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Health Sciences
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THE 2025 LIFE & HEALTH SCIENCES

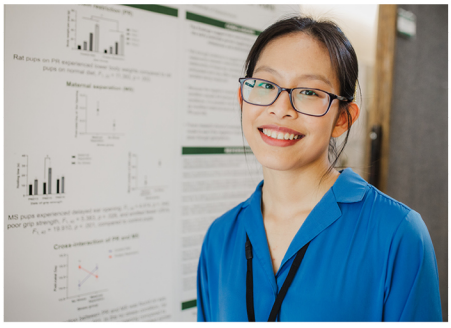
RESEARCH EXPO











ACKNOWLEDGING EXEMPLARY RESEARCH AND LEARNING AT THE UNIVERSITY OF SASKATCHEWAN

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Research competition abstracts

Agenda

09:00 – 11:30 a.m.	**STUDENT REGISTRATION*** D-Wing, outside Room 1B21, Health Sciences Building ***Registration and poster setup begin 30 minutes prior to each presentation session.***
9:30 – 11:00 a.m.	**RESEARCH POSTER SESSION #1** D-Wing Atrium, 3rd floor, Health Sciences Building • Undergraduate 1 • Basic Science 1 • Social & Population Health 1 • Translational, Clinical or Applied Science 2
10:00 a.m. – 11:30 a.m.	**RESEARCH POSTER SESSION #2** D-Wing Atrium, 2nd floor, Health Sciences Building • Undergraduate 2 • Basic Science 2 • Basic Science 3 • Translational, Clinical, or Applied Science 3
11:30 a.m. – 1:00 p.m.	**RESEARCH POSTER SESSION #3** D-Wing Atrium, 3rd floor, Health Sciences Building • Basic Science 4 • Basic Science 5 • Social & Population Health 2 • Translational, Clinical, or Applied Science 4
12:00 – 1:30 p.m.	**RESEARCH POSTER SESSION #4** D-Wing Atrium, 2nd floor, Health Sciences Building • Undergraduate 3 • Basic Science 6 • Translational, Clinical, or Applied Science 1
1:30 – 2:30 p.m.	**NETWORKING BREAK (COFFEE & SNACKS PROVIDED)** B-Wing Foyer (HLTH GB01), Health Sciences Building
2:30 – 3:45 p.m.	**AWARDS CEREMONY AND SPECIAL PRESENTATIONS** HLTH GB03, Health Sciences Building

2025 Best Supervisor Award

Congratulations to the winner of the
2025 Life and Health Sciences Research Expo
Best Supervisor Award

Dr. L. Dean Chapman BSc, PhD
Professor
College of Medicine

Nominated by Puja Rajesh

2025 Best Paper Awards

BEST PAPER – BASIC SCIENCE

Marina Carla Bezerra Da Silva
Western College of Veterinary Medicine

Supervisors: **Sarah Wood**
Western College of Veterinary Medicine

Elemir Simko
Western College of Veterinary Medicine

From larva to adult: In vitro rearing protocol for honey bee (Apis mellifera) drones

Bezerra da Silva MC, Kindopp MG, Sebastian Jose M, Obshta O, Edirithilake TLK, Tellarini Prieto EE, et al. (2025) From larva to adult: In vitro rearing protocol for honey bee (Apis mellifera) drones. PLoS ONE 20(2): e0314859. https://doi.org/10.1371/journal.pone.0314859

BEST PAPER – TRANSLATIONAL, CLINICAL, OR APPLIED SCIENCE

Robin Manaloor
College of Medicine

Supervisor: **Jon Gamble MD, FRCPC**
College of Medicine

Virtual multidisciplinary preoperative assessments: A multi-site formative evaluation and evidence-based guide for implementing change

Prystajecky M, Manaloor R, Barbour-Tuck E, Dyck H, Ermel D, Baerwald A, O'Brien J, Gamble J. Virtual multidisciplinary preoperative assessments: A multi-site formative evaluation and evidence-based guide for implementing change. Canadian Journal of General Internal Medicine. 2024 Dec 1;19(4):180-91. https://www.nature.com/articles/s41598-023-47861-8

BEST PAPER – SOCIAL & POPULATION HEALTH

Sierra Leonard
College of Medicine

Supervisor: **Scott Adams MD, PhD, MEd, FRCPC**
College of Medicine

Comparing Artificial Intelligence and Traditional Regression Models in Lung Cancer Risk Prediction: A Systematic Review and Meta-Analysis

Leonard S, Patel MA, Zhou Z, Le H, Mondal P, Adams SJ, Comparing Artificial Intelligence and Traditional Regression Models in Lung Cancer Risk Prediction: A Systematic Review and Meta-Analysis, Journal of the American College of Radiology (2025). https://doi.org/10.1016/j.jacr.2025.02.042

Undergraduate Research 1

1. PRION PROTEIN-MEDIATED REGULATION OF MGLUR1 & MGLUR5: IMPLICATIONS FOR GROUP I MGLUR RECEPTOR TRAFFICKING AND MEMBRANE COMPARTMENTALIZATION

Presenter:	**Kasra Khunjush**
USask Affiliation:	**Undergraduate student**
College:	**College of Arts and Science**
Collaborators:	Mohamed Taha Moutaoufik, Mohan Babu, Changiz Taghibiglou
Supervisor:	Changiz Taghibiglou, College of Medicine

Background:
Group I Metabotropic Glutamate Receptors (mGluR1/5) are involved in experience-dependent synaptic plasticity, in addition to regulating a variety of pathological conditions in the CNS. Cellular prion protein (PrPC), which is exclusively localized in lipid raft regions on the plasma membrane (PM), interacts with mGluR1/5 in some pathological cases. Previous studies have demonstrated that some CNS receptors (e.g. NMDARs) serve different roles depending on the specific PM domains in which they reside. This study investigates the impact of PrPC binding on the PM compartmentalization of mGluR1/5. This study hypothesizes that genetically knocking out PrPC reduces mGluR1/5 localization within PM lipid raft domains.

Methods:
Wild-type (WT) and PrPC knockout (Prnp –/–) mice were homogenized, then centrifuged to isolate total PM fractions. Sucrose density gradient ultracentrifugation separates homogenized tissue samples into detergent-resistant (lipid raft) and detergent-soluble (bulk-membrane) membrane fractions, with 0.5% Triton X-100 preserving lipid rafts. High-speed ultracentrifugation further refined PM compartment separation. Western blot analysis assessed PrPC, mGluR1/5, and PM domain markers, followed by co-immunoprecipitation (Co-IP) to assess interactions between mGluR1/5 and PrPC. Mathematical modelling determined possible interacting regions of mGluR1/5 and PrPC.

Results:
In PrPC KO mice, mGluR1/5 demonstrate significantly decreased compartmentalization in bulk-membrane domains and non-significant compartmentalization within Lipid raft domains. This effect is consistent across monomers and dimers for both receptor types. Moreover, this study used Co-IP and mathematical modelling to validate the existence of complex formation between PrPC and mGluR1 and provide a speculative binding domain region for this complex.

Conclusion:
PrPC and mGluR1/5 form complexes which impact the domain localization of mGluR1/5 within the PM. Deletion of PrPC from mouse models significantly diminishes the expression of mGluR1/5 within bulk-membrane domains of the PM.

2. EXPLORING THE ROLE OF AUTONOMIC NEUROTRANSMITTERS IN ANDROGEN-DEPRIVATION INDUCED NEUROENDOCRINE PROSTATE CANCER

Presenter:	**Jay Patel**
USask Affiliation:	**Undergraduate student**
College:	**College of Arts and Science**
Supervisor:	Anand Krishnan, M.Pharm, PhD College of Medicine

Background:
Neuroendocrine Prostate Cancer (NEPC) is a lethal and highly metastatic subtype of prostate cancer (PC) that arises due to neuroendocrine differentiation (NED) of PC cells. Although the exact underlying mechanism transitioning PC to NEPC is unknown, anti-androgen therapy resulting in androgen deprivation is a well-known trigger for NEPC. The PC cells undergoing NED display increased neurite-like outgrowth and express NED markers, such as, Chromogranin-A, Neuron-Specific Enolase, and Synaptophysin. Innervation of prostate tumors by sympathetic and parasympathetic nerves promotes prostate cancer growth via the neurotransmitters, Norepinephrine (NE) and Acetylcholine (ACh). In this study, we examined if these neurotransmitters promote NEPC in androgen-deprived conditions.

Methods:
LNCaP, a prostate cancer cell line positive for androgen receptor expression was used for in vitro culturing in this study. We cultured these cells with Testosterone+ACh or Testosterone+NE or Testosterone+ACh+NE for 14 days, followed by Testosterone deprivation for 48 hours or 72 hours. RT-qPCR was done to examine the expression of NED markers, and GraphPadTM Prism Software was used for data analysis.

Results:
Bright-field imaging showed increased neurite-like outgrowth in testosterone deprived groups under ACh and Ach+NE treatments suggesting neuroendocrine differentiation of cells. NE treatment groups showed little or no neurite-like outgrowth. RT-qPCR data for mRNA expression of NED markers showed that CHG-A was upregulated 48 hours after deprivation of testosterone (*$p<0.05$) in ACh group, however, no significant change was seen in NE groups post-deprivation compared to combination treatment. There was no significant changes in NSE and SYP between the testosterone withdrawn groups and the combination groups.

Conclusion:
Testosterone withdrawal in ACh supplemented prostate cancer cultures show enhanced neurite-like outgrowth and expression of NED marker CHG-A indicating their neuroendocrine transition. Overall, this study suggests that parasympathetic signaling driven by ACh has the potential to promote androgen-deprivation induced NEPC.

3. CHILLING INNOVATIONS: INVESTIGATING OSMOTIC RESPONSES OF IN SITU BOVINE OVARIAN CELLS TO PREDICT FUTURE MODELS FOR CRYOPRESERVATION

Presenter:	**Aunum Abid**
USask Affiliation:	**Undergraduate student**
College:	**College of Arts and Science**
Supervisor:	James Benson, PhD College of Arts and Science
Co-supervisor(s):	Iqra Azam, PhD

Background:

Cryopreservation is a process that preserves biological tissues at extremely low temperatures. While cryopreservation is widely used, it presents challenges including ice crystal formation, cytotoxicity, osmotic stress, and intracellular stress in cells and tissues. These injuries occur in pre-freezing and thawing conditions during equilibration of cryoprotective agents (CPAs). Currently, mathematical models of these stressors to optimize cell and tissue preservation with minimal cryoinjury to ovarian cells in monolayers or suspension exists. However, there is no data showing the effects of pre-freezing and thawing techniques on the structure, behaviour, and injury of ovarian cells in situ. Therefore, my project analyzed osmotic behaviour of ovarian cells in situ to help optimize future cryopreservation protocols.

Methods:

I sectioned and stained bovine ovaries with cellular membrane and nuclear dyes to identify changes in cell volume, injury, and intracellular features. These sections were then treated with varying concentrations of CPAs over time, were left to equilibrate, and assessed for osmotic behavioural and structural changes using 4D confocal microscopy.

Results:

Results supported structural and behavioural changes in ovarian cells exposed to varying anisosmotic CPA treatments over time. Addition of hyperosmotic treatments resulted in cell shrinking compared to hyposmotic treatments that resulted in cell swelling. Further changes due to osmotic stress caused structural changes in surrounding intracellular components, altering the natural state of the cells.

Conclusion:

Overall, osmotic-induced changes in ovarian cell volume and intracellular structures in situ were observed, supporting structural and behavioural changes during pre-freezing and thawing conditions. These findings are crucial towards understanding osmotic responses and cryoinjury for the first time in ovarian cells within tissues. This will dramatically enhance theoretical models of cryopreservation and advance practical methods for preserving ovarian tissue for biobanking, biodiversity conservation, and fertility restoration.

Self-declaration of research alignment with additional themes (optional):

Interdisciplinary/Interprofessional Collaboration

4. IDENTIFICATION OF ICP4 PROTEIN INTERACTING PARTNERS THROUGH BIOID PROXIMITY LABELING

Presenter:	**Sam Wihak**
USask Affiliation:	**Undergraduate student**
College:	**College of Arts and Science**
Collaborators:	Laura Kellerer, Western College of Veterinary Medicine
Supervisor:	Kristen Conn, Western College of Veterinary Medicine

Background:

Herpes simplex virus 1 (HSV-1) is a common viral infection that causes both oral and genital herpes. During lytic infection, HSV-1 genes are temporally regulated. Immediate early (IE) genes are first expressed, followed by early (E) and late (L) genes. E, and L gene expression are dependent upon IE expression, specifically Infected cell polypeptide 4 (ICP4). ICP4 is an IE protein and is the only essential transcriptional activator of E and L genes. ICP4 interacts with components of the host transcriptional machinery during infection, yet mechanistically, these interactions remain poorly understood. Additionally, ICP4 upregulates the rate of exchange of histones, destabilizing chromatin. The HSV1 genome in lytic infection is chromatinized, yet remains unstable and highly dynamic, suggesting that HSV1 genes are equally accessible. Despite this, HSV1 genes are temporally regulated. The destabilization of chromatin by ICP4 is consistent with this dynamic state of chromatin. However, currently identified protein interactions with ICP4 do not correlate with its chromatin regulatory function. As a starting point, we will identify more ICP4-interacting partners to further elucidate this function.

Methods:

Proximity ligation using BioID will be utilized to label ICP4-interacting partners. A miniTurbo biotin ligase will be fused to ICP4, ICP4 Δ760-1298, and a nuclear localization signal and inserted into a Tet-On inducible expression cassette. A stable cell line will then be generated through lentiviral transduction. Upon addition of biotin, proteins within 10 nm will be biotinylated. Biotinylated proteins will be purified and sent for identification through mass spectrometry.

Results:

Currently, two of the three fusion proteins have been cloned into a lentiviral transfer vector (Except miniTurbo-ICP4 Δ760-1298) for future co-transfection.

Conclusion:

Understanding the full range of ICP4-interacting proteins is the first step in understanding the mechanisms by which HSV1 gene expression is regulated. Characterizing key components in efficient HSV1 infection may present new targets for future treatment.

5. CYTOTOXIC AND MOLECULAR EFFECTS OF DISINFECTANT CHEMICALS IN HUMAN NEUROBLASTOMA SH-SY5Y CELLS

Presenter:	**Ivana Gulati**
USask Affiliation:	**Undergraduate student**
College:	**College of Arts and Science**
Supervisor:	Natacha Hogan, BSc, PhD College of Agriculture and Bioresources
Co-supervisor(s):	David Janz, BSc, MSc, PhD Western College of Veterinary Medicine

Background:

Production, use, and environmental releases of disinfectant chemicals have substantially increased since the COVID-19 pandemic. Benzalkonium chloride (BAC)-based disinfectants have seen the greatest increase in use. These compounds are reported to accumulate in the brain and disrupt lipid metabolism in rodents, leading to adverse neurodevelopmental outcomes; however, the neurotoxic potential of BACs in humans is poorly understood. The goal of this study was to characterize the in vitro toxicity of BACs using human SH-SY5Y neuroblastoma cells and assessing cytotoxicity, oxidative stress, and molecular changes associated with neurodevelopment, inflammation, and apoptosis. We also compared responses of BACs with triclosan (TCS), a legacy disinfectant with recent restrictions in use due to its environmental occurrence and toxicity, including behavioral disorders and neuronal damage in zebrafish and rodents.

Methods:

Undifferentiated cells were treated with either BAC or TCS for 24 h and assessed for various toxicological endpoints, including cell viability, cytotoxicity, and expression of target genes related to neurodevelopment, proinflammation and oxidative stress, and apoptosis. Cell viability was assessed using the MTT (3-(4,5-dimethylthiazolyl-2)-2, 5-diphenyltetrazolium bromide) assay, which involves reduction of a yellow tetrazolium salt to purple formazan crystals by metabolically active cells. Cytotoxicity was determined using the LDH (lactate dehydrogenase) assay, which involves the release of the LDH enzyme upon cell membrane damage in cells undergoing cellular death/damage. The relative expressions of target genes were evaluated using the comparative CT method, where B-Actin and GAPDH were used as the housekeeping genes.

Results:

Based on preliminary MTT (3-(4,5-dimethylthiazolyl-2)-2, 5-diphenyltetrazolium bromide) cell viability assay results, the median effective concentration (EC50) values were 2.126 and 2.202 µg/mL for BAC and TCS, respectively. Lactate dehydrogenase (LDH)-based median effective concentration (EC50) values were 3.048 and 2.843 µg/mL for BAC and TCS, respectively. Gene expression analysis showed that 1 µg/mL TCS upregulated the pro-apoptotic gene BNIP3, while 1 µg/mL BAC upregulated the proinflammatory and antioxidant gene Nrf-2.

Conclusion:

The 24h EC50s for cell viability and cytotoxicity were similar for BAC and TCS at 2-3 µg/mL, which suggests that the two chemicals are comparable in their cytotoxicity despite having potentially different mechanisms of action. These EC50s are 1-2 µg/mL lower than those causing cytotoxicity in

other human cell lines (H358 and MCF-7/B1), suggesting that SY5Y cells are similar in their sensitivity to these other cell lines. Upregulation of Nrf-2 by BAC (1 µg/mL) suggests toxicity mechanisms related to inflammation and oxidative stress, while upregulation of BNIP3 by TCS (1 µg/mL) suggests apoptosis-related mechanisms.

6. ART IN ANATOMY: USING FACE PAINTING AS A CREATIVE LEARNING TOOL

Presenter:	**Sophia Chiasson**
USask Affiliation:	**Undergraduate student**
College:	**College of Dentistry**
Collaborators:	Debora Lana Alves Monteiro, College of Dentistry
Supervisor:	Juliana Faquim, DDS, MSc, PhD College of Dentistry

Background:
The worldwide trend to modernize health education curricula emphasizes active and learner-centered approaches. Passive learning leads to disengagement and limited retention, failing to meet the needs of the new generation of learners. This is particularly important in anatomy education, where universities are increasingly replacing traditional methods, like cadaver dissections, with engaging and interactive tools to foster engagement and learning. This study aimed to enhance student engagement and retention in anatomy through interactive and hands-on teaching strategies.

Methods:
The Dental Hygiene Program at the College of Dentistry, USask, introduced face painting as a teaching tool. Students painted the facial and masticatory muscles onto their partner's skin, allowing them to visualize the origin, insertion, action, form, and surface landmarks of the anatomical structures. A post-activity survey was administered to assess satisfaction, engagement, ability to visualize anatomical structures, perceived value for clinical practice, and confidence in anatomical knowledge.

Results:
The face painting was well-received, fostering strong collaboration and teamwork through active participation and being perceived to be effective at reinforcing learning and knowledge retention. In a post-activity survey, learners (n=17/22) showed high praise for the face painting activity, with 94.1% of students satisfied and 100% engaged and interested in anatomy. It helped 88.2% better visualize anatomical structures, and 100% found it valuable for future clinical practice. Additionally, it enhanced the confidence of students, as reported by 81.2% of them. Qualitative analysis revealed that students found the activity essential for understanding facial muscles' anatomy and functions. One student reported discomfort, highlighting the need for voluntary participation, respect for personal boundaries, and an inclusive environment for all.

Conclusion:
Incorporating interactive activities like face painting enhances students' understanding of theoretical concepts and helps visualize complex structures. Multidimensional teaching tools improve comprehension and foster positive outcomes, such as stronger teamwork, communication, and collaboration skills.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

7. AMYLOID PRECURSOR PROTEIN IS ALTERNATIVELY SPLICED IN AN IN VITRO MODEL OF NEURODEGENERATION

Presenter:	**Annika Dixon**
USask Affiliation:	**Undergraduate student**
College:	**College of Arts and Science**
Supervisor:	Michael Levin, College of Medicine

Background:

Neurodegeneration underlies disease progression in multiple sclerosis (MS) but the mechanisms behind neurodegeneration are not fully understood. Recent research has implicated the RNA binding protein (RBP) heterogeneous ribonucleoprotein A1 (hnRNP A1) as being dysfunctional in MS, impacting its many functions in maintaining RNA homeostasis, RNA export, and alternative splicing. Alternative splicing mediated by hnRNP A1 has been shown to contribute to neurodegeneration in MS and its models, emphasizing the need to research aberrant alternative splicing as a mechanism contributing to disease progression; one of the aberrantly spliced RNA targets is the App transcript, encoding amyloid precursor protein (APP).

Methods:

We modeled hnRNP A1 loss-of-function by CRISPR/Cas9-mediated hnRNP A1 knockout in differentiated Neuro2A cells, a neuronal cell line, and verified the alternative splicing event by semi-quantitative RT-PCR. We will assess the functional consequences of the identified alternative splicing event by overexpressing the two different App isoforms tagged with the HA epitope to visualize the respective isoforms.

Results:

Nuclear depletion of hnRNP A1 resulted in alternative App splicing and upregulation of the APP751 isoform containing exon 7, with concomitant downregulation of the APP695 isoform, which excludes exon 7. Overexpression of HA-tagged APP751 and APP695 to assess functional consequences of this isoform switch showed no differences between the two isoforms as measured by immunofluorescence and western blot, likely due to the complex proteolytic processing and trafficking of APP that resulted in loss of the tag.

Conclusion:

Dysfunctional hnRNP A1, as modelled by hnRNP A1 knockout, resulted in upregulated APP751 and downregulated APP695 in a differentiated neuronal cell line, the functional consequences of which may be assessed using overexpression constructs of the affected isoforms. Ultimately, identifying the functional consequences of hnRNP A1-mediated alternative splicing events may lend insight into neurodegenerative mechanisms in MS.

8. ANTIMICROBIAL EFFECT OF HISTATIN-5, GK-17, AND INKL AGAINST ORAL PATHOGENS

Presenter:	**Mouaz Abdel-Radi**
USask Affiliation:	**Undergraduate student**
College:	**College of Dentistry**
Collaborators:	Luke Wandzura, College of Dentistry
	Walter Siqueira, College of Dentistry
Supervisor:	Eduardo Moffa, DDS, MSc, PhD
	College of Dentistry

Background:

Oral pathogens, including fungal Candida species and bacterial species such as Staphylococcus aureus, frequently cause infections within the oral cavity. The oral cavity may also serve as a reservoir for S. aureus, which can disseminate via the blood, leading to systemic infections. Traditional treatments rely on antifungal and antibiotic agents; however, their widespread use has contributed to the alarming rise in antimicrobial resistance. Thus, novel strategies are urgently needed to combat these oral pathogens effectively while mitigating resistance. Our objective was to evaluate the antimicrobial efficacy and cytotoxicity of Histatin-5 (His5), GK-17, and INKL against key oral pathogens (C. albicans and S. aureus), while also evaluating their resistance to proteolytic degradation by secreted aspartyl protease (SAP).

Methods:

A killing assay was performed using a 96-well plate, where pathogens were incubated with each peptide for 48 hours, followed by colony counting. Cytotoxicity was assessed using gingival fibroblasts incubated with the peptides in DMEM media. Additionally, the peptides were subjected to degradation by SAP at various times.

Results:

The results demonstrated significant antimicrobial activity for INKL and GK-17, with INKL showing superior efficacy in eradicating three strains of C. albicans, as well as methicillin-susceptible and -resistant strains of S. aureus, compared to His5. An MTT assay revealed minimal cytotoxicity across most concentrations, with only the two highest concentrations of GK-17and INKL exhibiting slightly cytotoxic effect. The degradation profiles, analyzed via HPLC, indicated that GK-17 exhibited substantial resistance to proteolytic degradation, unlike the other peptides

Conclusion:

These findings suggest that GK-17 and INKL hold promise as therapeutic agents for treating oral infections. Localized application may offer advantages over systemic drugs, including reduced side effects and enhanced efficacy. Further research into these peptides is warranted to explore their potential as innovative treatments in oral healthcare.

Undergraduate Research 2

9. EXAMINING THE MODERATING EFFECT OF MIND-BODY BELIEFS ON THE RELATIONSHIP BETWEEN TRENDING NORM MESSAGES AND ON-CAMPUS PHYSICAL ACTIVITY AND SITTING BEHAVIOUR

Presenter:	**Ami Klinger**
USask Affiliation:	**Undergraduate student**
College:	**College of Kinesiology**
Collaborators:	Lauren Hinz, College of Kinesiology
Supervisor:	Kevin S. Spink, College of Kinesiology

Background:
Trending norm messages (Mortensen et al., 2019) appear to be effective in influencing on-campus activity behaviour (Anderson et al., 2024). However, little is known about moderators that may influence these relationships. One possibility concerns one's intuitive understanding of how the mind and body relate-monism versus dualism (Burgmer & Forstmann, 2018). Those who believe that the mind and body are separate (dualists) report decreased engagement and a less positive attitude toward health behaviours compared to mind-body monists (Burgmer & Forstmann, 2012) while monists have an increased probability of engaging in physical and mental health behaviours (Ku et al., 2025). The purpose was to examine whether different understandings of how the mind and body relate would moderate the relationship between trending norm messages versus a control message for on-campus physical activity (PA) and sitting behaviour (SB).

Methods:
Students (N=89) completed surveys at two time points. Participants completed demographics, on-campus PA and SB, a mind/body dualism measure (Burgmer & Fortsmann, 2018) and were randomly assigned to receive either a trending norms or control message. One week later, on-campus PA and SB were reassessed.

Results:
Moderation was tested by examining the effects of the interaction between messages and mindset beliefs for on-campus PA and SB. Results revealed a significant moderation effect for PA ($p < .024$) and SB ($p < .007$). Individuals with a stronger monist belief receiving the trending norm message reported walking around while using phone more often and standing up to interrupt SB more often compared to those who received the control message. Differences between the trending norm and attention control message for PA and SB did not differ for dualists.

Conclusion:
These results provide preliminary evidence suggesting that mind-body beliefs may be a possible moderator of the relationship between trending norm messages and on-campus PA and SB.

10. EXAMINING THE EFFECTS OF TRENDING NORM MESSAGES ON UNIVERSITY STUDENTS' ON-CAMPUS ACTIVITY AND SITTING INTENTIONS AND BEHAVIOURS

Presenter:	**Lauren Hinz**
USask Affiliation:	**Undergraduate student**
College:	**College of Kinesiology**
Collaborators:	Ami Klinger, College of Kinesiology
Supervisor:	Kevin S. Spink, PhD College of Kinesiology

Background:

University students often report low physical activity (PA) (Scarapicchia et al., 2015) and high levels of sitting behaviour (SB) (Castro et al., 2020). Thus, examining how to increase movement in this environment becomes important. One approach to address this issue is using normative messages (Cialdini et al., 1990). Anderson et al. (2024) reported trending norm messages decreased on-campus SB, but did not increase PA. As students report that decreasing SB may be easier than increasing PA (Pachu et al., 2020), adding a positive outcome expectation (POE) to normative messages may be one way to increase on-campus PA. The purpose was to examine whether a trending norm message augmented with a POE would change students' movement intentions and behaviours for increasing PA and reducing SB while on campus.

Methods:

University students (N = 103) completed two online surveys. In the first survey, participants completed demographics and self-reported on-campus PA and SB, were randomly assigned one of two messages (trending norms or attention control), then completed intentions to increase PA and reduce SB while on campus in the next week. One week later, self-reported on-campus PA and SB were re-assessed.

Results:

Results from a MANCOVA revealed that messages significantly impacted intentions ($p=.003$) with both PA ($p <. 001$) and SB ($p < .005$) contributing. Those receiving the trending norms message reported greater intentions to increase PA and reduce SB. In terms of behaviour, the messages only significantly impacted SB ($p<.029$), with those receiving the trending norms message reporting they stood up more to break up sitting time ($p < .019$).

Conclusion:

These findings provide further experimental support for exposure to trending norms decreasing university students' on-campus sitting behaviours. While trending norm messages increased intention to be active, they did not increase PA.

11. AN EXPLORATION OF FACTORS AFFECTING DIETITIAN INVOLVEMENT IN RURAL PRIMARY HEALTHCARE MEMORY CLINICS

Presenter:	**Brianna Wickett**
USask Affiliation:	**Undergraduate student**
College:	**College of Pharmacy and Nutrition**
Collaborators:	Erin Fedusiak, College of Pharmacy and Nutrition Debra Morgan, College of Medicine Dana Klapak
Supervisor:	Allison Cammer, College of Pharmacy and Nutrition
Co-supervisor(s):	Julie Kosteniuk

Background:
Eating and drinking are often affected in individuals living with dementia, which can compromise nutrition status and increase risk for malnutrition. Although registered dietitians have an important role in the management of malnutrition, they are not always included in interprofessional teams. This study aimed to understand facilitators and barriers to dietitian involvement in interprofessional rural primary healthcare memory clinics which provide diagnosis and management for community-dwelling persons with suspected dementia.

Methods:
A qualitative descriptive approach was used. In June-July 2024, six focus groups were conducted with 23 participants: three with memory clinic teams, one with primary healthcare managers and facilitators, and two with dietitians. Data were analyzed using Braun and Clarke's six-step reflexive thematic analysis approach.

Results:
Four themes were developed that encompass barriers and facilitators to dietitian involvement in rural memory clinics: It's a matter of perspective, We are on the same team, What does rural have to do with it, and Structure is the key to success. The main barriers to dietitian involvement included low understanding among teams of the dietitian role and need for involvement, rural location of memory clinics, and need for structure to support involvement. The main facilitators included improved understanding among teams of the dietitian role and importance of nutrition care, teams' enthusiasm for collaboration and interprofessional approach to care, prior relationships between team members and dietitians, and recently added processes to include dietitians.

Conclusion:
Dietitian involvement in interprofessional rural primary healthcare memory clinics was influenced by several factors. Barriers specific to the rural location of the clinics as well as limited structures to include dietitians hindered dietitian involvement. Increasing exposure to dietitians may improve awareness of the dietitian role and nutrition issues experienced by persons living with dementia. Addressing barriers and capitalizing on facilitators is essential to improving dietitian involvement.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

12. AN EVALUATION OF AN ACTIVE LIVING PROGRAM FOR OLDER ADULTS IN RURAL SASKATCHEWAN: IMPLEMENTATION AND ACCEPTABILITY

Presenter:	**Erin Fedusiak**
USask Affiliation:	**Undergraduate student**
College:	**College of Pharmacy and Nutrition**
Collaborators:	Brianna Wickett, College of Pharmacy and Nutrition
	Debra Morgan, College of Medicine
	Sheila Szakács
Supervisor:	Julie Kosteniuk, PhD
	College of Medicine
Co-supervisor(s):	Allison Cammer, PhD
	College of Pharmacy and Nutrition

Background:
Health promotion initiatives can have important benefits for the physical health of community-based older adults. However, access to such opportunities is limited in rural areas. In 2023, an active living program for older adults was developed and implemented in seniors' housing apartments in two rural Saskatchewan communities. Using the 'downtime' (unassigned work time) of home care continuing care assistants (CCAs), the ongoing program provides in-person physical activity, cognitive stimulation, and social engagement. The study purpose was to examine the implementation and acceptability of the program.

Methods:
A qualitative descriptive study was performed between December 2023 and February 2024. One focus group and seven semi-structured interviews were conducted with a total of 10 participants including primary health care managers/directors, CCAs, and older adult participants of the program. Analysis was completed using six-phase reflexive thematic analysis.

Results:
Five themes were developed related to implementation and acceptability of the active living program: Mind the gap, The program that brings us together, Everyone gets a seat at the table, When staff step up to the plate, and The future is unclear. The study identified benefits of the program, including improved physical and mental well-being. The program supported a sense of purpose and agency among older adults and new social connections formed as a result of the initiative. CCAs also reported benefits, including satisfaction and empowerment to customize sessions to older adults' needs.

Conclusion:
The findings point to several benefits of an active living program for rural older adults, suggesting it has become an important community resource. This study highlights the value of considering older adults' needs and perspectives when developing health promotion programs for this population.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

13. EXAMINING GENDER DIFFERENCES IN FACULTY PROMOTION AMONG CANADIAN DENTAL SCHOOLS

Presenter:	**Roba Ramadan**
USask Affiliation:	**Undergraduate student**
College:	**College of Dentistry**
Collaborators:	Lauren Williams, College of Dentistry
	Michelle Siqueira, College of Dentistry
Supervisor:	Michelle Siqueira, College of Dentistry

Background:
Research is limited on gender differences in academic dentistry and leadership within Canadian dental schools. This novel study aimed to assess gender trends among dental school faculty, deanship positions, and student convocation, as well as explore faculty perspectives on institutional attitudes toward gender equality in Canadian dental schools.

Methods:
Data was gathered and analyzed from all ten Canadian dental schools' public websites for the categories of academic faculty, deans, and student convocation. An anonymous survey was sent to faculty members (n=518) through SurveyMonkey. Statistical analysis was performed through IBM SPSS 28.0 to determine if any statistically significant differences in gender occurred.

Results:
An average of 12.3% more women graduated than men in 2019-2024, a trend not yet present within academic faculty. A statistically significant gender gap exists when comparing assistant, associate, and full professor positions ($p = .019$). Additionally, the difference between men and women within the interim dean and dean positions is statistically significant ($p = <.001$). Survey results indicate a positive outlook on gender inclusion within institutions; yet a large proportion of respondents (>50%) either agreed or were unsure on whether gender influenced their career progression and their ability to negotiate wages.

Conclusion:
This study significantly contributes to the understanding of current gender trends and beliefs that exist in Canadian dental schools. While strides have been made to close the gender gap, there are instances in which these differences should not be ignored. Results emphasize a need for initiatives that support gender parity within the academic setting, such as female mentorship opportunities, greater institutional support for parents, and better data repositories that make gender trend data more easily accessible. Further research could investigate gender trends within dental specialties/residencies and possible wage disparities that affect dental schools' faculty.

