URSCA

URSCA 2018

4TH ANNUAL UNDERGRADUATE RESEARCH IN SCIENCE CONFERENCE OF ALBERTA

APRIL 29-30, 2018
UNIVERSITY OF LETHBRIDGE

Keynote Speaker: Dr. David Naylor, Department of Physics & Astronomy

University of
Lethbridge

FIAT LUX

CELEBRATING

UNDERGRADUATE SCIENCE RESEARCH
IN ALBERTA

CONTENTS

DR. DAVID NAYLO

PROFESSOR AND BOARD OF GOVERNORS' RESEARCH CHAIR | DIRECTOR, ASTRONOMICAL INSTRUMEN
DIVISION, INSTITUTE FOR SPACE IMAGING SCIENCE | DEPARTMENT OF PHYSICS & ASTRONOMY, UNIVE

As a Commonwealth Scholar David received his PhD in Physics from the University of Calgary in 1979. Following a Post Doctoral Fellowship at a European Space Agency Fellow in ESTEC, Noordwijk, he joined the Department of Physics at the University of Lethbridge in 1981. Over the last 36 years he has established an internationally recognized research program in the area of experimental astrophysics, specializing in the design and use of infrared and submillimeter, Fourier transform spectrometers and radiometers, in a variety of astronomical applications. He has held several prestigious research fellowships, NATO International Fellow (University College London), Smithsonian Fellow (Smithsonian Institute Washington), Perren Fellow (Queen Mary College London) and in 2003 was awarded a Board of Governors Research Chair at the University of Lethbridge.

David is the Director of the Astronomical Instrumentation Group and co-founder of the Institute for Space Imaging Science, formed in 2009 between the Universities of Calgary and Lethbridge. He attracts external funding for his research program of ~1M$ pa. David is the Canadian co-Investigator on ESA's Herschel/SPIRE mission and the SCUBA-2 project, for which his group developed an imaging Fourier transform spectrometer (FTS-2). He is also the Canadian co-Investigator on the ESA/JAXA SPICA mission. He has coauthored over 304 refereed publications with an i-index of 103, and h-index of 35 and two papers cited over 1000 times.

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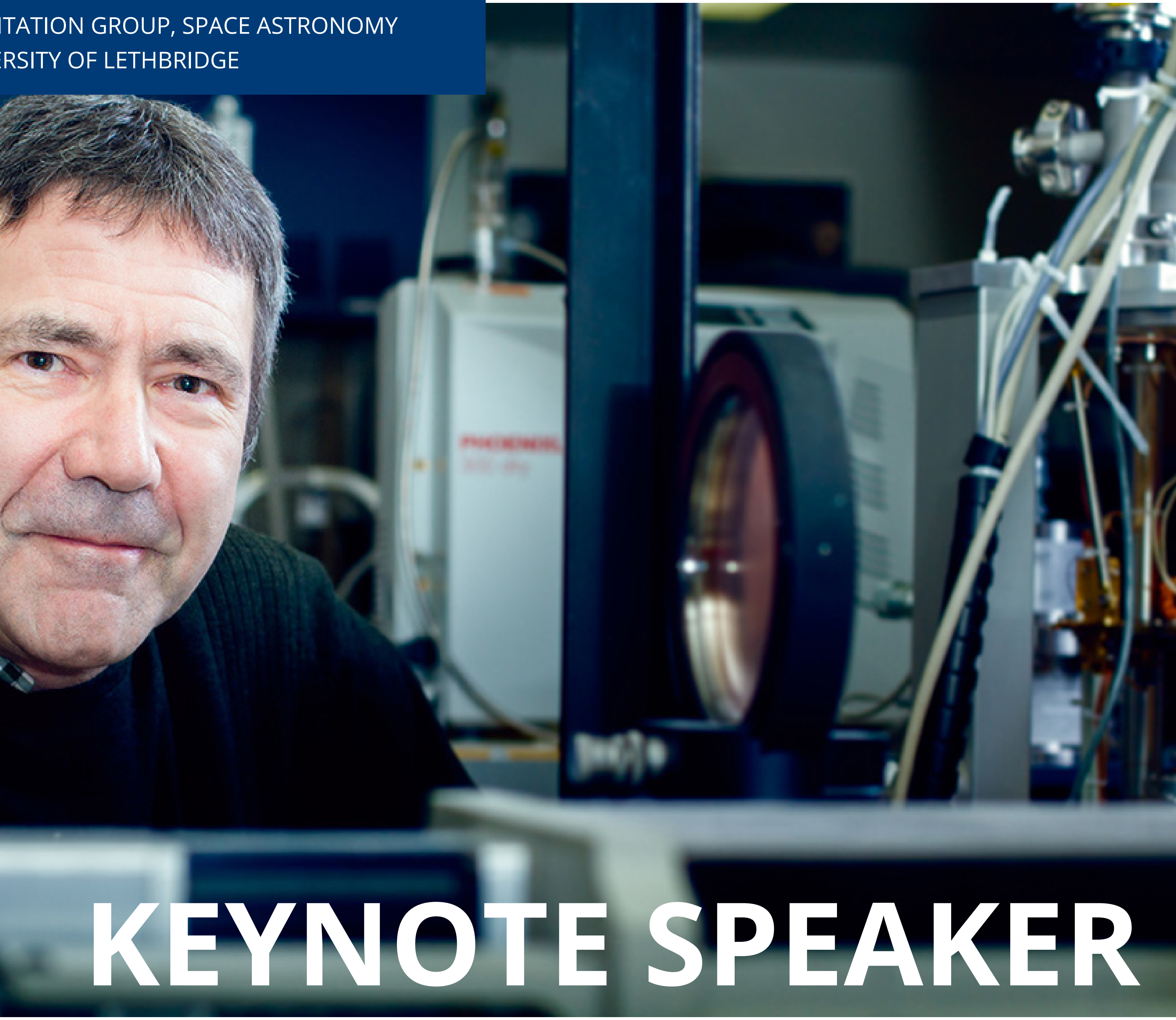
ITATION GROUP, SPACE ASTRONOMY
ERSITY OF LETHBRIDGE



KEYNOTE SPEAKER

David is a member of: American Astronomical Society, Astronomical Society of the Pacific, Canadian Association of Physicists, Canadian Astronomical Society, Optical Society of America and Society of Photo-optical Instrumentation Engineers. He has served on several (inter)national committees CTAG, NSERC GSC17, JCSA, NASA NGST, Herschel/SPIRE, Gemini and ALMA science steering committees, and regularly acts as a reviewer for granting agencies.

In 2003 David formed a high-tech spin-off company, Blue Sky Spectroscopy. Based in Lethbridge, Blue Sky specializes in custom instrumentation for the remote sensing markets. The company's heritage respects David's vision of providing exemplary training opportunities for students. Blue Sky has won several contracts from leading space agencies (NASA, ESA, CSA) and has delivered complex instrumentation to leading research teams at Harvard, Berkeley, CEA Paris, Chicago, Cardiff, the Max Planck Institute, NASA and NIST. Three of its systems are operating at the South Pole and the company recently delivered two systems to China. Blue Sky is gaining international recognition and was featured in a leading European aerospace magazine.

David actively recruits young scientists into his group and is particularly proud of the many students that have started their careers in his laboratory. When he is not traveling the globe, David is frequently found traveling with his wife Mavis to Calgary to visit their two children and three beautiful grandchildren.

Evidence of impact and contributions

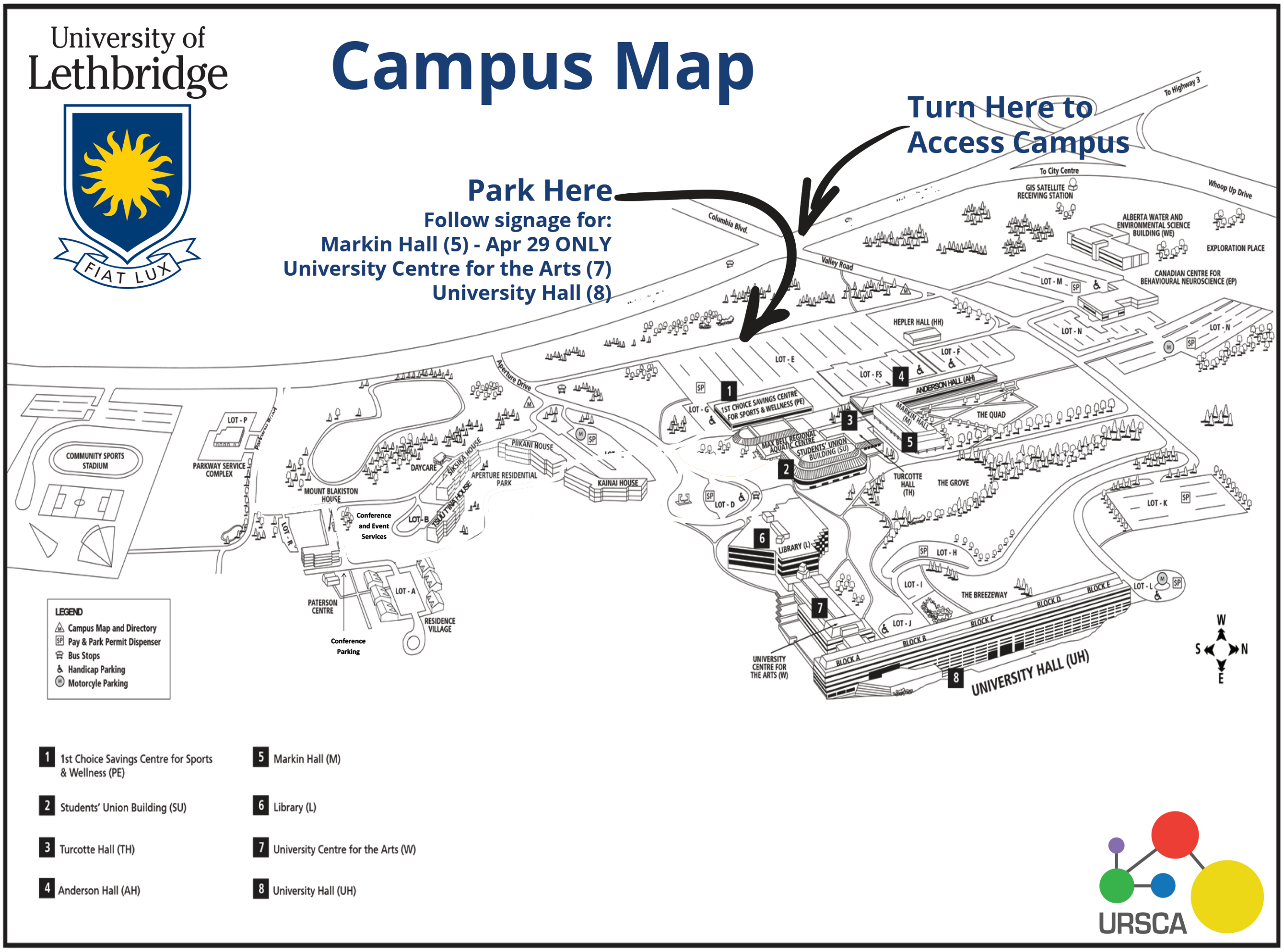
- Royal Astronomical Society of London group achievement award for the Herschel/SPIRE instrument (2014)
- Finalist in the Alberta Science and Technology (ASTech) provincial awards (2003, 2010, 2013)
- Named top 50 most influential people by Alberta Venture (July 2013)
- Recipient of Sir Arthur Clarke Award for academic study and research (July 2013)
- Awarded the key to the city of Lethbridge for contributions to science research (Nov 2009)
- Royal Astronomical Society of London group achievement award for the SCUBA instrument (2009)
- Co-founder of the Institute for Space Imaging Science (ISIS), a joint institute with Universities of Calgary and Athabasca, and Director of the Space Astronomy Division (2009)
- Canadian Principal Investigator for the ESA/JAXA SPICA/Safari mission (2008 - present)
- Awarded Alberta Centennial Medal for contributions to science (2005)
- Awarded Ingrid Speaker award for Distinguished Research (2003)
- Principal Investigator for imaging Fourier transform spectrometer, FTS-2 ((2003 – present)
- Member and Chair CSA-CASCA Joint Committee on Space Astronomy (2003-2006; 2010-present)
- Member of board of the Canadian Astronomical Society (2005-2008)
- Formed spin-off company Blue Sky Spectroscopy Inc. (6 permanent/4 part-time staff)(2003)
- Canadian Principal Investigator for the Herschel/SPIRE mission (2002 - present)
- Reviewer CFI, NSERC, CSA, CTAG, Ap.J., MNRAS, PASP, ICARUS, App.Opt., Meas. Sci. Tech., Opt. Let., JOSA
- Regularly gives public presentations to local groups (astronomy club, science fair, schools, seniors, churches, etc).

