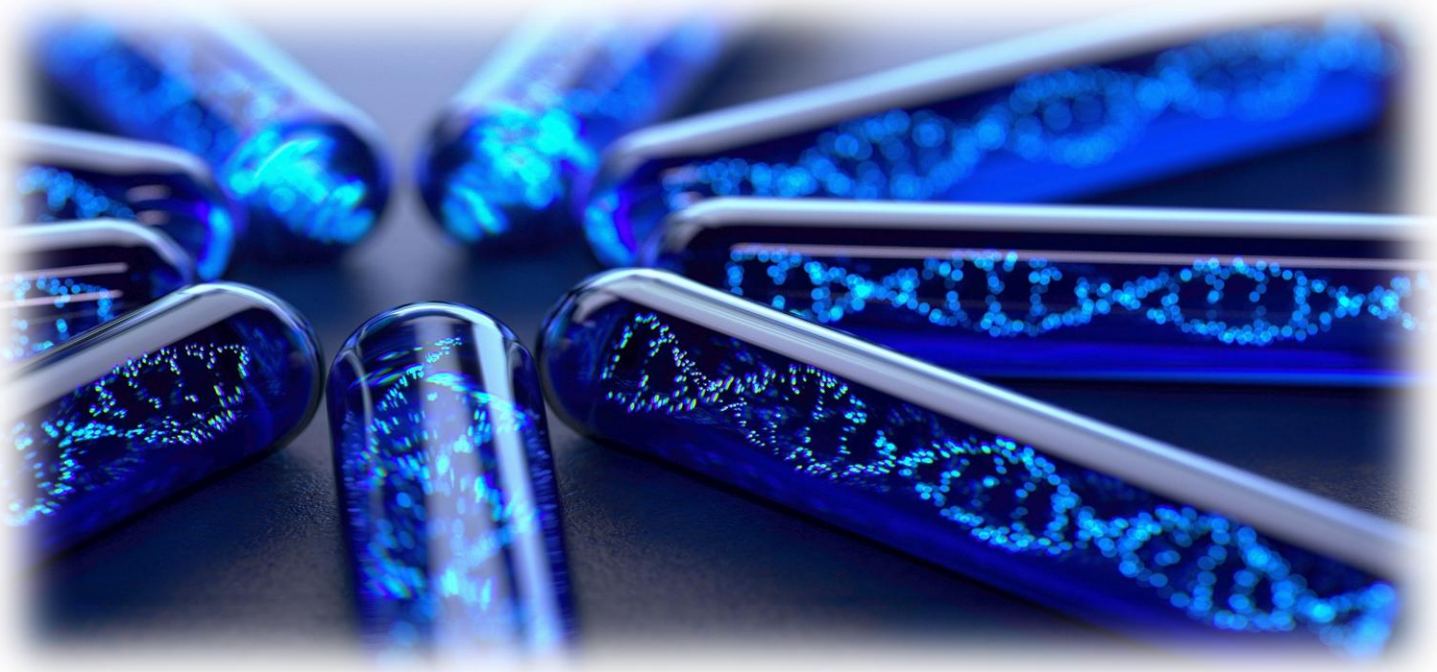
Graduate Student Research Day

Thursday June 4, 2026

Life Science Research Institute (LSRI)
Atrium & McNamara Boardroom
1344 Summer St. Halifax, NS



DALHOUSIE UNIVERSITY

FACULTY OF MEDICINE
MEDICAL RESEARCH DEVELOPMENT OFFICE

DALHOUSIE SUSTAINABLE EVENTS
PLATINUM

PREP Professional & Research Education Program

Welcome to the 2026 Graduate Research Day!

Graduate Student Research Day has been an annual tradition since 2005. This year, we proudly continue this tradition while recognizing the resilience and dedication of our graduate students during a year marked by significant academic and personal challenges.

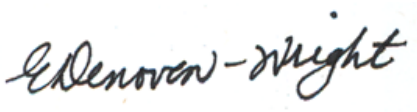
Graduate Student Research Day features over 60 abstracts presented through platform and poster sessions, adjudicated by experienced researchers who provide valuable feedback to support students' scholarly development. The event offers an important opportunity for knowledge exchange, interdisciplinary engagement, and collaboration across the health research community.

Graduate Student Research Day continues to highlight both the significance of graduate research and the determination of the students who carry it forward.

Our Objectives:

- **Increase Awareness:** Enhance understanding of ongoing research and emerging opportunities.
- **Critical Analysis:** Promote engagement with rigorous and innovative research.
- **Integrating Research and Education:** Strengthen connections between research and health education.

We invite you to join us in recognizing and celebrating the achievements of our graduate students.



Eileen Denovan-Wright, PhD
Associate Dean, Research

Faculty of Medicine

Schedule of Events

8:30-8:55	Registration & Light Refreshments
9:00-9:05	Welcome - Dr. Eileen Denovan-Wright, Associate Dean, Research
9:05-9:10	Opening Remarks – Dr. David Anderson, Dean of Medicine
9:10-9:15	Excellence in Research Award Introduction Dr. Kirill Rosen, Assistant Dean, Graduate and Postdoctoral Studies
9:15-9:45	Presentations – Faculty of Medicine, 2026 Excellence in Research Winners
9:15	**Zachary Long**, PhD Candidate
9:30	**Dr. Vanessa DeClercq**, Research Associate **Jack Case**, MSc Candidate - Presenting at a national conference **Dr. Elena Koning**, Postdoctoral Fellow - Presenting at the International Conference on Eating Disorders (ICED) in The Netherlands
9:45-9:50	Platform Presentations Introduction, Dr. Kirill Rosen, Assistant Dean, Graduate and Postdoctoral Studies
9:50-10:10	Platform Presentations Session #1
9:50	Daniel Basso, MSc Candidate
10:00	Jessica Latimer, PhD Candidate
10:10	Julia Fraiha-Pegado, PhD Candidate
10:20-11:20	Poster Presentation – Viewing and Judging Refreshments in the Atrium
11:20-12:00	Platform Presentations Session #2
11:20	Ahmed Ramadan, PhD Candidate
11:30	Brianna Latremouille, PhD Candidate
11:40	Claerwen Sladen-Dew, MSc Candidate
11:50	Ebadullah Kabir, PhD Candidate
12:00-1:15	Poster Presentation – Viewing and Judging Buffet Lunch in the Atrium
1:15-2:15	Keynote Presentations
1:15	**Dr. Ejemai Eboreime** MD; PhD; MSc; DLSHTM; PMP; FAPH
1:45	**Dr. Pegah Poursharifi** Ph.D.
2:15-2:55	Platform Presentation Session #3
2:15	Cameron Calder, MSc Candidate
2:25	Tanzima Fariha, MSc Candidate
2:35	Samuel Silva, PhD Candidate
2:45	Shannen Grandy, PhD Candidate
2:55-3:00	2nd Annual People's Choice Award Voting
3:00-3:30	Career Panel
3:30-4:00	Closing Remarks and Prizes Dr. Kirill Rosen, Assistant Dean, Graduate and Postdoctoral Studies

Keynote Speakers

Dr. Ejemai Eboreime MD; PhD; MSc; DLSHTM; PMP; FAPH

Assistant Professor

Department of Psychiatry

Closing the Gap: Implementation Science, Global Health, and the Making of a Research Identity

McNamara Boardroom, LRSI
1:15pm – 1:45pm, June 4, 2026

https://medicine.dal.ca/departments/department-sites/psychiatry/our-people/faculty/ejemai-eboreime.html

Dr. Pegah Poursharifi, Ph.D.

Assistant Professor

School of Biochemistry and Molecular Biology

The Glycerolipid Cycle at the Crossroads of Metabolism and Inflammation

McNamara Boardroom, LRSI
1:45pm – 2:15pm, June 4, 2026

https://medicine.dal.ca/departments/department-sites/biochemistry-molecular-biology/our-people/faculty/poursharifi--p--.html

Campus Partners (in alphabetical order)

Advancement

We work closely with our donor community and Dalhousie alumni to better understand what matters most to them and what impact they want to have through their engagement so we can introduce them to opportunities that align with our medical research and education excellence goals. It's important to us that we help our donors stay connected to the student learners and health research projects that they care about.

We build relationships with researchers, educators, and other key players within the faculty to better understand the work happening in and out of the lab and classrooms. We help scientists talk about their work in a way that we can all understand and help them tell their stories, make connections, and continue their laudable efforts.

The more we learn about the exciting advances taking place right here at Dal, the more we can share with our donor community and find opportunities for aligned interests to make greater impact, together.

https://medicine-advancement.dal.ca/

Career Service

Career Services at Dalhousie University supports students and recent graduates in exploring career paths, reflecting on skills, and navigating next steps. Through career advising, peer advising, and career counselling, students and recent alumni receive support with identifying career options, leveraging their degree, developing job search strategies, preparing for interviews, and refining application materials. With access to 1-to-1 appointments, workshops, and online resources, Career Services is here to help you set and work towards your career and employment goal(s).

https://www.dal.ca/life-at-dal/student-support/career-support.html

CORES

ADVANCE YOUR RESEARCH WITH STATE-OF-THE-ART FACILITIES AND SERVICES Through its strategic CORES program (Centralized Operations of Research Equipment and Supports), the Faculty of Medicine has developed a range of multi-user research facilities providing access to sophisticated equipment and services supported by trained experts. The CORES facilities welcome users from the Dalhousie community, other academic institutions, and external commercial groups.

https://medicine.dal.ca/research-dal-med/facilities.html

Faculty of Graduate Studies - GradPD

Dal GradPD is your go-to hub to learn about professional development designed for your specific needs as a graduate student. Together with partners across the university and external providers, the Faculty of Graduate Studies (FGS) assembles an ongoing schedule of free workshops and events aimed to help you prepare for a diversity of careers.

The four pillars of the Dal GradPD program are dedicated to building skills necessary for success in any career - Communication, Career Intelligence, Health and Wellbeing, and Leadership - and are offered exclusively to graduate students and postdoctoral fellows.

https://www.dal.ca/faculty/gradstudies.html

Dalhousie Libraries

Dalhousie Libraries have many online and in-person supports and services for graduate students. Our liaison librarians can help you navigate the resources and services available to you and offer individual research consultations relevant to various stages of the research process, including research data management advice, scholarly communications guidance, support for literature reviews, and more. Our Research Camp consists of training modules on a variety of subjects from library research to information management and more. (For more information and to register, follow this link: https://dal.ca.libguides.com/ResearchCamp). The Library provides access to physical and electronic books, journals, and other materials to support coursework and research. The document delivery service can also retrieve materials that are not held in our collections, at no cost to the requester. We also offer a variety of study spaces across our locations.

https://libraries.dal.ca/

Pulse

Pulse is a health innovation sandbox at Dalhousie University that brings together students, faculty, and external partners to identify gaps in healthcare and develop real-world solutions. It supports early-stage ideas through design thinking, mentorship, micro-grants, and venture development, with a focus on improving health outcomes through innovation.

https://dalinnovates.ca/pulse-hands-on/

Writing Centre

The Dalhousie Writing Centre offers confidential academic writing support and guided feedback for graduate, undergraduate, and professional program student writers across disciplines. We work with students one-one to discuss writing related to their academics, including dissertations, letters of intent, grant and scholarship applications, proposals, presentations, navigating questions around gen A.I, and more. Supports especially popular with grad students include mock defense practices, regular check-in appointments over time with a consistent advisor, and pomodoro-style writing sessions, which form a daily online writing community that provides consistency and gentle, non-evaluative accountability for completion of writing projects. We also offer a series of workshops on common writing concerns and dedicated writing weeks for grad students. Write to writingc@dal.ca for more information or visit us online at https://www.dal.ca/life-at-dal/student-support/writing-support.html

Career Panel

Welcome to our Career Panel!

This panel is a new addition to our Graduate Research Day. The session is designed to give graduate students the opportunity to explore the diverse career paths available after completing their graduate degree. Our panelists bring experience from academia, industry, and entrepreneurship, and are here to share insights from their own career journeys.

We encourage you to take full advantage of this session by asking questions, engaging in discussion, and reflecting on how your skills and interests might translate into different professional directions.

Career Panel Moderator

Sebastian Himbert - Department of Pediatrics, Dalhousie University

Career Panelists:

Erin MacKean - Founder & Chief Executive Officer, NeoLux Scientific

Dr. Christopher Hughes – Manager, Biological Mass Spectrometry Core Facility

Dr. Hamed Hanafi, PhD - Founder and CEO, NovaResp Technologies Inc; Adjunct Professor in the School of Biomedical Engineering and Dept. of Electrical and Computer Engineering, Dalhousie University

Dr. Amy Trottier, Hematologist, Nova Scotia Health; Assistant Professor, Division of Hematology and Hematologic Oncology, Dalhousie University

Student Presentation Schedules

Excellence in Research Awards

9:15-9:45 Presentations – Faculty of Medicine, 2026 Excellence in Research Winners

- 9:15 **Zachary Long**, PhD Candidate
- 9:30 **Dr. Vanessa DeClercq**, Research Associate
  Jack Case, MSc Candidate (Presenting at a national conference)
  Dr. Elena Koning, Postdoctoral Fellow (Presenting at the International Conference on Eating Disorders (ICED) in The Netherlands

Platform Presentations

9:50-10:10 Platform Presentations Session #1

- 9:50 Daniel Basso, MSc Candidate
- 10:00 Jessica Latimer, PhD Candidate
- 10:10 Julia Fraiha-Pegado, PhD Candidate

11:20-12:00 Platform Presentations Session #2

- 11:20 Ahmed Ramadan, PhD Candidate
- 11:30 Brianna Latremouille, PhD Candidate
- 11:40 Claerwen Sladen-Dew, MSc Candidate
- 11:50 Ebadullah Kabir, PhD Candidate

2:15-2:55 Platform Presentation Session #3

- 2:15 Cameron Calder, MSc Candidate
- 2:25 Tanzima Fariha, MSc Candidate
- 2:35 Samuel Silva, PhD Candidate
- 2:45 Shannen Grandy, PhD Candidate

Poster Presentations - 10:20am and 11:20am

Ahsan Malick, MSc Candidate
Supervisor: Dr. Francesca Di Cara, Department of Microbiology & Immunology

Alireza Aleali, MSc Candidate
Supervisor: Dr. Javeria Hashmi, Department of Medical Neuroscience

Aminat Mustapha, MSc Candidate
Supervisor: Dr. Alon Friedman, Department of Medical Neuroscience

Aryan Vesuna, MSc Candidate
Supervisor: Dr. Thomas Pulinilkunnil, Department of Biochemistry & Molecular Biology

Autumn Sweeney, MSc Candidate
Supervisor: Dr. Nelly Amenyogbe & Dr. Tobias Kollmann, Department of Microbiology & Immunology

Calvin Butler, MSc Candidate
Supervisor: Dr. Gabriela Ilie, Department of Community Health and Epidemiology

Claire Thiessen, MSc Candidate
Supervisor: Dr. Sanja Stanojevic, Department of Community Health and Epidemiology

Hala Obeid, MSc Candidate
Supervisor: Dr. Bahaa Abu-Raya, Department of Microbiology & Immunology

Harish Babu Kolla, PhD Candidate
Supervisor: Dr. Thomas Pulinilkunnil, Department of Biochemistry & Molecular Biology

Henok Andualem Tegared, PhD Candidate
Supervisor: Dr. Tobias Kollmann, Department of Microbiology & Immunology

Hugh Atkinson, MSc Candidate
Supervisor: Dr. Manuel Mattheisen & Dr. Mark Asbridge, Department of Community Health and Epidemiology

Jenysbel Hernandez Reyes, PhD Candidate
Supervisor: Dr. Jean Marshall, Department of Microbiology & Immunology

Kevin Nguyen, MSc Candidate
Supervisor: Dr. Xianping Dong, Department of Physiology & Biophysics

Lauren Over, MSc Candidate
Supervisor: Dr. Karen Lithgow & Dr. Zhenyu Cheng, Department of Microbiology & Immunology

Mariama Jammeh, MSc Candidate
Supervisor: Dr. Tobias Kollmann & Dr. Nelly Amenyogbe, Department of Microbiology & Immunology

Murtaza Lokhandwala, MSc Candidate
Supervisor: Dr. Greg Fairn, Department of Biochemistry & Molecular Biology