14. MAKING SOCIAL COMPARISON WORK FOR YOU TO GET MOVING

Presenter:	**Kate Korchinski**
USask Affiliation:	**Undergraduate student**
College:	**College of Medicine**
Collaborators:	Matthew Jarotski, College of Medicine
	Kevin S. Spink, College of Kinesiology
Supervisor:	Kevin S. Spink, College of Kinesiology

Background:
Social comparison is a powerful motivator (Festinger, 1954). The latest 'everything counts' physical activity (PA) messaging legitimizes all activity, which may allow individuals to compare more favourably to their peers, thus increasing their motivation to be active. This messaging has been demonstrated to be effective in increasing on-campus PA (Jarotski, 2024) and is associated with PA social comparison (Krammer et al., 2023). However, the relationship between these two variables has not been tested. The purpose of this study was to examine social comparison as a possible mediator of the 'everything counts' message and on-campus PA.

Methods:
University students (N = 42) completed two online surveys one week apart. Survey one assessed demographics, MVPA (Fowles et al., 2017), PA social comparison (Gitzel et al., 2023), and on-campus PA. Students were then randomly assigned one of two PA messages ('everything counts' or attention control) and PA social comparison was reassessed. One week later, on-campus PA was measured.

Results:
To minimize type II error in this exploratory study, a p value of .10 was selected (Maier & Lakens, 2022). Both relationships were significant and in line with establishing mediation (MacKinnon, 2008). The first revealed a significant relationship between the 'everything counts' message and post-message social comparison (beta = .129, p =.068).The second revealed a significant relationship between post-message social comparison and post-message on-campus PA (beta = .843, p = .028).

Conclusion:
This study provides experimental proof of concept evidence suggesting that social comparison could be a mechanism explaining why an 'everything counts' message increases on-campus PA. If supported with further research, this may shift the focus to targeting social comparison in PA messaging.

Undergraduate Research 3

15. EXPLORING THE UTILITY OF RESISTANCE TRAINING FOR CONGENITAL MIRROR MOVEMENT DISORDER

Presenter:	**Nisarg Shiroya**
USask Affiliation:	**Undergraduate student**
College:	**College of Kinesiology**
Collaborators:	Layla Gould, College of Medicine
	Gary Hunter, College of Medicine
Supervisor:	Jonathan Farthing, PhD
	College of Kinesiology

Background:
Congenital mirror movement (CMM) disorder is a very rare condition (<1 in a million) where voluntary limb movements trigger involuntary mirroring in the opposite limb. This study examined whether four weeks of unilateral resistance training, followed by 10 days of detraining, affects mirroring activity and cross-education effects (i.e., strength gain in the untrained opposite limb) in CMM.

Methods:
Two right-handed participants reporting CMM completed four weeks of maximal unilateral isometric grip training of the left hand, three times per week using a grip trainer (Digiflex), followed by 10 days of detraining. Training sessions increased from two to five sets of eight maximal repetitions per session. Participants completed testing for grip strength and muscle activation at baseline, mid-training, post-training, and after detraining. The Woods and Teuber scale was used to provide objective quantification of mirror movements (scored as 1, 2a, 2b, 3, 4) using video recordings of the hands. The scorer was blinded to the testing time point. Testing included three brief 3-second maximal voluntary contractions (MVC) and a 1-minute MVC contraction of each hand. MVC force (kg) was measured using Jamar and Biopac grip dynamometers, while simultaneous EMG recordings captured muscle activity from the flexor carpi radialis, extensor carpi radialis, and flexor digitorum superficialis of both arms.

Results:
Due to the low sample size in this study (on account of the rare condition), only descriptive results are reported. The objective quantification of mirror movements decreased for both participants after training (from level 2b to 2a and from level 3 to 2b). Trained left arm grip strength increased in the first participant by 12% and remained 6% above baseline after detraining. Untrained right arm strength improved 17% and increased to 23% above baseline after detraining, indicative of cross-education. The second participant showed a modest increase of ~6% by the end of detraining and no cross-education. Both participants showed substantial mirroring force and EMG activity in the opposite limb during 1-minute MVC contractions of either hand. Mirroring force in the right hand during a 1-minute left MVC was ~20% MVC for both participants at baseline and decreased by almost half at the end of detraining. Mirroring force in the left hand during 1-minute right MVC was ~40%

MVC and ~20% MVC for each participant, respectively, and decreased by almost half after detraining. EMG activation of the right hand during the left 1-minute MVC ranged from 67% to 82% MVC at baseline, with little change after training, and then increased after detraining. EMG activation of the left hand during the right 1-minute MVC was in the range of 80% MVC and tended to increase post-training, but reverted to baseline or lower after detraining.

Conclusion:

Unilateral grip training reduced mirroring force and improved strength, with signs of cross-education, and reduced clinical presentation of mirror movements. However, muscle activation responses varied, and detraining effects were inconsistent. Further research is needed to understand individual differences and long-term benefits for CMM.

16. ASSESSMENT OF SATISFACTION OF TOTAL KNEE ARTHROPLASTY PATIENTS USING CPAK CLASSIFICATION

Presenter:	**Thomas Goldade**
USask Affiliation:	**Undergraduate student**
College:	**College of Medicine**
Collaborators:	Janan Ashique, College of Medicine
	Evan Parchomchuk
	Cole Elaschuk
Supervisor:	Jans Van der Merwe, College of Medicine
Co-supervisor(s):	Mars Zhao

Background:
Total knee arthroplasty (TKA) is a successful procedure for osteoarthritis with high patient satisfaction rates. However, there are still factors contributing to decreased patient satisfaction leading to reduced quality of life. The Coronal Plane Alignment of the Knee (CPAK) classification, a novel system describing radiographic knee phenotypes, may offer insight into alignment related outcomes. This study evaluates whether specific pre- and post-operative x-ray CPAK combinations are associated with worse Patient Reported Outcome Measures (PROMs) after TKA.

Methods:
A retrospective chart review was performed on 346 patients who underwent primary TKA by a single surgeon in Saskatoon (2017-2023) and used CPAK classify pre- and post-operative radiographs. Patients were then asked to complete PROMs (OKS, KOOS-JR) to document satisfaction. Pearson correlation analysis was conducted to explore relationships between specific variables. Groups were created based on CPAK classifications to compare subgroup means to overall means, identifying significant differences using predefined thresholds.

Results:
The most common pre-operative CPAK classes were 2 (37.9%), 5 (19.6%) and 4 (12.6%), with 83.4% of post-operative patients in class 5. The mean KOOS-JR score was 62 (mild pain/difficulty) and the mean OKS score of 42 (satisfactory joint function).

Conclusion:
Our results suggest no statistically significant difference between pre- and post-op CPAK group combinations and KOOS-JR/OKS scores. The CPAK classification system was notably different pre- and post-operatively. Regardless of their pre-operative CPAK class, most patients were corrected to CPAK 5 postoperatively, which is the most phenotypical neutral alignment. Functional outcomes were consistent across most CPAK groups, suggesting tailoring alignment classification based on pre-op CPAK may not heavily influence short-term recovery. Surgeons may prioritize comorbidity management and standardized techniques, as CPAK classification did not strongly predict functional outcomes in this cohort.

17. SEROLOGICAL RISK FACTORS FOR ARTHROPLASTY COMPLICATIONS

Presenter:	**Nathan Oster**
USask Affiliation:	**Undergraduate student**
College:	**College of Medicine**
Collaborators:	Janan Ashique, College of Medicine
	Cole Elaschuk, College of Medicine
	Mikayla Rudniski, College of Medicine
Supervisor:	Jans Van der Merwe, MBChB, FRCSC
	College of Medicine
Co-supervisor(s):	Mars Zhao MD, BSc (Hons)

Background:
Post-surgical complications can have a devastating impact on patients' quality of life. Peri-operative bloodwork is routinely conducted and may predict post-operative complications. The purpose of this study is to understand if pre or post-operative serology is associated with post-operative complications arising from hip and knee arthroplasty.

Methods:
A retrospective chart review of 140 patients with post-operative complications and 120 controls was conducted between February 2022 and January 2025. Pre and post-operative absolute serological values as well as monocyte-lymphocyte, neutrophil-lymphocyte, platelet-mean platelet volume, and platelet-lymphocyte ratios. Surgical and comorbidity data were collected. The PJI and other post-operative complication group were compared to a control group. Logistic regression was used to assess whether pre-operative and post-operative laboratory values independently predicted post-operative complications. Receiver Operating Characteristic curves determined the sensitivity, specificity, area under the curve (AUC), and cutoff values for serological markers.

Results:
PJI and complication groups had higher age, comorbidity index, and lower hemoglobin compared to the control group ($P<0.05$). Pre-operative hemoglobin and lymphocytes had a negative relationship with post-operative complications (respectively: OR = 0.68, 0.45; $P<0.05$). Pre-operative Monocyte-Lymphocyte ratio and BMI (respectively: OR = 2.24, 2.61; $P<0.05$) and post-operative eosinophil count and monocyte-lymphocyte ratio (respectively: OR = 2.26, 1.79; $P<0.05$) had a positive relationship with post-operative complications. Post-operative eosinophil count had the highest AUCs (0.730-0.788) across comparisons indicating strong predictive power for complications, especially PJI.

Conclusion:
We identified multiple peri-operative serological risk factors for developing post-operative complications following hip and knee arthroplasty. Post-operative eosinophil count and monocyte-lymphocyte ratio had the most reliable predictors of post-surgical complications, particularly for PJI. These markers could be prioritized for monitoring high-risk patients. However, the predictive power of many routine bloodwork variables was limited, highlighting the need for multimodal risk assessment. Further validation is recommended to optimize cutoff values for clinical use.

18. EVALUATING THE ROLE OF THE SUPRAMAMMILLARY NUCLEUS IN TEMPORAL LOBE EPILEPSY

Presenter:	**McKenna Bolger**
USask Affiliation:	**Undergraduate student**
College:	**College of Medicine**
Collaborators:	Sarah Shaban, College of Medicine
	Alina Trofimova, College of Medicine
Supervisor:	Justin Botterill, PhD
	College of Medicine

Background:

Epilepsy is a chronic neurologic disorder characterized by seizure activity. Seizures manifest in many ways including loss of motor control, loss of awareness and convulsion. Temporal lobe epilepsy (TLE) is the most common form of epilepsy in adults. Most seizures associated with TLE involve the hippocampus and may result in neuronal loss. The supramammillary nucleus (SuM) of the hypothalamus is known to provide inputs to the hippocampus for the modulation of learning and memory; however, this correlation has yet to be established in the context of epilepsy.

Methods:

In the present study, Vesicular Glutamate Transporter 2 (VGlut2-Cre) transgenic mice were used to evaluate the SuM-hippocampal circuit in a chronic model of epilepsy. We used video electroencephalography (EEG) to determine whether activation or inhibition of the SuM-hippocampal circuit using Designer Receptors Exclusively Activated by Designer Drugs (DREADDs) will alter seizure severity and duration in chronic epilepsy. Spontaneous seizures were recorded for 5 days, followed by 5 days of recording while animals were given DREADDs agonist, deschloroclozapine (DCZ) (2 mg/kg/day), through drinking water to evaluate the effect of circuit manipulation.

Results:

Excitation of the SuM-hippocampal circuit with DREADDs increases frequency and duration of seizures in comparison to inhibition of the pathway. Percent change in EEG power is altered with circuit manipulation, specifically in the occipital cortex and hippocampus. Delta frequency is decreased when the pathway is excited compared to control in these brain regions. In the hippocampus, gamma frequency is increased with excitation compared to both the inhibitory and control conditions.

Conclusion:

Manipulation of the SuM-hippocampal circuit causes alterations in the presentation of seizures as well as changes to the EEG power of specific frequencies. These findings suggest that the SuM is involved in the modulation of the hippocampus in the context of TLE.

19. TITLE: COMPARATIVE DIAGNOSTIC VALUE OF SEROLOGICAL AND SYNOVIAL TESTS FOR PERIPROSTHETIC JOINT INFECTIONS: A COMPREHENSIVE ANALYSIS

Presenter:	**Jenna England**
USask Affiliation:	**Undergraduate student**
College:	**College of Medicine**
Collaborators:	Samuel Girgis, College of Medicine
	Thomas Goldade, College of Medicine
	Evan Parchomchuk, College Medicine
Supervisor:	Johannes van der Merwe, MBChB, FRCSC
	College of Medicine
Co-supervisor(s):	Mars Zhao, MD, BSc Hons

Background:
Prompt diagnosis of periprosthetic joint infections (PJIs) is crucial to providing optimal care. Currently, there are no gold standard tests available. An ideal test would be simple to implement, cost-effective, and readily available. We aimed to determine the best single or combined serological or synovial markers for diagnosing PJIs.

Methods:
There were 177 out of 313 patients who had PJIs between April 2012 and March 2023 and a control group of 60 patients who were included in this retrospective review. The PJIs were diagnosed using Musculoskeletal Infection Society (MSIS) and European Bone and Joint Infection Society (EBJIS) criteria. Serum (C-reactive protein (CRP), white blood-cell (WBC) count, neutrophil-lymphocyte ratio (NLR), polymorphonuclear neutrophil percentage (PMN%)) and synovial fluid (WBC, NLR, PMN%) parameters were compared between the two groups. We determined the sensitivity, specificity, area under the curve (AUC), and cut-off values (COV) for each marker. We determined the best combination of markers to diagnose PJIs. There was no statistical significance between the demographic data of the control and treatment groups.

Results:
The S-CRP had the highest AUC of 0.912 with a COV of 16.15 mg/dl (Sensitivity 79.6%, Specificity 97.8%). The combination of tests, S-CRP, SF-WBC, and S-NLR, demonstrated the highest AUC of 0.946 (Sensitivity 93%, Specificity 90.9%). The COV for SF-WBC was 5.75 cells/ul (AUC 0.803; Sensitivity 70.3%, Specificity 97.1%); S-NLR COV was 3.659 (AUC 0.803; Sensitivity 67.3%, Specificity 88%).

Conclusion:
We found the combination of S-CRP, SF-WBC, and S-NLR to be valuable in diagnosing PJI with high sensitivities and specificities. It can be easily implemented by clinicians without additional cost or equipment. It is important to use this with a thorough clinical and physical examination as well as other modalities (i.e., MSIS/EBJIS criteria).

20. QUANTIFICATION OF CEREBRAL EDEMA FOLLOWING ISCHEMIC STROKE

Presenter:	**Amber Jurke**
USask Affiliation:	**Undergraduate student**
College:	**College of Arts and Science**
Collaborators:	Huishu Hou, College of Medicine
	M. Jake Pushie, College of Medicine
	Michael E. Kelly, College Medicine
Supervisor:	Michael. E Kelly, MD
	College of Medicine

Background:

Cerebral edema is caused by various conditions such as traumatic brain injury, tumour, or stroke. This pathological swelling further complicates patients' recovery due to increased intracranial pressure (ICP) and blood-brain barrier (BBB) damage.

Methods:

Male and female C57BL/6 mice were randomly assigned to photothrombotic surgery, sham surgery, or naive control group. Photothrombotic stroke was induced using rose bengal and a laser to create ischemia in the right motor cortex. Brains were sectioned at 1-mm intervals and processed for wet/dry weight analysis, cryosectioning, and digital imaging. Tissue displacement was analyzed using a custom tool to measure displacement due to edema formation. Statistical analysis, including Pearson correlation, was conducted using Microsoft Excel, with significance at $p < 0.05$.

Results:

We determined that wet/dry weight analysis combined with the tissue displacement tool were efficient methods to quantify edema. Although acetazolamide did not prevent anatomical displacement or reduce swelling, we observed a positive correlation between water content and corpus callosum compression.

Conclusion:

Cerebral edema involves complex mechanisms that require targeted treatments. Precise quantification of edema is critical for reducing progression and advancing research. Overall, quantification will benefit in mitigating secondary injury and improving clinical outcomes.

21. CALF MUSCLE VOLUME AND FAT FRACTION CHANGES FOLLOWING BEDREST

Presenter:	**Kara Walz**
USask Affiliation:	**Undergraduate student**
College:	**College of Engineering**
Collaborators:	Malakeh Malekzadeh, College of Kinesiology
	Mary Masoomikhanghah, College of Engineering
	JD Johnston, College of Engineering
	Saija Kontulainen, College of Kinesiology
Supervisor:	Emily J McWalter, College of Engineering

Background:
Musculoskeletal changes associated with spaceflight are similar to those observed in patients confined to bedrest. Previous bedrest studies have shown that lower leg muscle volume decreases after bedrest and various countermeasures reduce changes. However, countermeasure effectiveness has only been studied in younger males. Although fat infiltration contributes to muscle atrophy, fat fraction has not been included in bedrest studies. This study aims to assess changes in muscle volume and fat fraction following 14 days of head-down bedrest (HDBR) in older adults.

Methods:
A 6° HDBR study was conducted including males and females in control (n=7, 3 female, mean age 57 SD 1 years) and exercise groups (n=8, 4 female, age 59, 3 years). Magnetic resonance imaging (MRI) scans were collected of the right lower leg before, and immediately, one week, and one month after bedrest. Muscles were segmented with an automatic segmentation software (Dafne, Basal, Switzerland). Muscle volume and fat fraction were calculated using custom code (Matlab, the Mathworks, Natick, MA). Differences over time were assessed using a Multivariate Analysis of Covariance (MANCOVA) with sex and exercise group as covariates.

Results:
Muscle volume varied significantly over time for 4/6 muscles examined ($p<0.05$); after bedrest, percentage volume decreased by 8.7 +/- 5.2% to 13.1 +/- 9.8%. Fat fraction varied significantly over time for 5/6 muscles examined ($p<0.05$) with the largest change pre- to immediate post-bedrest of 14.9 +/- 7.7% in the soleus. General trends were observed of muscle volume decreasing and fat fraction increasing immediately after bedrest and recovering at subsequent timepoints. There were no significant interactions with time and exercise intervention.

Conclusion:
The present study showed that muscle volume decreases and fat fraction increases after 14 days of HDBR and recovers towards baseline levels. These results present evidence of the potential role of fat infiltration in muscle atrophy in bedrest.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

22. SEASONAL TRENDS AND RISK FACTORS IN PROSTHETIC JOINT INFECTIONS: A RETROSPECTIVE ANALYSIS

Presenter:	**Mikayla Rudniski**
USask Affiliation:	**Undergraduate student**
College:	**College of Medicine**
Collaborators:	Mars Zhao, College of Medicine
	Johannes van der Merwe, College of Medicine
	Evan Parchomchuk, College of Medicine
Supervisor:	Johannes van der Merwe, MBChB, FRCSC
	College of Medicine
Co-supervisor(s):	Mars Zhao, MD, PGY2

Background:
Periprosthetic joint infection (PJI) is a major complication of joint arthroplasty. Occurring in 1-2% of cases, PJIs contribute negatively to patient morbidity, healthcare costs, and are the leading cause of revision surgery. Prior studies on the seasonal influence have yielded mixed results, with European studies linking warmer seasons to increased PJI rates, while North American data is less conclusive.

Methods:
A single-center retrospective review was conducted on patients presenting to a tertiary centre with PJIs of the hip, knee, ankle, shoulder, and elbow from April 2012 to May 2024. Eligible cases were diagnosed using Musculoskeletal Infection Society (MSIS) and European bone and joint infection society criteria (EBJIS). 114 cases of PJI were analyzed after exclusion. Data collection included demographic, comorbidity, and surgical details such as season of surgery, comorbidities, anesthesia type, and perioperative antibiotic use.

Results:
Among 114 patients with PJIs, acute PJIs were more common in winter (28%) and summer (26%), though findings were not statistically significant. Late PJIs had higher prevalence in winter and fall (31%). Total hip arthroplasty (THA) patients were significantly more likely to experience acute PJI, whereas late PJI was significantly more common in total knee arthroplasty (TKA) patients.

Conclusion:
No significant seasonal influence on PJI incidence was observed. However, an association between surgeon variability and PJI rates was identified. Future studies with larger samples are needed to clarify the seasonal impact and further investigate individual surgical practices to optimize outcomes.

Basic Science 1

23. COMPARATIVE ANALYSIS OF THE JEJUNAL MICROBIOME IN CONVENTIONAL VS RAISED WITHOUT ANTIBIOTICS BROILER PRODUCTION SYSTEMS

Presenter: **Ashani Palkumbura**
USask Affiliation: **Graduate student**
College: **Western College of Veterinary Medicine**
Supervisor: Susantha Gomis, Western College of Veterinary Medicine

Background:
The overuse of antimicrobials in broiler chicken production has contributed to antimicrobial resistance and the occurrence of antibiotic residues in broiler meat leading the Canadian broiler industry to adopt raised without antibiotics (RWA) programs. However, reducing antimicrobial use may increase susceptibility to economically important diseases like necrotic enteritis. Understanding the microbiome differences between RWA and conventional broiler systems is crucial for evaluating their effects on bird health and productivity. This study compared the jejunal microbiome composition in both production systems.

Methods:
Six commercial broiler farms, each operating both conventional (n=6 barns) and RWA (n=6 barns) systems, were selected. Jejunal content samples were collected from broilers (n=8/barn) at 33-35 days of age and analyzed using 16S rRNA gene amplicon sequencing to assess microbial composition. Additionally, serum samples were tested for antibodies against infectious bursal disease virus (IBDV) and chicken infectious anemia virus (CAV) using ELISA

Results:
Firmicutes was the dominant bacterial genus in the jejunal microbiome of both systems, followed by Pseudomonadota. None of the barns tested positive for CAV, while IBDV was identified in 5 of 6 farms.

Conclusion:
These results indicate that while the jejunal microbiome composition is largely similar between the two systems, RWA production may introduce additional health and management challenges. Further research is necessary to develop strategies that promote bird health in RWA systems while minimizing antimicrobial use

24. CHARACTERIZATION OF CORTISOL-DEPENDENT ANTIVIRAL RESPONSE IN PRIMARY BAT CELLS

Presenter:	**Manuela Pereira**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Rita Quintela-Tizon, Western College of Veterinary Medicine
	Ansil Basheer Rahmat
	Daniel J. Becker
Supervisor:	Arinjay Banerjee, College of Veterinary Medicine

Background:
Bats are natural reservoirs for various zoonotic viruses, including coronaviruses, often without exhibiting clinical disease. The spillover of these pathogens from bats to other animals in influenced by multiple ecological and physiological factors. Physiological stress, linked to increased glucocorticoid levels, has been associated with the modulation of metabolic and immune responses. While stress is known to modulate immune responses in humans, the impact of cortisol on viral infections in bats remains poorly understood. We hypothesize that elevated cortisol levels in bats lead to increased viral replication and viral shedding, potentially contributing to spillover events.

Methods:
To investigate the role of cortisol in viral replication, we will be developing primary bat cell lines from five New World bat species. As model systems for the optimization of cortisol experiments, we used CpLung (C. perspicillata lung-derived), Efk3B (E. fuscus kidney-derived), and PaKiT03 (P. alecto kidney-derived) cells. Cells were treated with cortisol at varying concentrations before infection with vesicular stomatitis virus expressing green fluorescent protein (VSV-GFP). Viral replication was assessed through fluorescence microscopy, $TCID_{50}$ assays, and immunoblotting for viral protein expression.

Results:
Two bat primary kidney cell lines have been succesfully generated. Our preliminary results indicate that cortisol treatment elevates viral protein (M protein) levels in CpLung cells, but it does not significantly increase the production of infectious VSV. This suggests that cortisol influences viral replication at a post-transcriptional level, however, unknown mechanisms in bat cells could be preventing the increase in the amount of infectious virus produced from these cells.

Conclusion:
Further experiments are needed to investigate the influence of cortisol in viral replication and shedding in bats. Upon the development of the all 10 primary cell lines proposed, we will evaluate the impact of cortisol on the expression of innate immunity genes and on the replication of HCoV-229E. By coupling laboratory and field experiments, our research aims to determine the mechanisms underlying viral tolerance and shedding in bats, contributing to a better understanding of factors that influence viral spillover events.

25. THE X FACTOR OF REPRODUCTIVE FITNESS: NEURONAL NUCB1'S ROLE IN SEX-SPECIFIC ENERGY STORAGE

Presenter:	**Narsimha Pujari**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Natalie Turriff, College of Arts and Science
	Kamea Chevrier, College of Arts and Science
	Vanessa Browne, College of Medicine
Supervisor:	Adelaine K.W. Leung, Western College of Veterinary Medicine

Background:
Metabolic disorders such as weight gain and diabetes affect men and women differently. This sex difference in metabolic regulation is evident between males and females across all metazoans. In females, energy storage mechanisms are fine-tuned for reproductive fitness, contributing to species survival. For example, in humans, adolescent males are more prone to developing obesity and diabetes, whereas in later age groups, postmenopausal women are more affected. These physiological sex differences are regulated by numerous proteins influenced by either sex chromosomes or sex hormones. To develop effective treatment strategies, it is essential to understand the regulatory proteins and mechanisms that mediate sexually dimorphic metabolism.

Methods:
Nucleobindin-1 (NUCB1) is a satiety- and insulin-regulating protein with potential sex-biased roles in metabolism. Although sex-specific associations between NUCB1 and obesity have been reported in both humans and mouse models, its cellular source and mechanism of action remain unexplored. Using the genetically tractable Drosophila melanogaster (common fruit fly) model, we aim to investigate the sex-specific roles of NUCB1.

Results:
NUCB1 is widely expressed in the neuroendocrine system. A pan-neuronal knockdown of NUCB1 resulted in increased body fat in females, while males were unaffected. This knockdown also depleted dILP expression (Drosophila insulin-like peptides, homologs of insulin) in males but had no effect in females. However, Akh (adipokinetic hormone, homolog of glucagon) expression was reduced in knockdown females but remained unchanged in males. To determine the cellular source of this difference, further knockdowns were performed in dILP- and Akh-producing neuroendocrine cells. Enzymatic analyses revealed that Akh-producing cells are responsible for NUCB1's role in sexual dimorphism. Notably, the female-specific changes in fat storage increased their egg production.

Conclusion:
These findings suggest that NUCB1 plays a critical role in regulating fat storage in a sex-dependent manner, ultimately contributing to reproductive fitness.

26. END OF THE LINE: TARGETING TELOMERASE OVEREXPRESSION VIA SYNTHETIC DOSAGE LETHALITY

Presenter:	**Mary Lazell-Wright**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Supervisor:	Franco Vizeacoumar, College of Medicine
Co-supervisor(s):	Andrew Freywald

Background:

While individual cancers display heterogeneity and diversity, 85% of these cancers share a common mechanism that allows them to maintain immortality; the hTERT pathway. Although directly targeting hTERT has been shown to be ineffective in the past, we hypothesize that the indirect targeting of hTERT via a synthetic dosage lethal (SDL) approach will allow for the selective killing of these high hTERT cancers. The hTERT pathway, usually only active in embryonic stem cells but reactivated in these cancers, allows for the transcription of unique enzymes, proteins, and RNA components that will continuously maintain telomere length, effectively immortalizing the cell. The SDL approach is a method in which the genetic dependencies on proteins of an overexpressed component are elucidated, and then inhibited. Due to the fact that only those cells with the overexpressed component (in this case, hTERT) will have a genetic dependency on the protein, regular cells with normal hTERT expression levels are predicted to remain minimally affected by the process. We hypothesize that four different nucleolus associated proteins (NAPs), will exhibit SDL interactions with these high hTERT cell lines, allowing for the selective killing of these cancers.

Methods:

The hypothesis was tested via in vitro colony formations and inhibitory drug assays.

Results:

Out of the 4 NAPs tested, only one was shown to have high hTERT selective SDL killing in the colony formations. The inhibitory drug data is still a work in progress.

Conclusion:

In conclusion, one of the four NAPs exhibited SDL killing in high hTERT cell lines. Further work is being done is establish a mechanistic link between the inhibition of the gene, and the death of the high hTERT cell lines.

27. MICROBUBBLE-ASSISTED DRUG DELIVERY FOR GLIOBLASTOMA

Presenter:	**Isabella Zittlau**
USask Affiliation:	**Graduate student**
College:	**College of Pharmacy and Nutrition**
Supervisor:	Ildiko Badea, College of Pharmacy and Nutrition
Co-supervisor(s):	Steven Machtaler

Background:

Microbubbles (MBs) are colloidal particles composed of a gas core surrounded by a protective shell, typically measuring between 1 and 10 µm in diameter. Widely utilized as contrast agents in medical imaging, MBs, when combined with focused ultrasound, cross physiological barriers, allowing the delivery of drugs to a specific area. This property makes them a promising strategy for treating brain tumors, including glioblastoma (GBM), the most prevalent and aggressive brain tumor in adults. A major limitation in GBM therapy is the blood-brain barrier (BBB), which tightly regulates substance passage into the brain. This study focuses on synthesizing MBs combined with ionizable gemini lipids (GL), a class of molecules presenting unique structures and properties compared to conventional surfactants. By optimizing this formulation, the goal is to enhance the transport of the chemotherapeutic agent temozolomide across the BBB into GBM cells while minimizing toxicity.

Methods:

MBs were formulated with various GLs and molar ratios. Size, bubble concentration, and surface properties were assessed.

Results:

The results revealed that the presence of GL in the formulation favored the formation of MBs, increasing the number of bubbles per mL and conferring a positive surface charge. In addition, a reduction in size from 1.2 to 0.9 µm was observed. Among the ionizable lipids, GL 16 yielded formulations with the highest concentration of bubbles, as well as favoring an increase of the positive surface charge of the formulations tested.

Conclusion:

MBs with optimal physicochemical properties were formulated. Since MBs enable the release of the drug through the BBB more easily, a lower drug concentration is necessary to be administered, thus minimizing drug adverse effects and circumventing drug resistance caused by high doses of drugs.

28. LEVERAGING SYNCHROTRON TECHNOLOGY TO ENHANCE DRUG DELIVERY SYSTEMS

Presenter:	**Jonathan Rekve**
USask Affiliation:	**Graduate student**
College:	**College of Pharmacy and Nutrition**
Supervisor:	Ildiko Badea, PhD
	College of Pharmacy and Nutrition
Co-supervisor(s):	Lee Wilson, PhD

Background:
Lipid nanoparticles (LNPs) are an advanced platform for nucleic acid delivery, offering protection and efficient cellular uptake. The incorporation of excipients such as glucose and sucrose can influence LNP structural integrity, stability, and nucleic acid release. This study explores the impact of lipid composition and excipients on LNP formulation and performance.

Methods:
LNPs were formulated with DNA, saRNA, or mRNA using Gemini lipids, incorporating either 5% glucose or 9.25% sucrose. Small-angle X-ray scattering (SAXS) was employed to analyze structural organization, lipid packing, and nanoparticle stability. The effects of varying lipid molar ratios were assessed to determine their influence on encapsulation efficiency and nucleic acid release kinetics.

Results:
SAXS analysis revealed that glucose-based formulations exhibited higher structural ordering and enhanced stability compared to sucrose-based LNPs. Increased peak intensities and hexagonal nanostructure formation in glucose formulations suggest improved nucleic acid loading and sustained-release potential.

Conclusion:
By optimizing LNP structural organization and stability, this study contributes to the development of more effective nucleic acid delivery systems. The findings have implications for improving therapeutic efficacy, patient compliance, and advancing targeted treatments for neurodegenerative diseases.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

29. INVESTIGATING SOX9 AND RUNX2 ACTIVITIES DURING OSTEOBLAST EVOLUTION

Presenter:	**Marziyeh Hassanzadeh**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Supervisor:	Brian F. Eames, College of Medicine

Background:

Changes in transcription factors and/or their binding sites cause evolutionary changes in gene expression. Osteoblasts of earlier-diverged vertebrates express more genes typical of chondrocytes than osteoblasts of later-diverged vertebrates, suggesting that the chondrocyte transcription factor Sox9 used to work more closely together with the osteoblast transcription factor Runx2 during early skeletal cell evolution. We hypothesized that changes in Sox9 and Runx2 caused changes in osteoblast gene expression during vertebrate evolution.

Methods:

To test the hypothesis, mouse pre-osteoblastic cells (MC3T3-E1.4) were transduced with recombinant FLAG-tagged Runx2 or Sox9 from either gar or mouse. Resultant gene expression and genomic binding sites were analyzed using RT-qPCR and ChIP-qPCR, respectively, on genes downstream of Sox9 and Runx2.

Results:

Transduction was confirmed by anti-FLAG western blotting and immunofluorescence. Overexpression of either mouse or gar Sox9 in osteoblasts induced the chondrocyte gene Col2a1. On the other hand, mouse Runx2 induced, but gar Runx2 did not, the osteoblast gene Sp7. Interestingly, mouse Sox9 reduced, whereas gar Sox9 increased, expression of mouse Runx2. ChIP-qPCR revealed that gar Sox9 was enriched on a mouse Col2a1 binding site, and mouse Runx2 was enriched on Col2a1 and Col1a2.

Conclusion:

These data begin to support the hypothesis that changes to Sox9 and Runx2 caused evolutionary changes in osteoblast gene expression. A simple explanation for cartilage gene expression in gar osteoblasts is Sox9 expression. However, induction of mouse Runx2 by gar Sox9 suggests that in earlier-diverged vertebrates, Sox9 and Runx2 used to work more synergistically, with Sox9 regulating both cartilage and bone genes. These data also support the evolutionary theory that osteoblasts evolved from chondrocytes. Subsequent compartmentalization of Sox9 and Runx2 transcriptional networks, seen in mouse, may have occurred in response to environmental factors associated with the transition from water to land.