Parking

Conference parking permits for Lot E are included in the registration fee.

Permits will be e-mailed out after registration has closed to all who identify that they require a parking permit.

An interactive campus map is available at ulethbridge.ca/campus-map.



Campus Map

Turn Here to Access Campus

Park Here

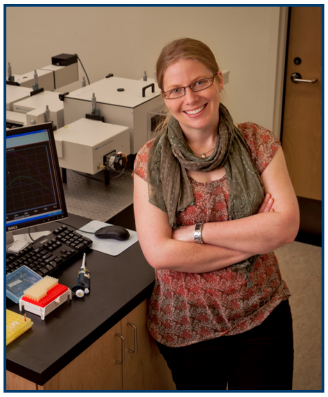
Follow signage for:
Markin Hall (5) - Apr 29 ONLY
University Centre for the Arts (7)
University Hall (8)

LEGEND
- ⚠ Campus Map and Directory
- SP Pay & Park Permit Dispenser
- Bus Stops
- ♿ Handicap Parking
- Ⓜ Motorcycle Parking

1. 1st Choice Savings Centre for Sports & Wellness (PE)
2. Students' Union Building (SU)
3. Turcotte Hall (TH)
4. Anderson Hall (AH)
5. Markin Hall (M)
6. Library (L)
7. University Centre for the Arts (W)
8. University Hall (UH)

Conference at a Glance

Day 1 | Sunday, April 29, 2018 7-9 p.m.
Opening Reception | Markin Hall Atrium
Guest Speaker: Dr. Ute Kothe



During the opening reception on April 29, Dr. Ute Kothe (Alberta RNA Research and Training Institute, Department of Chemistry & Biochemistry, University of Lethbridge) will present **The Citizenship of Being a Researcher**.

What does it mean to be a researcher? What does it mean to be a good citizen? And how are the two related? Based on Dr. Kothe's own experience in undergraduate research and her experience in supervising more than 50 undergraduate researchers in biochemistry, she will share how undergraduate research equips students with transferable skills to the benefit of students' careers as well as to our entire society. Dr. Kothe will inspire students to grow as researchers and as citizens by applying principles learned in research to all areas of their lives. She will argue that supporting early research experience thus fosters a knowledge-based, respectful and innovative society.

Dr. Ute Kothe is an Alberta Innovates Strategic Chair, elected Member of the College of New Scholars, Artists and Scientists of the Royal Society of Canada, winner of the U of Lethbridge Distinguished Teaching Award 2014 and supervisor of the Lethbridge Let's Talk Science program.

Day 2 | Monday, April 30, 2018 8 a.m.-5 p.m.
UCA/University Hall (Various Locations)

8-9:00 a.m. Urban Lounge
Registration & Welcome (continental breakfast)

9:00-10 a.m. uHall Classrooms B650, B660 & C610
Oral Presentations

10-10:15 a.m. Urban Lounge
Break (with snacks)

10:15-11:15 a.m. uHall Classrooms B650, B660 & C610
Oral Presentations

11:30 a.m.-12:30 p.m. Urban Lounge
Keynote Speaker: Dr. David Naylor

12:30-1 p.m. Urban Lounge
Lunch

1-3 p.m. UCA Atrium
Poster Viewing & Judging
Lab Tours (Naylor & Burg)

3-4 p.m. uHall Classrooms B650 & B660
Oral Presentations

4-4:15 p.m. Urban Lounge
Break

4:15-5 p.m. Urban Lounge
Reception & Awards* (appetizers served)
*Grand Prize sponsor: Gowling WLG
*1st place sponsor: uLethbridge, School of Graduate Studies
*2nd place sponsor: uLethbridge, Faculty of Arts & Science

Oral Presentation Schedule

SESSION A1 | B650 | 9:00-10:00 AM

9:00 a.m.
BEN HARTUNG | University of Lethbridge
Understanding the Functional Role of the C-Terminal Domain of the Conserved Protein LepA

9:12 a.m.
CERI HUGHES | University of Alberta
Retrospective Evaluation of PET/CT Scans of Intermediate Risk Prostate Cancer Patients

9:24 a.m.
ANNA J. RICHARDSON | MacEwan University
Balanced Scheduling to Reduce Procrastination: Can scheduling enjoyable activities increase productivity and satisfaction?

9:36 a.m.
JUSTIN SHARPE | University of Lethbridge
Rainbow trout (Oncorhynchus mykiss) chemosensory detection ability for copper nanoparticles

9:48 a.m.
JASON CHAN | Mount Royal University
Glucose Tolerance is Unchanged During Acute Normobaric Hypoxia

SESSION A2 | B660 | 9:00-10:00 AM

9:00 a.m.
MISHÉLLE SCOTT | MacEwan University
An aerial inventory of rock glaciers in the Southern Alberta Rocky Mountains

9:12 a.m.
BRITTNEY HERRINGTON | Mount Royal University
Normal and Elevated Blood CO2 Increased Anterior Blood Flow Responses During the Cold Pressor Test

9:24 a.m.
CHRISTIANNA CZYZ | The King’s University
Mind the Gap: Christian Faith in Decisions about Fertility Treatments

9:36 a.m.
DARREN GEMMILL | University of Lethbridge
Characterization of Engineered Protein Switches Using Intramolecular Disulfide Bridges

9:48 a.m.
WEIHAO LU | MacEwan University
Electrochromic opal-structure polymer sysem tactile E-skin sensor

SESSION A3 | C610 | 9:00-10:00 AM

9:00 a.m.
HOPE VIENNEAU | University of Lethbridge
Survival of the Fittest: Elucidating Fitness of Escherichia coli strains Lacking Pseudouridine Synthases

9:12 a.m.
MIGUEL MACARAIG & KAITLYN DRYDEN | MacEwan University
The Effect of Pace on the Performance of the Closers in the Kentucky Derby

9:24 a.m.
BRYNNE GOURLAY | Concordia University of Edmonton
Identification of Conserved Proteins in Nocardia brasiliensis and other Actinomycetoma causative agents using a Bioinformatic approach

9:36 a.m.
RYLEY CEJ | University of Lethbridge
Instrumentation for Photoactivated Cellular Biology

9:48 a.m.
AMANDA COYLE | MacEwan University
Primordial Sulfur and the Origin of Life

SESSION B1 | B650 | 10:15-11:15 AM

10:15 a.m.
ADAM SCHARNAU | University of Lethbridge
Selective Scratchers: An Analysis of Grizzly Bear Rub Tree Characteristics in SW Alberta

10:27 a.m.
NICOLE EWERT | University of Calgary
An analysis of mutational signatures in breast cancer among young women

10:39 a.m.
ALEX MACKIE | MacEwan University
Shining a Light on The Dark Side of Humanity: An Exploration of Edmonton’s Homicides Using Spatial Statistics

10:51 a.m.
JACOB GROENEVELD | University of Lethbridge
Custom FPGA Data Acquisition for Experimental Astrophysics

11:03 a.m.
RYAN GELDERMAN | The King’s University
Equipping People to be Citizen Scientists: Developing Water Quality Monitoring Sensors

SESSION B2 | B660 | 10:15-11:15 AM

10:15 a.m.
LEIF ELIASSON | MacEwan University
Applications of Discrete Markov Chains to Baseball Analysis

10:27 a.m.
TEAGAN WARKENTIN | Ambrose University
Abstract Design and Development of Natural Preservative

10:39 a.m.
JEFFREY MCDONALD | University of Lethbridge
Investigating Crosstalk Between DNA Repair and Ribosome Biogenesis

10:51 a.m.
RYAN HOFER | University of Calgary
Light Pollution: An Aerial Perspective

11:03 a.m.
ZAHRAH RAMPURI | Mount Royal University
Acute Hyperglycemia Decreases Neurovascular Coupling Magnitude in Healthy Females and Males

SESSION B3 | C610 | 10:15-11:15 AM

10:15 a.m.
MIRANDA LOHUES | University of Lethbridge
The Effects of Concussion on the Executive Function of Female Varsity Athletes

10:27 a.m.
SHAELYNN M. ZOUBOULES | Mount Royal University
Renal Acid-Base Compensation Demonstrates Plasticity During Incremental Ascent to High Altitude

10:39 a.m.
CRYSTAL ROSENE | University of Alberta
Source Detection Technique for Identifying Very Faint X-Ray Transients

10:51 a.m.
NICHOLAS ALGER | University of Lethbridge
Grasping numbers: How numerical magnitude affects kinematics of reach to grasp actions

11:03 a.m.
JAMES PRINCE | MacEwan University
A Markov Chain Analysis of John K. Samson’s music

SESSION C1 | B650 | 3:00-4:00 PM

3:00 p.m.
SIMMONE D’SOUZA | University of Lethbridge
Investigating the Interaction Between DDX17 and The Rift Valley Fever Virus 3’ Terminal Region Using a Nano-scale Structural Approach