Radka Sevcik, MSc Candidate
Supervisor: Dr. Alexander Quinn, Department of Physiology & Biophysics

Rhea Nickerson, PhD Candidate
Supervisor: Dr. Zhenyu Cheng, Department of Microbiology & Immunology

Sayanti Dey, PhD Candidate
Supervisor: Dr. Andrew Makrigiannis, Department of Microbiology & Immunology

Shirin Mehrpooya, MSc Candidate
Supervisor: Dr. Alexa Yakubovich, Department of Community Health and Epidemiology

Poster Presentations - 12:00pm and 1:15pm

Abbey Saunders, MSc Candidate
Supervisor: Dr. Morgan Langille, Department of Microbiology & Immunology

Andrew Michels, MSc Candidate
Supervisor: Dr. Robert Adamson, Department of Biomedical Engineering School

Anu Jose, PhD Candidate
Supervisor: Dr. Petra Kienesberger, Department of Biochemistry & Molecular Biology

Arash Mohammadi Matak, PhD Candidate
Supervisor: Dr. Francesca Di Cara, Department of Microbiology & Immunology

Bakhmala Khan, MSc Candidate
Supervisor: Dr. Paola Marcato, Department of Pathology

Berke Sahin, MSc Candidate
Supervisor: Dr. Sanja Stanojevic, Department of Community Health and Epidemiology

Brianna Samson, MSc Candidate
Supervisor: Dr. Corey Smith, Department of Biomedical Engineering School

Calum Blackwood, MSc Candidate
Supervisor: Dr. James Kramer, Department of Biochemistry & Molecular Biology

Cameron MacGillivray, MSc Candidate
Supervisor: Dr. Tomas Hajek, Department of Psychiatry

Haya Abdelwahab, PhD Candidate
Supervisor: Dr. Ketul Chaudhary, Department of Physiology & Biophysics

Ian Armstrong, MSc Candidate
Supervisor: Dr. Patrick McGrath, Department of Psychiatry

Jennika Veinot, PhD Candidate
Supervisor: Dr. Javeria Hashmi, Department of Medical Neuroscience

Kyle Medd, PhD Candidate
Supervisor: Dr. Locke Davenport Huyer, Department of Biomedical Engineering School

Mackenzie Searle, MSc Candidate
Supervisor: Dr. Kishore Pasumarthi, Department of Pharmacology

Mahdiye Mohati, MSc Candidate
Supervisor: Dr. Francesca Di Cara, Department of Microbiology & Immunology

Mark Hanes, PhD Candidate
Supervisor: Dr. Jean Marshall & Dr. Carman Giacomantonio, Department of Pathology

Meghana Janardhanan, PhD Candidate
Supervisor: Dr. Manuel Mattheisen & Dr. Ying Zhang, Department of Medical Neuroscience

Nathan Purvis, MSc Candidate
Supervisor: Dr. Nik Thomas, Department of Microbiology & Immunology

Parnian Jahanbani, PhD Candidate
Supervisor: Dr. Jun Wang, Department of Microbiology & Immunology

Parsa Kamali, MSc Candidate
Supervisor: Dr. Greg Fairn & Dr. Geoffrey Hesketh, Department of Biochemistry & Molecular Biology

Pedro Zavagli Suarez, PhD Candidate
Supervisor: Dr. Alexander Quinn, Department of Physiology & Biophysics

Riley MacKinnon, MSc Candidate
Supervisor: Dr. Alejandro Lomniczi, Department of Physiology & Biophysics

Saeideh Jamali, PhD Candidate
Supervisor: Dr. Jun Wang, Department of Microbiology & Immunology

Yatin Singh, MSc Candidate
Supervisor: Dr. Javeria Hashmi, Department of Medical Neuroscience

Abstracts

Excellence in Research Award Winners

Jack Case, MSc Candidate

Supervisor: Dr. Denys Khaperskyy, Associate Professor – Department of Microbiology and Immunology

Impaired host shutoff is a fitness cost associated with baloxavir marboxil resistance mutations in influenza A virus PA/PA-X nuclease domain

The polymerase acidic (PA) protein is a subunit of the influenza A virus (IAV) RNA-dependent RNA polymerase and the direct target of the anti-influenza drug baloxavir marboxil (BXM). As with other direct-acting antivirals, treatment with BXM selects for viruses carrying resistance mutations. If these mutations have negligible fitness costs, resistant viruses can spread widely and render cap-snatching endonuclease inhibitors like BXM obsolete. Multiple BXM resistance mutations in the nuclease domain of PA have been identified, with I38T and I38M amino acid substitutions occurring frequently. These mutations have minimal to no effects on viral polymerase activity, virus replication, or transmission. However, for reasons that are not well understood, viruses with BXM resistance substitutions have not been able to compete with parental wild-type strains. The IAV genome segment encoding PA also encodes the host shutoff nuclease PA-X, which shares the endonuclease domain with PA but has a unique C-terminal domain generated by ribosomal frameshifting during translation. Unlike their effects on PA activity, the effects of BXM or the I38T/M substitutions on PA-X function remain uncharacterized. In our work, for the first time, we directly examine the effects of baloxavir and I38T/M substitutions on PA-X activity. Most importantly, we demonstrate that the I38T/M resistance mutations significantly impair the host shutoff activity of PA-X proteins from different IAV strains of H1N1, H3N2, and H5N1 subtypes. Our work reveals that the deleterious effects of I38T/M on PA-X function may represent an important barrier to the spread of BXM-resistant viruses.

Zachary Long, PhD Candidate

Supervisor: Alexander Quinn, Professor – Department of Physiology and Biophysics

Mathematical Models of the Zebrafish Atrial and Ventricular Action Potential and Calcium Transient and Chamber-Specific Effects of Autonomic Control

Zachary Long[1], Ludovica Cestariolo[2,3], Arie Verkerk[4], Jose Rodriguez Matas[3], T Alexander Quinn[1,6]

[1]Physiology & Biophysics, Dalhousie University, Halifax, Canada
[2]Department of Biotechnology & Biosciences, Università degli studi di Milano-Bicocca, Milan, Italy
[3]Laboratory of Biological Structure Mechanics, Department of Chemistry, Materials & Chemical Engineering, Politecnico di Milano, Milan, Italy
[4]Medical Biology, Amsterdam UMC, Amsterdam, The Netherlands
[5]Centre for Research & Innovation in Bioengineering, Universitat Politècnica de València, Valencia, Spain
[6]School of Biomedical Engineering, Dalhousie University, Halifax, Canada

The zebrafish is an increasingly popular model for studying cardiac electrophysiology and autonomic control, due to its physiological similarity to humans and unique experimental accessibility. While computational modelling of the action potential (AP) and calcium (Ca^{2+}) transient (CaT) is advanced in mammals, zebrafish-specific models are lacking. We developed novel computational models of the zebrafish atrial and ventricular AP and CaT, then used them to investigate chamber-specific autonomic effects on electrophysiology, Ca^{2+} dynamics, and mechanical activity.

Ion current formulations from the 2004 Ten Tusscher and Panfilov model were re-parametrised using zebrafish patch-clamp data, with removal of the transient outward current and addition of the T-type Ca^{2+} current. The model was calibrated with microelectrode recordings and optical mapping of the AP and CaT in isolated adult zebrafish atria and ventricles. Simulations were compared to pharmacological experiments targeting sympathetic and parasympathetic receptors. Preliminary mechanical data were also collected to assess autonomic-induced changes in contractile force.

The new computational models reproduced the zebrafish AP, CaT, and rate-dependent responses. Pharmacological experiments showed responses largely consistent with mammalian data, though chamber-specific differences emerged: adrenergic stimulation prolonged the atrial AP and CaT but shortened the ventricular AP, while cholinergic stimulation caused AP shortening in the atrium and prolongation in the ventricle. Adrenergic stimulation increased peak contractile force while cholinergic stimulation reduced it, consistent with human data, informing future model development.

We present the first zebrafish-specific computational models of the atrial and ventricular AP and CaT, which represent valuable tools for future experimental-computational investigations of cardiac (patho)-physiology and pharmacological interventions using zebrafish.
We present the first zebrafish-specific computational models of the atrial and ventricular AP and CaT, which represent valuable tools for future experimental-computational investigations of cardiac (patho)-physiology and pharmacological interventions using zebrafish.

Dr. Elena Koning, Postdoctoral Fellow

Supervisor: Dr. Aaron Keshen, Associate Professor – Department of Psychiatry

Exploring the Therapeutic Potential of Psilocybin in Eating Disorder Treatment: Bridging Neurobiology, Lived Experience, and Advanced Clinical Study Design

Eating disorders are severe psychiatric illnesses affecting 1-3% of the global population. Cognitive behavioural therapy for eating disorders (CBT-ED) is the leading evidence-based treatment, but sustained recovery is only achieved in 40-50% of patients, and 25-50% drop out prematurely due to factors such as comorbid psychopathology, cognitive inflexibility, and experiential avoidance. Psilocybin treatment (PT) involves the administration of psilocybin with psychological support and has demonstrated robust antidepressant effects, increased neuroplasticity, and disruption of neural networks associated with cognitive rigidity. These mechanisms suggest PT may enhance engagement, learning, and behavioural change when delivered adjunctively with CBT-ED, thereby improving treatment outcomes.

Despite promising preliminary data in EDs, no studies have examined PT for bulimia nervosa (BN), or as an adjunct to evidence-based ED psychotherapy. Further, major knowledge gaps remain in patient perspectives and psychedelic trial design. The current postdoctoral research program aims to address these gaps through a two-phase approach. Phase 1 is a large-scale, deception-based online survey (N=300) of adults with an ED diagnosis. Through a mixed-methods approach, the survey will assess perspectives on psychedelics, perceived risks/benefits, expectations for a combined PT/CBT-ED intervention, and factors influencing adherence. Findings will directly inform modifications to the PT/CBT-ED protocol and clinical trial design. Phase 2 is a multi-site, double-blind feasibility RCT (N=70) evaluating therapeutic (25 mg) versus sub-therapeutic (5 mg, active comparator) PT delivered in two sessions during 10-week CBT-ED for BN. Primary outcomes include feasibility (enrolment, safety, tolerability, acceptability, blinding). Secondary outcomes examine preliminary effects on ED psychopathology and neurocognitive mechanisms.

Together, this is the first psychedelic research program for EDs in Eastern Canada. It will generate high-impact data to inform safe, acceptable, and effective PT protocols, advance mechanistic understanding, support definitive trials, and guide clinical guidelines and policy decisions for difficult-to-treat neuropsychiatric conditions.

Dr. Vanessa DeClercq, Research Associate

Supervisor: Dr. Morgan Langille

Leveraging microbiomes from multiple body sites to predict lung cancer outcomes

There is evidence that the gut microbiome can influence the effectiveness of cancer therapies and that some microbes directly cause specific types of cancers. Unique microbial profiles have also been described in tumours and other low-biomass samples; however, recent controversy has highlighted the challenges of utilizing these microbiomes for cancer diagnosis and treatment. This work aims to address current challenges with low-biomass samples and identify microbial biomarkers that can be used to predict lung cancer.

This is an observational prospective study of patients undergoing curative surgery for early-stage non-small cell lung cancer (NSCLC). Participants provided samples from multiple body sites (saliva, tumour, adjacent tissue, and blood). Extracted DNA underwent full length PCR amplification and PacBio sequencing of the 16S rRNA gene. Due to failed full length sequencing on low biomass samples, a second nested PCR amplification of the V6-V8 region and subsequent sequencing on the Illumina MiSeq was performed. A subset of samples was quantified using QIAcuity digital PCR and further analyzed by metagenomic sequencing on the NextSeq2000. Taxonomic profiles were analyzed in relation to clinical parameters including cancer stage, PDL1 status, and survival outcomes.

Our pilot data demonstrates that saliva and bronchoalveolar lavage fluid have over a hundred observed features while tumour, adjacent tissue, and blood have less than 10 features, similar to negative controls. Of concern is the lack of consistency and reproducibility with samples of low microbial biomass. On the other hand, microbially rich samples with robust profiles are associated with clinical variables.

Current methodologies present challenges with samples of low microbial biomass, making it difficult to detect signals that are distinct or above levels found in collection and processing environments. This study provides important insights into site-specific microbiomes and challenges when assessing the tumour microbiome and other low biomass samples as biomarkers for lung cancer.

Platform Presentations

Ahmed Ramadan, PhD Candidate

Supervisor: Dr. Alexander Quinn

Additional Authors: Matthew R. Stoyek

Optical Ablation with Optogenetics in the Whole Zebrafish Heart

Abstract

Catheter ablation is a widely used therapy for cardiac arrhythmias, involving the irreversible destruction of myocardium to disrupt pathological electrical circuits responsible for arrhythmia sustenance. Although often highly effective, this approach permanently scars cardiac tissue, alters its structure, and lacks the ability to dynamically adjust lesion size or location once ablation has occurred. Optogenetics, involving the use of genetically expressed light-activated ion channels ('channelrhodopsins') for the manipulation of cardiac electrophysiology with high spatiotemporal resolution, offers a fundamentally different anti-arrhythmic strategy. The recently discovered potassium-conducting channelrhodopsin ('HcKCR1') has emerged as a promising optogenetic tool for suppressing pathological electrical excitation, as it can drive membrane potential towards resting values ('repolarization') upon optical stimulation. To investigate the utility of HcKCR1 to target aberrant electrical activity, ventricular action potentials were recorded by microelectrode and fluorescence voltage imaging in adult zebrafish hearts with cardiac-specific expression of HcKCR1. HcKCR1 was locally activated by a 400 µm spot of LED light on the ventricular free-wall of varying intensity (0.02 – 0.9 mW/mm2). Results from both microelectrode and fluorescence voltage imaging showed intensity-dependent action potential shortening with HcKCR1 activation, due to accelerated repolarization, which returned to pre-light values post optical stimulation. In fluorescence voltage imaging experiments, propagating electrical waves were blocked in the optical 'lesion'; demonstrating spatial control as regions outside of the spot of light were unaffected. Overall, HcKCR1 stimulation can be dynamically adjusted to suppress electrical waves with high precision in a reversible manner.

Brianna Latremouille, PhD Candidate

Supervisor: Dr. Alexander Quinn

Effects of Increased Afterload on Left and Right Ventricular Cardiomyocyte Mechanical Function

Abstract

Background: The acute response of individual cardiomyocytes (CM) to stretch ('preload') is well-defined, however due to difficulties in the experimental control of the load against which CM contract ('afterload'), its direct effects are poorly understood. Hydrogel techniques are recently being employed to overcome this limitation. Yet, how CM respond to acute (patho)physiological increases in afterload and whether inter-chamber differences exist, is unknown.

Objective: Determine the responses of right and left ventricular CM to acute (patho)physiological increases in afterload.

Methodology: Adult rabbit isolated left (LV) and right (RV) ventricular CM were studied under varying levels of afterload using a gelatin-methacrylol (GelMa) hydrogel of different concentrations (7.5%, 10%, 12.5%). Hydrogels were cured with ruthenium-sodium persulfate exposed to 300W/m2 blue light (450?20nm) for 5 min and loaded cells were compared to blue-light exposed unloaded controls. Contractile function was measured by sarcomere length (SL) tracking at 10min intervals across 30min.

Results: Mechanical parameters of LV CM in 7.5% GelMa did not differ from control. At 0-10 min, LV CM in 10% GelMa had greater mechanical function than control ($p<0.05$). LV CM under high load conditions (12.5% GelMa), and RV CM under all levels of load took longer to initiate contraction but had increased mechanical function once they started (10-30 min, $p<0.05$).. Unloaded LV CM have greater mechanical function than unloaded RV CM ($P<0.05$), however CM from both ventricles respond similarly to loaded conditions.

Significance: This work will provide pathophysiological insight into the chamber-specific effects of increased ventricular afterload to help guide future novel therapeutic innovations

Cameron Calder, MSc Candidate

Supervisor: Dr. Javeria Hashmi

Chronic pain uncouples functional brain network segregation from cognitive performance in aging

Abstract

Background: Chronic pain disproportionately affects older adults and is bidirectionally linked with cognitive decline, yet the brain mechanisms connecting these processes remain an emerging area of investigation. We have recently shown that functional brain network segregation, the degree to which brain networks operate independently of one another, tends to decline with age while its preservation supports cognitive performance in healthy older adults (Calder et al). Whether chronic pain disrupts this relationship has not yet been examined.