30. TESTING ALPHAHERPESVIRUS TRANSCRIPTION REGULATOR BINDING TO CHROMATIN IN VITRO

Presenter:	**Laura Kellerer**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Kristen L Conn, Western College of Veterinary Medicine

Background:

During lytic infection alphaherpesvirus gene expression is temporally regulated such that immediate early (IE) genes are expressed first, then early (E), then late (L) genes. Alphaherpesviruses have essential transcription regulators. The IE proteins infected cell polypeptide 4 (ICP4) of Herpes Simplex Virus 1 (HSV1) or immediate early 1 (IE1) of equid alphaherpesvirus 1 (EHV1), required for productive infection and progeny virion production. Although critical for infection, we do not fully understand how they function. They regulate transcription. ICP4 or IE1 sequence-specifically bind IE promoters to repress transcription, whereas they bind non-sequence-specifically to E and L promoters to activate transcription. ICP4 destabilizes chromatin. This activity is consistent with the highly unstable lytic chromatin observed during HSV1 infection needed for progeny virion production. As IE1 is the only IE protein of EHV1 and EHV1 infection destabilizes chromatin IE1 may also destabilize chromatin. ICP4 or IE1 could destabilize viral chromatin by recruiting chromatin remodelers, by binding to DNA to block chromatin assembly or by binding to chromatin to promote its disassembly.

Methods:

As a first step to test a direct interaction between ICP4 or IE1 and alphaherpesvirus chromatin, we will evaluate whether ICP4 or IE1 bind viral chromatin in vitro. To this end, chromatin electromobility shift assays will be used. Representative HSV1 IE, E, or L promoters will be assembled into chromatin fragments with purified recombinant histone octamers to test direct ICP4 or IE1 chromatin binding. We will also test ICP4 or IE1 binding to chromatin fragments assembled with sequences without promoter elements and non-chromatinized sequences.

Results:

I am establishing conditions for the isolation of recombinant ICP4 from mammalian cells using an affinity resin and affinity-tagging IE1 through restriction enzyme cloning.

Conclusion:

Whether or not ICP4 or IE1 directly bind chromatin, this information will support the design of experiments to characterize their interaction with alphaherpesvirus chromatin.

Basic Science 2

31. THE IMPACT(S) OF HASKAP BERRY PHENOLIC COMPOUNDS ON HUMAN FIBROBLASTS: A STRUCTURAL INVESTIGATION INTO SYNERGY AND SIRTUIN 1

Presenter:	**Morgan Fleming**
USask Affiliation:	**Graduate student**
College:	**College of Agriculture and Bioresources**
Supervisor:	Christopher Eskiw, College of Agriculture and Bioresources
Co-supervisor(s):	Nicholas Low

Background:
Dietary intake is undeniably connected to health, although the depth and complexity of this connection is not well defined. A class of plant-produced chemical compounds hypothesized to contribute to this are phenolics which are recognized for their antioxidant activity. However, it is unclear if phenolics impact cellular functions beyond antioxidant activity. Recent research in our laboratory on the phenolic-rich, Saskatchewan bred, haskap berry indicated that complex phenolic fractions impact human fibroblast growth behaviour via mechanism(s) that are dependent on the deacetylase Sirtuin 1 (SIRT1). As these treatments are complex phenolic mixtures, it was unclear if individual phenolic structures were responsible for these impacts, or if phenolic combinations function synergistically.

Methods:
To address this, four structurally distinct phenolics from haskaps were selected and supplemented, individually or in combination, to male and female normal human fibroblasts. Initial investigations determining if the phenolics impact cell growth were done employing the population doubling time and cell viability assays. The phenolic treatment impacts on Sirtuin 1 transcript and protein abundance were determined by RT-qPCR and Western blot, respectively. Sirtuin 1 sub-cellular localization was investigated with Immunofluorescence and Sirtuin 1 activity levels with a Sirtuin 1 activity assay.

Results:
The phenolics demonstrated: (1) structure-dependent abilities to decrease cell proliferation and no cytotoxicity; (2) no observable impact on SIRT1 transcript abundance by RT-qPCR; (3) structure-dependent impacts on decreasing SIRT1 protein abundance by Western blot; (4) no observable impact on SIRT1 nuclear localization; and (5) structure and cell-line dependent impacts on SIRT1 activity.

Conclusion:
The phenolics that contain a catechol structure outperformed those without, indicating potential significance of this structural feature. Results also indicate potential sex and/or individual differences with respect to responses to phenolics. Finally, we observed that individual and simple phenolic

combination treatments were not as impactful as the complex phenolic extracts. This research highlights the potential significance of consuming whole foods and understanding individual genetic variance to achieve optimal levels of benefits from phenolics.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

32. ADVANCING THE UTILITY OF MICROTISSUES AS A MODEL OF THE TUMOUR MICROENVIRONMENT

Presenter:	**Breanne Bevelander**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Supervisor:	Dean Chamberlain, College of Medicine

Background:
Ovarian cancers are some of the most prevalent and deadly cancers among those assigned female at birth. In our research, we have developed a 3D model that recapitulates spatial complexities of this cancer, allowing us to gain a deeper understanding into the chemotherapeutic resistance, cell migration, and tumour microenvironmental architecture that contribute to this cancer's lethality. Our model (termed "microtissues") is unique in that it can be readapted to include other extracellular matrix (ECM) and cellular components as desired by the researcher and has proven successful for various cell types, cancerous and not. The product is a free-floating cylindrical microtissue that can better recapitulate the 3D tumour microenvironment than other models while being easy to maintain in lab. My primary goal is to expand the utility of these microtissues by characterizing them, establishing them as an in vivo model, and working to cryopreserve them.

Methods:
For my in vivo stream, I aimed to see how our model compares to others used in vivo, particularly injecting cells using either PBS or within a popular hydrogel. To improve the sustainability of our model and to make it easier to ship to collaborators, I have also been working to cryopreserve our model. Three days after generating the microtissues, I cryopreserve them. Once thawed, I subject them to viability and proliferation assays.

Results:
While more replicates are needed to draw conclusions for our in vivo work, it appears that cells injected into mice within microtissues develop tumours faster than other methods. With respect to cryopreservation trials, our microtissues survive cryopreservation, and appear to regain proliferative trajectories within 2 days of thaw.

Conclusion:
In summary, our innovative 3D microtissue model represents a significant advancement in modeling the tumour microenvironment as it offers spatial complexities and opportunities for cell migration and reorganization that remains absent in other models.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

33. MOLECULAR DIAGNOSTIC METHODS FOR BRUCELLA ABORTUS DETECTION IN WOOD BISON

Presenter:	**Kira Mudrey**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Muhammad Anzar, Western College of Veterinary Medicine
Supervisor:	Tim Dumonceaux, PhD Research Scientist Agriculture and Agri-Food Canada Adjunct professor, College of Veterinary Medicine

Background:
Wood bison, a species at risk globally, are threatened by a high prevalence of bovine brucellosis, a zoonotic bacterial infection caused by Brucella abortus that colonizes the reproductive tract and results in infertility and abortions. An estimated 25-37% of the Wood Buffalo National Park population, which is the largest and most genetically diverse in the world, are infected with bovine brucellosis. To support wood bison conservation efforts, B. abortus infection must be controlled and prevented from spreading to healthy herds. However, current diagnostic methods are time-consuming, require specialized equipment, or lack specificity. Newer molecular diagnostic methods present a promising alternative to traditional brucellosis diagnostics.

Methods:
We designed portable quantitative polymerase chain reaction (qPCR) and loop-mediated isothermal amplification (LAMP) assays and compared their performance characteristics with previously published LAMP and recombinase polymerase amplification (RPA) assays targeting Brucella species. We also developed a simplified DNA extraction protocol for bison semen and have begun assessing the performance of our DNA extraction and amplification methods outside of a traditional laboratory.

Results:
Our results indicate that all four assays can be performed with limited equipment, show good analytical specificity, and demonstrate diagnostic sensitivity greater than 90% and specificity greater than 80% compared to gold-standard culture results. qPCR showed the best analytical sensitivity (lowest limit of detection), followed by the cpn60 LAMP, the RPA assay, and then the bcsp31 LAMP.

Conclusion:
However, the RPA assay, when converted to a lateral flow format, is the fastest and most suitable for point-of-care applications, while still maintaining a low limit of detection. Further, using a short proteinase K treatment and syringe-based DNA extraction, we were able to extract amplifiable DNA in under ten minutes. Our initial field trials indicate that this method can feasibly be applied at the point-of-care to rapidly detect and help prevent the transmission of Brucella abortus.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

34. THE UNDEFINED ROLE OF HISTAMINE IN ACINETOBACTER BAUMANNII PHYSIOLOGY

Presenter:	**Emily Hein**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Tori Dauvin, College of Medicine
Supervisor:	Jessica R. Sheldon, College of Medicine

Background:

Acinetobacter baumannii is an opportunistic pathogen that causes a variety of infections such as those of the urinary tract, wounds, and burns, to more severe illnesses like sepsis and ventilator-associated pneumonia. A. baumannii was once considered relatively uncommon and predominantly an environmental microorganism but has quickly risen in prevalence in both community and hospital environments. While the reasons for this are not fully understood and currently under investigation in our lab, it is believed that part of this increase in incidence is due to its resistance to last-resort antibiotics which makes it difficult to eradicate. Further, like other Gram-negative bacteria, A. baumannii can produce histamine and I believe production of this chemical contributes to its pathogenicity and spread. Not only may A. baumannii be using histamine as a signaling molecule to sense changes in its environment, I also hypothesize that it metabolizes histamine as a nutrient and uses it in the acquisition of iron.

Methods:

I am currently working towards elucidating the role of histamine in host-pathogen interactions. My research includes identifying mechanisms of histamine sensing, response, and transport. In the case of the latter, the means of histamine uptake and efflux in bacteria is unknown and may represent potential therapeutic targets. More broadly, advancing our knowledge in understanding the pathophysiology of A. baumannii is essential to combating its antimicrobial resistance. To date, I have shown through bacterial growth curves and killing assays that high concentrations of histamine are inhibitory to the growth of A. baumannii, while low concentrations may support growth under iron restriction and in the absence of endogenous production (Figure 1). This is relevant as histamine is a key precursor to production of the iron-binding molecule acinetobactin, which is required for growth of the bacteria under nutrient limited conditions and in the host (Sheldon and Skaar 2020). Further, this indicates that A. baumannii is able to detect histamine. To identify the possible mechanisms that A. baumannii is using to sense and respond to histamine, RNA sequencing (RNAseq) was performed. The pathogen was exposed to two different histamine concentrations, 2 mM which is known to induce chemotaxis and virulence gene expression in some organisms, and 20 mM which has potential to inhibit these activities but has non-lethal impacts overall. A. baumannii was exposed to these concentrations of histamine for 15 minutes to evaluate transcriptional response to the biogenic amine. The extracted RNA was sent to SeqCoast Genomics for sequencing and determination of differentially expressed genes in the presence versus absence of histamine.

Results:

Our data shows that A. baumannii is indeed transcriptionally responsive to histamine, and that genes with differential expression when exposed to the molecule are clustered within loci putatively annotated to be involved in iron acquisition, drug efflux, and sulfate metabolism (Figure 2 and Table

1) Based on this RNAseq data, we have disrupted differentially expressed siderophore biosynthetic and regulatory genes, and as further analysis is performed, we plan to select an additional 3-5 targets for mutagenesis using an established recombineering technique that our lab has extensive experience with. I will perform genotype-phenotype analyses using mutants generated in genes showing significant expression changes in histamine by characterizing growth of these strains with and without histamine and under various conditions of nutrient limitation. Quantitative PCR (qPCR) was performed in the putative regulatory mutant to determine its involvement both in the response to histamine and control of siderophore biosynthesis. Further, I will screen for resistant mutants by plating our existing A. baumannii transposon mutant library on different histamine concentrations and identifying isolates that exhibit growth. Whole genome sequencing of resistant isolates will be performed to identify possible mutations that help to promote tolerance to histamine toxicity.

Conclusion:

Following our in vitro characterization, I will focus on defining the role of histamine responsive genes in A. baumannii infection. The survival and dissemination of these A. baumannii mutants will be assessed in vivo using an established pneumonia model for the pathogen. This model is preferred as histamine is the most prevalent in the lungs during infection. Bacterial fitness in this model will be determined by assessing the bacterial counts of derived mutants versus wild type A. baumannii in vital organs including the kidney, heart, liver, spleen, and lungs, as well as the blood. The overall accumulation of histamine in mice infected with wild type A. baumannii and its isogenic mutants, as well as uninfected control mice will be quantified by ELISA, and the in vivo transcriptional response assessed via NanoString technology (Figure 3). Together these results will help elucidate the role of histamine and histamine responsive genes at the host-pathogen interface. Overall, this project has already revealed responsiveness of A. baumannii to histamine, possible mechanisms of response and detoxification, and should provide significant insight not only into histamine metabolism in this important human pathogen, but also a better understanding of its basic biology. Together these results will help identify the means A. baumannii uses to survive and proliferate in the host and thus potential therapeutic targets.

Self-declaration of research alignment with additional themes (optional):

Interdisciplinary/Interprofessional Collaboration

35. CELLULAR STRESSORS ASSOCIATED WITH MULTIPLE SCLEROSIS TRIGGER RNA-BINDING PROTEIN MISLOCALIZATION IN PRIMARY MOUSE EMBRYONIC NEURONS

Presenter:	**Jay Gabriel Larga**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Supervisor:	Michael C. Levin M.D., FRCPC, FANA, FAAN College of Medicine

Background:
Multiple sclerosis (MS) is a neuroinflammatory and demyelinating disease characterized by chronic neurodegeneration. Dysfunction of the RNA-binding protein (RBP) heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) is associated with neurodegeneration in MS and MS animal models. A key pathological feature is the mislocalization of hnRNP A1 from its homeostatic nuclear location to the cytoplasm, disrupting RNA processing and neuronal homeostasis. Notably, cellular stressors are implicated in triggering RBP mislocalization in neurodegenerative diseases. Thus, we hypothesized that MS-associated stressors, including excitotoxic, oxidative, and endoplasmic reticulum (ER) stress will induce hnRNP A1 mislocalization and neurodegeneration.

Methods:
Primary mouse embryonic neurons were treated with glutamate, SIN-1, and Thapsigargin at varying concentrations to induce excitotoxic, oxidative, and ER stress, respectively. Following treatment, hnRNP A1 localization patterns were assessed using immunocytochemistry and quantitative fluorescent imaging to measure cytoplasmic/nuclear distribution and neurite morphology at different stressor paradigms. Cellular viability was also assessed using LDH and XTT assays.

Results:
Glutamate significantly induced hnRNP A1 mislocalization in a dose- (0.1–100 µM, $p < 0.0001$) and time- (10, 30, 60 min.; $p < 0.0001$) dependent manner, reaching 40.8 ± 3.08% mislocalization at the highest concentration and longest treatment time. Assays suggest that while glutamate did not significantly impact cell viability, SIN-1 and thapsigargin both induced mislocalization and reduced viability, suggesting cell death may contribute to the mislocalization observed.

Conclusion:
MS-associated stressors drive hnRNP A1 mislocalization, a process we previously linked with neurodegeneration. Ongoing analysis of neuronal phenotypes will further elucidate the impact of these stressors on MS neurodegeneration.

36. THE DUAL ROLE OF THE EPHB4 RECEPTOR IN REGULATING INVASIVENESS AND TUMOUR INITIATION IN CANINE AND HUMAN OSTEOSARCOMA

Presenter:	**Jessica Sharpe**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Frederick Vizeacoumar, College of Medicine
	Behzad Toosi, Western College of Veterinary Medicine
Supervisor:	Behzad Toosi, Western College of Veterinary Medicine

Background:

Osteosarcoma is an aggressive bone cancer with a high rate of metastasis and poor prognosis. Advances in treatment have been limited, highlighting the need for more effective therapeutic approaches. Recent evidence suggests that the EphB4 receptor regulates the invasion and metastasis of various human malignancies. However, the role of EphB4 in human and canine osteosarcoma has been poorly evaluated. Taking a comparative approach, we investigate the role of the EphB4 receptor in promoting osteosarcoma.

Methods:

EphB4 expression was evaluated by western blotting in multiple canine and human osteosarcoma cell lines and compared to normal osteoblasts. EphB4 expression was silenced using specific shRNAs, creating stable cell lines. Cellular invasion was assessed using transwell assays and propagation of tumour-initiating cells was assessed using the tumoursphere formation assay and Ki-67 proliferation marker. Tumour initiation was investigated using a xenograft model of human osteosarcoma. RNA sequencing of two human osteosarcoma non-silenced and EphB4-silenced cell lines was conducted to examine molecular pathways, followed by western blotting to assess pathway activation.

Results:

The EphB4 receptor was upregulated in both canine and human osteosarcoma cells compared to normal osteoblasts. EphB4 silencing reduced osteosarcoma cell invasion, yet enhanced tumoursphere expansion, and increased tumour initiation in mice. RNA sequencing revealed that molecular pathways involved in cellular invasion and tumour initiation were affected following EphB4 silencing. Western blotting of proteins within the relevant signaling pathways showed increased activating phosphorylation of Erk1/2, p90rsk, and p38 MAPK in the EphB4-silenced tumoursphere cells compared to the non-silenced controls, suggesting that these pathways regulate the growth and proliferation of tumour-initiating cells.

Conclusion:

The EphB4 receptor is overexpressed in both canine and human osteosarcoma, regulating critical aspects of tumour progression and invasive in both a tumour-promoting and tumour-suppressive manner. The consistent findings across species underscore the advantages of employing a comparative oncology strategy.

Self-declaration of research alignment with additional themes (optional):

Interdisciplinary/Interprofessional Collaboration

37. LIGAND BINDING PROPERTIES OF SUBSTRATE BINDING PROTEINS OF A MALTOSE UPTAKE SYSTEM IN GARDNERELLA SWIDSINSKII

Presenter:	**Agnes Truc Nguyen**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Janet E. Hill, PhD
	Western College of Veterinary Medicine

Background:
The MusEFGKI transporter system for uptake of glycogen breakdown products like maltose and malto-oligosaccharides has been observed in Gardnerella species from the human vaginal microbiome. This transport system includes substrate binding proteins (SBPs) that facilitate the uptake by binding to specific ligands. Unlike other Gardnerella species with only one MusE SBP, G. swidsinskii encodes two MusE SBPs. One (MusE1346) phylogenetically clusters with orthologs in other Gardnerella while the other (MusE1345) forms a separate cluster (~60% amino acid sequence identity). We hypothesized that these MusE SBPs differ in ligand-binding properties providing G. swidsinskii with a competitive advantage in accessing glycogen breakdown products. Our objective was to determine the specificity and affinity of G. swidsinskii MusE SBPs for maltose and malto-oligosaccharides.

Methods:
Predicted structures of MusE1345 and MusE1346 were visualized. Plasmids containing codon-optimized sequences for the SBPs fused with a His6 tag and/or a GST tag were constructed for protein expression in E. coli. Protein secondary structure and conformation were analyzed with circular dichroism (CD) and size exclusion chromatography with multi-angle light scattering (SEC-MALS). Affinities of purified SBPs for ligands were measured using isothermal titration calorimetry.

Results:
Predicted structures showed distinct N and C domains with a ligand-binding cleft. MusE1345 and MusE1346 were monomeric and comprised mainly α-helices (CD and SEC-MALS). Both SBPs exhibited high affinity (K_d 10^{-6} – 10^{-7} M) for maltose, maltotriose, and maltotetraose, and relatively weak affinity (K_d 10^{-3} – 10^{-4} M) for longer carbohydrates.

Conclusion:
G. swidsinskii encodes two MusE SBPs with similar affinities for maltose and malto-oligosaccharides under the same in vitro conditions. It remains a possibility that having two MusE genes confers an advantage to G. swidsinskii by producing more SBP relative to other Gardnerella species. Future studies co-culturing Gardnerella species and quantifying expression levels of MusE SBP genes will shed more light on the importance of these proteins.

38. DEEP DIVES INTO DENTAL CRYPTS: MOLECULAR AND MORPHOLOGICAL CONSERVATION OF THE PRIMATE TOOTH-BONE INTERFACE

Presenter:	**Amalya Babayan**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	A.J. Leece, PhD
	Tim D. Smith, PhD
Supervisor:	Julia Boughner, PhD
	College of Medicine

Background:
A key to understanding the evolutionary and developmental (evo-devo) processes that form the human dentition is to study the development of teeth and the surrounding jawbone (tooth-bone interface, or TBI) in non-human primates and human fossil ancestors. This study aimed to explore the developmental anatomy of the primate TBI through a comparative, qualitative approach integrating fossil data and molecular biology.

Methods:
Two methodologies were used. First, using CT-scanned (22–59 µm resolution) fossilized jaw fragments from n=3 Homo sp. (1.9–0.2 mya) and n=6 Paranthropus robustus (2.27–0.87 mya), we created 3D models of bony crypts and their encased teeth, scored tooth development stage, and described crypt form and position. Second, using immunohistochemistry (IHC) on sectioned, paraffin-embedded, slide-mounted jaws of perinatal Alouatta seniculus, Aotus nancymaae, Callithrix jacchus, Cebuella pygmaea, Papio anubis, and Saguinus oedipus (n=1 per species), we defined expression of bone (re)modeling pathway proteins RANK, RANKL, and OPG in tooth organs and follicles, and perifollicular tissues including the TBI.

Results:
For all teeth, relative to tooth size, corresponding crypts were more spacious and spherical before crown completion. As roots developed, crypt space shrank, and crypt shape traced tooth shape and tilt more closely. Regardless of tooth type, adjacent tooth crypts were interconnected. Gubernacular canals persisted throughout formation. Across primates and tooth types, RANKL, RANK and OPG were expressed in inner and outer enamel epithelium, follicle cells, osteoblasts, and osteoclasts.

Conclusion:
Our results suggest that the processes by which primate teeth form and fit within the jawbone are not specific to tooth class, jaw type, or species. Instead, crypt formation, migration, and TBI-related proteins are conserved across primates, offering new insight into craniodental integration and shared developmental processes.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

Basic Science 3

39. RMT1 LOSS SELECTIVELY ELIMINATES TELOMERASE OVEREXPRESSING CELLS THROUGH GENOME DESTABILIZATION

Presenter:	**Jared Price**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Vincent Maranda, Yue Zhang, Frederick Vizeacoumar
Supervisor:	Franco Vizeacoumar, PhD College of Medicine
Co-supervisor(s):	Andrew Freywald, PhD

Background:
The holoenzyme, telomerase, is frequently overexpressed in most cancer types and is generally associated with tumor survival. As a highly overexpressed biomarker, it implicates itself as a potential therapeutic target. Despite this potential, its direct inhibition has yet to produce a clinically relevant therapy against cancer. Here, we propose a novel strategy called synthetic dosage lethality (SDL) to overcome the deficiencies of previous efforts and apply it to models of telomerase over-expressing cancers. The identification of SDL interactions is of therapeutic interest because if a particular gene exhibits SDL with a tumor-driving molecular alteration, then targeting this SDL gene will cause lethality selectively in cancer cells harboring this alteration.

Methods:
The Vizeacoumar lab has utilized a pooled lentiviral CRISPR and shRNA screen against the entirety of the human genome to identify gene knockouts which was cross-referenced with cell line specific gene essentiality data from DepMap to create a short list of potential targets. These targets were then stratified according to canonical function, drugability, loss-of-fitness specificity, and essentiality. Here, I validate our top candidate gene, RMT1, as a telomerase-overexpression SDL partner. RMT1 loss was investigated along a TERT overexpression to underexpression axis using RNA and protein analyses and an array of microscopic techniques.

Results:
We identified key novel phenotypes dependent on RMT1 expression in telomerase positive and negative cell lines which likely contribute to the telomerase-specific loss of fitness. These include large-scale nuclear architecture alterations at the molecular and macro-structural level. We also investigated the role of the lncRNA TERRA in telomere homeostasis.

Conclusion:
This work is exceptionally exciting as RMT1 may have tumor-agnostic applicability due to the near-ubiquitous nature of telomerase expression in malignant solid tissue and key absence in normal somatic tissue. This could be a pivotal target in telomerase-expressing cancers.

40. THE ANTIVIRAL BREADTH OF BAT TRIM5A-LIKE RESTRICTION FACTORS

Presenter:	**Sauhard Shrivastava**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Cody Warren
	Nolwenn Jouvenet
	Linda Chelico, College Medicine
Supervisor:	Arinjay Banerjee, Western College of Veterinary Medicine

Background:
Bats are being recognized as reservoir hosts of several viruses yet show minimal or no negative effects of viral infections. This study investigates the mechanisms behind the tolerance of bat cells to viruses by examining TRIM5α-like proteins in two divergent bat species- Eptesicus fuscus and Pteropus alecto.

Methods:
We identified TRIM5α-like genes in the two bat species and compared with human TRIM5α gene expression levels and subcellular localization in respective cells. We tested the interactions of bat TRIM5α-like proteins with the capsids of various retroviruses -Hervey pteropid gammaretrovirus (HPG) -a Koala-Retrovirus (KoRV) related retrovirus, Human Immunodeficiency Virus (HIV), Simian Immunodeficiency Virus (SIV), Feline Immunodeficiency Virus (FIV), B- and N-tropic Murine Leukemia Virus (B-MLV and N-MLV). We also assessed the antiviral potency of bat TRIM5α-like proteins against flaviviruses -Tick-borne encephalitis virus (TBEV), Yellow fever virus (YFV), and Rio bravo virus (RBV).

Results:
The expression of bat TRIM5α-like gene is inducible by species-specific interferon-β with cytoplasmic localization like human TRIM5α, indicating that endogenous bat TRIM5α-like proteins function as interferon-stimulated genes (ISGs) in bat cells. Bat TRIM5α-like proteins restricted SIV, FIV, HPG and N-MLV pseudotyped viruses but did not inhibit the replication of TBEV, YFV, and RBV wildtype viruses.

Conclusion:
The study compares the efficacy of human TRIM5α with two bat-derived TRIM5α-like proteins against a panel of retroviral capsids and flaviviruses which enables the assessment of the breadth and specificity of the antiviral activities mediated by these proteins to seek insights into their evolutionary adaptations and capacity to block cross-species transmission. Significance - This study explores molecular factors that contribute to the occurrence of KoRV-related exogenous retroviruses in bat populations in Australia and provides insights into the role bats could play as reservoirs for KoRV-related gammaretroviruses during the ongoing KoRV epidemic in the Australian Koala population.

41. GENOME-WIDE ANALYSIS OF TRANSCRIPTIONAL NOISE IN MYCOBACTERIUM TUBERCULOSIS

Presenter:	**Nandini Chhabra**
USask Affiliation:	**Graduate student**
College:	**School of Public Health**
Supervisor:	Neeraj Dhar
	Adjunct Professor, School of Public Health

Background:

Tuberculosis (TB), caused by Mycobacterium tuberculosis (Mtb), is a leading cause of human mortality, responsible for 1.3 million deaths annually. Infection with Mtb results in a range of clinical outcomes, from latent infection to active disease. Even within an infected individual, Mtb exhibits remarkable heterogeneity due to the complex microenvironments it encounters, allowing it to adopt different physiological states. Recent studies have shown that Mtb uses phenotypic heterogeneity as a bet-hedging strategy to survive immune and antibiotic stress. Phenotypic heterogeneity refers to non-genetic variations within a clonal population, enabling microorganisms to thrive in fluctuating environments. This heterogeneity is often due to fluctuations in gene expression, known as "noise," which can result from promoter transitions between active and inactive states, leading to bursts of transcription. These fluctuations cause significant variations in protein levels among individual cells, promoting phenotypic diversity. Our hypothesis posits that gene expression noise in Mtb mediates antibiotic persistence, latency-reactivation, and cell-fate decisions.

Methods:

To globally analyze phenotypic noise and identify pathways driving heterogeneity in Mtb, we constructed a genome-scale promoter library. The experimental approach is summarized as: 1. Isolation and digestion of Mtb genomic DNA to generate promoter library fragments. 2. Construction of promoter library plasmid. 3. Cloning of promoter library fragments and electroporation of library into Mtb. 4. Screening of promoter library using flow cytometry and microscopy.

Results:

So far, I have isolated genomic DNA from Mtb and have prepared the DNA fragments of size 100-1500bp using Sau3AI for the library. I have successfully constructed a probe-based vector to clone the promoter fragments towards generating the library. I have cloned the and transformed promoter fragments clones into Mtb. till now I have assembled ~9000 strains and validated the library through fluorescence plate reader assays. I have analyzed ~5000 strains with flow cytometry and ~1700 strains through microscopy.

Conclusion:

The preliminary results confirm that there are genetic pathways that are noisier than the other pathways.

42. THE ROLE OF PITX2C IN METABOLIC DYSREGULATION AND REDOX IMBALANCE IN A ZEBRAFISH MODEL OF CARDIAC ARRHYTHMIA

Presenter:	**Mitra Sabetghadam**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Eli Wiens
	Ramaswami Sammynaiken
Supervisor:	Michelle Collins, College of Medicine

Background:

Genetics plays a pivotal risk factor for atrial fibrillation (AF), the most prevalent cardiac rhythm disorder. A non-coding region on chromosome 4q25, upstream of the gene encoding the transcription factor PITX2C, is strongly associated with AF. Recent data has suggested that PITX2C regulates cardiomyocyte metabolism and the antioxidant response to stress. However, how the absence of PITX2C leads to metabolic changes and the specific downstream metabolic alterations remain unclear.

Methods:

Transcript levels of selected genes encoding metabolic regulators were measured in a Pitx2c-deficient zebrafish model, which displays cardiac phenotypes similar to those seen in AF patients. RNA-seq analysis will be conducted to broadly assess transcript levels, focusing on identifying potential changes in metabolic pathways. Lipid accumulation in pitx2c-/- hearts was examined using Oil Red O staining in adult fish, with additional staining being performed on 3-month-old young adults to determine whether lipid accumulation is a secondary phenotype or directly associated with Pitx2c deficiency. Electron paramagnetic resonance (EPR) spectroscopy was used to evaluate superoxide (O2.-) levels in zebrafish hearts. To investigate the role of oxidative stress, we are modulating the expression of endogenous antioxidant genes, sod1 and sod2, which are potential targets of pitx2c, to assess whether their expression can mitigate cardiac arrhythmias.

Results:

Transcriptomic analysis during later cardiac maturation revealed a significant up-regulation of gapdh, associated with glycolysis, and a down-regulation of acsl1b and cpt1b, implicated in lipid metabolism. Notably, these changes were observed specifically in atrial tissue, not in the ventricles. Oil Red O staining indicated lipid accumulation in adult pitx2c-/- hearts, consistent with transcriptomic findings and alterations in fatty acid metabolism. EPR spectroscopy revealed significantly elevated O2.- levels in both adult and one-month-old juvenile pitx2c+/- and pitx2c-/- zebrafish hearts, suggesting a redox imbalance that may contribute to early metabolic dysfunction.

Conclusion:

In conclusion, this investigation suggests that PITX2C deficiency leads to metabolic and redox imbalances, contributing to cardiac dysfunction in AF.

43. IDENTIFICATION OF HIGHLY EXPRESSED GENES IN GARDNERELLA VAGINALIS ATCC 49145

Presenter:	**Divanthika Kularatne**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Janet E. Hill, PhD
	Western College of Veterinary Medicine

Background:
Gardnerella species are strongly associated with the gynecological disorder known as bacterial vaginosis, however, despite their clinical significance, the biology of these organisms is poorly understood. One of the major barriers to mechanistic research in Gardnerella is a lack of genetic tools. To identify strong promoters that could potentially be used in genetic tools for Gardnerella a transcriptomic study was performed using RNAseq.

Methods:
Gardnerella vaginalis ATCC 49145 was grown in 1% glycogen or 1% maltotriose in modified NYCIII medium as three biological replicates per condition on three consecutive days for each condition and the bacteria were harvested in the late exponential phase. RNA was extracted from bacterial pellets and the quality of the RNA was evaluated by A260/A280 ratio and RNA Integrity Number (RIN). cDNA and library preparation for sequencing was performed following the depletion of rRNA. The libraries were sequenced using paired-end reads (2 x 300bp) on the Miseq platform (Illumina). Quality trimmed reads were mapped to the reference genome of G. vaginalis ATCC 49145 using Bowtie 2. Read counts were normalized using the “reads per kilobase million” approach prior to the identification of the most highly expressed genes. Results from this study will lead to the identification of promoter sequences that may be useful in genetic tool construction.

Results:
The A260/A280 ratio of all extracts was 2.0 – 2.1, and the RIN value of all six samples was >9. An average of 3.8 million reads per sample were available following filtering for quality. Over 90% of the reads correspond to ribosomal RNA, and out of 1512 genes in the genome, more than 1400 genes were covered by the reads generated. The most abundant transcript in both growth conditions was a protein of unknown function.

Conclusion:
Good quality RNA was extracted from all the samples and the ribosomal RNA depletion with Ribo zero plus kit (Illumina) was inadequate. Seven of the top ten genes were relatively highly expressed in both conditions.