3:12 p.m.
JEFFREY STROM | MacEwan University
Visualizing Riemannian Surfaces in 3D Using OpenGL

3:24 p.m.
ABHI AGGARWAL | University of Alberta
Development and Characterization of Calcium Sensors for In vivo Neuronal Activity Imaging

3:36 p.m.
MAYA DEGROOD | University of Lethbridge
Investigation of myo-inositol Phosphates on Human Cells by Phenotypic Cell-Based Assays

3:48 p.m.
SHELDON KOLTER | MacEwan University
Microplastic Contamination of the Canadian Archipelago

4:00 p.m.
ZACK BAKER | The King’s University
Constructive Orderings on the Groups of Integers mod n

SESSION C2 | B660 | 3:00-4:00 PM

3:00 p.m.
KATE CHUA | University of Lethbridge
The Octagon Navigation Task Reveals Sex Differences in Spatial Ability

3:12 p.m.
YEONKYEONG LEE | MacEwan University
Stabilized Liposomes transdermal patch for loaded antioxidants skin therapy

3:24 p.m.
TIMOTHY VOS | University of Lethbridge
Investigating the function of snR30 during ribosome biogenesi

3:36 p.m.
KYLA DOHERTY | MacEwan University
Examining Correlates and Consequences of Implicit Theories of Social Anxiety

3:48 p.m.
YOUSSEF WAHBA | Ambrose University
Synthesis and Applications of Iron Nanoparticles Toward Environmental Remediation

Poster Schedule

GROUP A

1:00 p.m.
CLARISSA BEKE | University of Lethbridge
Mental tug of war: How does grasping and language affect each other?

1:06 p.m.
REBECCA MCHUGH | University of Lethbridge
Metabolomic Analysis of Prenatal Maternal Stress Effects on Offspring as a Result of the 2011 Queensland Flood

1:12 p.m.
BENNY RANA | Mount Royal University
Synthesis of Sunscreen Dendrimer

1:18 p.m.
KEARA CHEREDARYK | University of Lethbridge
Regulating gene expression through targeted RNA modification

1:24 p.m.
BHAVJOT GARCHA | University of Alberta
Effectiveness of Contact Lens Cleaning Solutions on the Disruption of Biofilms Formed by Different Microorganisms

1:30 p.m.
ELANI BYKOWSKI | University of Lethbridge
Using 1H NMR Spectroscopy to Compare Urinary Metabolites of Stroke and Spinal Cord Injury Patients Before and After Neurorehabilitation

1:36 p.m.
USMAN MOHAMMED | MacEwan University
Creating A Fitting Algorithm For Exoplanet Detection

1:42 p.m.
CLAIRE NIEHAUS | University of Lethbridge
The Effects of Adolescent WIN-55 Exposure: Assessing Changes in Neuroanatomy and Social Behaviour in Rats

1:48 p.m.
MELISSA GIDDY | University of Lethbridge
Dilbit toxicity: Behaviour changes in freshwater amphipods

GROUP B

1:00 p.m.
BRITTNI STEEVES | University of Lethbridge
Perception of Recreational Opportunities on a Campus to Increase Wellness

1:06 p.m.
NICOLE EWERT | University of Calgary
An analysis of mutational signatures in breast cancer among young women

1:12 p.m.
PRACHI SANGHAVI | University of Lethbridge
Metabolomic Profiling of Biomarkers Indicative of Ancestral and Lifetime Adversity in a Two-Hit Stress Model

1:18 p.m.
KIRSTI LONG | MacEwan University
Modelling Variations in Solar Irradiance

1:24 p.m.
KAMIKO BRESSLER | University of Lethbridge
The role of eukaryotic initiation factor 5B (eIF5B) in cell cycle regulation

1:30 p.m.
KYLE POFFENROTH & MICHAEL CORDARA | Mount Royal University
The effects of molecular crowding on the kinetics and small molecule inhibition of alkaline phosphatase

1:36 p.m.
DYLAN NIKKEL | University of Lethbridge
Computer Modeling of the Hydrogen-bonded Dimers Between O2-alkylthymine and the Canonical DNA Bases

1:42 p.m.
LUKE VANDERWEKKEN | The King’s University
The extraction of undecaprenol from sumac leaves

1:48 p.m.
DANIEL ROCCA | University of Lethbridge
Nucleotide Specificity Analysis in Universally Conserved NTPases

GROUP C

1:00 p.m.
NICHOLAS WAWRYK | The King's University
Analysis of Aspartame and its Degradation Using HPLC-MS/MS

1:06 p.m.
JUSTIN SHARPE | University of Lethbridge
Rainbow trout (Oncorhynchus mykiss) chemosensory detection ability for copper nanoparticles

1:12 p.m.
CYNTHIA FONDERSON | University of Lethbridge
Consequences of 1,3-butadiene DNA adducts – R,R-N6,N6-DHB-dA and R,S-1,N6-g-HMHP-dA – on DNA base pairing

1:18 p.m.
MARISSA BUCHAN | University of Lethbridge
Identifying Biomarkers for Assessing an Athlete's Readiness to Return to Play Following a Sport-Related Concussion Using 1H NMR Spectroscopy

1:24 p.m.
LORELEI BAQUIRAN | University of Alberta
I hear, therefore I perceive: Effects of speech accent on perception of physicians

1:30 p.m.
JOSH GARDEN | University of Lethbridge
Effects of Formaldehyde on DNA: A Molecular Dynamics Study of Formaldehyde Adducts

1:36 p.m.
KYLA DOHERTY | MacEwan University
Examining Correlates and Consequences of Implicit Theories of Social Anxiety

1:42 p.m.
DARREN GEMMILL | University of Lethbridge
Characterization of Engineered Protein Switches Using Intramolecular Disulfide Bridges

1:48 p.m.
ANDREA ABENOJA | University of Lethbridge
Development of culture medium for high density micropropagation of potato plants in vitro

GROUP D

2:00 p.m.
KATE CHUA | University of Lethbridge
The Octagon Navigation Task Reveals Sex Differences in Spatial Ability

2:06 p.m.
LINDSAY AMATTO | University of Lethbridge
Using cortical thickness and elevated plus maze as a means to assess brain and behaviour in adolescent rodents: Paternal preconception nicotine exposure and enriched housing

2:12 p.m.
ABHI AGGARWAL | University of Alberta
Development and Characterization of Calcium Sensors for In vivo Neuronal Activity Imaging

2:18 p.m.
KADEN FUJITA | University of Lethbridge
Modification of the Stripe Rust Resistance Gene Yr10 in Triticum aestivum

2:24 p.m.
MARIYA MARKOVINA | University of Lethbridge
Metabolomic Profiling of Gestational Diabetes Mellitus: A 1H-NMR Based Approach

2:30 p.m.
MISHÉLLE SCOTT | MacEwan University
An aerial inventory of rock glaciers in the Southern Alberta Rocky Mountains

2:36 p.m.
JOSH FRIESEN | University of Lethbridge
Development of a Cell-Free Synthetic Biology Platform

2:42 p.m.
MURDOCH MCKINNON | Mount Royal University
Mathematical Modelling of a Measles Outbreak in Pre-vaccine England and Wales

2:48 p.m.
DARREN VAN ESSEN | University of Lethbridge
Modifying the Stripe Rust Resistance Gene Yr10 in Wheat (Triticum aestivum L.) by PCR Mutagenesis

Poster Schedule cont.

GROUP E

2:00 p.m.
SIMMONE D'SOUZA | University of Lethbridge
Investigating the Interaction Between DDX17 and The Rift Valley Fever Virus 3' Terminal Region Using a Nano-scale Structural Approach

2:06 p.m.
KATRINA TAYLOR, HUNTER JOHNSON | MacEwan University | **MUHAMMAD SALEH** | University of Lethbridge
Single-dose UV-C irradiation induces formation of gamma-H2AX foci in cell line(MCF7) determined by immunofluorescence microscopy

2:12 p.m.
LINDSAY MULLER | Concordia University of Edmonton
Identification and Alignment of Human and Mouse SNPs in the DMD Gene using a Bioinfomatical Approach

2:18 p.m.
NADIA HAND | University of Lethbridge
The Effect of Varying Doses of UVC Radiation on the Viability of Human Cancer Cells

2:24 p.m.
JONATHAN ROVEREDO | Mount Royal University
Quantification of Tissue Specific Expression of ABC type B transporters in Eschscholzia californica

2:30 p.m.
MARINA GALATONOV | University of Lethbridge
Analysis of Potential Anti-Cancer Effects of Cannabinol and Cannabidiol using HCC1806 and HEK293 Cell Lines

2:36 p.m.
RABECCA THIESSEN | MacEwan University
Foraminifera: a tool for elucidating past and recent climate change in marine Arctic Canada

2:42 p.m.
JESSE HOLBEIN | University of Lethbridge
Implementation of a new method to identify Verticillium isolates affecting potato cultivars in Alberta

2:48 p.m.
NATASHA PATEL | University of Lethbridge
Synergistic Effects of Ancestral Stress and Aging on Anxiety-like Behaviours

GROUP F

2:00 p.m.
ANILEEN PAGENI | University of Lethbridge
Detecting chemical modifications of Ribonucleic Acid

2:06 p.m.
HUGH ALVAREZ | Mount Royal University
Potential sulfate sources for the Paskapoo aquifer of Alberta

2:12 p.m.
KEIRAN VANDEN DUNGEN | University of Lethbridge
Eukaryotic Initiation factor 5B (eIF5B) provides glioblastoma multiforme with resistance towards apoptotic agents

2:18 p.m.
RYAN HOFER | University of Calgary
Light Pollution: An Aerial Perspective

2:24 p.m.
MAYA DEGROOD | University of Lethbridge
Investigation of myo-inositol Phosphates on Human Cells by Phenotypic Cell-Based Assays

2:30 p.m.
LEORA HIAR | University of Lethbridge
Maternal Preconception Nicotine and Enriched Housing: The Effects on Offspring Anxiety Behaviour

2:36 p.m.
BRYNNE GOURLAY | Concordia University of Edmonton
Identification of Conserved Proteins in Nocardia brasiliensis and other Actinomycetoma causative agents using a Bioinformatic approach

2:42 p.m.
SYDNIE ERLENDSON | University of Lethbridge
The Wellness Value of Campus Landscapes

2:48 p.m.
GARRETT ROCKAFELLOW | University of Lethbridge
Sprouting behavior of potato seed tubers (cv. Russet Burbank) after the application of different plant growth regulators

Oral Presentation Abstracts

Abstracts are listed in the order of session and presentation with the presenter underlined (where needed).

