mediated isothermal amplification (LAMP) technique with PCR assays, with the objective of refining and validating a portable environmental DNA (eDNA) method for rapid field detection of wild pigs through a simple colorimetric reaction, eliminating the need for conventional DNA extraction and laboratory-based testing. Protocols for collecting environmental samples containing eDNA were developed and tested and different methods of eDNA extraction were trialed to establish which produced the strongest results. A LAMP-based concentration–extraction–identification device (CEID) will be validated using conventional PCR targeting a fragment of the mitochondrial D-loop region of Sus scrofa to confirm the presence of wild pigs in environmental samples. Protocols for the collection of environmental samples and subsequent DNA extraction methods were evaluated using Qubit and conventional PCR and confirmed using qPCR. A field protocol for water sample collection was evaluated and on-site testing will be evaluated using CEID. The colorimetric LAMP reactions were measured using Qubit fluorometry and positive samples confirmed in conventional PCR. The limit of detection (LOD) will be determined through serial dilutions and qPCR analysis. These findings will demonstrate that CEIDs enable rapid presence/absence detection of wild pigs within hours of sample collection and represent a portable, sensitive, and low-cost tool for improving surveillance and early detection of invasive wild pig populations, particularly in remote areas.

Evaluation of the safety, accuracy and helpfulness of common large language models in feline and canine veterinary emergency situations.

Bryan Kim, Mohammad Jokar, Diego Nobrega, Laura Osborne

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Keywords: *Artificial Intelligence, Veterinary Medicine, Veterinary Emergency*

Many pet-owners and veterinary clients depend on online sources to search information regarding their animals, especially when they begin to show symptoms of a disease and before visiting a veterinarian. Similarly, Artificial Intelligence (AI) or large language models (LLM) such as ChatGPT are being increasingly integrated into the way people search and ask questions, with conservative estimates of 8 billion AI searches per day. While previous studies in human medicine have discovered that LLMs can output unsafe information in the emergency situations, no research has been done in veterinary medicine from the client's perspective. This study aims to assess the safety, accuracy and overall helpfulness of five common large language models when provided scenarios of clients with feline or canine veterinary emergency situations. A question bank of 41 questions depicting common emergency scenarios of seven different clinical systems (Trauma, Cardiovascular, Respiratory, Gastrointestinal, Toxicology, Renal, Sepsis/Shock) and three time points (pre-emergency visit, Enroute/waiting for care, post-emergency) were created using simple, non-medical language to emulate public LLM usage. These were queried within a 24-hour window through ChatGPT, DeepSeek, Perplexity, Claude, and Google AI Overview (Gemini). Currently, the queried responses are under review by five emergency and critical care veterinary specialists to assess the safety and accuracy of the information provided. Preliminary results indicate that the Google AI overview which is the most frequently used AI tool, demonstrates some unsafe and conflicting advice while being the most difficult to read with the highest Flesch-Kincaid Grade level.

Assessing West Nile Virus Presence Across Calgary Microhabitats Using FTA Card-Based Surveillance

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[1]Faculty of Veterinary Medicine, University of Calgary

Keywords: *West Nile Virus, Surveillance, Mosquitoes*

Culex pipiens is an invasive mosquito species and a prominent vector for West Nile Virus (WNV) recently found in Alberta in 2018. It has spread to all major municipalities and is of increasing importance for animal and human health. Continued surveillance of Calgary mosquitoes through weekly trapping has provided samples to test for WNV through viral pathogen quantitative PCR as well as FTA cards, which is paper that can capture and preserve DNA/RNA effectively at room temperature. These FTA cards are soaked in honey and placed within gravid traps, which allows for any mosquitoes to feed on them while the trap is functional. This research focuses on the extraction from these cards to detect signs of WNV without testing mosquito samples. The results are expected to show positive results of WNV detection in cards corresponding with traps that caught positively identified Cx. pipiens samples because that would reinforce results of extraction from the mosquito. However, it is possible to have a negative result from a card within the same trap as a positively testing mosquito due to the nature of feeding being optional. Previous research has found positive FTA samples where no mosquito pools were positive as well, meaning FTA card testing might be more sensitive. The results should present us with a better understanding of where WNV is present across the six sites and three types of microhabitats, with next steps including further tracking and identification to determine changes of mosquito and virus patterns over time in Calgary.

Barking Up the Right Marker: Development of ITS1 Metabarcoding to screen for novel Canine Apicomplexans

Diana Abdolmaleki, Elizabeth Redman, Christian Savard, Christian Leutenegger, and John Gilleard

Faculty of Veterinary Medicine, University of Calgary; Antech Diagnostics

Keywords: *Apicomplexa; DNA metabarcoding; canine parasites*

Routine fecal examinations of North American dogs frequently reveal Eimeria-like oocysts, generally attributed to spurious passage of non-canine parasites acquired through coprophagy or scavenging rather than true infection. However, this interpretation remains molecularly unconfirmed, leaving open whether some oocysts represent unrecognized canine parasites. This study aims to develop a pan-apicomplexan fecal DNA metabarcoding assay that maximizes taxonomic coverage while limiting off-target amplification. An apicomplexan reference database was constructed using ITSx, a software that identifies and extracts internal transcribed spacer sequences, to locate internal transcribed spacer 1 (ITS1) between the conserved 18S and 5.8S ribosomal RNA genes. Candidate primers were evaluated computationally for coverage, amplicon length, and off-target amplification. Five primer pairs were tested on 11 canine fecal DNA samples identified as Eimeria-positive by genus-level quantitative polymerase chain reaction (qPCR). Amplicons underwent Illumina sequencing and classification against the custom database; unresolved sequences were assessed using BLASTn. All primer pairs recovered Apicomplexa from at least one sample, although target-read proportions varied substantially. Apicomplexa constituted up to 96.5% of reads in target-rich libraries, whereas others were dominated by fungi (up to 95.1%) or bacteria (up to 100%); unclassified reads reached 57.6%. Apicomplexan recovery was consistent at qPCR Ct values ≤24.28 but infrequent at values ≥24.52, indicating reduced sensitivity at lower parasite concentrations. These proof-of-concept results establish ITS1 as a promising target for broad apicomplexan detection. Next steps include screening primers against expanded non-target databases and refining polymerase chain reaction conditions to improve specificity and sensitivity before large-scale screening for novel canine apicomplexans.

New drugs against an old target: β-tubulin in parasitic nematodes

Elizabeth Rak, James Wasmuth

Faculty of Science, University of Calgary; Faculty of Veterinary Medicine, University of Calgary

Keywords: *Anti-nematode, drug discovery, parasites*

Parasitic nematodes (roundworms) cause significant burden to the global livestock industries. They reduce productivity through suppressing appetite, inducing anemia, and reducing fertility. In Canada, parasitic nematodes cost the cattle industry an estimated $2 billion annually despite the availability of current anti-nematode drugs. Furthermore, resistance has emerged in nematodes of livestock to all available drugs, and there is an urgent need to discover new nematode killing molecules.

To meet this need, the Wasmuth lab is using computational-assisted drug discovery approaches. Our approach is to use knowledge on how current drugs bind to proteins to identify novel molecules that target the same protein and overcome resistance mechanisms. This is termed ligand-based drug discovery. My starting point is the benzimidazole class of anti-nematode drugs. Benzimidazoles bind to the parasite's β-tubulin protein, disrupting microtubule polymerization essential for cell division, cytoskeletal structure, and nutrient uptake. This paralyses the nematodes, leading to their death.

Over the summer, I have been testing a ligand-based protocol designed to discover novel drugs against COVID-19. In brief: i) generate a virtual library of drug analogs; ii) dock these analogs against the target protein; iii) prioritize effective bindings based on predicted binding affinity and most desirable drug-like properties.

I am now adapting this protocol for use with benzimidazoles against nematode β-tubulin proteins. Nematode-killing effectiveness of top drug candidates will be validated using in vitro and in vivo assays.

BCoV Molecular Epidemiology in Western Canada: Enteric vs Respiratory Isolates

Elliott Brien, Aayush Poudel, Frank van der Meer

Faculty of Veterinary Medicine, University of Calgary

Keywords: *Coronavirus, Sampling, Sequencing*

Introduction:
Bovine Coronavirus (BCoV) causes respiratory and enteric disease in beef and dairy cattle, causing significant morbidity, mortality, and economic losses. The genetic, antigenic, environmental, or host factors contributing to distinct disease presentations remains unknown and further genetic characterization could contribute to a better understanding of BCoV pathogenesis. This study aims to genetically compare BCoV isolates from nasal and fecal swabs of calves suffering from neonatal calf diarrhea or respiratory tract diseases across Western Canada.