Methods: Resting-state functional MRI and cognitive assessments were completed by 60 healthy controls and 141 individuals with chronic pain. Cognitive performance was evaluated across working memory, cognitive inhibition, and pain expectation bias. Brain network segregation was quantified using the system segregation metric. PROCESS moderation analysis (SPSS) was used for exploring interaction effects.

Results: Overall measures of brain network segregation and cognition did not differ between age and sex matched groups. However, chronic pain patients showed greater age-related declines across multiple cognitive domains including working memory, inhibitory control, and processing speed, whereas healthy controls showed age-related decline only in inhibitory control. Despite this accelerated cognitive aging, the relationship between segregation and cognition was reversed in chronic pain: whereas higher segregation predicted better working memory in healthy controls, it predicted worse working memory in chronic pain patients. This reversal was particularly pronounced in younger adults with chronic pain.

Conclusions: Chronic pain is associated with an altered brain aging trajectory in which network segregation is relatively preserved but becomes functionally maladaptive, predicting worse rather than better cognitive performance. These findings suggest that preserved network segregation cannot be assumed to be neuroprotective in the presence of chronic pain, with important implications for interpreting neuroimaging biomarkers and developing cognitive interventions in this population.

Claerwen Sladen-Dew, MSc Candidate

Supervisor: Dr. Alexander Quinn

Additional Authors: Dr. Alexander Quinn

Determinants of Atrial Mechano-Arrhythmogenesis

Abstract

Feedback of mechanics to the heart's electrical system is essential for regulating cardiac output. However, in certain states this feedback may contribute to arrhythmia development ('mechano-arrhythmogenesis'). In the ventricle, it has been shown that arrhythmias may arise from mechanically-induced electrophysiological changes interacting with structural and functional alterations found in various cardiac diseases. In the atria, it has been suggested that atrial fibrillation – the most prevalent tachyarrhythmia – may be triggered by acute electrophysiological fluctuations, including altered excitability, repolarization, conduction, and calcium dynamics, driven by acute (patho-)physiological changes in the heart's mechanical load. Despite the growing appreciation for the potential importance of mechano-arrhythmogenesis in atrial fibrillation, underlying mechanisms remain poorly understood. Our goal was to explore the possible contribution of transient receptor potential ankyrin 1 channels (TRPA1), ATP-activated potassium channels (KATP; active in hypoxic conditions), acetylcholine-activated potassium channels (KAch), and microtubule density and detyrosination to atrial mechano-arrhythmogenesis.

Using freshly excised left atrial tissue from New Zealand white rabbits, functional fluorescence imaging of voltage and calcium, and controlled, transient tissue stretch, we targeted the potential modulators of mechano-arrhythmogenesis using pharmacological interventions. To date, we have observed that transient fluctuations in mechanical load result in acute arrhythmogenic events, which are mediated by the level of stretch, KAch activation and increased microtubule density and detyrosination.

While the causes of atrial arrhythmias are multi-faceted, mechano-sensitive mechanisms are hypothesized to be a key contributor. Through this study, we have begun to deepen our understanding of atrial mechano-arrhythmogenesis and explore molecular targets for novel anti-arrhythmic therapies.

Daniel Basso, MSc Candidate

Supervisor: Dr. Sherry Stewart & Dr. Jillian Filliter

Additional Authors: Farquhar, A., Chorney, J., Yakovenko, I., Okanya, A., Lunn, B.

Investigating the Substance Use Motives of Autistic Emerging Adults: A Mixed-Methods Participatory Study

Abstract

Background

Emerging research suggests: 1) autistic individuals may be at a higher risk for substance use; and 2) substance use may present differently in autistic individuals. However, little else is known about substance use in autistic populations, including why autistic people may choose to engage in substance use. To fill this latter gap, our participatory mixed-methods study recruited 13 autistic emerging adults to investigate their substance use motives.

Method

All participants: were 18-29; had a formal diagnosis of autism spectrum disorder (or equivalent); had used substances 6+ times in their lifetime; lived in Canada for most of adolescence; and did not display high-risk suicidality. First, they completed an online survey containing demographic questions, and validated autism, mental health, and substance use measures. Then, they completed an ~2-hour semi-structured interview focused on their substance use history. Thematic analysis was then used to identify substance use motives in interview transcripts, with survey data being used to help characterize the sample.

Results

Survey data revealed that alcohol, cannabis, and hallucinogens were the most common substance types used. Furthermore, 9 participants (69%) reported at least near-daily use of at least one substance during their 3-month peak use period. Interview data revealed two potential population-specific motives: camouflaging (societal conformity) and sensory-coping, as well as multiple potential population-specific presentations of established motive (e.g., a sensory-focused presentation of enhancement motives).

Conclusion

Results suggest population-specific motives and motive presentations for substance use, further supporting the need for autism-specific adaptations to substance use measures and interventions

Ebadullah Kabir, PhD Candidate

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Butyrylcholinesterase Activity as a Biomarker for Alzheimer's disease.

Abstract

Background:

Alzheimer's Disease (AD) is characterized by progressive memory and cognitive decline. Despite developments in diagnostic tools, the quest to identify an AD-specific biomarker continues. The enzyme butyrylcholinesterase (BChE) may be a suitable target for this research. BChE primarily associates with amyloid-β (Aβ) plaques in AD but not with plaques in cognitively normal brains with Aβ plaques (NwAβ), signifying the involvement of BChE in AD pathogenesis. Studies of the orbitofrontal cortex suggest that BChE may be a better diagnostic marker for AD.

Objective & Hypothesis:

We investigated the left temporopolar region (TPR), which, in AD, is associated with visual and language deficits. We quantitatively assessed the ratio of BChE-Aβ deposition and hypothesized that this ratio would be higher in AD brains compared to NwAβ.

Methods:

Sex- and age-matched TPR tissue blocks were obtained from the Maritime Brain Tissue Bank. Cases included 10 AD, 6 NwAβ, and 4 cognitively normal brains without Aβ plaques (N). TPR Brodmann areas (BA) were defined based on previous studies. Tissue sections were stained using immunohistochemical and histochemical techniques to identify Aβ and BChE pathology, respectively, and were photographed. Aβ- and BChE-positive plaque loads were quantitatively measured as percentages of the total area in each BA. We compared BChE/Aβ ratios across BAs between AD and NwAβ.

Results:

The ratio of BChE-Aβ deposition was higher, but not significant, in AD brains compared to NwAβ brains across all the BAs of the TPR.

Conclusion:

Although not significant, the higher proportion of BChE across all BA of the TPR suggests its potential as a better biomarker for AD than Aβ. Future work should investigate larger sample sizes, and more neuroimaging studies are required to further investigate BChE as a diagnostic tool for AD.

Jessica Latimer, PhD Candidate

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Co-Infection of Mirusviruses and Giant Viruses in a Marine Protist

Abstract

The thraustochytrids are single cell eukaryotes renowned for their production of polyunsaturated fats and recently gained attention as only known system to study mirusvirus expression in Aurantiochytrium limacinum. Here, we generate a long-read assembly of the well-known thraustochytrid Schizochytrium sp. 20888 that reveals three circular virus genomes: two mirusviruses and one Nucleocytoviricota. This is the second demonstration of mirusvirus in a protist and first evidence of mirusvirus co-infection with a Sicyoidochytrium minutum DNA virus (SmDNAV). The SmDNAV was first identified as a lytic virus with a very small host range constrained to S.minutum, but with increased genomic sampling it now appears to be present and expressed in several thraustochytrids, including culture collection strains, without crashing the cultures. The SmDNAV genomes are large (~200 kb) and lack numerous genes considered essential for the replication of giant DNA viruses, suggesting they rely on their hosts to replicate. This system presents a unique opportunity to study fine scale viral evolution to improve our understanding of co-infection and closely related viruses can be lytic or persistent.

Julia Fraiha-Pegado, PhD Candidate

Supervisor: Dr. Tomas Hajek

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Brain Structural Improvements Following Bariatric Surgery: A Coordinate-Based Meta-Analysis

Abstract

Introduction: Obesity is increasingly linked to reduced grey matter (GM) volume, white matter integrity, and functional connectivity, specifically within the hippocampus. While bariatric surgery is a highly effective intervention for significant weight loss and reducing mortality, its specific neuroanatomical impacts remain poorly synthesized. This study aimed to appraise available literature and quantify the extent of brain changes following surgical weight loss interventions.

Methods: We conducted a systematic search using Pubmed and Scopus to identify longitudinal MRI studies investigating brain structure changes after bariatric surgery. We used Seed-based d Mapping (SDM-PSI) to conduct a coordinate-based meta-analysis. Resulting GM volume changes were then visualized using MRIcronGL. Study quality was assessed using the Newcastle-Ottawa Scale (NOS)

Results: Five studies met inclusion criteria (n= 161, mean age= 27.6 – 51.1 years). Following surgical interventions individuals lost on average, between 8.5 to 11 BMI points. Meta-analysis results showed significant GM increases in the right cerebellum at an average follow-up of 8.4 months (SDM-Z= 2.59, p=0.019) even after family-wise error correction. At an uncorrected level, additional improvements were observed in right lenticular nucleus/putamen, right fusiform gyrus, BA48, left cerebellum and right lingual gyrus.

Conclusions: Our findings suggest that significant weight reduction following bariatric surgery is linked to overall improvement in several brain regions, most pronounced in the right cerebellum. Our findings indicate that surgical weight loss may reverse some obesity related neuroanatomical declines. Future research should focus on incorporating longer follow-up periods as well as cognitive assessments to determine if these structure changes translate into functional improvements.

Samuel Silva, PhD Candidate

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Did the 2023 wildfires affect emergency department visits for respiratory and cardiovascular causes in Nova Scotia? A time-series study

Abstract

Background:

Nova Scotia (NS) experienced the most destructive wildfire season on record in 2023 as measured by total forest area burned. The Western and Central health management zones were particularly affected by major wildfires (Barrington Lake and Tantallon wildfires). Particulate Matter 2.5 (PM2.5) emitted from wildfires has the potential to damage the respiratory and cardiovascular systems, thus, potentially increasing healthcare utilization.

Objectives:

To determine the associations between 1) wildfires and 2) daily PM2.5 levels with respiratory and cardiovascular emergency department (ED) visits in NS in 2023.

Methods:

For Objective 1, we conducted an interrupted time-series study. Our outcome was daily number of ED visits for respiratory and cardiovascular causes in the 30 days following the start of the wildfires in the NS Western and Central zones. ARIMAX models were fitted to the 1-year pre-wildfires data (separately by zone) and used to predict the number of ED visits in the wildfire period. Observed:expected ratios (OE) were generated. Excess visits were calculated.

For Objective 2, ground-level PM2.5 data was used from two air quality monitoring stations (one from each zone) to assess the association between daily PM2.5 levels and respiratory and cardiovascular ED visits following the start of the wildfires. Negative binomial models were used, and non-linear relationships and lag effects (up to 7 days) were investigated.

Results:

No evidence was found that wildfires were associated with respiratory and cardiovascular ED visits in the Western (excess visits:78; 95%PI:-508 to 472) and Central (excess visits:66; 95%PI:-795 to 753) zones. However, evidence was found that higher PM2.5 levels were associated with fewer ED visits on the same day (IRR 0.89; 95%CI 0.79-1.01), and greater visits 2 days later (exponential relationship; p=0.03) in the Western zone.

Conclusion:

Preparedness and mitigation strategies could consider using daily PM2.5 levels as indicators of daily fluctuations in respiratory and cardiovascular ED visits during wildfires.

Shannen Grandy, PhD Candidate

Supervisor: Dr. Zhenyu Cheng

Pseudomonas aeruginosa elastase B activates the integrated stress response and autophagy in lung epithelial cells

Abstract

Pseudomonas aeruginosa is a Gram-negative bacterium and opportunistic pathogen and the most common pathogen to cause chronic lung infection in CF patients. P. aeruginosa secretes an abundance of virulence factors including proteases and elastases that, in combination with exacerbated lung inflammation, cause significant damage to host lungs. Our lab has found that inhibiting the integrated stress response (ISR) reduces inflammation, making the ISR a promising therapeutic target. The ISR consists of sensor kinases HRI, PKR, PERK, and GCN2, which become activated through various forms of cellular stress. These kinases phosphorylate eIF2α, inducing expression of downstream effector proteins such as the transcription factor ATF4. We identified the P. aeruginosa secreted protease elastase B (LasB) to be a strong activator of the ISR. By using cell lines which lack one of the ISR kinases, we determined that GCN2 was required for LasB to activate the ISR. Activation of the GCN2-ATF4 signalling axis has been linked to autophagy which led us to assess the accumulation of the classic autophagy marker LC3-II. Wildtype (WT) and GCN2-/- 16HBE cells were pre-treated with chloroquine (Cq), an inhibitor of autophagic flux, and LasB. LasB in combination with Cq increased the accumulation of LC3-II compared to Cq alone and this was not dependent on GCN2. Additionally, we found that LasB was able to induce LC3-II accumulation in the macrophage cell line THP-1, indicating that this phenotype is not cell type specific. Finally, we have utilized an aqueous two-phase system (ATPS) to model P. aeruginosa infection with 16HBE cells for up to 16 hours. Using the ATPS model we have found that P. aeruginosa strains lacking LasB show delayed induction of autophagy compared to LasB expressing strains. These results suggest LasB has an important role in the timing of autophagy induction during P. aeruginosa infection.

Tanzima Fariha, MSc Candidate

Supervisor: Dr. Corey Baimel

Mapping the amygdala circuitry

Abstract

Motivated, goal-directed behaviours exist to sustain life and allow both humans and animals to learn to navigate the world while pursuing rewards and avoiding threats. While humans possess cognitive abilities that set us apart from other species, we share fundamental emotional behaviours with other species.

Responses to emotional stimuli are typically adaptive but can also be maladaptive. For example, in addiction, pursuit of the substance becomes excessive and harmful. One brain region that mediates such reward-driven behaviors is the basolateral amygdala (BLA). The BLA acts as a central hub, receiving inputs from and sending widespread projections to various brain regions. The BLA sends dense projections to the nucleus accumbens (NAc) which has been heavily implicated in reward-seeking behaviors. The NAc is divided into the medial and lateral shell, each related to different aspect in reward-driven behaviors.

Preliminary data suggest that distinct populations of BLA neurons project to these subregions and are differentially engaged during reward learning; however, the circuit level mechanisms driving these differences remain unclear. To assess projections from the BLA, we injected a retrograde viral tracer in the medial or lateral shell of the NAc and to identify inputs to the BLA, anterograde viruses were injected into the ventral hippocampus and prefrontal cortex, which are regions that send projections to this region.

Ongoing analyses are confirming that distinct populations of BLA neurons project to the medial and lateral shell of the NAc. In parallel, mapping efforts are underway to characterize distinct patterns of axonal distribution onto the BLA. Better understanding of the circuitry meditating reward-driven behaviors will aid in identifying better therapeutic treatment.

Poster Presentations

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Functional and dietary characterization of metagenome-assembled genomes in paediatric Crohn's disease following nutritional therapy

Abstract

Crohn’s disease (CD) exclusion diet with partial enteral nutrition (CDED+PEN) and exclusive enteral nutrition (EEN) effectively induce remission in mild-to-moderate pediatric CD1. In nutrition-responsive patients, prolonged dietary therapy shifts the gut microbiome and metabolome toward a healthy state; however, dysbiosis often persists despite sustained treatment, reflecting both excess abundance of Proteobacteria and reduced Firmicutes2. Alterations in microbial amino acid metabolism, including glutamate metabolism, have been associated with disease activity and sustained remission following dietary therapy3,4. Higher-resolution characterization of microbial metabolic capacity is therefore needed to elucidate microbial functions relevant to intestinal inflammation and response to dietary therapy.

We aim to use metagenome-assembled genomes (MAGs) to characterize genome-level differences in microbial amino acid metabolism pathways and asses their association with nutritional therapy-induced remission and dietary adherence in paediatric CD.