SESSION A1 | B650 | 9:00-10:00 AM

Understanding the Functional Role of the C-Terminal Domain of the Conserved Protein LepA

Ben Hartung, Harland E. Brandon, Rajashkhar Kamalampeta, Dylan Girodat, Hans-Joachim Wieden
University of Lethbridge, Department of Chemistry and Biochemistry

A large number of biochemical reactions that enable and regulate life are mediated by enzymatic proteins, which work by lowering the activation barrier of a biochemical reaction to increase the rate at which the reaction occurs. During translation, the ribosome is assisted by multiple different proteins which efficiently catalyze the formation polypeptides, to achieve a functional protein with as little error as possible. Many of the ribosomal associated proteins are GTPases, such as the Elongation Factors (EF-Tu and EF-G), which act as molecular switches by catalyzing the hydrolysis of GTP into GDP and an inorganic phosphate. For example, EF-G catalyzes the translocation of peptidyl-tRNA from the aminoacyl site, to the peptidyl site, as well as the movement of mRNA by one codon.

There are many translational GTPases whose functions are still unknown, one of them being LepA. LepA is a highly conserved GTPase, present in bacteria and eukaryotic mitochondria and chloroplasts. It is the third most highly conserved protein in bacteria, falling behind EF-Tu and EF-G, implying that it is likely serves a significant function in the cell. LepA is very similar in structure EF-G, apart from it's unique C-terminal domain (CTD). The role of the CTD and how it makes LepA different from EF-G in function are still unknown and is the basis for this study.

For my project, six variants of LepA were constructed to study the role of the CTD including C-terminal truncations and single point mutations. Initial data from our lab showed that several of these variants had altered GTP hydrolysis rates presumably because key functional amino acids in the CTD were removed or mutated. To ensure this was the case, several control experiments were carried out including measuring the binding affinity of LepA wild type and variants to nucleotides (GTP / GDP) were measured via rapid kinetics using a stopped flow. To do so, a fluorescent analog of GTP / GDP was used to monitor binding and unbinding to LepA. The results showed that all LepA variants tested were able to bind nucleotides with the same affinity, suggesting that altered nucleotide binding was not responsible for the change in GTP hydrolysis observed prior, and also that LepA has approximately 8 times higher affinity toward GDP when compared to GTP. Overall the work has contributed to the understanding of the CTD in LepA, and thereby helping to determine the functional role of LepA in protein synthesis.

Retrospective Evaluation of PET/CT Scans of Intermediate Risk Prostate Cancer Patients

Ceri Hughes
University of Alberta

Prostate cancer has a high incidence rate. Research into predictive factors for reoccurrence of prostate cancer can improve patient care and improve mortality rates. A clinical trial at the Cross Cancer Institute, aimed to determine if PET/CT scans using the radioactive tracer ^{11}C choline can predict the treatment outcome of intermediate to high risk prostate cancer patients. 30 patients were enrolled in the clinical trial, of which 25 continued on to successful data acquisition. After a baseline scan, treatment occurred over the next 7-8 weeks and patients were followed for up to 5 years. Chosen treatment outcome markers were the most recent PSA (prostate specific antigen) level and biochemical failure (PSA >2 over nadir). Quantitative PET data (standard uptake value – SUV) from interprostatic lesions was exported into Excel in the form of a time activity curves. A computer code, written in VBA (visual basic for applications), was used to sort, group, calculate and graph several parameters and values from patient data. Charts were visually inspected for correlation between any parameter and treatment outcome. Some separation was observed between high and low most recent PSA values and maximum SUV after 40 minute uptake time. Biochemical failure shows some correlation with integral SUV mean. Further evaluation of statistical power is required to determine significance. Biochemical failure occurred in only 4 patients during the 5 year follow-up period, thus limiting these findings. Furthermore, patient withdrawal during the trial limits statistical significance of later time points.

Balanced Scheduling to Reduce Procrastination: Can Scheduling Enjoyable Activities Increase Productivity and Satisfaction?

Anna J. Richardson
MacEwan University

The present research examined the effectiveness of a novel scheduling application in which the emphasis is paradoxically on scheduling leisure activities before scheduling work activities. According to the developer of this method, when we neglect to prioritize leisure activities, work activities can become tedious to the point that we begin to procrastinate. To assess this possibility, undergraduate students ($n = 27$) completed a two-week baseline of their study activities, during which they recorded both the duration and satisfaction level of each study session. This was followed by a four-week intervention in which the participants were randomly assigned to one of two conditions: (1) a traditional scheduling condition in which they scheduled their study activities for the coming week, and (2) a balanced scheduling condition in which they scheduled their leisure activities first and study activities second. We found no significant difference between the traditional scheduling and balanced scheduling groups in either study duration or satisfaction. For the combined group, however, we did find an overall effect of scheduling, with improvements from baseline to treatment in study duration ($p < .001$) and study satisfaction (marginally significant, $p = .07$), as well as an overall decrease in scores from pre-study to post-study on a standardized measure of academic procrastination ($p = .01$). These findings suggest that weekly scheduling, regardless of whether it includes scheduling one's leisure activities, may be an effective intervention for improving students' study behaviour and reducing procrastination. Limitations of the study include a small sample size and lack of appropriate controls for possible confounds.

Keywords: balanced scheduling, traditional scheduling, study time, satisfaction, procrastination

Rainbow trout (Oncorhynchus mykiss) chemosensory detection ability for copper nanoparticles

Justin Sharpe, Parastoo Razmara, Dr. Greg Pyle
University of Lethbridge, Pyle Lab

Metal nanoparticles (NP) have become increasingly prevalent in aquatic environments that receive effluents containing metal nanoparticles. Copper NPs are of specific interest for this study and have exhibited toxic effects for many different organisms. This study aims to identify if rainbow trout (Oncorhynchus mykiss) can detect copper NPs at first exposure to IC_{20} concentrations and what their response will be in a flow-through choice maze. A statistically significant avoidance response to copper NPs was observed. These findings indicate that rainbow trout can detect and avoid copper NPs at IC_{20} concentrations upon first exposure.

Glucose Tolerance is Unchanged During Acute Normobaric Hypoxia

JS Chan, AE Chiew, AN Rimke, G Chan, MD Kozak, MH Davenport, CD Steinback and TA Day
Mount Royal University

Blood glucose regulation is critical to support metabolism, particularly in contexts of metabolic stressors (e.g., high altitude). Data regarding insulin sensitivity and glucose tolerance in hypoxia are scant and inconclusive. We aimed to characterize the interactive effects of acute normobaric hypoxia and glucose regulation following an oral glucose tolerance test (OGTT) compared to normoxia. Following 12 hours of fasting on two separate days, 28 healthy participants (21.8±0.3 yrs; BMI 22.8±0.48 kg/m^2; 16 females) were randomly exposed to either normoxia (F_IO_2 0.21) or hypoxia (F_IO_2 0.148) in a normobaric hypoxia chamber. Blood glucose was tested from finger capillary samples via glucometer and sterile lancets. Following a 10-min baseline in normoxia or hypoxia, participants consumed an OGTT (75g, 300ml) and blood glucose was sampled every 10-min for 80-min. Peripheral oxygen saturation was lower at baseline in hypoxia (88.6±0.7 vs. 96.8±0.41%; $P<0.0001$), but fasted blood glucose was not different between trials (hypoxia=4.86±0.07 vs. normoxia=4.80±0.08 mmol/L; $P=0.47$). Blood glucose responses following OGTT were compared between oxygen conditions using a two-factor repeated measures ANOVA (2FRM-ANOVA; factors = oxygen condition x time) and area under the curve (AUC; paired t-test). Blood glucose responses were not different between trials (2FRM-ANOVA interaction, $P=0.765$; AUC normoxia vs. hypoxia, $P=0.227$). We conclude that glucose tolerance is unchanged with acute normobaric hypoxia, likely protecting the metabolic rate of organs that do not require insulin for uptake or storage (e.g., brain) during hypoxic stress.

Funding Sources: NSERC Discovery, MRU Faculty of Science and Technology

An aerial inventory of rock glaciers in the Southern Alberta Rocky Mountains

Mishélle Scott[1], Mark F.A. Furze[1], Nancy K. McKeown[1], Steven Pawley[2], Dan Utting[2]
[1]MacEwan University, Department of Physical Sciences; [2]Alberta Geological Survey, Edmonton

Rock glaciers are large lobes of rocky debris commonly found within alpine permafrost in the Alberta Rocky Mountains. Alpine permafrost is of significant scientific interest as it encompasses a large area and exhibits unique responses to climate change. Rock glacier falls from these increasingly unstable mountain slopes can represent significant geohazards, which makes mapping the spatial distribution of these features and classifying their morphology important. They can also be used to identify and understand past climatic change in these alpine regions, with relict (fossilized) rock glaciers indicating a past climate formerly able to create and support these features. Although a common feature within the Alberta Rocky Mountains, information on rock glacier characteristics and distribution within this region is rather limited. The inventory is based on the aerial classification of rock glaciers using high-resolution satellite imagery available through Google Earth and in ArcMap, a geospatial processing program. Geospatial mapping and remote sensing techniques were used for the quantitative and spatial analysis of these features to create an inventory that classifies, quantifies, and characterizes the rock glaciers within this region. Classification of talus-derived and glacier-derived rock glaciers was done using morphological characteristics as the elemental method for identification. Digital Elevation Models (DEM) and optical satellite imagery were used to quantify various attributes such as shape, state, slope, aspect, and elevation. A digital database with the findings from this research will be made publically available for future research through the Alberta Geological Survey.

Normal and Elevated Blood CO2 Increased Anterior Blood Flow Responses During the Cold Pressor Test

Brittney Herrington, LM Mann, SF Thrall, TA Day
Mount Royal University

The cerebrovasculature is responsive to acute alterations in blood gases (e.g., CO_2) and blood pressure. The brain is relatively pressure passive, with acute increases in mean arterial pressure (MAP) driving increases in cerebral blood flow (CBF). The superimposition of dynamic increases in MAP and controlled CO_2 perturbations on the regulation of anterior and posterior cerebral circulation is unclear. We aimed to characterize the effects of cold pressor test (CPT) on the anterior and posterior (middle and posterior cerebral arteries; MCA, PCA) with a background of different steady-state CO2 perturbations. Seventeen healthy participants were instrumented with electrocardiogram, finometer, mouthpiece/noseclip, and transcranial Doppler ultrasound (TCD) for measurement of MCA and PCA velocity (MCAv, PCAv). End-tidal CO_2 was measured using calibrated CO_2 analyzer. In a randomized order, a CPT was administered using 0-2°C water immersion of the lower limbs for 3-min under three coached, normoxic, steady-state end-tidal PCO_2 conditions: normocapnia (eupnea), hypocapnia (-10 Torr) and hypercapnia (+8 Torr). The CBV responses were calculated as the absolute difference (Δ) between baseline and the mean MCAv and PCAv during the 3-min CPT. The ΔMCAv response was larger in the hypercapnic trial compared to normocapnia and hypocapnia ($P<0.05$), but there were no differences in the ΔPCAv. The ΔMCAv CPT response was larger than the ΔPCAv during the hypercapnic trial ($P<0.001$) as well as the normocapnic trial ($P=0.017$), but there were no differences between ΔMCAv vs. ΔPCAv in the hypocapnic trials. Our data demonstrate that there was differential regional permissive hyperemia when acute increases in MAP and steady-state CO_2 are superimposed.