Methods:
BCoV-positive field samples will be used to isolate and propagate the virus using HRT-18 cells. 3-4 days post-inoculation, RNA will be extracted. RNA will be used for qRT-PCR using diagnostic primers targeting conserved regions in the spike (S) gene controlling for virus replication. Confirmed sample RNA will undergo reverse transcription, PCR amplification, and sequencing via Oxford Nanopore or Sanger platforms. Overlapping primers will amplify the entirety of the variable S gene, while single primer pairs will target the conserved N, M, and RdRp regions.

Expected findings:
Currently we have higher propagation success for nasal swabs (3/3) than fecal samples (2/6); processing of remaining field samples (5 fecal, 108 nasal) is ongoing. We hypothesize significant genetic diversity exists between respiratory and enteric Western Canadian field strains. Sequencing could reveal if distinct genetic variants are inducing different clinical presentations.

Discussion:
Differences in isolation success rates between nasal and fecal samples requires further optimization of our protocols. Isolation and sequencing will enable phylogenetic analysis of circulating strains in Western Canada, advancing our understanding of BCoV-induced disease pathogenesis.

Investigating A Reliable Oral Dosage For Complete Attack Rate In Prion Challenged Wild-type Mice

Ember, Chimoné, Ginny, Hermann

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Keywords: *Prion, Scrapie, Dosage*

Prions are proteinaceous infectious agents, distinct from typical viral and bacterial pathogens, that cause a variety of invariably fatal neurodegenerative diseases such as Chronic Wasting Disease in cervids, Creutzfeldt-Jakob Disease in humans, and Scrapie in sheep. Although oral uptake is typically the leading route for natural prion infections, experimental infection in mouse models is typically performed intracerebrally or intraperitoneally. Currently, an accurate infectious dose has not been elucidated for 100% clinical attack rate of wild-type mice when infecting them orally. Thus, we inoculated C57BL/6 mice via gavage with 100 uL of either high (N=8) or low (N=10) amounts of brain homogenate from terminally ill mice infected with mouse-adapted scrapie prions (20% or 5% w/v in phosphate buffered saline, respectively). Feces were collected to analyze prion shedding, and mice were euthanized upon reaching either clinical endpoints, or defined preclinical time points; with brain, spinal cord, and spleen tissues analyzed via immunoblots and real-time quaking-induced conversion assays to track disease progression within the mice. It is hypothesized that the group receiving a higher dose of infectious prions will have a 100% attack rate and develop clinical endpoints faster, though it remains to be seen how disease kinetics may shift with resultant survival time and initial inoculum load. Accurate assessment of sub-clinical and terminal mice could serve as an important step in characterizing an ideal single-case dosing model for future prion studies in wildtype mice.

Efficacy of lytic phages against Enterotoxigenic Escherichia coli F4-22774 in vitro

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Keywords: *ETEC, Bacteriophage, Antibiotic Resistance*

Background: Enterotoxigenic Escherichia coli (ETEC) causes post-weaning diarrhea in piglets, resulting in high morbidity and reduced weight gain that threatens Canada's billion-dollar pork industry. Increasing antimicrobial resistance necessitates the need for alternative treatments like bacteriophage (phage) therapy - viruses that lyse specific bacteria. Three phages - belonging to Autographiviridae (10B), Demerecivirdae (10F), and Caudoviricetes (10P) were previously isolated from Calgary sewage water. This study aimed to compare anti-ETEC efficacy of different phage combinations (single, double, and triple). **Methods:** Infection kinetics were assessed in a 5ml broth system using bacterial inocula of 103 and 105 CFU/ml at multiplicities of infection (MOI) of 1000 and 100. Optical density at 600nm was measured at 0, 4, 7, and 24h, followed by ETEC bacterial enumeration at 24h. Phage impact on bacterial growth was analyzed via a two-way ANOVA using GraphPad Prism (v11.0.2.). **Results:** At 105 CFU/ml, all phage treatments at both MOIs completely suppressed growth up to 7 hours ($p<0.0001$). At 10h, only 10B+10F (MOI 1000) and 10P+10F (MOI 100) reduced bacterial growth ($p<0.0001$). At 24h, only 10B+10P and 10P+10F (MOI 100) showed suppression ($p<0.05$). At 103 CFU/ml, all phage treatments completely suppressed bacterial bacterial growth until 10h ($p<0.0001$), although bacterial growth was minimal across all the experimental groups during the first 4h. **Conclusion:** Two phage combinations appeared to be most effective against ETEC. Further studies should assess phage resistance and potential antagonistic interactions among three-phage combinations.

Improving the monitoring and analyses of caribou in northern communities

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Keywords: *Filarioid nematodes, Caribou, Vector-Borne Diseases, Metabarcording, Climate Change*

Caribou (Rangifer tarandus sspp.) are fundamental for the food security and culture of Indigenous communities and are critical to ecosystem health. With climate change, caribou are being exposed to new and/or increasing amounts of vector-borne parasites, such as filarioid Setaria and Onchocerca species, that may affect their health and consequently ecosystems and the well-being of Indigenous communities. Whole blood has previously been used to detect filarioids but is not always available for testing. To better understand filarioid infection dynamics in caribou and set up better monitoring strategies, we determined the sensitivity of different caribou tissue samples for detecting infected individuals. To evaluate this, we tested all available sample types for each individual, including spleen, blood eluted from filter paper, skin, and joint fascia. We extracted DNA from 360 samples that were collected from different herds and seasons using the automated KingFisher Apex instrument. To detect parasite DNA, we implemented a panfilarioid metabarcoding approach: after PCR amplification targeting the ITS2 region, amplicons were sequenced on the GridION Nanopore device, and parasite presence was evaluated using a bioinformatic pipeline. These results were used to statistically assess the sensitivity of tissue types. With the samples still left to analyze, we anticipate that spleen and skin will be the most sensitive for the mosquito season. The results from this study will improve parasite monitoring, provide relevant insights on pathogen prevalence and distribution and in turn, improve health monitoring programs of caribou in northern communities, aid in conservation efforts, and improve food security in communities.

Evaluation of Glycyrrhiza Polysaccharides as a Candidate ProphylacticTreatment Against Infectious Laryngotracheitis Virus Infection in Chickens

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Keywords: *Infectious laryngotracheitis, antiviral response, chicken*

Infectious laryngotracheitis virus (ILTV) is an important respiratory pathogen of chickens that causes respiratory disease, reduced productivity, and mortality. Although vaccination against ILTV is practiced, outbreaks still occur. Glycyrrhiza polysaccharides (GPS), natural compounds extracted from licorice, have immunomodulatory properties and may help reduce viral infections. This study evaluated whether GPS could reduce clinical disease, viral shedding, and tissue viral load following ILTV infection.

Day old specific pathogen free chickens were divided into four groups: ILTV-challenged, GPS-treated, GPS treated +ILTV-challenged, and an untreated and uninfected control. All birds were pre-treated (6 hours before infection) with the GPS or PBS through intratracheal route. Challenged groups were infected with 1□105 embryo infectious dose (EID)50 of ILTV via the ocular nasal route. Clinical signs were monitored and scored daily. Five birds from each group were euthanized at 2, 4, and 7 days post-infection and tissues and swab were collected to assess viral shedding. Deoxyribonucleic acid (DNA) was extracted from swabs and tissues and ILTV genome loads were quantified with ILTV-specific quantitative polymerase chain reaction (qPCR).

The ILTV-challenged group developed clinical signs after infection. Clinical signs became significantly high at day 4 and continued through day 6 post infection before decreasing. In contrast, no clinical signs were observed in the GPS + ILTV-challenged group throughout the study, suggesting that GPS reduced disease severity. Ongoing qPCR analysis will determine whether GPS also reduces viral shedding, and ILTV genome loads in swabs and tissues. These findings will help evaluate the potential of GPS as a supportive antiviral treatment for improving the control of ILTV infection in chickens.

Engineering peptide aptamers to improve their anti-prion activity

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Keywords: *Prion disease, peptide aptamer, aptamer engineering*

Prion diseases are fatal neurodegenerative conditions caused by the conversion of cellular prion protein (PrPC) into the infectious isoform (PrPSc). Peptide aptamer 8 (PA8), a 16-amino-acid peptide displayed on the Escherichia coli thioredoxin A (TrxA) scaffold, blocks this conversion by directly binding PrPC. However, the bacterial scaffold limits therapeutic application, the contribution of individual residues remains unclear, and previous studies suggest there is scope for further improvement. We hypothesized that presenting PA8 on alternative scaffolds and substituting individual residues with alanine would reveal how these modifications affect its anti-prion activity.