44. BUILDING PATIENT AVATARS FOR PRECISION MEDICINE USING TISSUE ENGINEERING TECHNIQUES

Presenter: **Parnaz Soori**
USask Affiliation: **Graduate student**
College: **College of Medicine**
Supervisor: M. Dean Chamberlain, College of Medicine

Background:
Cancer, a complex and diverse disease, presents challenges such as genomic instability, tumour heterogeneity, and resistance to standard therapies. Despite the progress in precision medicine, many preclinical models struggle to accurately replicating human cancer biology, which limits their translational relevance. While rodent models have crucial integral role in cancer research, their inability to mimic human tumour complexity, including immune influences, tumour microenvironment (TME), and drug metabolism results in poor clinical translation, with less than 8% of preclinical findings applying to humans. In contrast, canine models (dogs) present a superior alternative due to their genomic, physiological, and environmental similarities to humans. Dogs share similar environmental exposures, diet, and immune system characteristics with humans, making them more relevant for translational research than rodents. Additionally, canines naturally develop spontaneous tumours with histopathological features closely resembling human cancers. These similarities, along with shorter lifespans, facilitate the accelerated study of tumour progression and therapeutic responses. The availability of veterinary clinical trials offers an ethical and cost-effective pathway for testing novel therapies, providing reassurance for support for our research

Methods:
Our project leverages canine models and tissue engineering techniques to develop a 3D canine soft tissue sarcomas (STS) model. Our model aims to faithfully recreate the TME, integrating extracellular matrix (ECM) components, stromal cells, and tumour heterogeneity. Our lab has developed a novel 3D tumour model known as microtissues. Microtissues are 2 mm-long collagen-based structures embedded with cancer cells, providing a physiologically relevant ECM. Unlike traditional 2D cultures, our 3D microtissue models provide a dynamic environment that better simulates in vivo tumour behaviour, offering a robust drug screening and therapeutic development platform. This model allows precise control over cell composition, enabling us to study interactions between specific cell populations. We process donated canine tumors into single-cell populations and culture them within microtissues. Within 5–10 days, we will test the samples against various concentrations based on the Cmax (the maximum concentration that can be safely administered to the dog) of 20 chemotherapeutic drugs such as Doxorubicin, Vincristine, etc.

Results:
So far, the experiments we have done with multiple drugs have proved that some tumors are more sensitive to some drugs than others.

Conclusion:
By observing the microtissue response to each drug, we can more precisely identify the most effective drug for a dog's tumour. This will enable future tests to determine the most beneficial treatments for that cancer, bringing promise for enhanced cancer treatments.

45. THE MODULATORY ROLE OF MYOGENIC TONE ON ALPHA-1 ADRENERGIC-MEDIATED CEREBRAL VASOMOTOR RESPONSES

Presenter: **Adam Luchkanych**
USask Affiliation: **Graduate student**
College: **Western College of Veterinary Medicine**
Supervisor: T. Dylan Olver, Western College of Veterinary Medicine

Background:
Myogenic reactivity and alpha-1 adrenergic signalling contribute to the regulation of cerebrovascular tone. Whether the level of myogenic tone influences alpha-1 adrenergic signalling in the cerebral circulation is unclear. It was hypothesized that myogenic tone and alpha-1 adrenergic-mediated vasoconstriction would act synergistically to enhance cerebral artery tone.

Methods:
Middle cerebral arteries from swine were harvested and downstream branches (1A and 3A) were isolated and mounted in a pressure myograph. Myogenic tone and vasomotor responses to alpha-1 adrenergic agonism (phenylephrine) were compared in 1A (n = 6) vs. 3A (n = 7) arteries at 60mmHg intraluminal pressure and in 1A arteries at high (80 mmHg; n = 4) vs. low (40 mmHg; n = 4) intraluminal pressure under control and L-type calcium channel blocker (nifedipine) pre-treatment conditions.

Results:
Myogenic tone was greater in 3A vs. 1A arteries (13 ± 8% vs. 24 ± 8%, P = 0.023) and alpha-1 adrenergic-mediated vasoconstriction was less (15 ± 9% vs. 30 ± 9%, P = 0.012). Myogenic tone was greater in high- vs. low-pressure conditions (35 ± 6% vs. 19 ± 14%, P = 0.036) and alpha-1 adrenergic-mediated vasoconstriction was lower (5 ± 9% vs. 16 ± 10%, P = 0.003). Differences in myogenic tone between the high (80 mmHg; n = 4) and low (40 mmHg; n = 4) intraluminal pressures were abolished in arteries pre-treated with the L-type calcium channel blockade (14 ± 14% vs. 9 ± 7%, P = 0.400) and differences in alpha-1 adrenergic-mediated vasoconstriction were likewise attenuated (3 ± 2% vs. 10 ± 8%, P = 0.105).

Conclusion:
Altogether, these data indicate increased myogenic tone is associated with reduced alpha-1 adrenergic-mediated vasoconstriction, and at a lower myogenic tone greater vasoconstriction may involve increased involvement of L-type calcium channels.

46. EMBRYONIC EXPOSURE TO BISPHENOL S CAUSES LONG-TERM BEHAVIOURAL ALTERATIONS IN ZEBRAFISH (DANIO RERIO)

Presenter:	**A K M Munzurul Hasan**
USask Affiliation:	**Graduate student**
College:	**College of Arts and Science**
Supervisor:	Douglas P Chivers, College of Arts and Science
Co-supervisor(s):	Som Niyogi

Background:
Bisphenol S (BPS) is a widely used synthetic compound known as an endocrine-disrupting chemical. It is commonly found in epoxy resins and polycarbonate plastics, materials frequently used for food storage containers and baby bottles. The ability of BPS to bind predominantly to estrogen receptors raises significant concern, as it can interfere with different neurological functions leading to neurobehavioural deficits. Despite extensive research documenting various adverse effects of BPS in larval fish, its its long-term neurodevelopmental effects remain poorly understood.

Methods:
Embryos were exposed to either 0.01% DMSO or 30 µg/L BPS from 4- 120 hours post-fertilization (hpf) and subsequently raised in clean water until adulthood (6 months). Social behaviour was assessed at 21 days post-fertilization (dpf), and the novel object recognition test was conducted at 25 dpf. At 6 months of age, behavioural tests including the novel tank, group preference, and shoaling test were performed. Neurotransmitter levels, including dopamine (DA), serotonin (5-HT), and acetylcholine (ACh), were measured in both 30 dpf juveniles and 6-month-old adult fish.

Results:
At the juvenile stage, BPS-exposed fish exhibited reduced social interaction at 21 dpf and impaired cognitive function in a novel object recognition test at 25 dpf. These behavioural alterations were accompanied by reduced DA levels and significantly increased 5-HT and ACh levels, indicating modulation of neurotransmitter systems during development. In adulthood, early-life BPS exposure resulted in persistent deficits in social behaviour, as evidenced by altered group preference, while no significant changes were observed in anxiety-like behaviour (novel tank test) or shoaling behaviour. Notably, DA levels remained significantly reduced in adults, although no alterations were found in 5-HT and ACh levels.

Conclusion:
These findings indicate that embryonic exposure to environmentally relevant concentration of BPS leads to persistent social behavioural impairments and long-term alterations in neurotransmitters levels in zebrafish, highlighting potential neurodevelopmental risks of BPS.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

Basic Science 4

47. CRISPR-CAS9 KNOCKOUT OF HNRNPA1 IMPACTS NEURON DIFFERENTIATION

Presenter:	**Miranda Messmer**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Kaitland Fior, College of Medicine
	Hannah Salapa
	Michael Levin, College of Medicine
Supervisor:	Michael Levin, College of Medicine
Co-supervisor(s):	Bogdan Popescu

Background:
Dysregulation of gene expression by RNA binding proteins (RBPs) is a pathogenic mechanism underlying multiple neurodevelopmental and neurodegenerative diseases. Heterogeneous nuclear ribonucleoprotein A1 (A1) is an RBP that regulates RNA metabolism and gene expression in neurons. A1 promotes neurite outgrowth, structural integrity, and regulates several pathways for synaptic function. Dysfunction of A1 in neurologic diseases contributes to neurodegeneration because these fundamental processes for neuronal health become impaired. These same processes are also key to neuron differentiation, a process required for neuron function and regeneration. Thus, our objective is to establish an in vitro model of A1 dysfunction through CRISPR-Cas9 knock-out (KO) to test the hypothesis that A1 regulates neuron differentiation.

Methods:
Cas9-expressing Neuro-2a cells and primary cortical embryonic neurons were treated with guide RNA targeting A1 (A1 KO) or Rosa26 (Control) for A1 KO. A1 protein was quantified to validate KO by western blot and immunocytochemistry. Expression of NeuN, a protein that promotes differentiation in cortical neurons, and synaptic genes were analyzed to evaluate differentiation in Neuro-2a cells following serum starvation.

Results:
A1 protein was reduced by 93-98% in Neuro-2a cells and progressively declined in primary neurons, reaching 78% KO at 10 days in vitro (DIV) and >90% KO by 14 DIV. Expression of synaptic signalling genes (Dlg4, Syt5, Syt1, Gabbr1, Ppfia3, Sema6a, Aplp1) were altered ($p<0.05$ for all targets) and NeuN was reduced ($p=0.005$) with A1 KO in Neuro-2a cells, suggesting impaired differentiation.

Conclusion:
We successfully generated an in vitro model of neuronal A1 dysfunction through CRISPR-Cas9 KO. Preliminary data suggests that A1 regulates gene expression for neuron differentiation, a key process for neuron development and maintenance of neuronal health and function.

48. FROM COW TO LAB: ASSESSING CYTOBRUSH-COLLECTED ENDOMETRIAL EPITHELIAL CELLS FROM POSTPARTUM COWS FOR IN-VITRO CULTURE SUITABILITY

Presenter:	**Sai Kumar B A A**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Jaswant Singh, Western College of Veterinary Medicine
Supervisor:	Dinesh Dadarwal, Western College of Veterinary Medicine

Background:
Bovine endometrial epithelial cells (BEEC) for in-vitro studies are typically obtained by dissection and enzymatic digestion of endometrial tissue from slaughterhouse-derived uteri. However, this lengthy and labor-intensive process can compromise cell viability and functionality. The cytobrush technique offers a rapid alternative to collect uterine cells from live cows for clinical assessment. This study aimed to isolate BEEC from postpartum cows using the cytobrush method for in-vitro culture and compare the effects of different proteolytic enzymes on the viability and apoptosis of in-vivo collected BEEC.

Methods:
BEEC were harvested from dairy cows (n=8, parity:1-4, age:2-5yr, five samples/cow) during early (12-15d) and late (40-44d) postpartum stages using triple-guarded cytobrush assemblies. Pooled samples from each cow were processed for phenotypic characterization, in-vitro culture, and digested enzymatically for 7.5- or 15-min using Collagenase I, Liberase™ TM or EDTA before assessing viability.

Results:
The mean (±SD) viable cell yield per cow was 1x106 (±0.15x106). Isolated BEEC expressed only cytokeratin, not vimentin, and exhibited swirling morphology up on in-vitro culture, reaching 85-100% confluency in 4-8d. Although not significant, fewer cows yielded culturable BEEC during early postpartum than the late postpartum stage (1/8 vs 5/8, $p>0.1$). BEEC treated with Liberase™ TM had higher viability ($p<0.01$) than those treated with EDTA during both early (93% vs 81%) and late (89% vs 63%) postpartum stages. Additionally, the percentage of non-apoptotic cells was higher ($p<0.02$) in the Liberase™ TM group (63%) than in the Collagenase I (41%) and EDTA (41%) groups during late postpartum period. Digestion duration did not affect the viability and apoptosis of BEEC harvested at both stages ($p>0.4$).

Conclusion:
The cytobrush technique is an efficient, and minimally invasive method to collect BEEC from postpartum cows for in-vitro culture. The findings confirm that enzymatic digestion negatively impacts BEEC viability, with Liberase™ being the most effective enzyme for maintaining cell viability.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

49. DIALYSIS MEMBRANE-INDUCED EPIGENETIC METHYLATION PATTERNS OF INFLAMMATION-RELATED GENES IN HEMODIALYSIS PATIENTS

Presenter:	**Hira Syeda**
USask Affiliation:	**Graduate student**
College:	**College of Engineering**
Collaborators:	Ahmed Shoker, College of Medicine
Supervisor:	Amira Abdelrasoul, College of Engineering

Background:

Hemodialysis (HD) is essential for end-stage renal disease (ESRD) patients, but dialysis membranes contribute to inflammation, immune response, and epigenetic changes, particularly DNA methylation. However, limited research explores how dialysis membranes affect DNA methylation patterns. This study explores DNA methylation alterations in pre- and post-dialysis states, identifying inflammation-related pathways and their correlation with dialysis membrane properties to better understand HD-induced inflammation and improve renal care

Methods:

• Sample Collection and Preparation • Illumina Infinium HumanMethylation450 BeadChip Analysis • Identification of Differentially Methylated Sites using Genome Studio • Functional Enrichment Analysis • Protein-Protein Interaction (PPI) Network Analysis

Results:

Results: We identified 595 genes in Group 1 and 516 genes in Group 2 with methylation changes between pre- and post-dialysis stages, with 178 shared molecular signatures. Group 1 showed 18 enriched biological processes and 4 KEGG pathways, while Group 2 showed 10 biological processes and 4 KEGG pathways. PPI analysis identified 93 genes with significant methylation changes, including TWIST1, CAV1, CDKN2A, and CXCL12, involved in inflammation and immune responses. Post-dialysis, inflammatory biomarkers (CRP, Serpin C1, Properdin, PF4, vWF-A2) significantly increased, linked to the key genes

Conclusion:

Conclusion: Our findings highlight DNA methylation and protein adsorption on dialysis membranes as key drivers of chronic inflammation in HD patients. Key hub genes (TWIST1, CAV1, CDKN2A, CXCL12) regulate inflammation and immune responses, while fibrinogen adsorption on membranes triggers complement and platelet activation, exacerbating inflammation. Targeted interventions are needed to reduce inflammation and improve HD outcomes

Self-declaration of research alignment with additional themes (optional):

Sustainable Progress

50. A NOVEL QPCR PROTOCOL FOR PAENIBACILLUS LARVAE IN HONEY: LEVERAGING SPORE GERMINATION DYNAMICS FOR RISK ASSESSMENT OF AMERICAN FOULBROOD

Presenter:	**Julia Tregobov**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Oleksii Obshta, Western College of Veterinary Medicine
	M. Fahim Raza, Western College of Veterinary Medicine
Supervisor:	Sarah Wood, DVM, PhD, Dipl. ACVP
	Western College of Veterinary Medicine
Co-supervisor(s):	Janet Hill, PhD

Background:

American Foulbrood (AFB), caused by Paenibacillus larvae, is a highly destructive disease of honey bees (Apis mellifera), resulting in significant economic losses for beekeepers. The bacterium produces resilient spores capable of surviving for decades, resisting heat, chemicals, and antimicrobials. As destruction of infected colonies remains the only reliable control, early detection is essential. However, traditional diagnostic methods based on symptom observation and culture assays are slow, labour-intensive, and often unreliable. Quantitative PCR (qPCR) has emerged as a preferred alternative due to its speed, sensitivity, and ability to detect asymptomatic infections. Despite these advantages, qPCR assays optimized for spore quantification in honey remain limited due to challenges in DNA extraction and inconsistent spore germination.

Methods:

This study develops a novel qPCR assay optimized for detecting P. larvae spores in honey by refining pre-treatment protocols informed by spore germination dynamics. Germination trials across multiple P. larvae isolates will improve DNA recovery consistency, enhancing assay sensitivity. The assay targets the highly conserved, single-copy chromosomal metalloproteinase (MP) gene to minimize false positives associated with multicopy genes.

Results:

A synthetic positive control and internal amplification control (eGFP) were successfully transformed into DH5α competent E. coli cells to generate stable stocks. These were incorporated into a duplex qPCR assay, which demonstrated reliable co-amplification and confirmed assay validity. P. larvae spore stocks, including oxytetracycline-resistant and susceptible isolates collected across Saskatchewan, were isolated and prepared for testing. Preliminary results indicate that the assay detects P. larvae spores with promising sensitivity in buffer and honey matrices.

Conclusion:

By addressing key diagnostic challenges, this research provides a reliable tool for early AFB detection, enabling proactive management strategies that reduce disease spread and economic losses. The optimized qPCR assay will help support sustainable apiculture practices, ultimately contributing to global efforts to protect honey bee populations and the agricultural systems they sustain.

51. MODELING RNA BINDING PROTEIN DYSFUNCTION AND NEURODEGENERATION IN MULTIPLE SCLEROSIS (MS) THROUGH NMDA RECEPTOR-MEDIATED GLUTAMATE EXCITOTOXICITY

Presenter:	**Fariba Karami**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Supervisor:	Michael Levin, College of Medicine

Background:
MS is characterized by demyelination and neuronal degeneration. One contributor to MS-related neurodegeneration is glutamate excitotoxicity due to excessive activation of N-methyl-D-aspartate (NMDA) receptors. Additionally, the dysregulation of the RNA binding proteins (RBP) heterogeneous nuclear ribonucleoprotein A1 (A1), has been implicated in the pathogenesis of MS. A key feature of neuronal A1 dysfunction is its mislocalization from the homeostatic nuclear location to the cytoplasm. This study investigates whether NMDA receptor-mediated excitotoxicity induces A1 mislocalization in neurons. Establishing this model could enhance our understanding of RBP dysfunction in MS-related neurodegeneration.

Methods:
To develop an in vivo model, NMDA (50 nM) or saline (control) were intracranially injected into the motor cortex of mice. Brain samples were collected at 1-, 2-, 3-, and 4-days post-injection (DPI). Serial brain sections were stained with: Nissl to identify the neuroanatomical location of the injection site, FluoroJade C, a neurodegenerative marker, and A1 with NeuN (a neuron specific marker) using immunohistochemistry to examine neuronal A1 localization.

Results:
Brain sections showed significant increases in neuronal FluoroJade C fluorescence in the ipsilateral compared to the contralateral side at 1, 2, 3 and 4 DPI (*$p<0.05$) indicative of successful NMDA injections causing neurodegeneration. In saline injected mice, there was no significant difference in FluoroJade C fluorescence between the ipsilateral and contralateral sides of the cortex suggesting that NMDA and not injection trauma mediated FluoroJade C staining. In NMDA injected mice, there was neuronal A1 mislocalization to the cytoplasm at all time points, in contrast to the contralateral side of the same brain and saline injected mice, where A1 maintained its homeostatic nuclear location.

Conclusion:
We successfully established an in vivo model of NMDA-induced RBP mislocalization, suggesting that NMDA excitotoxicity is a potential trigger for neuronal A1-mediated neurodegeneration and may provide new therapeutic targets for MS treatment.

52. SC-MANF – A POTENTIAL THERAPY FOR PERIPHERAL NERVE REGENERATION.

Presenter:	**Bhadrapriya Sivakumar**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Valeria Martinez, College of Medicine
	Anil Kumar, College of Medicine
	Anand Krishnan, College of Medicine
Supervisor:	Anand Krishnan, PhD
	College of Agriculture and Bioresources

Background:

Peripheral nerve injuries affect millions of people worldwide. Yet, no effective therapies are available to repair nerves and restore functions. The main challenge for natural nerve regeneration is the lack of local availability of growth factors in injured nerves. Thus, local, and sustained supplementation of potential growth factors should improve regeneration. We recently found a novel growth factor found in the peripheral nerves - Mesencephalic Astrocyte-Derived Neurotrophic Factor (MANF) promotes the outgrowth of neurons and plasticity of Schwann cells. This finding suggests that local supplementation of MANF may improve nerve regeneration in-vivo. Here, we generated SCs expressing MANF (SC-MANF) as a local delivery system and validated their potential to improve nerve regeneration using an explant model.

Methods:

SC-MANF was generated in-vitro and in explants by transducing SCs with lentiviral particles expressing Doxycycline(Dox) inducible MANF. Dox-induced expression and secretion of MANF was confirmed by western blot and ELISA, respectively. The effect of SC-MANF on neuroprotection and axon regeneration was evaluated using a novel DRG-nerve explant crush injury model. The regenerating axons in the explants were quantified using ImageJ software after staining the axons with βIII tubulin and GAP43.

Results:

Western blot showed that SC-MANF express significantly increased levels of MANF compared to SCs treated with lentiviruses carrying empty vector (L-EV). ELISA assay showed that MANF secretion is significantly higher in SC-MANF compared to L-EV. βIII tubulin stained 5-day DRG-nerve explant showed an increased number of intact axons in the proximal nerve stump in the SC-MANF group, showing neuroprotection, while GAP-43 stained 14-day explant showed an increased number of regenerating axons in the distal nerve stump of SC-MANF group, showing nerve regeneration. Immunostaining also confirmed the overexpression of MANF in the SC-MANF group.

Conclusion:

Our experiments showed that sustained local delivery of MANF can improve peripheral nerve regeneration.

53. MANIPULATION OF THE HOST IMMUNE SYSTEM IMPACTS BORRELIA BURGDORFERI TRANSMISSION TO IMMATURE TICKS AND PATHOGEN ABUNDANCE DURING TICK DEVELOPMENT

Presenter: **Cody Koloski**
USask Affiliation: **Graduate student**
College: **Western College of Veterinary Medicine**
Supervisor: Maarten Voordouw, Western College of Veterinary Medicine

Background:
The transmission of pathogens from infected hosts to uninfected vectors is crucial for the spread of vector-borne diseases. Borrelia burgdorferi (Bb), the Lyme disease pathogen, is transmitted in North America by Ixodes scapularis ticks. Once inside a rodent host, Bb establishes a chronic infection, but host-to-tick transmission often declines over time, suggesting a role for the adaptive immune system in limiting transmission. Mice with severe combined immunodeficiency (SCID) lack an adaptive immune response, leading to higher Bb loads than immunocompetent (IC) mice. By manipulating host Bb abundance, we can determine whether ticks acquire a proportional inoculum and track pathogen levels through multiple feedings and developmental stages.

Methods:
To investigate the relationship between host Bb load and transmission to immature ticks, we infected mice via tick bite and measured pathogen transmission across three larval infestations. We quantified Bb prevalence and abundance (qPCR) in replete larvae, 1-month-old nymphs, and 12-month-old nymphs to track changes in Bb load over tick development. We also assessed Bb abundance in mouse ear biopsies at each larval infestation.

Results:

To investigate the relationship between host Bb load and transmission to immature ticks, we infected mice via tick bite and measured pathogen transmission across three larval infestations. We quantified Bb prevalence and abundance (qPCR) in replete larvae, 1-month-old nymphs, and 12-month-old nymphs to track changes in Bb load over tick development. We also assessed Bb abundance in mouse ear biopsies at each larval infestation.

Conclusion:
This research provides insight into host-pathogen-vector interactions and the role of tick development in shaping pathogen dynamics.

54. TRANSGENERATIONAL INHERITANCE OF COGNITIVE DEFICITS INDUCED BY ANCESTRAL ARSENIC EXPOSURE IN ZEBRAFISH (DANIO RERIO) VIA MATERNAL AND PATERNAL LINEAGES

Presenter:	**Mahesh Rachamalla**
USask Affiliation:	**Graduate student**
College:	**College of Arts and Science**
Collaborators:	Markus Hecker
Supervisor:	Som Niyogi, College of Arts and Science
Co-supervisor(s):	Markus Hecker

Background:
Exposure to arsenic has been shown to impair learning and memory functions in both animal models and humans. However, the transgenerational inheritance of these cognitive deficits and the epigenetic mechanisms underlying them remains poorly understood, particularly in the context of both maternal and paternal ancestral exposure and its potential impact across up to three generations.

Methods:
The present study examined the intergenerational and transgenerational effects of ancestral arsenic exposure on cognitive performance specifically latent learning (using latent learning paradigm) in zebrafish, through both maternal and paternal lineages. In addition, the study assessed associated changes in brain biochemical parameters, neurotransmitter levels, and DNA methylation patterns of cognition-related genes. Adult male zebrafish (F0 generation) were exposed to dietary arsenic (30, 60, or 100 µg/g as arsenite) for 90 days and subsequently crossed with unexposed control females to produce the paternal lineage of F1 progeny. Similarly, exposed females were crossed with control males to generate the maternal lineage of F1 progeny. F1 males and females from the same exposure groups were then crossed to produce F2 offspring representing the continued maternal and paternal lineages of ancestral arsenic exposure.

Results:
Ancestral arsenic exposure resulted in cognitive impairments in both the F1 (intergenerational) and F2 (transgenerational) generations through maternal and paternal lineages. Notably, these effects emerged at lower ancestral arsenic exposure levels (30 and 60 µg/g) in the maternal lineage compared to the higher dose (100 µg/g) required to elicit similar effects in the paternal lineage. The observed cognitive deficits were accompanied by increased oxidative stress and disruptions in dopaminergic signaling. These neurobehavioral alterations were further linked to the downregulation of key cognition-related genes, including those involved in dopamine signaling and metabolism (Drd1 and MAO), as well as brain-derived neurotrophic factor (BDNF).

Conclusion:
In conclusion, the hypermethylation of promoter regions in key cognition-related genes (Drd1, MAO, BDNF) across generations highlights a potential epigenetic basis for the transgenerational inheritance of arsenic induced neurotoxicity, offering new insights into its long-term impact on brain function.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

Basic Science 5

55. INVESTIGATING TEMPORAL AND SPATIAL CHANGES IN PROTEINS INVOLVED IN MIGRATION OF BREAST CANCER CELLS IN A NOVEL 3D TUMOUR MODEL

Presenter: **Taylor Dzikowski**
USask Affiliation: **Graduate student**
College: **College of Medicine**
Supervisor: Dean Chamberlain, College of Medicine

Background:
Even among patients with the same subtype of breast cancer, there can be significant differences in the rate at which malignant cells migrate from the primary tumour to establish secondary tumours. This variation may be attributed to tumour heterogeneity and dynamic expression of invasive and metastatic proteins within primary tumours. 3D tumour models can be used to understand this phenomenon. Our lab recently developed a novel 3D tumour model called microtissues. Microtissues are free-floating collagen cylinders embedded with cancer cells, which provides a distinct advantage over traditional 3D models, particularly, microtissues do not experience rigidity from plastic, unlike other traditional 3D models like Matrigel domes. This prevents cell migration from being affected by plastic rigidity, making microtissues a potentially more accurate representation of cancer cell migration. Previous studies have demonstrated that breast ductal (luminal epithelial) cells fail to form natural ductal structures when cultured in collagen attached to plastic but successfully form these structures in free-floating gels. The use of collagen in our microtissues is particularly beneficial, as collagen is a vital component of the tumour microenvironment (TME) and plays an integral role in cancer progression, metastasis, and therapy response. The structural integrity of collagen enables the formation of free-floating microtissues and accommodates the growth of various cell types to recapitulate the TME. Our ongoing research aims to investigate the mechanisms behind the spontaneous migration of cancer cells within the microtissues.

Methods:
Data for this project has been acquired using RNA-sequencing, western blotting, and immunofluorescence confocal microscopy

Results:
Preliminary RNA-sequencing in HCC1806 and MDA-MB-231 cell lines has revealed opposite changes of specific epithelial-mesenchymal transition (EMT) markers, when comparing 2D to 3D microtissues between the two cell lines. Specifically, in HCC1806 microtissues ZEB1 and vimentin are upregulated, and SLUG and fibronectin-1 are downregulated, however in MDA-MB-231 microtissues, ZEB1 and vimentin are downregulated, while SLUG and fibronectin-1 are upregulated. Interestingly, occludin and claudin-1 become heavily downregulated in both cell lines from 2D to 3D. We utilized western blotting (WB) and immunofluorescent confocal microscopy (IF) to analyze the spatial and temporal

changes in proteins involved in cell migration. WB results have demonstrated that in HCC1806 cells, E-cadherin (a key protein in EMT and cell-cell adhesions) is greater in 2D cell culture than in 3D microtissues starts low in microtissues, and then gradually increases over time. Additionally, IF analysis of HCC1806 microtissues revealed that the number of E-cadherin positive cells starts low at early time points and increases as cells reach the microtissue surface. Moreover, live cell imaging techniques have allowed our lab to begin tracking HCC1806 cell migration within the microtissues to gain insights into how HCC1806 move within microtissues and interact with the TME.

Conclusion:

In summary, our research focuses on using microtissues to characterize the phenotypes of migratory breast cancer cells, paving the way for identifying potential drug targets against metastasis. Further investigation of EMT markers and other proteins involved in cell migration (i.e. integrins, matrixins, cytokeratins, etc.) will be conducted to determine if these markers follow the same changes observed in our preliminary RNA-sequencing data at the protein level and how these changes facilitate the migration of breast cancer cells.

56. INTERFERON BETA SPECIFICITY IN HUMANS AND BATS CONTRIBUTES TO DIFFERENCES IN VIRAL REPLICATION AND TOLERANCE

Presenter:	**Rita Quintela**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Arinjay Banerjee, PhD
	Western College of Veterinary Medicine

Background:
Bats are ancestral hosts of multiple zoonotic viruses, including betacoronaviruses (βCoVs) that cause severe disease and death in humans and livestock. Conversely, bats infected with these viruses do not show clinical signs of disease, making them a fascinating model to study the evolution of virus-host interactions. The innate immune response is the first line of defense against viral infections. Type I interferons (IFNs) are among the first cytokines to be released when an infection is detected in vertebrates. IFNs bind to the interferon-α/β receptor (IFNAR1/2) in host cells and induce the production of antiviral Interferon Stimulated Genes (ISGs). βCoVs have evolved to impair type I IFN activity in humans, increasing our vulnerability to infections. Little is known about how type I IFNs signal in bat cells and whether bats have evolved more efficient processes to better tolerate viral infections.

Methods:
We have identified that wildtype bat IFNβ do not protect human cells and vice versa, suggesting species-specific mechanisms. Based on computational modelling and positive selection analyses of IFNβ sequences from several mammals, we have produced mutant human and bat (Eptesicus fuscus and Pteropus alecto) recombinant IFNβ to test their antiviral potency against βCoVs.

Results:
Infection studies show that IFNβ with two specific point mutations have lower antiviral capacity compared to wildtype IFNβ in species-matched cells for both humans and bat species. Mutated IFNβ cannot effectively phosphorylate STAT transcription factors, suggesting a failure to prime IFNAR1/2. These results are supported by structural modelling showing significant changes on binding interface properties for mutated IFNβ-IFNAR1/2.

Conclusion:
The observed differential antiviral protection suggests that our identified amino acid residues are key determinants of IFNβ-mediated protection. Our study identifies remarkable species-specific adaptation of IFNβ and downstream antiviral processes which will inform basic and translational science for the development of IFNβ antiviral therapies for humans.

57. ENHANCING PESTICIDE SAFETY: REPRODUCTIVE FITNESS IN MALE HONEY BEES

Presenter:	**Marina Carla Bezerra da Silva**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Sarah Wood, Western College of Veterinary Medicine
Co-supervisor(s):	Elemir Simko

Background:
The widespread use of pesticides due to agricultural intensification has been associated with chronic pesticide exposure to honeybees. Current pesticide risk assessment for honeybees lacks standardized histopathological testing and established positive controls for reproductive safety in honeybee drones. To enhance pesticide safety, this study examined the effects of in vitro exposure to a miticide (amitraz) on drone survival and testicular weight, histopathology, and gene expression in germline and somatic cells.

Methods:
We reared honeybee drones in vitro from larva to adult and chronically exposed larvae to amitraz (0.6, 1.2, and 8.9µg/µL). Survival was recorded daily until adulthood when drones were euthanized for testis dissection and weighing. A subset was euthanized at the prepupal stage for histopathology and in situ hybridization chain reaction (HCR). Histopathology was used to quantify seminiferous tubules lacking rosettes (spermatogonia), while HCR measured testicular gene expression by fluorescence signal density (label count per μm^2) for germline (Vasa) and somatic (Castor) markers.

Results:
We observed a significant decrease in survival from larva to adulthood at medium and high amitraz doses, with survival rates of 63% and 52%, respectively; however, adult testicular weight was unaffected. Histopathology showed a dose-dependent increase in number of seminiferous tubules lacking rosette formation per testis: negative control (0.6 ± 0.5), solvent control (2.3 ± 2.5), low (2.9 ± 2.1), medium (6.7 ± 2.7), and high (13 ± 7.3). HCR analysis showed the medium dose significantly reduced fluorescence signals in the germline (0.5 μm^2) and somatic cells (1 μm^2) compared to controls (4 and 2.5 μm^2 respectively), while the high dose affected only germline cells (1.5 μm^2).

Conclusion:
We demonstrated that amitraz is a suitable positive control for reproductive safety testing in honeybee drones based on our preliminary histopathology results on loss of rosettes formation and decreased gene expression of germline and somatic cells.

58. LOSS OF PITX2C ALTERS ATRIAL MORPHOGENESIS AND SINOATRIAL NODE PATTERNING IN THE DEVELOPING ZEBRAFISH HEART

Presenter:	**Christopher Chivers**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Lorynn Labbie, Sebastien Gauvrit, Khizra Haq, Saanvi Mital, Maria Paz Cevallos Salvador, Jaclyn Bossaer, Manuel Vicente, Bea Dominguez, Juan Llopis, Didier Y.R. Stainier
Supervisor:	Michelle Collins, College of Medicine

Background:
The most common form of cardiac arrhythmia is atrial fibrillation (AF), which affects 2-3% of the population and can lead to stroke and heart failure. Several lines of evidence support a genetic basis for AF. The most significant risk locus is on chromosome 4q25, a region upstream of the gene PITX2, which encodes a crucial transcriptional regulator of cardiac morphogenesis. Altered PITX2 expression is reported in patients with AF, yet there is an incomplete understanding of how dysregulated PITX2 expression leads to AF.

Methods:
Atrial calcium handling was measured using the Twitch-4 Ca2+ biosensor (Tg(myl7:Twitch-4) Pitx2c+/-) zebrafish imaged with videomicroscopy by collaborators. Immunofluorescence imaging for atrial morphology by confocal microscopy in Tg(-0.8myl7:NLS-DsRed^hsc4; myl7:LA-GFP^s974; Pitx2c+/-). Transcription factor expression was examined by qPCR of embryonic heart tissue.