PacBio HiFi long-read and Illumina short-read shotgun metagenomic sequencing were performed on 42 longitudinal stool samples collected at weeks 0, 6, and 12 from treatment-naïve mild-to-moderate pediatric CD patients receiving either CDED+PEN (n=11) or EEN (n=7) from a prior randomized controlled trial (NCT01728870). Clinical remission is defined as a Pediatric Crohn’s Disease Activity Index ≤10 at week 6. Illumina data was taxonomically profiled using Kraken2 and Bracken, while PacBio HiFi data was processed using Anvi’o-based methods. Future functional annotation will focus on microbial pathways involved in glutamate metabolism and genes associated with adaptation to intestinal inflammation.

MAGs were obtained from long-read assemblies (MEGAHIT) using an Anvi’o based workflow with binning performed by MetaBAT2, MaxBin2, and CONCOCT, and dereplication of bins completed using DAS Tool. MAG quality was assessed using CheckM2 and taxonomic assignment was performed with GTDB-Tk. Anvi’o analyses yielded 0-13 high-quality MAGs per sample, with Bacteroides and Phocaeicola among the most recovered genera in high-depth samples.

This MAG-resolved framework will enable detailed characterization of microbial metabolic capacity and its relationship to diet-induced sustained remission.

Ahsan Malick, MSc Candidate

Supervisor: Dr. Francesca Di Cara

Role of taurine metabolism in inflammation and gut-brain communication in Drosophila melanogaster

Abstract

Neurodegenerative diseases (NDs) are conditions that cause strain to both healthcare and quality of life. Despite their burden, the aetiologies of NDs are poorly understood. Recent evidence points to changes in gut metabolism as an early mechanism influencing gut-brain communication and eventually onset of NDs. Under metabolically perturbed conditions, certain metabolites/nutrients could be endogenously upregulated or exogenously ingested to manage damage associated with metabolic deficiency. One such metabolite is taurine, an amino sulfonic acid with essential physiological and signaling functions. Previous lab work on Drosophila melanogaster (fruit fly) found that better aging flies with no ND symptoms produce higher taurine in their guts. Thus, I hypothesized that taurine would be a neuroprotective factor in the gut-brain axis that, when depleted, leads to ND-like symptoms. To test this hypothesis, I utilized the UAS-Gal4 system to create transgenic Drosophila melanogaster flies expressing small-interfering RNA sequences to knockdown a gene involved in peroxisome biogenesis, which are key metabolic organelles, as well as taurine synthesis enzymes through RNA-mediated interference. I utilized the negative geotaxis climbing assays (NGCA) to test for locomotor ability in wild-type and mutant flies treated with either taurine-supplemented food or a regular cornmeal diet (CMD). Results showed that flies climbed better over aging on a taurine diet compared to a CMD diet. Moreover, I performed immunofluorescence experiments on the guts of control and mutant flies fed with and without taurine, which indicated that taurine supplementation had noticeable changes on gut morphology. Finally, I looked at expression of neuropeptide signals in the different conditions, indicating taurine was affecting expression of known neuroinflammatory signals. Overall, my study in the fruit fly, a validated model to study neurodegeneration and inter-organ communication, helps identify conserved mechanisms that will help to define the onset of sporadic NDs in humans.

Alireza Aleali, MSc Candidate

Supervisor: Dr. Javeria Hashmi

Disentangling feature-domain and model-complexity contributions to chronic pain phenotype classification

Abstract

Chronic pain exhibits substantial inter-individual heterogeneity across sensory, functional, and affective dimensions, motivating phenotype-based approaches such as Pain-Disability-Affect (PDA) stratification. Machine-learning methods are increasingly used for chronic pain phenotyping; however, variability in feature selection, modality integration, and model architecture limits understanding of how predictive performance depends on feature domain, model complexity, and analytical strategy. In particular, the relative contributions of behavioural measures, quantitative sensory testing (QST), and neuroimaging features remain unclear, as does whether ensemble learning offers advantages over well-regularized single models.

We applied an agnostic, stepwise machine-learning framework to classify individuals with chronic pain (N = 140) into predefined high versus low PDA phenotypes. Predictor variables were organized into four feature baskets: (i) behavioural and clinical measures, (ii) behavioural plus schema-derived QST metrics, (iii) resting-state functional connectivity (rsFC) features summarized by principal components, and (iv) all features combined. Preprocessing, feature selection, and model training were conducted within cross-validation folds to prevent information leakage. Multiple classifiers were combined using a stacking ensemble, with performance evaluated using accuracy and weighted F1 score on a held-out test set. Model complexity and robustness were assessed using learning curves, reduced-feature models, and leave-one-out cross-validation.

Models trained on behavioural features alone demonstrated the most robust performance. Adding QST, rsFC, or multimodal features did not improve classification, and rsFC alone performed near chance. The stacking ensemble did not outperform the strongest individual classifier, with predictions largely driven by a tree-based model. Reduced behavioural models retained comparable performance.

These findings indicate that behavioural features primarily support discrimination of PDA phenotypes, while added feature and model complexity do not necessarily improve performance, supporting parsimonious strategies for chronic pain stratification. They further suggest that complex modalities such as neuroimaging require a clear hypothesis to be informative. Without such constraints, their inclusion may add noise without improving predictive performance.

Aminat Mustapha, MSc Candidate

Supervisor: Dr. Alon Friedman

CB_2 Modulation, Hypoxia, and Recovery After TBI

Abstract

Traumatic brain injury (TBI) initiates secondary injury cascades that critically shape functional outcomes, with cerebral hypoxia emerging as a central and potentially modifiable mechanism. Despite similar primary insults, affected individuals may diverge into susceptible or resilient recovery phenotypes, though the biological basis of this variability remains unclear. Cannabinoid receptor 2 (CB_2) signaling, a key regulator of inflammation and neurovascular function, represents a promising pathway through which hypoxia-related processes may be modulated.

This study investigated the relationship between hypoxia, CB_2-targeted intervention, and recovery phenotypes following TBI. Using a preclinical model, animals were stratified according to Neurological Severity Score (NSS) into susceptible and resilient groups. Experimental conditions included isoflurane-treated sham controls, TBI-only, and TBI animals treated with the selective CB_2 agonist JWH-133. Outcome measures included behavioral assessment and physiological indicators of oxygenation (peripheral oxygen saturation; SpO_2).

TBI induced significant alterations in blood oxygen saturation, demonstrating acute dysregulation of oxygen homeostasis following injury. Differences in SpO_2 dynamics across groups suggest that hypoxia is not only a consequence of TBI but also contributes to variability in recovery trajectories. Behavioral deficits were observed acutely post-injury, with trends indicating that CB_2 activation may modulate neurological outcome.

These findings position hypoxia as a central mechanism underlying divergent recovery phenotypes and suggest that early oxygen dysregulation may serve as a predictive marker of susceptibility versus resilience following TBI. They further support CB_2 signaling as a potential therapeutic target for modifying post-traumatic recovery trajectories.

Andrew Michels, MSc Candidate

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Freehand 3D Ultrasound Imaging of the Femoral Head

Abstract

Keywords: 3D imaging, arthroscopy, femoroacetabular impingement, segmentation, ultrasound

Objective: Femoroacetabular impingement (FAI) is a leading cause of hip pain. This orthopedic condition is commonly treated through arthroscopic resection of the femoral head, a minimally invasive surgical procedure. The current standard-of-care includes a pre-operative computed tomography (CT) scan to provide a 3D view of the target cam lesion and surrounding boney area. We are seeking to replace this CT with a non-ionizing and cost-effective modality: ultrasound.

Methods: The system attaches an optical tracker to a conventional ultrasound probe to locate 2D ultrasound image frames in virtual 3D space, enabling volumetric reconstruction. A convolutional neural network (CNN) segmentation model is applied to the 2D ultrasound images, extracting the bone surface as a 1-pixel wide contour. Points sampled from each contour are transformed into 3D space to generate a point cloud with a typical density of 250,000 points per scan. Finally, a best-fit surface generated from the point cloud visualizes the bone in 3D.

Results: System accuracy was assessed by comparing reconstructed bone surfaces to CT in four cadaveric hips and one in vivo hip, comparing specimens where femoral head cam lesions were present and absent. Ultrasound scans were co-registered with corresponding CT scans to assess their similarity. The 95th-percentile Haussdorf distance was calculated as $H_{95} = 0.91$ mm, SD = 0.21 mm, over the cam lesion area, sufficient to visualize typical cam lesions which have a prominence ≥2 mm. Additional testing was performed on live subjects to assess the impact of motion artefacts, noting no significant decreases in scan quality.

Conclusions: Our implementation of freehand 3D ultrasound imaging has sufficient accuracy and range to characterize cam lesions. This system has potential to be a viable alternative to pre-operative CT imaging for FAI assessment and surgical planning and is proceeding to clinical trials.

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Lysophosphatidic acid signaling promotes triacylglycerol and lipid droplet accumulation in cardiomyocytes

Abstract

Rationale: Lysophosphatidic acid (LPA) signaling contributes to metabolic complications of obesity and diabetes. Cardiac-specific overexpression of lipid phosphate phosphatase 3 (LPP3), which degrades LPA, lowers circulating LPA levels, attenuates cardiomyocyte LPA signaling, and protects female mice from high-fat diet (HFD)-induced metabolic cardiomyopathy. However, whether the LPA-LPP3 axis directly regulates cardiac lipid homeostasis remains unclear.

Objective: To determine how LPA signaling and LPP3 modulation influence cardiomyocyte lipid metabolism.

Methods: Untargeted lipidomics was performed in cardiomyocytes from male and female mice with or without cardiac-specific LPP3 overexpression (LPP3 OE) following low-fat diet (LFD) or HFD feeding. Neonatal rat cardiomyocytes (NRCMs) and human AC16 cells with LPP3 gain- or loss-of-function were treated with LPA and/or oleate, with or without LPA receptor inhibition. Forskolin was used to stimulate lipolysis. Lipid droplet content was assessed by microscopy, and lipolytic signaling was analyzed by immunoblotting and qPCR.

Results: Triacylglycerol levels were lower in female LPP3 OE mice following HFD, associated with increased HSL (S660) and PKA (T197) phosphorylation in ventricular tissue and cardiomyocytes. In NRCMs, LPA treatment or LPP3 knockdown reduced HSL phosphorylation, whereas forskolin or LPP3 OE prevented this suppression. LPA increased oleate-induced lipid droplet accumulation in AC16 cells and NRCMs and this effect was partially reversed by LPA receptor inhibition. LPP3 OE with or without forskolin significantly reduced, LPA-induced lipid droplet deposition.

Conclusion: LPA signaling promotes cardiomyocyte lipid accumulation through suppression of lipolysis, while LPP3-mediated LPA degradation mitigates this effect, providing a mechanism for LPP3-dependent cardio protection in metabolic disease.

Arash Mohammadi Matak, PhD Candidate

Supervisor: Dr. Francesca Di Cara

Defining the contribution of microbiota-derived signaling to intestinal inflammation and neurodegenerative diseases

Abstract

Introduction: Neuroinflammation is an inflammatory response within the central nervous system (CNS) that arises in response to neuronal injury, infection, or stress. While inflammation has a protective role, inappropriate or prolonged inflammation in the brain can lead to neurodegenerative diseases such as Alzheimer and Parkinson. Peroxisomes are essential metabolic organelles that maintain cellular redox balance and regulate lipid metabolism, processes that are closely linked to immune cell function and inflammatory control. Consequently, peroxisomal dysfunction can disrupt immune regulation and promote neuroinflammation. Consistently, peroxisomal metabolic alterations have been observed in patients with neurodegenerative diseases. Preliminary research found that peroxisome alterations affect how the gut processes lipids and, consequently, alter the gut microbiota. Recent evidence further links changes in intestinal microbiota to neuroinflammation and neurodegeneration over aging. We hypothesize that impaired peroxisome function within intestinal cells alters the gut microbiome, creating an inflammatory environment that contributes to neurodegenerative diseases.

Methodology: Drosophila melanogaster was used as a model to study neurodegeneration and host-commensal interactions. To explore the differences in gut microbes, metatranscriptomics, and metabolomics analysis were performed in flies that have no functional peroxisomes only in the gut cells compared to wild-type. To validate these findings, microbe-specific primers were designed to target the most significantly abundant bacterial taxa, and behavioral assays were used to assess neurodegenerative phenotypes in response to changes in microbiota.

Results: metatranscriptomics results revealed substantial shifts in microbial composition in mutant flies. The most notable differences were observed in the Acetobacter, Lactobacillus, and Pseudomonas families. qPCR results confirmed that Lactobacillus and Acetobacter are the two major genera consistently altered. Additionally, climbing assay comparing mutant and wild-type flies demonstrated impaired locomotion in male mutants.

Conclusions: By identifying key bacterial metabolites contributing to neurodegeneration, this research could lead to new treatments targeting the gut microbiome, potentially slowing or preventing these diseases. Ultimately, the goal is to validate the finding in patients' fecal samples to link changes in the metabolism of selected microbes to the onset of neurodegeneration. This research aims to improve the quality of life for affected individuals and reduce the global healthcare burden.

Aryan Vesuna, MSc Candidate

Supervisor: Dr. Thomas Pulinilkunnil

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SAR1 proteins remodel lipid droplet turnover and oxidative metabolism in muscle

Abstract

Background: Lipid droplets (LDs) store neutral lipids and buffer cellular energy demand. LD dysfunction contributes to myocardial steatosis, insulin resistance, and fatty liver disease. LD biogenesis is linked to endoplasmic reticulum (ER) export, but how lipid packaging is coupled to trafficking is unclear. Sar1A/Sar1B, COPII coat initiators, drive ER budding and can bind lipid-associated factors, suggesting roles in LD formation and turnover. Whether SAR1 isoforms regulate lipid handling in skeletal and cardiac muscle remains unknown.

Hypothesis: SAR1 promotes muscle lipid oxidation by regulating COPII trafficking of lipid-handling proteins and lipid cargo to bias lipid flux toward mitochondria.

Methods and Results: SAR1A/B were assessed by immunoblot in gastrocnemius and heart from male and female mice on low- or high-fat diet. Both paralogs were present in both tissues. In females, high-fat diet reduced SAR1A/B in gastrocnemius and reduced SAR1A in heart, but increased SAR1B in skeletal muscle; males showed no diet effect. In AC16 cardiomyocytes, SAR1A knockdown increased LD size/coalescence after oleate, whereas SAR1B knockdown increased LD number. Conversely, overexpression of SAR1A in oleate-challenged AC16 cells significantly reduced the number of LDs. In C2C12 myotubes, SAR1B knockdown decreased pyruvate-linked and maximal respiration, consistent with reduced oxidative metabolism.

Future Directions: BioID proximity labelling after oleate loading will map SAR1-dependent LD protein networks in CRISPR-Cas9 SAR1A/B knockout cells re-expressing WT, H79G, or T39N SAR1variants.

Significance: These data support a role for SAR1 in shaping LD morphology and muscle oxidative capacity, likely dependent on COPII trafficking. Disrupted SAR1 signalling may drive ectopic lipid storage and impaired oxidation in metabolic disease. Defining SAR1 effectors may identify targets for restoring lipid homeostasis and limiting lipotoxicity.

Autumn Sweeney, MSc Candidate

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If you give a Mouse Colostrum: Linking Early Nutrition to Neonatal Sepsis Outcomes

Abstract

Exclusive early breast milk (colostrum) feeding is the best-known prophylaxis against neonatal sepsis - a leading cause of neonatal mortality worldwide. However, the molecular mechanisms for colostrum's conferred protection are not understood. We deploy preclinical mouse models to investigate how colostrum deprivation impacts neonatal sepsis. Coupled with these models, non-invasive longitudinal assessment of vital organ function allows us to link early physiological perturbations to long-term clinical outcome. We thus aim to deploy a suite of non-invasive technologies called "NIMO" (non-invasive multi-omics) to enhance our understanding of disease course.

To model colostrum deprivation vs. physiological breast feeding, mouse pups are cross-fostered at birth to colostrum-producing or mature-milk producing dams. Pups are monitored until day of life 7, when they are challenged with different sepsis models: polymicrobial sepsis (cecal slurry), sterile bacterial inflammation (lipopolysaccharide), or sterile viral inflammation (poly I:C). Prior to challenge and continuing until clinical endpoint, pups will be non-invasively assessed via NIMO. This incorporates Indirect Calorimetry (IC) and Pulse Oximetry to track vital organ function and metabolic variables essential for determining overall trajectories that lead to immune resilience against infection.