PA8 presented on alternative protein scaffolds (mouse, human and Pyrococcus furiosus (Pf) TrxA, as well as human Stefin A-derived SQT scaffold) and alanine-substituted variants generated by site-directed mutagenesis were expressed in E. coli and purified by His-tag affinity chromatography. Persistently prion-infected mouse neuroblastoma cells were treated with engineered aptamers for five consecutive days and PrPSc levels were assessed by Western Blot.

Alternative scaffolds differentially affected PA8 activity. PA8 in PfTrxA showed enhanced anti-prion activity while human and SQT scaffolds maintained comparable or improved activity; in contrast, the mouse TrxA scaffold failed to support activity. These findings highlight the importance of scaffold context in determining aptamer function. Further, alanine scanning revealed residue-specific contributions to PA8 activity, with R2A reducing anti-prion activity while E4A, G9A, and V12A enhanced it.

Overall, we identified key PA8 determinants that can guide future aptamer optimization. Future studies will combine optimized alanine variants with PfTrxA scaffolds to further enhance PA8 activity and advance its therapeutic potential.

Feral Horse Parasite Abundance in Relation to Their Plant Communities

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Keywords: *Feral horses, Plant community composition, Gastrointestinal parasites*

Feral horses rely on available vegetation as their primary food source, making plant communities a potential driver of gastrointestinal parasite abundance through effects on grazing behaviour and diet composition. However, the relationship between plant community composition and parasite abundance in feral horses remains unclear. Understanding these interactions may inform management by identifying ecological drivers of parasite abundance. This study investigated whether plant community variation is associated with gastrointestinal parasite abundance in Alberta feral horses. A comparative observational study was conducted in the Sundre and Elbow River Equine Management Zones (EMZs). During the growing season (May–June 2026), McMaster fecal egg counts were performed on 18 fecal samples (nine per EMZ) to estimate parasite abundance. Vegetation surveys used nested transects and quadrats to characterize plant composition and percent cover, with sampling completeness assessed using species accumulation curves. Parasite abundance between EMZs was compared using a two-sample t-test. Preliminary analyses found no significant difference in parasite abundance between EMZs ($t(16) = 0.354$, $p = 0.728$). Vegetation surveys captured >80% of estimated species richness within each EMZ based on Chao estimates. Bray-Curtis dissimilarity plots indicated distinct plant community composition between EMZs. These findings suggest plant community variation may not correspond with parasite abundance during the growing season. A second sampling period in late summer (August–September) will determine whether seasonal changes reveal new relationships not initially detected. This research will contribute to understanding ecological factors influencing parasite abundance in feral horses and may provide insights into parasite management strategies in domestic grazing horses.

Documenting variation within the diplocaulid nectridean Diceratosaurus brevirostris from Linton and Five Points, Ohio

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Keywords: *lepospondyl, diplocaulid, Carboniferous*

Diceratosaurus brevirostris is a small newt-like aquatic tetrapod that lived 323-298 million years ago, discovered in natural molds from the coal mines of Linton and Five Points, Ohio. It has been classified within Lepospondyli, a paraphyletic assemblage of stem tetrapods and amniotes. We studied a new sample of specimens from the Carnegie Museum of Natural History, to evaluate variation within that population. Twelve complete and partial skulls, preserved as part and counterpart, were cast with silicone to create 24 peels in dorsal and palatal views. Using macro lens photography (Nikon D200 camera), anatomical drawings (Adobe Photoshop and Adobe Illustrator), and measurements (Image J), skulls will be analysed and compared with other prehistoric amphibians. Two distinct morphologies are observable: a 'narrow' snouted morph and a 'broad' snouted morph. The two morphs significantly differ in mean basal skull length (T-test, df= 8.264, p=0.004776). Both morphologies are highly modified, with the marginal dentition suggesting specialized feeding systems. The narrow morph is characterized by reduced tooth-bearing elements, long and slender vomers, and elongate nasals and frontals. Analysis is ongoing and skull reconstructions are under preparation. The holotype of *D. brevirostris* is based on the broad morph; the narrow morph represents a new species. A second species of diplocaulid nectridean at Five Points is consistent with modern ponds, which contain several different species of amphibians, and adds to our understanding of the ecology during the Late Carboniferous of Laurasia.

The Gut Remembers the Route: Divergent Dysfunction Despite Comparable Prion Seeding in Chronic Wasting Disease

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Keywords: *Chronic Wasting Disease, Gastrointestinal Dysfunction, RT-QuIC*

Prion diseases are fatal neurodegenerative disorders primarily affecting the central nervous system (CNS). Chronic wasting disease (CWD), however, is distinguished by peripheral replication, environmental shedding, and oral transmission. Previous work in knock-in mice expressing cervid prion protein, challenged with reindeer-CWD, revealed a route-dependent paradox: peripheral-originating CWD, modelled by oral inoculation, accelerated gastrointestinal transit and disrupted barrier function, whereas CNS-originating CWD, modelled by intracerebral inoculation, delayed transit and remodelled the distal gut. We asked whether these opposing phenotypes reflect differences in gastrointestinal prion burden.

Real-time quaking-induced conversion (RT-QuIC) amplifies minute quantities of prion seeds in tissues, enabling highly sensitive comparison of seeding burden. Using endpoint-dilution RT-QuIC data from archived stomach, cecum, colon, and spleen samples, we calculated the 50% seeding dose (SD50), an estimate of the relative abundance of seeding-competent prions. Gastrointestinal sections were also stained with hematoxylin and eosin to assess tissue architecture.

Robust prion seeding was detected throughout the gastrointestinal tract after both inoculation routes. Within each route, SD50 values were comparable among the stomach, cecum, and colon. Interestingly, SD50 values for each gastrointestinal tissue were also comparable between peripheral-originating and CNS-originating CWD. Across both routes, gastrointestinal tissues displayed higher seeding activity than the spleen.

Thus, opposing gastrointestinal phenotypes arise despite comparable local seeding burdens, indicating that prion load alone does not explain route-dependent dysfunction. Ongoing histological analysis will determine whether differences in intestinal architecture provide the missing link between disease origin and gastrointestinal response, positioning the gut as a biologically active and selectively engaged component of CWD pathogenesis.

Comparative Evaluation of the Discriminatory Power of Fourier-Transform Infrared Spectroscopy (IR Biotyper®) and Genotypic Methods in Classifying Staphylococcus aureus in Patients with Cystic Fibrosis

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Keywords: *Cystic fibrosis, Staphylococcus aureus, IR Biotyper*

Staphylococcus aureus is the most prevalent pathogen in cystic fibrosis patients with an increase of 20% in the last 30 years. Effective control strategies can be developed if the specific strains associated with infection are known. The IR Biotyper® (IRBT®) is a phenotypic microbial subtyping tool that uses Fourier Transform Infrared spectroscopy, providing a rapid and affordable method to track nosocomial outbreaks of S. aureus. We aim to optimize a standard operating procedure, validate the IRBT® through comparison with multi-locus sequence typing (MLST) and whole genome sequencing (WGS), and to evaluate its discriminatory power. We hypothesize that the IRBT® will be able to accurately cluster technical replicates and will have greater discriminatory power than MLST. We used 18 sputum isolates (15 patients) with a total of 6 sequence types determined using MLST. These were passaged twice onto blood agar and once onto tryptic soy agar (37°C-24 hours). Then for each isolate a suspension was created by adding distilled water followed by 70% ethanol. The isolates were spotted onto the IRBT® silica plate (4 replicates-2 biological repeats). A merged automatic cutoff of 0.151 was applied. 66.7% of isolates were stable across biological repeats, while six isolates were split, showing biological variability, which is a significant limitation of this technology. Each independent biological run demonstrated excellent clustering of its own four technical replicate spectra. Adjusted Wallace coefficients: 0.268 and 0.524 (stable only), show low agreement between MLST and IRBT®. Next steps include comparing the IRBT® to single nucleotide polymorphisms and core/accessory genomes.

Mapping the Role of Revascularization and Reinnervation in Regenerative Versus Fibrotic Wound Healing

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Keywords: *Skin tissue clearing, regenerative wound healing, innervation*

Introduction: After deep skin injury, mammals typically form scar that is stiff, painful, and prone to re-injury. The Biernaskie Lab is using a mouse model of large full-thickness skin wounds that partially regenerate (forming less scar and some new hair follicles/glands) to test potentially regenerative molecules. Restoring blood supply/innervation is critical in healing, but whether revascularization/reinnervation is required to initiate regeneration is unknown. Here, we used tissue clearing to determine how different spatial/temporal patterns of revascularization/reinnervation coincide with different healing outcomes.

Methods: Skin from mice under control or regenerative treatments (FD001, 02) was collected three months post-injury (n=20). Following our optimized Skin-iDISCO+[1] protocol, tissues were decolorized, cleared, and reconstructed using immunofluorescence staining for αSMA (vasculature) and PGP9.5 (innervation) with light sheet microscopy. We quantified blood vessel/cutaneous nerve total length and density using Ilastik machine learning with IMARIS' filament tracer.

