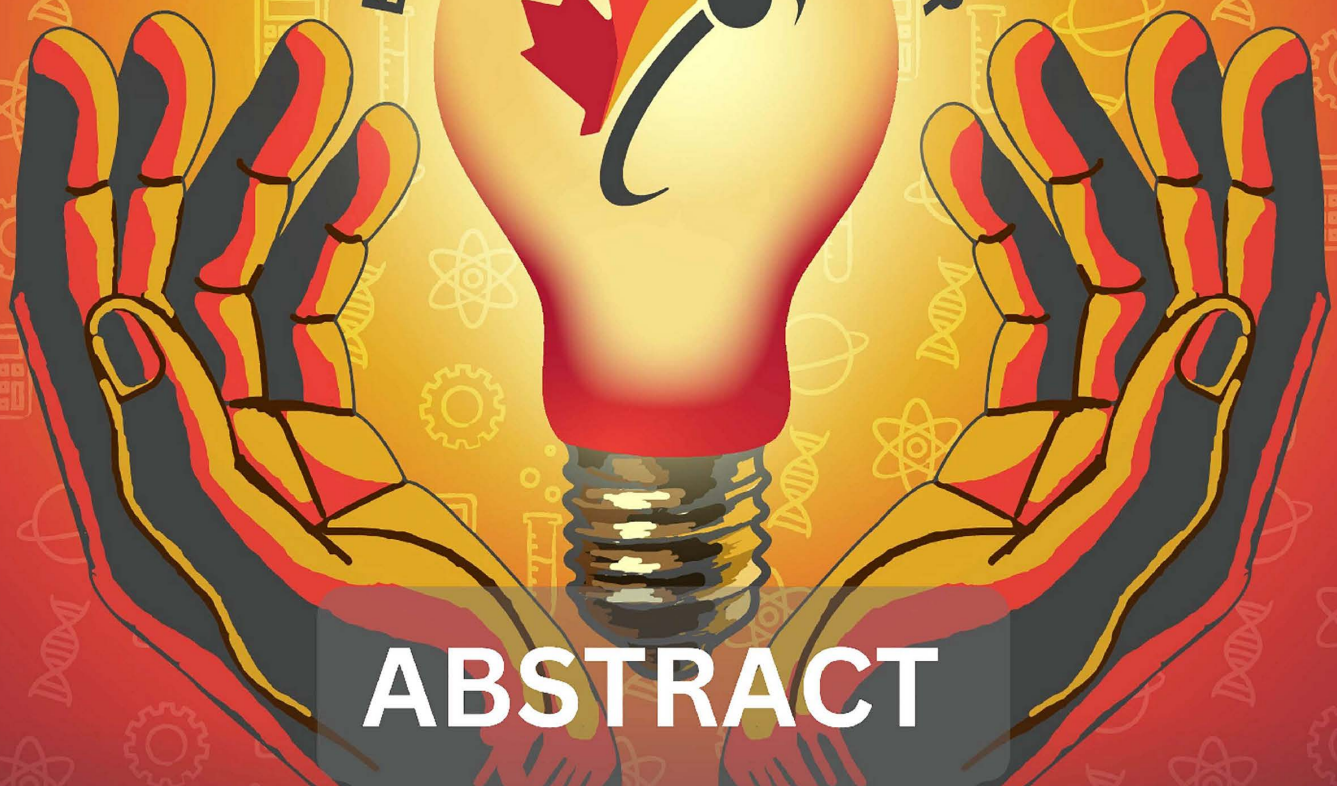
ABSTRACT BOOKLET

BE-STEMM 2024

2024 EN-STIMM

EMANCIPATE | ÉMANCIPER



ABSTRACT BOOKLET

July 30 - August 1

CBSN
RCSN

Canadian Black Scientists Network

Réseau canadien des scientifiques noirs

ABSTRACT BOOKLET

ABSTRACT BOOKLET

Table of Contents

Translational Research

Contributed Talks

Investigating the molecular mechanisms of insulin resistance in Myotonic Dystrophy type 1

Ofosu Adjei-Afriyie[1], Alexander Manta, Aymeric Ravel-Chapuis, Alexander MacKenzie, Sally Spendiff, Hanns Lochmuller
[1]Research Institute of Children's Hospital of Eastern Ontario, Ottawa, ON, CANADA; Department of Cellular and Molecular Medicine, University of Ottawa, Ottawa, ON, CANADA

Introduction
Myotonic Dystrophy Type 1 (DM1) is a multisystemic neuromuscular disease that presents with myotonia, skeletal muscle weakness, atrophy, and insulin resistance. While insulin resistance has been characterized within the context of type 2 diabetes (TD2), its pathomechanism in DM1 remains unclear. This project aims to investigate insulin resistance in DM1 and looks to evaluate what impact exercise could have on it.
Methods
Ingenuity Pathway Analysis was used to identify dysregulated proteins in the proteomic profile of exercised and sedentary DM1 mice, followed by western blotting to examine the insulin sensitivity pathway in DM1 patient myotubes. Finally, I determined exercise's impact on insulin signaling in DM1 tissue using western blotting and immunofluorescence techniques.
Results
Proteomic analysis indicates that PGC-1α, a protein integral to metabolic regulation, is downregulated in DM1 mice. Literature indicates that PGC-1α drives GLUT4 expression. GLUT4 is an insulin sensitive glucose transporter and its translocation to the cell surface is known to be downregulated in TD2. Western blotting indicates that both PGC-1α and GLUT4 are downregulated in DM1 mice compared to WT. Western blotting also revealed that GLUT4 translocation is diminished in patient derived DM1 myotubes, but rescued when subjected to an exercise mimetic.
Conclusion
In conclusion, insulin resistance can increase the incidence of TD2 in DM1 patients which can further diminish their quality of life. Elucidating insulin resistance mechanisms in DM1 could unveil potential therapeutic targets. Exploring exercise as a therapeutic can increase the validity for prescribing this non-invasive treatment for DM1 patients.

Lay Abstract This study looks into Myotonic Dystrophy Type 1 (DM1), a complex neuromuscular condition characterized by many muscle complications and insulin resistance. While insulin resistance is well-understood in type 2 diabetes, its mechanism in DM1 remains murky. This research aimed to shed light on this and explore the effects of exercise.
A predictive computer model and literature review pointed to several proteins that act abnormally in DM1. Of interest is GLUT4, a protein that is critical for allowing the entry of sugar into the cell. Our experiments showed that cell surface levels of GLUT4 and total GLUT4 can be lowered in DM1, but exercise can mitigate this.
These insights are crucial as insulin resistance can worsen patient quality of life. By unraveling these mechanisms, we can identify potential treatment targets. Moreover, considering exercise as a therapy could offer a promising avenue for enhancing the health of DM1 individuals.

The effects of tendon vibration on balance control and electromyography in chronic ankle instability.

Emmanuel Zangio [1], Grant Handrigan
[1]University of Moncton

Introduction: Tendon vibration has been extensively studied in terms of postural effects and is a possible rehabilitation technique for patients with chronic ankle instability (CAI). The objective of this project is to explore tendon vibration of the lower leg and to compare with postural variables and electromyography of the lower leg in healthy adults and adults with chronic ankle instability.
Methodology: This project uses a cross-sectional quasi-experimental design. Fifteen participants with and 15 participants without CAI were recruited for this project. Participants completed the FAAM (""Foot and ankle ability measure"") and CAIS (""chronic ankle instability index"") questionnaires. Balance control (pressure centre variables) and muscle responses (EMG) were measured under different tendon vibrator placements (At, Fl, Ta) and under visual and non-vision conditions. Each trial was performed twice, resulting in a total of 28 trials. Each test lasted 30 seconds and contained 10 seconds of vibration in the central part, creating three phases per test (NoVib, ViB, NoVib).
Results: The 15 participants with sprains had the following anthropometric measurements: 23.2±5.6 years, 1.77±0.1m, 73.6±10.5kg. The 15 participants without ankle sprains had the following anthropometric measurements: 20.3±1.6 years, 1.76±0.1m, 72.2±13.1kg. There was a significant difference between the FAAM and CAIS results for the injured group (values are x± SD, 61.6±14.8%, and 78±10.7% respectively) compared to the non-injured group (99.9±0.7%, and 100±0%).
Conclusions: Data analysis is in progress and preliminary data for balance and EMG activity monitoring will be presented at the conference.

Lay Abstract In this study, we investigated the effects of tendon vibration on posture in both healthy adults and those with chronic ankle instability (CAI). Tendon vibration has been explored as a potential rehabilitation method for CAI patients. We recruited 30 participants, half with CAI and half without, to compare their balance control and muscle responses using electromyography (EMG) under different tendon vibrator placements and visual conditions. Participants completed questionnaires assessing foot and ankle ability as well as chronic ankle instability. Balance control and muscle responses were measured during trials with and without tendon vibration. Preliminary analysis showed significant differences between the two groups in terms of their functional ability and ankle instability index. Our findings contribute to understanding the potential role of tendon vibration in rehabilitating chronic ankle instability. Further data analysis is ongoing, and we anticipate presenting additional results at upcoming conferences.

Relationship between adipose tissue cellular heterogeneity, obesity, and metabolic disease

Kafi Ealy[1,2]
[1] *Toronto Metropolitan University* [2] *Toronto Hospital for Sick Children Research Institute*

Adipose tissue is regarded as a very flexible organ that responds dynamically to nutritional, metabolic and environmental cues. In response to chronic overnutrition, adipose tissue undergoes cellular remodeling to enable healthy and unhealthy fat mass expansion to maintain homeostasis. Pathological adipose tissue remodeling underlies inflammatory responses, insulin resistance and obesity-associated cardiometabolic dysfunction but the specific coordinated changes in cellular populations within various adipose depots is not well characterized. The objective of this work was the identification and functional characterization of heterogeneous cell populations within adipose tissues that mediate metabolic dysfunction associated with obesity and aging.
We performed single cell mass cytometry high-throughput proteomics analysis (CyTOF) of visceral and subcutaneous fat depots in mouse models of obesity and aging. We observed distinct phenotypic shifts in pro-inflammatory and pro-fibrotic immune and adipose progenitor cell populations under obesogenic and aging conditions. Further, in mice undergoing intermittent fasting, a dietary intervention known to improve metabolic health, we observed improved metabolic health and rejuvenation of cellular senescent phenotypes in adipose progenitor cells.
Our ongoing work extends these findings to human populations to identify biological and functional differences in adipose tissues that may underlie ethnic-specific increased susceptibility to T2DM and its associated complications.

Lay Abstract Fat tissues in our body are very flexible as they expand and remodel in healthy and unhealthy ways in response to chronic overnutrition. This process of remodeling of fat tissues under obesogenic conditions is associated with whole-body inflammation, insulin resistance and cardiometabolic disease. This work aimed to identify and functionally characterize the cell populations within fat tissues that are associated with metabolic dysfunction. We also aimed to identify nutritional interventions that could alter cell function and improve metabolic health. We found that intermittent fasting rejuvenated fat stem cells and led to remodeling of specific immune cell subsets. These findings identified diet-associated alterations in the cell composition of fat which could help predict cellular parameters that correlate with prevalence of human metabolic disease and response to dietary treatments.

Roles for Kaiso and p120ctn in intestinal inflammation and colitis-associated cancer

Lindyann Lessey[1], Roopali Chaudhary, Robert W. Cowan, Geoffrey Wood and Juliet M. Daniel
[1]McMaster University

Inflammatory bowel disease (IBD) is characterized by chronic inflammation of the gastrointestinal tract and is known to increase the likelihood of developing colitis-associated cancer (CAC) in patients. However, the molecular mechanisms underlying the IBD-to-CAC transition remain unknown. Our lab previously reported that intestinal-specific overexpression of the transcription factor Kaiso induces a chronic inflammatory phenotype characterized by crypt hyperplasia, increased infiltration and activation of neutrophils, and increased permeability of the intestinal epithelium. A similar inflammatory phenotype was observed following the loss of p120ctn, a binding partner and inhibitor of Kaiso. However, the role of Kaiso and p120ctn in IBD and CAC have not been fully explored. Since inflammation and genetic alterations drive progression from an inflammatory phenotype to hyperplasia and sometimes to colon tumours, we hypothesize that Kaiso overexpression in conjunction with p120ctn depletion induces severe intestinal inflammation and tumour formation. To investigate this, Kaiso overexpressing mice (KaisoTg) were mated with p120ctn conditional knockout (p120CKO) mice and intestinal tissues from the progeny (KaisoTg;p120CKO) were collected and examined for intestinal inflammation and polyp formation. We found increased hyperplasia and mass formation in 6 and 12-month-old KaisoTg;p120CKO mice respectively compared to controls. Immunofluorescence revealed that areas of p120ctn loss were associated with decreased E-cadherin and β-catenin expression and increased ZO-1 expression, but not changes in their subcellular localization. Collectively, these findings suggest that p120ctn loss in KaisoTg mice leads to cell-cell adhesion defects that may exacerbate intestinal inflammation and lead to polyp formation.

Lay Abstract Inflammatory bowel disease (IBD) is characterized by chronic inflammation of the intestine. Patients with IBD have an 2 times greater chance of developing a colon cancer subtype that is associated with intestinal inflammation. The protein Kaiso has been implicated in the development of intestinal inflammation and cancer through its regulation of other proteins that function within these processes. Kaiso's inhibitor, the p120ctn protein, has been shown to protect against intestinal inflammation and carcinogenesis. This study aims to examine the opposing roles of Kaiso and p120ctn in intestinal tissues to determine their roles in inflammatory bowel disease and the progression to colon cancer. Findings from this study would help shed light on the complex roles of both Kaiso and p120ctn in intestinal diseases.

Lightning Talks

Role of the transcription factor Kaiso in TGFβ-mediated triple-negative breast cancer metastasis

Hanad Adan[1], Lindyann Lessey, Stephanie Ali-Fairbairn, Juliet Daniel
[1]McMaster University

Triple-negative breast cancer (TNBC) is a highly aggressive and metastatic breast cancer subtype and is characterized by the absence of three predictive biomarkers. Consequently, traditional targeted therapies are ineffective, and TNBC patients have a poor prognosis and shorter survival rates. TNBC is prevalent in young premenopausal women of African ancestry (WAA). WAA in West Africa, the Caribbean, and the U.S.A. experience high TNBC rates, which suggests a link between African ancestry and TNBC and many postulate that WAA have a genetic predisposition to developing TNBC. In elucidating the underlying causes of this racial disparity in TNBC incidence, our lab identified Kaiso, a dual-specificity transcription factor, as a key player in TNBC aggressiveness and poor outcomes. WAA TNBC tissues have significantly higher levels of nuclear Kaiso compared to white women, and higher total Kaiso levels correlate with low TNBC survival. However, the mechanism underlying Kaiso's role in TNBC remains largely unknown. We recently identified a positive feedback loop between Kaiso and Transforming Growth Factor Beta (TGFβ) signaling, which promotes TNBC metastasis. Our goal is to examine the Kaiso-TGFβ feedback loop to elucidate Kaiso's mechanism of action in TNBC aggressiveness and metastasis. To date, we demonstrated that TGFβ increases Kaiso expression in TNBC cell lines and that conversely, Kaiso depletion induces decreased expression of TGFβ signaling effectors. We also determined that Kaiso may be a downstream target of TGFβ signaling. Ongoing studies are examining this Kaiso-TGFβ feedback loop to elucidate Kaiso's mechanism of action in TNBC aggressiveness and metastasis.

Lay Abstract Triple-negative breast cancer (TNBC) is an aggressive breast cancer that is difficult to treat in part due to the lack of effective treatments. Notably, TNBC develops more often in Black women compared to white women. Several studies have linked a protein named Kaiso to low patient survival of various cancers, including TNBC. Notably, Kaiso associates with high rates of TNBC in Black women. How Kaiso contributes to TNBC development is not well understood but we have data showing that Kaiso interacts with TGFβ, another protein that promotes TNBC and tumor metastasis. Our study seeks to determine Kaiso's role in TGFβ function and TNBC using tissues from Black women from Nigeria, Barbados, and the United States. This can help with the identification of new targets for therapies and provide a better understanding of the factors that contribute to the racial disparities in TNBC outcomes.

Kaiso, androgen receptor and increased mortality of women of African ancestry with triple-negative breast cancer

Stephanie Ali Fairbairn[1],Robert Cowan ,Salija Golamari , Ryan Rattan , Melody Pan and Juliet Daniel
[1]McMaster University

Women of African ancestry (WAA) experience a disproportionate burden of the highly aggressive, metastatic triple-negative breast cancer (TNBC) subtype and high mortality rates compared to women of European ancestry (WEA). Our lab previously showed that the transcription factor Kaiso may be linked to this racial disparity seen in WAA TNBC patients. Recent studies have indicated that WAA TNBC tissues also express less androgen receptor (AR) than WEA TNBC tissues, supporting the existence of a novel BCa subtype – quadruple-negative breast cancer (QNBC). Notably, in silico analysis revealed that high Kaiso and low AR expression correlated with poorer overall survival in BCa patients. Thus, we hypothesized that high Kaiso and low AR expression could be contributing to the increased mortality in WAA with TNBC. Using tissue microarrays and immunohistochemistry, we found reduced and cytoplasmic AR expression concomitant with increased Kaiso expression in WAA compared to WEA. Moreover, western blot and qRT-PCR analyses showed an increase in AR expression in response to Kaiso depletion in TNBC cells, and chromatin immunoprecipitation revealed that Kaiso associates with the AR promoter region. These findings suggest that AR could be a bona fide Kaiso target gene and that there may be clinical relevance of high Kaiso, and low AR expression in BCa survival, especially in patients with an African heritage. Findings from this study will strengthen the potential to specifically target Kaiso and AR for TNBC treatment.

Lay Abstract Triple-negative breast cancer (TNBC) is an aggressive breast cancer (BCa) subtype that spreads rapidly to vital organs and for which there are no specific treatments. Thus, women diagnosed with TNBC are more likely to die than those diagnosed with other types of BCa. Notably, TNBC is more common in young Black women than in White women. Our lab found that a protein named Kaiso was more highly expressed in TNBC tissues from Black women compared to White women, and these Black women with high Kaiso levels were less likely to survive. Kaiso also seems to regulate the Androgen receptor, whose low expression correlates with poor survival in Black women with TNBC. Collectively our findings suggest that high Kaiso and low Androgen receptor levels contribute to the racial difference in BCa outcomes in Black women, and these proteins may be useful markers to target for TNBC treatment.

Poster Presentations

Fabrication of bone marrow extracellular matrix scaffolds with 3d printed predefined internal microarchitecture promoting vascularization

Joab Ogato[1], Alex Czekanski, Eleftherios Sachlos
[1]Department of Mechanical Engineering, York University

INTRODUCTION: The application of three-dimensional (3D) bioprinting techniques has revolutionized the development of tissue analogs. These engineered tissues hold immense potential as alternatives for transplantation and as disease models, facilitating advanced biomedical research. While strides have been made in successfully creating thin tissues ($<$ 1mm), the engineering of viable thick tissues ($>$ 1mm) remains a formidable challenge due to the absence of a functional microvascular system.
METHODS: We present a novel approach that repurposes a conventional 3D printer into a bioprinter. By employing biocompatible 3D printing materials, we fabricated a sacrificial mould into which a slurry of type I collagen is poured and allowed to solidify. Once the sacrificial mold is dissolved chemically, examination through optical computed tomography and scanning electron microscopy (SEM) illustrates the presence of defined microchannels within the collagen scaffold. To enhance the functionality of the scaffold, immortalized human umbilical vein endothelial cells (HUVEC-hTERT2) were introduced into the microchannels and cultivated for 72 hours.
RESULTS: Assessment using SEM and fluorescent microscopy demonstrates the successful attachment and proliferation of cells on the scaffold's microchannel surface.
CONCLUSION: By employing this method, we can fabricate scaffolds containing predefined microvasculature. This breakthrough offers a potential solution to the long-standing challenge of creating functional microvascular systems within thicker tissue constructs. Beyond this, a vast array of stem cells could be introduced to the bulk of the vascularized scaffold, leading to a more biomimetic culture system. Thus, allowing for a more in-depth understanding of stem cell interactions with the supporting cell systems.

Lay Abstract Including functional vasculature in engineered constructs has been a technical challenge preventing fabrication of thick (>1mm) viable tissue. Using proprietary 3D printing raw materials, a sacrificial mould is printed into which a type I collagen slurry is cast. After the sacrificial mould is removed, Human umbilical vein endothelial cells(HUVECs) are seeded in the scaffold microchannels and thereafter, incubated for 72 hours. Scanning electron micrographs show differentiated HUVECs attached to the microchannel surface. Future work is focused on co-culturing bone-marrow cells in the interstitial space while perfusing the HUVEC-lined 3D printed microchannels with cell culture media for bone marrow tissue engineering.

Identifying Mediators of Invasive Lobular Carcinoma (ILC) Metastasis

Josephine Elugbaju[1], Christina Addison
[1]University of Ottawa/Ottawa Hospital Research Institute

Invasive Lobular Breast Cancer (ILC) is often diagnosed at more advanced stages with 30% of ILC patients being diagnosed with multiple concurrent metastatic sites. ILC also has higher recurrent rates post-surgery and responds poorly to chemotherapy hence identification of more effective therapies to prevent or treat metastatic ILC is urgently needed. We recently isolated the more invasive VIVA1 cells from the representative ILC cell line MDA-MB-134VI. Orthotopic VIVA1 tumor cell administration in NSG mice, showed robust tumor growth in mammary ducts with spontaneous metastasis to the spleen, ovary, liver, adrenal gland and bone. RNAseq analysis showed Sox9 (SRY box transcription factor 9) was one of the most highly upregulated genes in VIVA1 cells. KEGG pathway analysis suggested significant alterations in a number of metabolic pathways including calcium signaling which had the highest number of altered genes. Interestingly, 7/16 genes in this KEGG pathway are predicted Sox9 targets. We thus hypothesize that Sox9 promotes ILC cell invasion and metastasis in part by altering metabolic signalling. We have confirmed that siRNA-mediated depletion of Sox9 results in impaired VIVA1 cell invasion in vitro, concomitant with reduced gene expression of the calcium signaling proteins. Our findings to date in our metastatic ILC model suggest that Sox9 may play an integral role in promoting metastatic growth of ILC in part via its ability to alter tumor cell metabolism. Given that ILC does not readily respond to chemotherapy, understanding the role of and targeting these metabolic vulnerabilities may lead to novel effective therapies for metastatic ILC.

Lay Abstract Invasive lobular breast carcinoma (ILC) is the second most common type of breast cancer, efficient treatments are needed, however, few metastatic ILC models exist. We thus developed a metastatic model (VIVA1 cells) isolated from the representative ILC cell line MDA-MB-134VI. Injecting VIVA1 cells into the mammary ducts led to significant tumor growth and spontaneous spread (metastasis) to similar sites in the body as those observed in ILC patients. Genetic analysis showed that a gene called Sox9 was higher in VIVA1 cells, cellular pathway analysis found a significant alteration in Calcium signalling with 7/16 altered pathway genes being predicted Sox9 targets. We thus hypothesize that Sox9 promotes ILC invasive and metastatic properties by altering Calcium signalling which concurrently promotes the growth and survival of ILC cells that have spread to new organ sites. Understanding the role of and targeting these metabolic vulnerabilities may lead to novel effective therapies for metastatic ILC.

Development of co-culture spheroids as potential models for atherosclerotic disease modelling

Ibukunoluwa Naiyeju[1]
[1]*McGill University*

Atherosclerosis is a chronic, systemic, inflammatory disease associated with the build-up of fatty deposits ("plaques") in arteries. Atherosclerotic plaques are characterized by the accumulation of low-density lipoproteins (LDL) in macrophages and smooth muscle cells, resulting in foam cells which make up the bulk of the lesion. How these two cell types and their foamy counterparts interact and contribute to plaque growth and inflammatory signalling remains poorly understood. To address this knowledge gap, we have developed a novel co-culture spheroid model using cells representative of those found within the plaque microenvironment. Co-culture spheroids were fabricated using THP-1-derived M0 macrophages and human aortic smooth muscle cells (SMCs) at co-culture ratios of 1:1 and 1:2 under varying co-culture conditions (varying culture media ratios and supplementation with or without extracellular matrix). Immunostaining was conducted to assess the morphology of the spheroids and confirm the presence of both cell types, alongside size distribution measurements over time. The formation of spheroids which retain their compactness for up to 10 days was observed, with the supplementation of extracellular matrix (collagen Type 1 within the concentration range of 5-7.5 μg/mL). Furthermore, immunostaining revealed the presence of both cell sub-types in within the spheroids, and the Alamar Blue assay showed that the spheroids remained metabolically active for up to 10 days. This model demonstrates the potential of spheroid models for atherosclerosis studies and we anticipate that future investigations into protein expression, proliferation, and apoptosis within the model will provide additional insights.

Lay Abstract Atherosclerosis is a chronic disease where fatty plaques grow inside arteries and block the blood flow to the organs which these arteries supply. Unmanaged atherosclerosis can progress to heart disease and other life-threatening events such as heart attacks and strokes. One of the key processes which we know sustains the progression of atherosclerosis is inflammation. However, our knowledge of this process is limited because there is a paucity of 3D plaque models. In my project, I am working to address this knowledge gap by developing a novel three-dimensional (3D) demo model to understudy inflammation inside a fatty plaque. I will fabricate this model using spheroids, which are 3D constructs where cells exist in a spatial orientation like how they occur naturally. After this, I will study how inflammation progresses in the model. Through these experiments, we will gain insights into the lesser-known factors that promote or hinder the process of inflammation, and we are optimistic that these insights will advance knowledge for the treatment of atherosclerosis in the field of biomedical engineering.

Equity and Justice

Contributed Talks

Caregivers' perception of their children's health in canada: a nationwide study

De-Lawrence Lamptey[1]
[1]*Holland Bloorview Kids Rehabilitation Hospital*

Introduction and Objective
The purpose of this study was to explore the extent to which the intersectionality of racial identity/ethnicity and childhood disability influenced caregivers' perception of their children's health.
Materials and Methods
This study involved an analysis of a population-representative survey collected across Canada by Statistics Canada. Caregivers rated their children's health as excellent, very good, good, fair and poor. Multinomial regressions were performed to assess the effects of race/ethnicity and childhood disability on caregivers' rating of their children's health.
Results
The preliminary results showed that childhood disability was significantly associated with caregivers rating their children's health as poor. However, there was no significant association between racial identity/ethnicity and caregivers rating their children's health as poor. The preliminary interaction effects of racial identity/ethnicity and childhood disability on caregivers' perception revealed that the extent to which a caregiver rated their children's health as poor was significantly highest for Black, Chinese, "other Asian", Indigenous, non-Indigenous, "not a visible minority" and South Asian children with disabilities respectively compared to "not a visible minority" and non-Indigenous children without disabilities.
Conclusion and Significance/Implication
The preliminary study findings suggest that caregivers' perception of their children's health can be significantly influenced by the intersectionality of racial identity/ethnicity and childhood disability.