Results:
We previously reported that loss of pitx2c in zebrafish leads to cardiac arrhythmia during larval stages. Here we characterize an atypical chamber morphology in pitx2c-/- atria compared to wild-type siblings affecting chamber size and cardiomyocyte density, potentially indicating a rise in non-cardiomyocyte cell types, and is associated with an increase in expression of the sinoatrial node precursor gene shox2. Using the Ca2+ biosensors GCaMP and Twitch-4, we observed reduced Ca2+ amplitude, rise time, and rise/decay slopes in pitx2c+/- and pitx2c-/- atria compared to wild-type siblings, with no differences in ventricular Ca2+ handling.

Conclusion:
We conclude that loss of Pitx2c derived calcium overload phenotype in cardiomyocytes related to changes in electrophysiology in consequence of altered sinoatrial node development. We hypothesise that altered chamber morphology and sinoatrial node expansion synergize to alter electrical activity in the heart to drive the arrhythmia phenotype, further impairing cardiac development leading to a more severe phenotype over time. We are currently examining other aspects of cardiac development and the conduction system including cardiac looping and atrial trabecular network as well as investigating the potential immune or epicardial-derived adipose infiltration of the myocardium in pitx2c-/- zebrafish, both previously associated with atrial fibrillation.

59. OXIDIZED PHOSPHATIDYLCHOLINE FOUND IN MULTIPLE SCLEROSIS ARE MEDIATORS OF NEURODEGENERATION

Presenter:	**Ruoqi Yu**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Supervisor:	Jeff Dong, College of Medicine

Background:
Multiple Sclerosis (MS) is a chronic neuroinflammatory and neurodegenerative disease affecting 2.9 million worldwide. People living with MS (pwMS) can have a range of symptoms including muscle weakness, vision impairment, impaired sensation, and cognitive dysfunction. Accumulating evidence have suggested a role of oxidative stress in MS pathology. Indeed, oxidative phosphatidylcholines (OxPC), products of lipid peroxidation, accumulate in white matter (WM) as well as grey matter (GM) lesions in the brains from pwMS. While we recently found that OxPC deposition in the mouse spinal cord WM induces axonal loss, demyelination, and neuroinflammation, the role of OxPC in GM lesions during MS remains unknown.

Methods:
To determine the function OxPC accumulation in the GM, I stereotaxically injected POVPC, a purified MS-relevant OxPC, into the spinal cord GM of mice and performed quantitative immunofluorescence microscopy analysis after 3, 7, and 14 days.

Results:
I found that OxPC deposition in the GM induced significant NeuN+ cell loss which associated with cleaved-caspase 3 upregulation, as well as significant E06+ OxPC deposition. Additionally, IBA1+ cells expressing NADPH oxidase accumulated at the lesion center whereas GFAP+ astrocytes surrounded the lesion edge. Notably, this pathology persisted from day 3 to 14.

Conclusion:
These results indicate OxPC accumulation in the GM of the CNS promotes neuroinflammation and neurodegeneration. Further investigations into OxPC-mediated cellular and molecular responses in GM will advance our understanding of GM pathology during MS.

60. SERINE PHOSPHORYLATED HSPB1 LEVELS AND CELLULAR LOCATIONS ARE ALTERED IN HUMAN MYOMETRIAL CELLS UNDER TENSION STRESS.

Presenter:	**Shayla Jesse**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Daniel J. MacPhee, Western College of Veterinary Medicine
Supervisor:	Daniel J. MacPhee, Western College of Veterinary Medicine

Background:

The myometrium, or uterine muscle, undergoes cellular adaptation during pregnancy to enable the future production of labour contractions and delivery of a baby. Fetal growth induced uterine stretch increases detection of small Heat Shock Protein Beta 1 (HSPB1) in the myometrium during pregnancy, particularly serine phosphorylated forms of HSPB1. However, the precise responses of phosphorylated forms of HSPB1 and their specific cellular locations in human myometrial cells following tension are unknown. We hypothesized that increased tension applied to myometrial cells will increase the detection of serine phosphorylated forms of HSPB1 and that cellular locations of these proteins will be altered with tension over time.

Methods:

The hTERT-HM immortalized human myometrial cell line was seeded on collagen I-coated flexible bottom 6-well plates and cultured in DMEM/F12 media containing 10% FBS and antibiotics. A Flexcell FX-6000T system was used to induce different unrestrained tensions (0, 10, 15, 20, 25% elongation) on myometrial cells, followed by lysis in RIPA buffer, SDS-PAGE, and detection of phosphorylated forms of HSPB1 by immunoblot analyses. For time course experiments following elongation at 25%, cells were immediately fixed in 4% paraformaldehyde/phosphate buffered saline (PBS), permeabilized with PBS containing 0.1% Triton X-100, then immunostained for specific forms of phosphorylated HSPB1.

Results:

For experiments with different tensions, immunoblot analyses demonstrated that phosphoserine-15-HSPB1 (pS15-HSPB1) and pS78-HSPB1 were significantly elevated at 25% elongation relative to 20%, 15%, 10%, and 0%. In contrast, pS82-HSPB1 detection was only significantly elevated at 25% elongation relative to 10% and 0%. Over a time course of 25% cell elongation, immunofluorescence detection of pS78-HSPB1 was markedly diminished in focal adhesions at actin stress fibre termini, compared to pS15-HSPB1, while pS82-HSPB1 remained in perinuclear locations.

Conclusion:

Our results indicate that pS15-HSPB1, pS78-HSPB1, and pS82-HSPB1 may have distinctive roles within myometrial cells exposed to tension stress.

61. HOST RESTRICTION FACTORS ZAP AND APOBEC3G INTERACTION, RESULTS IN ENHANCED RESTRICTION OF HIV-1.

Presenter:	**Shreoshri Bhattacharjee**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Supervisor:	Linda Chelico, College of Medicine

Background:
The APOBEC3 family of cytidine deaminases acts as an intrinsic antiviral defense mechanism against various viruses and retroelements. These enzymes are well-established for their independent antiviral actions; however, the impact of their protein-protein interaction network on antiviral activity remains unexplored.

Methods:
Using an existing APOBEC3 affinity purification and mass spectrometry (AP-MS) dataset, we investigated interactions involving APOBEC3G (A3G). This analysis revealed a protein-protein interaction between A3G and ZAP, a zinc-finger antiviral protein (also known as ZCCHV). ZAP, a Pattern Recognition Receptor (PRR), binds single-stranded RNA and restricts viral replication through mechanisms such as RNA degradation and translation inhibition by targeting CpG dinucleotides. Both A3G and ZAP are independently known to interact with HIV-1 RNA.

Results:
Our investigation identified a synergistic effect when A3G and ZAP were co-expressed. While ZAP alone reduces HIV-1 titres and A3G mutates newly formed HIV-1 (-)DNA, their combined expression led to a significant reduction in HIV-1 infectious titres in producer cells. This synergy suggests that the A3G-ZAP interaction enhances co-restriction beyond their independent antiviral mechanisms.

Conclusion:
The observed A3G-ZAP protein-protein interaction facilitates a unique co-restriction mechanism that effectively suppresses HIV-1 replication. This finding broadens our understanding of the interaction networks within the APOBEC3 family and their contribution to antiviral defense. Mechanistic details underlying this synergy warrant further investigation.

62. THE ROLE OF DDX41 IN STRESS GRANULE FORMATION AND MYELOID MALIGNANCIES

Presenter: **Harmony Grainger**
USask Affiliation: **Graduate student**
College: **College of Medicine**
Supervisor: Yuliang Wu, College of Medicine

Background:
Stress granules (SGs) and processing bodies (P-bodies) are membraneless RNA granules that function to balance storage, translation, splicing, and degradation of mRNA, especially during environmental stress. Dysregulation of RNA granules is linked to myeloid malignancies, including myelodysplastic syndrome (MDS) and acute myeloid leukemia (AML). DDX41 is a DEAD-box helicase, mutations in which are implicated in MDS and AML. Our preliminary results suggest that DDX41 is essential for P-body formation. Despite its established role in P-bodies, the role of DDX41 in SG dynamics remains elusive, and the consequences of its dysfunction in oncogenesis are not fully understood. Given that SGs and P-bodies form docking interactions, we hypothesize that DDX41 is essential for P-body and SG formation and their dysfunction contributes to the development of MDS and AML.

Methods:
To investigate this, we will use HeLa wild-type (WT) and DDX41 knockout (KO) cell lines, along with mouse primary dendritic and macrophage cells (both WT and DDX41 KO), and expose them to stress conditions, including oxidative stress from sodium arsenite treatment. Then we will determine the formation and dynamics of SGs (using marker G3BP1) by immunofluorescence (IF). We will extend this analysis to patient-derived MDS and AML samples to determine whether DDX41 mutations affect the formation of SGs and P-bodies under stress conditions. RNA sequencing of HeLa WT, p.R525H, and DDX41 KO cells will enable us to assess how DDX41 mutation and deficiency impact gene expression and splicing events associated with P-body and SG pathways.

Results:
So far, investigation in HeLa cells has shown robust SG formation in response to sodium arsenite treatment, with DDX41 KO cells displaying persistent SGs that failed to disassemble in the same time that WT did, suggesting that DDX41 is essential for SG resolution following stress

Conclusion:
This project aims to clarify DDX41's role in the formation of P-bodies and SGs during cellular stress, enhancing our knowledge of the molecular mechanisms that govern the stress response and the consequences of mutations in essential genes.

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63. UNRAVELING THE REGULATORY NETWORK OF A CRUCIAL PROTEIN INVOLVED IN LYME BORRELIOSIS

Presenter:	**Supriya Ramesh**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Kerri Kobryn, College of Medicine
Supervisor:	Jenny Wachter, College of Medicine

Background:

Lyme disease, caused by the spirochete Borrelia burgdorferi, is the most prevalent tick-borne illness in the Northern Hemisphere, with over 400,000 new cases annually in the United States. Despite its significant public health impact, no effective human vaccine exists. This bacterial infection is transmitted through tick bites and thrives in a complex enzootic cycle involving a hard tick vector and a vertebrate host. The transition between these hosts necessitates tight regulation of gene expression and protein profiles in response to varying environmental cues. Central to this regulatory process is the alternate sigma factor RpoS, essential for host infection. Overexpression of RpoS is lethal to the spirochetes, necessitating precise regulatory mechanisms.

Methods:

Preliminary data strongly suggests that BBD18 is a DNA or RNA binding protein and directly effects the expression of 15 genes. We would like to confirm the ability of BBD18 to bind nucleic acids and will start by performing electromobility shift assays using DNA/RNA probes of the 15 genes found to be differentially regulated in the absence of BBD18. To determine additional targets, substrates, and binding partners of BBD18 we plan to perform co-immunoprecipitation experiments followed by sequencing and mass spectrometry.

Results:

The bbd18 gene with pET30a vector backbone was obtained from GenScript. The expression vector was used to isolate and purify recombinant BBD18 protein. The 16 DNA probes were amplified using their respective primers and further purified. Currently, we are optimizing the conditions for gel shift assays.

Conclusion:

As this plasmid-encoded protein is essential for spirochete survival and infectivity, we seek to further define the regulatory network utilized by BBD18 to control the critical component of the spirochete's adaptive response to vertebrate infection, RpoS.

64. DEVELOPMENT OF SARS-COV-2 REPLICATION TOOLS TO STUDY HOST-PATHOGEN INTERACTIONS

Presenter:	**Megha Rohamare**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Anil Kumar, College of Medicine
	Darryl Falzarano
Supervisor:	Joyce Wilson, College of Medicine

Background:

The development of SARS-CoV-2 replication tools is crucial for understanding the complex host-pathogen interactions that drive COVID-19. SARS-CoV-2, a novel coronavirus responsible for the global pandemic, has unique mechanisms for infecting human cells and evading immune responses. However, the specific interactions between the virus and host cell factors remain underexplored. This project aims to create and optimize tools, including replicative systems and viral reporter constructs, to study the virus's replication cycle and its impact on host cells. By establishing these tools, the project will provide a platform for screening potential therapeutic agents. Ultimately, this work will contribute to a deeper understanding of SARS-CoV-2 biology, support the development of antiviral therapies, and inform strategies to manage future coronavirus outbreaks.

Methods:

In Vitro Transcription: The full-length SARS-CoV-2 cDNA is transcribed in vitro to produce RNA, which is then used for transfection into host cells to generate virus particles. Transfection of Host Cells: The RNA generated from the cDNA is transfected into a suitable cell line (often Vero cells or other permissive cell types) to produce the SARS-CoV-2 virus. Selection of Viral Variants: The reverse genetics system allows for the introduction of mutations or deletions in the SARS-CoV-2 genome to study the impact of specific genes or mutations on viral replication and pathogenesis. RNA-Seq for Genome Stability: To assess the impact of SARS-CoV-2 infection on host cell genome stability, RNA sequencing is performed to analyze changes in maintaining genome integrity during infection. TCID50 (Tissue Culture Infectious Dose 50%) is the amount of virus required to infect 50% of cultured cells, used to quantify viral infectivity and determine viral titers.Growth kinetics- performed by infecting cultured cells with virus, incubating for a set period, and collecting supernatants at various time points for viral titration. Antiviral assays- conducted by treating infected cells with compounds and measuring their effect on viral replication or cytopathic effects.

Results:

We successfully generated full-length molecular clones for SARS-CoV-2 Delta WT and Omicron WT variants, confirming their replication in VERO cells. Viral titers increased over multiple passages, with Delta WT showing a consistent rise from 1×10^6 PFU/mL to 6×10^6 PFU/mL, and Omicron WT from 6.9×10^5 PFU/mL to 2.9×10^6 PFU/mL. Delta exhibited stronger cytopathic effects, while Omicron showed delayed CPE. Nano-luciferase reporter viruses (Delta NLuc and Omicron NLuc) were used for rapid antiviral screening, with Remdesivir, Molnupiravir, and Nirmatrelvir showing dose-dependent inhibitory effects in both viruses. Whole genome sequencing revealed high sequence stability in Delta strains, while Omicron strains accumulated mutations, particularly in genes associated with replication and the spike protein, which correlated with enhanced viral replication in later passages.

Conclusion:

The generation of the SARS-CoV-2 Delta and Omicron molecular clones and their corresponding Nano-luciferase reporter viruses provides valuable tools for studying viral replication, evolution, and antiviral drug screening. The observed mutations in Omicron suggest potential adaptations for improved replication, while stable Delta variants highlight consistent viral characteristics. The use of these reporter viruses in antiviral assays confirmed the efficacy of approved drugs, making them promising candidates for future therapeutic research.

65. GLP-1R/GIPR DUAL AGONISM ON GUT LIPID HANDLING IN RATS

Presenter:	**Farnoosh Tabatabaeian**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Rita Wang, College Medicine
	Kundanika Mukherjee, College Medicine
	Changting Xiao, College Medicine
Supervisor:	Changting Xiao, College of Medicine

Background:
Metabolic diseases, such as obesity and type 2 diabetes, are associated with atherogenic dyslipidemia, a condition with high levels of harmful blood lipids that cause atherosclerotic cardiovascular disease (ASCVD) and death. The gut mis-handles lipids in metabolic diseases by generating a larger amount of harmful lipid particles known as chylomicrons. Tirzepatide is a peptide that simultaneously activates the glucagon-like peptide receptor (GLP-1R) and the glucose-dependent insulinotropic polypeptide receptor (GIPR). It is an effective treatment for obesity and type 2 diabetes. It has also shown to improve blood lipids and lower ASCVD risks. However, it remains unclear whether these effects result from weight loss, improvement in systemic metabolism, or direct modulation of lipid handling in the gut.

Methods:
This study assesses the effects of tirzepatide on gut lipid secretion and metabolic regulation using a rat model. Male Sprague-Dawley rats were fed either a high-fat diet (to induce compromised metabolism) or a control diet for eight weeks and were injected subcutaneously with tirzepatide or placebo for the final week. Intraperitoneal glucose tolerance tests (IPGTT) were performed at week six to assess glucose metabolism. Rats then underwent surgical catheter implantation for lipid infusion into the small intestine and mesenteric lymph collection. Lymph flow rate and triglyceride levels were analyzed.

Results:
High-fat feeding causes glucose intolerance, indicating compromised metabolism. Preliminary findings suggest that high-fat feeding increases gut lipid output compared with control diet, and tirzepatide treatment attenuates gut lipid output regardless of diets. Underlying cellular and molecular mechanisms are being investigated through assessments of gut morphology and gene expression (qPCR and spatial transcriptomics).

Conclusion:
These findings will provide insights into the regulation and metabolic adaptation of gut lipid secretion and whether GLP-1R/GIPR dual agonism by tirzepatide directly modulates gut lipid metabolism. This research may help identify therapeutic targets in the gut for dyslipidemia and ASCVD.

66. PROTEOMICS CHARACTERISATION OF PERINEURAL INVASION COMPETENT CANCER CELLS USING AN EX-VIVO MODEL

Presenter:	**Nickson Joseph**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	George Katselis, College of Medicine
	Paulos Chumala, College of Medicine
Supervisor:	Anand Krishnan, PhD
	College of Medicine

Background:
Perineural Invasion (PNI) is the invasion of cancer cells into peripheral nerves, particularly into the perineural space. PNI is identified as a risk factor for cancer recurrence and metastasis. The exact mechanism that drives PNI is still unknown. Here, using our newly developed ex-vivo PNI model, we characterised the proteomics profile of PNI competent breast cancer cells to study the characteristic molecular features of PNI competent cells.

Methods:
Dorsal Root Ganglion (DRG)-nerve preparations were embedded in Cultrex in a 24-well plate and eGFP+ MDA MB 231 breast cancer cells were seeded into each well for creating a 3D co-culture. After 2 weeks, the preparations were isolated for immunostaining to detect the spatial orientation of PNI competent cancer cells within the DRG-nerve cellular environment. Additional preparations were used for generating individual cell suspension after enzymatic digestion of the tissues. The eGFP+ PNI competent cancer cells were then sorted from the icell suspension using a cell sorter and proteins isolated from the purified cells were used for LC-MS/MS analysis.

Results:
MDA MB 231 cells that invaded the DRG-nerve preparations were found around sensory neurons, not Schwann Cells and axons, indicating that sensory neuron-derived tropic signals might facilitate PNI. Proteomics characterisation of purified PNI competent cancer cells showed the unique upregulation of ciliogenesis and planar polarity effector-1 (CPLANE-1).

Conclusion:
Our results indicate that tropic signals derived from sensory neurons may promote PNI. Our result also indicates that CPLANE-1 may serve as a molecular target or biomarker for PNI competent breast cancer cells.

67. PITX2C TRANSCRIPTIONAL REGULATION OF CARDIAC RHYTHM

Presenter:	**Andy Kim**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Jared Stevenson, College of Arts and Science
	Sebastian Gauvrit, College of Medicine
Supervisor:	Michelle Collins, College of Medicine

Background:

Atrial fibrillation (AF) is the most common cardiac arrhythmia, and patients with AF are faced with increased morbidity and mortality. Recently, genetic variants associated with AF populations have been identified near the paired-like homeodomain transcription factor 2 (PITX2) gene. PITX2C is known to be crucial in maintaining cardiac rhythm through transcriptional regulation of key cardiac rhythm genes. However, how PITX2C acts as a central regulator of cardiac rhythm, and how its dysregulation drives arrhythmogenesis is not completely understood. I hypothesize that decreased PITX2C function will cause transcriptional changes in key cardiac rhythm genes, leading to global tissue-level consequences that sustain arrhythmogenesis.

Methods:

Here, we aim to knockdown Pitx2c in isolated neonatal rat atrial myocytes (NRAMs) and characterize key readouts of impaired cardiomyocyte function. One of the crucial processes we hypothesize to be disrupted is excitation-contraction coupling. This will be examined by live cell imaging of intracellular Ca2+ dynamics using a fluorescent indicator. Additionally, key contractile proteins will be assessed by immunofluorescent imaging using antibodies against a-actinin, myomesin, and titin. Cardiac metabolism, supplying the energy to beat, will be examined using Seahorse XFp to assess mitochondrial energetics.

Results:

We have observed that Pitx2c knockdown NRAMs display decreased contractile function owing to an increased frequency of abnormal oscillations, highlighting early afterdepolarizations, a marker of arrhythmias. In further detriment of contractility, we have observed mis-localization of Titin, an integral protein to the sarcomeres, the basic units responsible for shortening upon contraction. Additionally, Pitx2c knockdown NRAMs display reduced oxidative phosphorylation, a highly efficient energy production process within the mitochondria.

Conclusion:

Development of this NRAM Pitx2c knockdown model that recapitulates arrhythmic phenotypes is crucial to understand the orchestral role of PITX2C in cardiac function. Future studies will determine the gene regulatory network downstream of PITX2C to link gene expression changes and AF pathogenesis.

68. EVOLUTION AND ROLE OF BETACORONAVIRUS TRANSCRIPTION REGULATORY SEQUENCE (TRS) IN DISEASE PATHOGENESIS

Presenter:	**Arkadeb Bhuinya**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Arinjay Banerjee, Western College of Veterinary Medicine

Background:
Zoonotic coronaviruses like severe acute respiratory syndrome coronavirus (SARS-CoV), SARS-CoV-2, and Middle East respiratory syndrome (MERS-CoV) have caused significant human outbreaks and have cumulatively claimed the lives of seven million people in the 21st century. All three coronaviruses are speculated to have evolved in bats and transmitted to humans zoonotically through unknown intermediate hosts. While both SARS-CoV-2 and MERS-CoV share a bat origin, they have different case fatality rates of 0.4-15% and 37%, respectively in infected humans. Factors that drive this differential pathogenicity between zoonotically transmitted highly pathogenic coronaviruses remain unknown. Transcription regulatory sequence (TRS) is a short motif present in coronavirus genomes that regulate viral transcription. Although SARS-CoV-2 and MERS-CoV proteins contribute directly to disease pathogenesis by inhibiting cellular antiviral response, little is known about role of these TRSs on viral protein expression.

Methods:
Expression of TRS regulated transcription intermediates are quantified using quantitative polymerase chain reaction from in vitro and in vivo samples. To demonstrate the dependence of coronavirus gene expression on TRS, I have developed an in vitro reporter model using several molecular techniques to screen the transcriptional strengths of coronavirus TRSs. I will generate weak TRS mutant viruses using a reverse genetics platform that I am optimizing to demonstrate that TRS is critical for infection and pathogenesis in in vivo model.

Results:
In SARS-CoV-2, the accessory gene ORF6 exhibits reduced expression at transcript levels in infected samples. This pattern of lower expression is consistent across both the wildtype virus and its variants. Utilizing a reporter assay, we have identified that the TRS of ORF6 demonstrates diminished activity at both the RNA and protein levels. We are presently investigating the underlying mechanisms responsible for this observation.

Conclusion:
The findings from my research will develop an advanced framework for investigating viral TRSs in zoonotic coronaviruses that are not yet well understood.

69. INVESTIGATING THE ROLE OF INHIBITORY FACTOR-1 (IF1) IN OZONE- INDUCED LUNG INFLAMMATION.

Presenter:	**Mohammad Umar**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Gurpreet K. Aulakh, Western College of Veterinary Medicine

Background:
ATP Synthase Inhibitory Factory 1 (IF1) prevents the mitochondrial ATP Synthase (ATPSV) hydrolyzing activity. Neutrophils are known to express ATPSV on the plasma membrane during lung inflammation. It is not entirely clear how IF1 and its mimic molecule BTB06584 function in the process of neutrophil recruitment in O3-induced lung inflammation. We sought to determine the role of BTB and IF1 in neutrophilic lung inflammation in vitro and in vivo using an IF1 KO mice model.

Methods:
To study the interaction of the ATPSV-β subunit with BTB06584, we performed a DARTS assay. We proceeded to study the role of IF1 in neutrophil migration using a neutrophil-specific IF1 knockout mice model, developed using the Cre-LoxP system. We imaged the neutrophil migration in vivo using the lung intravital imaging and in vitro by chemotaxis assay.

Results:
The results from the DARTs assay revealed that BTB induces the proteolytic degradation of ATPSV-β subunit in a concentration-dependent manner ($p<0.01$). We further studied the effect of BTB on neutrophil migration and found that BTB increases fMLP-induced neutrophil migration by 2 folds in a dose-dependent manner ($p<0.01$). Further, we have developed knockout mice using Myeloid Related Protein (MRP8) Cre-IF1Lox technology to understand the role of IF1 in neutrophil activation and migration using lung intravital imaging and neutrophil chemotaxis assays. We also observed a 2-fold increase in neutrophils in the lungs exposed to the ozone as compared to the non-exposed in wild-type C57BL/6J and IF1 floxed mice. The genotyping and immunocytochemistry from the bone marrow-derived neutrophil reveals 7 out of 19 germline IF1 knockout mice that are being used for BALF, blood & Tissue collection.

Conclusion:
We conclude that BTB assist in proteolytic degradation of β-subunit and increases the migration of the bone marrow neutrophils. The genotyping data reveals germline knockouts instead of desired neutrophil-specific IF1 knockouts in F2 generation.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

70. HYPOXIA-INDUCIBLE FACTOR-1A AS A POTENTIAL CONTRIBUTOR TO GINGIVAL OVERGROWTH

Presenter:	**Asmaa Fadl**
USask Affiliation:	**Graduate student**
College:	**College of Dentistry**
Supervisor:	Andrew Leask, PhD College of Dentistry

Background:
Gingival overgrowth, an excessive enlargement of gum tissue around the teeth caused by certain medications, genetic mutations, or chronic inflammation, can obscure teeth, hinder speech and mastication, compromise oral hygiene, and affect esthetics, ultimately diminishing quality of life. High recurrence rates after surgical intervention underscore the need for non-invasive approaches. Fibrotic gingival overgrowth, characterized by extracellular matrix (ECM) accumulation, has been associated with microvascular alterations observed in drug-induced cases and fibrosis induced by smoking or chronic periodontitis, indicating a hypoxic microenvironment. The contribution of hypoxia, through the key regulator hypoxia-inducible factor (HIF)-1α, to gingival overgrowth remains unexplored. Therefore, we investigated HIF-1α's role in fibrotic responses of human gingival fibroblasts (HGFs), proposing it as a potential therapeutic target for fibrotic gingival overgrowth.

Methods:
HGFs were treated with or without dimethyloxallyl glycine (DMOG), a hypoxia-mimetic agent, for 6 hours. Western blotting and immunofluorescence were used to assess the expression of HIF-1α protein and fibrosis-related transcription factors. Changes in profibrotic and ECM gene expression following HIF-1α stabilization were evaluated using real-time PCR (RT-PCR). To further confirm findings, small-interfering RNA (siRNA) was employed to knock down HIF-1α and assess changes in profibrotic gene expression in HIF-1α's absence.

Results:
In response to DMOG, HIF-1α protein was significantly stabilized and translocated to the nucleus, accompanied by increased protein expression of fibrosis-related transcription factors, particularly early growth response 1 (EGR1) (N = 3). RT-PCR revealed upregulation of profibrotic and ECM collagen-encoding genes following HIF-1α stabilization, most notably connective tissue growth factor (CTGF) and type IV collagen alpha 3 chain (COL4A3). These genes were downregulated upon HIF-1α knockdown using siRNA (N = 3, p-value <0.05).

Conclusion:
This study demonstrates that HIF-1α stabilization promotes the expression of fibrosis-related genes in HGFs, highlighting the potential role of hypoxia, via HIF-1α, in fibrotic gingival overgrowth and positioning HIF-1α as a novel therapeutic target.

71. DNA DAMAGE TOLERANCE: NOVEL INTERACTIONS OF THE SIR SILENCING COMPLEX WITH INTEGRAL DAMAGE TOLERANCE PATHWAYS

Presenter:	**Josephine Rybchuk**
USask Affiliation:	**Graduate student**
College:	**College of Arts & Science**
Supervisor:	Wei Xiao, College of Arts and Science

Background:

DNA Damage Tolerance Response The Proliferating Cellular Nuclear Antigen (PCNA) dependent tolerance response is initiated once PCNA encounters a lesion on the DNA strand during replication. Failure to address damage leads to replication fork stalling, collapse, and ultimately cell death due to replication failure. The resultant pathway (right) can be modulated by mono- or poly-ubiquitination of PCNA allowing for direction between the lower fidelity translesion DNA synthesis (TLS) or the higher fidelity homology directed/error-free DNA damage repair. The Silencing Information Regulator Complex Although responsible for mating type expression in yeast, the Silencing Information Regulator (SIR) complex is also associated with interaction with and promotion of DNA damage responses through multiple mechanisms (left). As yeast Sir proteins mimic their human counterpart Sirtuin proteins, which are involved in cellular aging and DNA damage responses, ideally our understanding of yeast Sir functions can be extrapolated to higher level mammalians.

Methods:

Targeted gene disruption in 10D (W303 MAT□) yeast strains via PCR generated disruption cassettes for the gene of interest with a YDP plasmid selectable marker. Phenotypic assays such as serial dilutions, live-killing and recombination efficiency experiments to clarify the alterations in cell responses in the presence of variable DNA damaging agents: Methyl-methanesulfonate (MMS) – DNA double-strand break (DSB) induction 4-nitroquinoline oxide (4NQO) – DNA adduct formation, DNA DSB induction Ultraviolet radiation (UV) – DNA lesion formation, single-strand DNA breaks

Results:

Fig 2.1. Serial dilution assay showing rescue of cell sensitivity for knockouts of known sensitive DDT mutant rad5 with sir deletion mutants, where sir3 and sir4 can rescue sensitive mutants but not sir2
Fig 2.2 Serial dilution assay showing the change in phenotype upon gene knockouts of DDT mutants rad5, sir4 and rad51 indicating interaction and alteration in cell survival between sir4 and rad51(a). Further experiments including a live killing assay (b), a recombination efficiency assay (c) and a NHEj vs. HR event assay (d) further clarify the extent of Rad51 and Sir4 involvement with DDT mutant rad5.

Conclusion:

When investigating the DDT pathway and potential interactions of the peripheral Sir complex with DDT, we found a novel interaction for Sir3 and Sir4 with DDT branches, but not Sir2. When exploring this interaction further, we see that Sir3/Sir4 influence sensitivity of Rad5/Rad18 mutants in a Rad51 mediated manner, indicating preference for homologous recombination facilitated repair.

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72. SENSITIVITY ASSESSMENT FOR PAENIBACILLUS LARVAE DETECTION: A COMPARISON OF YARD AND BARREL SAMPLING METHODS

Presenter:	**Rosephine Enadeghe**
USask Affiliation:	**Postdoctoral fellow**
College:	**Western College of Veterinary Medicine**
Collaborators:	Belarmino Lopez Neto, Western College of Veterinary Medicine
	Oleksii Obshta, Western College of Veterinary Medicine
	Elemir Simko, Western College of Veterinary Medicine
Supervisor:	Elemir Simko, Western College of Veterinary Medicine
Co-supervisor(s):	Sarah Wood

Background:
A total of 212 honey samples collected from Yard (n=125) and 5th barrel (n=87) extraction were analyzed using culture-based and matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS) techniques RESULTS: Samples from yard extraction reveal low concentration of P. larvae spores <100 CFU/g whereas Samples from every 5th barrel revealed more spore concentration when compared American foulbrood (AFB) is a devastating disease in honey bees (Apis mellifera) caused by Paenibacillus larvae known to infect the larval and pupal stages of honey bees. Risk assessment of AFB is focused on adult bees samples collected from the individual hives. Accordingly this may not be feasible for large commercial operations which consequently rely on indiscriminate antibiotic metaphylaxis to control AFB thus a need for herd medicine. Our Objective was to compare

Methods:
A total of 212 honey samples collected from Yard (n=125) and 5th barrel (n=87) extraction were analyzed using culture-based and matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS) techniques

Results:
Samples from yard extraction reveal low concentration of P. larvae spores <100 CFU/g whereas Samples from every 5th barrel revealed more spore concentration when compared with samples collected from individual yards.

Conclusion:
This result demonstrates that Barrel samples seem to be more sensitive/representative however linking samples to a specific yard may be a challenge

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

73. GENETIC AND OCCUPATIONAL DETERMINANTS OF LUNG HEALTH TRAJECTORIES IN GRAIN WORKERS: A LONGITUDINAL MULTILEVEL MEDIATION STUDY

Presenter:	**Barada Mohanty**
USask Affiliation:	**Graduate student**
College:	**School of Public Health**
Collaborators:	Zhiwei Gao
	James Dosman, College of Medicine
	Punam Pahwa, College of Medicine
Supervisor:	Punam Pahwa, PhD
	College of Medicine
Co-supervisor(s):	Zhiwei Gao, PhD

Background:
Both genetic and environmental factors, including gene-environment interactions, influence changes in lung function over time. Certain genotypes may mediate or suppress the association between occupational exposures and lung function decline. This study investigates how genetic polymorphisms interact with years of exposure in the grain industry to influence longitudinal changes in forced vital capacity (FVC) and forced expiratory volume in one second (FEV1) among Canadian grain elevator workers.

Methods:
Longitudinal data from the Saskatchewan Grain Workers' Surveillance Program (1978–2005), comprising 1,195 observations from 213 individuals, were analyzed. Multilevel modeling was applied to account for repeated measures across nine data collection cycles. A stacked data approach was used, combining the dependent variable (DV) and mediator into a single stacked response variable. This variable was used to fit a mixed-effects model, incorporating indicator variables for the DV and mediator to derive all necessary estimates for the mediation analysis. Based on the levels of time-dependence for exposure (X), mediator (M), and outcome (Y), four analytical scenarios were considered: 1-1-1, 2-1-1, 1-2-1, and 2-2-1. For instance, in the 1-2-1 scenario, the M was time-independent (higher level), while X and Y were time-dependent (lower level).

Results:
The TNF-alpha genotype demonstrated a suppressing effect on the relationship between years of grain industry exposure and both FVC and FEV1. No significant ($p > 0.05$) mediation or suppression was observed for other genotypes. The indirect effects accounted for 25% of the total effect on FVC and 14% on FEV1, both acting in the opposite direction of the direct effects- indicating suppression, where TNF-alpha offset the negative impact of occupational exposure on lung function.