Results: Preliminary data suggests wound site innervation is increased with FD001 and FD001+FD002 compared to control and FD002 alone. We hypothesize vascularization will increase under regenerative treatments. 3D reconstructions will be presented to illustrate differences.

Discussion: Preliminary data suggests our regenerative treatments increase revascularization/reinnervation post-injury, potentially promoting functional skin regeneration. Revascularization supports oxygen/nutrient supply, while reinnervation modulates immune-inflammatory responses and restores sensation. This mirrors literature describing transiently increased post-injury vascularization/innervation in mice treated with regenerative agents IL10/TGFβ. To further understand revascularization/reinnervation's temporal role, we are currently processing samples from 15 (n=7) and 35 (n=6) days post-injury. Understanding regenerative competence could lead to treatments improving wound healing outcomes for humans and animals.

Identification of the Sexually Active Group in Beef Heifers Using Automated Monitoring Devices

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Keywords: *Sexually Active Group (SAG), Heifers, Automated Monitoring Device (AMD)*

The Sexually Active Group (SAG; i.e., a cohesive group of active animals engaging in vulva sniffing, chin rubbing, and mounting behaviors) was previously described as a behavioral proxy to identify cycling cattle. However, identifying the SAG through visual observation is impractical in cow-calf operations. This study aimed to assess whether behaviors measured by an automated monitoring device (AMD) could be used to identify beef heifers in the SAG. Eighty Angus heifers of the University of Calgary's W.A. Ranches, aged 13.8±0.4 months (mean ±SD) and weighing 371.72±28.98 kg, were fitted with AMD ear-tags. The tags transmitted data via satellite and provided a daily time budget for grazing (GR), walking (WA), and resting and ruminating (RR), as well as distance travelled per day, and average velocity. Visual observations were conducted twice daily for six days to identify heifers composing the SAG and expressing estrus behaviors. Heifers that did not present these behaviors were classified as Non-SAG. A total of 25 heifers were observed engaging in the SAG in six days. Preliminary results suggest that SAG heifers spent 576±106 minutes GR, 125±60 WA, 630±97.4 RR, and travelled 2200±868 m at 0.0331±0.0243 m/s. Non-SAG heifers spent 590±94.3 GR, 85±42.1 WA, 669±93.8 RR, and travelled 1966±1341 m at 0.0299±0.0250 m/s. Analyses comparing the behaviors of the SAG and Non-SAG heifers will be presented at the SURE symposium. This study will provide evidence on the potential of an AMD to identify animals in the SAG to remotely monitor herd cyclicity.

RNA Virus Surveillance in Wild American Martens Across Canada

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Keywords: *RNA Virus, Martens, Molecular Surveillance*

Many emerging infectious diseases originate in wildlife, and RNA viruses account for a disproportionate number of zoonotic spillover events. Their high mutation rates enable rapid adaptation to new hosts, increasing the likelihood of cross-species transmission. Recent coronavirus outbreaks highlighted mustelids, including mink, as potential bridge hosts that facilitate viral adaptation between wildlife and humans. However, the diversity of RNA viruses circulating in wild Canadian mustelids remains poorly characterized. We hypothesized that intestinal samples from American martens (Martes americana) harbour RNA viruses from one or more targeted viral families, revealing previously underrecognized viral diversity in this wildlife species.

To test this hypothesis, intestinal samples collected from American martens across Canada between 2016–2017 were screened for RNA viruses. RNA was extracted from each sample, assessed for quality, converted to complementary DNA (cDNA), and analyzed by RT-PCR using pan-family primers targeting conserved regions of the coronavirus, rotavirus, astrovirus, and calicivirus genomes. Putative positive amplicons will be confirmed by Sanger sequencing to determine viral identity.

Screening of the marten samples will generate a molecular survey of RNA viruses from the targeted viral families, enabling the identification and characterization of viruses circulating in wild Canadian martens. The findings will provide baseline information on the diversity of RNA viruses in this understudied wildlife species and improve our understanding of viruses with zoonotic potential. This work will strengthen wildlife virus surveillance in Canada and provide foundational data for future studies investigating the ecology, evolution, and spillover risk of RNA viruses in mustelids.

Canine Nausea: A Scoping Review

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Keywords: *dog, nausea, perioperative*

Introduction
Nausea is difficult to assess, especially in non-human animals. Although vomiting is the focus of published research, nausea itself may be more distressing. Nausea assessment is uncommon in veterinary practice, risking under-diagnosis and inadequate treatment. This scoping review maps evidence relating to canine nausea, focusing on the perioperative period, to identify knowledge gaps.

Methods
A modified Joanna Briggs Institute scoping review methodology was used. MEDLINE, CAB Abstracts, and Scopus were searched to identify peer-reviewed articles investigating the mechanisms, assessment, prevention or treatment of canine nausea. Titles, abstracts, and full texts were screened independently by two reviewers. Data were extracted using a predefined tool.

Results
A total of 12,477 records were identified. Following deduplication and screening, 337 full-text articles were assessed for eligibility. Agreement between reviewers during full-text screening was substantial (Cohen's $\kappa = 0.70$). Data extraction is underway for the 129 included studies. Preliminary findings suggest canine nausea involves multiple neurotransmitter pathways (serotonin, dopamine, histamine, and substance P), with postoperative and opioid-associated nausea representing a major focus of the literature. Assessment methods are highly heterogeneous and frequently rely on behavioural proxies, such as retching and hypersalivation, or use vomiting as a surrogate outcome rather than assessing nausea directly.

Discussion
This review maps the current evidence relating to canine nausea, identifies evidence gaps, including the lack of standardized nausea assessment methods and the reliance on vomiting as an indirect measure of nausea, and guides future research aimed at improving nausea assessment and management, particularly during the perioperative period.

Testing a Gondwanan origin for Aedini, the most species-rich mosquito tribe

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Keywords: *Biogeography, ancestral range reconstruction, Aedini*

Aedini is the most species-rich mosquito tribe, spans all six biogeographic realms, and contains the principal vectors of human arboviruses, yet its geographic origin remains unknown. Crown Aedini dates to approximately 91 Ma, when Gondwana was fragmenting and separating South America from Australia. A Gondwanan origin predicts an austral ancestral range and old trans-Gondwanan connections via Antarctica and the South Atlantic.

We analyzed 100 dated trees generated in TACT, adding unsampled species only within tribes having molecular data, and each pruned to 1244 Aedini tips. Ancestral ranges were reconstructed in BioGeoBEARS under DEC ±J, in unstratified and time-stratified analyses under a six-stratum scheme (3, 20, 34, 50, 66, 120 Ma). Pre-specified strata weigh dispersal by the presence or absence of intercontinental connections, notably an Afro-Neotropical corridor before 66 Ma and an austral South America–Antarctica–Australia route before 34 Ma. Twenty stochastic maps and visualization used the maximum clade credibility tree.

DEC+J was preferred on every tree, by a wide margin over DEC (ΔAICc 32–105). Of 1243 cladogenetic events, 695 were sympatric, 280 subset, 174 vicariant, and 93 founder-event, while anagenetic range expansions numbered 794 and range extinction was estimated at zero. Crown Aedini was reconstructed as austral, with the Neotropics present at 0.97 and 72% probability on Gondwanan-only ranges (Neotropical, Afrotropical, Australasian), though probability was diffuse across many range combinations. This austral reconstruction supports a Gondwanan origin, though dispersal outweighed vicariance, suggesting Aedini spread across a fragmenting Gondwana rather than being divided by it.

Identifying Priority Learning Outcomes for Clinical Educators in Distributed Veterinary Clinical Education: A Modified Delphi Study

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Keywords: *Veterinary, Education, Delphi*

Clinical educators play a critical role in distributed veterinary clinical education but often receive limited training on teaching. Although faculty development programs exist, there is little evidence identifying which learning outcomes should be prioritized. This study aims to identify and prioritize outcomes for clinical educators within distributed veterinary clinical education using a modified Delphi consensus process. Experts in distributed veterinary clinical education rate learning outcomes in two questionnaire rounds, with round two informed by round one's responses. The learning outcomes were developed from Consortium on Workplace-Based Education and Learning (COWBEL) member schools training for their clinical educators and refined by the research team. Participants rate each outcome using a five-point Likert scale and provide qualitative feedback. Round one will be used to refine the questionnaire before redistribution in round two to establish consensus. At the time of submission, round one data collection was ongoing with six participants completing the survey. Preliminary findings indicated that two learning outcomes met the predefined consensus threshold of greater than 80% agreement. All six participants rated two outcomes 'very important' (100%): Incorporating students into clinical practice while supporting learning, workflow, and patient care; and providing timely, specific, and actionable feedback to support student improvement. The analysis also considered whether consensus was reached that any learning outcomes were not important. These preliminary findings indicate early training priorities identified by experts. Completion of the modified Delphi process will inform evidence-based training resources to better prepare clinical educators and support workplace-based veterinary education.