Lay Abstract The study investigated the extent to which the intersection of racial identity/ethnicity (e.g., Black and Indigenous) and childhood disability influenced caregivers' perception of their children's health. Caregivers rated their children's health as excellent, very good, good, fair and poor. The preliminary results showed that childhood disability was directly connected to caregivers rating their children's health as poor. There was no direct connection between racial identity/ethnicity and caregivers rating their children's health as poor. The extent to which a caregiver rated their children's health as poor was highest for Black, Chinese, "other Asian", Indigenous, non-Indigenous, "not a visible minority" and South Asian children with disabilities respectively compared to "not a visible minority" and non-Indigenous children without disabilities. The preliminary study findings suggest that caregivers' perception of their children's health can be influenced by the intersection of racial identity/ethnicity and childhood disability.

Perceived racism and maternal mental health outcomes of Black mothers in Ontario

Titilola Omotosho[1]
[1]*University of Toronto*

Black mothers face significant disparities in mental health outcomes during the perinatal period, including higher rates of postpartum depression. As part of a project, this study answered the question: Does racism impact postpartum mental health outcomes for Black mothers in Ontario? The study provided a comprehension of how Anti-black racism, exhibited in the form of microaggressions, discrimination, and inequality, affects the postpartum mental health outcomes of Black mothers.
A sequential mixed-methods research design combined surveys, interviews and FGD. The instrument was designed with a section for the adapted version of EPDS. 30 Black mothers who had given birth within the last three years were purposively sampled for the study. All participants completed the survey, 15 were selected for FGD and 5 for the in-depth interview. The theoretical framework is Black Canadian Feminist Thought and CRT.
Anti-Black racism and racial discrimination are prevalent in Ontario's healthcare facilities during the perinatal period. Most respondents felt they were not treated with the same level of care as other patients. 25% of Black mothers screened positive for postpartum depression. Concerns over healthcare providers' attitudes and inadequate education were reported by 80% of participants. Mistrust was seen due to the misdiagnosis of babies.
This study emphasizes the need for interventions and policies to promote health equity for Black mothers, by addressing Anti-black racism and promoting cultural humility. Healthcare providers should prioritize client-centered services and continuous education. Urgent advocacy for policy changes, healthcare reforms, and investments in affected communities is crucial.

Lay Abstract This study investigated how racism affects the mental health of Black mothers after giving birth in Ontario, Canada. The researcher used surveys, interviews, and group discussions with 30 Black mothers. They found that racism and discrimination are common in healthcare during and after pregnancy. Many mothers felt they did not get the same care as others, and 25% screened positive for postnatal depression. Issues like repelling healthcare providers' attitudes, embarrassment, and discourtesy 80% of participants. The study suggests that policies and interventions are needed to tackle racism in healthcare and provide better support for Black mothers. Healthcare providers should focus on understanding diverse cultures and prioritize the needs of their clients. It's also important to push for changes in policies, healthcare systems, and investments in communities to address these issues.

Dismantling healthcare inequities: anti-racism and anti-oppression training for systemic change

Abimbola Saka[1], Zita A. Seshie
[1] D.A.S Innovative Hub, Scarborough

Introduction: Across diverse communities such as African, Black, Caribbean, Indigenous, and other People of Color, shared experiences of oppression underscore the need for collective action. Compounded by intersecting identities, including race, religion, ability, sexual orientation, socioeconomic status, gender, and gender identity, systemic biases exacerbate exclusion and discrimination. Within the Canadian healthcare system, these ingrained inequities manifest in disparities affecting marginalized groups' access, treatment, and outcomes. Addressing these deeply rooted issues demands equipping healthcare professionals with the knowledge and tools to recognize and dismantle racism and oppression within their practice. These training modules respond proactively to this, empowering healthcare providers to challenge discriminatory practices and foster equitable healthcare delivery. Methods: The training approach encompasses a multifaceted strategy to engage participants effectively. Combining didactic instruction, interactive exercises, case studies, and group discussions, we cultivate a dynamic learning environment that fosters active participation and critical reflection. Tailoring content to address healthcare professionals' specific challenges ensures its relevance to real-world clinical scenarios. Discussion/Results: Initial assessments of the training modules demonstrate promising outcomes, including heightened awareness of racism and oppression in healthcare, improved understanding of implicit biases, and enhanced cultural competency. Participant feedback underscores the content's relevance and effectiveness, highlighting its role in fostering advocacy and organizational change. Conclusions: These anti-racism and anti-oppression training modules are instrumental in cultivating inclusive and equitable healthcare environments. Empowering healthcare professionals to challenge discrimination can enhance patient outcomes and bolster staff morale. Ongoing evaluation and refinement will ensure its sustained efficacy in dismantling barriers to equitable care.

Lay Abstract This presentation introduces comprehensive training developed by D.A.S Innovative Hub to help healthcare workers tackle racism and oppression. The training aims to fill gaps in knowledge and provide tools for promoting change and advocacy within healthcare settings. The modules focus on understanding how systemic discrimination affects patients and staff and offer practical strategies for breaking down oppressive structures and promoting inclusivity. Key topics include understanding racism and oppression, addressing implicit bias and microaggressions, and providing culturally competent care. Additionally, the training covers recognizing intersectionality and health disparities, advocating for equity, and creating inclusive healthcare environments. This training empowers healthcare workers with the knowledge and skills to deliver fair and inclusive patient care.

Black women and the nonprofit sector

Timi Idris[1]
[1]*Dalhousie University*

Introduction: Society depends on charitable non-profit organizations for food, shelter, education, and so many other social services. The health and global economic crisis caused by COVID-19 highlighted how important nonprofit organizations are as they were tasked with providing even more support to the communities they serve. Whilst employee health and wellness are integral to the successful operation of a nonprofit, there is a growing problem of mental and emotional burnout among nonprofit workers which has negatively impacted employee retention.
Methods: I aim to conduct in-depth semi structured interviews with 20 Black Women who live in the Nova Scotia. The interviews will focus on participants' experiences in nonprofit; effect of workplace wellness policies; and the ways these experiences are perceived in relations to their intersectional identity. This study draws on the work of Kimberlé Crenshaw on intersectionality and critical race theory, which will theoretically ground the methodology of the study.
Anticipated results: One primary outcome expected from this research is the identification and exploration of challenges specifically faced by Black women within nonprofit settings. These challenges may encompass barriers to career progression, disparities in treatment, and the intricate intersectionality of race and gender.
Significance: With an understanding of the challenges faced by nonprofit employees presented through the lens of Black women, this study can help inform social policies and practice that seeks to improve employee wellbeing and also provides an avenue for organizations to think of ways to improve the health of their staff.

Lay Abstract Charitable nonprofit organizations are crucial for providing food, shelter, education, and other social services. The COVID-19 crisis underscored their importance, as nonprofits were called upon to offer even more support. Despite their vital role, nonprofit workers, especially Black women, face significant mental and emotional burnout, affecting employee retention. This study seeks to explore the barriers to wellbeing for Black women in nonprofit organizations and the impact on service delivery. Focusing on the intersections of race and gender, the study aims to highlight the unique challenges Black women encounter in the nonprofit sector. Using critical race theory and intersectionality, this qualitative research is situated in Nova Scotia, home to Canada's largest indigenous Black community. By centering Black women's experiences, the study aims to inform social policies and practices that enhance employee wellbeing, offering insights for organizations to improve staff health and retention during a critical period for Black communities in Canada.

Lightning Talks

Exploring multifactorial barriers and resources for accessing equitable mental health care among African Nova Scotians (EMBRACE-ANS)

Temitayo Sodunke[1], Ejemai Eboreime, Cinera States, Mutiat Sulyman, Vincent Agyapong
*[1]TBC**

Introduction and Objective: African Nova Scotians (ANS), representing one of Canada's oldest Black communities with a 400-year history, face disproportionate mental health challenges stemming from intergenerational trauma, racism, and social inequities. Despite up to 40% of ANS suffering from undiagnosed and untreated mental illness, current understandings of multifactorial barriers and enablers from provider and health system perspectives remain limited. This study aims to holistically investigate the structural, social, and interpersonal factors influencing equitable access to appropriate, affordable, and culturally safe mental healthcare for the ANS community.
Materials and Methods: The study will employ a participatory mixed-method approach, consisting of a Scoping review, Qualitative and quantitative methods (including interviews, focus groups, and surveys), and Integrated Knowledge Translation. The research questions will explore barriers and facilitators to equitable mental healthcare access, considering perspectives from care providers, healthcare organizations, and Black communities. The study will also examine how the Nova Scotia mental-health system can be optimized to better align with the needs and priorities of Black communities.
Results: The expected results will elucidate understudied supply-side gaps and opportunities, unveil root causes of disparities, and center community voices in solutions.
Conclusion and Significance/Implication: EMBRACE-ANS will provide empirical evidence on multilevel barriers and facilitators, opening new avenues of research to dismantle structural inequities and tailor care models to the diverse needs of African Nova Scotians while accessing mental healthcare. The findings will contribute to the development of targeted interventions and policies aimed at improving mental health outcomes and reducing disparities for the ANS community.

Lay Abstract This project aims to address inequitable access to mental health care experienced by African Nova Scotians in Nova Scotia. Compared to other groups, African Nova Scotians face greater barriers reaching appropriate, affordable, and culturally relevant mental health services when needed. Reasons include systemic racism, discrimination, lack of cultural sensitivity by providers, mistrust of health systems, stigma, and logistical obstacles like transportation difficulties. This leads to undiagnosed and untreated mental illness within the community. To better understand these barriers from all perspectives, we will conduct interviews and focus group discussions with African Nova Scotians to hear about their experiences firsthand and get their ideas for change. Interviews with mental healthcare providers and organisational leaders will uncover training gaps, biases, and provider-level barriers they face delivering high quality care to this population. The goal is to develop practical solutions that align services with African Nova Scotians' needs and priorities.

**To Be Confirmed (TBC)*

Poster Presentations

Enhancing diversity in STEMM: the role of predictive analytics and mobile technology in supporting black participation

Dara Dillon[1], Romain Williams
[1]The Inclusivity Institute for Better Data, Toronto

Introduction and Objective: This scoping review addresses the persistent underrepresentation of Black individuals in Science, Technology, Engineering, Mathematics, and Medicine (STEMM) fields. Despite increased diversity initiatives, significant gaps remain, impacting the development of inclusive educational and professional environments. The objective of this review is to evaluate the application of predictive analytics as a strategic tool to identify barriers and enhance participation rates of Black students and professionals in STEMM.
Materials and Methods: The review synthesizes existing literature on barriers to Black participation in STEMM, the use of predictive analytics to forecast educational and career outcomes, and the development of mobile applications that utilize these predictions to support Black individuals in STEMM. This approach consolidates research findings to assess the efficacy and potential of technological interventions in promoting inclusivity.
Results: The findings reveal that predictive analytics effectively identify key success factors and obstacles faced by Black individuals in STEMM. The review highlights several case studies where predictive models have informed the development of support systems, significantly improving engagement and retention rates.
Conclusion and Significance/Implication: The review concludes that predictive analytics and mobile technology hold substantial promise for reducing racial disparities in STEMM fields. By providing targeted support and personalized guidance, these technologies foster an environment that is more conducive to success for Black individuals. The implications of this work suggest a transformative approach to diversity initiatives, urging further collaboration to refine and implement these technologies broadly.

Lay Abstract This review looks at how we can use technology, specifically predictive analytics, to help more Black individuals succeed in fields like science, technology, engineering, mathematics, and medicine—collectively known as STEMM. Despite efforts to bring more diversity into these important areas, Black students and professionals are still not as represented as they should be. This work explores the challenges they face, such as unfair treatment, fewer resources, and lack of guidance, and how a specially designed mobile app can make a difference. This app would use data to give personalized advice and support, aiming to make STEMM fields more welcoming and supportive for Black individuals. The goal is to ensure they have the opportunities and tools needed to thrive. This paper encourages a team effort from teachers, policymakers, and community leaders to test and improve this technological solution, making a significant step toward equality in education and professional fields.

The impact of race, culture, and income inequality on literacy practices in the black communities of Montreal

Tanya Matthews[1]
[1]*McGill University*

Introduction: Children in low-income situations face financial, mental, and self-esteem challenges that negatively impact their learning and language outcomes (Bradley & Corwyn, 2002, 2012; Roberts et al., 2005). In Canada, there needs to be more ethnocentric research exploring home-based literacy practices, which is a critical area where the intersectionality of these social determinants can be examined and further determine their impact on educational outcomes.
Objective: This study explores oral language and literacy practices in low-income Black communities, aiming to understand how these vary due to income inequality and cultural differences. It sheds light on the implications for early language and reading skills and educational outcomes.
Methods: The first phase of this study involved meticulously recruiting six participants from Montreal. A community-based participatory research method was employed, which included ethnographical measures, literacy questionnaires, and shared book-reading dyads.
Results: Families prioritize education but need help accessing resources in their neighbourhoods. There are differences and similarities in literacy practices across households, comparable to those of middle-class white families in Canada.
Conclusions and Significance: The participant data reveals significant findings about pre-literacy practices. Differences in these practices may be linked to income inequality and cultural differences, providing valuable insights into how these factors affect literacy practices and academic success. This research can inform educational policies and practices regarding the impact of race, culture, and income on literacy practices and academic success.

Lay Abstract

Introduction: In Canada, there is a lack of culturally relevant research examining how income, race, and culture affect the literacy practices used in Black families.
Objective: This study examines how race, income, and culture affect oral language and literacy practices in low-income communities.
Methods: Six participants were recruited. A community-based participatory research method was employed, which included ethnographical measures, literacy questionnaires, and shared book-reading dyads.
Results: Families prioritize education but need help accessing resources in their neighbourhoods. There are differences and similarities in literacy practices across households, comparable to those of middle-class white families in Canada.
Conclusions and Significance: The data reveals existing differences and similarities in the literacy practices employed across households and some similarities with literacy practices used in mainstream homes.

Equitable access to mental health care for black and indigenous peoples in Canada: a scoping review

Yolanda Watungwa[1], Nomusa Mngoma, Barbara Hamilton-Hinch, and Matthew Numer
[1]Dalhousie University

Introduction and Objective
Mental wellbeing is a fundamental component of one's health, and in the words of Dr. Vikram Patel, "there is no health without mental health". Access to appropriate mental health services, and interventions that recognize the Canada's diverse population are critical to the health of Black and Indigenous peoples as they experience oppression in many areas of life, often because of racial stigma and discrimination. The inter-relationship between systemic racism, stigma and discrimination is significant because the three phenomena actively impair the health and quality of life. Understanding the nuanced experiences of Black and Indigenous peoples with the Canadian healthcare system, is key to providing health for all.
Objective: To map academic literature on access to mental health services for Black and Indigenous peoples in Canada with a focus on barriers and/or facilitators.
Materials and Methods
This scoping review followed the Arksey and O'Malley scoping review framework. The search strategy included five databases (CINHAL, APA PsychInfo, the Social Work Abstracts, MEDLINE. We used narrative synthesis, iteratively, and summarized the results in quantitative and qualitative forms, following the Arksey and O'Malley (2005) protocol.
Results
The results can be captured in three key themes as follows; cultural incongruence, representation, and mental health care that recognizes Black and Indigenous experience.
Conclusion/Significance
Barriers and facilitators to accessible mental health care exist at every level of the socio-ecological model, and therefore, comprehensive and multidimensional approaches are required to meet the needs of the Canadian Black and Indigenous peoples.

Lay Abstract Mental wellbeing is a fundamental component of one's health, and in the words of Dr. Vikram Patel, a leading mental health researcher, "there is no health without mental health". Access to appropriate mental health services, and interventions that recognize the Canada's diverse population are critical to the health of Black and Indigenous peoples as they experience oppression in many areas of life, often because of racial stigma and discrimination. These phenomena interact to greatly compromise the quality of one's life. Our study exposed three areas of importance to access, namely, mental health care that recognize Black and Indigenous experience, are culturally aligned, and demonstrate representation. Barriers and facilitators to accessible mental health care exist at every level of the socio-ecological model and comprehensive, multidimensional and culturally appropriate mental health care is important to ensure health for all.

Exploring the perspectives of Liberian frontline health workers on ethical tensions experienced during the Ebola epidemic and COVID-19 pandemic

Parnor Madjitey[1], Anne Andermann, Matthew Hunt
[1]McGill University

Introduction: Virulent contagions like Ebola and COVID-19 can have devastating consequences on populations and healthcare systems, including possible exposure of health workers resulting in harms in the line of duty. Insufficient measures to support health workers during such crises may amplify ethical tensions as they perform their duties. Although studies have considered various measures to assist health workers deal with ethical tensions during public health crises, few have explored the perspectives of health workers in under-resourced healthcare systems. This study therefore aimed to explore the ethical tensions faced by frontline healthcare workers who cared for Ebola and COVID-19 patients in health facilities in Liberia.
Methods: Guided by interpretive description methodology, data was gathered through audio recorded interviews, and by reviewing collateral documentary sources. Participants included 9 healthcare administrators and 45 primary health workers. A framework method was used to analyze the data and generate themes.
Results: Liberian health workers experienced a range of ethical tensions, including their professional duty to care for patients being at conflict with personal needs including concern for family well-being. They reported experience of stigma from family and community members, particularly during the Ebola epidemic and to a lesser extent during the COVID-19 pandemic.
Significance: Assisting health workers in resource-limited settings with psychosocial services, and financial incentives would promote their wellbeing and support the quality of care provided to patients during contagions.
Conclusion: Ethical tensions for health workers are likely an unavoidable dimension of public health emergencies. Taking steps to minimize and mitigate these tensions is critically important.

Lay Abstract During epidemics like Ebola or pandemics like COVID-19, doctors, and nurses face many challenges including taking care of many patients at the hospital, working longer hours than usual and not having adequate safety materials like gloves, gowns, boots to protect themselves at work. Due to this situation many health workers get worried about contracting the disease, becoming sick and possibly dying. They also become worried about carrying the disease home and spreading it to their family members who could fall sick and die. As a result of these concerns, the health workers are faced with a choice between caring for patients during infectious disease outbreaks or staying away from work to protect themselves from the diseases. During such situations, it is important to provide health workers with the necessary support to address their concerns so they can continue to take care of patients and keep the healthcare system alive.

Medical and Public Health Research

Contributed Talks

Food insecurity, pandemic related pregnancy stress, and maternal-infant health outcomes

Landry Kalembo[1], Shannon Bainbridge, Bénédicte Fontaine-Bisson
[1]Interdisciplinary School of Health Sciences, Department of Cellular and Molecular Medicine, School of Nutrition Sciences, University of Ottawa, Institut du savoir Montfort, Hôpital Montfort

Adverse psychological, and environmental exposures during early life can result in undesirable health, including increased risk of chronic diseases in adulthood. Food insecurity (FI) and heightened stress are well-established gestational exposures known to initiate adverse developmental programming events which were exacerbated for many Canadians during the pandemic. We aimed to examine the relationships between maternal FI and stress during the COVID-19 pandemic, and how they were associated with maternal gestational weight gain (GWG) and newborn birthweight in a Canadian pregnant cohort.
Data was collected retrospectively from 273 individuals that were pregnant and delivered an infant between March 2020 - March 2023. Participants responded to an online survey derived from previously validated questionnaires addressing FI, stress, and self-reported GWG and infant birthweight.
Over half (55%) of participants experienced FI, a fifth (20%) reported heightened stress related to pregnancy preparedness and over a third (34%) related to COVID-19 infection during the pandemic. Participants from food secure and insecure households differed significantly in age, sexual orientation, household type and housing status ($p < 0.001$). Heightened stress was associated with sexual orientation, household type and unplanned pregnancies ($p < 0.05$). Infant birthweight extremes (32%) were associated with heightened stress related to both pregnancy preparedness and COVID-19 infection ($p < 0.02$).
Results from this study provide a better understanding of the scope of FI, gestational stress, and their potential drivers during the pandemic in a Canadian cohort, which could lead to tailored interventions aimed at improving maternal and infant health and wellbeing during emergency/pandemic contexts.

Lay Abstract The COVID-19 pandemic exacerbated Food Insecurity (FI) among vulnerable pregnant populations, while also amplifying their stress levels – likely contributing to adverse developmental programming events and pregnancy outcomes. Given that an infant's short and long term health and well-being can be influenced by maternal exposures during pregnancy, more research is needed to better understand these exposures, their causes, consequences, and how they associate with health inequalities. Investigating these associations could provide crucial information on the importance of perinatal screening and implementing targeted interventions to enhance lifelong offspring health outcomes, especially during emergency or pandemic contexts.

Understanding mortality differentials of Black adults in Canada

Toyib Olaniyan[1], Tanya Christidis, Mathew Quick, Tafadzwa Machipisa, Tolulope Sajobi, Jude Kong, Kwame Mckenzie, Michael Tjepkema

[1] *Statistics Canada, Ottawa*

To understand the paths contributing to differential mortality patterns, standard Cox-proportional hazard models was used to assess the incidence risk of diagnosis (uterine and prostate cancer) and incident hospitalization (HIV and diabetes) among Black adults. Competing risk regression was used to evaluate the cumulative risk of death for the four disease outcomes since diagnosis/hospitalization. For the observed differential cancer mortality, mediation analysis was conducted to investigate the role of cancer diagnosis at follow-up (a proxy for delayed diagnosis that is not entirely indicative of late-stage cancer). Across all examined outcomes, except for uterine cancer, Black adults had elevated incident diagnoses or hospitalizations compared to White adults. Notably, Black males demonstrated a two-fold increased risk of incident prostate cancer and hospitalizations due to HIV and diabetes, while Black females had a 12-fold increased risk of incident HIV hospitalizations and were 15% less likely to be diagnosed with uterine cancer compared to White females. Cumulative mortality risk analysis showed a two-times significantly lower survivability among Black females diagnosed with uterine cancer relative to White females. Delayed diagnosis mediated a marginally higher proportion of the total differential uterine cancer mortality among Black females (14.9%, 95%CI: 10.5% to 23.1%) compared to White females (8.9%, 95%CI: 6.3% to 13.9%). This study unveils substantial parallels between heightened incidence risk and relative mortality for most of the four explored outcomes between Black and White adults in Canada. This underscores the need for targeted interventions and early detection strategies to address health disparities in this population.

Lay Abstract To understand the paths contributing to differential mortality patterns, standard Cox-proportional hazard models was used to assess the incidence risk of diagnosis (uterine and prostate cancer) and incident hospitalization (HIV and diabetes) among Black adults. Across all examined outcomes, except for uterine cancer, Black adults had elevated incident diagnoses or hospitalizations compared to White adults. Notably, Black males demonstrated a two-fold increased risk of incident prostate cancer and hospitalizations due to HIV and diabetes, while Black females had a 12-fold increased risk of incident HIV hospitalizations and were 15% less likely to be diagnosed with uterine cancer compared to White females. This study unveils substantial parallels between heightened incidence risk and relative mortality for most of the four explored outcomes between Black and White adults in Canada.

Differences in aspirin use among high-risk pregnancies and associated maternal-fetal outcomes - a retrospective cohort study.

Leonet Reid[1], John Snelgrove, John Kingdom, Valeria Rac, Hilary Brown, Kelsey McLaughlin
[1]Dalla Lana School of Public Health- University of Toronto

Preeclampsia affects 1 in 20 pregnancies in Canada, adding 3.1 million dollars to healthcare costs due to its maternal-fetal complications. Daily aspirin has been demonstrated to reduce the risk of preterm birth associated with preeclampsia when initiated in screen-positive individuals between weeks 11-16 of pregnancy. Despite this evidence favoring aspirin prophylaxis, this preventive strategy is currently underutilized in Canada, due to challenges in identifying at-risk patients and limited publicly-funded preeclampsia screening resources. Descriptive and explorative analysis was utilized to examine a retrospective cohort of 641 individuals to determine patterns of aspirin use based on maternal characteristics and associated maternal-fetal outcomes. Logistic regression was used to estimate the factors associated with increased odds of not receiving aspirin and the odds of non-use by combined and cumulative risk factors. The study revealed that only 34% of the sample population had a documented history of aspirin usage. The common aspirin dosage was 81 mg/day, whereas a higher dosage of >100 mg/day was reported to have higher efficacy rates in preventing preterm pre-eclampsia. The odds of non-use decreased as the number of risk factors increased. Moreover, the study found significant differences in the incidence rates of preterm births between aspirin users and non-users. The study emphasizes the underutilization of aspirin prophylaxis in high-risk pregnancies, with only 34% receiving it despite clear indications. Optimized aspirin utilization can mitigate adverse maternal-fetal outcomes, as the reduced rates of preterm births reveal the potential benefits of aspirin to patients and health systems.

Lay Abstract Preeclampsia is a serious pregnancy complication, affecting 1 in 20 pregnancies in Canada, leading to increased healthcare costs. Daily aspirin has been shown to reduce the risk of preterm birth associated with preeclampsia. However, this preventive strategy is underutilized in Canada due to challenges in identifying at-risk patients and limited publicly-funded screening resources. A study examined patterns of aspirin use in high-risk pregnancies and associated maternal-fetal outcomes. The findings revealed that only 34% of the sample population had a documented history of aspirin usage, despite clear indications. The study demonstrated an overall underutilization of aspirin among high-risk pregnant individuals, with varied usage among maternal characteristics. By increasing awareness and access to aspirin prophylaxis, we can improve the health outcomes of pregnant individuals and their newborns.

Factors affecting the implementation of interventions to eliminate silicosis in the South African mining industry

Chinyelu Patrick[1], Zodwa Ndlovu, Oludoyinmola Ojifinni, Vanessa Govender
*[1]TBC**

Introduction
Silicosis is an incurable occupational lung disease caused by exposure to respirable crystalline silica (RCS). In South Africa (SA), mineworkers' silicosis is important because of its association with tuberculosis. Silicosis can be prevented through control of RCS exposure. The mining industry has set milestones for RCS dust reduction and silicosis elimination by 2024. Elimination has been partially successful.
Objective
To explore existing implementation strategies, facilitators and barriers that might affect the implementation of silicosis reduction interventions in the SA mining industry.
Materials and Methods
A cross-sectional exploratory qualitative study was conducted. We used an implementation science framework, Consolidated Framework for Implementation Research (CFIR), to guide the development of interview guides and data analysis. In-depth interviews were conducted with 18 purposively selected participants. Transcribed data were coded using inductive and deductive coding to derive themes and sub-themes.
Results
The emerged themes were intervention-related factors, implementation-related factors, human-related factors, health-related factors and contextual factors. Strategies for implementation were engineering controls, best practices, industry milestones and compensation. Facilitators were communication, supportive role of Minerals Council South Africa, legislation, monitoring and evaluation. Barriers were lack of implementation practices and inadequate enforcement of best practices. The collection of data was systematically done using the CFIR. This created a better understanding of the factors that have contributed to implementation.
Conclusion/Significance
Communication with mineworkers must be key and continuous to ensure that mineworkers are getting the right information. Enforcement of implementation strategies was found lacking. Thus enforcement of legislation and policies needs to be improved.