Conclusion:
The suppressive role of TNF-alpha highlights the potential for genetic factors to buffer adverse occupational exposures. Incorporating gene-environment interactions within a mediation framework may enhance risk assessment and guide occupational health policies.

74. REVEALING CHANGES OF GENE-GENE RELATIONSHIPS IN CHRONIC OBSTRUCTIVE PULMONARY DISEASE THROUGH GENE NETWORK ANALYSIS OF SINGLE-CELL RNA SEQUENCING DATA

Presenter:	**Jing Wang**
USask Affiliation:	**Graduate student**
College:	**School of Public Health**
Collaborators:	Yang Guo
	Li Xing
	Xuekui Zhang
Supervisor:	Li Xing, College of Arts and Science

Background:
Chronic obstructive pulmonary disease (COPD) is a major cause of mortality and disability worldwide, with genetic factors playing a crucial role. Gene-gene relationships influence cellular processes and disease progression. By comparing these relationships in COPD patients versus healthy controls, this research aims to identify key genes involved in COPD mechanisms.

Methods:
We apply the Peeling Algorithm (PA)—an iterative method for feature selection in high-dimensional data—to examine changes in gene coreness across four cell types: cMonocyte, ncMonocyte, Macrophage, and Macrophage Alveolar. Multiple dissimilarity measures are used to evaluate gene relationships, and PA is performed at varying thresholds to pinpoint significant gene-gene relationship differences. To further explore the biological role of identified genes, gene set enrichment analysis is conducted to detect pathways that may be relevant to COPD.

Results:
By analyzing differences in gene-gene interaction between control and COPD groups, the PA successfully highlights genes with notable changes in coreness. Subsequent gene set enrichment analyses reveal pathways potentially linked to COPD pathophysiology, providing insights into the disease's underlying molecular mechanisms.

Conclusion:
Our findings underscore the importance of gene-gene interaction networks in understanding COPD. The integrated use of the Peeling Algorithm and gene set enrichment analysis offers a powerful approach for pinpointing critical genes and pathways involved in COPD progression.

75. REIMAGINING HEALTH EDUCATION: A SOTL APPROACH TO ANTI-OPPRESSIVE PEDAGOGY IN A MASTER OF PHYSICAL THERAPY PROGRAM

Presenter:	**Sara Reena**
USask Affiliation:	**Graduate student**
College:	**School of Public Health**
Collaborators:	Carrie Stavness, Mya Duong, Sarah Oosman
Supervisor:	Sarah Oosman, School of Rehabilitation Science

Background:
Racism is a key determinant driving health inequities among Indigenous populations in Canada. Canadian healthcare professional graduates are entering a health system requiring enhanced critical reflexivity, cultural humility, and anti-oppressive skills. Educators must develop these skills in our students and build professionals that are equipped to address decolonizing practices in their work. Our Master of Physical Therapy (MPT) program is engaging in curricular renewal during a time of expansion and growth, providing a unique opportunity to augment anti-oppressive pedagogy (AOP). Through an MPT summer research project, our team explores student's experiences of and perspectives on current existing pedagogies in MPT curriculum and barriers to decolonizing in their MPT journey. We sought to understandHow faculty and clinical instructors can meaningfully incorporate anti-oppressive pedagogy (including decolonization, reconciliation, cultural humility) into MPT curriculum.

Methods:
The team conducted student focus groups exploring MPT student experiences with learning anti-oppressive professional practice skills, including student-driven recommendations, essential to collectively informing our teaching/learning pathway. Principles such as student-educator partnerships and co-creation from the Scholarship of Teaching and Learning (SoTL) characterized the application of AOP within the program and the study methodology.

Results:
Analysis of data utilizing Simmons 4M framework (2020) revealed: Desire for land-based learning led by Indigenous Knowledge Holders, Need for dismantling self-identified barriers to reflection and decolonization, Support for un-grading to promote learning in the absence of grades, Importance of instructors being explicit about scaffolding anti-oppressive approaches, Support to dismantle fears when calling out racism within power hierarchies

Conclusion:
Results inform AOP-inclusive pedagogy, preparing MPT graduates to apply essential skills in the health system. MPT students recognize the need to self-decolonize and critically reflect on their knowledge and practice. These findings are applicable to health care professional educators and researchers engaging in curriculum re-design, both nationally and internationally.

Self-declaration of research alignment with additional themes (optional):
Indigenous Health Research

76. CULTURAL CONTINUITY AND POSITIVE MENTAL HEALTH AMONG ON-RESERVE FIRST NATIONS ADULTS IN RURAL SASKATCHEWAN: GENDER-SPECIFIC INSIGHTS

Presenter:	**Humaira Anjum**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Reynaldo Lindain, Warren Seesequasis, Nicole Bird
Supervisor:	Bonnie Janzen, PhD College of Medicine

Background:
Rooted in historical and ongoing colonial injustices, many Indigenous people in Canada experience substantial challenges to their mental well-being. Cultural continuity may be a protective factor for Indigenous people's mental health by reinforcing a sense of identity and solidarity. However, limited research has explored how cultural continuity may be associated with self-reported positive mental health among adult First Nations people living on reserve, and whether such relationships differ by gender. To bridge these knowledge gaps, this study adopts a strengths-based approach to investigate the association.

Methods:
Data were drawn from a community-based cross-sectional survey, the most recent iteration of a 12-year collaboration between three rural Saskatchewan First Nations communities and the University of Saskatchewan, which involved 832 participants (55% women), aged 18 years and above. Ethical approval from the University and community consent were also obtained for this secondary data analysis.

Results:
Initial descriptive analyses showed that 57% of participants self-reported positive mental health; men (67%) were significantly more likely than women (49%) to report so ($p \leq 0.001$). Preliminary results also suggested associations between positive mental health and key aspects of cultural continuity including traditional language use, connection to land, community belonging, and participation in cultural activities. For both women and men, positive mental health was linked to a stronger connection to the land, a greater sense of community belonging, and participation in storytelling. Gender differences in the mental health correlates were evident, with making clothes and plant gathering associated with positive mental health in women, and Indigenous language proficiency, storytelling, and singing/dancing associated with positive mental health in men.

Conclusion:
These initial observations suggest a relationship between cultural continuity and positive mental health among First Nations adults with possible gender-based variation. Further analyses, including exploratory factor analysis and multivariable regression, are planned to clarify these relationships.

Self-declaration of research alignment with additional themes (optional):
Indigenous Health Research

77. LIMITING CONTINUOUS SITTING BEHAVIOUR WHILE ON CAMPUS: FOCUS ON MOVING VERSUS MINUTES

Presenter:	**Bailey Gitzel**
USask Affiliation:	**Graduate student**
College:	**College of Kinesiology**
Collaborators:	Brittany Krammer
	Jantz Sawatsky
	Darren Nickel
Supervisor:	Kevin S. Spink, College of Kinesiology

Background:
Engaging in physical activity (PA) and reducing sedentary behaviour are associated with health benefits (CDC, 2020), but different paths to achieving these health benefits have been identified. The traditional messaging approach suggests that adults should accumulate at least 150 minutes of moderate-to-vigorous PA each week as well as limit long periods of sitting (CESP, 2021). In contrast, WHO (2020) now suggests changing our PA messaging to highlight that health benefits come from moving regardless of the intensity or duration. However, the effectiveness of these two message types has not been tested. The purpose of this experimental study was to examine whether 'movement' or 'minute' messages would be more effective in limiting on-campus sitting behaviour.

Methods:
In an online study, university students completed two surveys. Survey one assessed demographics, perceived PA adequacy for health (Zahrt & Crum, 2020), and on-campus sitting behaviour. Students were then randomly assigned to receive either a 'move' (n=46) or '150 minute' (n = 42) message. One week later, survey two reassessed on-campus sitting behaviour.

Results:
Results from an ANOVA revealed that the messages significantly affected sitting behaviour, $F(1,84) = 8.86$, $p=.004$, partial eta squared =.10, while controlling for pre-message on-campus sitting and perceived PA adequacy for health. Those receiving the 'move' message reported limiting the time they remained continuously seated at any one time significantly more than those receiving the 'minute' message.

Conclusion:
This study provides initial evidence suggesting that 'move' messaging may be more effective in limiting on-campus continuous sitting behaviour than the traditional 150 'minute' message. If these results can be replicated, they may have implications for future messaging.

78. MATERNAL NEAR-MISS AND QUALITY OF CARE IN FIRST - LEVEL REFERRAL HOSPITALS IN INHAMBANE, SOUTHERN MOZAMBIQUE – A MIXED-METHODS STUDY

Presenter: **Fernanda Andre**
USask Affiliation: **Graduate student**
College: **College of Medicine**
Supervisor: Nazeem Muhajarine, College of Medicine

Background:
Pregnancy-related complications continue to significantly affect the lives of women worldwide. Women in sub-Saharan Africa, account for nearly two-thirds of global maternal deaths. The WHO recommends monitoring maternal near-misses (MNM) (of deaths), as this approach provides a better understanding of the quality of care women receive at the health facility. Mothers who experience severe complications, such as severe pre-eclampsia, or postpartum hemorrhage, often share common risk factors.

Methods:
A cross-sectional, explanatory sequential designed mixed-methods study was conducted from June 6 to December 9, 2022, using the Mozambique-Canada Maternal Health project criteria for MNM at two regional hospitals in Mozambique. Six hundred thirty-eight participants were enrolled in the study, and 43 of them participated in qualitative interviews. We performed a multivariable logistic regression analysis after checking for multicollinearity using the VIF and standard error. The intra-facility correlation was adjusted using the Huber-White standard error estimator. We used grounded theory methodologies to analyze the qualitative data.

Results:
The incidence proportion of MNM is 147 per 1,000 live births (14.7%). Age, distance travelled, ANC visits, labour onset, and multiple deliveries were significantly associated with MNM. Older mothers (>35 years), with multiple deliveries, referred for care before labour were more likely to experience an MNM. Mothers living more than eight kilometres from the hospital had lower odds of an MNM. Women's experiences of an MNM fell under four themes: becoming near-miss, co-morbidities, distance travelled, and poor risk awareness of maternal complications.

Conclusion:
The quality of ANC care women receive needs improvement. Unlike maternal deaths, women who survive an MNM have a story to tell. These narratives provide a better understanding of the underlying factors contributing to MNM cases.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

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79. - STRATEGIES TO PROMOTE ORAL HEALTH EQUITY FOR IMMIGRANT POPULATIONS IN CANADA AND THE USA: A SCOPING REVIEW PROTOCOL

Presenter:	**Rutik Isai**
USask Affiliation:	**Graduate student**
College:	**School of Public Health**
Collaborators:	Debora Lana Alves Monteiro, Jessi Robinson, Amrinderbir Singh
Supervisor:	Juliana Faquim, DDS, MSc, PhD College of Dentistry

Background:
Global migration resulted in an estimated 281 million international migrants in 2020. North America, particularly Canada and the United States, continues to be a main destination for migrants, and Canada has hosted more than 3 million non-permanent residents as of 2024. While migrants may have opportunities for improved quality of life, they also encounter barriers to dental care access, including financial distress, lack of insurance, language barriers, and cultural unfamiliarity. The purpose of this scoping review is to map existing evidence related to dental care, interventions and strategies for immigrants in Canada and United States.

Methods:
Following the PRISMA-ScR and JBI guidelines, we will systematically search MEDLINE (PubMed), Scopus, Web of Science, EBSCO, and grey literature (Open Grey, Google Scholar) for English-language studies (2014-2024). Inclusion criteria focus on immigrants, refugees, asylum seekers, and non-permanent residents in Canada/USA, excluding the long-term residents & non-English publications. The protocol is registered with OSF.

Results:
Preliminary findings will aim to categorize effective interventions (e.g., culturally tailored programs, policy changes), systemic barriers (financial, linguistic, geographic), and facilitators (community-based approaches, health literacy initiatives). Results will be presented thematically with supporting tables/figures to visualize key patterns in dental care equity strategies.

Conclusion:
This review will identify interventions and strategies in promoting dental care equity for immigrant populations. The synthesized evidence aims to inform policymakers and healthcare providers in developing more accessible, culturally competent dental services.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

80. THE ASSESSMENT AND UTILITY OF THE PHARMAZZZ TRAINING PROGRAM AND PROVISION OF COGNITIVE BEHAVIORAL THERAPY FOR INSOMNIA (CBTI)

Presenter:	**Melissa Neudorf**
USask Affiliation:	**Graduate student**
College:	**College of Pharmacy and Nutrition**
Collaborators:	Karen Jensen
	Holly Mansell, College of Pharmacy and Nutrition
	Alfred Remillard, College of Pharmacy and Nutrition
Supervisor:	Katelyn Halpape BSP, ACPR, PharmD, BCPP
	College of Pharmacy and Nutrition

Background:
CBTi for insomnia is recommended as first-line therapy over pharmacotherapy, however, one of challenges to the accessibility of this treatment is limited providers. PharmaZzz is a program that trains healthcare professionals to provide CBTi. This study describes the impact of the PharmaZzz program and the current practices of PharmaZzz-trained healthcare professionals.

Methods:
An electronic, cross-sectional questionnaire was emailed to all healthcare professionals that completed the PharmaZzz program. Data collection was open from November 25th, 2024 to January 20th, 2025. The questionnaire explored program experience, implementation of CBTi services in their practice, and perceived patient response. Data was collected in REDCap and analyzed using descriptive statistics and content analysis for open-text responses.

Results:
Eighteen healthcare professionals responded to the survey and met the inclusion criteria. Most healthcare professionals found the program useful (94.4%), applicable to their practice (72.2%), and user-friendly (94.1%). All respondents indicated the course was an efficient use of time. The number of respondents that provide CBTi in practice is high (61.1%). All perceive their provision of CBTi as beneficial and improving patients' sleep patterns. A common challenge found by respondents was the lack of time to implement CBTi into practice. In terms of improvement of the program, respondents requested that it include more real-world examples.

Conclusion:
There was an overall positive response to PharmaZzz. There were many aspects that respondents liked about the course, however, there were suggested areas for improvement. Due to the low response rate and most of the respondents being pharmacists, the results are not representative of non-pharmacist healthcare professionals.

81. HOW DENTAL PROFESSIONALS CAN IDENTIFY, REPORT, ADDRESS, AND TREAT DOMESTIC VIOLENCE VICTIMS? A QUALITATIVE STUDY TOWARDS CREATING GUIDELINES

Presenter:	**Ana Beatriz Cantao**
USask Affiliation:	**Graduate student**
College:	**College of Dentistry**
Collaborators:	Ana Beatriz Cantao, College of Dentistry
	Liran Levin, College of Dentistry
Supervisor:	Liran Levin, College of Dentistry

Background:
Domestic violence (DV) represents a critical public health concern with widespread impact across diverse populations, particularly affecting children, women, LGBTQI+ individuals, and those residing in rural areas. DV manifests in various forms, including physical, emotional, sexual, and financial abuse, often resulting in severe injuries, notably to the head, face, and oral cavity. Dental professionals are uniquely positioned to identify signs of abuse, such as traumatic dental injuries; however, barriers, including insufficient training, lack of standardized protocols, and uncertainty regarding intervention strategies, hinder their ability to effectively recognize, document, and report suspected cases.

Methods:
The aim of this study is to develop an evidence-based guide to support dental professionals in identifying, reporting, and managing DV cases in clinical practice. Using a qualitative research method, this research will integrate insights from dental professionals, physicians, psychologists, social workers, and legal experts to identify gaps in knowledge, training, and response protocols. The study will examine key clinical indicators of abuse, explore challenges faced by dental professionals, and establish best practices for incorporating DV response strategies into dental care.

Results:
Through semi-structured interviews, the research will generate data-driven recommendations to enhance dental professionals' roles in multidisciplinary DV interventions. This study will address clinical, ethical, and legal considerations related to DV identification and management, offering evidence-based strategies for recognizing signs of abuse, documenting cases, and facilitating appropriate referrals. Strengthening interprofessional collaboration is essential for an effective, coordinated response.

Conclusion:
The findings will contribute to bridging gaps in dental education and practice, equipping dental professionals with the necessary tools and expertise to address DV effectively. Results will be disseminated through open-access publications, conference presentations, and training materials. Multimedia tools, including animation clips, will be developed to promote knowledge mobilization and enhance the role of dental professionals in DV intervention.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

82. WHOLE GENOME SEQUENCE ANALYSIS OF GLOBAL PAENIBACILLUS LARVAE POPULATIONS

Presenter:	**Oleksii Obshta**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Tayab Soomro, College of Agriculture and Bioresources
	Midhun Jose, Western College of Veterinary Medicine
	Thanuri Eridithilake, Western College of Veterinary Medicine
Supervisor:	Sarah Wood, PhD, DACVP
	Western College of Veterinary Medicine

Background:

American foulbrood (AFB) is a fatal infectious disease of honey bee brood caused by the bacterium, Paenibacillus larvae. Infected colonies with clinical signs of AFB must be destroyed by burning. In North America, prevention of AFB outbreaks heavily relies on oxytetracycline metaphylaxis, resulting in sustained selective pressure for oxytetracycline resistance in P. larvae populations. In contrast, the use of antibiotics in prohibited in EU and New Zealand.

Methods:

To investigate the presence of antimicrobial resistance genes (ARGs) and genetic diversity of global P. larvae populations, publicly available P. larvae genomes (23 from Canada, 163 from New Zealand, 154 from EU) were analyzed using the Nullarbor bioinformatics pipeline to detect the presence of ARGs and virulence genes. Genetic diversity was assessed using single nucleotide polymorphism (SNP)-based phylogenetic analysis and core-genome multi-locus sequence typing.

Results:

The tetL tetracycline resistance gene was identified in 13 Canadian isolates; however, multiple other ARG`s (vanF, dfrC, mgrA, norA) were found in P. larvae isolates around the world. Multiple genotype-specific virulence genes were detected; however, presence of virulence genes was not associated with either ERIC type I or ERIC type II P. larvae genotype. Phylogenetic analysis revealed a clustering of the isolates based on their respective genotype and geographic location, with distinct P. larvae populations identified in NZ, the EU and Canada.

Conclusion:

Overall, this pilot study highlights the suitability of WGS analysis as a part of global P. larvae surveillance for monitoring the emergence and spread of antibiotic-resistant and highly-virulent isolates and tracing the geographic origin of these P. larvae variants.

83. REALIST EVALUATION OF FOOD WASTE DIVERSION PROGRAMS ACROSS CANADA

Presenter:	**Caitlin Olauson Barlas**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Supervisor:	Nazeem Muhajarine, College of Medicine
Co-supervisor(s):	Wanda Martin

Background:
Food loss and waste (FLW), including food grown and produced but not consumed, harm the environment and human health through air and water contamination. Up to one-third of global food is wasted, with 13% lost between harvest and retail. Reducing FLW improves food availability, reduces pollutants, and benefits the environment.

Methods:
A realist evaluation (RE) of existing food rescue organizations across Canada will explore how, why, under what circumstances and to what extent these organizations effectively divert edible food waste from private businesses like restaurants, retail, and event centers into organizations that support individuals experiencing food insecurity. This study will use purposeful sampling and a combination of methods to investigate factors influencing success for FLW reduction programs, including infrastructure, financial incentives, and regulatory support, while examining barriers like affordability and ease of implementation. This research is nested within a larger 5-phase research project called Second Chance Food that aims to develop a circular economy food system that meets environmental and social needs.

Results:
Research results and analysis have not yet been conducted; the research poster will focus on the purpose and protocol.

Conclusion:
The results of this research will be shared through traditional academic and non-academic means with the goal of contributing the global and scholarly discourse regarding food waste reduction and food insecurity through peer-reviewed publications and presentations, while also advance practical changes through stakeholder engagement to development municipal policy and practice recommendations.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

84. WHAT CAN BE LEARNED FROM ACCOUNTS OF THE EXPERIENCES OF IRANIAN IMMIGRANTS WITH LONG COVID IN CANADA: AN INTERPRETIVE DESCRIPTION APPROACH

Presenter:	**Mehrdad Askarian**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Tracey Carr, College of Medicine
	Gary Groot, College of Medicine
Supervisor:	Tracey Carr, College of Medicine
Co-supervisor(s):	Gary Groot

Background:
Long COVID (LC) is a global health challenge characterized by persistent and multifaceted symptoms that disproportionately affect marginalized populations. This thesis investigates the lived experiences of Iranian immigrants in Canada who are suffering from LC to provide a detailed understanding of how this specific group navigates the challenges associated with LC and to gain insights into their specific healthcare needs and preferences.

Methods:
The research engaged twenty Iranian immigrants in Canada suffering from LC, who were recruited through purposive sampling methods via Telegram groups utilizing an Interpretive Description (ID) methodology. Semi-structured interviews underwent thematic analysis.

Results:
Six principal themes were identified and interpreted through a rigorous analytical process: the phenotypes and trajectories of LC symptoms, healthcare challenges and the need for holistic care, emotional and psychological impact, economic and workplace vulnerabilities, role of social and online support networks and finally cultural and traditional healing practices. The results underscore notable deficiencies within the healthcare system, emphasizing the necessity for culturally adjusted, interdisciplinary interventions. Despite the difficulties stemming from cultural stigma and language barriers, participants demonstrated resilience through their community and cultural practices. These revelations enhance the comprehension of how LC intersects with health, culture, and immigration.

Conclusion:
This study advocates for pragmatic recommendations aimed at addressing the unfulfilled requirements of immigrant populations. Elevating the perspectives of Iranian immigrants with LC furnishes essential knowledge for healthcare practitioners and policymakers to formulate inclusive and equitable strategies. These discoveries contribute to the ongoing discourse surrounding LC and lay a foundation for systemic reforms to improve healthcare access for immigrant communities living with chronic conditions.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

85. WEIGHT STIGMA EXPERIENCED FROM HEALTHCARE PROFESSIONALS SEEN IN RELATION TO A BREAST CANCER DIAGNOSIS BY BREAST CANCER SURVIVORS IN SASKATCHEWAN

Presenter:	**Abby Lehmann**
USask Affiliation:	**Graduate student**
College:	**College of Pharmacy and Nutrition**
Supervisor:	Allison Cammer, RD, PhD College of Pharmacy and Nutrition
Co-supervisor(s):	Soo Kim, BScPT, PhD

Background:

In Canada, breast cancer is the most common cancer diagnosis among females, accounting for one-quarter of all cancer diagnoses. Being overweight or obese are risk factors for breast cancer development and recurrence. Breast cancer has subsequently been characterized as a weight-associated cancer. Weight stigma towards individuals with obesity is highly prevalent in the healthcare setting and is associated with further weight gain, increased incidence of chronic disease and avoidance or delay in seeking medical care. Weight stigma is experienced by women with breast cancer along their care continuum and can be associated with negative consequences to their cancer care.

Methods:

A 43-question survey was developed by the research team to meet the objectives of the study. Breast cancer patients diagnosed with breast cancer on or after January 2012 and subsequently treated (chemotherapy, radiation therapy, immunotherapy, endocrine therapy) in Saskatchewan were surveyed. A modified validated questionnaire, the Stigmatizing Situations Inventory (SSI), was used to determine if participants had experienced weight stigma from healthcare professionals seen in relation to their breast cancer diagnosis.

Results:

In total, 70 participant responses were analyzed. An average SSI score of 1.31 was found, indicating low levels of stigma experienced. Participants were more likely to experience higher levels of stigma if they had treatment-induced weight gain. SSI scores increased as BMI value increased. Obese participants had a 0.3 higher average SSI score normal weight or overweight participants

Conclusion:

The results of this study showed that participants experienced low levels of weight stigma from healthcare professionals seen in relation to their breast cancer diagnosis. This was contrary to the hypothesis of the research team. However, further research is needed to understand the experiences of participants with high SSI scores and participants who have a higher BMI with a goal of improving patient care outcomes.

Self-declaration of research alignment with additional themes (optional):

Interdisciplinary/Interprofessional Collaboration

Translational, Clinical, or Applied Science 1

86. DESIGNING A MUCOSAL RNA VACCINE AGAINST BOVINE ALPHA HERPESVIRUS-1 INFECTION IN CATTLE

Presenter: **Alaa Ibrahim**
USask Affiliation: **Graduate student**
College: **School of Public Health**
Supervisor: Aneesh Thakur, School of Public Health

Background:
Bovine alpha herpesvirus-1 (BoAHV-1) is a significant pathogen in the global cattle industry infecting both upper respiratory and genital tract mucosa leading to severe respiratory problems as well as reproduction defects like infectious rhinotracheitis and abortion, respectively. Vaccination is crucial for controlling BoAHV-1 infection in cattle. The available vaccines for BoAHV-1 in market are based on inactivated or live attenuated pathogens but these vaccines do not completely protect cattle from the risks of BoHV-1. The risk of reversion to virulence of live attenuated vaccines highlights the need to develop more safer and effective vaccines against BoAHV-1. Recently, nucleic acid-based vaccines especially messenger RNA (mRNA) have gained significant interest over traditional inactivated or live attenuated vaccines because mRNA vaccines can be easily and rapidly manufactured on a larger scale, induce robust immunity, and are safer due to lack of the pathogen reactivation like traditional vaccines. Self-amplifying mRNA (saRNA) is a special type of mRNA that can replicate once it gets into a cell and requires a much lower dose and frequency to induce immune responses.

Methods:
The aim of this project is to design a nasal saRNA vaccine encoding for transmembrane glycoprotein D of BoHV-1 using lipid-based delivery systems. The nanoparticles will be designed to improve the saRNA stability, delivery, and cellular uptake in the lungs and subsequently improving the saRNA immunogenicity and efficacy against BoHV-1. The innovative vaccine will be able to induce mucosal immunity in the lungs where the BoAHV-1 infection starts and due to dose sparing of saRNA will require less frequent dosing of animals, thereby reducing the overall vaccination costs. So firstly, saRNA LNPs will be prepared and optimized using microfluidic technique following by the in-vitro characterization for measuring; particle size, PDI, surface charge, entrapment efficiency, saRNA encapsulation and recovery percent. Following by in-vitro biological assessment then in-vivo evaluation for testing the efficacy.

Results:
Expected results: saRNA loaded LNPs will be developed in nanosize range, improving targeting activity and delivery to lung tissue after the inhalation providing robust and prolonged immunization for cattle against bovine alpha herpes virus.

Conclusion:
This innovative nanovaccine will help in producing cost-effective, convenient, safe and effective vaccine for cattle vaccination against bovine alpha herpes virus, improving cattle industry worldwide.

87. INVESTIGATING THE IMMUNOSUPPRESSIVE EFFECTS OF CLASSICAL AND VARIANT INFECTIOUS BURSAL DISEASE VIRUSES IN THE BURSA OF FABRICIUS (BF) OF BROILER CHICKENS

Presenter:	**Yasodha Basnayake**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Ayumi Matsuyama, Western College of Veterinary Medicine
	Shelly Popowich, Western College of Veterinary Medicine
	Shanika Kurukulasuriya, Western College of Veterinary Medicine
Supervisor:	Susantha Gomis, BVSc, MVetSc, PhD, Dip ACPV
	Western College of Veterinary Medicine

Background:

Infectious bursal disease (IBD) is an economically important immunosuppressive disease in chickens. The two serotypes of IBDV, 1 and 2 can naturally infect avian species. Serotype which is the pathogenic is classified into classic (cIBDV), variant (varIBDV), and very virulent (vvIBDV) strains. The most common strain of the IBD virus (IBDV) circulating in Canada is SK09 (varIBDV-SK09) however common IBDV vaccines in Canada contain cIBDV strains. Therefore, the objective of this study was to compare the immunogenic effects of varIBDV SK09 compared to classical IBDV (cIBDV) at the cellular level

Methods:

Maternal antibody free broiler chickens were exposed to varIBDV SK09 or cIBDV D78 and ST-12 at day 7 of age by the oral route. The BF (n=3/group) were obtained at 5 days post-infection from IBDV-maternal antibody free broiler groups 1. no IBDV challenge 2. varIBDV-SK09 challenge 3. ST-12 and D-78 challenged. Flow cytometry was performed to profile and compare B cells, T cells and monocytes/macrophages in the BF in four groups

Results:

According to the statistical analysis of flow cytometric results of the BF, B cells, T cells and monocyte/macrophages were significantly higher in the varIBDV SK09 infected group in comparison with the ST-12 and D-78 infected groups and the control group ($P < 0.05$). B cell depletion in the BF was significant in the varIBDV SK09 infected group in comparison with the control group ($P < 0.05$). Further, there was no statistically significant difference detected in B cells, T cells and monocyte/macrophages in the D-78 and ST-12 infected groups and the control group ($P > 0.05$)

Conclusion:

In conclusion, it is suggested that circulating strains of varIBDV-SK09 are challenging and are a threat to the Canadian poultry industry. An enhanced anti-IBDV approach with vaccines using circulating variant strains is required to address this issue surfaced by the varIBDV strains.

88. DETECTING CHANGES IN NEUROMUSCULAR FUNCTION AFTER LEG IMMOBILIZATION: RELIABILITY OF STRENGTH AND CONTRACTILE PROPERTIES OF THE KNEE EXTENSORS AND PLANTAR FLEXORS

Presenter:	**Aryan Kurniawan**
USask Affiliation:	**Graduate student**
College:	**College of Kinesiology**
Collaborators:	Emily McWalter, College of Engineering
	Joel Lanovaz, College of Kinesiology
Supervisor:	Jon Farthing, PhD
	College of Kinesiology

Background:
Immobilization causes a rapid loss in muscle strength and size. While many have studied these effects in the knee extensors (KE) through a knee brace model, no study has also immobilized the ankle to concurrently compare the effects on the upper and lower leg. The purpose of this study was two-fold: 1) to assess and compare the reliability of neuromuscular measures in both the upper and lower legs, and 2) to determine whether these measures are sensitive enough to detect change in muscle strength and size following disuse.

Methods:
Ten participants (5 females, 5 males, 24 ± 4 years) completed two reliability sessions involving twitch contractile properties, and isometric and dynamic strength tests in both the KE and plantar flexor (PF) muscles. Reliability was determined using ICC based on poor (<0.5), moderate (0.5-0.75), good (0.75-0.90), and excellent (>0.9). Six participants (4 females, 2 males, 21 ± 2 years) completed 14 days of leg immobilization using a knee brace and ankle boot on the left leg. The same battery of measures was completed pre and post disuse, with the addition of MRI scans to quantify the amount of atrophy.

Results:
KE reliability ranged from moderate to excellent, and PF reliability ranged from poor to good, with percent minimal detectable change ranging from 12.2% to 70.2%. The best reliability was shown for KE isometric strength (ICC =.958). In the immobilized leg, averaged across all contraction types, PF and KE strength decreased by 14.5% ($p=.001$, $\eta^2_p=.921$), and 18.1% ($p=.003$, $\eta^2_p=.916$) respectively, but remained unchanged in the non-immobilized PF ($p= .077$, $\eta^2_p=.496$) and KE ($p=.525$, $\eta^2_p=.085$). KE twitch contractile properties were impaired for both sides (time main effects: $p<.05$, $\eta^2_p=.582$-$.665$), where peak twitch-force decreased by 13.3% and 7.0%, half-relaxation time increased by 15.2% and 8.5%, and twitch rate-of-torque-development decreased by 4.2% and 12.1% for the left and right sides respectfully. Immobilized knee extensor muscle volume decreased by 5.4% ($p=.003$, $\eta^2_p=.856$).

Conclusion:
Reliability was overall better for KE than PF, but it depended on the measures. Upper and lower leg strength decreased similarly after immobilization. Impaired twitch contractile properties on both legs after the intervention suggests a decrease in overall physical activity. To our knowledge, this study is novel by directly comparing changes in neuromuscular function of the upper and lower leg after unilateral immobilization.

89. BIOPROSPECTION OF BACTERIAL SECRETOMES FROM STINGLESS BEES' LARVAL FOOD AS A SOURCE OF ANTI-NEURODEGENERATIVE MOLECULES

Presenter:	**Serena Malta**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Tamiris Sabrina Rodrigues, Carlos Ueira-Vieira
Supervisor:	Ana Paula Mendes-Silva, College of Medicine
Co-supervisor(s):	Ana Maria Bonetti

Background:
Alzheimer's disease (AD) is a leading cause of dementia, with an estimated 135 million cases by 2050. It is characterized by neuronal loss and cognitive decline, with β-amyloid (Aβ) plaque accumulation playing a key role. Aβ results from amyloid precursor protein (APP) cleavage by β-secretase (BACE1) and γ-secretase. BACE1 inhibition is a therapeutic strategy, but clinical trials with synthetic inhibitors have failed. Given that microorganisms from stingless bees' larval food produce bioactive compounds, this study evaluated the BACE1 inhibitory activity of bacterial secretome from Melipona quadrifasciata.

Methods:
Bacterial secretomes underwent proteomic analysis and bioprospection of bioactive peptides. Computational analyses predicted physicochemical properties, toxicity (ToxinPred), solubility (Innovagen), and molecular targets (SwissTargetPrediction). Peptides with bioactivity >0.5, non-toxicity, and predicted BACE1 interaction were selected for molecular docking (AutoDock Vina). BACE1's 3D structure (PDB ID: 3TPJ) was prepared, and ligands were modeled and energy-minimized. Docking covered the entire receptor, and the ten lowest-energy poses were analyzed for interactions (Chimera, LigPlot+). Secretomes' neuroprotective effects were assessed in a Drosophila melanogaster rough eye AD-like model (APP/BACE1 overexpression). Eye morphology was qualitatively analyzed via scanning electron microscopy (SEM) and histology ($n \geq 3$ per group). Aβ levels were quantified ($n = 30$) for statistical comparisons.