Assessing Cytoskeletal Organization in Testicular Organoids

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Keywords: *Testicular Organoids, Cytoskeletal Organization, Spermatogenesis*

Three-dimensional testicular organoids (TOs) have emerged as promising in vitro models for studying spermatogenesis because they more closely replicate the cellular organization and microenvironment of the testis than conventional two-dimensional culture systems. However, robust methods are needed to evaluate the structural organization of testicular organoids in response to experimental perturbations. This study aimed to optimize methods to assess the cytoskeletal architecture of porcine testicular organoids. TOs were cultured in Organoid Formation Media (OFM) for 6-12 days prior to fixation and stained using Phalloidin to visualize filamentous actin (F-actin). Confocal microscopy was utilized to visualize cytoskeleton organization. Images were analyzed to evaluate cytoskeletal organization, tissue morphology, and overall structural organization within the three-dimensional constructs. Phalloidin staining successfully labeled F-actin throughout the organoids, revealing cytoskeletal organization within the three-dimensional tissue. Confocal microscopy showed structural features and cellular organization across intact organoids, allowing qualitative assessment of tissue morphology. Reliable assessment of porcine testicular organoid structure is an important step toward determining how closely these models resemble the biological testicular microenvironment. The methods established in this study provide a foundation for future investigations examining cellular interactions during testicular development. Continued refinement of structural characterization techniques will enable further analysis of cytoskeletal responses to experimental perturbations in testicular organoids, improving their application in reproductive biology research.

Comparison of Stride Parameters Between Racing Quarter Horses and Thoroughbreds Using Wearable Sensor Technology

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Keywords: *Equine biomechanics, Wearable sensors, Injury Prediction*

Introduction: Catastrophic musculoskeletal injuries remain a welfare concern in horseracing. Continuous monitoring of stride parameters using wearable sensors has shown promise in identifying horses at increased risk of injury in Thoroughbred racing. However, Quarter Horses differ substantially from Thoroughbreds in conformation, race distance, acceleration, and racing strategy. This raises the question of whether existing Thoroughbred injury models can be generalized to Quarter Horses. We aim to characterize stride parameters in racing Quarter Horses and compare them with Thoroughbreds to determine whether Quarter Horses represent a continuation of Thoroughbred stride dynamics or a distinct biomechanical profile.

Methods: Global Navigation Satellite System (GNSS) recordings were collected during routine Quarter Horse races at Century Racetracks in Alberta using wearable sensors to obtain continuous measurements of horse speed and position. Stride length, stride frequency, and acceleration were derived from this data. Stride characteristics and acceleration were analyzed across race phases and race distances using linear mixed-effects models. Quarter Horse stride characteristics were then compared with previously collected Thoroughbred data obtained using identical wearable sensor methodology.

Results: Data analysis is currently in progress. Stride parameters will be analyzed to compare locomotion mechanics between Quarter Horses and Thoroughbreds and to examine the effects of race stage, race distance, and acceleration on their strides.

Conclusion: This work will establish the first quantitative database of in-race Quarter Horse stride parameters using wearable sensors. Comparing these data with Thoroughbred stride characteristics will help determine whether discipline-specific biomechanical models are required to improve prospective injury prediction.

Development and Validation of a High Throughput UV Plate-Reader Workflow for Rapid Microbial Contamination Detection in Mammalian Cell Culture

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Keywords: *Cell culture contamination; Plate reader; Nicotinamide; Escherichia coli; Microbial detection; High-throughput screening*

Mammalian cell cultures are biomedical research tools but are vulnerable to microbial contamination, which can spread, alter cell behaviour, and invalidate experiments before changes. Current checks by microscopy, turbidity, or media colour are intermittent and subjective. Recent cell-therapy work showed that contamination can change culture-media UV patterns because most bacteria carry nicotinamidase, which converts nicotinamide into nicotinic acid, whereas mammalian cells lack this enzyme. However, that workflow used cuvettes, measuring samples one at a time. We adapted this concept into a 96-well plate-reader workflow and hypothesized that UV/visible absorbance would provide an earlier contamination signal than colour change or cloudiness.

After screening plate formats, UV-transparent 96-well plates were selected for low background UV absorbance. Nutrient medium (DMEM), alone or with fibroblast cells, was added to wells at 150 µL/well. Wells were assigned to sterile control or E. coli contamination from 10^1–10^6 CFU/mL (n=5/condition), with outer wells excluded or water-filled to reduce evaporation and edge effects. Plates were read on a SpectraMax i3x at 0 h, incubated at 37°C, then every 30 min from 12-24 h. Readings at 255-276 nm tracked the UV fingerprint, 560 nm tracked colour change, and 660 nm tracked cloudiness.

Preliminary results showed that UV-transparent plates reduced background noise, and contaminated samples showed the expected UV fingerprint before stronger colour or cloudiness changes, especially at higher E. coli concentrations. Together, these findings support a scalable plate-reader workflow for contamination screening, with analysis focused on confirming low-level detection and expanding testing across media types and microbes.

Effects of Host Genotype and Tissue-Specific Microenvironment on Chronic Wasting Disease Strain Evolution

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Keywords: *Prion, Chronic Wasting Disease, Strains*

Prion diseases, including Creutzfeldt-Jakob disease (CJD) in humans and Chronic Wasting Disease (CWD) in cervids, are fatal neurodegenerative diseases caused by the misfolding and aggregation of the cellular prion protein (PrP^{C}) into its infectious isoform (PrP^{Sc}). Different conformations of PrP^{Sc} give rise to prion strains with unique biochemical characteristics. The evolution of strains is thought to be driven by selective pressures, such as the tissue microenvironment and host genotype. PRNP genotype can vary due to single nucleotide polymorphisms (SNPs), including the S138N SNP in caribou. We hypothesize that tissue-specific microenvironment (spleen versus brain) and host PRNP genotype (138SS versus 138SN) will result in strain evolution, detectable through changes in the prion's biochemical properties. To test this hypothesis, gene-targeted mice expressing the 138SS genotype were inoculated with infectious brain or spleen homogenates derived from 138SN or 138SS reindeer. Brain homogenate from each group was assessed for Proteinase K (PK) resistance and/or for seeding activity using real-time quaking-induced conversion (RT-QuIC). Preliminary results from PK differentials suggest a trend towards greater PK resistance in prions originating from the 138SS reindeer compared with those from 138SN. Results from RT-QuIC analyses are currently ongoing. As no cure for CWD exists, a thorough understanding of strain evolution is crucial for developing effective mitigation strategies and assessing the risk of proposed solutions such as selective breeding and vaccination. This research will provide valuable insight into how host genotype and tissue-specific microenvironment influence CWD strain evolution.

Chronic Wasting Disease Vaccines: Comparing Vaccine Delivery Platforms

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Keywords: *chronic wasting disease, vaccination, mRNA lipid nanoparticles*

Chronic wasting disease (CWD) is a highly contagious fatal neurodegenerative disease in deer and related species (cervids) with no approved treatments. Experimental vaccination with PLGA nanoparticles (PLGA-NP) transporting our recombinant immunogen has induced immune responses that reduce transmission and prolong survival, but boosting is required. Messenger RNA lipid nanoparticle (mRNA-LNP) vaccines are known to sustain often stronger responses through in vivo expression of protein. We hypothesize that an mRNA-LNP vaccine of our immunogen will provide a more sustained protective immune response compared to the PLGA-NP vaccine. Vaccines will be intramuscularly injected into 50 transgenic mice expressing elk prion protein, with 15 receiving the mRNA-LNP vaccine, 15 receiving a negative control mRNA-LNP, 15 receiving the PLGA-NP vaccine, and 5 unvaccinated. After prime-boost immunization, mice will be intraperitoneally infected with CWD prions. Disease progression will be assessed through clinical signs. Immune response will be evaluated through serum antibody titer using ELISA and antibody neutralizing activity in cell culture. Infectivity will be measured by immunoblot and prion amplification assays, and neuropathology will be measured by immunohistochemistry. We expect that the mRNA-LNP vaccine will result in increased antibody titers and neutralizing activity, and decreased clinical signs, infectivity and neuropathology. Slower disease onset and prolonged survival is expected in vaccinated mice. These results will illuminate how vaccine formulations affect efficacy against CWD for wild and farmed cervids. Creating a vaccine with a long-lived and effective immune response is crucial for long-term protection in cervid populations where frequent vaccination is problematic.