Preliminary findings reveal that colostrum-deprived pups are significantly more susceptible to all three models of sepsis, having more severe clinical scores and a higher degree of weight loss compared to control pups. Additionally, colostrum-deprived pups have a significantly reduced resting energetic expenditure (measured via IC) than colostrum-fed pups prior to challenge. Future studies will employ NIMO technologies early in the challenge course to identify the physiological drivers of sepsis susceptibility in colostrum-deprived animals.

The NIMO platform will enable us to bridge preclinical to clinical insight into how disruptions to early-life feeding impact homeostatic physiology. Hence, this research addresses a fundamental knowledge gap with direct translational potential and the potential to inform public health strategies to improve neonatal health.

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non-coding RNAs, antigen presentation, immunoproteasomes, interferon signaling, breast cancer

Abstract

Introduction:

Breast cancer is a leading cause of cancer-related deaths in women. Despite advances in immunotherapies, breast cancers are often resistant to these treatments due to inefficient antigen presentation, often caused by downregulated immunoproteasomes. We have identified long non-coding RNA LINC01929 is overexpressed in breast cancer tissues and associated with worse patient survival, reduced T cell tumor infiltration, and gene expression changes associated with dysregulated antigen presentation. To investigate the underlying mechanism, our study focuses on deciphering the effect of LINC01929 on type I interferon (IFN) signaling and immunoproteasome activity.

Methods:

MCF7 and MDA-MB-231 breast cancer cell lines are treated with antisense oligonucleotides (ASO) to reduce LINC01929 levels and then used in the following assays: qPCR for antigen presentation-associated genes, western blots of immunoproteasome- and type I IFN-associated proteins, and fluorogenic substrate assays to assess immunoproteasome activity. We use Anifrolumab, a monoclonal antibody that blocks type I IFN signaling, in combination with the ASO to confirm LINC01929 mediates antigen presentation through type I IFN signaling.

Results:

Targeting LINC01929 upregulates the expression of key immunoproteasome subunits, including proteasome subunit beta type-8 (PSMB8), and increases overall immunoproteasome activity. This coincides with upregulation of STAT1 and its phosphorylated forms at tyrosine-701 and serine-727. Anifrolumab treatment blocks all these effects induced by LINC01920 knockdown in the breast cancer cells.

Conclusions:

LINC01929 suppresses antigen presentation and induces a cold breast tumor microenvironment through suppressing type I IFN signaling. Targeting LINC01929 may be a novel therapeutic avenue to overcome breast cancer resistance to immunotherapy.

Berke Sahin, MSc Candidate

Supervisor: Dr. Sanja Stanojevic

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The Association Between Socioeconomic Status and Geographic Distance with Health Outcomes in People with Cystic Fibrosis in Nova Scotia

Abstract

Background: In Nova Scotia, a province with Canada's largest urban-rural income gap, CF care is centralized in Halifax, potentially creating barriers for its dispersed population. While low socioeconomic status (SES) and distance to clinic are independently associated with worse CF outcomes internationally, their synergistic effect in universal healthcare settings remains understudied. This study estimated the associations between area-level SES and geographic distance with annual clinic visits, lung function (FEV_1% predicted), and hospitalization rates in the Nova Scotia CF cohort.

Methods: A retrospective longitudinal cohort study (2015-2019) used probabilistically linked Canadian CF Registry and Health Data Nova Scotia data (N = 178; 1,340 person-years). Mixed-effects Poisson and linear mixed models with random intercepts and slopes for time were fitted, adjusting for age, sex, and pancreatic sufficiency status. Canadian Index of Multiple Deprivation (CIMD) quintiles (Q1 = least deprived; Q5 = most deprived) were modelled as categorical predictors with Q1 as the reference.

Results: No statistically significant deprivation gradient was detected for any outcome across any CIMD dimension. However, for Material Deprivation and Economic Dependency, Q3 and Q4 showed consistently larger FEV_1 deficits relative to Q1 than Q5, suggesting a non-linear pattern. FEV_1 declined approximately 1.0 percentage point per year (95% CI: -1.57 to -0.49), with no differential decline by deprivation level. Biological determinants dominated clinical variance: female sex (IRR = 0.35) and pancreatic insufficiency (IRR = 0.09) were the strongest predictors of hospitalization.

Conclusion: Area-level deprivation was not associated with worse CF outcomes in Nova Scotia, likely reflecting the attenuating effect of the single-payer system on financial access barriers. The non-linear quintile pattern suggests moderately deprived patients may face unaddressed barriers despite not meeting thresholds for active clinical support. Structured, deprivation-aware allocation of travel assistance and social work resources may reduce inequities the current reactive model fails to capture.

Brianna Samson, MSc Candidate

Supervisor: Dr. Corey Smith

Quantifying the Compressive Mechanical Properties of Retinal Tissue Using Spherical Indentation

Abstract

Introduction: Quantifying the compressive mechanical behaviour of retinal tissue is essential for understanding the role of mechanical forces in healthy tissue and during disease progression. Existing approaches focus on nanoscale surface mechanics and do not capture depth-dependent or region specific mechanical behaviour, resulting in limited data at the tissue scale. The aim of this study is to develop a methodology for quantifying the apparent compressive modulus of retinal tissue using spherical indentation.

Methods: Rabbit retinal tissue samples were subjected to indentation testing using the Biomomentum Mach-1 system, equipped with a 0.5mm spherical indenter at a velocity of 0.07 mm/s. Samples were mounted photoreceptor-side down onto a polydimethylsiloxane substrate to ensure stability. Using force–displacement data, the apparent compressive modulus was calculated using the Hayes model, incorporating thickness measurements from optical coherence tomography.

Results and Discussion: Indentation mapping was performed over 15-25 locations per retina (~21mm diameter), in central and peripheral regions. Testing was conducted in PBS at two time points, <6 hours or 24-hours post-dissection. The methodology enabled separation of tissue and substrate response and supports analysis of regional and time-dependent variations in apparent compressive modulus.

Conclusion: This framework enables tissue-scale characterization of retinal mechanics and may inform biomechanical modelling and calibration of robotic and microsurgical systems that require precise force control.

Calum Blackwood, MSc Candidate

Supervisor: Dr. James Kramer

Identifying dynamic protein interactions for G9a and Brm in Drosophila melanogaster during stress and memory.

Abstract

The Drosophila proteins G9a and Brahma (Brm) are conserved regulators of gene expression, with essential roles in stress response, learning and memory. Mutations in the human orthologs of G9a (EHMT1/2) or Brm (SMARCA2/4) are linked to neurodevelopmental disorders, and dysregulation of either factor is frequently observed in cancer. Despite their importance, how G9a and Brm are targeted to specific genomic loci, particularly in response to environmental cues, is poorly understood. To address this, we developed Localized Fusion of TurboID (LoFTI), a novel genetic system in Drosophila, that enables tissue specific proximity labeling while preserving native regulatory elements. Using endogenous expression of G9a and Brm-TurboID fusion constructs, we previously established baseline interactomes under normal conditions. Building on this foundation, we applied LoFTI to examine G9a interactions during oxidative stress, using both ubiquitous and fat body-specific expression. Although oxidative stress produced only modest changes in G9a's interactome, integrating this experiment with our prior datasets allowed us to define a set of high-confidence G9a interactors consistently enriched across experiments and conditions. This list includes both known and previously uncharacterized interactors, notably several transcription factors that may contribute to the genomic targeting of G9a. Gene ontology analysis revealed enrichment for expected categories such as "gene regulation" and "chromatin binding," as well as unexpected enrichment terms, such as "RNA splicing," suggesting roles for G9a beyond its established functions. Building on the success of LoFTI in identifying stable and condition-specific interactors, we are now applying this system to investigate dynamic G9a and Brm interactions during memory formation. Together, these studies will provide new insight into how tissue- and context-specific protein interactions guide the activity of G9a and Brm, ultimately informing their roles in human disease.

Calvin Butler, MSc Candidate

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Evaluating the Cost-Effectiveness of the Pictou County Personal Empowerment Program: Evidence from a Rural Chronic Disease Cohort

Abstract

Background: Chronic disease and multi-morbidity are widespread in Canada, with Nova Scotia among the highest rates nationally. The Pictou County Personal Empowerment Program (PEP) is a six-month, home-based intervention targeting mental well-being, quality of life, and self-management. This study evaluated PEP's effectiveness in reducing psychological distress and improving quality-adjusted life years (QALYs), its impact on healthcare costs, and its cost-effectiveness from the healthcare payer perspective.

Methods: A prospective economic evaluation was conducted using data from a single-arm longitudinal cohort (n=151) linked with Nova Scotia Medical Services Insurance physician billing data. Participants were enrolled between December 2023 and January 2024. Generalized estimating equations were used to model with-in subject changes in two effectiveness outcomes–Kessler Psychological Distress Scale (K10) and SF-6D health utility scores–and healthcare utilization costs. QALYs were calculated from health utilities using an area-under-the-curve approach. Incremental cost-effectiveness ratios (ICERs) were calculated using adjusted within-participant changes in costs and outcomes, with uncertainty assessed through non-parametric bootstrapping and cost-effectiveness acceptability curves.

Results: The cost of delivering PEP was $57.92 CAD per person. Healthcare costs remained stable at both follow-ups (6-month difference: +$47.20, p=0.473; 12-month difference: +$57.62, p=0.595), yielding total incremental per-person costs of $105.12 at 6 months and $115.54 at 12 months. K10 scores declined by 2.85 points at 6 months (95% CI: −3.73, −1.97) and 3.27 points at 12 months (95% CI: −4.19, −2.34). SF-6D utility improved by 0.026 (95% CI: 0.010, 0.043) and 0.035 (95% CI: 0.017, 0.053) at 6 and 12 months, yielding net QALYs of 0.007 and 0.022. QALY-based ICERs were $15,927/QALY at 6 months and $5,274/QALY at 12 months, well below Canada's $50,000/QALY threshold.

Conclusions: PEP is a low-cost, potentially cost-effective intervention that produces sustained improvements in psychological distress and health-related quality of life, supporting PEP's value as a scalable model for chronic disease management.

Cameron MacGillivray, MSc Candidate

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Body Mass Index and Regional Brain N-Acetylaspartate:

A Meta-Analysis of ^{1}H-MRS Studies

Abstract

Introduction:

Obesity is highly prevalent in bipolar disorder (BD) and has been increasingly associated with alterations in brain structure, yet the neurobiological mechanisms underlying these changes remain poorly understood. Proton magnetic resonance spectroscopy (^{1}H-MRS) provides a mechanistic approach by quantifying neurometabolites such as N-acetylaspartate (NAA), a suggested marker of neuronal integrity. Although emerging evidence suggests that obesity may be associated with altered neurometabolite profiles, findings remain limited and methodologically heterogeneous.

Methods:

To clarify whether obesity, measured by body mass index (BMI), is reliably associated with altered brain NAA levels, an effect-size meta-analysis of adult ^{1}H-MRS studies was conducted. A systematic search of PubMed, Embase, and Scopus identified studies reporting neural NAA concentrations and BMI. Due to variability in reporting practices, two analytic approaches were employed: categorical comparisons between healthy-weight and overweight (BMI ≥ 25) and continuous analyses examining the full BMI range.

Results:

Across eligible studies, higher BMI was associated with lower NAA in frontal regions in both models (categorical: d = -0.49, 95% CI [-0.95, -0.03], p = .03, k = 6; continuous: r = -0.24, 95% CI [-0.35, -0.12], p < .001, k = 6). An additional categorical difference was observed in the right hippocampus (d = -0.52, 95% CI [-0.85, -0.19], p = .002, k = 4), though based on fewer studies.

Conclusions:

Overall, these findings provide preliminary evidence that higher BMI is associated with reduced NAA, particularly in frontal regions, further motivating standardized region-specific MRS research, especially in high-risk populations, such as those with BD.

Claire Thiessen, MSc Candidate

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Immigration and rate of lung function decline among Canadian adults

Abstract

Background: Early life exposures impact lung development and lung function trajectories. Impaired lung function in adulthood is a biomarker of overall health. Immigrants to Canada may have been exposed to early life risk factors that predispose poor lung development compared to Canadian born individuals and may therefore be at risk of steeper lung function decline in adulthood. The association between immigration status and lung function decline is unknown in the Canadian population.

Objective: To estimate the association between immigration status and lung function decline in a Canadian adult population.

Methods: Longitudinal data from the Canadian Longitudinal Study of Aging (CLSA) was used. Over 30,000 participants aged 45-85 at baseline in 2011 completed a comprehensive physical assessment and in-home interview. Follow-up assessments were completed in 2015 and in 2018. Linear mixed effects models were used to estimate the association between immigration status and lung function (as measured by spirometry outputs FEV1, FVC, and FEV1/FVC). An interaction between immigration status and age was used to determine whether the rate of lung function decline differed between immigrants and Canadian born participants.

Results: 12,201 participants met the inclusion criteria for this analysis, 55% of whom were female. The average age was 61 (sd: 9.6). 2,080 (17%) participants were immigrants. Immigrant lung function (mean FEV1 % predicted: 1.00 (0.16)) was not significantly different from non-immigrant (mean FEV1 % predicted: 1.01 (0.16)) lung function. Similarly, the trajectory of lung function decline did not vary between immigrants and non-immigrants (interaction with age = 0.0002, 95% CI: -0.0004, 0.0007).

Conclusion: Initial lung function measures and lung function trajectories were similar between immigrants and non-immigrants. Results may not be generalizable to the broader Canadian immigrant population, as the CLSA is more representative of high SES individuals than the Canadian population and those who can speak English or French.

Hala Obeid, MSc Candidate

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Evaluating the safety and immunogenicity of concurrent versus sequential Tdap and RSV vaccine administration in pregnancy: a pilot feasibility trial.

Abstract

Introduction: To protect infants from RSV and pertussis diseases, RSV (RSVpreF) and pertussis (Tdap) vaccines are advised in pregnancy. Non-pregnancy studies suggest that giving the 2 vaccines together may result in reduced antibody responses transferred to infants. Given the need for and complexity of coadministration pregnancy vaccine trials, we sought to determine feasibility of conducting this trial at Canadian institutions.

Methods: This is a multicenter, randomized, observer-blinded placebo-controlled phase 4 trial (NCT07097012). Intervention and visits: Concurrent group: Visit 1: Normal saline at 28-29+6 wks gestation (WG); Visit 2: Tdap and RSVpreF vaccines 4 wks later; Sequential group: Visit 1: Tdap at 28-29+6 WG, Visit 2: RSVpreF and placebo 4 wks later. Visit 3 is 4 wks after visit 2 and visit 4 is at delivery (mothers and newborns). Blood is collected during visits 1-4. Target is 30 participants/group. Outcomes: Feasibility: Screening, consent, randomization, retention, and protocol compliance rates; Safety: Adverse Event Following Immunization (AEFI), pregnancy and birth Adverse Events of Special Interest (AESI) and Serious Adverse Event (SAE) after vaccination; Immunogenicity: Seroconversion of anti-B. pertussis and RSV preF IgG 4 wks after vaccination; Anti- B. pertussis, RSV preF IgG levels at birth.

Results: As of April 7, 2026, the team at Canadian Center for Vaccinology, has consented and randomized 13. The team at the Vaccine Evaluation Center, BC, has randomized 8. As well, the team at Ottawa Hospital Research Institute, ON, has randomized 4. And ethics approved at CHU Sainte-Justine, QC. Current retention and compliance with trial protocol rates are 100%. No SAE (related to study product), AESI or AEFI has been reported.

Conclusions: A complex pregnancy vaccine trial is successfully underway at several Canadian institutions. Future work will test samples for RSV and pertussis antibodies levels and functions.

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TFEB Acetylation Is Dispensable for Basal Insulin Signaling and ER Stress in AC16 Cardiomyocytes

Abstract

Background: Transcription factor EB (TFEB) coordinates autophagy and lysosomal biogenesis and is regulated by post-translational modifications. In obesity, saturated fatty acids activate mTORC1, increasing TFEB phosphorylation, blunting autophagy and insulin signaling, and promoting organelle stress. The role of TFEB acetylation in cardiomyocytes remains unclear.

Hypothesis: Enhancing TFEB acetylation will drive nuclear localization and improve insulin signaling and stress resilience in cardiac cells.