Lay Abstract Silicosis, an incurable lung disease caused by exposure to respirable crystalline silica (RCS), poses a significant health risk to South African mineworkers, due to its association with tuberculosis. Despite industry efforts to reduce RCS dust and eliminate silicosis by 2024, progress has been partial. This study aimed to assess facilitators and barriers to the implementation of silicosis interventions in the SA mining sector. Employing a cross-sectional exploratory qualitative approach, we utilized the Consolidated Framework for Implementation Research (CFIR) to structure interviews and analyze data. Eighteen purposively selected participants underwent in-depth interviews, with resulting data coded to unveil themes and sub-themes. Key findings were engineering controls, industry milestones, and communication emerging as crucial elements. Inadequate enforcement and implementation gaps served as prominent barriers. This study underscores the necessity for ongoing communication with mineworkers and strengthened enforcement of policies to enhance silicosis prevention efforts in the SA mining industry

**To Be Confirmed (TBC)*

Stopping enteric illnesses early through environmental surveillance

Lawrence Goodridge[1], Hailey Davidson, Charles Chettleburgh, Anxin Zhao, Valeria Pinto, Opeyemi Lawal, Amber Fedynak
[1]University of Guelph

In Canada, consumption of contaminated food causes 4 million illnesses, 14,150 hospitalizations and 323 deaths each year, with an estimated annual economic burden of approximately $4 billion. The current foodborne outbreak surveillance approach is passive in nature and relies on sick individuals to seek medical care, meaning that public health officials are not alerted of an outbreak for an average of 3-5 weeks post-exposure. This allows contaminated food to remain in circulation, sickening increasing numbers of people. An active surveillance system was developed through the establishment of Sentinel sampling sites in Quebec City, Guelph, and Winnipeg. Wastewater was collected from each site for a period of 2 years to establish population structure and baseline levels of circulating bacterial, viral pathogens using real time Polymerase chain reaction assays. When pathogen wastewater signals indicated an increase in a target pathogen, the sample was further analyzed using meta-genomic sequencing for viruses, or alternatively, for bacterial pathogens, wastewater samples were cultured to isolate the target pathogen followed by whole genome sequencing to investigate potential linkages to ongoing or previous outbreaks. In several instances, increases in the wastewater signal occurred before reported increases in human foodborne illness cases, and genomic linkages were made to pathogens previously implicated in outbreaks or contamination events. These results demonstrate the potential usefulness of the Sentinel approach for early detection of foodborne outbreaks.

Lay Abstract In Canada, contaminated food causes 4 million illnesses, over 14,000 hospitalizations, and 323 deaths annually, with an economic impact of about $4 billion. Traditionally, detecting foodborne outbreaks has been slow, as it relies on affected individuals seeking medical care, leading to delays of 3-5 weeks in identifying such outbreaks. To combat this, a proactive approach using Sentinel sampling sites was developed in Quebec City, Guelph, and Winnipeg. This method involved collecting and analyzing wastewater over two years to monitor bacterial and viral foodborne pathogens. When an increase in pathogens was detected, further specific analyses was conducted to determine linkages with existing foodborne outbreaks. This approach has proven effective, identifying pathogens before they are reported in human cases and linking them to previous outbreaks. The Sentinel system offers a significant advancement in public health protection, enabling faster responses to contaminated food and reducing both health impacts and economic losses.

Lightning Talks

Identification of the transition point of COVID-19 from a pandemic to an endemic disease through respiratory viruses surveillance

Jim Ayukekbong[1]
[1]*Canadian Journal of Infection Control, Toronto*

The emergence of Coronavirus Disease 2019 (COVID 19), caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), has led to an unprecedented global health crisis. The pandemic was declared in the Spring of 2020 and declared over in 2023. To-date, SARS-CoV-2 has been associated with more than 7 million deaths out of more than 700 million confirmed cases worldwide. However, before the COVID-19 pandemic other respiratory viruses caused seasonal outbreaks of disease in the population, but this was disrupted at the start of the pandemic. The aim of this study was to assess the burden of respiratory viruses during and post pandemic and compare trends with pre-pandemic data.
Participants presenting with one or more respiratory symptoms such as fever, cough, general weakness/fatigue, headache, myalgia, sore throat, coryza, dyspnea, anorexia from March 2020 to December 2023 were tested for respiratory viruses by polymerase chain reaction.
From March 2020 to December 2022, SARS-COV-2 (causative agent of COVID-19) was the main virus implicated in more than 99% of all respiratory diseases. From December of 2022 to December 2023, other respiratory viruses such as Rhinovirus, Respiratory Syncytia Virus, Influenza virus, Para-Influenza virus, Seasonal Coronavirus and Human Metapneumovirus accounted for over 70% of all respiratory viruses detected during outbreaks.
This change in the incidence of respiratory virus circulation marked the shift of COVID-19 from a pandemic to an endemic disease and highlights the need to re-calibrate public health measures to control not just COVID-19 but all other respiratory infections.

Lay Abstract The aim of this study was to assess the burden of respiratory viruses during and post pandemic and compare trends with pre-pandemic data. Participants presenting with one or more respiratory symptoms such as fever, cough, general weakness/fatigue, headache, myalgia, sore throat, coryza, dyspnea, anorexia were tested for respiratory viruses. From March 2020 to December 2022, COVID-19 was the main virus implicated in more than 99% of all respiratory diseases. From December of 2022 to December 2023, other respiratory viruses such as Rhinovirus, Respiratory Syncytia Virus, Influenza virus, Para-Influenza virus, Seasonal Coronavirus and Human Metapneumovirus accounted for over 70% of all respiratory viruses detected during outbreaks. This change in the incidence of respiratory virus circulation marked the shift of COVID-19 from a pandemic to an endemic disease and highlights the need to re-calibrate public health measures to control not just COVID-19 but all other respiratory infections.

Understanding the social and structural factors impacting people of African descent with uterine fibroids in Nova Scotia

Keisha Jefferies[1], Josephine Etowa, Bukola Salami, Megan Aston, Angela Alleyne, Shane Austin, Bukola Oladimeji, Melissa Rothfus, Emma Stirling-Cameron, Lisa Bland, Crenda Marfo, Ashley Osa-Peters, Elizabeth Nkrumah
[1]Dalhousie University

INTRODUCTION
Evidence suggests that Black women are three times more likely to experience uterine fibroids compared to the general population. Black women experience larger fibroids with earlier onset, and more severe or debilitating symptoms. Symptoms include pelvic pain, bladder issues, and heavy or abnormal menstrual bleeding. Understanding the state of the literature informs primary research on uterine fibroids among Black people of African descent (BPAD).
OBJECTIVES
The objective of this scoping review is to describe the extent and type of literature available regarding BPAD with uterine fibroids globally.
METHODS
This scoping review follows JBI scoping review methodology and the PRISMA-ScR Checklist. Inclusion criteria for this review includes sources that involve BPAD and uterine fibroids. This review does not include jurisdictional, geographical, regional, or study setting restrictions. A comprehensive search strategy developed in collaboration with a health sciences librarian was used to retrieve peer-reviewed. Databases were searched from inception. Title and abstract screening, full text review, and data extraction will be completed by two independent team members.
RESULTS
Extracted data will be classified into conceptual categories. The analysis will identify study methods, location, results including statistical information or thematic findings, and recommendations.
SIGNIFICANCE
Growing attention on the debilitating and disproportional impacts of uterine fibroids reinforces both the timeliness and necessity of a review of the literature regarding BPAD with uterine fibroids globally. To better address this ongoing health issue, it is necessary to understand the current state of knowledge, identify evidence gaps, and develop recommendations for future research.

Lay Abstract Uterine fibroids are non-cancerous growths in the uterus that are generally considered harmless. In reality, many people with uterine fibroids experience symptoms such as heavy menstrual bleeding, pelvic pain or pressure, bladder issues, and a reduced quality of life. The cause of uterine fibroids is not fully understood however, research indicates that Black women are disproportionately impacted and experience more severe symptoms compared to the general population. The purpose of this scoping review is to gather and describe the available literature regarding People of African descent with uterine fibroids. The review will describe current literature as well as identify current knowledge gaps and opportunities for future research. An interdisciplinary team will conduct the scoping review using a systematic approach to screen, review, extract, analyze, and combine information from the literature. The findings will be presented narratively along with charts or tables, where necessary.

Development and evaluation of a training program to enhance care and support of victim/survivors of sexual violence

Nomusa Mngoma[1]
[1]*Queen's University*

Introduction and Objective
Gender-based violence (GBV), a universal social problem affecting millions globally, leaves long-lasting psychological, emotional and physical health consequences. When sexual assaults occur, those in remote rural villages have poor or no access to healthcare and social services. Frontline healthcare and community workers can play an important role in such contexts, particularly, with adequate evidence-based, trauma-informed care and support training. Sexual assaults are underreported with only 16% of rapes reported to the police. Commonly held but untrue beliefs about sexual assault - rape myths - contribute to survivors' reluctance to report for fear of not being believed. Therefore, addressing rape myths is key to supporting survivors.
Objective: To evaluate changes in frontline workers' knowledge and beliefs about sexual assault.
Materials and Methods
A convenience sample of 115 nurses, social workers, and community caregivers participated in a tailored program to enhance capacity to respond to sexual assaults. Before and after the training, participants completed a 10-item questionnaire of commonly held rape myths relevant to the local context. A focus group discussion (n=16) followed.
Results
Knowledge and attitudes improved, with some scores reaching statistical significance (Chi-squares, $p<0.005$). Before the training 58% believed that the "stranger" posed the greatest danger to children and 31% said drinking and skimpy clothing excuse rape.
Conclusion and Significance/Implication
Participating in an evidence-based trauma-informed training program can improve knowledge, attitudes and beliefs about rape. Non-specialist community caregivers and other frontline workers can, with basic training, provide survivors and their families with accurate information, advice and support.

Lay Abstract Sexual assault is a serious universal social problem that leaves lasting psychological, emotional and physical scars. When sexual assaults occur, those in remote rural villages have poor or no access to healthcare or social services. In addition to shame and stigma, sexual assaults often go unreported for fear of not being believed. Rape myths - commonly held but untrue beliefs about rape – are part of the problem and are important to dispel so that people may be more inclined to report and receive care and support. We developed a program designed to address these myths, and 115 frontline workers participated. We were able to see some improvements in knowledge and attitudes. We are encouraged that, with basic training, frontline workers and community caregivers can provide adequate care and support for survivors of sexual assault. In places where access to health and support services is limited, this represents much-desired hope.

The impact of gender on pediatric surgical care in Africa

Sacha Williams[1], Olivia Serhan[2] Jenny Wang[2] Christian Guindi[2] Elena Guadagno[1] Maeve Trudeau[1,2] Emannuel Ameh[3] Kokila Lakhoo[4] Nirav Patel[5] Dan Poenaru[1,2]

[1]Montreal Children's Hosp, Dept of Pediatric Surgery; [2]McGill Faculty of Medicine; [3]National Hosp, Nigeria; [4] Oxford University, UK; [5]Chris Hani Baragwanath Hosp, South Africa

Introduction

Currently, 1.7 billion children globally lack access to surgical care. A significant proportion of these children reside in Africa. Girls, whose care is often affected by barriers steeped in gender inequity, may be at higher risk of poor surgical outcomes.

Objective

This study explores the impact of gender on pediatric surgical care in Africa.

Methods

Differences in access to care and clinical outcomes for boys and girls were examined for pediatric surgical conditions that do not differ by physiological sex. A systematic review of African pediatric surgical studies ensued, followed by a random effects meta-analysis, and risk of bias assessment.

Results

Of the 12281 records retrieved, 54 were selected for review. Most studies were retrospective (57.4%), single-site (94.4%), from Egypt, Nigeria, Ghana, or Ethiopia (55.6%), focused on pediatric surgical gastrointestinal conditions (63.0%), published in 2010 or sooner (85.1%), had study durations of 5 years or less (68.5%), and cohorts of less than 200 children (57.4%). Sixty percent reported the outcome of mortality, while 38.9% studies reported other complications. Meta-analysis odds ratios revealed surgery was performed 3.6 times more often on boys (95% CI: 2.6, 4.9); and mortality was 1.6 times greater for girls (95% CI: 1.3, 2.0).

Conclusion

There appear to be gender disparities in pediatric surgical care. Findings will be further explored and validated in an onsite multinational, multi-site, mixed-methods study, involving community participatory focus groups.

Lay Abstract

Introduction: Millions of African children lack access to surgery. Girls may be more at risk.

Objective: Exploring the impact of gender on African pediatric surgery.

Methods: Reports on children's surgical diseases equally affecting boys and girls, were evaluated to assess surgical access and postoperative outcomes.

Results: Fifty-four papers were reviewed. Most involved one hospital, in Egypt, Nigeria, Ghana, or Ethiopia, up to 200 children, from 2010 onward, and lasted 5 years or less. Sixty percent reported on death as an outcome. Statistical analysis revealed surgery occurred 3.6 times more often on boys, and girls' mortality was 1.6 times higher.

Conclusion: These findings suggest a gender gap in African pediatric surgery in which girls are disadvantaged. This will be further explored in an onsite, collaborative study.

Poster Presentations

Characterizing salmonella enterica serovars from dry foods

Dharamdeo Singh[1], Opeyemi U. Lawal, Carlos G. Leon-Velarde, Valeria R. Parreira, Lawrence Goodridge
[1]University of Guelph

Introduction
Salmonella enterica poses serious public health risks. Elucidating the genomic dynamics of Salmonella strains within various food matrices is vital for reinforcing food safety measures and managing hazards linked to low-moisture foods (LMFs). Two Salmonella enterica isolates, sourced from dry hazelnuts (serovar Muenchen) and chia seeds (serovar Cubana) were characterized using genomic approaches.
Method
DNA was extracted from isolated colonies using Qiagen's DNeasy Blood & Tissue Kit and long-read whole genome sequencing (WGS) was conducted with the Oxford Nanopore Minlon platform. Post-sequencing, low-quality sequences and adapters were removed, and De Novo assembly was conducted using Geneious Prime. Genome annotation was executed with PROKKA, while genes encoding antimicrobial resistance and virulence factors were detected using CARD and VFDB, respectively. PHASTER tools helped identify prophage regions.
Results
Whole genome sequencing of Salmonella serovar Muenchen identified 4,737 genetic features and 4649 predicted coding sequences, inclusive of four intact prophage regions and 26 antimicrobial resistance genes, with a gene for aminoglycoside antibiotic inactivation. Additionally, S. Muenchen harbored 163 virulence genes, including the spvB gene critical for Salmonella pathogenesis. Salmonella serovar Cubana had 5,004 predicted genetic features and 4904 predicted coding sequences, and three intact prophage regions. Twenty-two antimicrobial resistance genes were identified, including the sidA gene for fluoroquinolone efflux, and 172 virulence genes were identified, including the spvB gene.
Significance
Examining antimicrobial resistance, virulence factors, and prophage contents of S. Muenchen and S. Cubana provides important data for risk assessments, outbreak investigations, and focused interventions for decreasing Salmonella contamination in LMFs.

Lay Abstract Salmonella enterica is a significant public health concern in low-moisture foods (LMFs). Genomic characteristics of Salmonella strains found in hazelnuts (serovar Muenchen) and from chia seeds (serovar Cubana), were characterized using genomic methods. The results showed that both strains contained genetic elements that could contribute to their ability to cause disease and resist antimicrobial treatment. For example, S. Muenchen had 26 antimicrobial resistance genes, as well as 163 virulence genes. Similarly, S. Cubana had 22 antimicrobial resistance genes and 172 virulence genes. Both strains also contained intact prophage regions. These findings provide valuable insights into the genomic makeup of Salmonella strains found in LMFs, and can inform efforts to reduce the prevalence of these bacteria in the food supply. By understanding the specific genetic features that are associated with increased virulence or antimicrobial resistance, it may be possible to develop more targeted strategies for controlling Salmonella contamination in LMFs.

Uterine fibroids and black people of African descent: a scoping review

Keisha Jefferies[1], Keisha Jefferies, Josephine Etowa, Bukola Salami, Megan Aston, Angela Alleyne, Shane Austin, Bukola Oladimeji, Melissa Rothfus, Emma Stirling-Cameron, Lisa Bland, Crenda Marfo, Ashley Osa-Peters, Elizabeth Nkrumah
[1]Dalhousie University

INTRODUCTION
Evidence suggests that Black women are three times more likely to experience uterine fibroids compared to the general population. Black women experience larger fibroids with earlier onset, and more severe or debilitating symptoms. Symptoms include pelvic pain, bladder issues, and heavy or abnormal menstrual bleeding. Understanding the state of the literature informs primary research on uterine fibroids among Black people of African descent (BPAD).
OBJECTIVES
The objective of this scoping review is to describe the extent and type of literature available regarding BPAD with uterine fibroids globally.
METHODS
This scoping review follows JBI scoping review methodology and the PRISMA-ScR Checklist. Inclusion criteria for this review includes sources that involve BPAD and uterine fibroids. This review does not include jurisdictional, geographical, regional, or study setting restrictions. A comprehensive search strategy developed in collaboration with a health sciences librarian was used to retrieve peer-reviewed. Databases were searched from inception. Title and abstract screening, full text review, and data extraction will be completed by two independent team members.
RESULTS
Extracted data will be classified into conceptual categories. The analysis will identify study methods, location, results including statistical information or thematic findings, and recommendations.
SIGNIFICANCE
Growing attention on the debilitating and disproportional impacts of uterine fibroids reinforces both the timeliness and necessity of a review of the literature regarding BPAD with uterine fibroids globally. To better address this ongoing health issue, it is necessary to understand the current state of knowledge, identify evidence gaps, and develop recommendations for future research.

Lay Abstract Uterine fibroids are non-cancerous growths in the uterus that are generally considered harmless. In reality, many people with uterine fibroids experience symptoms such as heavy menstrual bleeding, pelvic pain or pressure, bladder issues, and a reduced quality of life. The cause of uterine fibroids is not fully understood however, research indicates that Black women are disproportionately impacted and experience more severe symptoms compared to the general population. The purpose of this scoping review is to gather and describe the available literature regarding People of African descent with uterine fibroids. The review will describe current literature as well as identify current knowledge gaps and opportunities for future research. An interdisciplinary team will conduct the scoping review using a systematic approach to screen, review, extract, analyze, and combine information from the literature. The findings will be presented narratively along with charts or tables, where necessary.

Blazing a trail - validation of a cannabis health literacy tool

Queen Jacques[1], Jennifer Donnan, Lisa Bishop, Rachel Howells, Dr. Zhiwei Gao, Maisam Najafizada
[1]Memorial University of Newfoundland

Background
Cannabis health literacy involves seeking and understanding information on cannabis to make informed decisions about its use. Since the legalization of cannabis, considerable effort has been placed into improving public knowledge and awareness about minimizing the potential harm and risks with cannabis use. However, there is no validated or established method to measure the public's cannabis health literacy, thus hindering the evaluation of cannabis awareness initiatives. Our study aimed to create and validate a questionnaire that measures cannabis health literacy.
Methods
Our cannabis health literacy questionnaire (CHLQ), developed in consultation with stakeholders, comprises four dimensions: knowledge of cannabis, knowledge of risks, understanding of harms and risks of cannabis use, and ability to seek and access cannabis information. Using the Rasch model to validate a questionnaire, we examined the reliability and construct validity by assessing separation reliability, item difficulty, item fit statistics, and unidimensionality. The validation exercise consisted of administering the CHLQ in three adult Canadian population samples, modifying it after each iteration.
Results
In the final iteration, three of the four dimensions of the CHLQ comply with the criteria for reliability and construct validity, with one subscale showing poor unidimensionality. Our findings showed that each CHLQ dimension had a well-distributed range of question difficulties and high item separation reliability.
Conclusions
The CHLQ can be applied to assess the public's cannabis health literacy. It can help researchers, educators, and policymakers identify areas where public awareness may need improvement and guide the development of targeted educational messaging and programs.

Lay Abstract With cannabis now legal in Canada, understanding its use and risks is crucial. Our study introduces the Cannabis Health Literacy Questionnaire (CHLQ), a tool designed to measure people's knowledge about cannabis harms and risks, and their ability to evaluate and apply cannabis health information. Our results show that the tool effectively measures various aspects of cannabis health literacy. By identifying gaps in cannabis health literacy, the CHLQ can guide targeted educational initiatives, helping ensure that individuals make informed decisions about cannabis use. This research is essential for shaping effective public health strategies, ensuring the safety and well-being of the public.

Insights from the ground: a qualitative investigation of specific factors influencing cannabis retailers in NL

Tanisha Wright Brown[1], Dr. Dina Gaid, Dr. William Newell, Dr. Thomas Cooper, Dr. Elizabeth Schwartz, Dr. Maisam Najafizada, Dr. Lisa Bishop, Dr. Jennifer Donnan
[1]Memorial University of Newfoundland

Introduction and Objectives: Legalizing recreational cannabis in Canada was intended to protect public health and safety while creating new business opportunities. However, opening and operating a cannabis store is not without challenges, and protecting public health is reliant on a functioning retail market. This study aims to identify specific factors influencing the cannabis retail operations in Newfoundland and Labradors (NL) as perceived by licensed and unlicensed retailers.
Materials and Methods: Using a qualitative research design, we conducted in-depth semi-structured Zoom interviews with nine licensed and nine prospective retailers in NL. Guided by our newly developed Comprehensive Cannabis Retail Framework (CCRF), the interviews were transcribed verbatim, and thematic analysis was applied to identify both pre-existing and emergent themes that shed light on specific factors influencing the cannabis retail market in NL.
Results: Our study identified several key factors influencing the cannabis retail market in NL, including government regulations, supply chain, and economic, and socio-cultural factors. It revealed that licensed retailers were mostly influenced by advertising and price restrictions, high taxation, inventory and logistics management, and mentorship from family and friends. Prospective retailers' barriers to entry included high licensing fees, licensing inequity, and the ability to obtain financing.
Conclusions and Significance/Implications: These findings have the potential to shape policy decisions in NL and underscore the need for ongoing discussions and regulatory adjustments to better support the success of licensed cannabis retailers and attract new entrants to the legal market, while prioritizing public health and safety.

Lay Abstract Legalizing recreational cannabis in Canada was a big step toward balancing public health and economic growth, yet. running a cannabis store presents unique challenges. Understanding these challenges is crucial for a safe and successful retail market. This study explores the factors influencing cannabis retail operations in Newfoundland and Labrador, as perceived by both licensed and unlicensed retailers. Through interviews and thematic analysis, key factors were identified, including government regulations, supply chain issues, and economic and socio-cultural factors. Licensed retailers faced challenges like advertising restrictions, high taxes, and inventory management, with mentorship playing a crucial role in their success. Conversely, prospective retailers faced barriers like steep licensing fees and difficulty securing financing, hindering their entry into the legal market. Our findings highlight the need for ongoing discussions and policy refinement to support licensed retailers and prospective retailers to enter the legal market, all while prioritizing public health and safety.

Risk of comorbidity with cardiovascular diseases in people living with diabetes in Africa

Divine-Favour Ofili[1], Regina Idu Ejemot-Nwadiaroa, Stephen Chukwuma Ogbodod, Henshaw Okoroiwuf, Ugochinyere Vivian Ukahh

[1]Department of Epidemiology, Biostatistics & Occupational Health, McGill University, Canada

Introduction: Diabetes mellitus (DM) and cardiovascular diseases (CVD) share similar risk factors, thereby increasing the likelihood of comorbidity. However, the risk of CVD, based on the interaction of key risk factors, among people living with DM is less understood. Thus, this study quantified the composite CVD risk and its association with socio-demographic characteristics in people living with DM in Africa. Methods: Using data from the World Health Organization STEPwise approach to non-communicable diseases risk factor Surveillance (STEPS), and generalized linear mixed models for clustered ordinal responses, we assessed the association between CVD risk and socio-demographic characteristics in non-pregnant African adults living with diabetes. CVD risk was measured using a composite score (STEPS-CARDIO index) of five key CVD risk factors – smoking, overweight/obesity, hypertension, physical activity, and diet. Results: In this sample of 4738 individuals, older age was significantly associated with higher CVD risk (OR, 1.03; 95% CI, 1.02-1.04), and this was consistent for both sexes. Women had 1.20 times higher CVD risk than men (OR, 1.20; 95% CI, 1.05-1.38). Although education, marital status, occupation, and household size, were generally positively associated with CVD risk, being a student (OR, 0.51; 95% CI, 0.31-0.86) or religious education graduate (OR, 0.97; 95% CI, 0.68-1.37) were protective; the latter presented an increased CVD risk for men. Significance: The findings highlight gendered and social differences in CVD risk among people with DM. Tailored preventive interventions are therefore required to address the specific needs, and significantly reduce the CVD risk, of populations living with diabetes in Africa.

Lay Abstract Diabetes mellitus (DM) and cardiovascular diseases (CVD) often occur together due to shared risk factors. However, understanding CVD risk in people with DM remains limited. Using data from the World Health Organization STEPwise approach to non-communicable diseases risk factor Surveillance (STEPS), this study assessed the CVD risk in non-pregnant adults with diabetes living in Africa. The risk of CVD was measured using a score (STEPS-CARDIO index) that combined five key CVD risk factors – smoking, overweight/obesity, hypertension, physical activity, and diet. We found that older age increased CVD risk, with women having higher risk than men. Factors like higher education and occupation also increased risk of CVD, but being a student or religious education graduate appeared to reduce the CVD risk in people with diabetes. These findings highlight the need for tailored interventions to reduce CVD risk among African populations living with diabetes, by considering gender and other social factors.

Impact of Health Inequity-Induced Risk Factors on Midline Brain Malformations

Yumi Dille[1], Author2
[1]Your Affiliation

Introduction/Hypothesis: Midline brain malformations encompass a spectrum of congenital anomalies affecting structures along the midline of the brain, including the corpus callosum, pituitary gland, and optic nerves. These malformations can lead to significant neurological deficits and developmental delays. The etiology of midline brain malformations is complex and multifactorial, involving both genetic and environmental factors. This study examines patients with septo-optic dysplasia, a rare congenital condition characterized by underdevelopment of the optic nerves, pituitary gland and septum pellucidum or corpus callosum, as a model to elucidate this multifactorial interplay. Understanding the risk factors associated with these malformations is crucial for early detection, intervention, and adequate follow-up.
Materials/Methods: A retrospective cohort study of children with septo-optic dysplasia was conducted using medical records from the McGill University Health Centre and Genova University, Italy over a ten-year period. Patients diagnosed with septo-optic dysplasia based on neuroimaging or clinical findings were included. Demographic data, family history, maternal health records, and genetic testing results were analyzed. Statistical analysis included logistic regression to identify significant risk factors associated with the development of midline brain malformations.
Results: Out of 50 patients included in the study, almost all patients exhibited abnormalities of the septum pellucidum or corpus callosum and had pituitary gland anomalies. Young maternal age under 20 years, risk behaviour (e.g. alcohol usage/smoking/substance abuse), first trimester bleeding were identified as significant risk factors ($p < 0.05$) associated with midline brain malformations. Furthermore, inadequate follow-up by either a midwife or gynecologist was noted in a large amount of cases. The yield of genetic testing was very low, showing chromosomal anomalies in less than 2% of cases. This indicates that the disease is likely the outcome of interactions among biological, behavioral, and social factors.
Significance: This research highlights how prenatal care and risk behaviors are associated with septo-optic dysplasia. Identifying particular risk factors can assist in focused screening and counseling approaches, potentially lowering the occurrence of these brain malformations through timely intervention and enhanced prenatal healthcare.