Funding Sources: NSERC Discovery, MRU Faculty of Science and Technology.

Mind the Gap: Christian Faith in Decisions about Fertility Treatments

Christianna Czyz, Heather Looy, Heather Prior
The King's University, Edmonton

Infertility is an increasingly common health concern that affects at least one in six couples trying to conceive. This interdisciplinary qualitative research and bioethics project at The King's University explores the role that faith plays in the decision-making process for Christian couples experiencing infertility, especially in relation to using assisted reproductive technologies (ARTs) such as in vitro fertilization. Our research shows that there is a "disconnect" (gap) between the academic bioethical discussions, denominational statements, and couples' personal decision-making about ARTs. A thorough website search confirmed that online resources available are primarily fertility clinic websites, general support websites and alterative treatment websites, and that Christian resources are both sparse and difficult to access. A survey of nine clergy from different denominations in Edmonton also confirmed that couples do not seek their support and that clergy feel ill-equipped to address this issue. To make current resources more accessible for couples and to encourage dialogue between different areas of infertility support, a website has been launched to help address the gap many couples experience.

Characterization of Engineered Protein Switches Using Intramolecular Disulfide Bridges

Darren Gemmill, Dylan Girodat, Hans-Joachim Wieden
University of Lethbridge, Alberta RNA Research and Training Institute (ARRTI), Department of Chemistry and Biochemistry

Protein engineering is the process of developing proteins that can perform functions that often are novel and do not occur in nature. Development of proteins with new properties is critical for a wide range of biotechnology applications including new metabolic pathways, biosensors, and molecular scaffolds. Engineered proteins are frequently used in the food industry, medicine, nanobiotechnology, and environmental applications. One of the limits of protein engineering is the lack of ability to rationally design molecular switches. Here we report on the development of a molecular switch which utilizes cysteine disulfide bridges.

Our model system for the development of a designer molecular switch is the translation elongation factor (EF) G. EF-G stimulates translocation of tRNA through the ribosome, a process that requires a conformational change in EF-G. We have developed and implemented a Molecular Dynamics simulation pipeline to design 3 EF-G variants (G163C-T650C, P121C-K675C, and T125C-S679C) with disulfide bridges that limit the conformational changes of EF-G to specific functional states. To assess correct folding of these conformationally restricted EF-G variants, we have used circular dichroism and determined key enzymatic properties such as nucleotide binding and GTP hydrolysis rates for these EF-G variants.

The reported data validates the ability of our Molecular Dynamics pipeline to rationally design novel molecular switches.

Electrochromic opal-structure polymer sysem tactile E-skin sensor

Weihao Lu
MacEwan University (Under Dr. Sam Mugo)

We developed a versatile, highly sensitive and wearable skin-like sensor with electrochromic color-changing system to measure the human (or pets and livestock)'s heart and pulse as well as the fast response for clinic metabolites from sweat. The transduction system of the e-skin sensor will be based on color and capacitance changes of the tailor-made molecule receptor integrated in the sensor. These dual transduction mechanism of the sensing elements are based on integration of opal polymer nanostructures (hollow nanogels), which diffract different wavelength of light based on Braggs diffraction. The opal polymer structures will also be redox responsive and as such capacitance and impedance changes of the sensor will also be investigated using PalmSense 4 potentiostat. The range of characterization techniques such as SEM, TEM and Raman spectroscopy also applied to fabricate the surface morphology.

SESSION A3 | C610 | 9:00-10:00 AM

Survival of the Fittest: Elucidating Fitness of *Escherichia coli* strains Lacking Pseudouridine Synthases

Hope Vienneau, Emily Soon & Ute Kothe
University of Lethbridge, Alberta RNA Research and Training Institute (ARRTI), Department of Chemistry and Biochemistry

The ribosome is a fundamental component of gene expression, producing proteins from corresponding mRNA sequences. The ribosome is comprised largely of ribosomal RNA (rRNA), which is known to contain various nucleotide modifications. The most abundant of these modifications is pseudouridine, the 5-ribosyl isomer of uridine, whose isomerization is catalyzed by pseudouridine synthases. The peptidyltransferase center (PTC) of the *E. coli* ribosome contains 6 pseudouridines generated by four pseudouridine synthases.

The objective of this study is to examine the contributions of ribosomal pseudouridine synthases to bacterial fitness by characterizing growth phenotypes of knockout strains. Each of the four pseudouridine synthases acting on the ribosomal PTC were sequentially deleted from wild type *E. coli*, and the effects on cellular fitness were assessed using competition assays and growth curves in both minimal medium and in the presence of antibiotic. The competition assays revealed that each knockout strain (single, double, triple, and quadruple) exhibited a severely reduced fitness, as they were quickly outcompeted by the wildtype strain. The growth curves showed that certain pseudouridine synthases became more important under different stress conditions. In minimal media, it was found that RluB and RluF are more important than the alternative pseudouridine synthases in counteracting the effects of nutrient limitation, both with and without antibiotic present. Additionally, deleting RluE seemed to rescue the growth phenotype in the multiple knockouts. Together, these findings suggest that pseudouridines play different roles in ribosomal activity within the cell depending on the growth conditions, and provide selective advantages for *E. coli* when competing for limited resources.

The Effect of Pace on the Performance of the Closers in the Kentucky Derby

Miguel Macaraig and Kaitlyn Dryden
MacEwan University

The Kentucky Derby is the longest held sporting event in America, and is often referred to as "The Most Exciting Two Minutes in Sports." In horse racing, the closers or the horses that are coming from the back of the pack excite most viewers. This study attempts to establish the effect of early speed to the performance of closers in the Kentucky Derby based from Kentucky Derby races from 1933 to 2017. The study is designed such that effect of pace is isolated from other factors of the race and is analyzed through different linear models. The results of the study are also used to emphasize the greatness of the late Secretariat, who is considered as one of the greatest horse that ever lived.

Identification of Conserved Proteins in *Nocardia brasiliensis* and other Actinomycetoma causative agents using a Bioinformatic approach

Brynne Gourlay
Concordia University of Edmonton

Mycetoma, a neglected tropical disease, is caused by a multitude of different microorganisms. This condition may be caused by both bacterial and fungal species, with the bacterial species suggested to spread more quickly through the body. Often untreated due to lack of medical access, amputation is ultimately a commonly relied upon resolution to avoid further complications in patients. *Nocardia brasiliensis*, although a rare pathogen, is the main culprit of actinomycetoma (bacterial-caused mycetoma). This underreported disease has not been fully explored. Currently, actinomycetoma has no preventative measures. Given the difficult patient accessibility of medical care, an effective, practical, pre-emptive approach is worth exploring. One such measure is the implementation of a broad-spectrum vaccine aimed at most, even all, mycetoma causative bacterial agents by targeting a conserved motif. I hypothesize that at least one *Nocardia brasiliensis* encoded protein is conserved amongst other actinomycetoma bacteria. Using a bioinformatical approach, identified *Nocardia brasiliensis* proteins were used to search for homologs in other potential mycetoma-causative agents. Three key DNA replication proteins have been identified as potential candidates. Interestingly, homologs were identified in other *Nocardia* species, as well as *Rhodococcus*, *Actinobacteria*, and *Corynebacteriales* species. Furthermore, nucleotide sequences encoded by the three most common causative agents of mycetoma were compared. From these analyses, the 16S ribosom was identified as partially conserved amongst them. These identified elements can now serve as a platform for future studies exploring them as a potential vaccine candidate.

Instrumentation for Photoactivated Cellular Biology

Ryley Cej
University of Lethbridge

Local ranchers observed livestock becoming ill after consuming the berries of local flora. The University Lethbridge was asked to investigate why or how the berries were causing the illness. Upon investigation the biology department determined a molecule in the berries which was photoactivated, demonstrated the potential for photodynamic therapy.

The precise calibration of a Photoactivation apparatus is an essential step towards successful utilization of photosensitizers. Using an integrating sphere and a spectroradiometer the spectral and radiometric properties of the LED can be determined. These properties of the LED coupled with a monochromator can be used to accurately calibrate a consumer grade DSLR camera. This DLSR camera can then be used to determine the spectral distribution of the LED when in the photoactivation apparatus. The calibration of the photoactivation apparatus allows for the various properties of the LED to be explored and thus accurate conclusions can be drawn about the photoactivation of the molecule.

The goal of this research is to better understand the exact conditions necessary for photoactivation of this molecule and others.

Primordial Sulfur and the Origin of Life

Amanda Coyle
MacEwan University (Under the supervision of Dr. Robert Hilts)

The study of meteorites can give insight regarding the chemical composition that was present when the solar system was being created. The elements in meteorites have not undergone extensive changes since they were formed billions of years ago, so they are thought to resemble those on Earth before the formation of the hydrosphere. This can lead to information regarding the formation of the solar system, Earth, and consequently, life. Sulfur is of interest because it has essential roles in biochemistry and a prevailing theory regarding the origin of life is that it began in an iron-sulfur world. By determining the sulfur composition of meteorites and the isotopic ratios – ratio of atoms of the same element with different atomic masses – we hope to determine the processes behind for formation of the form of sulfur responsible for the creation of life. This first stage of the project was to perfect wet chemistry and analytical techniques to extract and quantify sulfur species from meteorites. The development of the techniques required reading research literature, testing, and altering the techniques while working with a meteorite simulant. Multiple extractions with different solvents were used to differentially separate the sulfur species based on their chemical and physical properties. The extractions were pure with high yields. These techniques will be used to extract sulfur from the meteorites in the MacEwan collection, which will then undergo isotopic analysis.