Effect of Infectious Bronchitis Virus Challenge on Vaccinated and Unvaccinated Broiler Chickens

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Keywords: *Infectious Bronchitis Virus, Broiler Chicken, Vaccine Response, Maternal Antibody, Immune Response.*

Infectious bronchitis (IB), caused by infectious bronchitis virus (IBV) is a viral disease of poultry causing respiratory illness, reduced weight gain, and economic losses. Vaccination is the primary control strategy, but maternal antibodies can interfere with the vaccine induced immune response.

One hundred and twenty broiler chickens were assigned to vaccinated-challenged (VC), non-vaccinated challenged (NVC), and vaccinated non-challenged (VNC) groups. At day 1, birds received 110 µL of the recommended dose of a live attenuated IBV vaccine containing Massachusetts and Connecticut serotypes by the ocular–nasal route. Birds were challenged ocular–nasally with 10^5 EID_{50} of DMV/1639 at 2 or 4 weeks. At 3 and 7 days post-infection (dpi), lung, trachea, and kidney were collected for nucleocapsid-gene qPCR. Additionally, 0.5 mL blood was collected via brachial vein, and then serum was collected to measure anti-IBV antibodies by a commercial ELISA kit. Birds were scored daily for general and respiratory signs on a 0–3 scale; a combined score of 5 was the humane endpoint.

Following the 2-week challenge, vaccinated-challenged birds had lower viral loads in the lungs and kidneys at 3 and 7 dpi, whereas after the 4-week challenge, a significant reduction was observed only in the lungs at 7 dpi. Control antibody titers declined below the ELISA cut-off by 3 weeks. Following the 4-week challenge, VC birds had significantly higher titers than NVC birds at 3 and 7 dpi. NVC birds had significantly higher clinical scores after both challenges, while VC birds showed minimal to no clinical signs.

Assessing Anxiety-Like Behaviour Through Environmental Novelty and Innate Stress Using a Group-Housed Novelty-Induced Hypophagia Paradigm

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Keywords: *Novelty-induced Hypophagia, Anxiety, Refinement*

The novelty-induced hypophagia (NIH) assay assesses anxiety-like behaviour in rodents by measuring approach-avoidance conflict toward a familiar, palatable food under novel or anxiogenic stimuli. Increased latency to consumption indicates increased anxiety-like behaviour. However, obtaining individual measurements often requires chronic individual housing, introducing a social isolation confound. To solve this, we developed a modified NIH paradigm that maintains group-housing while enabling individual assessment across home, novel, and predatory contexts.

Adult male and female C57Bl/6J mice were trained to consume diluted sweetened condensed milk while group-housed. During testing, mice were transferred together into a holding cage, and mice were randomly selected for sequential testing. Following each trial, mice were placed into a post-test cage before returning to their home cage. Anxiety-like behaviour was evaluated under home cage, novel cage, and synthetic predator odour (2,4,5-trimethylthiazoline; 2MT) conditions. For predator testing, mice were exposed to 2MT in a separate chamber before assessment in the home cage. The paradigm was then used to evaluate acute PD-0325901 (Mirdametinib) treatment, a candidate therapeutic for autism. Latency to consumption was recorded for all tests.

The modified protocol enabled individual assessment while maintaining group-housing. Novel environment increased latencies, while 2MT exposure elicited comparable responses despite testing in the home cage. No sex differences were observed. Evaluation of Mirdametinib treatment is underway.

This modified NIH protocol aligns with the refinement principle of the 3Rs by preserving group-housing while allowing for individual assessment. Incorporating environmental novelty and an innate stressor provides a broader assessment of anxiety-like behaviour and candidate anxiolytic therapies.

Sex-Specific Myelin Differences in Auditory Brain Regions of a Fragile X Syndrome Mouse Model

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Keywords: *Fragile X syndrome, Myelin, Auditory Hypersensitivity*

Fragile X Syndrome (FXS), characterized by loss of the FMR1 gene on the X chromosome and subsequent loss of Fragile X Messenger Ribonucleoprotein, is the leading monogenic cause of autism spectrum disorder (ASD) and inherited intellectual disability. Auditory hypersensitivity, defined by heightened response to auditory stimuli and increased neuronal excitability within auditory circuits, is a common and clinically significant feature of both FXS and ASD. Despite this, little is known about how myelin abnormalities contribute to functional differences in FXS, or how they manifest by sex. This project examines how FMRP loss impacts myelination of auditory circuits in a sex-dependent manner at postnatal day 20 (P20), a developmental stage associated with peak auditory hypersensitivity in mice, as demonstrated by susceptibility to audiogenic seizures. Brain sections from P20 wildtype and FMR1-knockout mice of both sexes (n=5/group) were immunostained for myelin basic protein (MBP), a major structural component of myelin, and imaged in the inferior colliculus (IC) and auditory cortex (AC) under standardized conditions. Mean MBP fluorescence intensity was quantified using ImageJ and compared between genotype and sex groups within each region. Preliminary data show reduced MBP expression in FMR1-knockout mice of both sexes relative to controls, with a more prominent difference in females; ongoing analyses will determine whether this difference, or any sex-specific pattern, is statistically significant. This work will provide insight into how myelination of auditory circuits is altered in FMR1-knockout mice. Understanding sex-dependent differences in myelin could further explain variability across sexes in FXS and inform future diagnostic approaches.

Value and outcomes of collared caribou mortality investigations in the Northwest Territories

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Keywords: *caribou mortality, wildlife health, diagnostics*

Caribou are an important part of northern ecosystems and are connected to the culture and livelihoods of Indigenous communities in northern Canada. The barren-ground and boreal woodland caribou (*Rangifer tarandus groenlandicus* and *R. t. caribou*, respectively) occupy these regions, though some populations have declined in recent decades, with climate change, predation, and human disturbance implicated as contributing factors. In the Northwest Territories (NT), caribou deaths are typically detected using GPS collars; however, delayed access to remote sites due to logistical and financial constraints often limits confidence in determining cause of death and biological sample quality. This project characterizes causes of caribou mortalities, evaluates how investigation timing influences sample viability, and identifies spatial, temporal, and environmental factors associated with biological sample collection. We compiled field data from 211 boreal woodland and 251 barren-ground collared caribou mortalities investigated across the NT since 2013. Biological samples were collected opportunistically from 31 boreal woodland and 48 barren-ground caribou mortalities. Post-mortem analyses will use collected samples, including jaw and teeth evaluations, long bone morphometrics and marrow assessment, hair, and internal organs, to investigate health and mortality causes. Spatial analyses will compare locations of all investigated mortality events with those where samples were collected. We expect analyses to quantify relationships between investigation timing, sample quality, and diagnostic confidence. These findings are expected to strengthen wildlife health surveillance by informing prioritization of resource-intensive investigations to improve sample quality and determine proximate causes of mortality. This work supports conservation and health surveillance of free-ranging caribou in the NT.

Limit of Detection of Chromogenic Culture Media for On-Farm Culture of Bovine Mastitis Pathogens

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Keywords: *Culture, Bovine Mastitis*

Bovine mastitis is the leading cause of antimicrobial use on dairy farms. Antimicrobial stewardship could be improved by using an on-farm diagnostic test. A tool that could make this possible is culturing milk samples on-farm using chromogenic media, producing different coloured growth for different species. Although the diagnostic characteristics of chromogenic media have been explored in the past, the analytical sensitivity (or limit of detection) has not been defined for major mastitis causing pathogens. To find this, we cultured 6 isolates of 5 major mastitis causing species (*Escherichia coli*, *Klebsiella pneumoniae*, *Streptococcus dysgalactidae*, *Streptococcus uberis*, *Staphylococcus aureu*s) on 4 different chromogenic media (CHROMagar gram negative, CHROMagar orientation, CHROMagar streptoccoccus, CHROMagar staphylococcus) compared to blood agar and MacConkey media, the gold standards. Created a serial dilution of 0.5 McFarland of each species in pasteurized milk, plating the dilution and incubating at 37°C, counting growth after 24hrs. The results were later analyzed using a Kaplan-Meier curve and compared using a chi-squared test. No significant difference was found between the limits of detection between all the culture media for any of the species. The limit of detection of the chromogenic media is comparable to that of the gold standard, indicating that it is a reliable diagnostic for detecting bacteria in milk. In the future, we will run qPCR on the last samples in each dilution that exhibit growth to quantify the analytical sensitivity.