Lay Abstract In this study, we looked at the prenal risk factors and clinical outcomes associated in patients with septo-optic dysplasia, thereby contributing to the field's understanding and clinical management of these complex congenital brain malformations. This study, based on ten years of data from the McGill University Health Centre and Genova University, Italy aimed to identify key risk factors associated with these midline brain malformations.

Population-level effect of COVID-19 vaccination coverage on transmission and mortality during Omicron variant dominance: a global longitudinal analysis

Stephen Ogbodo[1], Author2
[1]Your Affiliation

Introduction: Given the high transmissibility of the SARS-CoV-2 Omicron variant and concerns about reduced vaccine effectiveness, we assessed the population-level impact of countries' COVID-19 vaccination campaigns during this period of global Omicron dominance.
Methods: We used a panel dataset of 110 countries over 16 months (January 2022 to April 2023). Using random effects negative binomial regression models, we assessed the effect of monthly full vaccination coverage on new COVID-19 cases and deaths, adjusting for a range of country characteristics and non-pharmaceutical policy interventions. Data were obtained from open access databases, including Our World in Data and the Oxford COVID-19 Government Response Tracker.
Results: On average, each 1 percentage point increase in vaccination coverage was associated with a 1.4% reduction (95% confidence interval [CI]: 0.1–2.8%, p=0.035) in the rate of new cases and a 5% reduction (95% CI: 3.6–6.4%, p<0.001) in deaths. This association was dose-dependent: compared to a vaccination coverage of <50%, coverages of 50-59%, 60-69%, 70-79% and ≥80% were associated with 20.5% (95% CI: -16.4% to 45.7%, p=0.20), 53.8% (22.6–72.5%, p=0.003), 54.3% (15.5–75.3%, p=0.01), and 69.6% (38.7–84.9%, p<0.001) lower rates of new cases, respectively. Similar gradients were observed for the rates of deaths. Furthermore, herd immunity appeared to be achieved at vaccination coverages of 60% or more, in line with expert predictions.
Significance: Our findings underscore the crucial role of vaccination in mitigating the impact of pandemics, particularly during the emergence of highly transmissible variants like Omicron.

Lay Abstract
Objectives: We aimed to assess the population-level effect of countries' COVID-19 vaccination campaigns during the period of global Omicron dominance: January 2022 to April 2023.
Methods: Our sample was a panel dataset of 110 countries over 16 months obtained from open access databases. Using random effects negative binomial regression models, we assessed the effect of monthly full vaccination coverage on new COVID-19 cases and deaths.
Results: On average, each 1 percentage point increase in vaccination coverage was associated with a statistically significant 1.4% reduction in the rate of new cases and 5% reduction in deaths. This association was dose-dependent: progressively higher levels of vaccination coverage were associated with greater reductions in COVID-19 cases and deaths. Furthermore, herd immunity was achieved at vaccination coverage of 60%.
Significance: Our findings underscore the crucial role of vaccination in mitigating the impact of pandemics, particularly during the emergence of highly transmissible variants like Omicron.

Mathematics and Statistics

Contributed Talks

Mathematical study of multi-scale atmospheric wave interactions

Lucy Campbell[1]
[1] *Carleton University*

I will discuss a mathematical problem that describes multi-scale interactions between different types of waves in an atmospheric fluid flow, namely planetary Rossby waves that result from the rotation of the earth and internal gravity waves that result from the gravitational and buoyancy forces. These waves play important roles in the development of a number of phenomena observed in the atmosphere, which affect weather and climate. In my research I use mathematical and computational methods to solve mathematical models for these wave interactions, based on the laws of physics, and this presentation will cover some recent progress.

Leveraging artificial intelligence and mathematical modelling for diseases outbreak support

Jude Kong[1]
[1]*University of Toronto*

Real-time delivery of credible information is critical throughout disease outbreaks to predict changes in the outbreak as early as possible and guide public health measures. However, too little data, collected too slowly, can affect the accuracy of these predictions and the efficacy of mitigation efforts. Advances in artificial intelligence (AI) and mathematical methodologies can fill gaps in data and improve disease outbreak response at every stage. Mathematics- and AI-powered tools have enabled monitoring the spread of diseases at local, state, and national levels; predicting upcoming peaks and their intensities; identifying hot spots; guiding the purchase and allocation of healthcare resources; informing decisions and policies, both for closing down facilities and for reopening them; and optimizing vaccination rollout strategies. In this talk, I will discuss harnessing mathematics and AI to fill gaps in data and improve disease outbreak response at every stage. In particular, I will present some of the mathematics- and AI-based frameworks that we designed and deployed during COVID-19 to support the efforts of decision-makers, the medical community, and the public in managing every stage of the COVID-19 crisis. These frameworks utilize innovative mathematics and AI models to integrate both conventional (e.g., historical data) and unconventional data (e.g., Google Trends, Google Trends Rate, social media, satellite data, and economic activity data).

Lay Abstract Real-time delivery of credible information is critical throughout disease outbreaks to predict changes in the outbreak as early as possible and guide public health measures. However, too little data, collected too slowly, can affect the accuracy of these predictions and the efficacy of mitigation efforts. Advances in artificial intelligence (AI) and mathematical methodologies can fill gaps in data and improve disease outbreak response at every stage. Mathematics- and AI-powered tools have enabled monitoring the spread of diseases at local, state, and national levels; predicting upcoming peaks and their intensities; identifying hot spots; guiding the purchase and allocation of healthcare resources; informing decisions and policies, both for closing down facilities and for reopening them; and optimizing vaccination rollout strategies. In this talk, I will discuss harnessing mathematics and AI to fill gaps in data and improve disease outbreak response at every stage.

Nonstationary autoregressive modeling of time series count data with covariates: addressing seasonality in branching negative binomial

Bakary Traore[1]
[1]*University of N'Zerekore*

Various models for time series of count data account for discreteness, overdispersion and serial dependence. In addition to these, accounting for covariates incorporation pattern are the complexities that arise while dealing with data which involve seasonality aspects. Specifying a model that can handle such kind of time series of count data is very important in several real-life application. However in this paper, we present a non-stationary autoregressive model where covariates informations are incorporated in the Branching Negative Binomial (bNB) autoregressive model in order to asses the seasonality in the process of time series event. A simulation study is done to evaluate how well the proposed strategy performs, and inference is based on maximum likelihood estimate. The model is used to analyze a real-world dataset, which is an infectious disease with covariates, including temperature and rainfall.

Lay Abstract Time series data with count observations often exhibit complexities like overdispersion and serial dependence. Incorporating covariates into models for such data, especially when dealing with seasonal patterns, is crucial for real-life applications. This paper introduces a non-stationary autoregressive model that incorporates covariates into a Branching Negative Binomial (bNB) model to assess seasonality in count time series data. A simulation study assesses the performance of this approach, with inference based on maximum likelihood estimation. The model is applied to analyze a real-world dataset of an infectious disease, considering covariates such as temperature and rainfall. This methodology offers insights into understanding and predicting the dynamics of count time series events affected by seasonal factors.

Parametrizable dataset for the classification of ice hockey power plays

Ken Nsiempba[1], John Zelek, David Clausi
[1]University of Waterloo

The advent of deep learning tools has significantly enhanced researchers' capabilities in analyzing spatio-temporal data. This type of data analysis holds relevance across various domains. For instance, it aids in detecting and preventing potential cyber or financial attacks and is crucial for studying and forecasting traffic patterns in cities. More specifically to our study, spatio-temporal data analysis plays a vital role in detecting specific sporting events.
Improving the ability to identify and cluster patterns within sporting events has profound implications. It can aid in automatic highlight detection and is especially beneficial for coaching, particularly in underfunded and minor leagues. While the insights presented in this paper can be applied to numerous team sports, our focus primarily lies on ice hockey.
This paper makes three significant contributions: 1) We introduce a simple, parametrized ice hockey formation dataset, facilitating the development and benchmarking of baseline models. 2) We investigate the impact of two spatio-temporal parameters from the dataset on the accuracy of event classification. 3) We compare the accuracies of three models: K-Nearest-Neighbours, Graph Networks, and Convolutional Neural Networks.

Lay Abstract Deep learning tools have made it easier for researchers to understand spatio-temporal data, which is data that changes over both space and time. This kind of analysis is useful in many areas. In our case, we use it to find specific moments in sports games. Finding and grouping patterns in sports can help with things like picking out the best moments of a game or helping coaches, especially in smaller or less-funded leagues. While our ideas could work for many team sports, we're focusing on ice hockey here. In this paper, we do three main things:
1.We create a simple dataset for ice hockey formations that can be easily adjusted, making it easier to build and compare basic models.
2.We look at how two specific parts of our dataset affect how well we can tell different events apart.
3.We test three different A.I. algorithms.

On the Alexandrov's estimate

Kennedy Idu[1], Robert Jerrard, Charles Griffin
[1]University of Toronto

A classical fact due to Alexandrov states that if Ω is a bounded open convex domain in ^{n}, and $u : \bar{\Omega} \to$ is a convex function such that $u = 0$ on Ω, then

$$[u]_{1/n}^n \leq C(\Omega)|u(\Omega)|.$$

Here $C(\Omega)$ is a constant, depending only on Ω, and

$$[u]_\alpha := \sup_{x,y\in\Omega, x\neq y} \frac{|u(x) - u(y)|}{|x - y|^\alpha}. \tag{1}$$

and u denotes the subgradient of u. The estimate is not only crucial to regularity theory of the Monge-Ampere equation, but also main tool in some linear elliptic PDE estimates. In this talk, will discuss some extensions and refinements of the estimate depending on the geometry of Ω. This is a joint work with Charles Griffin and Robert L. Jerrard (University of Toronto).

Lay Abstract We revisit the Alexandrov's theorem and investigate problems of optimality and sharpness of conditions and parameters such as geometry of domain, range of Holder exponent and estimate-constant

Risk Factors of Human Mpox (Monkeypox) Infection: A Systematic Review and Meta-Analysis

Chigozie Ugwu[1]
[1]*Laboratory for Industrial and Applied Mathematics (LIAM), Department of Mathematics and Statistics, York University*

Background: Mpox (formerly Monkeypox) is a disease caused by the monkeypox virus. Before the May 2022 outbreak, Mpox infections were sporadically endemic in Central and Western Africa. Due to its rapid decline and scarce epidemiologic data, the zoonotic disease has been relatively understudied.
Objective: This review aims to synthesize evidence on risk factors associated with the transmission of human Mpox in humans both in endemic and non-endemic countries.
Methods: The Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines were followed in conducting the systematic review. Electronic databases were searched. Two reviewers sifted the articles that were included in the review: firstly, by title and abstract, and secondly, by full text. The included articles were assessed for bias. Evidence from the included articles was synthesized qualitatively and quantitatively (meta-analysis).
Results: 947 articles were identified from the database search and 31 articles were eligible to be included in the systematic review. The findings of the meta-analysis showed that interaction with animals (OR=5.61,95%CI=2.83,11.13), HIV (OR=4.46,95%CI=3.27,6.08), other STIs (OR=1.76,95%CI=1.42,2.91), sexual contact (OR=1.53,95%CI=1.13,4.82), close contact with an infected person (OR=2.39,95%CI=1.87,3.05,p=0.009), being identified as men who have sex with men (MSM) (OR=2.18,95%CI=1.88,2.51), and having multiple sexual partners (OR=1.61,95%CI=1.24,2.09) were associated with an increased risk of contracting Mpox. In addition, the presence of co-morbidities was found to be associated with a high risk of Mpox (OR=1.58,95%CI=1.31,1.91), and patients who had been vaccinated against smallpox had a lower risk of Mpox infection (OR=0.24,95%CI=0.11,0.55). Higher education level was associated with a low risk of Mpox although not statistically significant.
Conclusion: This study identified that sexually transmitted infections (STIs), the presence of comorbidities, sexual contacts, and being identified as MSM are highly associated with an increased risk of Mpox infection.

Biomedical and Molecular Research

Contributed Talks

MicroRNA (mir)-299a-5p promotes apoptosis of tubular cells through ERK5 inhibition

Ifeanyi Nmecha[1], Jason Choi, Bo Gao, Melissa MacDonald, Joan C. Krepinsky
[1]McMaster University

Diabetic kidney disease (DKD) is the leading cause of end stage renal failure in North America. Tubular epithelial cell apoptosis was shown to contribute to the pathogenesis of DKD by promoting interstitial fibrosis, which leads to the increased production of extracellular matrix proteins. Previously, we showed that microRNA (miR) 299a-5p promotes the fibrosis response in mesangial cells. Here we studied the role of this miR in regulatingtubular apoptosis. Immortalized human kidney proximal tubular cells (HK2) were treated with high glucose; miR-299a-5p was detected by qPCR. HK2 cells were transfected with miR overexpression and inhibition plasmids using Transfectamine reagent. Apoptosis was detected using the Annexin V kit. Immunoblotting and immunohistochemistry showed protein expression. A bioinformatics screen of four databases showed that miR299a-5p targets MAP3K2, a protein primarily expressed in the tubules. MAP3K2 is an activator of ERK5, an anti-apoptotic and anti-inflammatory kinase. miR-299a-5p overexpression reduced the protein expression of MAP3K2 and phosphorylation of ERK5, while augmenting the expression of apoptotic markers and endoplasmic reticulum stress. Conversely, miR299a-5p inhibition restored MAP3K2 expression and ERK5 phosphorylation to basal levels, while attenuating HG-induced apoptosis. In type-1 diabetic Akita mice, miR299a was increased in association with reduced expression of MAP3K2 and phosphorylated ERK5. These data support an important role for miR-299a-5p in regulating tubular cell apoptosis in HG. Future studies will determine whether inhibition of this miR in vivo attenuates apoptosis and reduces tubulointerstitial fibrosis in DKD.

Lay Abstract Diabetic kidney disease is the leading cause of kidney failure in North America due to cell death and scarring. Our previous work showed that miR-299a-5p worsens kidney scarring. In this study, we looked at how it affects cell death. Kidney cells were treated with sugar to mimic diabetes and found that miR-299a-5p levels increased. Boosting of miR-299a-5p levels in these cells, increased cell death and stress. Conversely, blocking miR-299a-5p decreased cell death. We found that miR-299a-5p targets MAP3K2, which helps protect cells from damage. In diabetic mice, we saw increased miR-299a-5p levels, less MAP3K2, and more cell stress. This shows that miR-299a-5p plays a big role in cell death in response to sugar levels. Future studies will see if stopping miR-299a-5p in mice helps prevent cell death and reduces kidney scarring.

Establishing an optogenetic model of exercise-induced damage and repair in Drosophila melanogaster

Tiara Mulder[1], Francesca Di Cara , Nicanor Gonzalez-Morales
[1]Dalhousie University

Striated muscles are composed of myofibres, each containing myofibrils built from sarcomeres, the basic contractile unit. During exercise, repeated contractions result in muscle damage, which is repaired, restoring the sarcomere structure. However, the specifics of this repair process are poorly understood. Due to limitations in studying human muscle directly, model organisms like Drosophila melanogaster are invaluable due to their shared muscle structure and sarcomeric proteins, simplified genetics, and rapid generation times.
However, exercising Drosophila presents challenges; traditional methods like flipping or tapping machines do not adequately simulate the direct relationship between muscle contraction and damage. To address this, we utilized an optogenetic approach, expressing light-sensitive ion channels called Channelrhodopsins in Drosophila femur muscles via the UAS-Gal4 system to stimulate muscle contractions. Our results show that Drosophila femur muscles undergo substantial damage, characterized by loss of Z disc structure, within 1-2 hours of light stimulation. However, this Z disc structure is restored within 3-5 days post-stimulation. To further test our model, we investigated the role of filamin, a protein shown to be involved in muscle repair in humans and mice that accumulates at the damage sites. Our results revealed that Drosophila filamin accumulates at the damaged sites within 2 hours of stimulations, similar to what is shown in previous studies. In conclusion, our study shows an optogenetic approach can induce muscle damage within Drosophila femur muscles and that this method can be utilized to understand further muscle damage and repair mechanisms and the role of sarcomeric proteins in these processes.

Lay Abstract Muscles are built from fibers that contract during exercise, causing damage that is naturally repaired over time. Understanding this repair process is challenging in human studies, making fruit flies (Drosophila melanogaster) a valuable alternative due to their similar muscle composition and rapid life cycle. Traditional exercise methods for these flies fail to mimic natural muscle stress accurately. Our study employed an innovative optogenetic technique, activating muscles in fruit flies using light-sensitive proteins, allowing us to directly observe muscle damage and repair. We found that light stimulation rapidly damaged the flies' femur muscle structure, specifically the Z discs, which was restored within 3-5 days. Additionally, we tracked the protein filamin, crucial for muscle repair, observing its accumulation at injury sites within two hours of damage. This approach provides a new way to study muscle repair, offering insights that could enhance our understanding of similar processes in humans.

Arl8b-KD cells have altered lysosome characteristics reducing ebola entry

Redaet Daniel[1], Elizabeth LaMarche and Dr. Marceline Cote
[1]University of Ottawa

To infect cells, the Ebola virus (EBOV) requires internalisation and endosomal trafficking to late endosomes/lysosomes, where viral fusion occurs. This process is mediated by the EBOV glycoprotein, which is triggered by cleavage by pH-dependent cathepsin proteases and interaction with its viral receptor, the lysosomal-resident protein Niemann-Pick C1 (NPC1). Interestingly, lysosomes are not homogenous in cells, and their functions and acidity are modulated by their position in cells. The mobility of the lysosomes is facilitated by ADP ribosylation factor-like protein 8B (Arl8b), working in complex with other proteins to move the lysosome throughout the cell. It is unknown if and how Arl8b-positioned NPC1+ lysosomes impact Ebola entry. Here, we used Arl8b siRNA-transfected HeLa cells to localize lysosomes to the perinuclear area. We found that Arl8b knockdown inhibited entry by EBOV viral-like particles (VLPs) but not VLPs harbouring the vesicular stomatitis virus glycoprotein. Using fluorescently labelled EBOV VLPs, we observed that EBOV reached NPC1+ compartments in Arl8b KD cells, suggesting that VLP trafficking to lysosomes is not impaired but rather that the perinuclear NPC1+ lysosomes themselves are non-conducive to viral entry. As Ebola virus relies on cathepsins to cleave its GP, we examined the protease activity in the Arl8b KD cells. We found that, compared to control cells, lysosomal protease activity was reduced in the Arl8b KD cells. Taken together, our study suggests that Arl8b-positioned lysosomes vary in their characteristics thus altering their functions specifically in Ebola virus entry.

Lay Abstract Ebola virus heavily relies on the acidic environment of lysosomes to enter cells. For the cells overall function, lysosomes must be able to move around which requires the presence of protein Arl8b. How the positions of lysosomes impact Ebola virus entry remains unclear. Through our research we have identified that perinuclear lysosomes reduce Ebola virus entry. Subsequent results have shown that the virus is still able to enter the cells and go to the lysosomes but for some reason the lysosomes are not functionally able to faciliate Ebola virus entry.

Protein coalation: a novel role of Coenzyme A in redox regulation of human sperm capacitation

Chika Onochie[1], Cristian O'Flaherty
[1]McGill University

INTRODUCTION
Infertility is rising worldwide, affecting 17% of couples, half due to male factors. Sperm capacitation, the process through which spermatozoa gain fertilizing function in the female reproductive tract, relies on precise redox signaling, and any dysregulation may result in infertility. We discovered that protein CoAlation, a novel protein modification by Coenzyme A, is involved in the spermatozoon's antioxidant defense, but its role in redox signaling during capacitation is unknown. We aim to determine the localization of protein CoAlation and the impacts of altered CoASH biosynthesis on sperm capacitation.
METHODS
Highly motile spermatozoa from healthy volunteers were used. CoAlated proteins, PANK2, and COASY enzymes were localized by subcellular fractionation followed by immunoblotting or immunocytochemistry. The effect of CoASH biosynthesis on capacitation was studied by incubating spermatozoa in capacitating media with fetal cord serum ultrafiltrate (FCSu), in the presence of pantothenic acid or PANK2 inhibitor.
RESULTS
CoAlated proteins are primarily present in the treated Triton-soluble and -insoluble fractions, the flagellum, and the post-acrosomal region of spermatozoa under oxidative stress. PANK2 and COASY were in all sperm fractions. PANK2 inhibition increased, and pantothenic acid supplementation decreased Phospho-Tyrosine levels in capacitating spermatozoa compared to FCSu-alone controls.
CONCLUSION
CoASH levels modulate sperm capacitation. CoAlated proteins localized in the sperm head and flagella suggest an alteration of sperm chromatin and flagellar proteins impacting sperm functions. Ongoing proteomic analysis aims to identify capacitation-related proteins prone to coAlation and to characterize the sperm CoAlome during oxidative stress. These will aid in developing diagnostic tools for male infertility.

Lay Abstract Infertility is rising worldwide, affecting 17% of couples, with half due to male factors. Male fertility depends on sperm capacitation, the process through which sperm become fertile in the female reproductive tract. This process depends on well-regulated redox signaling; any imbalance can lead to infertility. Our study focuses on protein CoAlation, a modification by Coenzyme A that plays a role in sperm defense against oxidative stress. Using sperm from healthy volunteers, we investigated where this modification occurs in sperm and whether changes in Coenzyme A synthesis affects capacitation. The findings reveal that protein coAlation is widespread all over the sperm when exposed to oxidative stress, and that levels of coenzyme A determine sperm capacitation. The next phase of this research is to identify which proteins undergo protein CoAlation during sperm capacitation and to assess their roles, potentially leading to new ways to diagnose and treat male infertility.

Lightning Talks

Functional significance of food-derived peptides in inhibiting islet amyloid polypeptide (IAPP) fibrillation in type 2 diabetes management

Raliat Abioye[1], Martha S. Yiridoe, Chenyang Wang, Tamer A.E. Ahmed, Maxwell T. Hincke, Riadh Hammami, Chibuike C. Udenigwe

[1]Department of Chemistry and Biomolecular Sciences, University of Ottawa; School of Nutrition Sciences, University of Ottawa, Canada

Introduction and Objective: Islet amyloid polypeptide (IAPP) fibrillation has been commonly associated with the exacerbation of type 2 diabetes. Consequently, inhibition of IAPP fibrillation to minimize β-cell cytotoxicity is an important approach towards β-cell preservation and type 2 diabetes management. Three tetrapeptides, TNGQ, MANT, and YMSV, were initially studied for their effect on IAPP fibrillation and cellular membrane integrity.
Materials and Methods: Using thioflavin T (ThT) fluorescence assay, circular dichroism (CD) spectroscopy, dynamic light scattering (DLS), molecular docking, and membrane leakage and cell viability assays, we evaluated the potential anti-fibrillation mechanism and cytoprotective effects of the tetrapeptides.
Results: ThT fluorescence kinetics and microscopy and transmission electron microscopy showed that all three tetrapeptides showed varying anti-fibrillation activity, with TNGQ being the most effective inhibitor. Molecular docking showed that TNGQ and MANT interact with monomeric IAPP via hydrogen bonding and electrostatic interaction. Giant unilamellar vesicles were used to demonstrate the cytoprotective effects of the tetrapeptides in the presence of IAPP. Following the trend, TNGQ produced the lowest fluorescence intensity and percent leakage and was the best at maintaining membrane integrity over 12 h, suggesting the role of peptide structure on anti-fibrillation activity. Molecular docking of the tetrapeptides to oligomeric IAPP fibrillar intermediate highlights the importance of binding to the C-terminal region for fibrillation inhibition.
Conclusion and Significance/Implication: The findings provide insight into the preferred structural interactions of anti-IAPP fibrillation peptide inhibitors, towards the rational development of novel anti-diabetic peptides with anti-fibrillation mechanisms.

Lay Abstract Islet amyloid polypeptide (IAPP) is a naturally occurring hormone that regulates blood glucose levels. However, IAPP commonly self-interacts, causing the formation of aggregates. These aggregates are toxic to pancreatic b-cells and are tied to type 2 diabetes (T2D) progression. Thus, using inhibitors to discourage IAPP aggregation is a promising avenue for managing T2D. Furthermore, the focus on natural disease treatment methods finds food-derived peptides an excellent source of natural inhibitors. Thus, this research aims to identify aggregation inhibiting natural peptides and evaluate their effects on preventing b-cell death by understanding the relationship between peptide interactions and inhibitor function. In this study, three peptides, TNGQ, MANT, and YMSV were discovered for their ability to prevent IAPP aggregation and associated toxic effects on pancreatic b-cells through unique interactions with IAPP. Findings from this study will significantly advance the field in developing targeted natural peptide inhibitors as novel T2D treatment methods.

Investigating the impact of host physiology on anti-tumor immunity

Sheri McDowell[1]
[1] *University of Geneva*

The immune system possesses the ability to target and eliminate neoplastic disease, but myriad factors can impact this process. Identifying such factors is a pillar of cancer immunology research, with great emphasis on endogenous host physiology that can potentially boost the efficacy of immunotherapeutic agents. During my doctoral degree I investigated how obesity-associated inflammation influences tumor immunology with the objective to describe how inflammatory alterations influenced immune populations within the systemic circulation and secondary metastatic organs. Using in vivo preclinical models, I found that obesity enhanced cancer progression, and inflammatory alterations within adipose tissue resulted in systemic perturbations of myeloid cell populations. This consequentially increased cancer cell spread to secondary metastatic organs. These findings highlight how underlying host physiology, can perturb immune populations to influence cancer progression. For my postdoctoral training I will continue investigation into host factors that influence anti-tumor immunity. For example, it is well established that cytotoxic T cells can directly kill tumor cells, with such tumor elimination events being influenced by various factors. While great advances have been made to understand how cytotoxic cells eliminate tumors, greater understanding of the role of host physiology in this process is needed. To address this, we will use real-time intravital microscopy, coupled with tumor models to validate any findings. Given the importance of the immune system in regulating anti-tumor responses, better understanding of how host physiological factors influence immune cells within tumors is fundamental to advance cancer immunology research and improve immunotherapy outcome for patients.

Lay Abstract The immune system possesses the ability to target and eliminate neoplastic disease, but myriad factors can impact this process. Identifying such factors is a pillar of cancer research, with great emphasis on host physiology that can potentially boost the efficacy of therapeutic agents. Within the past few years exciting advances have been made in the field, highlighting numerous, previously unidentified endogenous host factors that influence immune response and immune targeting therapies including metabolic factors such as obesity, bacterial microbiome composition and the sleep cycle, also termed the circadian system. Given the importance of the immune system in regulating anti-tumor responses, my research aims to better understand how host physiological factors influence immune cells within tumors to improve immunotherapy outcomes for patients and death from this disease.