SESSION B1 | B650 | 10:15-11:15 AM

Selective Scratchers: An Analysis of Grizzly Bear Rub Tree Characteristics in SW Alberta

Adam Scharnau, Mike Verhage & Cameron Goater
University of Lethbridge

Grizzly Bears (*Ursus arctos*) have been shown to exhibit rubbing behavior on "rub trees" as a form of intra-specific communication. By leaving chemical cues on trees, the signaling individual can convey information in the absence of physical contact with conspecifics. The criteria that bears use to select rub trees is unclear, especially within characteristic bear habitats in SW Alberta. We surveyed rub tree characteristics in Alberta's BMA5 (1685km^2), near Crowsnest Pass. Analyses of these characteristics showed that the majority of rub trees were located on flat ground, with a slight south-facing orientation (58.7%) and within 3.3m of a trail. Bear hair was found on 99.4% of trees, with 88% featuring discoloured and smooth bark. The most common rub tree species was Lodgepole Pine (56.3%), followed by White Spruce (15.9%) and Engelmann Spruce (8.7%). By comparing rub tree characteristics to those of trees in adjacent stands, we found the presence of "rare" rub tree species. The most common rare rub tree species was Lodgepole Pine (8.6% gross species composition), followed by White Spruce (7.4%) and Subalpine Fir (6.1%). Overall, 30.2% of all rub trees were rare in their stand, demonstrating a significant selection for conspicuous tree species. The results of this study show that Grizzly Bears in SW Alberta rely primarily on well-used trails and uncommon tree species to ensure an increased probability of scent transmission.

An analysis of mutational signatures in breast cancer among young women

Nicole Ewert
University of Calgary (under the supervision of Dr. Darren Brenner and Dr. Edwin Wang)

BACKGROUND. Approximately 7% of breast cancer cases are diagnosed among women 40 years of age or younger, and over 40% of all cancer diagnoses in this population are breast cancer. In 1969-2012, there was an increasing incidence of breast cancer among young (≤40 years) Canadian women, and in 1995-2006 there was also an increase in incidence of 3% and 1% among European women 20-29 years and 30-39 years respectively. Younger age is related to later stage at diagnosis, and worse outcomes even when controlling for disease stage and other prognostic features. The most aggressive tumour subtypes, human epidermal growth factor receptor 2 positive and triple-negative breast cancer have a higher prevalence among young women. Clinical and molecular differences between tumours diagnosed at different ages motivates study of differences in patterns of mutations at a genomic level. Mutational signatures are patterns in the type and three-nucleotide neighbourhood of somatic single-nucleotide variants across the exome, which may provide insight into the exposures and processes leading to carcinogenesis.

METHODS. Clinical and variant call data for 1098 breast cancer patients was taken from The Cancer Genome Atlas. Cases were separated into young (≤40 years) and old (>40 years) age groups, and the mutational load was found for each. The *SomaticSignatures* R package was used to determine the mutational spectrum of one young patient. This package will be used to construct mutational spectra for each age group, then decompose them into mutational signatures.

RESULTS. There were 91 and 951 patients in the young and old categories respectively. The young group had a median mutational load of 166.5 mutations, slightly less than the median of 198 in the older group. The mutational spectrum showed a high frequency of TCA>TTA and TCT>TTT variants, which is similar to the previously identified Signature 2, and similarly a high frequency of TCA>TGA and TCT>TGT transitions which resembles Signature 13. These two signatures are commonly found in the same tumour, and are thought to be caused by cytidine deaminase activity of AID/APOBEC proteins.

CONCLUSIONS. Patterns in a mutational spectrum suggest that Signatures 2 and 13 may be present in at least one young breast cancer tumour, but this approach should be continued to confirm this hypothesis. Further research should be conducted with a larger sample of young breast cancer patients with known exposures to risk factors.

Shining a Light on The Dark Side of Humanity: An Exploration of Edmonton's Homicides Using Spatial Statistics

Alex Mackie
MacEwan University

Prior to 2011, Edmonton had never experienced 40 homicides in a single year. Since then, there have been three separate years to experience 40 or more murders. With this knowledge, it seems prudent to explore any relationships that may exist regarding homicide events. While there has been research done into what types of people are involved in such events, little research can be found on spatial trends associated with homicide locations. Using spatial statistics, it is our goal to explore the possible existence of a spatial relationship between homicide events. More specifically, point pattern analysis will be used to investigate possible clustering of events and areal analysis will be used to check for spatial autocorrelation. We will follow up these analyses by building linear models and testing the residuals for spatial autocorrelation.

Custom FPGA Data Acquisition for Experimental Astrophysics

Jacob Groeneveld, Locke Spencer, Vince Weiler
University of Lethbridge, Astronomical Instrumentation Group

Field-Programmable Gate Array (FPGA) technology is becoming more advanced and commercially accessible with many off-the-shelf options available for a variety of applications ranging from the casual hobbyist to leading edge hardware development research requiring precision real-time operation. FPGAs allow for task-configurable, customizable designs, which can be highly optimized for specific applications. FPGAs are also very easily reconfigurable for other appications via software modification, and are thus very useful for use in an experimental physics laboratory. The Digilent Cmod A7 available for ~$90 USD was selected as an ideal solution for an application requiring 43 digital I/O pins, sub-microsecond level timing accuracy, and a state-machine cycle rates in excess of 100 kHz. This work presents the use of the CmodA7 FPGA module as part of a custom electronic data acquisition system for a laboratory-based interferometry testbed supporting the development of instrument concepts and techniques for experimental astrophysics. Using serial communication over a custom Universal Asynchronous Receiver-Transmitter (UART) designed in the Verilog hardware descriptive language, we demonstrated non-standard serial baud rates up to 4 Mbps, allowing for serial transmission rates over 2 Mbps. This work presents the validation of this data acquisition (DAQ) system, and identification of the barriers to higher data rates through the UART interface. We also present preliminary results from other FPGA interface options using USB and ethernet communication which all significantly higher data rates, at the cost of increased complexity in FPGA design and the associated development and validation cycle(s).

Equipping people to be citizen scientists: developing water quality monitoring sensors

Ryan Gelderman, Kristopher J. Ooms, Peter G. Mahaffy
The King's University

The quality of a community's water supply is an important factor for determining the health of individuals and the community as a whole. An important way of equipping local citizens to take control of their local water supplies is to provide tools that allow them to monitor key parameters that can be used to assess water quality. We have developed a low cost set of water sensors that can be operated using a smart device and be built by citizen scientists around the world to perform water quality measurements. This water sensor currently tests the pH, temperature, and turbidity of a given water sample and can be set up for single tests as well as longer term monitoring. This project is part of a larger effort in collaboration with the Organization for the Prohibition of Chemical Weapons (OPCW) and funded by the European Union to equip global citizens to monitor their chemical environment.

Applications of Discrete Markov Chains to Baseball Analysis

Leif Eliasson
MacEwan University

There are two fundamental notions which justify the use of Markov chains in the analysis of baseball game outcomes. The first is simply a statement of the consequences of the rules of Baseball itself-- namely that for any batter, exactly one of three possible outcomes will have occurred by the time their turn at bat is finished. They will have scored a run, or they will find themselves on base, or they will be "out". As a consequence, the evolving state of a game of baseball can be entirely characterized in terms of batters in sequence moving from their turn at bat into the appropriate variation of one of these three foundational "states". In particular, from the beginning of a half-inning to its conclusion, every single possible configuration of bases occupied, number of outs, and number of points scored can therefore be arranged sequentially and, as I will demonstrate, the discrete Markov chain is the perhaps the most natural framework in which to do this.

The second fundamental notion is the justification for why, if we create a matrix of transition probabilities representing the transition from one "state of the field", or "arrangement of players on bases" to the next, this matrix should in fact be a Markov chain. The key is this: since the states being transitioned through in this proposed matrix are exactly the state of the field of play at the time a given batter takes their turn at the mound, and the subsequent state after a batter has taken his turn depends solely upon the performance characteristics of that batter (this is a crucial point, as indeed the next state de facto depends upon the performance of the defenders in the field, but statistically their effects and any others may be aggregated into some "average" performance of the batter), it is logically equivalent then to say that the past states of the game have no bearing on what state will be reached next. The Markov property is satisfied precisely because the state of the game after a batter has taken their turn rests entirely on the shoulders of that batter, without regard to what the batters before have done.

Taken together, these two notions suggest a way to construct a Markov chain which will model each state of play which the game passes through from the start of a half-inning to its conclusion.

Abstract Design and Development of Natural Preservative

Teagan Warkentin
Ambrose University

Personal care products employ a wide variety of chemicals. Preservatives are essential chemicals used in personal care products to prevent microbes from growing.   It's quite common to use a wide variety of preservatives to achieve broad-spectrum protection against mold, fungi, gram positive and gram negative bacteria. These include parabens, formaldehyde releasers, isothiazolinones, and phenoxyethanols. However, formaldehyde releasers are carcinogens and parabens are known endocrine disrupters that affect reproductive health, leading to problems related to fetal growth. An average person gets exposed to a number of such chemicals on a daily basis. This research is an attempt to design and develop safer preservatives through innovative strategies.

There are results for a gram positive bacterium, staphylococcus and E. coli a gram negative bacterium 6 essential oils and 2 lipids were chosen because they had shown to have antimicrobial effects.   The six essential oils are: cinnamon, clove, eucalyptus, oregano, thyme and lavender. The two lipids tested are octanoic acid and lauric acid which are fatty acids. The different concentrations tested, were ratios of 1:1. 1:10, 1:100, and 1:1000 each compound was with the organic solvent DMSO (dimethyl sulfoxide) Data for E. Coli with potassium sorbate, Vitamin E and another essential oil wild orange was obtained. The methods used were similar to that of the Kirby Bauer method, instead of using a sterile paper disc a 5 microliter drop each solution was put directly onto the plate. The size of the incubation zone was measured and used for the data collected.

Investigating Crosstalk Between DNA Repair and Ribosome Biogenesis

Jeffrey McDonald, Erin Kelly, and Ute Kothe
University of Lethbridge, Alberta RNA Research and Training Institute (ARRTI), Department of Chemistry and Biochemistry

Although typically perceived as separate pathways, DNA repair and ribosome biogenesis have surprisingly been associated with one another by the reported interaction between the human DNA repair enzyme SMUG1 and the pseudouridine synthase dyskerin (DCK1, Cbf5 in yeast). Specifically, this interaction has been shown to excise 5-hydeoxylmethyl deoxyuridine, but not uridine or pseudouridine from RNA molecules.

Uracil glycosylases, such as SMUG1, remove damaged bases from DNA, leaving an abasic site open for repair. In particular, uracil glycosylases serve a role in protecting the genome from mutation in the event of cytosine deamination to uracil. Unrepaired U:G mismatches can give rise to transition mutations in replication, resulting in altered gene expression.

Dyskerin, a ribosome biogenesis factor, is part of a ribonucleoprotein complex that modifies ribosomal RNA by catalyzing the isomerization of uridine to pseudouridine. The function of dyskerin offers an interesting link to cancer, in which large ribosome quantities are generated within an enlarged nucleolus for rapid protein synthesis. Additionally, RNA pseudouridine synthases have been found to be overexpressed in many cancers and linked to a poor prognosis. Following the overexpression and purification of SMUG1 and Cbf5 (dyskerin homologue), the study looks to establish an electrophoresis and fluorescence based uracil-DNA glycosylase assay utilizing fluorescently labelled DNA molecules and DNA endonucleases. In light of the unclear SMUG1-dyskerin interaction, this fluorescence based assay, will be used to characterize the effect of Cbf5 on SMUG1 activity and vice versa. The affinity of SMUG1 to RNA in the presence and absence of Cbf5 will also be investigated via binding studies, with the aim of testing the hypothesis that dyskerin acts as an RNA tether for SMUG1.