Methods and Results: AC16 cardiomyocytes were treated with the HDAC inhibitor SAHA to increase acetylation and TFEB abundance/localization. SAHA increased global acetylation and total TFEB but did not promote TFEB nuclear accumulation. To test the functional dependency of cardiomyocytes on TFEB acetylation, AC16 cells were transfected with an acetylation-deficient TFEB mutant (Ad TFEB.7KR) or a control (Ad mCherry) and assessed for insulin and ER-stress signalling. Insulin-stimulated AKT and IRS1 phosphorylation and tunicamycin-induced CHOP accumulation were comparable between groups, indicating TFEB acetylation is dispensable for basal insulin responsiveness and ER-stress signaling.

Future directions: We will test whether TFEB acetylation influences lipotoxic injury by challenging AC16 cells and primary cardiomyocytes expressing control or TFEB.7KR with saturated fatty acids.

Significance: This work aims to determine the role of TFEB acetylation in TFEB trafficking and in metabolic stress pathways in cardiomyocytes. These findings will inform whether targeting TFEB acetylation is a viable strategy for cardioprotection in obesity and diabetes.

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Role of Stem Cell Antigen-1 Expressing Cells in Right Ventricular Remodelling in Chronic Hypoxia-Induced Pulmonary Hypertension

Abstract

Background: Most stem cell antigen-1 expressing cells (Sca-1+ cells) are cardiac-resident endothelial progenitor cells (CEPCs) and may contribute to angiogenesis. Importantly, angiogenic response is critical for right ventricular (RV) adaptation and survival in pulmonary hypertension (PH). In this study, we examined the relevance of Sca1+ cells in RV remodelling using two rat chronic hypoxia model.

Methods: To assess the effect of RV pressure overload, male and female Fischer CDF rats were subjected to 3 weeks of hypoxia (10% O2). In both models, cardiac structure, and function were assessed using echocardiography. Heart samples were collected, and Fulton index was measured to assess RV hypertrophy. Immunofluorescence straining of RV samples was performed to assess abundance and localization of Sca-1+ cells.

Results: In response to hypoxia, RV systolic pressure was increased significantly in male and female rats compared to controls, along with significant elevation in the RV hypertrophy. Importantly, these rats demonstrated adaptive RV remodelling and preserved RV function in response to chronic hypoxia as indicated by similar RV fractional area change and cardiac index in hypoxic rats. Adaptive RV remodelling in hypoxic rats was associated with an increase in the abundance of Sca-1+ cells in the RV of male and female rats compared to control rats. Immunofluorescence staining demonstrated localization of Sca-1+ cells to vascular endothelium in the RV.

Conclusion: The cardiac Sca-1+ cells in the heart may be the resident endothelial progenitor cells may contribute to angiogenesis and RV adaptation.

Henok Andualem Tegared, PhD Candidate

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Host age determine BCG systemic dissemination

Abstract

Introduction: Despite the known pathogen agnostic benefits of Bacille Calmette–Guérin (BCG) vaccination in preventing neonatal sepsis, critical knowledge gaps remain that must be addressed to optimize this approach for global benefit. Remarkably, despite Calmette's discovery of rapid-onset BCG bacteremia in human newborns after oral vaccination, whether systemic dissemination is a prerequisite for pathogen-agnostic protection has remained unanswered for ~100 years. This issue has regained prominence now that systemic dissemination of BCG in adults has been shown to be essential for protection from TB. This project will determine whether BCG's ability to enter the bloodstream underlies its protective efficacy in newborns. This project will focus on neonatal sepsis as a model.

Design and Methods: To determine age-dependent BCG systemic dissemination (bacteremia), blood was collected at 6, 12, and 24 hours post-vaccination across neonatal, juvenile, and adult mice following skin administration. We also evaluated BCG dissemination following subcutaneous and intravenous routes in adults. BCG bacteremia was quantified using ddPCR and culture. Given that BCG seeding of the bone marrow drives granulocyte colony stimulating factor (G-CSF)-mediated emergency granulopoiesis and confers protection from neonatal sepsis, G-CSF levels were measured using ultrasensitive assays and correlated with bacteremia to elucidate the mechanistic link between systemic BCG dissemination and host immune activation.

Results: Subcutaneous BCG administration resulted in bacteremia at 6 hours post-vaccination in all neonates and juveniles, but not in adults. G-CSF induction followed a sequential rather than parallel trajectory, surging at 12 hours after bacteremia onset.

Conclusion: Following vaccination, BCG spreads into the bloodstream in an age-dependent manner, rapidly occurring in neonates but not in adults. Bacteremia precedes G-CSF induction. This is the first experimental confirmation of Calmette's startling discovery. The relationship of bacteremia to protection can now be assessed in this model, including contrast of age vs route.

Hugh Atkinson, MSc Candidate

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Khat Use and Anxiety in Rural Ethiopia: Seasonal Patterns and Measurement Validation

Abstract

Khat (*Catha edulis*) is an amphetamine-like stimulant consumed daily by over 20 million people in East Africa and the Arabian Peninsula. Despite widespread use and hypothesized links to anxiety, rigorous evidence remains limited by inadequate measurement tools and unexamined seasonal variation.

This study employed a three-stage framework among 632 males aged 18-40 in rural Ethiopia across dry and rainy seasons. Stage 1 validated amphetamine immunoassay and assisted self-report (ASR) against HPLC-measured urinary norephedrine (n=119). The ASR 0–2 day recency window achieved the strongest diagnostic performance (sensitivity=0.96; κ=0.69), outperforming both full-week recall and immunoassay detection.

Stage 2 demonstrated that ASR sensitivity remained stable across seasons (McNemar's p=0.62) despite significant increases in khat prevalence and intensity during the rainy season, supporting year-round field deployment.

Stage 3 found no association between khat use and SRQ-20 anxiety scores across all exposure definitions, model specifications, and seasonal contexts. Somatic health burden was the strongest predictor of anxiety (IRR 1.26-1.35 per symptom), with scores 28-37% lower during the rainy season independent of khat use.

These findings validate a low-cost exposure framework for khat research in LMICs and implicate somatic health burden, rather than khat consumption, as the primary driver of anxiety in this population.

Ian Armstrong, MSc Candidate

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'So, where are you from?' Sense of belonging to Canada and to Islam as moderators of mental distress due to trauma and discrimination for Muslims living in Canada

Abstract

Muslims in Canada suffer discrimination and high rates of trauma. Despite this, Muslims make less use of mental health services than other Canadians and face barriers to accessing care. Muslim mental health outcomes are under-studied in Canada, hindering efforts to support this community. Identifying factors that help Muslims mitigate mental distress from trauma and discrimination is an important part of supporting the mental health and well-being of the Muslim community in Canada.

Sense of belonging has been shown to protect mental health. However, very few studies have unpacked the different spheres of life in which a person may or may not feel they belong. This issue may be especially pertinent to Canadian Muslims, as Islamophobic rhetoric can give the impression that Islam itself does not belong in Canada, creating tension between Muslim Canadians' national and religious identities.

This study will use a survey to investigate how sense of belonging to Canada and to Islam each mitigate mental distress related to trauma and discrimination. Researchers will distribute the survey through both secular and religious organisations that serve Muslims in Canada. Secular organisations are important as many Canadian Muslims are non-practicing, and even practicing Muslims may not be affiliated with a mosque, whether because there is none close by or for other reasons.

Descriptive statistics and correlations between variables of interest and demographic factors will shed light on the makeup and mental health of a national sample of Canadian Muslims. Moderation analysis will explore the role of each sense of belonging in buffering mental distress related to trauma and discrimination. Results will help clarify how Canadian Muslims' sense of national and religious belonging relate to each other and to mental distress from trauma and discrimination, contributing to an understanding of how to support Muslim mental health in Canada.

Jennika Veinot, PhD Candidate

Supervisor: Dr. Javeria Hashmi

Working memory and Trauma-Related Phenotypes of Chronic Pain Are Linked to Distinct Brain Connectivity Patterns

Abstract

Chronic pain (CP) is a heterogeneous disease, comprised of pain severity and pain affect symptoms. CP is commonly associated with comorbidities such as trauma, post-traumatic stress, and impaired working memory, yet the relationship between these conditions and how they contribute to CP remains poorly understood. Historically, CP conditions are categorized based on pain localization, but emerging research is suggesting this method may not be effective, and rather stratifying based on associated symptoms and comorbidities may result in more clinically meaningful groups. Previously, we have shown that impaired working memory is associated with increased chronic pain severity, independently of trauma. In another study, we demonstrated that post-traumatic stress is associated with increased pain affect, but this relationship was not associated with working memory. Here, we aimed to test whether we could identify clinically relevant orthogonal phenotypes within a CP population, and whether these phenotypes were associated with any patterns in brain network connectivity.

159 participants with CP underwent resting-state functional MRI, working memory assessment, and completed clinical questionnaires assessing chronic pain expression, depression, anxiety, trauma, and post-traumatic stress.

A principal components analysis identified two factors: PCA1 showed high-loadings for pain severity, pain-related disability, widespread pain, and impaired working memory. PCA2 showed high-loadings for pain affect, posttraumatic stress, and trauma exposure. PCA1 was associated with increased connectivity between the language/memory network and the subcortical and sensory networks, whereas PCA2 was associated with decreased within-network connectivity of the sensory network, and increased connectivity between the language/memory network and the attention/executive network.

Overall, these findings provide preliminary work identifying two emerging phenotypes in a CP population – one with heightened pain affect, associated with trauma and posttraumatic stress, and one with heightened pain severity, associated with decreased working memory – each linked to distinct underlying patterns of brain connectivity.

Jenysbel Hernandez Reyes, PhD Candidate

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Mast cells with a mission: harnessing the tumor microenvironment in ovarian cancer.

Abstract

Ovarian cancer remains a highly lethal gynecologic malignancy. In Canada, approximately 3,100 women are diagnosed each year, with only about 45% surviving beyond five years post-diagnosis. Emerging evidence suggests that IgE-bearing cells—including mast cells, monocytes, and macrophages—may contribute to anti-tumor activity in ovarian cancer. Notably, mast cells are potent immune cells resistant to radiation and many chemotherapeutic agents, making them attractive targets for combination therapies. Robust anti-tumor immune responses require both local effector $CD8^+$ T cells and activated natural killer (NK) cells. The recruitment and activation of these effector populations require localized production of cytokines and chemokines, including type I interferons and interleukin-2 (IL-2). We hypothesized that mast cells can be engineered to function as regulated delivery vehicles for immune-activating cytokines, enabling spatially and temporally precise modulation of the tumor microenvironment. To test this concept, we developed a murine model in which bone marrow–derived mast cells are genetically modified to express selected immune mediators under doxycycline-inducible control, allowing tunable cytokine release. IFN-α, and IL-2 have well-established roles in promoting anti-tumor immunity, enhancing immune cell activation, and shaping inflammatory responses. We have performed both in vitro and in vivo studies employing genetically modified mast cells expressing these cytokines in the ID8 murine ovarian cancer model. Therapeutic outcomes assessed included tumor progression, overall survival, and recruitment and activation of anti-tumor immune populations. This approach aims to determine whether engineered mast cells can be leveraged as a programmable cellular platform to enhance immune-mediated control of ovarian cancer.

Kevin Nguyen, MSc Candidate

Supervisor: Dr. Xianping Dong

A Novel Approach to Treating Triple-Negative Breast Cancer

Abstract

Breast cancer is the most common cancer worldwide and the second leading cause of cancer-related deaths among Canadian women. Triple-negative breast cancer (TNBC) is an aggressive subtype characterized by a high tendency to metastasize and limited treatment options. Recent evidence shows that ATP released into the tumor microenvironment (TME) plays an important role in TNBC progression. However, the source of ATP and the mechanisms by which it accumulates in the TME remain unclear.

Lysosomes are enzyme-containing organelles that digest large biological components and produce nutrients crucial for cell survival and growth. SLC17A9 or VNUT is an ATP transporter located on the lysosomal membrane that imports ATP into the lysosome to maintain lysosomal function, which is required for tumor growth. In addition, lysosomes can fuse with the cell membrane and release ATP into the TME, where ATP activates cell membrane proteins on neighboring TNBC cells and lead to metastasis.

We investigate the role of SLC17A9 in TNBC progression by exploring the following questions: (i) Does SLC17A9 promote TNBC growth by accumulating lysosomal ATP levels and improving lysosomal function? (ii) Does SLC17A9 facilitate TNBC metastasis by elevating ATP in the TME and activating cell membrane proteins? and (iii) Can SLC17A9 inhibitors reduce TNBC progression and improve the effectiveness of chemotherapy drugs for TNBC?

By uncovering the molecular mechanisms of TNBC progression regulated by SLC17A9 and exploring its inhibition, this study will advance our understanding of TNBC biology and offer a new treatment strategy for patients with TNBC and potentially other cancer types. Given that SLC17A9 is commonly found in many different cell types, it is also a potential target for other diseases.

Kyle Medd, PhD Candidate

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Electrospinning Polyester Fibre Meshes for Controlled Delivery of Anti-Inflammatory Itaconate

Abstract

Implantable polymeric fibrous mesh medical devices are a mainstay in many reconstructive medical procedures including ligament/muscle tears, pelvic floor reconstruction, and abdominal hernia repair. Although effective in providing therapeutic reconstructive support due to their tensile strength and flexibility; mesh devices suffer complications arising from prolonged inflammatory reactions termed the foreign body response (FBR). Here, chronic inflammation drives pathological fibrotic phenotypes, resulting in loss of device function through fibrosis and contracture. The use of hydrolytically liable polymeric materials (polyesters) can subvert these long-term fibrotic outcomes through material resorption. However, the increased reactivity of the inflammatory layer (e.g. reactive oxygen species, degranulation/enzyme release) driven by the FBR may pre-maturely degrade the device, causing reconstructive support failure. In our study, we aim to deliver a potent anti-inflammatory metabolite, itaconate, to effectively manage FBR inflammation and increase the success rates of reconstructive fibre meshes. To do this, we fabricated novel anti-inflammatory poly(alkylene itaconate) variable comonomer materials into fibre mesh devices. Here, itaconate is synthesized into the backbone of the polyester, comprising 50% molecular make-up. Additionally, the variable comonomer diol species provides tunability of critical material properties including degradation rate, the primary mechanism dictating itaconate delivery kinetics. Through a design of experiments, we fabricated poly(dodecylene itaconate)/PCL blended fibre mesh devices through electrospinning, a technique which provides simple benchtop tunability of nano-scale fibre formation. These optimized parameters were translated to poly(hexylene itaconate) and poly(nonylene itaconate) PCL blended materials, fabricating 3 diol distinct itaconate/PCL blended fibrous mesh devices with limited morphological differences. Finally, we found that the degradation by-products of these materials demonstrated regulation of nuclear factor kappa-light-chain-enhancer of activated B cells (NF-κB) activity in stimulated macrophages in a diol dependent manner. Importantly, we highlight the feasibility of translating this comonomer variable polyester platform to precisely tune delivery of itaconate based therapeutics in a new fibre mesh form-factor.

Lauren Over, MSc Candidate

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Bacterial activation of proteinase-activated receptors as a trigger of infection-induced preterm labour

Abstract

Introduction: Preterm birth (<37 weeks) is the primary cause of neonatal mortality worldwide, affecting over 15 million pregnancies each year. Mechanisms leading to preterm labour (PTL) are poorly understood, but it is estimated that up to 60% of PTL cases arise from uterine bacterial infection from the ascension of dysbiotic vaginal microbiota including Prevotella bivia. However, the pathways through which these bacteria contribute to PTL initiation remain unknown. Labour pathways can be triggered by activating uterine proteinase-activated receptors (PARs). Select human proteases cleave the PAR extracellular domain, exposing a tethered ligand that binds back to the receptor to initiate signalling pathways. In pregnancy, uterine PAR signalling can trigger inflammatory and contractile labour cascades. Our previous work shows that protease activity of PTL-associated Prevotella bivia degrades collagens and elastin; structural components of pregnancy tissues remodelled during labour. We hypothesize that P. bivia proteases additionally contribute to labour initiation through human uterine PAR activation.