Investigating covalent HDAC inhibitors for the treatment of Duchenne muscular dystrophy

Mulu Geletu[1], Yasir Raouf, Abootaleb Sedighi, Geordon Frere, Rebecca Allan, Nabanita Nawar, Elvin de Araujo, and Patrick Gunning

[1]University of Toronto Mississauga

Duchenne muscular dystrophy (DMD) is a genetic disorder caused by mutations in the dystrophin gene that result in protein loss or truncation, causing muscle weakness and degeneration. Histone deacetylases (HDACs), a type of enzyme that has existed throughout evolution, cause chromatin condensation by removing the acetyl group from histones and other protein regulatory factors. Our goal is to investigate HDAC inhibitors for DMD treatment that increase histone acetylation and regulate muscle-specific genes. We have developed a first-in-class series of molecules that selectively and potently engage Class 1 HDACs via a covalent mechanism of action. To evaluate these molecules in vitro, we cultured C2C12 skeletal myoblasts in a complete medium. To induce differentiation to myotubes, confluent cultures were treated with HDAC inhibitors for 72 hours and cells with 2% horse serum were used as a positive control. Cells were fixed and immunofluorescent staining was performed. Western blotting analysis was performed by lysing the cells with RIPA and total proteins were resolved on a polyacrylamide-SDS gel, Bands were visualized using clarity western ECL substrate at a 1:1 ratio for HRP secondary antibody and analyzed. Our results show that C2C12 myoblasts can effectively differentiate into myotubes by using HDACi YSR734 to activate muscle-specific biomarkers like myogenin, Cav3, and AC-alpha-tubulin. This process also sheds light on how these biomarkers contribute to muscle regeneration. The current study aims to advance our inhibitors toward preclinical covalent HDAC inhibitors.

Lay Abstract Duchenne muscular dystrophy (DMD) is a genetic disorder characterized by progressive muscle degeneration and weakness that predominantly affects young males. It is caused by a mutation in the X chromosome in the gene encoding a protein called 'dystrophin'. There is currently no cure for this disease. We and others have identified that using a class of drugs called HDAC inhibitors can help rescue some of these effects. For example, just this year (2024), the FDA approved the drug, givinostat, as an HDAC inhibitor for the treatment of DMD. We created a series of inhibitors that have a unique mechanism of action and selectively and potently inhibit HDACs. We have used cell biology experiments to show that these inhibitors help regenerate muscle cells in a test tube. The current study aims to advance our inhibitors to treat patients with Duchenne muscular dystrophy.

Poster Presentations

Tanycytes in sensory circumventricular organs

Amirah-Iman Hicks[1], Masha Prager-Khoutorsky, PhD
[1]McGill University, Department of Physiology

Tanycytes are specialized glial cells found in regions of the brain, called circumventricular organs (CVOs), featuring an incomplete blood-brain barrier due to the presence of fenestrated vasculature. Tanycytes have a unique morphology with cell bodies contacting the cerebral spinal fluid (CSF) and long processes extending into the brain parenchyma. OVLT and SFO are sensory CVOs involved in regulating hydromineral balance and cardiovascular function, containing neurons activated by increases in blood osmolality and Na+. Given their strategic location, we hypothesize that tanycytes in sensory CVOs communicate with neurons, and modulate neuronal activity in response to changes in the composition of the CSF and the peripheral circulation.
Visualization of tdTomato expression in tanycytes showed that they feature numerous small protrusions along their processes, and branch to contact both fenestrated blood vessels and neuronal cell bodies. Tanycytic expression of GCaMP6f showed that OVLT and SFO tanycytes display transient elevations in intracellular Ca2+ in response to increases in extracellular Na+, ATP, and glutamate. In addition, we found that tanycytes in sensory CVOs express components of purinergic and glutamatergic signaling. To examine if ATP can act as a gliotransmitter in these regions, extracellular ATP indicator GRABATP was expressed on the surface of OVLT neurons. Our data show that increases in extracellular glutamate and Na+ elevate ATP in the OVLT.
Our findings suggest the presence of bidirectional communication between tanycytes and neurons in the sensory CVOs, potentially mediated by glutamate release and/or purinergic signaling, and modulated in response to changes in hydromineral balance.

Lay Abstract The brain is isolated from the peripheral blood circulation by a barrier that protects it from the entrance of harmful substances (pathogenic or inflammatory agents) and prevents excessive fluctuations in the levels of circulating molecules. However, a few specialized brain areas located in the hypothalamus are not fully isolated from the peripheral circulation and thus can directly sense the composition of the blood (e.g. levels of glucose, ions, and hormones). These specialized brain areas are of key importance for the organism as they respond to the levels of circulating molecules by controlling vital functions, such as food intake, energy metabolism, plasma sodium detection, water balance, and blood pressure. This research project characterizes the properties of key cells that constitute the barrier between the peripheral circulation and these specialized hypothalamic areas, and provide evidence of bidirectional communication between glial cells and neurons in these regions.

Alternative oxidase unlocked: developing an experimental tool for protein expression in saccharomyces cerevisiae

Anissa Francis[1]
[1]*Wilfrid Laurier University*

The alternative oxidase (AOX) is a terminal enzyme found within the electron transport system of different organisms. AOX was originally discovered in plants but is also present in protists, fungi, and animals. Although its presence has been confirmed in all domains of life; excluding archaea, its purpose and importance have yet to be definitively established. Our current knowledge indicates that this enzyme acts as a terminal oxidase to support bioenergetics, while simultaneously acting as a regulator in organisms to influence the response to biotic and abiotic stressors. Investigating the post-translational regulation of AOX may lead to a better understanding of the physiological function of AOX. The goal of my project is to create a tool to study the post-translational regulation of AOX enzymes from different organisms. This involves identifying, amplifying, and cloning AOX cDNA from Dictyostelium discoideum, Cryptosporidium parvum, Selaginella moellendorffii, Candida albicans, and Amphimedon queenslandica into a plasmid for the expression of these AOX proteins in the yeast Saccharomyces cerevisiae. This will allow for cross-organismal comparisons to be made as we will have created a tool capable of producing AOX proteins from various eukaryotic organisms.

Lay Abstract The alternative oxidase (AOX) is located within the electron transport system. AOX was originally discovered in plants but is also present in protists, fungi, and animals. Although its presence has been confirmed in almost all domains of life, its purpose and importance have yet to be definitively established. Current literature indicates that this enzyme supports energy transformations in living organisms experiencing high-stress situations. If we can investigate the different levels of control that regulate this enzyme after it is produced, we can better understand the function of AOX. My project aims to create a tool to study and investigate these regulatory controls across various organisms by identifying, amplifying and cloning AOX cDNA from organisms that represent all domains of life, excluding archaea. This will allow cross-organismal comparisons to be made as we will have created a tool capable of producing AOX proteins from various organisms.

The role of tmed2 in craniofacial development

Cassandra Millet-Boureima[1], Hannah Gordon, Loydie A. Jerome-Majewska
[1]McGill University Health Centre

TMED2 is a member of the transmembrane emp24 domain protein family required for cargo transport between the ER and Golgi. We identified a mutant mouse line with a loss of function point mutation in the Tmed2 signal sequence (Tmed299J) in a screen for genes required for proper morphogenesis. We found that Tmed299J homozygous mutant embryos die at E11.5 due to placental defects. These mutants display developmental delay, failure to turn, posterior truncations, abnormal heart looping, and abnormal head development. Recently, we generated mutant mouse lines with LoxP sequences flanking exons 2 and 3 of Tmed2 to investigate its tissue-specific requirements during embryogenesis. Using beta-actin Cre, we generated mice with heterozygous deletion of Tmed2 and confirmed that the two mutant alleles failed to complement. While Tmed2 heterozygous mice (Tmed2+/-) resembled controls, Tmed2 homozygous mice (Tmed2-/-) arrested at E8.5 and showed developmental delay with a significant decrease in mRNA levels. Furthermore, knockout of Tmed2 in neural crest cells with Wnt1-Cre2 resulted in microcephaly and micrognathia. Cartilage and skeletal preparation of E14.5 and E18.5 neural crest mutant embryos showed reduced frontonasal cartilage and poor ossification in the mandible and bones of the head derived from neural crest cells. These results indicate that TMED2 is required in the neural crest cells for normal development of the head. Future studies will focus on identifying the TMED2 cargoes important for craniofacial development.

Lay Abstract TMED2 is involved in protein transport between key parts of a cell, the ER and the Golgi. A point mutation in the Tmed2 gene in mice leads to embryonic death by E11.5 due to abnormal placental development. These mice also show a growth delay, and abnormal heart development and head formation. We created a new mutant mouse line to understand how the Tmed2 gene affects specific tissues. When Tmed2 was knocked out in neural crest cells—a group of cells important for forming facial structures—mutant mice developed microcephaly (small head) and micrognathia (small jaw). Additionally, skeletal and cartilage examination of these mice showed poor bone development in the head and reduced frontonasal cartilage. Our findings suggest that TMED2 plays a critical role in the proper development of the head and face. Ongoing studies aim to uncover which specific cargoes transported by TMED2 are crucial for normal craniofacial development.

Loss of the DNA repair protein, polynucleotide kinase phosphatase potentiates type-i interferon response via ros-induced damage to DNA

Wisdom Kate[1], Mesfin Fanta, Michael Weinfeld
[1]University of Alberta

Introduction
DNA damage is implicated in the activation of the type-I interferon (T1IFN) response. This opens the possibility of using DNA repair inhibitors to stimulate the immune system against tumours. PNKP is a DNA end-processing enzyme that possesses both 5'-kinase and 3'-phosphatase activities, and its downregulation sensitizes cancer cells to ionizing radiation (IR) and H2O2. We, therefore, hypothesize that loss of PNKP will increase IR- and reactive oxygen species (ROS)-induced damage to DNA and consequently mediate the T1IFN response.
Materials and Methods
Cells were depleted of PNKP using RNA interference prior to exposure to IR, ROS scavengers, or inhibitors. Immunoblotting, immunofluorescence, ELISA, and RT-qPCR were used to analyze changes in protein and/or gene expression levels.
Results
Our data showed that loss of PNKP in breast cancer cells causes a robust phosphorylation of STAT1, upregulation of interferon (IFN)-stimulated genes, as well as accumulation of cytosolic DNA. We also found that STAT1 activation and the consequent induction of pro-inflammatory genes in PNKP-depleted cells was dependent on the DNA sensor, cGAS in co-operation with ZBP1. Lastly, depletion of mtDNA, using 2',3' dideoxycytidine or treatment with ROS scavengers indicated that leakage of mtDNA into the cytosol and ROS-induced damage to DNA, respectively were indeed driving T1IFN response following PNKP loss.
Conclusion and significance
The data above provide evidence that PNKP inhibition might help to mediate the T1IFN response leading to enhanced immunogenic targeting of tumours.

Lay Abstract Breast cancer is the most diagnosed cancer in North American women, accounting for about 25% of all new cases of cancer. Although radiotherapy has shown clinical benefits, some tumours still retain the capacity to repair the toxic DNA damage caused by radiation, which ultimately leads to tumour spread and relapse. There is, therefore, the need to target certain proteins within tumours that are involved in repairing damaged DNA. To this end, our research is focused on developing an inhibitor against the DNA repair protein called polynucleotide kinase phosphatase (PNKP). Together with other DNA repair proteins, PNKP makes tumours resistant to the effect of radiation by repairing the DNA damage induced by radiation. In this study, we aim to further improve the therapeutic effects of radiation in boosting the immune system by inhibiting PNKP. We, therefore, speculate that PNKP inhibition will potentiate the immune system to better recognise and attack tumours.

Modeling cerebro-costo-mandibular syndrome (CCMS) with tamoxifen-induced Snrpb deletion

Yanchen Dong[1], Sabrina Shameen Alam, Jennelle Smith, Eric Bareke, Loydie A. Jerome-Majewska
[1]Research Institute of the McGill University Health Centre at Glen Site, Montreal, QC H4A 3J1, Canada, Department of Human Genetics, McGill University, Montreal, QC H3A 0G1, Canada

Heterozygous mutations in SNRPB, a core component of the major spliceosome, are responsible for Cerebro-costo-mandibular Syndrome (CCMS). CCMS is a rare congenital disorder commonly characterized by microcephaly, micrognathia, cleft palate, and varying degrees of rib abnormalities. Previously, we found that Snrpb heterozygous mouse embryos arrest shortly after implantation. Although mutants from our previous model, with heterozygous deletion of Snrpb in the developing brain and neural crest cells, exhibited craniofacial malformations resembling those observed in CCMS patients, a model that can capture the full spectrum of CCMS symptoms remained elusive.

To bridge this gap, we employed the tamoxifen (TAM) inducible Cre recombinase system to induce heterozygous deletion of Snrpb during mid-gestation and subsequently characterized the phenotypes of mutant embryos across various developmental stages. Skeletal preparation of E17.5 mutant embryos revealed characteristic hallmarks of CCMS, including posterior rib gaps, a bell-shaped thorax, and scoliosis, in addition to the previously described craniofacial phenotypes. These rib and vertebral defects have not been previously modeled, highlighting the novelty and clinical relevance of this CCMS model.

With this model, we aim to investigate the molecular mechanisms underlying CCMS-like abnormalities. Starting with axial skeletal anomalies, we conducted bulk RNA sequencing on somite tissues isolated from early-stage (E9.5) mutants. Our preliminary analysis revealed altered splicing of epigenetic modifiers in mutant somites. We hypothesize that this splicing alteration in somites could disrupt the expression of downstream target genes essential for axial skeletal development. To further validate this hypothesis, we intend to conduct ATAC-Seq to assess changes in chromatin accessibility.

Lay Abstract Cerebro-Costo-Mandibular Syndrome (CCMS) is a rare genetic condition causing microcephaly (small head), micrognathia (small jaw), cleft palate, and rib abnormalities. It is caused by mutations in the SNRPB gene, which plays a key role in processing RNA. To study CCMS, we generated a mouse model with temporally-controlled Snrpb deletion. Mutant embryos showed many typical CCMS traits, including a posterior rib gap, a bell-shaped thorax, scoliosis, and craniofacial malformations. Using this model, we aim to investigate the molecular mechanisms underlying CCMS-like abnormalities, with the goal of developing new treatment strategies for CCMS.

Mechanisms of salt taste detection and modulation in Drosophila melanogaster

Sasha McDowell[1]
[1]*University of British Colombia*

TBC*

Lay Abstract TBC*

**To Be Confirmed (TBC)*

A phosphoinositide and cAMP crosstalk regulate quorum sensing in trypanosomes

Abdoulie Touray[1]
[1]*Division of Experimental Medicine, McGill University, Montreal, QC, H4A 3J1, Canada*

Quorum sensing is a mechanism by which cells sense density to control cell division and gene expression. African trypanosomes' control of cell density during infection is associated with host protection from lethal parasitemia and development to transmissible stages. Trypanosoma brucei is an extracellular protozoan parasite that causes sleeping sickness in humans. In the host bloodstream, the parasite replicates as a proliferating long slender form, which differentiates into cell cycle-arrested short stumpy forms adapted for vector transmission. cAMP signaling is involved in quorum sensing in trypanosomes, but the mechanisms are poorly understood. Here, we show that a cytosolic phosphatidylinositol phosphate 5-phosphatase 2 (PIP5Pase 2) enzyme regulates quorum-sensing in T. brucei. PIP5Pase 2 knockdown results in cell density-dependent G1/S growth arrest and development of long slender forms into short stumpy-like forms, characteristic of quorum sensing. Moreover, PIP5Pase 2 knockdown results in parasites cleared from infection. PIP5Pase 2 has an N-terminal 5-phosphatase and a C-terminal RhoGAP-like domain. Enzymology with recombinant 6xHis-tagged PIP5Pase 2 showed that the enzyme dephosphorylates preferentially PI(3,4,5)P3 with KM of 46.2 μM. Isothermal titration calorimetry kinetics revealed that rPIP5Pase 2 binds cAMP compared to cGMP, with KD of 0.66 nM and 1.6 mM, respectively. Affinity chromatography and mass spectrometry analysis of PIP5Pase 2 in the presence of cAMP analog, 8-pCPT-2'-O-Me-cAMP, showed differential PIP5Pase ubiquitination and interaction with receptor-type adenylate cyclase, revealing a phosphoinositide regulatory system responsive to cAMP. Our model indicates that PIP5Pase 2 negatively regulates quorum sensing, and cAMP controls PIP5Pase 2 activities to initiate cell density sensing. The data reveal a crosstalk between cAMP and phosphoinositide signaling in eukaryote quorum sensing.

Lay Abstract Quorum sensing is a mechanism by which cells sense density to control cell division and gene expression. During the mammalian bloodstream stage, African trypanosomes tightly regulate cell density to prevent the host from lethal parasitemia and enhance differentiation to the insect transmissible stage. This is important in terms of disease progression and transmission. Trypanosome brucei, a subspecies of the African trypanosomes, causes sleeping sickness in humans. During the mammalian infection, the parasite replicates as a proliferating long slender form, that differentiates into cell non-dividing short stumpy forms adapted for vector transmission. cAMP signaling is involved in density sensing in trypanosomes, but the mechanisms are not fully elucidated. In this study, we have shown that, a phosphatase enzyme called, phosphatidylinositol phosphate 5-phosphatase 2 (PIP5Pase 2) enzyme regulates density-sensing in T. brucei. PIP5Pase 2 removes phosphate from a range of phosphoinositides and binds cAMP indicating a signaling cascade involving the two pathways to regulate cell density during T. brucei infection.

Physical and Applied Sciences

Contributed Talks

Drugging the undruggable: Harnessing AI for discovery of novel DCAF1 WD40 domain ligands

Serah Kimani[1], Julie Owen, Alice Li, Brian Wilson, Stuart Green, Fengling Li, Yanjun Li, Aiping Dong, Suzanne Ackloo, David Kuter, Cindy Yang, Miranda MacAskill, Stephen MacKinnon, Matthieu Schapira, Mahmoud Noureldin, Héctor González-Álvarez, Ahmed Mamai, Laurent Hoffer, John Guilinger, Ying Zhang, Moritz von Rechenberg, Jeremy Disch, Christopher Mulhern, Belinda Slakman, John Cuozzo, Gennady Poda, Mohammed Mohammed, Punit Saraon, Manish Mittal, Pratik Modh, Vaibhavi Rathod, Bhashant Patel, Vijayaratnam Santhakumar, Magdalena Szewczyk, Dalia Barsyte-Lovejoy, Richard Marcellus, Marie-Aude Guié, Anthony Keefe, Cheryl Arrowsmith, Peter Brown, Rima Al-awar, Masoud Vedadi, Vijay Shahani, Levon Halabelian
[1]Structural Genomics Consortium, University of Toronto, Toronto, ON M5G 1L7, Canada. 2. Princess Margaret Cancer Centre, University Health Network, Toronto, ON M5G 2C1, Canada.

DCAF1 (DDB1 and CUL4 Associated Factor 1) is the substrate recognition subunit of Cullin 4 RING ubiquitin E3 ligase (CRL4) complex that is involved in the host ubiquitin proteasome-mediated protein degradation pathway, and is implicated in various cellular processes including DNA replication, transcription, cell cycle progression, among many others. It has been identified as a driver of tumorigenesis and other disease processes, as well as a potential target to enable the proteasome-mediated degradation of therapeutic targets. DCAF1, a 1507 residue multi-domain protein utilizes its WD40 repeat (WDR) domain to recruit substrate proteins to the CRL4 E3 ligase complex; a key process we aim to modulate or exploit using small-molecule chemical probes for development of proteolysis-targeting chimeras (PROTACs). We used two AI-driven approaches to discover small-molecule ligands targeting the WD40 domain of DCAF1: DNA-encoded library (DEL) screening combined with ZebiAI's Machine Learning (ML) technology and a proteome-wide drug-target interaction prediction ML technology implemented in Recursion's MatchMaker. Hits emerging from these efforts were tested experimentally using Surface Plasmon Resonance (SPR), which resulted in the identification of two chemical classes of DCAF1 binders. Co-crystallization studies coupled with structure-activity relationship efforts have led to the synthesis and development of more potent compounds from one of the chemical series, with binding affinities in the lower nanomolar range. Further extension of this hit has led to the development of a PROTAC molecules that targets another WDR protein, WDR5 for proteasomal degradation. Progress on this work will be presented.

Lay Abstract The human DCAF1 protein is a component of a ubiquitin E3 ligase (CRL4) complex, where it recruits proteins for degradation. Based on this role, DCAF1 can be hijacked to degrade unwanted proteins in the cell using bifunctional molecules, that have one end binding to DCAF1 and the other end binding to the unwanted protein. In addition to this, DCAF1 has been shown to drive development of certain cancers and can therefore be targeted to develop anti-cancer drugs. Despite these crucial roles, DCAF1 has for a long term been classified as undruggable. The invention on artificial intelligence has however changed this narrative. In this study we used two AI-driven approaches to find two classes of small molecule binders of DCAF1. We have further developed a DCAF1-recruiting bifunctional molecule that enables degradation of a protein that causes various human diseases, WDR5. Progress in this work will be presented.

Investigating sintering of metal aggregates during laser-induced incandescence on metal nanoparticles

Stephen Robinson-Enebeli[1]
[1] *University of Waterloo*

Time-resolved laser-induced incandescence (TiRe-LII) allows for in situ measurements that can provide both temporal and spatial information on nanoparticles in the gas phase. The technique involves heating the nanoparticles with a nanosecond laser pulse, commonly at 1064 nm, and measuring their incandescence at different wavelengths as they cool down. A measurement model is regressed to the data to infer quantities such as the size distribution of the nanoparticles, and their concentration. Unfortunately, current measurement models are unable to capture some commonly-observed phenomena in TiRe-LII data. These include excessive absorption, where the peak experimental temperatures reached by laser-heated nanoparticles exceed predicted values, and anomalous cooling, where nanoparticles cool faster immediately after reaching their peak temperature than can be explained by current heat transfer models. In this work, we propose that prompt signals from metal aerosols originate from metal nanoparticle aggregates with minimal sintering of the primary particles, and upon laser heating, the primary particles sinter, during which the absorption cross-section and heat transfer characteristics of the aggregate change. We compare the experimental time-resolved spectrally resolved incandescence of an iron nanoparticle aerosol to those obtained from simulations to examine trends predicted for aggregate sintering during TiRe-LII. Furthermore, we regress the standard TiRe-LII model, to the experimental data to determine the time at which full sintering occurs, and aggregate and sintering effects are minimized. Our results show sintering effects, including increased absorption and change in particle distribution within the probe volume, dominate the peak LII signal and gradually dissipate with time.

Lay Abstract Time-resolved laser-induced incandescence (TiRe-LII) allows for in situ measurements that provide both temporal and spatial information on nanoparticles. The technique involves heating the nanoparticles with a nanosecond laser pulse, commonly at 1064 nm, and measuring their incandescence at different wavelengths as they cool down. Unfortunately, current measurement models are unable to capture some commonly-observed phenomena in TiRe-LII data. These include excessive absorption, where particles reach higher-than-predicted temperatures, and anomalous cooling, where particles cool faster than predicted. We propose that prompt signals from metal aerosols originate from metal nanoparticle aggregates with minimal sintering of the primary particles, and upon laser heating, the primary particles sinter, during which the absorption cross-section and heat transfer characteristics of the aggregate change. Through simulations and analysis of experimental data, we show sintering effects, including increased absorption and change in particle distribution within the probe volume, dominate the peak LII signal and gradually dissipate with time.

Correlated shapeshifting and conformational isomerization

Burhan Hussein[1], Aisha Bismillah, Mary-Kate Rylands, Will Maturi, Yuzhen Wen, Conor Rankine, Juan Aguilar, Paul McGonigal
[1]Concordia University

This work explores how shapeshifting isomerization of fluxional carbon cages such as bullvalene can be correlated to conformational changes such as E/Z stereoisomerism. The rapid, successive Cope rearrangements of bullvalenes produce a series (Figure 1a) of constitutional isomers. Recent advances in the synthesis of substituted derivatives, alongside the development of related fluxional cages, have led to renewed interest in exploiting these 'shapeshifting' structures as part of functional molecules and materials. To exploit the shapeshifting isomerization of bullvalenes in larger collective motions of extended structures, we need to understand how its fluxional Cope rearrangements are influenced (Figure 1c) by conformational changes of surrounding groups (Figure 1b). Here, we report the isomeric distribution of carbamate-functionalized bullvalenes and demonstrate that, even in this structurally simple case, conformational changes can become correlated to shapeshifting isomerization. The presence of rotationally hindered single bonds with partial double bond character (e.g., amide C–N bonds) from a carbamate functional group allows for conformational changes to be slowed down and observed by dynamic NMR spectroscopic techniques at accessible temperatures, allowing us to measure distributions of conformational and constitutional isomers experimentally. Through-space interactions of the carbamate rotation to the bullvalene carbon cage subtly tune the energetics of the dynamic system. As part of this investigation, we have also assessed how this isomer distribution can be accurately modelled by comparing the calculated energies of just a small number of conformers instead of performing a global conformational analysis.

Lay Abstract This study explores the world of shapeshifting molecules, focusing on bullvalene, a carbon cage that undergoes rapid changes in its structure. By examining its isomerization process and relating it to conformational alterations like E/Z stereoisomerism, we aim to understand how these dynamic molecules can be harnessed for practical applications. Recent advancements in synthesizing modified versions of bullvalene have reignited interest in exploiting their unique properties in designing functional materials. Through experiments with carbamate-functionalized bullvalenes, this study reveals how even subtle changes in molecular configuration can impact their shapeshifting behaviour. By analyzing the distribution of different isomers using dynamic NMR spectroscopy and computational modelling, we gain insights into the complex interplay between molecular structure and dynamics. These findings pave the way for leveraging shapeshifting molecules in designing innovative materials with tailored properties.

The effect of pre-calcination temperature on property and activity of molybdenum-based catalyst

Femi Oloye[1]
[1]*University of Pittsburgh*

Developing new materials are crucial for the growing world and tremendous progress has been made in this regard. However, the properties of materials generated from different labs vary to some degree. Since every step-in catalyst preparation plays a significant role in the performance of the final catalyst, it is important to investigate the effect of pre-calcination temperature on the activities of catalysts. The temperature monitored varied from 673 K to 973 K and the synthesized catalyst was molybdenum oxide supported sulphated zirconia (MoO3/SZ) catalysts. Calcination affected the surface area. The diffraction patterns of the support and the supported catalyst were amorphous when calcined at 673 K. In contrast, the support calcined between 823 and 923 K exhibited only a tetragonal phase, while calcination at 973 K resulted in the transformation of the tetragonal phase to monoclinic. The XRD patterns of all catalysts were similar to their respective supports, with minor contributions from molybdenum oxide. The support calcined at 673 K showed no Raman active features due to the zirconia phase but showed low-intensity features after loading of Mo precursor, followed by calcination at 823 K. The catalysts with largely amorphous support exhibited the least activity towards n-heptane hydroisomerization and the highest selectivity to methane. The tetragonal phase of zirconia appears to play a beneficial role in the hydroisomerization of n-heptane using MoO3/SZ catalyst. Thus, pre-calcination of support before loading of active material plays a significant role in the activity of the final catalyst.