Studying these protein-protein and RNA-protein interactions will provide insight into the crosstalk between the two important, and previously thought to be unrelated, cellular pathways of DNA repair and ribosome biogenesis with potential implications for new cancer treatment strategies.

Light Pollution: An Aerial Perspective

Ryan Hofer, Phil Langill
University of Calgary, Astrophysical Observatory

Artificial Sky glow is a growing obstacle for both the public to enjoy the night sky, and Astronomers to make accurate measurements of the universe around us. Given Calgary’s expanding urban geography and population, light pollution and resulting sky glow has continued make the stars less accessible. In this first aerial light pollution observation in Canada, this study will give quantifiable resolution to which areas of the SW quadrant of Calgary and area surrounding the Rothney Astrophysical Observatory create Sky Glow. Measuring Sky glow from above and below the plane using a sky quality meter, giving results in magnitudes per square arcseconds, and further instruments on the bottom giving photon counts from ground sources via digital CCD and a wide lens optics. Resulting in measurements of Sky Glow from above and tying them with sources from below to see if there is a correlation. Further using this data, we will explore the impact of urban development on our night sky.

Acute Hyperglycemia Decreases Neurovascular Coupling Magnitude in Healthy Females and Males

ZH Rampuri[1], JE Soriano[1], JE Lorida[1], TK Joki[1], MH Davenport[2], CD Steinback[2] and TA Day[1]
[1]Mount Royal University; [2]University of Alberta

Neurovascular coupling (NVC) is the link between neural activity and the corresponding changes to regional cerebral blood flow. Chronic hyperglycemia associated with diabetes has deleterious effects on vascular function. However, the potential effects of acute hyperglycemia on NVC in healthy humans is unknown. We aimed to characterize the effects of acute hyperglycemia on NVC response magnitude in females and males, and hypothesized that acute hyperglycemia would reduce NVC response magnitude. 40 healthy participants (21.6±1.7 yrs; BMI 24.1±4.1 kg/m^2; 20 females) were instrumented with electrocardiogram (ECG) to measure heart rate (HR), Finometer to measure mean arterial pressure (MAP), transcranial Doppler ultrasound (TCD) for measurement of posterior cerebral artery velocity (PCAv). Blood glucose was tested using a glucometer and capillary draw via sterile lancet. NVC responses were elicited using a standardized strobe light visual stimulus (VS; 6Hz, 360rpm; 5x30sec on/60sec off) before (fasted) and 30-min after an acute hyperglycemic load (75g glucose, 300ml; 4.8±0.4 vs. 7.5±1.2 mg/dl; P<0.0001). NVC magnitude was quantified as the difference (delta) and percent (%)-change between the mean baseline (2-min average) and the mean of five responses over the 30-sec VS. Acute hyperglycemia reduced delta NVC responses (4.8±3.9 vs. 3.3±3.4 cm/s; P=0.004) and %-change NVC responses (12.5±9.6 vs. 8.1±7.9%; P=0.002). Neither delta nor %-change NVC responses were different between women and men while fasted (P=0.98; P=0.74), nor when hyperglycemic (P=0.42; P=0.34). Our data suggest that acute hyperglycemia decreases NVC response magnitude in healthy adults equally in females and males.

Funding Sources: NSERC Discovery, MRU Faculty of Science and Technology

SESSION B3 | C610 | 10:15-11:15 AM

The Effects of Concussion on the Executive Function of Female Varsity Athletes

Miranda Lohues and Claudia L.R. Gonzalez
University of Lethbridge

This study examines the effects of previous concussions on executive function (decision making) and memory abilities of female varsity athletes (n=31 age range 18-27). Participants were included if they have suffered at least one concussion within the past five years. Their performance was compared to that of 29 non-athlete female controls without a concussion. We used subjective and objective tests of executive function. Subjective tests included the Behavior Rating Inventory of Executive Function (BRIEF-A), and the Amsterdam Executive Function Inventory (AEFI). Objective measures included reconstructing Lego models, the Tower of Hanoi puzzle, Snap card game, and the Stroop test. Memory was assessed with the well-known Wechsler Short-Term Memory test. Executive function was worse in the concussed athletes but only in the subjective measures. Objective measures yielded no differences between the groups. Surprisingly, concussed athletes showed better memory ability than non-concussed controls. Research is underway to determine if this result is because varsity athletes possess better cognitive abilities. Previous research has found positive correlations between these cognitive abilities and exercise, participation in high level sport, and participation in team sport. Further research is also focusing on testing older (55+) athletes and non-athletes to determine if concussion in youth affect cognition but only in later stages.

Renal Acid-Base Compensation Demonstrates Plasticity During Incremental Ascent to High Altitude

Shaelynn M. Zouboules[1], Heidi Nysten[2], Tom D. Brutsaert[3], Cassandra E. Nysten[1], Ken D. O'Halloran[4], Craig D. Steinback[5], Mingma T. Sherpa[6] and Trevor A. Day[1]
[1]Mount Royal University; [2]Red Deer Regional Hospital; [3]Syracuse University; [4]University College Cork; [5]University of Alberta; [6]Kunde Hospital

Ascent to high altitude, and the associated hypoxic ventilatory response, imposes an acid-base challenge, namely chronic hypocapnia and respiratory alkalosis. The kidneys act to compensate for this respiratory alkalosis via bicarbonate (HCO_3-) excretion in urine to induce a compensatory metabolic acidosis. The time course and extent of plasticity of this important renal response during incremental ascent to altitude is unclear. We developed a practical index of renal reactivity (RR), indexing the relative change in arterial HCO_3- concentration ($[HCO_3\text{-}]_a$; i.e., response) against the relative change in arterial partial pressure of CO_2 ($PaCO_2$; i.e., stimulus) during ascent (i.e., $RR=\Delta[HCO_3\text{-}]_a/\Delta PaCO_2$). We sought to assess if RR increased over time and with incremental ascent to altitude, and if RR was correlated with relative changes in arterial pH (ΔpH_a) throughout ascent. During ascent to 5160m over 10 days in the Nepal Himalaya, arterial blood was drawn from the radial artery for measurement of acid-base variables (Abbott iSTAT portable blood gas/electrolyte analyzer; CG4+ and CHEM8+ cartridges) in lowlanders at 1045/1400m (baseline) and at four different altitudes following one-night sleep: 3440m, 3820m, 4370m and 5160m. At 3820m (day five) and higher, RR significantly increased and plateaued in comparison to 3440m (day three; $P<0.04$), suggesting plasticity in renal acid-base compensation. At all four altitudes, we observed a strong correlation (range: $r=-0.71$ to -0.98; $P<0.001$) between RR and relative ΔpH_a from baseline, suggesting that the RR index accurately quantified renal acid-base responsiveness throughout ascent. In conclusion, renal acid-base compensation mechanisms demonstrate plasticity during incremental ascent to high altitude, which was detected using a novel RR index. The extent of plasticity and plateau in renal responsiveness may predict severity of altitude illness or acclimatization at higher or more prolonged stays at altitude.

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Source Detection Technique for Identifying Very Faint X-Ray Transients

Crystal Rosene[1] and Gregory R. Sivakoff[2]
[1]University of Alberta, Augustana Faculty; [2]University of Alberta

Very faint X-ray transients (VFXTs) are a rare type of X-ray binary with a distinctly low luminosity of L_x<10^6 erg/s. Accurate identification of VFXTs from typical X-ray surveys is challenging due to their minimal luminosity and low likelihood of occurrence. The Swift X-ray Telescope Survey of the Galactic Bulge aims to scan a large area of the sky in search of VFXTs while detecting shallow photon data. The faint nature of VFXTs makes them difficult to differentiate from random astrophysical background events or noise, thus, VFXTs are more susceptible to mis-identification. This research project involved developing a method for accurate source identification given limited photon data using Poisson statistics to differentiate between source and background photons. A Python 3 code was developed for which Swift Xray or simulated data is input, and the locations of detected astrophysical sources is returned. It is predicted that this source detection technique will allow for the accurate identification of VFXTs from shallow Swift Galactic Bulge Survey data, and can be extended for use in future surveys of a similar nature.

Grasping numbers: How numerical magnitude affects kinematics of reach to grasp actions

Nicholas Alger, Nancy Foesier, Nicole van Rootselaar, Claudia Gonzalez
University of Lethbridge (The Brain in Action Lab)

The SNARC (spatial-numerical association of response codes) effect is a well-studied phenomenon showing a spatial organisation of the magnitude of numbers. Smaller numbers (0-4) are associated with the left side of an individuals perceived surroundings, while larger numbers (6-9) are associated with the right side of an individuals perceived surroundings. The goal of our study was to determine if a larger numerical value on an object will increase the maximum distance between the thumb and index finger when reaching for the object also known as the maximum grip aperture. Further, it was of interest if the effect would be seen when using a cluster of small shapes as an indicator of numeracy as opposed to an Arabic numeral.

Two sets of blocks were used: one with Arabic numerical values (1, 2, 8, 9) written on them and the other with heart-shaped stickers on them. For each set of blocks the values 1 and 9 were on the faces of the smaller block, while the values 2 and 8 were on faces of the larger block which served as a foil. A control block the same size as the smaller blocks with nothing on its face was also used. University students were recruited for the study, each participant was only tested using one set of blocks. Participants were tasked with grasping blocks after an audio cue. While reaching for the block, participants were instructed to say the number of hearts or Arabic numeral on the block. This was done for both the left and right hand of each participant. During each grasp of the block maximum grip aperture was recorded. Research is still undergoing with results to be finalized in the coming weeks.

Based on prior experiments we hypothesize that maximum grip aperture should be altered depending on the size of the numerical value on the object. A tendency to have a larger maximum grip aperture when reaching for the larger number should occur, even though the objects are the same size. Using a cluster of shapes as an indicator of numeracy should also result in a similar difference to the one seen with numerical values. Since numerical processing occurs in the right hemisphere of the brain, the effect should be more pronounced in the left hand than the right.

A Markov Chain Analysis of John K. Samson's music

James Prince
MacEwan University

Music is an important part of the human experience. Artists may have a tendency towards certain chords due to their vocal range, the mood of certain chords, or just habit. We study the progression of one chord sequence to another within two albums by the Canadian artist John K Samson. Based on the movement between chords we construct a finite Markov chain. We analyze the properties of this Markov chain, and we interpret the results in musical terms.