Methods: PAR proteolysis was evaluated with fluorometric protease assays using pooled, sequential fluorophore-quenched (FQ) peptides corresponding to the extracellular domain sequences of PAR1 and PAR2. FQ peptides were incubated with P. bivia cell-free supernatant in kinetic assays to screen for secreted proteolytic PAR1 or PAR2-targeting activity. Metallo-, cysteine, and serine class-specific protease inhibitors were incorporated into the assay to confirm the protease class conferring the observed activity.

Results: P. bivia cell-free supernatants proteolyzed PAR1 and PAR2 FQ peptide pools; indicated by increasing fluorescence over time. The metalloprotease inhibitor, 1,10-phenanthroline, abrogated P. bivia PAR1 and PAR2 proteolysis, confirming secreted metalloproteases are conferring PAR-proteolyzing activity.

Conclusions: Our findings show that P. bivia secreted metalloprotease activity target peptides corresponding to the extracellular domains of PAR1 and PAR2. Bacterial targeting of uterine PARs would be a novel mechanism by which dysbiotic vaginal bacteria might contribute to preterm labour initiation.

Mackenzie Searle, MSc Candidate

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Investigating the Effect of High-Fat Diet and Hypertension on Thoracic Aortic Aneurysm in male and female mice lacking NPRA

Abstract

Thoracic aortic aneurysms (TAA) involve the progressive weakening and dilation of the thoracic segments of the aorta and can lead to rupture and sudden death. Because there are no reliable biomarkers or treatments to slow or reverse disease progression, surgical repair remains the only definitive treatment. While hypertension, hyperlipidemia and genetic factors are known risk factors for TAA, it is not known whether these interactions can modify the aortic disease probability in male Vs. female patients. Our preliminary studies revealed an increased incidence of thoracic aortic dilatation in aged female mice lacking the natriuretic peptide receptor A (NPRA) gene. Our ongoing studies aim to determine whether high-fat diet accelerates aneurysm formation in young male and female NPRA knockout (KO) and wild-type mice. To date, high-fat diet has increased body weight, fat mass, and corrected body fat percentage in both sexes compared to control diet irrespective of the genotypes. NPRA KO mice show higher systolic, diastolic, and mean blood pressures than wild-type mice. We anticipate accelerated TAA development in high-fat diet-fed KO mice, with a higher incidence of thoracic aortic dilatations, compared to normal-det fed KO mice and their respective wild-type controls. In mice with aneurysm formation, we expect to observe increased inner aortic diameter and decreased wall thickness, as measured by echocardiography, consistent with the progressive weakening of the aortic wall. Ongoing studies will include histology and staining of the thoracic aorta and microRNA profiling, with a specific focus on miR-21 and its downstream targets associated with aneurysm development. Together, we expect these studies to support the hypothesis that NPRA loss paired with diet-induced metabolic stress will accelerate early TAA development.

Mahdiye Mohati, MSc Candidate

Supervisor: Dr. Francesca Di Cara

Diacylglycerol A Key Regulator Of IMD Signaling Activation

Abstract

Introduction: Chronic inflammatory diseases affect millions of Canadians, with conditions like inflammatory bowel disease and arthritis causing significant health and socioeconomic burdens. Chronic inflammation is characterized by elevated cytokine levels, particularly tumor necrosis factor-alpha. While anti-TNF therapies can offer relief to some patients, their limited effectiveness and loss of response highlight the need for alternative treatment strategies.

Immune signaling pathways, including the TNF pathway, rely on the physical assembly of adaptor proteins into amyloid-like structures. In this pathway, the RIPK1 and RIPK3 form amyloid-like necrosomes that amplify inflammatory signaling. Similarly, the IMD pathway in Drosophila melanogaster, which is analogous to the mammalian TNF pathway, forms functional amyloids upon immune stimulation, thereby activating the signaling cascade and inducing the expression of distinct immune mediators. Our lab discovered that peroxisomes, organelles central to lipid metabolism, are vital for IMD activation. In this research, we focused on exploring a new regulatory mechanism that targets the assembly of immune signaling proteins during pathway activation.

Methodology: We employed Drosophila as a model system to investigate the molecular mechanisms underlying IMD pathway activation. Lipidomic analyses were conducted to assess changes in lipid composition in wild-type and peroxisome-deficient Drosophila macrophage-like cells, followed by targeted genetic manipulations to restore specific lipid species in peroxisome-deficient cells. Results were visualized with immunofluorescent microscopy, and pathway activation was confirmed by qPCR.

Results: Our findings reveal that peroxisome dysfunction disrupts IMD amyloid-like structures, thereby impairing immune activation. Lipidomic profiling indicated alterations in cellular lipid composition, particularly in glycerolipid intermediates. Remarkably, restoring diacylglycerol levels rescued IMD aggregation and immune mediator expression in peroxisome-deficient cells, demonstrating that specific lipids can directly modulate immune signaling by influencing protein assembly.

Conclusion: These results identify a previously unrecognized lipid-dependent regulatory mechanism controlling amyloid-like immune signaling complexes. This mechanism could open new avenues for developing innovative lipid-based strategies to manage chronic inflammatory diseases.

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Colostrum Deprivation Impairs BCG-Induced Neutrophil Expansion: Implications for Global Vaccine Efficacy

Abstract

Introduction: Bacille Calmette-Guérin (BCG) vaccination reduces neonatal sepsis mortality within days of administration by triggering G-CSF-driven emergency granulopoiesis and neutrophil expansion. Yet globally, 50% of neonates do not receive timely BCG vaccination, and similarly, fewer than half receive colostrum, the bioactive-rich early milk critical for neonatal immune programming. Our prior work demonstrates that colostrum-deprived neonatal mice are more susceptible to polymicrobial sepsis than colostrum-fed counterparts. Whether colostrum deprivation also impairs the neonatal immune response to BCG is unknown. Critically, no human BCG trial has systematically accounted for early feeding status, representing a major gap in understanding vaccine efficacy in real-world settings. Therefore, we investigated whether colostrum deprivation diminishes BCG-induced neutrophil expansion.

Methods: Neonatal mice were cross-fostered at birth to either colostrum-producing (CL) or mature milk-producing (MM, colostrum-deprived) dams. At day of life (DOL) 3, pups were vaccinated with BCG. At DOL 6, spleen and blood samples were harvested for flow cytometry and multiplex immunoassay (BioPlex) analyses, quantifying peripheral neutrophil expansion and plasma G-CSF levels respectively across CL and MM groups.

Results: Colostrum-deprived (MM) pups mounted an equivalent G-CSF response to BCG as colostrum-fed (CL) pups, indicating intact upstream cytokine signalling. However, MM pups exhibited significantly attenuated neutrophil expansion following BCG vaccination compared to CL pups, suggesting that colostrum deprivation impairs the downstream translation of G-CSF signalling into granulopoiesis.

Conclusions: These findings indicate that colostrum deprivation uncouples G-CSF production from neutrophil expansion in response to BCG, the very mechanism responsible for vaccine-mediated sepsis protection. This raises the critical possibility that BCG may be less effective in colostrum-deprived neonates, a population that overlaps substantially with those at highest risk of sepsis mortality. Survival studies and functional neutrophil phenotyping are underway to determine the clinical significance of this impairment.

Mark Hanes, PhD Candidate

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B CELL-DEFICIENCY MODIFIES TUMOR ONSET AND IMMUNOSURVEILLANCE IN MICE

Abstract

Introduction: About 40% of melanomas harbor oncogenic BRAF mutations. With immune checkpoint and small-molecule inhibitors achieving limited benefit for advanced disease, new strategies for managing melanoma are urgently needed. B cells are enriched in BRAF-mutant melanomas, but their role remains controversial. Anti- and pro-tumor roles for B cells have been identified in humans and mice. Fundamental knowledge on the role of B cells in melanoma will provide novel insight into how B cells may be therapeutically manipulated to improve clinical benefit. Here, we defined the function of B cells using a BRAF-mutant spontaneous melanoma model.

Methods: The development of melanoma in B cell-deficient and B cell-containing BRAF-mutated spontaneous melanoma mice was assessed over time. Cellular immune profiling was performed using high-dimensional flow cytometry. NK cell-mediated killing of RMA and RMA-S lymphoma target cells was measured using a peritoneal clearance assay. To determine the contribution of NK cells to immunosurveillance against melanoma onset, NK cells were depleted in vivo via intraperitoneal injections of anti-NK1.1.

Results: B cell-deficiency significantly delayed the onset of spontaneous melanoma and resulted in fewer tumor-infiltrating CD8+ T cells and dendritic cells in secondary lymphoid tissues. The absence of B cells was not associated with a change in total NK cell numbers but was associated with an increased frequency of mature NK cells and decreased frequency of immature NK cells in peripheral lymphoid tissues of tumor-bearing hosts. NK cells from B cell-deficient mice exhibit similar lytic-capability against MHC-devoid target cells. Phenotypically, NK cells from B cell-sufficient mice chronically exposed to melanoma displayed profiles consistent with exhaustion including downregulation of NKG2D. Importantly, melanoma onset was accelerated in B cell-deficient mice depleted of NK cells.

Conclusions: The absence of B cells is associated with delayed BRAF-mutant spontaneous, murine melanoma onset and altered nature and responses of NK cell populations.

Meghana Janardhanan, PhD Candidate

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Anxiety Disorders in the Canadian Longitudinal Study on Aging: Genome-wide association study and meta-analyses

Abstract

Anxiety disorders are one of the most common classes of mental disorders worldwide, with a lifetime prevalence of up to 30%. Characterized by excessive and enduring fear, anxiety or avoidance of perceived threats and panic attacks, anxiety disorders represent various expressions of underlying dysregulation of the basic threat-response systems. Given the prevalence, associated impairments, and significant societal and economic impact of these disorders, identifying their risk factors is of substantial interest. Evidence from family and twin studies suggests that genetic variation contributes significantly to susceptibility, accounting for approximately 30–50% of the variance in risk. Although early linkage and candidate gene studies did not identify consistent susceptibility loci, genome-wide association studies using large-scale samples have begun to reveal several associated genetic loci and shared genetic influences across anxiety-related traits. Advancing this research, this ongoing project focuses on identifying additional loci and examining the contribution of genetic factors to anxiety disorders through a genome-wide analysis in the Canadian Longitudinal Study on Aging, followed by meta-analysis with other cohorts. Beyond primary association testing, the project also employs calculating polygenic scores and cross-trait genetic correlation analyses, to characterize the complex genetic architecture of anxiety and its common comorbidities within an aging population.

Murtaza Lokhandwala, MSc Candidate

Supervisor: Dr. Greg Fairn

ACYL-COA SYNTHETASE INHIBITION ATTENUATES mTORC1 SIGNALLING WITHOUT SUPRESSING LAMTOR1 PALMITOYLATION

Abstract

Mechanistic target of rapamycin complex 1 (mTORC1) is a central regulator of cellular growth and metabolism and is frequently hyperactivated in many cancers. Amino acids activate mTORC1 through the Ragulator-Rag GTPase pathway at the lysosomal membrane; however, how lipid metabolism intersects with this signaling axis remains poorly defined. LAMTOR1, an essential Ragulator component, is irreversibly myristoylated and reversibly S-palmitoylated, and lipidation of LAMTOR1 is required for amino acid-dependent mTORC1 activation. We investigated whether cellular acyl-CoA availability links fatty acid metabolism to amino acid sensing by mTORC1. Inhibition of the acyl-CoA synthetases was used to disrupt intracellular acyl-CoA pools, which were monitored in live cells using a fluorescent biosensor LACSerHR. In various cell types, Inhibition of acyl-CoA synthesis impaired amino acid-stimulated mTORC1 signaling. Notably, disruption of acyl-CoA synthesis did not alter LAMTOR1 lysosomal localization, indicating that acyl-CoA's regulates mTORC1 activity downstream to Ragulator recruitment. Collectively, these data identify fatty acid-derived acyl-CoAs as important modulators of amino acid-dependent mTORC1 activation and support a model in which lipid metabolism contributes to nutrient sensing independently of LAMTOR1 membrane targeting.

Nathan Purvis, MSc Candidate

Supervisor: Dr. Nik Thomas

A Conserved G-Loop Motif in Tir Mediates ATP Binding and Contributes to EPEC Virulence

Abstract

Enteropathogenic and Enterohemorrhagic Escherichia coli (EPEC/EHEC, respectively) are major causes of diarrheal disease and rely on a type III secretion system (T3SS) to inject multiple effector proteins into host cells during infection. Host colonization requires EPEC to phosphorylate its CesT chaperone. Furthermore, an EPEC translocated intimin receptor (the Tir effector) mediates intimate attachment to intestinal cells. The molecular mechanisms controlling this process remain undefined, including how CesT phosphorylation occurs and what bacterial kinase is involved.

To that end, we searched the EPEC virulence-associated proteome for proteins with potential ATP-binding sites. We identified that the Tir effector contains a strictly conserved glycine-rich (GxGxxG) 'G-loop' motif that is known to mediate ATP-binding in eukaryotic protein kinases (e.g., Protein Kinase A). We therefore asked whether the Tir G-loop functions as a bona fide ATP-binding motif, and whether the Tir G-loop is required for EPEC virulence.

To experimentally address this, we investigated Tir G-loop ATP-binding capacity using an in vitro ATP-binding assay and explored its role in EPEC infection. Using a fluorescent ATP analog (TNP-ATP), we demonstrate that recombinant Tir binds TNP-ATP in a G-loop-dependent manner. Moreover, targeted Tir G-loop mutations (predicted to impair ATP binding) markedly reduced TNP-ATP binding affinity. To assess the Tir G-loop's relevance to EPEC virulence, we evaluated bacteria expressing Tir G-loop variants in an in vitro cell culture infection model. Notably, Tir G-loop mutations demonstrated to disrupt TNP-ATP binding resulted in a virulence defect, indicating that the Tir G-loop contributes to EPEC pathogenesis.

These data support a model in which a conserved G-loop in Tir functions as an ATP-binding motif and contributes to EPEC virulence. The findings reveal a previously unrecognized EPEC virulence mechanism with potential for therapeutic targeting through small-molecule ATP-binding site inhibition.

Parnian Jahanbani, PhD Candidate

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CHLAMYDIA-DRIVEN MACROPHAGE REPROGRAMMING AS A POTENTIAL LINK TO OVARIAN CANCER

Abstract

Ovarian cancer is the deadliest gynecological malignancy, with High-Grade Serous Carcinoma(HGSC) accounting for most deaths. While genetic mutations such as BRCA1/2 only explain a proportion of cases, non-genetic contributors remain underexplored. Chronic Chlamydia trachomatis(Ct) infection has emerged as a potential risk factor, with epidemiological and genetic evidence confirming a causal link to HGSC. While Ct induces DNA damage, impairs DNA repair, and degrades p53 in fallopian tube epithelial cells, how infection-driven immune remodeling contributes to tumor development remains poorly understood.

We hypothesize that Chlamydia infection induces long-lasting immunosuppressive alterations in the female reproductive tract(FRT) that facilitate ovarian tumor development. Using a murine model of intravaginal Chlamydia infection, we profiled immune cell dynamics across acute, resolution, and post-resolution phases(Days 17–91).

While bacterial clearance occurred by Day32, CD45+ immune cell counts in the FRT remained significantly elevated even at Day91,indicating persistent inflammation beyond active infection. Using established markers to distinguish bone marrow-derived macrophages(BMDMs) from tissue-resident macrophages(TRMs), we found BMDMs rapidly dominated the FRT and remained the predominant macrophage population through Day91. Both pro-inflammatory(M1) and anti-inflammatory(M2) BMDM phenotypes persisted long-term, with a notable M1/M2 hybrid population enriched in BMDMs. Since M2 macrophages are known drivers of tumor progression, we investigated whether Chlamydia antigens alone could induce this polarization; in vitro treatment with heat-killed Chlamydia upregulated M2 markers in macrophages, confirming active infection is not required.

These findings demonstrate that Chlamydia infection alters macrophage composition both quantitatively and qualitatively in the FRT, establishing a durable immunosuppressive environment that may link chronic infection to ovarian cancer susceptibility.