Optimizing Oxford Nanopore-Based DNA Metabarcoding for Arctic Insect Surveillance

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Keywords: *Metabarcoding, Nanopore, Biting Insects*

Arctic environmental change is altering the distribution of biting insects and the pathogens they carry, creating new risks for wildlife health, food security, and ecosystem stability. However, the distribution of many Arctic biting insect species and their associated pathogens remain poorly documented, limiting our ability to detect emerging disease risks. This study aims to optimize an Oxford Nanopore-based DNA metabarcoding workflow for rapid, cost-effective identification of Arctic biting insects and their pathogens to strengthen wildlife disease surveillance in the Kitikmeot region. Samples collected by community members through the Kitikmeot Biting Insect Monitoring Program (KBIMP) were sorted for biting insects, followed by DNA extraction and PCR amplification of an insect barcode marker. Amplicons were sequenced with the GridION Oxford Nanopore platform and analyzed using bioinformatic pipelines to identify insect species. This optimized, highly multiplexed approach offers significantly reduced costs relative to traditional Sanger methods, while providing significant improvements in DNA barcode length relative to Illumina methods. To evaluate these advantages, workflow efficiency, sequencing throughput, and cost per sample will be assessed to determine the performance of Oxford Nanopore sequencing for large-scale Arctic insect surveillance. Optimizing this workflow will expand Arctic biting insect surveillance across remote regions and strengthen our ability to monitor changing vector distributions and emerging wildlife disease risks.

Trends in herd-level seropositivity of Salmonella Dublin in Alberta dairy herds

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Keywords: *prevalence, Salmonella Dublin, seropositivity*

Introduction: *Salmonella enterica* subsp. *enterica* serovar Dublin is a cattle-adapted, Gram-negative bacterium that poses significant risks to the dairy industry in Alberta by causing increased calf morbidity, mortality, and abortion, and decreasing milk production. Although herd-level seropositivity data are available, whether this positivity has changed over time remains unknown. This study aimed to identify trends in herd-level seropositivity of *S.* Dublin at the provincial level, as well as when stratified by regions, herd size, herd type, and milking system type.

Methods: In a serial cross-sectional study, bulk tank milk samples were collected from all licensed dairy herds in April 2026 (n=458). Samples were tested for antibodies against *Salmonella* Dublin using an indirect enzyme-linked immunosorbent assay (iELISA). Data on herd status for *Salmonella* Dublin seropositivity in April 2022 and June 2024, along with herd characteristics, were obtained from previous studies. Changes in herd-level apparent prevalence across these years were assessed using Cochran's Q test.

Results: Herd-level positivity increased from 6.6% (95%CI: 4.5-9.2) in 2022 to 10.4% (95%CI: 7.7-13.5) in 2024 and 12.4% (95%CI: 9.6-15.8) in 2026 (Cochran's Q, $p = 0.001$). When stratified by herd characteristics, significant increases in positivity were observed in the South and Central regions, in medium-sized herds, in non-Hutterite herds, and in herds with automatic milking systems.

Discussion and Significance: These findings suggest that *Salmonella* Dublin is becoming increasingly concerning in Alberta, indicating increasing herd-level exposure. Continued monitoring is essential to enhance understanding of disease dynamics, and these results will aid in prioritizing surveillance and control.

Development of a Ferritin-Nanoparticle Based Mpox Vaccine Displaying Viral Proteins

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Keywords: *Mpox, emerging virus, nanoparticle vaccines*

Poxviridae is a family of double-stranded DNA viruses that infect humans and animals. Among its most recognizable members is Variola virus, the causative agent of smallpox, which was eradicated in 1980 through international vaccination efforts. Recently, outbreaks of MPXV (formerly Monkeypox virus) which causes the disease Mpox, have highlighted the public health need for improved poxvirus vaccine strategies. Although existing smallpox vaccines are currently used to protect against mpox and MPXV infection, development of pathogen-specific vaccines remains an important area of research. This project aimed to develop an MPXV vaccine using a ferritin-nanoparticle platform. Ferritin-nanoparticles self-assemble into particles displaying viral antigens such as MPXV proteins B6, M1, A29, and A35, as 8 trimeric antigens (24 antigens total). This multivalent array has been shown to enhance immune responses. To develop this vaccine, plasmids encoding ferritin protein fused to the MPXV antigens B6, M1, A29, and A35 were designed and cloned. A His-tag was included for downstream protein purification and analysis. The plasmids were propagated in bacteria, purified, and analyzed for correct orientation and cloning by restriction digestion and DNA sequencing. Expi293 mammalian cells were then transfected with the plasmid encoding the MPXV-ferritin fusion proteins for protein expression. Expressed protein was analyzed by SDS PAGE, western blot analysis, and quantified by BCA Assay. Western blots were probed with anti-his to identify the his-tag fused to the protein of interest. Preliminary findings demonstrate the feasibility of using ferritin-nanoparticle constructs for mpox vaccines and establish a foundation for future protein expression and immunogenicity studies.

Prevalence of West Nile Virus in Mosquitoes Around the Calgary Area

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Keywords: *West Nile Virus, Culex pipiens, RT-qPCR*

The common house mosquito, *Culex pipiens*, is invasive to North America and has driven the spread of West Nile virus (WNV) across eastern North America. It has recently appeared in Alberta. WNV is a mosquito-borne virus whose primary vectors in Alberta are mosquitoes of the genus *Culex*. These species are opportunistic feeders that bite both mammals and birds, increasing their potential to transmit the virus to incidental hosts such as humans and horses. With no direct WNV surveillance active in Alberta, regional data on transmission risk and seasonality remain limited. With *Cx*. *pipiens* present, WNV poses a greater risk to public and veterinary health. This project aims to monitor WNV prevalence in the Calgary area and characterize its prevalence. In coordination with the City of Calgary and the Wilder Institute/Calgary Zoo, mosquitoes are collected from urban and rural habitats using CO2 traps, targeting host-seeking females, and gravitraps, targeting gravid females. Collection has occurred annually during peak season (June–September) since 2024 and continues through 2026. Specimens are morphologically identified and processed for DNA/RNA extraction, pooling material from up to 50 individuals of the same species and trap. Pools undergo reverse transcriptase qPCR with a fluorescent dye to detect WNV RNA, and pool positivity rates are calculated to assess prevalence and risk. To date, 659 samples have been tested. Preliminary results show *Culex tarsalis*, *Culex pipiens*, and *Aedes vexans* have the highest infection rates. These findings help assess transmission risk, inform public health management, and improve understanding of WNV disease ecology in the region.

Herd-level prevalence of Neospora caninum in Alberta dairy herds using ELISA on bulk tank milk samples

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Keywords: *Alberta dairy herds, Neospora caninum, prevalence*

Introduction: Neospora caninum is a protozoal parasite that is recognized as one of the leading causes of abortion in dairy cattle worldwide. Neospora caninum spreads horizontally via dog feces infected with the parasite's eggs, or through vertical transmission from dam to calf. The objective of this cross-sectional study was to estimate herd-level prevalence of N. caninum in Alberta dairy herds.

Methods: Bulk tank milk samples were collected in April 2026 from all licensed dairy herds (n = 459) in Alberta and tested for antibodies against N. caninum using a commercially available ELISA (IDEXX Neospora X2) following the manufacturer's recommendations. After incubating the samples for 30 minutes at 18-26°C, plates were washed four times before adding conjugate. Wash and incubation steps were repeated for the TMB substrate and stop solution. Samples with a Sample-to-Positive ratio (S/P ratio) ≥0.50 were considered positive. Herd-level prevalence was calculated as the proportion of ELISA-positive herds out of total tested herds. The Chi-square test was used in RStudio to determine if N. caninum status and herd characteristics were associated.

Results: The apparent provincial herd-level N. caninum prevalence was estimated at 16.8% (95% CI: 13.6 –20.5%). At the regional level, the prevalence was 27.6% (95% CI: 20.3–36.3%), 16.3% (95% CI: 11.5– 22.5%), and 8.7% (95% CI: 5.2–14.4%) for herds in the North, Central, and South regions of Alberta, respectively. Hutterite colony herds were less frequently N. caninum-positive than non-colony herds (8.4% vs. 20.3%; p=0.002). N. Caninum prevalence did not differ (p=0.70) between herds with a conventional milking system and an automatic milking system (17.1% vs. 15.7%) or between small, medium, and large-sized herds (17.6, 14.7, and 18.7%, respectively; p=0.70).

Conclusion: These estimates provide up-to-date data on herd-level prevalence of N. caninum in Alberta across different regions and herd characteristics, guiding future surveillance and control efforts.

Investigating the Role of Proteases in the Host-Immune Response during Swine Dysentery

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Keywords: *Swine dysentery, protease, Brachyspira hyodysenteriae*

Brachyspira hyodysenteriae is a Gram-negative spirochete that colonizes the large intestine and causes swine dysentery, a mucohemorrhagic colitis characterized by diarrhea resulting in significant economic losses to the swine industry. Despite well-characterized clinical signs, the host inflammatory response responsible for tissue damage remains poorly understood. We hypothesize that host-derived proteases, which regulate tissue remodeling and immune responses, contribute to disease progression by exacerbating colonic injury.