Lay Abstract Catalysts are crucial in many industries, as they help to speed up chemical reactions. However, the synthesis of catalysts is more of an art than a science. Since starting from the same material does not guarantee to have a catalyst of the same property or activity. Therefore, paying careful attention to each step in the synthesis process becomes crucial. In this study, the effect of pre-calcination was tested. It was found that a simple step, such as calcination of the precursor before loading of the active metal, plays a significant role in the property and activity of the final catalytic material.

Lightning Talks

Effect of Temperature on FeNi Particle Growth During Thermal Treatment of Ultramafic Ni Concentrates

Brian Makuza[1], Sam Marcuson, Mansoor Barati
[1]University of Toronto

The depletion of the high-grade Ni sulfide ores has resulted in efforts aimed at processing the alternative low-grade ultramafic ores. However, these ultramafic ores contain considerable MgO, silica, and gangue rocks, challenging their processing. Smelting has been predominantly used for Ni extraction from sulfide ores as hydrometallurgical methods are associated with vast chemical usage and wastewater. However, high smelting temperatures (>1300 °C), refractory corrosion, and significant emissions remain the main smelting drawbacks. Thus, we explored the thermal treatment (<1000 °C) of the ultramafic Ni concentrates blended with Fe additive as a promising approach with mild processing conditions for upgrading these concentrates. The heat-treated product primarily comprises a magnetic FeNi alloy and a non-magnetic gangue suitable for subsequent physical separation. However, the formed FeNi particles are fine and dispersed in the gangue, lowering magnetic separation efficiency. Thus, adequate growth of the FeNi particles is imperative to guarantee their effective separation from the gangue. This work systematically investigated the effect of various heating temperatures to decipher its impact on FeNi particle growth.

Lay Abstract Nickel is a key ingredient in lithium-ion batteries and its demand has overgrown supply. The primary nickel sources (rocks) are sulfides and laterite. The sulfides accounted for about 70% of global nickel production in the 90's, decreasing to about 30% by 2022. Such a decline is attributed to their depletion and the increasing mining depth, which affects mining economics. Although the laterites are abundant, they face significant drawbacks due to their low grade and wet and stick nature, affecting material handling. Thus, the current focus has been on ultramafic deposits to meet the increasing demand. Although Canada alone has several hundred million tonnes of mineralization, these ultramafics have high magnesium content, affecting nickel recovery efforts. Moreover, the significant asbestos poses a safety, health and environmental risk. Thus, this work proposes a promising approach for nickel extraction from ultramafic ores using mild and environmentally benign process steps.

Experiment and theory of azo isomerization photo-disassembly

Kayrel Edwards[1], Coral Hillel, Mikhail Kim, William Pietro, Ozzy Mermut, Christopher Barrett
[1]McGill University

Azo food dyes are commonly used in many of our favorite foods to add color, such as Kool Aid and Skittles, which contain Allura Red (E129) and Amaranth (E123). Outside of its use as a food dye, azo molecules can act as the 'perfect' photo-switch. Azo dyes can isomerize between the E and Z (trans and cis) stereoisomers upon irradiation, through rotation around the –N=N– bond. This change in geometry on the molecular scale can translate to a micro/macroscale movement of a material when the azo dye is embedded into its matrix. Previous studies by the authors showed that it was possible to fabricate photo-reversible materials via the self-assembly of two water-soluble starting components, crosslinked to create a water-insoluble material. Herein we set out to fabricate fully recyclable, water-insoluble polyelectrolyte multilayer (PEM) films from water-soluble polyanions (polyallylamine hydrocholoride (PAH) and azo food dye crosslinkers, Amaranth (AMA) and Allura Red (ALR). It was observed that visible light irradiation at sunlight intensities triggered complete disassembly of the films into their water-soluble starting components over several days, with the relative rate of disassembly 57 x and 14 x faster in light than in the dark. Additionally, Density Functional Theory calculations demonstrated that ALR thermal cis-trans isomerization proceeds through facile rotation about the weakened double bond, and the activation free energy was estimated as 24 kJ/mol, suggesting rapid isomerization occurring on the order of microseconds or less.

Lay Abstract Azo food dyes are commonly used in many of our favorite foods to add color, such as Kool Aid and Skittles. Outside of its use as a food dye, azo molecules can act as the 'perfect' photo-switch, utilizing light as a clean source of motion. Previous studies by the authors showed that it was possible to prepare materials such as films and coatings, which revert between strong and intact materials vs. disassembled individual components, in response to the light. These materials can be self-assembled using building blocks such as modified cotton, to become water-resistant. Building on this work, herein we set out to prepare fully recyclable materials using azo food dyes Allura Red and Amaranth. Using the different colors in sunlight, such as the green and blue colors seen in a rainbow, the materials disassembled at a much faster rate (50 x) than when kept in the dark.

Inverse design of metamaterial waveguide gratings using machine learning

Norman Israel[1], D. Blankespoor, D.-X. Xu, Y. Grinberg and L. Ramunno
[1]University of Ottawa

Periodic metamaterials are composed of a periodic array of alternating dielectric materials. They are important in the design of photonic devices. They are often described using the effective medium theory (EMT). However, for our grating coupler designs of interest, it is found that EMT does not predict the metamaterial behaviour well.

3D simulations are typically required for the design of grating couplers that incorporate the metamaterial gratings but they are time consuming. If 2D simulations can be made analogous to the 3D models without sacrificing overall performance, it would bring significant cost reduction, and enable different optimization strategies. This requires knowledge of the effective refractive index versus wavelength, something that we cannot reliably obtain from EMT approximation.

In this work we use neural networks to predict the effective refractive index of a metamaterial grating within the environment of a grating coupler, over a large range of parameters and wavelength. In addition, we go in the inverse direction, where, for a desired effective refractive index, predict the required metamaterial grating geometry.

We validate our results with Ansys Lumerical 3D simulations. We found that our deep neural network forward models predict the transmission spectra better than 2% (2D models) and 5% (3D models). We also found that the inverse map gives excellent agreement between 2D transmission spectra and the 3D transmission spectra.

Our work demonstrates that for some type of metamaterial gratings, we can reduce a 3D simulation to a 2D simulation, shrinking computational cost quite significantly.

Lay Abstract Much of the devices we use rely mostly on electric current to transmit data through the device. This method lacks efficiency. This can be overcome by using light to carry information in the device. This is what is done in integrated photonic devices. These devices consist of components called waveguides and grating couplers. The waveguides guide light in a desired direction, like how wires guide electric current in electrical devices. The grating couplers allow light from a source (such as a laser) to integrate with the other components.

Designing these waveguides can be a time-consuming process. We use artificial intelligence and other optimization techniques, to design waveguides in a manner that makes the process less time-consuming. Our work reduces the amount of time and energy spent in the design process, while still giving efficient designs for photonic devices.

Poster Presentations

Noise Exposure Assessment of Montreal Metro's Orange Line

Peter Mensah[1]
[1]*McGill University*

Background: Noise exposure is increasingly becoming a nuisance to users of trains at the Montreal Metro network. This survey assessed the level of noise exposure to users within Montreal's orange metro line (from McGill to Lionel Grouix).
Objective: The main objectives were to determine noise exposure levels, assess compliance with regulatory limits, identify risks to metro users, recommend corrective actions.
Methods: Sound surveys were conducted using a calibrated sound level meter to measure noise levels in decibels (dB) at strategic sampling points. Measurements were taken systematically during peak and off-peak periods to capture fluctuations in noise levels.
Results: The maximum recorded noise level was 83 dB(A), with an average noise level of approximately 79 dB(A). The highest noise levels were observed near train arrivals and departures, particularly during peak hours. Noise levels inside moving trains reached up to 82 dB(A). These levels of noise exposure may result in temporary hearing loss and in severe situations, permanent hearing loss.
Conclusion: The survey revealed high noise levels, particularly during peak hours and near train movements which may lead to hearing loss. Recommendations to mitigate this risk include installing noise barriers, routine noise monitoring, improving maintenance culture and increasing public awareness about noise hazards.

Lay Abstract This study assessed noise exposure levels to users in the Montreal Metro, focusing on the orange line from McGill to Lionel Grouix. We measured noise at various locations, including stations, platforms, and inside trains, during both busy and quiet times. The highest noise level recorded was 83 decibels (dB), with an average of 79 dB. The loudest areas were near train arrivals and departures, especially during peak hours and exposure to these noise levels may lead to temporary or permanent hearing loss. Noise levels inside moving trains reached up to 82 dB. To reduce the risk of hearing loss to users, noise reduction measures, such as installing noise barriers, regular noise monitoring and good maintenance culture must be considered and implemented.

Overview of C2MCI research and opportunities

Jyoti Kotecha[1]
[1] *TBC**

TBC*

Lay Abstract TBC*

**To Be Confirmed (TBC)*

Neuroscience and Psychology

Contributed Talks

Impact of pre-implantation alcohol exposure on brain development and functions: an implication for gabaergic interneurons

Aboubacrine Mahamane Touré[1], Lisa-Marie Legault, Michelle Robb, Serge McGraw and Elsa Rossignol
[1]CHU Sainte-Justine Research Center/Université de Montréal

Introduction: Exposure to alcohol at critical periods of prenatal life can alter DNA methylation profiles of brain cells and contribute to the molecular mechanisms by which Fetal Alcohol Spectrum Disorder emerges. However, the effects of alcohol exposure at the very beginning of gestation on brain development remain largely unexplored.
Methods/Results: Using a translational mouse model, we show that pre-implantation alcohol exposure (PAE) induces a neurobehavioral phenotype with autistic-like behaviors in a sex-dependent fashion in adult mice. Males display reduced anxiety with no hyperactivity while females are anxious and hypoactive. Regarding social interactions, males display altered sociability with an intact preference for social novelty while the opposite scenario is seen in females. Analysis of PAE embryonic brains shows no overt effect on cortical thickness but reveals a strong reduction in GABAergic interneuron (IN) density in the dorsal migratory streams. This reflects a reduction of IN precursor proliferation in the medial ganglionic eminence, together with a delay in tangential migration of IN towards the dorsal pallium. Disorders of IN migration or proliferation have been previously associated with autistic-like phenotype, suggesting a contribution of this cellular deficit to the overall phenotype. Mechanistically, we find that PAE induces lasting stage-/sex-specific changes in DNA methylation of multiple brain-expressed genes, including regulators of IN development. Interesting candidate genes are currently being further investigated and validated.
Conclusion: Altogether, our results provide new insights on the impact of PAE on IN development/functions before and after birth and on the disease mechanisms of alcohol-related neurodevelopmental disorders.

Lay Abstract The effects of alcohol exposure at the very beginning of gestation on brain development remain largely unexplored. Using a translational mouse model, we show that pre-implantation alcohol exposure (PAE) induces autistic-like behaviors in a sex-dependent fashion in adult mice. Males display reduced anxiety with no hyperactivity while females are anxious and hypoactive. Regarding social interactions, males display altered sociability with an intact preference for social novelty while the opposite scenario is seen in females. Analysis of PAE embryonic brains reveals reduced proliferation of GABAergic interneuron (IN) precursors, together with a delay in tangential migration of IN towards the cortical plate. Mechanistically, we find that PAE induces lasting stage- and sex-specific epigenetic changes of multiple genes that regulate IN development. Our results provide new insights on the disease mechanisms of alcohol-related neurodevelopmental disorders.

Impact of perinatal insults in the cerebellum of premature infants

Mamadou Dia Diagne[1]
[1]*University of Montreal*

In Canada, around 8% of babies are born prematurely each year, before 37 weeks of pregnancy. During the latter part of pregnancy, the cerebellar cortex undergoes a crucial period of development, characterized by the formation of intricate neural connections through processes like neurogenesis, neuronal migration, and maturation. This developmental phase is particularly sensitive to any insults that might occur. We believe that perinatal insults, such as infections or bleeding around the time of birth, can disrupt the normal growth and migration of cells in the granular layer of the cerebellum.
Our main goal is to understand the changes in cerebellar neurons caused by these insults. To do this, we use a special transgenic mouse model that allows us to mimic perinatal insults, including infection and hemorrhage, in a controlled manner. By depleting microglial cells, a type of immune cell in the brain, we can specifically study the immune response to these insults. We inject substances like Lipopolysaccharide (LPS) and bacterial collagenase into the brains of these mice shortly after birth to induce insults.
We'll be comparing mice with depleted microglia to normal mice, exposing them to various insult conditions and analyzing their cerebellums at different stages of early postnatal development (P3, P7, and P15). By staining for specific proteins associated with different types of neurons and cellular processes, such as calbindin for Purkinje cells and Pax6 for granule cells. We hope to gain insights into the mechanisms underlying cerebellar injury in premature infants and explore potential therapeutic interventions.

Lay Abstract In Canada, about 8% of babies are born prematurely every year. Premature birth can affect the development of the brain, particularly the cerebellum, which is responsible for balance and coordination. We believe that insults during this critical developmental phase can lead to problems in how neurons in the cerebellum grow and connect.
To study this, we're using a special mouse model where we can manipulate the immune cells in the brain. We're injecting substances to mimic infections or bleeding that can happen around the time of birth. Then, we're looking at how the brain cells, especially those in the cerebellum, are affected.
We'll use different stains to see changes in specific types of brain cells and their connections. By doing this, we hope to better understand how these insults affect brain development and how the immune system in the brain responds.

Long-term functional brain outcomes in youth with enterovirus-71 central nervous system involvement: a multi-echo resting-state fmri study

Jasmine Ali-Gami[1], Dr. Hsiang-Yuan Lin
[1]National Taiwan University Hospital, University of Toronto, CAMH

Background: An Enterovirus (EV) infection, particularly the EV-71 strain, is a common pediatric infectious disease. Numerous studies have shown the correlation between an EV-71 CNS infection and the development of ADHD. However, no published evidence has studied the longitudinal brain development in this unique population of youth who are at a three times greater risk of developing ADHD.
Objective: Our research investigated the longitudinal brain features of youth with a pediatric EV-71 CNS infection earlier in life. Specifically, our research aimed to address the following: "Are there abnormalities in functional connectivity of the midbrain and striatum that would link to the increased risk of developing ADHD?".
Methodology: This cohort study included 31 youths with a previous EV-71 CNS infection 6-18 years ago. Sixteen of them developed ADHD later in life. This study included 53 age- and sex-matched youth with idiopathic ADHD and 37 matched neurotypical youth. Our methods utilized multi-echo resting-state functional magnetic resonance imaging to examine the functional connectivity.
Results: Compared to youth who had an EV-71 infection and did not develop ADHD, the group that developed ADHD showed lower functional connectivity between the right substantia nigra pars compacta, right ventral tegmental Area, the left dorsal caudate and the left calcarine.
Conclusion: This is the first study investigating longitudinal functional brain patterns following a severe EV-71 CNS infection. We found that generally, youth with Enterovirus-facilitated ADHD had a similar intrinsic functional connectivity pattern at cortical and striatal levels. Altered midbrain functional connectivity is unique in Enterovirus-facilitated ADHD.

Lay Abstract The Enterovirus-71 (EV-71) infection, known as the strain of the Enterovirus invading the central nervous system, is a common pediatric infection within the Asia-Pacific region and beyond. Colloquially referred to as hand, foot and mouth, the EV-71 strain of the virus has resulted in the development of ADHD later in life. With this unique psychological sequelae, the mechanistic cause to why many EV-71 survivors are at a greater risk of developing ADHD remains unknown. In the present study, we aim to highlight areas of potential atypical connectivity in regions such as within the brain stem and subcortex between EV-71 survivors who developed ADHD and those who did not develop ADHD later in life. Our study suggests a possible avenue of later research being dopamine dysregulation contributing to ADHD symptomology, which may facilitate the development of targeted intervention and rehabilitation strategies to enhance the quality of life and reduce disabilities.

The long-term and multi-generational impact of chronic psychological stress during adolescence

Tamara Franklin[1]
[1]*Dalhousie University*

Introduction: Adolescent stress is associated with heightened risk factors for several psychiatric diseases with social symptoms including depression, schizophrenia, and social anxiety disorder. Interestingly, there is increasing evidence that stressful events may also affect the well-being of future offspring, and this may be observed several generations after the initial stressful exposure. The mechanisms underlying such multi-generational effects are not currently known, but are likely a combination of social (e.g., maternal care) and biological (e.g., epigenetic regulation) mechanisms.
Methods: My lab is working with a psychological stress model in mice. This model involves exposing mice to a predator (a rat) for 30 minutes each day during periods of adolescent development. We then observe the behaviour of these mice and additionally breed these mice to observe the behaviour of their offspring. Currently, we are also examining the effects of this stress treatment on epigenetic regulators in the brain.
Results: We have found that this adolescent stress treatment results in an increase in adult anxiety-like behaviours and post-partum depressive-like behaviours.The offspring of mice previously exposed to stress also show anxiety-like and depressive-like behaviours.
Conclusion/Significance and Implication: These findings highlight the persistent and multi-generational effects of stress experienced during adolescence, and provide a rodent model to ask mechanistic questions related to the brain changes underlying these behavioural effects.

Lay Abstract Adolescence is a critical period for brain development and exposure to psychological stressors experienced during this developmental period can have long-lasting consequences for both the individual, and for their offspring. My lab is asking questions around the brain changes that occur as a result of exposure to adolescent stress, how this could be associated to stress-induced psychiatric diseases like post-partum depression, and how this can have consequences across multiple generations. We expose mice to a psychological stressor during their adolescent period and observe the behaviour of these mice and their offspring. We have found that adolescent stress increases anxiety-like and post-partum depressive-like behaviours in mice, and that their offspring also show anxiety-like and depressive-like behaviours. We are currently investigating how brain function is altered as a result of this stressor, and how this might lead to the behavioural changes observed.

Examining the healthy immigrant effect on alcohol use in emerging adults

Lydia Muyingo[1], Sean Mackinnon, Fakir Yunus, Aida Saade, Simon B. Sherry, Patricia J. Conrod, Matthew Keough, Marvin Krank, Kara Thompson, Sherry H. Stewart
[1]Dalhousie University

Introduction and Objective: Prior research in the healthy immigrant effect (HIE) on alcohol use hasn't explored the impact of the heterogeneity of the immigrant population related to assimilating into a country's mainstream culture (acculturation), adherence to original culture's values (enculturation), or country of origin (COO) drinking rates. We examined whether the HIE on alcohol use in emerging adults is moderated by acculturation/enculturation.
Materials and Methods: We compared four alcohol indicators (quantity, frequency, binge drinking, and alcohol-related problems) across undergraduates from five universities (N=1016) of differing immigration statuses defined by participants' and parents' birthplace. We extended previous work on by analyzing main effects and interactions of acculturation and enculturation with immigrant status on alcohol indicators, and the impact of COO drinking rates.
Results: Immigrant groups differed in ways consistent with the HIE; 1.5 generation immigrants reported the lowest alcohol involvement, followed by 2nd generation, then 3+ generation immigrants. The HIE was generally not moderated by levels of acculturation or enculturation; however, we found significant interactions between immigrant status and enculturation on alcohol frequency and alcohol-related problems. Unexpectedly, enculturation was positively associated with alcohol frequency and alcohol-related problems in 1.5 generation students. COO per capita alcohol consumption was mostly unrelated to alcohol outcomes but was positively associated with alcohol frequency and binge drinking among 1.5 and 2nd generation students.
Conclusion and Significance/Implication: While more recent immigration status is associated with lower alcohol involvement in emerging adult undergraduates, enculturation may be a risk for more frequent and problematic drinking in 1.5 generation students.

Lay Abstract This study focusses on alcohol use in immigrants (1.5, 2nd, 3+ generation) attending Canadian universities. Past research has shown that new immigrants tend to report better health compared to the majority population in the early years of immigration. To test this, we compared levels of 4 different aspects of alcohol use among the 3 immigrant groups. We also considered how much 1.5 and 2nd generation immigrants reported identifying with Canadian values and their original culture values to see if that would impact alcohol use levels. We also considered the drinking levels of their original country. Overall, we found 1.5 generation immigrants had the lowest involvement with alcohol compared to 2nd and 3+ generation immigrants. Surprisingly, we found that identifying with original cultural values may put 1.5 immigrant generation university students at risk for frequent and problematic drinking. This study supports culturally-appropriate alcohol use programs in universities.

Assessing baseline tms-eeg markers of anxiety symptoms in patients with major depressive disorder (mdd)

Renée Lawson[1], Reza Zomorrodi, Daniel Blumberger, Ishrat Husain, Daphne Voineskos
[1]University of Toronto

Background: 45-67% of major depressive disorder (MDD) patients are diagnosed with a comorbid anxiety disorder. Dysfunctional cortical inhibition systems within the brain play significant roles in both MDD and anxiety symptoms. Measuring these changes at the neurophysiological level has been made possible with the use of transcranial magnetic stimulation and concurrent electroencephalography (TMS-EEG). While markers of cortical inhibition have been investigated in MDD, neurophysiological markers of anxiety have not yet been investigated using TMS-EEG to date.
Objective: To identify neurophysiological markers of anxiety symptoms at baseline using GAD-7 scores and ROI TMS-evoked potential (TEP) amplitudes.
Methods: Secondary data analysis was conducted using the demographic, neurophysiological (TMS-EEG), and anxiety scale (GAD-7) data from Blumberger and colleagues' 2021 CARTBIND study. Participants were separated into two groups based on GAD-7 scores (high and low anxiety at baseline). Area-Under-Curve (AUC) values of specific frontal electrodes' TEP amplitudes were used to assess neurophysiological markers of anxiety at baseline.
Results: 114 Participants had available TMS-EEG data at baseline. 63 participants were categorized as 'high anxiety' at baseline, while 51 were categorized as 'low anxiety' at baseline. No significant differences were found between any of the selected frontal electrodes between the high anxiety and low anxiety group at baseline. Analysis is ongoing.
Conclusions: The results of this study will provide significant insight regarding neurophysiological markers of anxiety. This study has the potential to be the foundation for further investigation of EEG markers that could be used as a diagnostic tool in the future.

Lay Abstract
Background: 45-67% of major depressive disorder (MDD) patients are diagnosed with an anxiety disorder. Dysfunctional cortical inhibition systems within the brain play significant roles in both MDD and anxiety symptoms. Measuring these changes at the neurophysiological level has been made possible with the use of transcranial magnetic stimulation and concurrent electroencephalography (TMS-EEG). While markers of cortical inhibition have been investigated in MDD, neurophysiological markers of anxiety have not yet been investigated using TMS-EEG to date.
Objective: To identify neurophysiological markers of anxiety symptoms at baseline
Methods: Secondary data analysis was conducted using the demographic, neurophysiological (TMS-EEG), and anxiety scale (GAD-7) data from Blumberger and colleagues' 2021 CARTBIND study.
Results: 63 participants were categorized as 'high anxiety' at baseline, while 51 were categorized as 'low anxiety' at baseline. No differences were found between any of the selected frontal electrodes between the high anxiety and low anxiety group at baseline.

Poster Presentations

The impact of repetition on the development of memory functions

Bailey Agard[1], Amy S. Finn
[1]University of Toronto

After decades of developmental research characterizing children as ever-curious explorers of their environments, researchers are slowly shifting focus to a converse aspect of development—the tendency to engage in things repeatedly. Interestingly, during a free-play paradigm younger children explored less than older children; instead they preferred engaging with the same things repeatedly (Pelz & Kidd, 2020), pointing to underlying benefits of early repetition. In adults, repetition has been found to degrade memory specificity (Yassa & Reagh, 2014), but the role it plays in children's memory remains unclear. Notably, factors such as the protracted development of the hippocampus and increased forgetting rates, could counterintuitively diminish this effect in young children. The current study developed a child-friendly version of Yassa & Reagh's paradigm to investigate this effect at different developmental stages, and whether young children's memory may protect them from experiencing degradation via repetition. Adults and children 5-10 years old were shown repeating and non-repeating items during exposure before being asked to make old/new judgements about items that were identical, similar-looking, or completely novel. Pilot results (adults: n=37, children: n=19) found that adults displayed degraded specificity for highly similar repeated items. Children showed a curious U-shaped pattern whereby younger children behaved like adults, but older children's specificity was actually improved by repetition. This demonstrates that our novel paradigm is able to replicate previous adult findings. Full data collection is currently ongoing, but we predict a less deleterious impact (or even a benefit!) of repetition in children, indicating its role in early learning.

Lay Abstract Current literature often characterizes children as ever-curious explorers of their environments, but this contrasts older work showing that young children sometimes stubbornly perseverate on the same thing. Anecdotally, caregivers also often report their children requesting the same media repeatedly. In order to understand why this is such a common occurrence, this study aims to determine how repetition impacts children's memory and learning at different stages of development, and how they compare with adults. Thus, adults and children 5-10 years old were shown repeating and non-repeating images before being asked whether they saw subsequent images that were identical, similar-looking, or completely novel. This work aims to inform educators about learning techniques that are most beneficial across development. Ultimately, it is important for reducing assumptions that children are simply lesser adults and can help us understand the ways children are perhaps even better equipped for learning certain things in our environment.

Ecology, Sustainability and Evolution

Contributed Talks

Plastic waste-to-hydrogen: accelerating a low-carbon circular economy

Emmanuel Galiwango[1], James Butler, Weiguo Ma, Samira Lotfi, Kevin Austin
[1]Clean Energy Innovation, National Research Council, Ottawa,Canada

Problem statement: post-consumer and industrial wastes involving plastics quickly lose their physicochemical integrity and utility value, hence becoming a global environmental pollutant damaging the entire ecosystem. Heterogeneity and low-end value have hampered recycling; Only 9 % plastics is recycled globally, with Canada and US recycling 6 and 4 %, respectively. Conventional technologies such as incineration solves mass to volume waste problem but adds to pollution levels. Like other world economies, Canada and US diverts 82 and 73% plastic wastes to landfills. However, landfills have become pollution hubs due to soil and water leachates, and air pollution, thus the need for a paradigm shift to sustainable safe approaches to waste management. The purpose of this study is to investigate the hybrid conversion process of unsorted waste streams and non-hazardous reaction media to produce low carbon fuels (H2) and materials (char and oil).
Method & Experimental procedure: Leveraging on superior water sub-and-supercritical properties, and the negation for the feedstock drying step, competitive hydrothermal conversion technology in a batch reactor system was investigated at different reaction conditions.
Results: Preliminary results revealed 0.041g H2/g feed and 0.005g CH4/g feed; 88.2 wt.% char yield with improved thermal stability; up to 16.22 wt.% liquid yield containing high value components.
Conclusions & Significance: Hybrid hydrothermal conversion addresses environmentally unsafe and challenging heterogenous wastes by converting them to green high value products in a circular economy model. Further studies on continuous scale and various waste feedstocks are underway to fully optimize the operation parameters for future commercial adoption.