Results:
Proteomic analysis identified six peptides predicted to inhibit BACE1. Secretomes S9 and S27 improved ommatidia organization, reducing tissue roughness and increasing inter-ommatidial bristles, while histology indicated a more preserved retina in treated groups compared with control, but all these findings were qualitative. A quantitative Aβ analysis showed no statistically significant differences between the group treated with S27 and S9 compared to untreated control ($p=0.3153$ and $p=0.0546$ respectively).

Conclusion:
Bacterial secretomes from stingless bees' larval food contain bioactive peptides with anti-neurodegenerative potential. Further studies should quantitatively assess observed morphological changes and validate therapeutic relevance.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

90. ERGONOMIC RISK ASSESSMENT IN TELEROBOTIC ULTRASOUND SONOGRAPHERS: AN OBSERVATION STUDY

Presenter:	**Leonardo Mauad**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Scott Adams, College of Medicine
Supervisor:	Angelica Lang, College of Medicine

Background:

Introduction: Ultrasound sonographers experience risk factors during work that contribute to pain and disability. The prevalence of pain amidst this occupation can reach 84.9%-87.7% in the USA and Canada. An emerging technology to increase the accessibility of healthcare is telerobotic remote ultrasound. However, there have been no assessments of the ergonomic risks for telerobotic ultrasound sonographers despite important differences in set up and task demands. Objective: To assess the ergonomic risk factors experienced by sonographers during telerobotic ultrasound exams.

Methods:

Methodology: Two sonographers were assessed during 40 ultrasound exams over 60 days. Before the first session, they filled out QuickDASH questionnaire. For each data collection session they were equipped with 10 IMUs to record upper body movement. Videos were also recorded and analysed by one rater using 3 ergonomic risk questionnaires (HARM (Hand Arm Risk Assessment Method), RULA (Rapid Upper Limbs Assessment) and REBA (Rapid Entire Body Assessment)). Outcomes were analyzed descriptively.

Results:

Results: Varying degrees of postural exposures (arm elevation, axial rotation, elbow flexion, and wrist deviation) were present during telerobotic ultrasound scanning. Amongst the anatomical regions analysed, the biggest difference between sides was during ulnar deviation, with the right hand using more ulnar deviation than the left side (90th percentile: 17.6° vs 8.0°). For the elbows, both sides showed similar flexion in the lowest risk range for elbow disorders. Humeral elevation presented as a moderate risk factor for injury for both sides (90th percentile: 63.5° and 61.6°). Analysis with the ergonomic risk questionnaires is ongoing.

Conclusion:

Conclusion: Humeral elevation and wrist deviation postural exposures may be risk factors for injury during telerobotic ultrasound scanning, indicating possible areas to lower the injury risk. More complete ergonomic analyses are underway to determine the risk level for telerobotic ultrasound sonographers.

91. SUPRAMAMMILLARY NUCLEUS OF THE HYPOTHALAMUS CONTRIBUTES TO HIPPOCAMPAL DENTATE GYRUS AND CA2 EPILEPTIFORM ACTIVITY IN A MOUSE MODEL OF TEMPORAL LOBE EPILEPSY

Presenter:	**Sarah Shaban**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Alina Trofimova, College of Medicine
	McKenna Bolger, College of Medicine
	Dara Kwochka, College of Arts and Science
Supervisor:	Justin Botterill, College of Medicine

Background:

Temporal lobe epilepsy (TLE) is the most common adult-onset form of epilepsy often caused by brain injuries, tumours, and malformations. It manifests through seizures characterized by abnormal, synchronized neural activity and includes symptoms ranging from confusion to severe convulsions with loss of motor control. The hippocampus is broadly implicated in TLE as approximately 80% of seizures originate in the hippocampus or adjacent regions. However, the circuitry contributing to seizure activity in TLE is not fully understood. Recent studies show that the supramammillary nucleus (SuM) of the hypothalamus sends projections to the hippocampal dentate gyrus (DG) and CA2 to influence hippocampal activity and functions. Although the SuM-hippocampal circuit is well-characterized in healthy mice, there is limited data on this circuit in TLE.

Methods:

Vesicular Glutamate Transporter 2 (VGluT2-Cre) transgenic mice were used to evaluate SuM-hippocampal circuitry. Optogenetic slice electrophysiology examined SuM-DG and SuM-CA2 synaptic activity under seizure-like conditions. Multi-site jGCaMP8m fiber photometry tracked Ca2+ dynamics in these circuits. Cre-dependent GFP injections detected axonal sprouting in the hippocampus post-status epilepticus. Bidirectional chemogenetics and video electroencephalography (EEG) evaluated how SuM circuit activation or inhibition influences seizure activity, severity, and duration in an acute model.

Results:

Optogenetic electrophysiology showed that SuM-DG and SuM-CA2 synapses are normally weak but can drive epileptiform-like activity. Fiber photometry revealed aberrant, synchronized Ca2+ activity in SuM-DG and SuM-CA2 circuits at seizure onset. GFP labeling confirmed hippocampal axonal sprouting. EEG power analysis highlighted significant changes in delta frequency in the hippocampus with excitation of the SuM.

Conclusion:

SuM projections to the hippocampus may contribute to seizure severity. This work may potentially offer insight into understanding, managing, and advancing treatments of epileptic conditions and disorders.

92. EFFECTS OF CB1 ALLOSTERIC MODULATORS ON EPILEPTIFORM ACTIVITY IN TEMPORAL LOBE EPILEPSY

Presenter:	**Alina Trofimova**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Robert Laprairie, College of Pharmacy and Nutrition
	Justin J. Botterill, College of Medicine
Supervisor:	Justin J Botterill, College of Medicine

Background:

Two-thirds of patients with temporal lobe epilepsy (TLE) are resistant to anti-seizure medications. One promising approach for epilepsy treatment is modulating network activity via endogenous cannabinoid receptors. Previous work found that a positive allosteric modulator of the cannabinoid receptor type 1 (CB1R) reduced epileptic discharges in a genetic model of epilepsy. However, the electrophysiological effects of CB1R allosteric modulators in neurons remain unclear. Here, we investigated the effects of the newest CB1R modulators on the intrinsic properties and epileptiform activity of entorhinal cortex neurons, structure involved in the generation of seizures in TLE, in control and epileptic mice.

Methods:

We used 3-6-month-old C57BL/6J mice treated with pilocarpine to induce seizures and assessed neurons a month later using local field potential and whole-cell patch clamp electrophysiology on 300 µm slices. The control group were C57BL/6J mice with no history of seizures. We tested two CB1R modulators: GAT591 (positive) and GAT358 (negative) at 1µM concentration.

Results:

GAT358 reduces the frequency and duration of ictal discharges in the entorhinal cortex of mice with no prior history of seizures by suppressing pyramidal neuron activity. In contrast, GAT591 makes principal neurons more resistant to excessive stimulation. In epileptic mice, suppressing FS-IN activity by GAT358 further increases hyperexcitability in the entorhinal cortex, leading to a higher frequency of interictal events while maintaining ictal activity.

Conclusion:

Under normal conditions, positive modulation of CB1R enhances excitability in the entorhinal cortex, while negative modulation reduces it by suppressing pyramidal neurons, but in the TLE model, the opposite effect occurs, likely due to suppression of FS-IN activity in this region.

Self-declaration of research alignment with additional themes (optional):

Interdisciplinary/Interprofessional Collaboration

93. UTILIZATION OF A SYNTHETIC ANTI-EGFR ANTIBODY FOR TUMOR IMAGING IN HUMAN AND CANINE MALIGNANCIES

Presenter:	**Adalia Lopes**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Jessica Sharpe, Western College of Veterinary Medicine
	Kris Barreto, College of Medicine
	Eric Price, College or Arts and Science
Supervisor:	Behzad Toosi, PhD
	Western College of Veterinary Medicine
Co-supervisor(s):	Eric Price, PhD

Background:
Nuclear imaging can be used to detect early-stage tumors and micrometastases, leading to earlier and more accurate diagnoses and, consequently, better clinical outcomes. Epidermal growth factor receptor (EGFR) is upregulated in various types of human and canine tumors and its overexpression is associated with tumor progression and invasion. To improve early detection of small tumors, new nuclear imaging strategies using antibodies that specifically bind to tumor cells must be developed.

Methods:
We conjugated a synthetic anti-EGFR antibody (nimotuzumab) and an isotype IgG control with the CHX-A''-DTPA chelator and assessed yield and purity. The antibodies were then radiolabeled with 177Lu, and the radioactive signal was monitored using a Radio-TLC reader. The radiolabeled antibodies were injected into the tail veins of immunodeficient mice bearing EGFR-expressing xenograft tumors of canine osteosarcoma (ABRAMS) or human breast cancer (MDA-MB-231) in the flank area. Tumor uptake and retention of 177Lu-EGFR and 177Lu-IgG were evaluated using microSPECT-CT imaging at 24, 48, 72, and 168 hours post-injection. After the final imaging session, mice were euthanized, and biodistribution and potential organ toxicity studies were performed.

Results:
Biodistribution and imaging analyses showed high tumor uptake of 177Lu-EGFR at all four time points in both xenograft models. Dosimetry identified the tumor, spleen, lungs, and liver as the organs with the highest uptake.

Conclusion:
These results suggest that 177Lu-EGFR can be further investigated for imaging EGFR-high tumors in both species.

94. : THE EPHA2 RECEPTOR EXPRESSION AND ITS IMPACT ON CANINE MELANOMA PROGRESSION

Presenter:	**Shabnam Abdi**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Arata Matsuyama, Western College of Veterinary Medicine
	Kaylee Jo, Western College of Veterinary Medicine
	Behzad M. Toosi, Western College of Veterinary Medicine
Supervisor:	Behzad Toosi, Western College of Veterinary Medicine

Background:
Melanoma is a deadly type of skin cancer in dogs because it spreads quickly throughout the body. Despite treatment options such as tumor removal combined with chemotherapy and/or radiotherapy, survival rates remain low, highlighting the need for more effective therapies. The EphA2 receptor, a member of the erythropoietin-producing hepatocellular (Eph) receptor family, is overexpressed in various human cancers and is associated with aggressive tumor progression. This makes EphA2 a promising target for cancer therapies aimed at blocking its activity. However, the role of the EphA2 receptor in melanoma progression in dogs remains poorly understood. This study aims to investigate the oncogenic role of EphA2 in canine melanoma progression.

Methods:
Normal canine melanocytes were isolated from the eye, skin, and oral tissues of dogs to assess baseline EphA2 expression. Western blotting, immunofluorescence, and transmission electron microscopy were used to confirm and characterize these normal melanocytes. The expression of the EphA2 receptor in canine melanoma cell lines was evaluated using Western blotting. Melanoma cells were transduced with lentiviral particles encoding EphA2-targeting shRNAs to silence EphA2 expression. Transduction with non-silencing scrambled shRNAs was performed to generate non-silencing controls. Silencing was confirmed by Western blotting and immunofluorescence. The effects of EphA2 silencing on melanoma cell survival, apoptosis, invasion, colony formation, and tumorspheres propagation were analyzed.

Results:
Western blotting and immunofluorescence confirmed the presence of MLANA/MART-1, a melanocyte marker, in normal canine melanocytes. Electron microscopy revealed distinct stages of melanosome development. Canine melanoma cell lines showed significantly higher EphA2 expression levels compared to normal melanocyte cells. Moreover, stable EphA2 silencing consistently and significantly reduced colony formation, invasion, and tumorsphere formation in canine melanoma cells. In addition, EphA2 silencing increased apoptosis in canine melanoma cells.

Conclusion:
Our data provide functional evidence that the EphA2 receptor contributes to the malignant biological behavior of melanoma cells in dogs. This suggests that EphA2 inhibition could potentially aid in suppressing melanoma invasiveness.

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95. COMPARISON OF THE ACCURACY OF A PRESSURE TIP CATHETER AND TWO CLINICALLY USED TECHNIQUES TO MEASURE INTRAVESICULAR, INTRAABDOMINAL PRESSURE IN A CANINE CADAVERIC MODEL .

Presenter:	**Elroy (niko) Williams**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Jennifer Loewen,Cindy Shmon, Anthony Carr
Supervisor:	Cindy Shmon, DVM, DVS, DACVS, CCRP Western College of Veterinary Medicine
Co-supervisor(s):	Jennifer Loewen, DVM, MSc, DACVEEC

Background:
Abdominal compartment syndrome (ACS) can result in new-onset multi-organ dysfunction and sometimes failure. Accuracy and timely therapeutic interventions are vital for successfully managing critically ill patients. Despite the predominant use of external pressure transducers (ExtT) and water manometry (WM) for Intravesicular Pressure (IVP) measurements in human and veterinary medicine, the accuracy of these two clinically approved techniques have not been comparatively assessed. The utility of pressure tip catheters (PTC) catheters over fluid-filled line transduction systems such as ExtT and WM for IVP has also never been evaluated.

Methods:
Twenty-two canine cadavers had IVP measured by WM, ExtT, or PTC in a randomized fashion. A Foley urinary catheter was placed and attached to either a WM or ExtT for IVP measurements. A PTC was placed similarly into the urinary bladder for IVP measurements. Pneumoperitoneum was achieved via laparoscopic insufflation. IVP measurements were recorded, following incremental increases in laparoscopic insufflation pressure.

Results:
When compared to the insufflated, direct intraabdominal pressure- a statistically significant difference in accuracy was appreciated with the ExtT technique, showing an average overestimated of indirect IAP by ± 2.63mmHg (p-value= 0.0041). Water mannometry and the PTC techniques showed no significant difference in accuracy.

Conclusion:
Water manometry IVP technique appears to be a more accurate & feasible means of indirect IAP monitoring compared to other labour and cost-intensive techniques.

96. EXPLORING UPPER LIMB MUSCULOSKELETAL SYMPTOMS AFTER GENDER-AFFIRMING TOP SURGERY

Presenter:	**Sarah Fitzgerald**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Angelica Lang, College of Medicine
Supervisor:	Angelica Lang, College of Medicine

Background:
While 1 in 300 Canadians 15 and over identified as transgender and/or gender diverse (TGD) in 2021, this community continues to experience substantial barriers preventing access to equitable healthcare. A lack of TGD specific research contributes to this inequity. For example, to date, no research has been conducted examining potential musculoskeletal symptom development following gender affirming top surgery. These surgeries are important procedures for many TGD individuals and are often necessary to alleviate gender dysphoria. It is vital that these surgeries, and required post-surgical care, remain safe and accessible. Therefore, the purpose of this study was to define the scope and scale of potential post-surgical upper limb musculoskeletal symptoms following gender affirming top surgery.

Methods:
Adults living in Canada who had undergone any form of gender-affirming top surgery were recruited to complete an online survey about post-surgical musculoskeletal and healthcare navigation experiences.

Results:
Seventy-eight individuals participated. All but two participants indicated the presence of at least mild effects of at least one musculoskeletal symptom. Commonly reported symptoms included changes in front of chest sensation (83%), chest tightness (71%), chest pain (55.7%), and shoulder pain or tightness (55.7%). Additionally, only 28% of participants felt their musculoskeletal symptoms were fully resolved, and 29% received post-surgical musculoskeletal treatment. Participants indicated an immediate need for increased access to safe, TGD specific healthcare, and post-surgical rehabilitation resources, but also widely reported improved overall quality of life and gratefulness to have had access to surgical intervention.

Conclusion:
These findings indicate a need for improved post-surgical care. Bearing in mind that access to gender-affirming surgery is a medical necessity which leads to improved mental health, awareness of the potential musculoskeletal symptoms, combined with enhanced TGD-specific resources and care pathways, would help to maintain high quality of life.

97. HOW TOTAL METABOLOME COMPARES TO CREATININE NORMALIZATION FOR LC-MS BIOMARKER ANALYSIS IN A RESPIRATORY DISEASE MODEL FOR CHILDREN SAMPLES

Presenter:	**Emma Finch**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Maryam Alyari, College of Pharmacy and Nutrition
	Deborah Michel, College of Pharmacy and Nutrition
Supervisor:	Darryl Adamko, College of Medicine
Co-supervisor(s):	Anas El-Aneed, College of Pharmacy and Nutrition

Background:
Liquid chromatography mass spectrometry (LC-MS) is the gold standard method for the quantification of metabolites. The quantification of metabolites is the method of choice for biomarker-discovery research and holds promise in diagnostics. Urine biomarkers are ideal as urine can be collected non-invasively and is metabolite rich. Urine analysis requires a method of normalization to determine accurate metabolite concentrations unrelated to hydration level. Creatinine is a commonly used method of LC-MS urine data normalization as its excretion is usually constant from the body and thus, can be used to normalize metabolite concentrations. However, in our previous work creatinine has shown to be an inaccurate method of normalization when comparing between children's samples. Taking an overall concentration of metabolites from a urine sample and utilizing the overall signal from a variety of metabolites to normalize is an alternate method of normalization called the total metabolome. The method uses derivatization to determine the total signal from a representative subgroup of the metabolome, namely amine and phenol-containing metabolites, using HPLC-UV and uses this value to normalize. The purpose of our study is to evaluate the total metabolome normalization within cohorts of children's samples ages 3 and 5 to determine its ability to improve a biomarker diagnostic model regardless of age.

Methods:
Based on a published method, a modified approach is used with a mixture of 24 anime or phenol containing metabolites to act as the representative sub metabolome for the total metabolome. 90 children's urine samples were collected. These urine samples were previously analyzed for LC-MS biomarkers for asthma.

Results:
These biomarker values were normalized using creatinine and total metabolome to compare the total metabolome normalization method to creatinine.

Conclusion:
An improved diagnostic model in children of various ages was seen as a result of total metabolome normalization.

98. POSTOPERATIVE INFECTION IN PREGNANT WOMEN WHO UNDERGO CESAREAN SECTION AT A TERTIARY HOSPITAL IN DHAKA, BANGLADESH: A DESCRIPTIVE CROSS SECTIONAL STUDY.

Presenter:	**Sumaiya Zahan Dolon**
USask Affiliation:	**Graduate student**
College:	**School of Public Health**
Collaborators:	Alfa Ibne Rafi, Ajima Jahan Dihan
Supervisor:	Fahim Kabir Monjurul Haque

Background:
Cesarean sections are common in emerging and industrialized nations. About 15% of individuals worldwide have CS. Due to advances in anesthesia, blood transfusion, pain management, and infections, major cesarean section complications have decreased during the last 30 years. Even high-tech institutions risk postoperative infection. Post-operative complications including surgical site infection extend hospital stays, necessitate readmission, and raise hospital expenses by 10–20%, increasing morbidity. High-income nations report 2% to 7% Cesarean Section-Surgical Site Infection (CS-SSI), whereas low- and middle-income countries do not. CS-SSI risk factors include BMI above 25, anemia, longer operating time, early membrane rupture, emergency surgery, pre-existing medical conditions, and young surgeons. SSI after CS ranges from 0.3% in Turkey to 24% in Tanzania. The most frequent post-cesarean section consequence is infectious morbidity (18-83%). Fever, bacteremia, wound infection, endometriosis, UTI, and pelvic abscess are common in cesarean moms.

Methods:
The descriptive cross sectional study included 1117 patients undergoing cesarean section in Maternal and Child Health Training Institute (MCHTI), Azimpur, Dhaka, Bangladesh. Patients' demographics, antibiotics used with dosages were recorded. Investigations like pus culture, blood and urine culture were recorded for patients with postoperative complications. Change of antimicrobial following culture sensitivity which occurred at 3rd party laboratory outside of the hospital; report was noted.

Results:
Most of the patients were upper lower class (45.33%), C the common risk factor can be Body Mass Index (BMI) and along with that anemia and hemoglobin can also be considered as risk factors for those who have undergone Cesarean Section(CS). Hence, the most common pathogen was Escherichia coli 22 (37.93%) and the second most common pathogen was Klebsiella 17(29.32%). The use of third generation cephalosporin (ceftriaxone) in the majority of the patients was observed. Two drugs combination commonly included third generation cephalosporin and metronidazole and in addition gentamicin was added when three drugs combination was used.

Conclusion:
This study found risk variables for postoperative infection in Cesarean Section (CS) women. Higher body weight, diabetes, anemia, and hemoglobin were risk factors. Overall, the statistics were similar to other countries. As others have shown, research-backed risk-reduction techniques boost performance.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

99. REAL-TIME PATHOGEN DETECTION WITH NANOPORE SEQUENCING

Presenter:	**Tayab Soomro**
USask Affiliation:	**Graduate student**
College:	**College of Agriculture and Bioresources**
Collaborators:	Sam Horovatin
	Tim Dumonceaux
	Matthew Links, College of Agriculture and Bioresources
Supervisor:	Matthew Links, College of Agriculture and Bioresources

Background:
Rapid and precise pathogen detection is vital for agriculture, wildlife conservation, and clinical diagnostics. Traditional methods, such as PCR, target specific genes effectively but struggle to detect unexpected pathogens. PCR relies on predefined primers, which may not bind if a pathogen's gene sequence varies, leading to false negatives. It can also produce false positives when the target gene appears in non-pathogenic organisms. These limitations can cause inaccurate diagnoses. Nanopore sequencing offers an alternative by quickly generating long-read data, though it needs tools for real-time analysis to be fully effective.

Methods:
We developed nanoCAS (Nanopore Classification and Alerting System), a web-based tool paired with a nanopore DNA sequencer. nanoCAS lets users create a custom database of reference sequences and set alert thresholds for pathogens or specific sequences. As sequencing occurs, it aligns the data to the database in real-time and sends alerts when thresholds are met. A key feature is its ability to detect multiple pathogens at once, giving a full picture of a sample's makeup beyond just targeted sequences.

Results:
nanoCAS has proven effective in agriculture, identifying pathogens like Xylella fastidiosa in grapevines, which causes Pierce's disease, and Brucella spp. in cattle and bison, linked to brucellosis. It is also being tested for Sclerotinia in canola. In performance tests, nanoCAS reliably detects pathogens in environmental DNA samples using minimal data. Its ability to spot a wide range of bacterial and fungal pathogens across plant and animal hosts highlights its edge over PCR, which is limited to predefined targets.

Conclusion:
These findings show nanoCAS is precise and adaptable, making it a promising tool for pathogen detection. Its real-time, broad-spectrum analysis outshines traditional methods. With uses in clinical diagnostics, agriculture, and beyond, nanoCAS strengthens pathogen detection strategies and stands as a valuable asset for researchers and practitioners.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

100. ADENINE AS A BIOMARKER TO DETECT ESCHERICHIA COLI SEPTICEMIA IN BROILER CHICKEN

Presenter:	**Asha Ranaraja**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Susantha Gomis, BVSc, MvetSc, PhD, Diplomate Western College of Veterinary Medicine

Background:
Pathogens cause a range of metabolic alterations upon entry into the host which can be effectively detected using metabolomics. The metabolome is sensitive to subtle physiological changes in the body and, are therefore useful as an early diagnostic tool to detect diseases even before clinical symptoms appear. Such metabolic biomarker-based studies are widely applied in human medicine, but are still in their infancy in veterinary medicine. In this study, we focused on characterizing the serum metabolomics profile of broiler chickens following Escherichia coli challenge to identify potential biomarkers for early disease detection. E. coli is the major cause of yolk sac infections and septicemia in neonatal broiler chickens, which is associated with significant economic losses to the industry. Morbidity, mortality as well as the and the inability to detect disease at the acute stage poses great challenges to animal welfare and productivity.

Methods:
We infected three-day-old commercial broiler chicks with E. coli while the control birds remained uninfected. Serum was collected at 8- and 24-hours post E. coli challenge and analyzed using liquid chromatography-mass spectrometry.Data were analyzed using an integrated approach involving univariate, multivariate, machine learning, and pathway analysis.

Results:
We were able to identify a clear difference in the metabolomics profiles of the infected and non-infected groups. Out of 457 altered differential metabolites, Adenine was significantly and consistently downregulated across both 8 and 24 hours post infection.

Conclusion:
These findings highlight the potential use of Adenine as serum biomarker for early diagnosis of E. coli septicemia in the broiler chicken. Early disease detection will enable timely veterinary interventions to help reduce economic losses and improve animal welfare and human food safety.

101. AMOXICILLIN: AN ALTERNATIVE FOR TREATING EUROPEAN FOULBROOD DISEASE IN HONEY BEE LARVAE.

Presenter:	**Thanuri Edirithilake**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Maria Janser, Western College of Veterinary Medicine
	Marina de Silva, Western College of Veterinary Medicine
	Midhun Jose, Western College of Veterinary Medicine
Supervisor:	Sarah Wood, DVM,PhD, ACVP
	Western College of Veterinary Medicine

Background:

European foulbrood disease (EFB) caused by the bacterium <i>Melissococcus plutonius<i>, kills honey bee larvae, impacting colony health and strength. In North America, the only approved antibiotic for managing and treating European foulbrood disease is oxytetracycline. Recent studies have raised concerns about M. plutonius developing resistance to oxytetracycline which poses a significant challenge for disease management and underscores the need for another treatment options. Here, we investigated the use of amoxicillin as an alternative treatment for European foulbrood disease.

Methods:

We grafted newly hatched honey bee larvae and infected them with (<i>M. plutonius<i>. Each plate consists of four groups; a control group with uninfected larvae, an infected control group, a group treated with amoxicillin and a group treated with oxytetracycline. The larvae received amoxicillin (in three different doses- 1□g/mL, 10 □g/mL, 100 □g/mL) with larval diet through day two to day five. Larvae were reared until day six and their daily survival was monitored. Larval weight and health status (categorized as either sick or healthy) on day six were recorded.

Results:

We found that all doses of amoxicillin significantly prolonged the larval survival than the infected control group (P <0.001). At day six, the median larval weight of the amoxicillin treated group, on average 85.8 mg greater than the infected group. There was no significant different in the survival, weight and health status of larvae between amoxicillin treated and oxytetracycline treated group.

Conclusion:

At all concentration tested, amoxicillin can be used as a treatment for European foulbrood disease in honey bee larvae. The efficacy of amoxicillin in treating EFB is comparable to that of oxytetracycline. It is a potential alternative for treating EFB in beekeeping.

102. SPRAYING PROBIOTICS ON CHICKEN EGGS DURING INCUBATION ENHANCES GUT HEALTH IN CHICKENS AFTER HATCH

Presenter:	**Mihiprabha Rathnayake**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Supervisor:	Susantha Gomis, Western College of Veterinary Medicine

Background:
Understanding the effects of early gut colonization by spraying probiotics on incubating eggs is important. This method is a noninvasive and industry feasible method of introducing probiotics to embryos and therefore chicks at hatch. The objective of this study was to understand the spray application of probiotics during incubation, on microbiome development of specific pathogens free (SPF) chickens.

Methods:
SPF eggs were grouped as 1-9 (n=50). Groups 1-5 were sprayed with bacterial broths (1x109 colony forming units (CFU)/ml) of Enterococcus faecalis, Bifidobacterium pullorum sp gallinarum, Lactobacillus plantarum, Ligilactobacillus salivarius, Pediococcus acidilactici at 15 and 17 days of embryonation (DOE). Group 6 was sprayed with probiotic mixture at 15 and 17 DOE. Group 7 was given a probiotic mixture of 1x108 CFU/bird at 1 and 2 days post hatch (PH) and group 8 was given the probiotics mixture during the first week PH. Group 9 was incubated and raised separately without administering probiotics. Jejunal content was collected at 2-, 10-, 20- and 30-DPH. The16S rRNA amplicon sequences were obtained using nanopore and analyzed using EPI2ME.

Results:
The microbial composition at 2 DPH was different compared to 10 DPH, 20 DPH and 30 DPH. The group which probiotic mixture was sprayed during the incubation showed early establishment of a healthy gut microbiota at an age early as 10 days of age. A normal bird will take 30 days to establish a healthy gut microbiome which consist of beneficial bacteria. This study showed early establishment of gut microbiota with pre hatch application of probiotics.

Conclusion:
Spraying probiotics on incubating chicken eggs is feasible technique to promote colonization of probiotics in the intestine of embryos. This method facilitates establishment of probiotic bacteria in the intestine of chicks at the beginning of their life.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

Translational, Clinical, or Applied Science 3

103. INSIGHTS INTO HONEY BEES' POLLEN DIET ACROSS SASKATCHEWAN'S PRAIRIES

Presenter:	**Emilio Tellarini Prieto**
USask Affiliation:	**Graduate student**
College:	**Western College of Veterinary Medicine**
Collaborators:	Marcelo Polizel Camilli, Western College of Veterinary Medicine Justin Slobodian, Western College of Veterinary Medicine Adriana Martinez Arias
Supervisor:	Sarah Wood, Western College of Veterinary Medicine
Co-supervisor(s):	Elemir Simko

Background:
Pollen is the primary source of proteins, lipids, vitamins, and minerals for honey bees (Apis mellifera L.). The nutritional composition of pollen can vary significantly between plants. Furthermore, the diversity of pollen collected has a direct impact on honey bee health. Studies have shown that bees are more resistant to pesticides and disease when fed a mixed pollen diet. However, monoculture areas have been associated with a decline in pollen diet quality. Therefore, we decided to investigate the plant composition of the pollen diet of hives in Saskatchewan and its relationship to the landscape.

Methods:
40 honey bee colonies were distributed in ten sites across Saskatchewan in June 2024. Each of the sites randomly received four hives. The proportion of main crops and land use types within a 2km radius of the hives was determined using Geographic Information System. We use Shannon index to measure the landscape diversity of each site. Three pollen collections were made, corresponding to June, July and August 2024. Plastic pollen traps were used for the collection of corbicular pollen. Three grams pollen samples were then sorted by color. The 18 most collected pollen colors were submitted for plant taxa identification using DNA metabarcoding analysis.

Results:
Canola (Brassica) pollen was the most collected overall (18%), especially in August (34%). Clovers contributed a large proportion of the diet (16% Melilotus and 6% Trifolium). Pollen collected in July was the most diverse (1.7 ± 0.68 [Shannon-index, median ± IQR]), and there was no statistical difference between July and August. A positive and statistically significant correlation was found between landscape diversity within a 2 km radius from hives and pollen diversity (r=0.258, p=0.006).

Conclusion:
The analysis of collected pollen revealed that, with the exception of canola, the honey bees' pollen diet is mainly composed of non-cultivated species, such as weeds and shrubs.

104. STABILIZING MRNA-LIPID NANOPARTICLES WITH CARBOHYDRATES FOR INHALATION

Presenter: **Naga Suresh Kola**
USask Affiliation: **Graduate student**
College: **School of Public Health**
Supervisor: Aneesh Thakur, College of Medicine

Background:
Pulmonary delivery of messenger ribonucleic acid (mRNA) vaccines via inhalation holds promise for eliciting comprehensive mucosal and systemic immunity, which is pivotal for providing frontline protection against respiratory pathogens. However, delivering mRNA to the lungs presents challenges, particularly with conventional lipid nanoparticles (LNPs) that are prone to instability during nebulization owing to high shear stress. To address this challenge, we aimed to test carbohydrates as excipients in LNPs to improve their stability during nebulization. We hypothesized that incorporating saccharides into LNP formulation would prevent nanoparticle aggregation and protect the encapsulated mRNA from degradation during nebulization.

Methods:
We formulated firefly luciferase (FLuc) encoding mRNA-loaded LNPs by microfluidic mixing and incorporated carbohydrates as excipients during dialysis. The FLuc mRNA-LNPs were aerosolized into fine mist by vibrating mesh nebulizer. mRNA-LNPs were characterized for size, polydispersity, morphology, and mRNA encapsulation. To assess the efficacy of nebulized LNPs for mRNA transfection, we performed in vivo bioluminescent imaging in mice following intranasal administration.

Results:
FLuc mRNA-LNPs exhibited monodispersed, spherical oligolamellar structures with size<150 nm. Nebulization differentially impacted LNPs stability: conventional LNPs without excipients, i.e., salt-based formulations underwent significant physicochemical alterations with almost 50% of encapsulated mRNA degradation. Formulations incorporating mono- and disaccharide excipients effectively preserved LNPs integrity. In vivo, luciferase expression studies in mice demonstrated sustained protein expression for 7 days. Notably, the lactose-based mRNA-LNPs resulted in higher expression ($p<0.001$) within the nasal cavity, while the sucrose-based formulation predominantly yielded a 3-fold higher expression in the lungs compared to unmodified mRNA-LNPs.

Conclusion:
Our findings demonstrate that incorporating non-reducing disaccharides as excipients is a promising strategy to mitigate nebulization-induced mRNA-LNPs degradation and promote higher protein expression in the mice lungs. This suggests that the strategic selection of excipients can significantly improve the efficacy of inhaled LNP-based mRNA therapies by promoting both LNP stability and efficient mRNA transfection across the lungs.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

105. VALIDATING MUSCLE ACTIVITY ESTIMATES IN PERSONS WITH SUBACROMIAL PAIN SYNDROME WITH MUSCULOSKELETAL MODELLING

Presenter: **Lauryn Campbell**
USask Affiliation: **Graduate student**
College: **College of Engineering**
Supervisor: Angelica Lang, College of Medicine

Background:
Compensations from chronic shoulder pain can affect mobility. However, kinematic (movement) and muscle activation patterns associated with pain, namely subacromial pain syndrome (SAPS), are highly varied. Consequently, more work is needed to further understand the shoulder movement and muscle activity compensations that occur with SAPS. Measuring scapular movement and muscle activity can be difficult, but musculoskeletal modeling offers a way to comprehensively examine these factors.

Methods:
The Thoracoscapular OpenSim musculoskeletal model is used to investigate how scapular kinematics are associated with changes in muscle activity in persons with SAPS. Kinematic data collected from 7 individuals with SAPS performing a functional task protocol will be evaluated using a full-factorial approach that decreases the maximum activation capacity of the lower trapezius, middle trapezius, supraspinatus, and serratus anterior muscles.