Swine dysentery pathogenesis was investigated in weaned pigs orally challenged with *B. hyodysenteriae* or an inert solution (n = 10 per group). Disease progression was monitored daily over two weeks, and fecal samples were analyzed by qPCR to confirm bacterial shedding. Protease activity was assessed using transcriptomic bioinformatics, protease activity assays of colonic tissue and luminal contents, and an IPEC-J2 intestinal epithelial cell model to investigate host epithelial protease responses during infection.

Infection was confirmed by detection of *B. hyodysenteriae* DNA in feces. Transcriptomic analysis demonstrated upregulation of matrix metalloproteinases (MMPs), followed by serine and cysteine proteases. Proteomic analysis revealed reduced abundance of structural proteins in the colon, while gene ontology analysis identified enrichment of protease-related pathways. Consistent with these findings, protease activity assays demonstrated increased host protease activity in colonic tissue, luminal contents, and IPEC-J2 cell supernatant during infection.

These findings indicate that *B. hyodysenteriae* infection stimulates host-derived protease activity, contributing to tissue destruction and the development of mucohemorrhagic colitis. This work advances our understanding of swine dysentery pathogenesis and identifies host proteases as potential therapeutic targets to reduce disease severity and improve swine health.

Evaluating zoonotic potential of chronic wasting disease through disease progression in transgenic mice

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Keywords: *Zoonosis, Prion, Chronic Wasting Disease*

Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy of deer and other cervids, caused by misfolding of cellular prion protein to disease-causing prions, resulting in neurodegeneration. Due to zoonotic disease caused by transmission of bovine prions and ongoing human consumption of venison, concerns about zoonotic potential of CWD are growing. Recent work in our lab showed clinical evidence of CWD transmission to cynomolgus macaques, a relevant primate model for zoonotic transmission. Transgenic mice carrying the cellular prion protein from deer (TgDeer), elk (TgElk), and humans (TgHuman) were inoculated with macaque-passaged CWD (macCWD). Initial inoculations were below the detection limit for pathological prion protein at clinical endpoints without amplification despite an increasing attack rate across subsequent passages. However, after passaging into bank voles, a universal model for prion disease, prions were detectable in bank voles and subsequent TgDeer passages in pre-amplifcation immunoblot. To better understand macCWD prions, we performed a time-point experiment to monitor disease progression and predict zoonotic potential. Tissues from both rodent groups were used to inoculate TgDeer, TgElk, TgHuman, and prion protein knockout mice. Mice were harvested at two pre-clinical time-points and at clinical disease, and tissue samples screened for prions. Clinically sick cervidized mice were positive in pre-amplification immunoblot, but earlier time points are inconclusive, so prion amplification assays will be completed. As endpoint groups for TgHuman and knockout mice are still ongoing, these assays could compare pre-clinical CWD development between species. This work will be used to select mice for further work in spatial transcriptomics.

Evaluation of the Use of Human ELISA to Detect Bovine GDF9 in Follicular Fluid

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Keywords: *Ovarian reserve; bovine follicular fluid; GDF9*

Current estimations for the ovarian reserve in cattle primarily reflect the population of growing follicles, rather than representing the follicles within the dormant reserve. Identifying novel markers that directly reflect the ovarian reserve is critical for livestock management to best inform upon the fertility potential of a heifer. This study aims to explore whether a human growth differentiation factor 9 (GDF9) ELISA (AnshLabs, TX) can detect this oocyte-derived analyte in cattle follicular fluid (FF). An in-silico conformation comparison and homology assessment using multiple sequence alignments between human and bovine GDF9 protein sequences was carried out using Jalview software (version 2.11.5.2). The assay's ability to detect GDF9 was tested with serially diluted (1:10) ovarian FF and discarded in-vitro maturation (IVM) supernatant fluid to test assay parallelism. FF aspirated from small (SF, n=5), medium (MF, n=2), and large (LF n=2) antral follicles was collected to measure GDF9 concentrations. Preliminary results demonstrated an observed homology of 95.5% between human and bovine GDF9 mature protein sequences. Correspondingly, test linearity was demonstrated using serial dilutions of FF and IVM supernatant fluid (r^2 = 0.99). Follicular size and GDF9 concentrations displayed an inverse relationship (SF: 5809±260.9 pg/ml; MF: 176.2±9.4 pg/ml; LF: 59.3±5.5 pg/ml; $p<0.001$). Both the homology assessment and serial dilution findings support the use of a commercially available human GDF9 ELISA to detect GDF9 in bovine FF. Future work using this human GDF9 ELISA for bovine FF is to investigate the potential use of GDF9 to serve as a marker for ovarian reserve in cattle.

Movement Asymmetry of the Head and Pelvis Before and After Routine Hoof Care in Shod and Unshod Horses

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Keywords: *Equine movement asymmetry; routine hoof care; markerless gait analysis*

Background: Routine hoof care alters hoof conformation and hoof-ground interaction, but evidence of its immediate effects on objective movement asymmetry, a key component of veterinary lameness examinations, is conflicting. We tested whether head and pelvic movement asymmetry changed after hoof care and differed between shod and unshod horses.

Methods: This observational pre/post study included 44 horses and 85 matched hoof-care cycles (54 shod, 31 unshod; 170 observations; mean 1.9 cycles/horse). Sleip, a smartphone-based markerless system, quantified maximum and minimum head and pelvic movement asymmetry during straight-line, in-hand trot before and after hoof care. Linear mixed-effects models tested pre/post differences with random intercepts for horse and hoof-care cycle. Secondary models adjusted for stride frequency and tested pre/post × hoof-management interactions. Stride frequency was analyzed with a separate mixed-effects model. Statistical significance was set at $p<0.05$.

Results: Maximum head movement asymmetry increased by 0.0435 Sleip units (~1.7 mm; $p=0.0499$), and minimum head movement asymmetry increased by 0.0741 units (~3.0 mm; $p=0.0294$). There was no evidence of pre/post changes in maximum pelvic movement asymmetry ($\beta=-0.0141$, $p=0.6226$) or minimum pelvic movement asymmetry ($\beta=0.0035$, $p=0.8761$). Stride-frequency adjustment did not alter findings. Stride frequency showed no pre/post change (post-pre $\beta=0.0074$ Hz, $p=0.2474$), and no pre/post × hoof-management interaction was identified for any outcome.

Conclusion: Routine hoof care was associated with small increases in maximum and minimum head movement asymmetry, with no evidence of corresponding pelvic changes. Recent hoof-care history should be considered when interpreting objective movement asymmetry during veterinary lameness examinations.

Investigating the Effects of Systemic Inflammation Following Ependymal Cell Dysfunction

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Keywords: *Ependymal Cells, Systemic Inflammation, Glut1*

Introduction: Ependymal cells are multiciliated glial cells that line the cerebral ventricular surface, where they maintain a semi-permeable barrier between the cerebrospinal fluid and brain, propel cerebrospinal fluid flow, and regulate transport of ions and other molecules. Ependymal dysfunction is seen in many disorders such as hydrocephalus and Alzheimer's disease. Recent work from our lab demonstrated that impairment of ependymal cell metabolism through deletion of the glucose transporter 1 (Glut1) results in cognitive impairment and broad neuropathology resembling Alzheimer's disease (Sharma et al, in revision). Because these effects are at least partly due to impaired ventricular barrier function, we hypothesize that this ependymal dysfunction may render the brain more vulnerable to systemic inflammatory challenge (e.g. viral or bacterial infection). **Materials & Methods:** To test this, two cohorts of mice (n=24) were used, consisting of wild-type controls and Glut1 conditional knockout (Glut1-cKO) mice. Glut1 conditional depletion was induced at postnatal day 21, followed by three injections of either lipopolysaccharide (LPS), polyinosinic:polycytidylic acid (Poly I:C), or sham at postnatal day 30 to model systemic inflammatory challenge. Brains and spleens collected 1, 2, and 8 weeks after treatment were frozen, cryosectioned, and immunostained for quantification of glial and inflammatory responses using confocal microscopy. Unpaired t-tests was used to analyze glial and microglial changes in response to challenge. **Results:** We anticipate that in response to inflammatory insult, Glut1-cKO mice will have greater ependymal disruption, increased CD45+ peripheral immune cell infiltration, and enhanced microglial and astrocytic reactivity. **Discussion/Significance:** This work will shed new light on ventricular cell biology and how ependymal cell dysfunction impacts overall brain homeostasis and healthy brain aging.

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