Parsa Kamali, MSc Candidate

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Examining the role of S-acylation on the PUFA-TAG lipase activity of PNPLA3

Abstract

The patatin-like phospholipase domain-containing 3 (PNPLA3) I148M variant substantially increases the risk of metabolic dysfunction-associated steatotic liver disease (MASLD), yet the molecular mechanisms governing PNPLA3 catalytic activity at lipid droplet membranes remain poorly understood. PNPLA3 functions as a triacylglycerol lipase with specificity for polyunsaturated fatty acid-containing substrates, but how this lipid droplet-resident enzyme achieves catalytic competence at the membrane interface is unknown. Recent studies demonstrate that PNPLA2, also known as adipose triglyceride lipase (ATGL), requires S-acylation—reversible palmitoylation of cysteine residues—for lipase activity. This dynamic post-translational lipidation modulates protein-membrane interactions and catalytic function, suggesting that PNPLA3 may employ similar regulatory mechanisms. Using acyl resin-assisted capture, we detected S-acylated PNPLA3 in Huh7 cells under basal conditions. Pharmacological inhibition with 2-bromopalmitate and cyanomyracrylamide significantly reduced S-acylation. Next, guided by AlphaFold predictions, we generated a series of Cys-to-Ser mutants predicted to reside in the catalytic site. Using confocal microscopy, we examined these PNPLA3 mutants for their ability to localize to lipid droplets and mobilize polyunsaturated fatty acids in Huh7, HeLa, and ATGL-knockout HeLa cells. Our findings reveal that S-acylation regulates PNPLA3 activity at the lipid droplet interface, possibly by modulating enzyme orientation or conformational dynamics at the triacylglycerol-phospholipid boundary. Ongoing investigations into whether the pathogenic I148M variant disrupts this lipidation machinery may uncover reversible mechanisms underlying MASLD pathogenesis.

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Impact of Nandrolone Decanoate and Exercise Training on Cardiac Morphofunction, Mast Cell Recruitment, and Molecular Signaling

Abstract

Supraphysiological administration of anabolic-androgenic steroids (AAS), such as nandrolone decanoate (ND), has surged among athletes and recreational users seeking performance enhancement. However, chronic misuse is related to severe cardiovascular consequences, including advanced heart failure 1. While exercise training usually leads to physiological adaptations, evidence suggests that ND administration reduces innate protective mechanisms and triggers pathological cardiac remodeling, especially when combined with strenuous exercise 2. This maladaptive process is often driven by a shift toward a pro-inflammatory state and altered molecular signaling, leading to possible pathologic hypertrophy 3.

Our study evaluated the interaction between ND and exercise training (TR) on cardiac function and signaling. Echocardiographic analysis revealed that the group ND-TR developed significant systolic dysfunction, evidenced by reduced Ejection Fraction (75.2%) and Fractional Shortening (39.8%) compared to non-trained ND rats (85.7% and 50.6%, respectively). Structurally, the ND-TR group exhibited increased interventricular septum thickness and end-systolic diameter.

These functional impairments were associated with local inflammation and altered protein expression. The ND-TR group showed the highest mast cell recruitment (32.8 ± 5.7), indicating a strong pro-inflammatory environment. Protein analysis confirmed that ND administration shifts the cardiac environment toward a pro-inflammatory state by reducing IL-10 levels. Furthermore, pathological remodeling was emphasized by the upregulation of Calcineurin (859.04 pg/mL) and reduced AKT2 expression in ND-treated groups. In conclusion, the interaction between ND and exercise promotes systolic disfunction and exacerbated inflammation, highlighting that AAS misuse during training facilitates irreversible tissue damage.

Radka Sevcik, MSc Candidate

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Optogenetic Action Potential Modulation for Arrhythmia Prevention in Long QT Zebrafish Hearts

Abstract

Background: Long QT syndrome (LQTS) is a potentially lethal condition in which repolarisation of the cardiac action potential (AP) is impaired due to decreased outward repolarising current (e.g., rapidly-activating delayed rectifier K+, IKr) and/or an increase in inward depolarising current (e.g., L-type Ca2+, ICa,L). These changes in ionic currents and the resulting AP prolongation can lead to early after depolarisations (EAD) and ectopic excitation, which may result in deadly re-entrant arrhythmias. Current therapeutic options for LQTS, however, are limited, warranting the exploration of novel treatment options.

Goal: The goal of my work is to develop a drug-induced experimental model of LQT induced EADs in the zebrafish isolated heart and use optogenetics to normalise AP morphology to demonstrate its potential as an anti-arrhythmic therapy.

Methods: Zebrafish represent a powerful experimental model based on the ease of their genetic alteration and the similarity of their cardiac electrophysiology to human. Hearts isolated from AB strain zebrafish were exposed to dofetilide (IKr blocker) and Bay K8644 (ICa,L activator) to cause AP prolongation and EAD generation. Effects on the AP were measured with sharp electrode recordings and voltage optical mapping. The established experimental protocol was then applied to isolated hearts expressing the light-activated repolarising K+ channel HcKCR1, with green LED light of controlled intensity and duration applied to regions of the heart for AP modulation.

Significance: By demonstrating the utility of optogenetics for local AP modulation and the prevention of EADs, this work supports the potential future use of optogenetics for treatment of LQTS.

Rhea Nickerson, PhD Candidate

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Role of the integrated stress response in modulating the host immune response to Pseudomonas aeruginosa lung infection

Abstract

Pseudomonas aeruginosa is a highly adaptable environmental Gram-negative bacterium which causes diverse opportunistic infections in humans, particularly chronic lung infections in people with cystic fibrosis (pwCF), where it drives persistent inflammation leading to respiratory failure. P. aeruginosa is highly antibiotic-resistant, and during its transition to chronicity adapts to exploit the lung niche and evade immune clearance, making it very difficult to treat. My project aims to deepen our understanding of this host-pathogen interaction and develop novel treatments by exploring the relationship between P. aeruginosa infection and the host integrated stress response (ISR). The ISR is a highly-conserved eukaryotic stress response mediated by eIF2α phosphorylation leading to general translation inhibition and activation of transcription factor ATF4 to promote cellular stress adaptation or cell death depending on stress intensity and duration.

Based on previous literature, our lab is using P. aeruginosa-embedded agar beads to model extended lung infection in C57BL/6 mice. We have extended infection for up to 1 week, with sustained production of inflammatory cytokines and neutrophil recruitment, recapitulating hallmark features of the persistent inflammation which drives lung damage in human chronic infection. Using this model, we treated mice daily with specific ISR-inhibiting drugs ISRIB and 2Bact. Treatment with 2Bact significantly improved weight recovery and clinical symptoms beginning at 3 days post-infection. ISRIB resulted in an intermediate but non-significant phenotype. Interestingly, this protective effect of 2Bact was only seen in male mice. Complementarily, we used a RAW264.7 cell-based infection model to corroborate that P. aeruginosa infection activates the ISR, indicated by upregulation of ATF4 via western blot. Pre-treatment of cells with 2Bact strongly decreased this activation. Together, these observations position ISR inhibition as a potential novel strategy to modulate the host response to P. aeruginosa lung infection and reduce infection-associated morbidity and mortality in pwCF and other chronic lung diseases.

Riley MacKinnon, MSc Candidate

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Investigating New Pathways in the Metabolic Control of Puberty

Abstract

Background/aims: In rodents, hypothalamic KNDy neuron activation during late-juvenile development triggers puberty. Metabolic alterations during the perinatal period can affect the development of hypothalamic KNDy neurons, thereby altering the timing of puberty. Here, we aim to identify the molecular networks of metabolically induced changes in hypothalamic developmental trajectories.

Methods: We used a model of nutritional status by raising female Wistar rats in three conditions (overnutrition, normal nutrition, and undernutrition) starting at postnatal day (P)0. Pubertal timing was determined as the day of vaginal opening and first estrus. RNA sequencing of the arcuate nucleus-median eminence (ARC-ME) at P14, followed by a battery of systems biology approaches, identified metabolically altered gene networks. Networks were further validated at P14-28 by qPCR. Finally, networks were validated at the protein level by immunofluorescence.

Results: Overnutrition (ON) rats showed advanced puberty, increased Kiss1 expression, and increased arborization of KNDy neurons. Undernutrition (UN) rats showed delayed puberty, reduced Kiss1 expression, and decreased arborization of KNDy neurons. RNAseq analysis of the ARC-ME revealed altered Gene Ontology Pathways: Extracellular Matrix Formation, Extracellular Matrix Organization, and Oligodendrocyte (OL) Differentiation. An ARC-ME single-cell transcriptomic database showed cell-specific enrichment in perineuronal net (PNN) components. Select PNN and OL gene expression changes were validated in the ARC-ME across development before puberty. Immunofluorescent staining of PNNs showed a marked increase in ARC-ME density in ON and a reduction in UN animals. Moreover, ON animals showed enhanced OL maturation, whereas UN animals showed diminished OL maturation.

Conclusions: Early-life nutritional alterations disturb hypothalamic OL and PNN developmental trajectories, potentially impacting KNDy neuron development and pubertal maturation.

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Early Innate Immune Signatures Imprint Clinical Outcomes of Bordetella pertussis challenge in a Controlled Human Infection Model

Abstract

Background: Despite widespread vaccination, Bordetella pertussis continues re-emerging globally, highlighting gaps in understanding vaccine-induced protective immunity. Controlled human infection models (CHIMs) offer powerful platforms to interrogate host-pathogen interactions, define protection correlates, and inform next-generation vaccine design.

Methods: This open-label, phase 1, dose-escalation CHIM trial was conducted at the Canadian Center for Vaccinology. Healthy adults (18-40 years) were intranasally inoculated with B. pertussis isolate D420. Blood, serum, PBMCs, and nasal washes were collected at baseline and post-challenge. Innate immune responses were assessed using multicolor flow cytometry and Luminex assays, analyzed by clinical outcome, sex, and vaccination history.

Findings: Although infection followed dose-dependent patterns, 22% (11/50) of participants remained non-infected across all challenge doses, indicating intrinsic resistance to colonization of B. pertussis. Non-infected participants exhibited sustained expansion of circulating NK cells together with early mucosal production of granzyme A, granzyme B, IL-29 (type III interferon lambda 1), and MCP-2, reflecting rapid cytotoxic and antiviral-like effector programming associated with spontaneous clearance. In contrast, symptomatic participants displayed robust complement activation and mucosal production of eotaxin-2 and MIP-1δ, accompanied by depletion of circulating neutrophils and expansion of monocytes, eosinophils, and NK cells in peripheral blood. Asymptomatic individuals displayed a distinct intermediate phenotype, characterized by early I-TAC and TRAIL production with concurrent depletion of circulating neutrophils. In vitro assays further demonstrated that B. pertussis directly induced NK cell activation and degranulation, promoting production of granzymes, perforin, and IFN-γ together with CD16 upregulation. Importantly, NK responses induced by in vitro stimulation followed an intrinsic functional hierarchy aligned with clinical outcomes, being strongest in non-infected participants, intermediate in asymptomatic individuals, and weakest in symptomatic participants.

Interpretation: Distinct early innate immune programs are mechanistically linked to divergent clinical trajectories following B. pertussis challenge.

Sayanti Dey, PhD Candidate

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NKR-P1B Restrains Glycolytic and Inflammatory Reprogramming of Alveolar Macrophages

Abstract

Alveolar macrophages (AMs) are the primary sentinel immune cells in the alveolar niche that protect against pathogens but are also uniquely adapted for debris clearance and surfactant metabolism to maintain lung homeostasis. We previously observed that the NK cell-associated receptor, NKR-P1B, is expressed by AMs and is critical for AM survival and metabolic reprogramming. To further elucidate the underlying mechanisms, we investigated the role of this receptor in AM metabolism and inflammation. Nkrp1b-/- mice display dramatically altered AM metabolism compared to wild-type (WT) mice. At steady state, while AMs from WT mice rely on mitochondrial oxidative phosphorylation, AMs from Nkrp1b-/- mice derive about 80% of their ATP through glycolysis. This metabolic shift is driven by the upregulation of the glucose transporter GLUT1 and hexokinase 1 (which is the key rate-limiting enzyme for glycolysis) in Nkrp1b-/- AMs. To characterize their phenotype further, we performed single-cell RNA sequencing of the AMs. Transcriptomic analysis revealed five major AM subpopulations in the lungs. The Ki67hi proliferating AM subpopulations are dramatically reduced in Nkrp1b-/- mice, explaining the decline of AM numbers. Another AM subset, which exhibits upregulated expression of genes related to hallmark inflammatory pathways and oxidative stress, is markedly enriched in the Nkrp1b-/- mice. We next validated the pro-inflammatory phenotype of these AMs through their phospho-kinome profiling, where we found that AMs from Nkrp1b-/- mice have several upregulated phosphorylated targets associated with inflammatory signalling. Together, our findings indicate that NKR-P1B restrains the glycolytic and inflammatory reprogramming of alveolar macrophages, thereby maintaining lung homeostasis.

Shirin Mehrpooya, MSc Candidate

Supervisor: Dr. Alexa Yakubovich

Knowledge and preparedness to respond to domestic and sexualized violence against women among emergency care professionals: A mixed methods study in Nova Scotia

Abstract

Emergency care settings are critical points of entry to care for women experiencing domestic and sexualized violence. Yet little is known about professionals' knowledge and preparedness to respond in Nova Scotia, where rates of violence against women (VAW) are high and the emergency care system is under strain. This mixed methods study examines emergency care professionals' readiness to identify and respond to VAW at a system level.

As part of the larger parent study, we conducted a brief online survey between November 2023 and February 2024 with 1649 health professionals across Nova Scotia, including 205 working in emergency care. Using a modified version of the Physician Readiness to Manage Intimate Partner Violence Survey (PREMIS), we assessed knowledge, opinions, preparation, and practices related to VAW. Nine emergency care professionals were purposively selected to participate in semi-structured follow-up interviews to further explore factors shaping their readiness. Quantitative data were analyzed using descriptive statistics; qualitative data will be analyzed using reflexive thematic analysis within a feminist poststructuralist framework. Both strands will be weighed equally and integrated using joint-display tables.

Nearly two-thirds of emergency care participants (59%) reported encountering at least one case of domestic or sexualized violence in the past six months, half of whom said that addressing violence was either not a team priority or were unsure if it was. Survey responses revealed several gaps in knowledge and preparation: 65% reported little to no knowledge of VAW prevalence in Nova Scotia, and 45% reported limited understanding of their role in addressing VAW. Qualitative analysis is currently underway.

This study will provide a comprehensive snapshot of emergency care professionals' readiness to manage VAW in Nova Scotia. Findings will inform interventions and policy aimed at strengthening emergency responses at a system level and establish a benchmark for future research evaluating intervention effectiveness.

Yatin Singh, MSc Candidate

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Childhood Trauma and Body Mass Index as Predictors of Systemic Dysregulation and Sensory Abnormalities in Fibromyalgia

Abstract

Fibromyalgia (FM) is a chronic pain condition characterized by widespread pain, fatigue, and sensory hypersensitivity. FM is increasingly recognized as involving systemic dysregulation beyond the central nervous system. Mild inflammation, insulin resistance, thyroid dysfunction, and elevated body mass index (BMI) have all been reported in FM as potential markers of broader physiological disturbance, although findings across studies remain inconsistent. These abnormalities have also been implicated in relation to childhood trauma, which is a known risk factor for greater symptom severity and altered stress regulation in FM. However, no studies to date have examined whether childhood trauma and BMI jointly explain variance in FM symptoms, nor whether these factors are linked to markers of system wide dysregulation and sensory abnormalities.

31 FM patients and 25 healthy control (HC) participants; these groups were age matched and all participants were females. Blood samples were collected for FM patients to measure levels of various substances such as insulin, insulin resistance, high-sensitivity c-reactive protein (hsCRP), cortisol and white blood cells (WBC). Trauma exposure was measured using Childhood Trauma Questionnaire (CTQ) and Brief Trauma Questionnaire (BTQ). To address sensory mechanisms we examined pain ratings during a schema based heat pain task involving heat stimuli preceded by expectancy cues of varying intensity.

BMI had significant negative correlations with CTQ sexual abuse and CTQ emotional abuse but BMI was not significantly correlated with BTQ total. A significant positive correlation was found between BMI and pain ratings in the schema task, but correlations were significant only in the low intensity cue range. BMI was significantly positively correlated with insulin, insulin resistance, hsCRP and the functional total of the Fibromyalgia Impact Questionnaire.

Our findings demonstrate system wide dysregulation in a majority of our FM sample. The extent of dysregulation is indicative of abnormalities in sensory pain processing.