Results:
The subject-specific models were scaled based on anatomical marker data, resulting in root-mean square errors below 50mm for all models. A 180 combinations of muscle capacity reductions were simulated for each subject's model to generate activation estimates for all muscles in the shoulder complex. Parallel computing was used to reduce processing time from approximately 10080 hours to only 105 hours. A finalized model will be determined by comparing normalised experimentally collected electromyography (EMG) with predicted outputs of the model. A multivariate repeated-measures ANOVA will determine if there are significant differences in muscle activity across the tasks and muscles.

Conclusion:
Differences in muscular activations will identify harmful adaptations associated with injury and act as a first step to understanding if adaptations are the cause or result of damage. For future applications, the OpenSim model can be applied to a larger sample of SAPS subjects and be compared against controls.

106. DEVELOPMENT AND OPTIMIZATION OF 3D-PRINTED NASAL CAVITY REPLICAS FOR EVALUATION OF NASAL SPRAY DEPOSITION PATTERN

Presenter:	**Arash Amanlou**
USask Affiliation:	**Graduate student**
College:	**College of Pharmacy and Nutrition**
Collaborators:	James Oxman, College of Medicine
	David Kuang, College of Arts and Science
Supervisor:	Azita Haddadi, College of Pharmacy and Nutrition
Co-supervisor(s):	Scott Adams

Background:
Nasal drug delivery is a widely used non-invasive route of administration for local and systemic treatments. Nasal cavity models can be created using 3D printing technology, providing a cost-effective approach to studying nasal spray deposition. However, producing these models can be complex and time-consuming, lack anatomical precision, and may not adequately account for patient variability. This study aims to improve the development of these models using stereolithography (SLA) and fused deposition modeling (FDM), focusing on enhancing segmentation precision, manufacturing methods, and deposition evaluation.

Methods:
CT images were used to generate nasal cavity models through a novel segmentation approach to reduce the processing time and achieve anatomical accuracy. The models were then created using SLA and FDM, with various material selections, optimized print parameters, and post-processing considerations to enhance transparency, durability, and reusability. An experimental setup was designed to create a physiologically relevant nasal cavity and airway model. Deposition analysis of nasal sprays was conducted using a semi-automatic 3D-printed nasal spray actuator device, and deposition patterns were visualized using luminous particles and colorimetry techniques.

Results:
The proposed segmentation methodology reduced processing time and enhanced the model's accuracy. SLA-printed models had higher transparency and precision, but required additional post-print processing steps compared to FDM models. For models intended for regional delivery, FDM-printed models offer higher durability and reusability compared to SLA-printed models but lacked clarity.

Conclusion:
This study successfully developed and optimized 3D-printed nasal cavity models for evaluating nasal spray deposition patterns. The models provide a reproducible, cost-effective alternative to existing methods, allowing a better understanding of nasal spray dynamics and supporting improved drug delivery strategies.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

107. INVESTIGATION OF COMMERCIAL LNP COMPOSITIONS FOR MRNA DELIVERY ACROSS RESPIRATORY MUCOSA

Presenter:	**Dhruv Patel**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Anil Kumar, College of Medicine
	Ekaterina Dadachova, College of Pharmacy and Nutrition
	Arinjay Banerjee, Western College of Veterinary Medicine
Supervisor:	Aneesh Thakur, College of Medicine

Background:

Parenteral messenger RNA (mRNA)-lipid nanoparticle (LNP)-based vaccines e.g., mRNA-LNP vaccines against COVID-19 effectively induce systemic immunity but suboptimal mucosal immunity in the lungs. Mucosal immunity, particularly through IgA and resident memory T cells, is essential for protection against respiratory pathogens. It is not known if commercial LNPs used in parenteral mRNA therapeutics or vaccines can be used for mRNA delivery in the lungs. Here, we evaluated commercial mRNA-LNP compositions for their safety and RNA delivery following respiratory mucosal immunization.

Methods:

Lipid nanoparticles (LNPs) encapsulating firefly luciferase (Fluc) protein-encoding mRNA was prepared by microfluidic mixing. SM-102 (SpikeVax®, Moderna), ALC-0315 (Comirnaty®, Pfizer-BionTech), MC3 (Onpattro®, Alnylam), and C12-200 were selected as ionizable lipids to formulate LNPs. In vitro protein expression was evaluated in cell lines such as A549, BHK21, RAW 264.7, and Calu3. In vivo protein expression was assessed in BALB/c mice via intranasal (i.n.) (by micropipette) and intrapulmonary (i.pulmon.) (by PennCentury™ Microsprayer® aerosolizer) routes.

Results:

In vitro FLuc protein expression levels in cell lines were found to be highest ($p<0.0001$) for C12-200 LNPs across all the cell lines. In vivo protein expression upon i.n. immunization showed no significant difference among SM-102, ALC-0315, and C12-200 LNPs, whereas MC3 LNPs showed lowest ($p<0.05$) expression. In vivo protein expression in the lungs upon i.pulmon. delivery demonstrated non-comparable FLuc expression levels between SM-102 and C12-200 LNPs, whereas the expression in ALC-0315 and MC3 LNPs was significantly lower ($p<0.05$). Among LNPs, C12-200 LNPs induced the highest inflammatory cytokine IL-1β production in the lungs.

Conclusion:

Overall, FLuc mRNA-loaded SM-102 LNPs generated the highest protein expression in cells and in mice upon i.n. and i.pulmon. administration, and induced the least inflammatory cytokine response in the lungs. Further in vivo immunogenicity studies will assess if this high protein expression by SM-102 LNPs promotes antigen-specific T cells and antibody responses following respiratory mucosal immunization.

108. 3D TUMOROID MODEL FOR STUDYING MACROPHAGE POLARIZATION AND THERAPEUTIC STRATEGIES

Presenter:	**Reza Javan**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	R. Santamaria Cuevas, College of Medicine
	B. Bevelander, College of Medicine
Supervisor:	Dean Chamberlain, College of Medicine

Background:

Breast cancer affects over 2.3 million women worldwide annually and despite advancements in therapies, treatment often fails, leading to high mortality rates. The tumor microenvironment (TME) plays a crucial role in cancer progression, with immune cells significantly influencing tumor behavior and contributing to drug resistance. Among these immune cells, monocytes not only contribute to cancer progression but also play a key role in drug resistance in breast cancer patients. The monocyte upon entering into the tumor microenvironment (TME) can differentiate into M2 macrophages. M2 macrophages can play a critical role in promoting tumor development and drug resistance in various cancers, including breast cancer. For example, by secreting interleukin-6 (IL-6), they can enhance the expression of multidrug resistance (MDR) proteins on the surface of cancer cells, thereby contributing to the development of chemoresistance. As the monocytes migrate into the tumor microenvironment, cytokines and other TME components polarize them into specific macrophage subtypes. Since the differentiation of monocytes into macrophages and their subsequent polarization primarily occur in tissues, traditional 2D cell culture systems are not ideal for studying macrophage-related drug resistance in breast cancer patients. Using a 3D tumor model is one approach that allows us to study the interaction between TME and macrophages.

Methods:

Our lab has developed a novel 3D tumor model, known as microtissues, to address this limitation. Microtissues are 2 mm-long collagen-based structures embedded with cancer cells, providing a physiologically relevant extracellular matrix. Studies have shown that collagen expression increases in breast cancer patients as the disease progresses, contributing to a worse prognosis. This is due to collagen remodeling, which alters the tumor microenvironment and impacts tumor cell biology and metastasis. Unlike synthetic matrices like alginate or PEG, which can influence macrophage polarization, microtissues are free from synthetic materials, minimizing potential interference with macrophage polarization. This model allows precise control over cell composition, enabling us to study interactions between specific cell populations.

Results:

Our lab has developed a novel 3D tumor model, known as microtissues, to address this limitation. Microtissues are 2 mm-long collagen-based structures embedded with cancer cells, providing a physiologically relevant extracellular matrix. Studies have shown that collagen expression increases in breast cancer patients as the disease progresses, contributing to a worse prognosis. This is due to collagen remodeling, which alters the tumor microenvironment and impacts tumor cell biology and metastasis. Unlike synthetic matrices like alginate or PEG, which can influence macrophage polarization, microtissues are free from synthetic materials, minimizing potential interference with

macrophage polarization. This model allows precise control over cell composition, enabling us to study interactions between specific cell populations. Recent findings from our model demonstrate that key cytokines involved in monocyte recruitment, such as monocyte chemoattractant proteins (MCPs), IL-16, and MIP (Macrophage Inflammatory Protein) and those promoting M2 macrophage polarization, including interleukin-4 (IL-4) and IL-10, are released by the microtissues at significantly higher levels on Day 5 compared to those released by a 2D model on the same day. Notably, cytokines important for monocyte recruitment to the TME, such as MIP and IL-16, align with our RNA sequencing data, further validating the model's ability to accurately reflect cytokine expression dynamics. This highlights the suitability of our model for studying M2 macrophage polarization at early time points.

Conclusion:

We are currently investigating how these cytokines influence macrophage polarization by co-culturing classical monocytes, isolated from peripheral blood, with microtissues and analyzing polarization using immunofluorescence and confocal microscopy. The future aim of this research is to explore strategies such as repolarizing macrophages to the M1 phenotype and utilizing dsRNA nanoparticles to activate macrophages against cancer cells within microtissues, with the ultimate goal of applying these findings to breast cancer treatment.

109. ANALYZING THE EFFECTS OF CANNABINOL AS AN INDIVIDUAL COMPOUND IN MICE

Presenter: **Alayna Jones**
USask Affiliation: **Graduate student**
College: **College of Pharmacy and Nutrition**
Supervisor: Robert Laprairie, College of Pharmacy and Nutrition

Background:
Δ9-tetrahydrocannabinol (THC) is the compound in cannabis that produces the 'high' associated with cannabis use. When THC degrades from air, heat, or light, it produces cannabinol (CBN). The intoxication levels and psychoactive effects of CBN are still unknown. The primary objective of this project was to determine whether CBN is intoxicating and therefore should be regulated similar to THC and cannabidiol content are currently regulated in Canadian cannabis products.

Methods:
There were two parts to this project. First was a battery of tests known as the "tetrad" to study the behavioral effects of 0.1-10 mg/kg CBN in C57Bl/6 mice. Second was a pharmacokinetic time course to quantify the amount of CBN in mouse blood 10 min - 8 h following administration.

Results:
The data collected shows that CBN produced effects in the behavioral tetrad, with some sex differences observed. Dose-dependent effects were observed with lower potency but similar efficacy to THC. Blood levels of CBN suggest a Tmax for CBN of approximately 6 h.

Conclusion:
The data collected to date indicate CBN is an intoxicating cannabinoid that should likely be regulated in cannabis products.

110. ASSESSING HUMERAL KINEMATIC DIFFERENCES IN FARM TASK PERFORMANCE: LABORATORY VS. FIELD SETTINGS IN SASKATCHEWAN

Presenter:	**Denise Balogh**
USask Affiliation:	**Graduate student**
College:	**College of Medicine**
Collaborators:	Loukas Sherlock
	Angelica Lang, College of Medicine
Supervisor:	Angelica Lang, PhD
	College of Medicine

Background:
Farmers are at high risk for the development of musculoskeletal disorders of the shoulder due to the performance of physically demanding work involving high force, high humeral elevation demands, repetitive movement, exposure to vibration, and extended periods spent in driving postures. Certain humeral kinematics, such as high elevation and internal rotation, are considered to be risk factors for shoulder injury, but the humeral kinematic requirements for many farm work tasks need to be better defined. Measuring authentic farm work in many participants can be difficult, as farm work and farm tools are not standardized from farm to farm, and travel to farms can be difficult. There remains a need to determine whether simulating farm work in a lab setting will fully capture the movement demands of high-risk farm tasks. This study assessed kinematic variability during farm task performance across three locations. It was hypothesized that variability would be lowest in the lab and higher on natural farms, and that location would elicit differences in task performance.

Methods:
Three Inertial Measurement Units (XSens, Awinda) placed on the sternum and bilateral humeri tracked upper limb kinematics during 4 simulated farming work tasks (overhead drill, shovel, climb ladder, seed bag lift), and in 3 different locations; 1) laboratory (10 participants, 6F/4M, average age = 33.2); 2) an agricultural tradeshow, 'Ag in Motion' (10 farmers, 6F/4M, average age = 34.9); 3) grain/cattle farms (10 farmers, 6F/4M, average age = 33.9). Three repetitions of each task were recorded. Mean and peak humeral elevation and axial rotation (mean, peak internal and external) angles were evaluated for the primary 'mover' arm during each of the tasks. Coefficient of variation was calculated to assess the rep to rep (within) variability for each outcome and was compared between locations with 1-way ANOVAs ($p < .05$). Median absolute deviation (MdAD) was derived to assess between participant variability and descriptively compared between locations. Finally, 1-way ANOVAs ($p < .05$) tested the effect of location on mean and peak angles during task performance.

Results:
The results for the overhead drill and shovel tasks are reported in this abstract. Within participant variability for peak internal rotation during the shovel task was lower in the lab than at the individual farms or Ag in Motion ($F_{2,27}=5.594$, $p=.009$). Between participant variability for all outcomes ranged from 4.7-19.2 MdAD in the lab, 6-14.2 MdAD at Ag in Motion, and 3.8-25.8 MdAD on the individual farms. The MdAD was lowest across all outcomes in either the lab or Ag in Motion locations, except for the mean axial rotation during the overhead drilling, in which the MdAD was lowest on the individual farms. As hypothesized, variability was generally lower in the controlled settings (lab and Ag

in Motion), however for many outcomes the within and between variability were comparable across all three locations. When comparing task performance across locations, mean ($F_{2,27}=17.1$, $p<.001$) and peak ($F_{2,27}=6.0$, $p=.007$) humeral elevation were higher on the individual farms than in the lab or Ag in Motion during the overhead drill. Peak internal rotation ($F_{2,27}=4.4$, $p=.023$) was greater when drilling at Ag in Motion compared to when simulating this task in the lab. For the shovel task, peak external rotation ($F_{2, 27} = 5.6$, $p = .017$) was greater on the individual farms and Ag in Motion than when simulating this task in the lab.

Conclusion:

Simulating an occupational task in-lab may not fully reflect the demands of the task when performed in a real-world settings. Humeral axial rotation in particular may differ between in-lab and in-field performance work tasks.

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111. CIRRHOSIS-RELATED READMISSION RATES AND PREDICTORS OF MORTALITY: INSIGHTS FROM SASKATOON

Presenter:	**Adedamola Bello**
USask Affiliation:	**Resident**
College:	**College of Medicine**
Collaborators:	Talha Salman, College of Medicine
	Rachel Alvi, College of Medicine
	Sushila Pathak, College of Medicine
Supervisor:	Mina Niazi, MD
	College of Medicine

Background:
Cirrhosis is a major global cause of hospitalization, readmission, and mortality, accounting for 1.5 million deaths annually. Between 1999 and 2016, cirrhosis-related deaths in the United States increased by 65%. In Canada, cirrhosis cases are projected to double by 2040, driven by rising rates of metabolic-associated and alcohol-related liver disease. Frequent hospitalizations and readmissions occur due to complications such as ascites, hepatic encephalopathy, variceal bleeding, infection, and renal failure. Understanding the factors contributing to readmissions and mortality is critical for optimizing care.

Methods:
A retrospective cohort study was conducted at Royal University Hospital and St. Paul's Hospital in Saskatoon, Saskatchewan between 2016 and 2022 to evaluate predictors of readmissions and mortality in adult patients hospitalized with cirrhosis. Patients were identified through diagnostic codes, and those with hepatocellular carcinoma or receiving palliative care for end-stage liver disease were excluded. Data collected included demographics, etiology of cirrhosis, portal hypertension-related complications, MELD scores, readmissions at 30, 60, and 90 days, and one-year mortality. Statistical analyses included correlation and regression models to identify factors associated with adverse outcomes.

Results:
Our preliminary data show that among 320 patients, cirrhosis-related readmission rates were 19.4% at 30 days, 25.3% at 60 days, 28.4% at 90 days, and 44.4% beyond 91 days. Alcohol-related liver disease (49.7%) and hepatitis C virus (9.7%) were the most common etiologies, with 12.5% of patients having combined alcohol and HCV-related cirrhosis. Overall mortality within one year was 44.4%; however, in patients with MELD-Na ≥30, mortality was 54.5%. Patients with four or more complications demonstrated the highest mortality rate (59.3%) and were more likely to experience readmissions. Complications such as hepatorenal syndrome ($P < 0.0001$) and hepatic encephalopathy ($P = 0.021$) were significantly associated with increased mortality. Hepatorenal syndrome was also a strong predictor of adverse outcomes, including higher readmissions.

Conclusion:

This study highlights the substantial burden of readmissions and mortality in patients with cirrhosis, particularly those with advanced liver dysfunction, multiple complications, and alcohol-related liver disease. Our findings align with existing literature and emphasize the need for targeted interventions, including enhanced management of portal hypertension-related complications, comprehensive discharge planning, and structured outpatient follow-up. Future efforts should prioritize reducing readmission rates and improving outcomes for this high-risk population while addressing underlying drivers such as alcohol use, HCV and metabolic liver disease.

112. CO-DEVELOPING A MULTIDISCIPLINARY DELIRIUM PREVENTION PATHWAY TO REDUCE POSTOPERATIVE DELIRIUM IN OLDER ADULTS WITH COGNITIVE FRAILTY

Presenter:	**Ava Bayat**
USask Affiliation:	**Resident**
College:	**College of Medicine**
Collaborators:	Ali AlQatan, Heather Dyck
Supervisor:	Peter Hedlin, College of Medicine
Co-supervisor(s):	Jennifer O'Brien

Background:
Older adults with cognitive frailty, including those living with Alzheimer's disease and related dementias, are at significantly increased risk of postoperative delirium (POD) and other adverse outcomes following surgery. Despite available guidelines, the implementation of structured, patient-centered interventions to prevent POD remains inconsistent across healthcare settings. This study aims to co-develop a multidisciplinary, evidence-based clinical pathway to reduce the incidence and impact of POD in older surgical patients across Saskatchewan.

Methods:
Using a Participatory Design approach, this study engages knowledge users—including patients, caregivers, clinicians, and healthcare administrators—as equal partners in the co-development process. Ten interdisciplinary workshops were conducted by a professional facilitator to identify key pathway components. Prior to participation in workshops, participants reviewed a virtual "Gallery of Findings" provided in PDF and video formats. This "Gallery of Findings" included summaries of professional guidelines, delirium prevention strategies from other institutions, educational materials, and patient narratives. Data were collated and synthesized across all workshops to produce a Process Map and identify Key Ideas for developing a POD pathway.

Results:
The ten facilitated workshops were held with 44 participants, including 19 physicians (anesthesiology, internal medicine, psychiatry, geriatrics, surgery, emergency medicine), 15 nurses, nurse practitioners, educators, or managers, 3 patient partners, 3 resident physicians, and 4 who did not self-identify. Participants identified 36 Key Ideas for developing a POD pathway and co-developed a Process Map to visually outline the POD Pathway.

Conclusion:
This study presents a novel, collaborative approach to designing a multidisciplinary, patient-centered clinical pathway to prevent postoperative delirium in older adults with cognitive frailty. Our next steps include implementing and evaluating the POD pathway. Through meaningful engagement with patients, caregivers and healthcare professionals, we aim to transform perioperative care for vulnerable older adults and establish a sustainable and patient-centred model.

Self-declaration of research alignment with additional themes (optional):
Interdisciplinary/Interprofessional Collaboration

113. SEMINAL BACTERIAL ISOLATES AND THEIR ASSOCIATIONS WITH SEMEN QUALITY IN RAMS

Presenter:	**Devinda Wickramasingha**
USask Affiliation:	**Resident**
College:	**Western College of Veterinary Medicine**
Collaborators:	Dinesh Dadarwal, Western College of Veterinary Medicine
	Fritz Schumann, Western College of Veterinary Medicine
	Kamal Gabadage, Western College of Veterinary Medicine
Supervisor:	Dinesh Dadarwal, Western College of Veterinary Medicine

Background:
Bacterial infections of the reproductive tract have been reported to be associated with infertility and subfertility in rams. Our objective was to identify common bacterial isolates in ram semen and evaluate their associations with semen quality parameters.

Methods:
A total of 150 rams of various breeds, aged 1–5 years, from nine different flocks in Saskatchewan, underwent breeding soundness evaluation during the summers of 2022 or 2023. Semen ejaculates were collected via electroejaculation and assessed for semen quality parameters, including gross and individual motility, sperm morphology (Eosin-Nigrosin stain) and the presence of leukocytes (Feulgen stain). A portion of each semen ejaculate was submitted to Prairie Diagnostic Services, Saskatoon, for aerobic and anaerobic bacteriological culture, including Brucella ovis. Binomial and percentage outcomes were analyzed using logistic regressions and Wilcoxon rank sum tests, respectively, in Stata/BE17, with $P<0.05$ considered significant.

Results:
Bacteria were present in all but two samples. The most common isolate was Staphylococcus equorum (43%). Among 95 rams, nine potential reproductive pathogens were identified: Corynebacterium spp. (14.7%), Pasteurella multocida (12%), Streptococcus spp. (11.3%), Brucella ovis (10%), Acinetobacter spp. (10%), Staphylococcus spp. (8%), Trueperella pyogenes (4%), Pseudomonas spp. (2.6%), and Actinobacillus seminis (2.6%). Only B. ovis and Acinetobacter spp. were significantly associated with poor semen quality. Rams infected with B. ovis and Acinetobacter spp. exhibited lower percentages of normal sperm (40.5% ± 26 and 48.5% ± 27, respectively), reduced live sperm counts (46.7% ± 29 and 64.3% ± 13 respectively), and decreased motility (35.7% ± 28 and 40.7% ± 29, respectively). Leukospermia was found in all 15 rams positive for B. ovis, with 2.5 times higher odds ($P<0.001$) of having ≥5 leukocytes per high-power field.

Conclusion:
The significant impact of B. ovis and Acinetobacter spp. on semen quality highlights the need for routine bacteriological screening in rams with poor semen quality and fertility.

114. IMPLEMENTATION OF AMERICAN FOULBROOD SURVEILLANCE IN COMMERCIAL BEEKEEPING IN SASKATCHEWAN: A TWO-YEAR ASSESSMENT

Presenter:	**Belarmino Lopes Neto**
USask Affiliation:	**Postdoctoral fellow**
College:	**Western College of Veterinary Medicine**
Collaborators:	Rosephine Enadeghe, Western College of Veterinary Medicine Oleksii Obshta, Western College of Veterinary Medicine Elemir Simko, Western College of Veterinary Medicine
Supervisor:	Elemir Simko, Western College of Veterinary Medicine
Co-supervisor(s):	Sarah Wood

Background:

American foulbrood (AFB) is a destructive disease of honey bees caused by the spore-forming bacterium, Paenibacillus larvae. Consequently, as antibiotic-resistant strains of P. larvae continue to emerge, accessible tools are crucial to minimize antibiotic surveillance, including AFB surveillance, while ensuring sustainable beekeeping practices. This study aimed to analyze the concentrations of P. larvae spore in end-of-season pooled, extracted honey collected from commercial beekeeping operations in Saskatchewan, Canada.

Methods:

To assess AFB risk in commercial BKO, a total of 1471 honey samples were analyzed using quantitative P. larvae bacterial culture method over two-year period (2023 and 2024). P. larvae spores have been detected 287 and 331 honey samples from 2023 and 2024, respectively, representing 70% of tested beekeeping operations (30 out of 42).

Results:

Out of 620 positive honey samples, 348, 245 and 27 were associated with low (23%), moderate (16%), and high (2%) AFB risk, based on previously established threshold, respectively. Moreover, antimicrobial resistance test showed 4% and 1% of tested samples from 2023 and 2024 contained oxytetracycline-resistant P. larvae isolates, respectively.

Conclusion:

These findings offer an in-depth surveillance of AFB in commercial beekeeping operations on SK, aiming to reduce use of antimicrobials and prevent AFB Outbreaks by using evidence-based approach. Ultimately, this project will improve collaborative efforts between academia and beekeeping industry to for prevent AFB in SK.

115. EFFICACY OF OVERWINTER MITICIDE TREATMENTS AGAINST VARROA DESTRUCTOR IN HONEY BEE COLONIES IN WESTERN CANADA

Presenter:	**Alvaro De la Mora**
USask Affiliation:	**Postdoctoral fellow**
College:	**Western College of Veterinary Medicine**
Supervisor:	Sarah Wood, Western College of Veterinary Medicine
Co-supervisor(s):	Elemir Simko

Background:
Honey bees contribute to more than 30% of the food that is consumed in Western societies, however, honey bees are affected by different stressors, including the external parasitic mite Varroa destructor, which is the main biotic factor associated with more than 30% of colony losses in North America. Many beekeepers use synthetic products (like amitraz) to control Varroa infestation rates in their colonies, however these products have different disadvantages: Varroa can develop resistance against these compounds, these products are toxic to the bees, and they can contaminate honey and wax. Thus, there is a need of alternative solutions to control Varroa. One approach is the use of natural compounds such as organic acids like oxalic acid, but there is a need of more research on using these compounds because their efficacy will depend on evaporation, which requires specialized equipment for their application and personal protection equipment for the beekeepers. Thus, this project aims to evaluate the efficacy of a new slow-released oxalic acid method inside the overwinter indoor facilities in Western Canada.

Methods:
This project took place in two overwinter indoor facilities, one in Kinistino, Saskatchewan and the other one in Starbuck, Manitoba. Also, this project was in collaboration between commercial beekeepers in Saskatchewan and Manitoba, the Knowledge & Research Transfer Team of the Manitoba Beekeepers' Association, and the University of Saskatchewan. Five treatments were stablished: 1. Negative control, chemical free cardboard strips. 2. Positive control, amitraz slow-release strips. 3. Oxalic acid slow-release strips, low dose. 4. Oxalic acid slow-release strips, mid dose. 5. Oxalic acid slow-release strips, high dose. Treatments will be applied during eight weeks. After eight weeks, honey bee colonies were evaluated for Varroa infestation levels in adult bees, Varroa natural fall on sticky boards, colony survivorship, and honey bee population size.

Results:
There were differences between treatments for Varroa natural fall, Varroa infestation levels, colony survivorship, and honey bee population size.

Conclusion:
Using a slow-release method for the natural compound oxalic acid seems to reduce the negative impact of honey bee colony losses in overwintering indoor facilities in Western Canada.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

116. ARE HONEY BEES SAFE IN SASKATCHEWAN CANOLA FIELDS?

Presenter:	**Marcelo Camilli**
USask Affiliation:	**Postdoctoral fellow**
College:	**Western College of Veterinary Medicine**
Supervisor:	Elemir Simko, Western College of Veterinary Medicine
Co-supervisor(s):	Sarah Wood

Background:
Canada is the largest producer and exporter of canola, with Saskatchewan (SK) accounting for over 50% of this production. There is a strong relationship between this crop and honey bees: canola honey represents approximately 70% of all honey extracted in Western Canada, and pollination services significantly contribute to increased canola yields. However, around 95% of canola is grown from seeds treated with neonicotinoid insecticides to protect crops from insect pests but may also pose risks to insects pollinators, including honey bees. In this study, we aim to document comparatively pesticide residue levels in samples of honey, pollen, and bees collected from Saskatchewan canola fields and from the northern boreal forest during the canola blooming period.

Methods:
A total of 80 colonies were used in the summer of 2024, with 60 colonies placed in canola fields (15 apiaries × 4 hives) and 20 colonies placed in the boreal forest region (5 apiaries × 4 hives) as a control group, far from agricultural crops. Samples of honey, pollen, and bees were collected in July of 2024 and submitted to the Agriculture and Food Laboratory (AFL) at the University of Guelph for pesticide screening, targeting over 500 active ingredients.

Results:
A total of 7 pesticide residues were detected in honey samples (5 fungicides, 1 insecticide, and 1 herbicide), 10 in bees (9 fungicides and 1 herbicide), and 24 in pollen (17 fungicides, 4 insecticides, and 3 herbicides).

Conclusion:
This ongoing study will determine whether honey bee colonies are exposed to potentially harmful levels of pesticide residues while foraging in Saskatchewan's canola fields.

Self-declaration of research alignment with additional themes (optional):
Sustainable Progress

117. DEVELOPMENT OF A LIPID NANOPARTICLE-BASED ADJUVANT WITH THE TLR3 AGONIST POLY(I:C) FOR MUCOSAL VACCINATION

Presenter:	**Tasson da Costa Rodrigues**
USask Affiliation:	**Postdoctoral fellow**
College:	**Vaccine and Infectious Disease Organization (VIDO)**
Collaborators:	Azita Haddadi, College of Pharmacy and Nutrition
	Jeffrey M. Chen
	Mark Fenton, College of Medicine
Supervisor:	Aneesh Thakur, Vaccine and Infectious Disease Organization (VIDO)

Background:
Currently nanostructured lipid-based adjuvanted vaccines are administered via parenteral route, which induces poor immunological response in the mucosa. Mucosal immunity is critical for protection against pathogens. However, few mucosal vaccines are licensed for human use, mainly due to the lack of adequate mucosal adjuvants. Lipid nanoparticles (LNPs) have emerged as promising nanocarriers for many therapeutics and vaccines. We hypothesized that the incorporation of polyinosinic-polycytidylic acid (poly(I:C)), an agonist of the toll-like receptor 3 (TLR3) in LNPs, would induce robust mucosal immunity in the lungs.

Methods:
LNPs were produced by microfluidic mixing method containing C12-200:DOPE:Cholesterol:DMG-PEG 2000 (35:16:46.5:2.5 mol%) in the organic phase and 25, 50, and 100 □g (19.2, 38.5 and 76.9 □g/mL, respectively) of poly(I:C) high (HMW) or low molecular weight (LMW) in the aqueous phase. The size, polydispersity index (PDI) and surface charge of the LNPs were assessed by dynamic light scattering. The poly(I:C) was quantified by the Quant-iT RiboGreen RNA kit. TLR3 activation was assessed after incubating formulations with HEK-Blue™ murine TLR3 reporter cells for 24 hours and cell viability was determined by flow cytometry.

Results:
LNPs encapsulating poly(I:C) LMW showed 83-96 nm for size and 0.142 - 0.085 for PDI, while LNPs with poly(I:C) HMW showed 96-107 nm for size, and 0.151-0.249 for PDI. The TLR3 stimulation was higher for poly(I:C) encapsulated LNPs. In fact, using 25 □g of poly(I:C) LMW for LNPs induced TLR3 stimulation 3.0 and 5.5 times higher than poly(I:C) LMW alone and empty LNPs, respectively. The LNP-poly(I:C) LMW formulation did not induce cytotoxicity and showed cell viability around 80%.

Conclusion:
Overall, we found that LNP-formulated poly(I:C) LMW exhibited optimal physicochemical properties, induced high TLR3 activation, and maintained cell viability. These results support our ongoing work to evaluate the mucosal adjuvant effect of LNP-poly(I:C) LMW in a tuberculosis model in vivo.

118. BREAST CANCER SURVIVORS ALTER SCAPULAR KINEMATICS DURING A PROGRESSIVE LIFTING TASK

Presenter:	**Kenzie Friesen**
USask Affiliation:	**Postdoctoral fellow**
College:	**Centre for Canadian Rural and Agriculture Health**
Collaborators:	Angelica Lang, College of Medicine
Supervisor:	Angelica Lang, College of Medicine

Background:

Breast cancer survivors (BCS) may experience shoulder issues after treatment. Elucidating movement deficiencies post-surgery can inform intervention strategies to improve shoulder function and health longevity. Following breast cancer surgery, upper limb strength is affected and fatigue can ensue which can hinder quality of life. Therefore, we examined shoulder motion among BCS during a progressive overhead lifting task with increasing loads.

Methods:

Twenty-one female BCS (53±11 years; 17 right-handed) who underwent either mastectomy and/or reconstruction were assessed. Participants were fitted with reflective markers tracking thorax and upper limbs. Each participant performed a progressive overhead lifting task, involving lifting a crate from waist height to forehead height. Four sets of 5 repetitions were completed. Load was increased for each set.Scapular internal rotation (IR) and upward rotation (UR) were calculated bilaterally [3]. Scapular angles were extracted per repetition cycle which represented the bottom of the lift (near wasit height) to the top of the lift (when the hand reached peak position) and normalized to 100 data points. Statistical parametric mapping (SPM) repeated measures analysis of variance tests were used to compare the entire cycle between repetitions and sets per scapular angle and side.

Results:

SPM analyses indicate there is a main effect for repetition and set. Right ($F_{4,80}=4.19$, $p<0.001$, range: 27-55% cycle) and left ($F_{4,80}=4.06$, $p=0.004$, range: 25-42% cycle) scapular IR increased over repetitions within a set (Figure 1). Left side IR ($F_{3,60}=4.96$, $p=0.013$, range: 20-29% cycle) decreased between sets, as did left side UR ($F_{3,60}=4.79$, $p=0.002$, range: 80-100% cycle) while right side UR increased ($F_{3,60}=4.78$, $p<0.001$, range: 70-100% cycle).

Conclusion:

BCS alter scapular motion between repetitions and sets with increasingly loaded lifts. These adaptations may impact abilities or injury risk in daily life.

Special thanks

The organizing committee of the 32nd annual Life and Health Sciences Research Expo would like to thank the following people for playing instrumental roles in the delivery and execution of this important University of Saskatchewan event.

Thanks to their commitment to supporting the next generation of health professionals, the expo has been able to continue its mission of bridging disciplinary gaps and enhancing discovery while championing efforts that can improve the health of people across Saskatchewan, Canada, and the world.

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