Lay Abstract Post-consumer and industrial wastes involving plastics quickly lose their physicochemical integrity and utility value, hence becoming a global environmental pollutant damaging the entire ecosystem. Heterogeneity and low-end value have hampered recycling; Only 9 % plastics is recycled globally, with Canada and US recycling 6 and 4 %, respectively. Conventional technologies such as incineration solves mass to volume waste problem but adds to pollution levels. Like other world economies, Canada and US diverts 82 and 73% plastic wastes to landfills. However, landfills have become pollution hubs due to soil and water leachates, and air pollution, thus the need for a paradigm shift to sustainable safe approaches to waste management. The purpose of this study is to use hydrothermal technology to convert end-of-life organic or fossil-based carbonaceous wastes to low carbon fuels (H2) and materials (char and oil). Increasing hydrogen production sources and carbon management is key to accelerating low-carbon circular economy.

A mutualism-parasitism gradient plus control over nodule access leads to trait variation in bacteria-plant mutualists

Abdel Halloway[1], Liana T. Burghardt, Katy D. Heath
[1]Case Western Reserve University

Basic theory suggests that mutualisms may struggle to sustain functional trait variation for a number of reasons. These reasons include the advantages of cheating, population declines due to positive feedbacks, mutualistic pairs outcompeting other species, and stabilizing selection leading to trait convergence. And yet, mutualism variation persists, even within a local environment. Here, we seek to explore how a mutualism-parasitism gradient and control over nodule access may lead to and maintain between-species variation. We then compared our model with experimental data from the Sinorhizobium-Medicago system. Our model shows that between species coexistence is possible when traits are sufficiently different from another, otherwise variation collapses. When traits are sufficiently different, the pairs evolve away from each other until they are isolated. Both the mutualism-parasitism gradient and control over access are necessary for this coexistence; without either, the system would collapse to a single species pair. Our model results comport with the experimental data. Specific clades of Sinorhizobium seem to exist on separate adaptive peaks which correlate to groupings of Medicago species.

Lay Abstract Mutualisms, relationships where two species benefit from interacting with each other, are key to the functioning of ecosystems. Mutualisms provide numerous services like pollination of plants, dispersal of seeds, or in the case of microbes and plants, the trade of key resources that help each other grow. Such mutualisms are found everywhere on earth with nearly every species. Understanding the processes driving relationships between mutualist species is critical to make sure that these relationships can persist in the face of global and anthropogenic change. Our theoretical analysis of mutualisms shows that they tend to form isolated pairs. For example, only one insect species pollinates a plant species and no other, and that plant is only pollinated by that one insect. This is important since the survival of one heavily relies on the other. If these relationships break down, then there would be little else to help the species persist.

Phylogenomics of novel clones of aeromonas veronii recovered from a freshwater lake reveals unique biosynthetic gene cluster

Opeyemi Lawal[1], Noah Bryan[1,2], Valeria R. Parreira[1], Rebecca Anderson[1], Yanhong Chen[1], Melinda Precious[1], Lawrence Goodridge[1]

[1]Canadian Research Institute for Food Safety, University of Guelph, Guelph, ON, Canada N1G 2W1; [2]Bayview Secondary School, 10077 Bayview Ave, Richmond Hill, ON L4C 2L4.

Introduction and Objective - Aquatic ecosystems harbor clinically relevant pathogens and antimicrobial resistance genes, posing a global health risk. This study focused on Aeromonas veronii in Lake Wilcox, Ontario, recognizing its significance in pathogen surveillance.

Materials and Methods - Freshwater samples from Kettle Lake, Ontario, were analyzed using microbiological, biochemical, and whole-genome sequencing techniques.

Results - Eleven bacterial colonies were isolated, predominantly A. veronii (n=9), with discrepancies between identification methods. Notably, 67% of A. veronii isolates were human pathogens. Genomic analysis revealed high diversity, with 41 novel alleles and seven new sequence types, indicating the lake as a reservoir for various pathogenic clones. A comparison with global A. veronii genomes suggests potential cross-border dissemination. All isolates carried genes (OXA-912, cphA) conferring resistance to β-lactams. Virulence gene content varied between human and non-human pathogenic strains, with human pathogenic isolates associated with the type III secretion system. Mobilome analysis indicated the absence of plasmids but the presence of intact P22-like phages and diverse insertion sequences. Novel biosynthetic gene clusters were identified, hinting at unique secondary metabolite production potential.

Conclusion and Significance - This study highlights the importance of continual surveillance of aquatic ecosystems to understand pathogen evolution, human pathogenicity potential, and the ecological significance of genetic elements, shedding light on their impacts on human health.

Lay Abstract This study assessed the microbial landscape of Lake Wilcox, Ontario, revealing its role as a potential reservoir for harmful bacteria like Aeromonas veronii. By analyzing freshwater samples from Kettle Lake using advanced genetic techniques, we uncovered a concerning trend: a majority of A. veronii strains were found to be potential human pathogens. Moreover, genetic analysis revealed a diverse array of bacterial strains, indicating the lake's role in fostering various pathogenic clones, with implications for global spread. Of note, these bacteria carry genes that confer resistance to common antibiotics, further complicating treatment. The differences in virulence gene content suggest varying risks associated with different strains. The study also identified novel genetic elements hinting at the potential for unique toxin production. Ultimately, these findings underscore the urgent need for continuous monitoring of aquatic environments to better understand the evolution and impact of pathogens on human health.

Quantifying wildfire carbon emissions: a machine learning approach leveraging combustion measurements

Chinyere Ottah[1], Zilong Zhong, Cheryl Rogers, Jose Bermudez Castro, Alemu Gonsamo
[1]School of Earth, Environment, and Society, McMaster University, 1280 Main Street West, Hamilton, ON L8S 4K1, Canada

In the context of climate change, wildfires have emerged as the primary disturbance agent in Canadian forests and peatlands ecosystems. Accurate mapping of these ecosystems is crucial for understanding carbon losses, refining carbon accounting methods, and devising effective mitigation strategies. In this study, we employed a random forest model to estimate carbon emissions resulting from wildfires across Canada's forests and peatlands, integrating field measurements of combustion with remotely sensed data.
Our analysis indicates substantial carbon emissions from both aboveground and belowground combustion processes. Specifically, wildfires occurring in 2023 resulted in the emission of 117.45 Tg of carbon from aboveground biomass in peatlands and forests, with an additional 486 Tg emitted from belowground consumption.
These findings highlight the pressing need for improved monitoring and management strategies to address the impact of wildfires on carbon dynamics in boreal ecosystems. By leveraging a combination of field measurements and remote sensing data, our statistical models provide valuable insights into the carbon budget of these vital ecosystems, enabling more informed decision-making for sustainable land management and climate change mitigation efforts.

Lay Abstract Wildfires are increasingly shaping Canadian forests and peatlands due to climate change. Our study focuses on quantifying the carbon emissions resulting from these fires, which is crucial for grasping their broader impact on the environment. By combining on-the-ground measurements with satellite data, we developed statistical models to estimate the carbon released during wildfires in 2023 across Canada's forests and peatlands. Our findings reveal a significant amount of carbon emitted from both the burning vegetation and the underlying peat. In total, wildfires released 117.45 Tg of carbon from aboveground sources and an additional 486 Tg from belowground consumption. Understanding these emissions is essential for addressing climate change and its impact on our ecosystems. This research not only sheds light on the carbon dynamics in Canadian landscapes but also helps to design strategies for managing wildfires and mitigating their environmental consequences.

Optimizing Dairy Cow Health and Productivity with Efficient Movement Monitoring Using Data Augmentation and Computer Vision

Francois Gonothi Toure[1]
[1]*Université du Québec à Montréal (UQAM)*

Monitoring the health and emotions of dairy cows is critical for enhancing productivity and ensuring animal welfare. This study focuses on detecting, predicting, and tracking cow movements using videos collected by static cameras installed in barns. The challenge lies in gathering sufficient data for training machine learning models, as traditional methods require extensive datasets to achieve high performance. Current techniques are limited by the need for large amounts of annotated data, which is time-consuming and expensive to collect.

The hypothesis is that a small dataset, when properly augmented, can achieve high precision and accuracy in cow movement tracking. This research uses a small initial dataset of brief video clips, with frames at 640x640 resolution and various frame rates, annotated using bounding boxes. Cameras are placed at different positions: center (ceiling, left, right), front (ceiling, left, right), and rear (center, left, right). The dataset is enlarged using various augmentation techniques, including horizontal and vertical flips, rotations, crops, shears, brightness adjustments, exposure adjustments, blurring, and noise addition. This augmented dataset is used to train neural networks using YoloV8, achieving a model with 85-95% precision and accuracy. The trained model, validated with 5% of the data and tested with 2%, shows excellent performance with high precision and accuracy. The confusion matrix and performance curves indicate robust results.

This approach bypasses the current limitations of needing large datasets for training, demonstrating that high-performance models can be achieved with minimal initial data through effective data augmentation techniques.

Lay Abstract Ensuring the health and well-being of dairy cows is crucial for better milk production and animal welfare. This study monitors cows' movements using videos from static cameras in barns. Traditional methods need a lot of video data to train computer models, which is hard to collect and expensive. By using and enhancing a small amount of video data, we can create an accurate model to track cow movements. This study uses short video clips with frames at 640x640 resolution, annotated with bounding boxes, and enhances them using techniques like flips, rotations, and brightness adjustments. This larger dataset is then used to train models with YoloV8, achieving high accuracy in tracking cow movements. The trained model shows excellent accuracy and precision, even with a small amount of initial data. This approach overcomes the need for large datasets, showing that high accuracy can be achieved with minimal initial data through effective augmentation.

Lightning Talks

Shedding light on shadow effects: assessing vegetation indices across different lightning conditions

Angela Kross[1], Vitoria Barbosa, Dulce Hernandez, David Fargey
[1]Concordia University

Shadows pose a significant challenge in optical remote sensing across satellite, airborne, and drone-acquired imagery. Shadowed pixels distort surface reflectance, requiring specialized processing to extract usable information. While moderate to high spatial resolution imagery (e.g., drone) has addressed topographic and cloud shadows, very-high resolution imagery introduces new challenges, demanding adaptation of existing techniques.

The main problem caused by shadows is the loss or reduction of information in images, potentially compromising derived biophysical and structural parameters through pixel values and vegetation indices (VIs). Within this context, we investigated how shadows affect spectral signatures and vegetation indices, aiming to identify VIs that accurately detect vegetation from both shaded and sunlit areas.

We collected hyperspectral images (Pika L sensor) of basil and corn plants in a greenhouse over several weeks, processed them for reflectance, and selected sunlit and shaded spectral samples from leaves. Various VIs were extracted and analyzed visually and statistically to assess differences between sunlit and shaded leaves.

Preliminary findings revealed lower reflectance in shaded leaves across all wavelengths. Several VIs (e.g., Atmospherically Resistant Vegetation Index, Modified Chlorophyll Absorption Ratio Index Improved, Normalized Difference Vegetation Index) showed promise in capturing similar information from both sunlit and shaded leaves.

Understanding how shadows affect spectral signatures and VIs is crucial for the effective use of high-resolution imagery in vegetation monitoring. By identifying vegetation indices that accurately detect vegetation from both shaded and sunlit areas, our findings contribute to improving the accuracy and reliability of drone-based assessments of vegetation characteristics and health.

Lay Abstract Shadows present a significant challenge in remote sensing, affecting images from satellites, aircraft, and drones. They distort surface reflectance, making it difficult to extract accurate information. While moderate to high-resolution drone imagery has addressed some shadow issues, very high-resolution images introduce new challenges. Shadows cause a loss of information, affecting measurements of vegetation presence, structure and health. In this study, we examined how shadows impact spectral signatures and vegetation indices. By analyzing images of basil and corn plants in a greenhouse, we found that shaded leaves had lower reflectance across all wavelengths. Some vegetation indices, such as the Atmospherically Resistant Vegetation Index and Normalized Difference Vegetation Index, showed promise in detecting vegetation in shaded areas. Understanding shadow effects is crucial for accurately identifying vegetation and monitoring vegetation health using high-resolution imagery, improving our ability to assess plant characteristics and health from drone images.

A synthesis of the state of fast fashion in the top garment-producing countries: China, Turkey, India, Bangladesh, Vietnam, and Indonesia.

Kerrice Bailey[1], *Sapna Sharma*
[1]*York University*

The growth of the fast fashion industry has accelerated over the last 5 decades leading to serious environmental repercussions. This industry has placed immense pressure on natural water resources impacting both water quantity and quality, generating 20% of global wastewater, in addition to contributing 8% of global greenhouse gas emissions. In this systematic review, we explore the environmental impacts of the fast fashion industry in the top garment-producing countries, specifically, China, Turkey, India, Bangladesh, Vietnam, and Indonesia. More specifically, we review the predominant environmental impacts, research fields, and policy changes related to fast fashion in each of the top garment-producing countries. Additionally, we identify knowledge gaps and barriers to implementation of sustainable garment production. Finally, we offer potential solutions with respect to policies, guidelines or infrastructures that could aid in movement towards a more sustainable garment-producing industry. In our systematic review, we identified 2318 studies, of which 210 studies were relevant to our research questions. We provide a complete synthesis of the water and environmental state of the top garment-producing countries and summarise the current approaches to reducing barriers in sustainable garment production.

Lay Abstract The growth of the fast fashion industry has accelerated over the last 5 decades leading to serious environmental repercussions. This industry has placed immense pressure on natural water resources impacting both water quantity and quality, generating 20% of global wastewater, in addition to contributing 8% of global greenhouse gas emissions. We review the predominant environmental impacts, research fields, and policy changes related to fast fashion in each of the top garment-producing countries, specifically, China, Turkey, India, Bangladesh, Vietnam, and Indonesia. Finally, we offer potential solutions with respect to policies, guidelines or infrastructures that could aid in movement towards a more sustainable garment-producing industry. In our systematic review, we identified 2318 studies, of which 210 studies were relevant to our research questions. We provide a complete synthesis of the water and environmental state of the top garment-producing countries and summarise the current approaches to reducing barriers in sustainable garment production.

City living: the influence of urban stress on early rates of neurogenesis in eastern grey squirrels (sciurus carolinensis)

Alannah Grant[1], Amy Newman
[1]University of Guelph

As the fastest growing habitat type on the planet, urban environments encroach upon existing ecosystems at a pace never seen before, yet the severity and implications of these alterations are greatly unexplored. One means through which we may gain insight on the impact of urbanization on wildlife is through the hypothalamic-pituitary-adrenal (HPA) axis, a mechanism that connects organisms with their environment via the stress response and glucocorticoid (GC) production. Furthermore, the multi-generational impact of living in an urban setting may be revealed through the examination of maternal effects, and how a mother's stress, in response to urban stimuli, shapes offspring neurological development, specifically neurogenesis. Eastern grey squirrels (Sciurus carolinensis) are abundant throughout urban and habitats, making them a fitting representative population, for both their success in these environments and their reliance on neurogenesis, an integral part of their caching behaviour. Using urban and natural populations, our study applies a comparative approach to investigate potential trade-offs of an urban lifestyle in wildlife. With physiological methods, we examine the stress of mothers and offspring, and its effects on the rates of neurogenesis in juveniles. Preliminary results may highlight influence of maternal programing as suggested by generational differences in GC production. By testing novel theories related to the ecological and physiological outcomes of environmental stress, this research helps illuminate the specific mechanisms that are influenced by rapid, anthropogenic, environmental changes and moreover, contribute to the development of conservation strategies associated with modified landscapes.

Lay Abstract Currently, the urban landscape is the fastest growing habitat type on the planet. This rapid expansion presents new challenges and stressors that wildlife must respond and adapt to. The vertebrate stress response is a vital mechanism that kick starts behavioural and physiological processes that help animals deal with stressful situations and increase their survival. However, if the animal is consistently facing stressors and the stress response happens too frequently, this can hold long-term concequences for the animal's physiology and development. This is especially a problem for one common city slicker, the eastern grey squirrel, that relies on a particular stage of brain development (neurogenesis) which allows them to remember and find their hidden nut stashes every winter. My research aims to understand how stress brought on by an urban lifestyle can impact neurogenesis in grey squirrels and how stress may even be shaped by previous generations.

A mechanistic stage structure model to estimate the growth and mortality parameters of five fish species in canadian waters

Sherif Shuaib[1]
[1] *York University*

In this study, we present a stage-structured discrete-time model to estimate growth and mortality parameters for five economically significant fish species in Canadian waters: Atlantic Salmon (Salmo salar), Rainbow Smelt (Osmerus mor-dax), Capelin (Mallotus villosus), Cod (Gadus morhua), and American Eel (Anguilla rostrata). In theory, we computed the net reproduction number and conducted an in-depth stability analysis of both the trivial and non-trivial equilibrium points. In application, the model was fitted to data (2002-2021) for all five fish species and yielded very good results. The parameter estimation revealed consistent mortality rates for juveniles and young adults across all species, with notable variability among adults. Significant growth transitions were observed during the shifts from juvenile to young adult and from young adult to adult stages, with Atlantic Salmon and Cod displaying remarkable increases during these transitions. Capelin exhibited distinct growth transitions, while Rainbow Smelt and American Eel showcased unique patterns. Additionally, our study employs both local and global sensitivity analyses to identify pivotal parameters crucial to the extinction and non-extinction of each fish population. This study contributes new information on fish species with limited or no available information on their parameters. Thus, insights gained from this study could lead to the formulation of new policies or the adjustment of existing ones to better manage fish populations, ensuring both ecological balance and economic benefit. Furthermore, our analysis points out the need for more researchers to apply mechanistic models to understand climatic effects on fish distribution.

Lay Abstract

Development of a stage-structured discrete-time model for estimating growth and mortality parameters of five economically significant fish species in Canadian waters.

- Identification of significant growth transitions during the shifts from juvenile to young adult and from young adult to adult stages, with Atlantic Salmon and Cod displaying remarkable increases.
- Utilization of local and global sensitivity analyses to identify pivotal parameters crucial to the extinction and non-extinction of each fish population.

Poster Presentations

Application of Hollow fiber membranes (HFMs) for optimized CO2 delivery for algal biofilm growth

Eboseremen Ebewele[1], Jay Werber, Grant D Allen, Stewart Aitchison
[1]University of Toronto

As microalgal biotechnology advances toward sustainable and clean bioenergy production, optimizing both yield and kinetics of microalgal cultures becomes imperative. This study investigates the utilization of hollow fiber membranes (HFMs) to optimize CO2 delivery for algal biofilm growth. Air enriched with CO2 in varying concentrations (5% - 20%) was supplied through dense and porous HFMs to algae media in a photobioreactor. Dissolved CO2 in the reactor was quantified alongside algal biomass productivity to assess CO2 transfer efficiency and utilization. Results demonstrated a significant increase in dissolved CO2 and enhanced biofilm growth on membrane surfaces, indicating HFMs' efficacy in facilitating CO2 delivery and subsequent biofilm formation. Thus, HFMs offer a promising approach for effective CO2 delivery, leading to increased biofilm productivity in algal cultivation systems.

Lay Abstract This study focuses on enhancing the productivity of algal biofilms within photobioreactors. Our central hypothesis proposes that the synergistic integration of Hollow Fiber Membranes (HFMs) will create optimal conditions for algal biofilm growth. Through the implementation of HFMs, our aim is to streamline the delivery of CO2, a crucial factor in fostering robust algal biofilm development. This innovative approach holds the potential to significantly augment the availability of CO2 within the reactor, ultimately leading to heightened productivity.

Fundamental and applied research in skeletal biology: evo-devo to space biology

Tamara Franz-Odendaal[1]
[1]*Mount Saint Vincent University*

This poster will summarize the two main arms of research in my laboratory. Our fundamental research projects involve understanding the evolution and development of particular bones in the ocular skeleton of fossil and extant vertebrates. A series of flat bones circumvent the eyeball of most reptiles and develop via an intriguing induction signaling mechanism that involves FGF, BMP, Wnt/Bcatenin, and EDA. These genes interact in a reaction diffusion manner to initiate 13-15 signaling centres around the eye. Each center induces an individual bone that then grows to overlap one another to form the scleral ossicle ring. Our fundamental research first documented the presence and absence of the ocular skeleton over vertebrate phylogeny and more recently is focused on investigating the interactions of these gene players over development using the chicken embryo as model. The applied research in our lab centers around the effects of vibration and simulated microgravity on skeletal development using zebrafish as a model organism. Through various exposure durations and experimental start and end points, we are beginning to understand how bone cells interact with one another in response to these perturbations. Funding for our research is primarily from the Natural Sciences Engineering Research Council and the Canadian Space Agency and is supported through Canadian Foundation of Innovation grants and provincial funding from Research Nova Scotia.

Lay Abstract This research poster summarizes our fundamental and applied research in the field of skeletal biology. All vertebrate animals have a skeleton composed of bones and cartilages. Bones fossilize well and there is a rich history of vertebrate evolution in Canada and globally. How the skeleton develops in the correct orientation, size and shape has intrigued researchers and forms the basis of our research. Through an assessment of particular bones in fossil and living vertebrates, we documented when these bones evolved. We are now studying how they develop. This fundamental knowledge contributes to our greater understanding of the evolution of animals. On the more applied side of our research, we are intrigued by the effects of vibrations and microgravity on bone develop. These two phenomena have opposing impacts on the developing skeleton and could provide significant insight into bone disorders that involve an over or under production of bone.

Microbiome transmission mode influences host capacity for adaptation

Kenzie Givens[1], *Armin Moczek*
[1]*Indiana University*

Introduction:
It is well known that the microbiome contributes to host fitness and phenotype. Yet, the degree to which vertical and horizontal microbiome transmission modes influence host evolution has not received robust theoretical treatment. Here, we describe an evolutionary model that investigates how the strategy for acquiring a microbiome influences the host's capacity for adaptation.
Methods:
We developed an agent-based simulation in which hosts must evolve novel traits by forming partnerships with microbes. We explore three strategies for microbiome transmission: horizontal transmission, where microbes are randomly sampled from the environment each generation; vertical transmission, where offspring inherit a random sample of the parental microbiome; and hybrid transmission, where offspring inherit a blend of parental and environmental microbiomes.
Results:
Populations with horizontal transmission evolve novel traits more slowly and do not readily develop specialized partnerships with specific microbe species. In populations that engage in vertical transmission, we find that specialized partnerships evolve rapidly but may result in lower mean host fitness when there is significant environmental variation. Host organisms that engage in a hybrid transmission mode exhibit a higher mean fitness in the long term. When targeted disturbances disrupt specialized partnerships, such as may occur when organisms are exposed to antibiotics, hybrid transmission modes allow hosts to recover faster.
Conclusion:
Our findings demonstrate that the way in which organisms acquire their microbiome has significant effects on the rate of adaptation, long term fitness, and resilience in unpredictable environments.

Lay Abstract Many species engage in vertical microbiome transmission, whereby offspring inherit the microbiome from parents at the time of reproduction. Other species engage in horizontal transmission, whereby each generation acquires its microbiome from the environment. Still others engage in a hybrid strategy, where parental and environmental microbes are blended. It is not yet known if and how these three strategies differentially influence the host organisms' capacity to adapt. Here, we describe an evolutionary model that investigates how each strategy influences host fitness, the rate of adaptation, and robustness to environmental perturbations. We find that specialized partnerships evolve faster under vertical transmission than horizontal transmission, but vertical transmission decreases host fitness in unpredictable environments. Hybrid transmission improves host fitness in unpredictable environments and makes organisms more resilient to targeted disturbances because the environmental microbiome acts as a reservoir.

The lake ice pump: a conceptual model for carbon delivery from inland waters to the coastal ocean

Samantha Jones[1], Patrick Duke, Araleigh Alexander, Zoe Walker, Brent Else
[1]University of Calgary, Department of Geography

What happens in the lake, doesn't stay in the lake! The lake ice pump is a seasonal carbon transport pathway that connects a tundra lake to the coastal ocean—two systems that are typically studied separately. It relies on lake water compartmentalization by freshwater ice to create conditions favourable for carbon dioxide (CO2) and methane (CH4) accumulation. The gases are released later when spring breakup reconnects the lake to the river, which rapidly moves the gas-rich water across the terrestrial-marine interface. These interconnected processes are observed in Iqaluktuuttiaq (Cambridge Bay), Nunavut, in the Greiner Lake-Freshwater Creek-Cambridge Bay coastal ocean continuum. Shallow areas in Greiner Lake near the outlet to Freshwater Creek are isolated over winter by thick lake ice that can grow all the way to the lake bottom. Pockets of lake water can become anoxic and accumulate significant amounts of CO2 and CH4 that can't be ventilated to the atmosphere or released into the river until the following spring. During breakup, CO2- and CH4-rich water enters Freshwater Creek and moves the short distance downstream to Cambridge Bay. The river emits gases directly to the atmosphere and delivers dissolved gases to the coastal ocean where they move under sea ice still present in the bay. This cycle repeats annually, moving greenhouse gases generated in a terrestrial setting to the ocean. Lakes and streams are common in tundra lowlands, so the lake ice pump may be a useful framework when considering carbon movement through similar Arctic systems.

Lay Abstract What happens in the lake, doesn't stay in the lake! The lake ice pump describes a unique way that greenhouse gases can move from the Arctic tundra to the ocean. It is observed in Iqaluktuuttiaq (Cambridge Bay), Nunavut, where the relatively short Freshwater Creek connects Greiner Lake to the coastal ocean. Ice that freezes to the bottom in shallow parts of the lake creates compartments that can accumulate carbon dioxide and methane during the winter. When the ice melts in the spring, the gases are released into the river and travel downstream to the bay. Carbon dioxide and methane are emitted from the river to the atmosphere and flow into the ocean where sea ice is still present. This cycle repeats every year, behaving like a pump that moves greenhouse gases from the land to the ocean.

Enhancing green roof performance through native plant diversity: implications for urban ecosystem services

Patrick Ndayambaje[1]
[1]*University of Toronto Scarborough*

Green roofs are increasingly integrated into urban design as natural solutions, offering numerous ecosystem services. However, the selection and management of plant species on these roofs remain constrained. Promoting plant diversity is advocated as a method to enhance ecosystem services. While the advantages of plant mixtures over monocultures have been extensively studied in other ecosystems, research on green roofs is still limited.
Although the perennial succulent Sedum is commonly used on green roofs, incorporating native plants may enhance biodiversity. In a green roof experiment, six native plant species were compared both in monoculture and mixed plantings, with and without the presence of Sedum. Ecosystem service indicators, including aboveground biomass, plant traits, thermal regulation, and carbon sequestration, were assessed.
We observed a weak interaction among plant communities in terms of plant diversity, with Evening Primrose exhibiting divergent traits and indications of Common Yarrow facilitation during drought stress. However, Sedum had a negative effect on native plants, with native-only mixtures outperforming those with Sedum in terms of temperature reduction and CO2 sequestration. This study suggests that Sedum may hinder CO2 fixation efficiency and the cooling effects of other plants, while incorporating diverse plant species and mixtures can enhance green roof performance. The observed biodiversity–ecosystem function relationships in natural ecosystems may also manifest in engineered ecosystems like green roofs

Lay Abstract Green roofs are becoming increasingly common in cities, offering natural solutions and various benefits to urban environments. However, the way we choose and manage plants on these roofs is still limited. This study looked at how adding native plants alongside the commonly used Sedum could improve green roof performance. We found that while Sedum is popular, it might actually hinder the ability of other plants to cool the environment and absorb carbon dioxide. By mixing native plants with Sedum, we discovered that we could enhance the roofs' ability to regulate temperature and sequester carbon. This suggests that incorporating diverse plant species can significantly improve the overall effectiveness of green roofs in providing essential services to urban areas. In essence, our work highlights the importance of considering plant diversity in designing sustainable urban landscapes.

Immunology and Micrbiology

Contributed Talks

Applying methods in flow virometry to study viral surface proteins

Jonathan Burnie[1], Christina Guzzo
[1]University of Toronto Scarborough

Introduction – The importance of studying viruses in preparation for emerging public health threats has been appreciated globally since the COVID-19 pandemic. One particularly important aspect of viral pathogens to study are their surface proteins since these proteins influence viral entry and tropism. Viruses such as HIV and SARS-CoV-2, which have caused major public health crises, have been well studied using traditional virology techniques. However, applying new methodology to these pathogens allows the possibility to address new experimental questions.
Methods – Over the last decade, flow cytometry has been applied increasingly to study viruses (termed flow virometry). Flow virometry allows for high throughput analysis of individual virus particles and permits the visualization of virus heterogeneity through dot plots. Herein, we describe advancements in the emerging technique flow virometry to study proteins on the surface of HIV.
Results – We show that flow virometry can be used for a variety of applications, including screening the surface of viruses for host proteins, evaluating differences in cellular models of virus production and assessing changes in protein confirmation on single virions. While this work was done exclusively on HIV, we also highlight how this tool can be applied to other enveloped viruses like coronaviruses.
Significance– Taken together, we demonstrate new advances in flow virometry as a tool to provide sensitive, high throughput characterization of viral envelope proteins in a quantitative manner. We anticipate that this tool will have broad applications ranging from protein discovery and characterization to vaccine quality control.

Lay Abstract The importance of studying viruses in preparation for emerging public health threats has been appreciated globally since the COVID-19 pandemic. One particularly important aspect of viral pathogens to study are their surface proteins since these proteins initiate viral infection. Viruses such as HIV and SARS-CoV-2, which have caused major public health crises, have been well studied using traditional scientific techniques. However, applying new techniques to study these viruses allows the possibility to address new experimental questions. Herein, we describe the use of the technique flow virometry to study proteins on the surface of HIV. While this work was done exclusively on HIV, we also highlight how this tool can be applied to other viruses like coronaviruses. Taken together, we demonstrate new advances in flow virometry as a tool which can have broad applications ranging from protein discovery and characterization to vaccine quality control.

Site of antibody affinity modification in the gut of zebrafish (Danio rerio)

Emmanuel Alimo[1], Brad Magor
[1]University of Alberta

The humoral adaptive immune system, mediated by B cells, produces antibodies that are capable of binding to pathogens, and this binding can be improved through a process called Antibody Affinity Maturation (AAM). For a long time, it has been known that only warm-blooded vertebrates can affinity mature their antibodies at a site known as Germinal centers. However, recent studies indicate that cold-blooded vertebrates, though lacking histologically distinct germinal centers, yet have a functional Immunoglobulin gene mutator enzyme called Activation-induced cytidine deaminase (AID), which is a key initiator of the AAM process. In fish, for instance, clusters of AID+ cells encircled by pigmented Melano-macrophages (MMCs) were found in the kidney and spleen. We test the hypothesis that these clusters are present in the gut and functionally analogous to germinal centers. Fluorescence microscopy was used to detect and isolate the MMCs from the gut that auto fluoresce due to high amounts of lipofuscin. Transcripts of B-cells expressing IgM and IgT isotypes that are prominent in the gut were targeted with specific primers and then amplified with PCR, followed by High-throughput next-generational sequencing. We show evidence of B-cells within the MMCs that are undergoing Clonal expansion, Somatic Hypermutation, and antigen-driven selection, which are hallmarks of B-cells undergoing antibody affinity maturation in germinal centers. These findings provide insights into the evolution of the affinity maturation process and the improvement of fish vaccines.

Lay Abstract The humoral adaptive immune system, mediated by B cells, produces antibodies to fight against pathogens, and this binding can be improved through a process called Antibody Affinity Maturation (AAM). For a long time, it has been known that only warm-blooded animals have this system where they can improve the efficacy of the antibodies at a site known as Germinal centers. However, recent studies indicate that cold-blooded animals, though lacking histologically distinct germinal centers, yet have the enzyme called Activation-induced cytidine deaminase (AID), which plays a role in the AAM process. In fish, for instance, clusters of AID+ cells encircled by pigmented Melano-macrophages (MMCs) were found in the kidney and spleen. We test the hypothesis that these clusters are present in the gut and functionally analogous to germinal centers.

Unveiling novel protein translation inhibitors against mycobacteria through reporter-guided analysis

Maya George[1], Michael Cook, Gerard Wright
[1]McMaster University

Translation is a fundamental process for bacterial survival, facilitating the synthesis of essential proteins for growth, metabolism, and adaptation to diverse environmental conditions. Disrupting translation is a prevalent mechanism of action for antibiotics, essential in controlling the growth of pathogenic bacteria, including Mycobacterium tuberculosis, for which known translation inhibitor such as Streptomycin is commonly used. In the next 35 years, drug-resistant TB is estimated to kill around 75 million people and cost the global economy $16.7 trillion. As resistance continues to rise, the development of antimicrobial agents is crucial. In this project, we aimed to develop a novel reporter-guided approach for identifying antimycobacterial compounds specifically targeting protein translation. Based on the discovery of a cysteine-responsive regulatory mechanism in Mycobacterium smegmatis, we developed a translation inhibition reporter strain by coupling this cysteine attenuator with a luciferase gene and high-level promoter. This innovative approach allows for the direct detection of translation inhibition in a 12-hour assay, enabling rapid screening of potential antimicrobial compounds. Using this reporter, we identified Pheganomycin, a peptide antibiotic with specific activity against mycobacteria, from our Wright Actinomycete Collection. Historically linked to a mechanism of action surrounding the cell membrane and mycobacterial lipid components, Pheganomycin presents intriguing prospects for further investigation. Overall, the isolation of Pheganomycin highlights the efficacy of our reporter-guided approach in identifying antimycobacterial-specific translation inhibitors. This study lays the groundwork for future investigations into the antimicrobial properties and mechanisms of action of Pheganomycin and related compounds and fundamental processes of protein synthesis in mycobacteria.

Lay Abstract Understanding how bacteria survive is crucial for developing antibiotics to treat infections effectively. One way antibiotics work is by disrupting a process called translation, which bacteria need to make essential proteins. While we've discovered numerous antibiotics with different ways of treating bacterial infections, bacteria have become increasingly resistant through a natural process called antibiotic resistance, creating a dire need for new antibiotics. To address this challenge, we developed a new method to identify compounds that target bacterial translation, focusing on the Mycobacterium species, including the bacteria causing tuberculosis (Mycobacterium tuberculosis). Using this method, we uncovered Pheganomycin, a natural compound produced by soil bacteria that has shown effectiveness against TB bacteria. This discovery opens exciting possibilities for understanding new targets and developing treatments against TB and Mycobacterium-related bacterial infections. Our study marks a crucial step forward in discovering novel natural products and sets the stage for future research in this field.

Ninein is required for phagocytosis in macrophages

Safia Omer[1], Rene E. Harrison
[1]Department of Biological Sciences, University of Toronto Scarborough

Phagocytosis by macrophages is a highly polarized process to destroys large target cells. Binding to particles induces extensive cortical actin-generated forces that drive the formation of elaborate pseudopods that extend out and around the target- particle. Post-internalization, the resultant phagosome is driven towards the cell interior on microtubules (MTs) by cytoplasmic dynein. However, it is unclear whether dynein and cargo-adaptors contribute to the earlier steps of particle internalization and phagosome formation. Here we reveal that ninein, a MT minus-end-associated protein that localizes to the centrosome, is also present at the phagocytic cup in macrophages. Ninein depletion impairs particle internalization by delaying the early F-actin recruitment to sites of particle engagement and cup formation, with no impact on F-actin dynamics beyond this initial step. Ninein forms membrane-bound clusters on phagocytic cups that do not nucleate acentrosomal MTs but instead mediate the assembly of dynein-dynactin complex at active phagocytic membranes. Both ninein depletion and pharmacological inhibition of dynein activity reduced inward displacement of bound particles into macrophages. We found that ninein and dynein motor activity were required for timely retrograde movement of phagosomes and phagolysosome formation. Taken together, these data show that ninein alone and with dynein play significant roles during phagocytosis.

Lay Abstract Macrophages specialize in clearing microbes such as bacteria and parasites. Following contact with these elements, macrophages extend their plasma membranes to surround and encapsulate these particles within an enclosed-membrane compartment known as the phagosome. The resultant phagosome is then subjected to pushing and pulling mechanical forces to translocate the phagosome to the cell center. My work examines dynein and how and when it is associated with the phagosome. I identified that ninein, an adaptor protein, is required for the recruitment of the dynein complex to the phagocytic membrane. Inhibition of dynein activity or depletion of ninein protein from macrophages reduces the inward movement of the phagosome. I found that this early phagosome movement is required to promote downstream processes that result in the degradation of the engulfed particle. This work highlights the importance of the adaptor protein ninein and motor dynein and their role in pulling pathogen-containing phagosome inside macrophages.

Science Education

Contributed Talks

The visible and the hidden: racism, whiteness and epistemic oppression in the Canadian academy

Nathan Andrews[1], Akalya Kandiah, Annie Duchesne, Joseph Shea, Sadia Diriye, Maria Chadid Hernandez, Ulaş Taştekin
[1]McMaster University

Scholars have highlighted that Canadian higher education encompasses issues such as racism, which have impacts such as the underrepresentation of BIPOC (Black, Indigenous and Persons of Colour) scholars and the 'leaky pipeline'. While often considered to be objective and value-free, science itself is also situated in social and political contexts. What, then, are the impacts of racism, whiteness, and epistemic oppression on how science is "done" in the Canadian academic context? Using a triangulation of approaches, such as syllabi analyses, interviews, and event ethnography (of discipline-specific annual conferences), this transdisciplinary study contributes to an understanding of the intersections of racism, whiteness, epistemic oppression, and their connection with the institutional inertia to diversity and meaningful transformation. The findings underpin the colonial roots of the sciences and the marginalization of BIPOC scholars, which manifests in faculty experiences of systemic barriers, the 'leaky pipeline', and disproportionate division of labour among other outcomes. This study emphasizes not only the importance of trans/cross-disciplinary work to better understand the nuanced impacts of racism, whiteness and epistemic oppression on BIPOC scholars in different fields but also highlights that these impacts can occur in both visible and hidden ways.

Lay Abstract While often considered to be value-free or objective, science is 'done' in social and political contexts. What, then, are the impacts of racism, whiteness, and epistemic oppression on how science is "done" in the Canadian academic context? Using multiple approaches, such as the analysis of university-level course syllabi, interviews, and an ethnographic study of the annual conferences of three specific academic disciplines, we present findings that expose the colonial roots of the sciences and the marginalization of BIPOC (Black, Indigenous and Persons of Colour) scholars which manifests in faculty experiences of systemic barriers, the 'leaky pipeline', and disproportionate division of labour among other outcomes. The study also emphasizes the relevance of trans/cross-disciplinary collaboration as a way to examine the multiple expressions and impacts of racism, whiteness, and epistemic oppression across the broader academic context in Canada.

Exploring effective teaching practices for black students learning science in Nova Scotia – initial findings

Eddia Copeland Solas[1]
[1]*Mount Saint Vincent University*

Three decades after the publication of the Black Learners Advisory Committee (BLAC) on Education report in Nova Scotia, Black students are still being underserved in the province. The BLAC report's directives—for educators to adopt a sensitive, responsible approach tailored to the unique needs of Black learners—remain partially unfulfilled. This paper reveals initial findings of a qualitative study, comprising teacher and student interviews and classroom observations, aimed at meticulously gathering and analyzing the pedagogical practices of educators who are effectively educating Black students in science, in order to assist in filling the gaps. The findings show that the teachers have high expectations of students, are heavily involved in community engagement, recognize inequities and have an unwavering commitment to change, practice reflective and adaptive teaching, build relationships and are lifelong learners. It is hoped that this work will result in a framework for broader application within Nova Scotia's educational systems. By presenting these preliminary insights, the paper invites a critical examination of how these practices can be universally adopted in Canada to serve the needs of Black students, thereby catalyzing systemic change in the pursuit of equity and excellence for all students.

Lay Abstract Three decades after the publication of the Black Learners Advisory Committee (BLAC) on Education report in Nova Scotia, Black students are still being underserved in the province. The BLAC report's directives—for educators to adopt a sensitive, responsible approach tailored to the unique needs of Black learners—remain partially unfulfilled. This paper reveals initial findings study, comprising teacher and student interviews and classroom observations, aimed at analyzing the teaching practices of educators who are effectively educating Black students in science, in order to assist in filling the gaps. The findings show that the teachers have high expectations of students, are heavily involved in community engagement, recognize inequities and have an unwavering commitment to change, practice reflective and adaptive teaching, build relationships and are lifelong learners.

Assessing the impact of accessible experiential learning for bipoc students at FREED

Alannah Grant[1], Candace Goodwin, Aranya Iyer, Mariel Terebiznik, Rachel Giles, Vanessa Nhan, Jamie Grimm
[1]Field Research in Ecology and Evolution Diversified (FREED), Guelph, Ontario

There is a clear underrepresentation of Indigenous, Black and/or Racialized (BIPOC) individuals in conservation spaces that only intensifies higher up the career ladder. Field Research in Ecology and Evolution Diversified (FREED) is an organization whose mandate is to address barriers to accessing field work alongside creating a curriculum that is led by majority BIPOC early-career professionals for BIPOC undergraduate students. In our presentation, we will discuss how our organization is assessing the impact of accessible, experiential learning experiences for BIPOC undergraduate students in field work and ecology and evolutionary biology. We will present results from surveys conducted during our 2023 event that assessed student experiences before and after participating in FREED. Specifically, we surveyed how student perceptions of their own skills and confidence in field work, their sense of community in conservation and ecology sectors, and their likelihood of pursuing a conservation-based career changed after participating in FREED. We will also share how our FREED curriculum integrates accessibility, multiple knowledge systems, including Indigenous knowledge, and diverse learning opportunities into our events that make FREED a unique and meaningful experiential learning experience for students.

Lay Abstract An essential part of connecting to the natural world – and one of the most appealing aspects of studying it – is having the opportunity to see a textbook come to life. One way to do this is by gathering knowledge on the world around us and immersing in nature through what is known as field work. However, field work experience is a privilege that is not afforded to all, and many students, especially those from marginalized groups, face barriers that exclude them from participating in field work and furthering their careers in ecology and the natural sciences. To address these barriers, FREED hosts weeklong naturalist workshops, led primarily by BIPOC (Black, Indigenous and people of colour) graduate students and early career professionals. We center equity and accessibility and strive to make our events safe spaces where students from diverse backgrounds can explore field work, ecological research, and naturalist hobbies.

Opening the eyes of undergraduate students to hidden impacts of bias in STEM

Maydianne Andrade[1]
[1]*Department of Biological Sciences, University of Toronto Scarborough*

Research and practice in Science, Technology, Engineering, Mathematics, Medicine and Health (STEMM) often rest on the unquestioned assertion of the objective analysis of facts, a bedrock to most aspects of undergraduate STEMM education. Yet there is ample evidence that unchecked, unacknowledged bias among individual STEMM educators, researchers and practitioners intersects with and perpetuates systemic discrimination based on flawed scientific reasoning. Consequences range from the negative impacts of 'race norming' in medical technologies to the pervasive use of AI trained on biased data, to the under-representation of marginalized groups in clinical trials and STEMM careers. We describe our approach to expanding undergraduate understanding while sidestepping some of the common objections to such education in STEMM. We created a new senior, multi-disciplinary course in Biology that provides a data-informed understanding of concepts such as biological essentialism, colonialism and biopiracy, eugenics, erroneous beliefs about race and gender, and how historical prejudices are woven into modern scientific norms. The term project requires students identify practices, structures, and individual actions that could ensure that science disrupts, rather than enables, social inequities. We then used student projects to create tutorials for introductory biology courses, building student understanding without adding to already heavily circumscribed program requirements. One strength of this approach is ensuring a specific focus on STEMM, rather than providing a more general understanding of discrimination and bias which students struggle to connect to their STEMM learning. Approaches and challenges with garnering administrative support and collegial buy-in for such a course will be discussed.

Lay Abstract Many undergraduates with a BSc in biology have never learned about the ways in which prejudice and bias can affect every dimension of science, from research to teaching and practice. Despite the common emphasis on objectivity, scientists are as susceptible to bias as are other people, and the negative effects of unacknowledged individual and systemic bias can be substantial. In this talk, we discuss how small changes in the curriculum can help ensure undergraduates are aware of, and can act to counter, these effects. We describe a new course that links topics in biology to real-world data and examples of how flawed assumptions and understanding of concepts such as inheritance, 'race' and gender can lead to negative impacts on marginalized populations. We outline a pilot program to use student projects from this senior-level course to education first-year undergraduates.

Poster Presentations

Homemade spectrophotometer: affordable science for educational innovation

Ryan Bossou Tihoun[1]
[1]*Paul-Gérin-Lajoie d'Outremont (École Secondaire/Secondary School), Montreal, Canada*

Science has significantly transformed numerous sectors, yet the escalating costs of high-level scientific research tools have placed a strain on many educational institutions. Spectrophotometers, despite being among the more affordable devices in modern labs, typically cost around 5,000 CAD—still prohibitively expensive for most schools worldwide. To bridge this financial divide, we developed a method to construct a functional spectrophotometer using inexpensive materials, reducing the cost to about 100 CAD—a dramatic decrease by a factor of 50 compared to commercial models. Our spectrophotometer comprises a flashlight as the light source, a toilet paper roll to channel the light beam, a cuvette for holding samples, grating paper for diffraction, and a smartphone camera as the detector. Data analysis was performed using Python programming. We constructed the rest of the device using cardboard and wood. We tested our spectrophotometer's effectiveness by measuring the molecular concentration of Allura Red in Gatorade Fruit Punch. This project demonstrates how combining expertise and principles from various scientific fields, such as chemistry, physics, and computer science, can innovatively address challenges and conduct significant research. Through this initiative, we aim to demonstrate that sophisticated scientific investigations can be accessible and affordable, inspiring educational institutions worldwide to engage in practical science learning and experimentation.

Lay Abstract In an innovative effort to make scientific research tools more affordable, we successfully built a functional spectrophotometer for around 100 CAD, drastically reducing the commercial 5,000 CAD cost. Using everyday items such as a flashlight, a toilet paper roll, grating paper, and a smartphone camera, we constructed a device capable of performing scientific analyses. The spectrophotometer, which uses the flashlight to project light through a sample in a cuvette, measures light intensity variations with the phone's camera. We demonstrated the device's reliability by measuring the dye content in a popular sports drink (Gatorade). This project showcases the integration of multiple scientific disciplines—chemistry, physics, computer science, etc.—to solve practical problems affordably and effectively. By doing so, we hope to inspire educational institutions worldwide to explore hands-on science, making advanced experiments accessible and encouraging a hands-on approach to learning.

Assessments in Anatomy: Exploring Faculty Perspectives, Challenges, and Solutions Through a Focused Group Discussion

Terkuma Chia[1], Izuchukwu Okafor, Michael I. Oraebosi, Oluwatosin Oyeniran, Victoria Chukwu
[1]Institute of Health Sciences Education, McGill University, Montreal, Quebec, Canada

Introduction: Assessments constitute a major responsibility of faculty. In anatomy, various assessment methods impact both students and faculty. This qualitative study aimed to understand the perspectives of anatomy faculty regarding assessments. The primary objective is to explore faculty viewpoints on assessment methods, the challenges they face, and potential solutions to these challenges.
Methods: This qualitative study was conducted using focused group discussions to gather perspectives from anatomy faculty. Two focused group discussions were conducted, each involved eight participants with varying years of teaching experience from both public and private institutions. The discussions, held over Zoom each for 90 minutes, were audio-recorded and transcribed verbatim. Thematic analysis was performed to identify emerging themes related to assessment practices and challenges.
Results: The analysis revealed that assessment in education is crucial for evaluating student performance and providing faculty feedback. Significant challenges include resource constraints, fairness in exams (both practical and viva formats), and managing large class sizes. Maintaining fairness requires adherence to marking schemes and standardized criteria. The varying rigor of assessment methods between medical and non-medical programs necessitates tailored approaches across disciplines. Additionally, improved resources such as internet access, ICT integration, cadavers, facilities, and staffing were emphasized. These efforts put together can strengthen assessment practices and uphold educational standards.
Significance: Understanding anatomy faculty experiences and challenges in assessments is vital for improving educational practices. This study offers insights to enhance assessment methods and support faculty and students. It fosters collaboration among faculty to find solutions, inform policy changes, support professional development, and allocate resources to improve the quality of anatomy education.

Lay Abstract Assessments are a major responsibility for anatomy faculty, impacting both students and teachers. This study aimed to understand faculty perspectives on assessment methods, challenges, and potential solutions. Using focused group discussions, two sessions were held over Zoom, each lasting 90 minutes with eight participants from public and private institutions. The sessions were recorded, transcribed, and analyzed to identify key themes. The analysis showed that assessments are crucial for evaluating student performance and providing faculty feedback. Major challenges include limited resources, fairness in exams (practical and viva), and managing large class sizes. Ensuring fairness requires strict marking schemes and standardized criteria. Differences in assessment methods between medical and non-medical programs need tailored approaches. Improved resources like better internet, ICT tools, cadavers, facilities, and staffing were highlighted as necessary. Understanding faculty experiences and challenges in assessments is essential for improving educational practices and informing better resource allocation.

Art Submission

Poster Presentation

The Enduring Struggle of Endometriosis: Art as Advocacy

Ezinne Ekediegwu[1]
[1]*McGill University*

Artwork Description

Central Figure: Adorned in traditional Nigerian attire, representing the societal challenges faced by individuals grappling with endometriosis in Nigeria.

Symbolism

Crimson Garments: Symbolize the profound suffering endured due to the disease

Hands on Abdomen: Highlights the locus of her anguish

Seeds Scattered into the Wind: Represent her tireless efforts to raise awareness and enlightenment regarding her condition

Wind as Metaphor: Represents societal currents of ignorance and indifference that hinder her efforts

The Enduring Struggle of Endometriosis: Art as Advocacy

Ezinne Ekediegwu[1]
[1]*McGill University*

Introduction:

This evocative artwork narrates the profound struggle of a patient suffering from endometriosis, whose life is marked by persistent pain and weakness. The artist poignantly conveys the individual's unwavering commitment to raising awareness and fostering understanding of this debilitating disease within her societal context.

Statistics and Reality:

Prevalence: One in ten women is afflicted by endometriosis, yet awareness remains alarmingly scarce
Nigeria:Limited access to specialized medical practitioners with no more than two Endometriosis specialists
Global Context:Lack of definitive knowledge and cure casts a shadow over countless lives worldwide

Challenges in Medical Practice

Dismissal of Symptoms:Medical practitioners often dismiss patients' symptoms as imaginary
Ineffective Treatment:Patients are prescribed ineffective treatments, leading to delayed diagnoses
Ridicule and Mockery:Sufferers face ridicule, exacerbating their plight and leading to preventable tragedies

Hope and Advocacy:

Amidst the darkness, a beacon of hope emerges through the protagonist's resolute advocacy and unwavering determination. Her indomitable spirit serves as a rallying cry, urging society to confront its ignorance and apathy. Through her courageous crusade, she endeavours to sow the seeds of awareness and understanding, nurturing a brighter future for future generations.

Conclusions:

Amidst the darkness, a beacon of hope emerges through the protagonist's resolute advocacy and unwavering determination. Her indomitable spirit serves as a rallying cry, urging society to confront its ignorance and apathy. Through her courageous crusade, she endeavours to sow the seeds of awareness and understanding, nurturing a brighter future for future generations.

Science Education

Poster Presentation

Two Bugs / One Stone: Breaking Barriers to Biology for Underserved Students Through Interactive Invertebrate Behaviour Experiences

Luciana Baruffaldi, Susheen Mahmood, Laini Taylor and Maydianne C.B. Andrade University of Toronto Scarborough, Scarborough, ON, Canada

Introduction: Although STEM education is an important part of school curricula the quality of STEM programming in schools is variable, and more than 50% of Canadian students drop science in senior high school. We worked to use outreach methodologies to enrich the grade nine curriculum, while building relationships between students and diverse STEM role models. Methods & Results. Researchers, graduate, and undergraduate students from the Andrade lab at the University of Toronto Scarborough (UTSC) acted as scientist-mentors and worked with STEM teachers from West Hill Collegiate (WHC, low socio-economic status public high school in Scarborough, ON) to co-develop an in-class science enrichment program that was integrated into and supported the curriculum of grade 9 STEM classes. Scientist-mentors facilitated discussions and activities focusing on 4 overarching themes: 1) the importance of diverse perspectives from different cultures and backgrounds in science, 2) the importance of studying animal behaviour, 3) the process of designing a novel experiment, collecting, and interpreting real data, and 4) the different careers paths in STEM. WHC students conducted several research experiments in labs at UTSC, and scientist-mentors visited the WHC school repeatedly over the course of a semester. The initiative culminated in students presenting their research findings to their community at WHC's annual 'STEM Day'. Significance. By providing students from under-represented and under-served communities with an opportunity to actively participate in science, we hope to increase the enrollment and retention of marginalized youth in STEM. The next phase of this initiative will involve expansion to more schools, more formal assessment of student responses.

BE-STEMM 2024 was made possible by the generous support of our sponsors

Diamond Sponsor & Network Host

University of Toronto Scarborough

Platinum Sponsors

University of Calgary

CIHR IRSC
Canadian Institutes of Health Research / Instituts de recherche en santé du Canada

NSERC CRSNG

The University of British Columbia

Gold Sponsors

GenomeCanada

University of Toronto

University of Guelph
Improve Life.

Québec
Fonds de recherche – Nature et technologies
Fonds de recherche – Santé
Fonds de recherche – Société et culture

Silver Sponsors

Public Health Agency of Canada / Agence de la santé publique du Canada

McGill

University of Waterloo

McMaster University

Queen's University

NSERC CRSNG
Chairs for Women in Science and Engineering
Chaires pour les femmes en sciences et en génie

WIMA Women in Science

WWEST

Women in Science and Engineering
NSERC Chair – Atlantic Region

CFSG
Chaire pour les femmes en sciences et en génie

WISE Planet

NSERC CRSNG
Chairs for Inclusion in Science & Engineering Atlantic

Bronze Sponsors

metrix

University of Toronto | BRN Black Research Network

University of Windsor

Canadian Science Publishing