Investigating the Interaction Between DDX17 and The Rift Valley Fever Virus 3' Terminal Region Using a Nano-scale Structural Approach

Simmone D'souza[1], Tyler Mrozowich[1], Justin Vigar[1], Hans-Joachim Wieden[1], Trushar R. Patel[1,2,3]
[1]University of Lethbridge, Alberta RNA Research and Training Institute, Department of Chemistry and Biochemistry; [2]University of Alberta, DiscoveryLAB, Faculty of Medicine & Dentistry; [3]University of Calgary, Department of Microbiology, Immunology & Infectious Diseases, Cumming School of Medicine

Rift Valley Fever (RVF) is a currently an untreatable disease that affects both humans and livestock in sub-Saharan Africa. This disease is viral in origin and the Rift Valley Fever virus (RVFV) is transmitted primarily through mosquito vectors Aedes and Culex. RVFV is a part of the *Bunyaviridae* family, and the genus *Phlebovirus*. Recent studies have indicated that RVFV interacts with the human DEAD-box RNA helicase protein DDX17. There is minimal research on the specific interactions between this host protein and the viral RNA, although DDX17 has been shown to inhibit RVFV replication. The DDX17 helicase performs a critical role in viral replication, and we are trying to dissect the specific role by which it inhibits RVFV replication. In addition, we are also studying two regions of the RVFV which forms a stem-loop structure that is proposed to interact with DDX17. Using selective 2'-hydroxy acylation analyzed by primer extension (SHAPE) and small-angle x-ray scattering (SAXS) techniques we aim to gain both secondary and 3-dimensional structural information. To identify specific domains of DDX17 that interact with both viral constructs, we require a highly pure preparation of full-length DDX17 and its truncated domains. Thus, the primary objective of my project is to establish protocols for large scale preparation of full-length and individual domains of DDX17 to identify a specific domain of DDX17 that interacts with the RVFV RNA using Electrophoretic mobility shift assays (EMSA) and study interactions using microscale thermophoresis (MST).

Visualizing Riemannian Surfaces in 3D Using OpenGL

Jeffrey Strom
MacEwan University

Using a hand-written C++ program, I will explore visualizations of Riemann surfaces in OpenGL. These surfaces will be plotted by visualizing discrete points in the complex plane. This will allow exploration of these surfaces in a first-person 3D environment.

Development and Characterization of Calcium Sensors for In vivo Neuronal Activity Imaging

Abhi Aggarwal
University of Alberta

Genetically-Encoded Fluorescent Calcium Indicators for Optical Imaging (GECOs), that modulate their fluorescence intensity in response to changes in calcium ion concentration, are powerful tools for the investigation of cell biology. These fluorescent indicators are vital when it comes to cellular imaging because they allow the non-invasive study of cells, tissues, and sub-cellular structures at a detail that was previously not possible. The focus of this project is engineering a new GECO that exhibits favourable characteristics, such as increased brightness and a higher fold change. To develop this new GECO, we started from mNeonGreen, the brightest monomeric fluorescent protein currently available. An initial prototype construct was made using rational design, following the precedent of the GCaMP series of indicators. This construct was further improved using directed protein evolution with colony-based screening of libraries of randomly generated variants. We observe the brightness of promising new variants and perform tests to see how new mutations have affected the brightness and the fold change of the variant. After many rounds of screening, our latest variant of mNeonGreen-GECO exhibits a Ca2+-dependent change of eight. When compared to the original construct, this indicator appears significantly brighter with higher contrast between Ca2+-bound and Ca2+-free states. Directed evolution is ongoing and we expect to produce a fluorescent indicator that will be used for in vivo imaging of intracellular Ca2+ dynamics. We will further image its calcium dynamics directly in Zebrafish and compare our variants with mNeonGreen fluorescent protein and the GCaMP series. Using mNeonGreen, we hope to create a calcium indicator that researchers can use to investigate the physiological activity of organs, understand the signaling patterns within tissues, and use to study the various disease states which may lead to the development of new therapies.

Investigation of myo-inositol Phosphates on Human Cells by Phenotypic Cell-Based Assays

Maya Degrood, Jan Tuescher, Steven Mosimann, Roy M. Golsteyn
University of Lethbridge

Myo-inositol phosphates (IPs) are a large family of compounds that are ubiquitous in eukaryotes. They are involved in many critical cellular functions, from signal transduction to DNA repair in eukaryotes. *Myo*-inositol hexa*kis*phosphate ($InsP_6$), commonly known as phytic acid, is the most abundant cellular IP and previous studies have suggested that exogenous $InsP_6$ has anti-proliferative effects on multiple cancer cell lines. By contrast, derivatives of $InsP_6$ with lower phosphate number, such as *myo*-inositol (1,2,4,5,6)-penta*kis*phosphate ($InsP_5$), have not been studied due to their costly preparation. Here we investigated the effects of $InsP_6$ and $InsP_5$ on the human bone osteosarcoma cell line, U2OS, by phenotypic assays. After 48 h after treatment with either $InsP_6$ and $InsP_5$ at 15 or 50 µM, cells display a striking vacuole formation, as observed by light microscopy. By staining with acridine orange and observing by fluorescence microscopy, the vacuolated cells showed acidic vesicle accumulation, indicative of increased autophagy. By staining with the non-permeant fluorescent dye Lucifer yellow and fluorescence microscopy we observed that vacuolated cells showed higher levels of the fluorescent dye, indicative of endocytosis, than non-treated cells. Vacuoles observed by phase contrast microscopy are frequently stained with Lucifer yellow and acridine orange. These findings suggest that $InsP_5$ and $InsP_6$ affect endocytosis, which subsequently leads to increased lysosomal degradation the engulfed material. Understanding the effects of IPs on human cells is important in understanding inositol signalling pathways and may lead to the discovery of novel anticancer compounds.

Microplastic Contamination of the Canadian Archipelago

Kolter, S. Pieńkowski, A. Furze, M. & Ross, M.
MacEwan University, Physical Sciences Department

Microplastics (MPs) are considered to be synthetic polymeric material <5mm in size and originate from either primary sources, those manufactured to be <5mm in size, or from the breakdown of larger pieces by physical, chemical and radioactive processes. These fragments may become small enough to allow them to be ingested and bio-accumulate. MP pollution has been recorded in marine sediments in nearly all of the Earth's oceans and has been recently quantified in Greenlandic sea ice and Greenlandic sea way sediments. An independent research project with Drs Matthew Ross, Anna Pieńkowski and Mark Furze in the Fall of 2017 quantified MP pollution in Frobisher Bay sediments.

Eleven samples were collected during the 2017 summer expedition aboard the CCG Amundsen ice breaker. They were taken in a linear fashion within Frobisher Bay allowing for the correlation of MP deposition and proximity to anthropogenic habit in the area. Extraction procedures were based on modifications of standard methods developed by the National Oceanic and Atmospheric Administration. This includes four procedures which aimed to separate MPs from sediments and micro-organic materials by exploiting differing density and dissolution properties. We collected sieved MPs of five size ranges via vacuum filtration onto 0.45μm filter paper for analysis. Subsequent visual mapping allowed large scale processing of data and pinpoints areas of interest for spectral analysis. Using Raman microscopy, polymer identification may allow us to understand sources and migratory patterns of MPs. This process allowed us to quantify MP contamination in Arctic sediments enhancing global data sets for future research into MP source, transport and fate.

We can conclude that MP contamination is found at higher concentrations nearest the City of Iqaluit relative to mouth of Frobisher Bay with averages ranging between 13.08 MPs per gram of sediment (mp/gs) and 5.31 mp/gs respectively. This suggests that relatively small communities can have a significant impact on MP contamination levels in secluded oceanic bays.

I look forward to the opportunity to further disseminate microplastic contamination research as it is vital in increasing public awareness and pressure on policy makers to initiate mitigation and reclamation of this very important global issue.

Constructive Orderings on the Groups of Integers mod n

Zack Baker

The King's University

Abstract

This research is motivated by the desire to extend the traditional idea of the factorial into the structure of groups, specifically the groups of integers mod n. To accomplish this, we first create an inequality $\prec$ for the group $\mathbb{Z}/n\mathbb{Z}$, which cololoquially defines what we call an ordering on $\mathbb{Z}/n\mathbb{Z}$. Then, to define the factorial for some element g of $\mathbb{Z}/n\mathbb{Z}$, which we denote $g\dagger$, we simply take the sum of all elements smaller than or equal to g mod n. That is, $g\dagger = \sum_{x \in S} x$ where $S = \{h | h \preceq g, h \in \mathbb{Z}/n\mathbb{Z}\}$. From this, we can study the structure of the group under this ordering. We define the function $D_{\preceq} : \mathbb{Z}/n\mathbb{Z} \to \mathbb{Z}/n\mathbb{Z}$ by $D_{\preceq}(\mathbb{Z}/n\mathbb{Z}) = \{g \dagger | g \in \mathbb{Z}/n\mathbb{Z}\}$, and we call $D_{\preceq}(\mathbb{Z}/n\mathbb{Z})$ the *dagger subset* of $\mathbb{Z}/n\mathbb{Z}$. The main focus of this research is the study of these dagger subsets, and their relation to the original group $\mathbb{Z}/n\mathbb{Z}$.

SESSION C2 | B660 | 3:00-4:00 PM

The Octagon Navigation Task Reveals Sex Differences in Spatial Ability

Kate Chua
University of Lethbridge

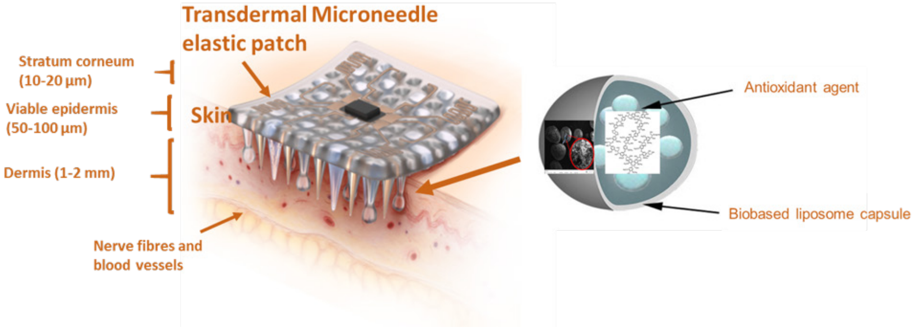
The Morris Water Maze (MWM) is commonly used in research for investigating spatial cognition and hippocampal-dependent learning in nonhuman animals. One of the most consistent findings in the literature is the male advantage in spatial ability. Usually, the MWM is adapted as a virtual reality for testing in humans. In our lab, we constructed a real-world navigation task and found that by default, men implemented an allocentric strategy whereas women adopted an egocentric strategy when finding the target location. Based on these findings, the present study designed a table-top version of the MWM. The goal of each subject is to locate a hidden target by navigating on an octagonal board using different spatial navigation strategies. The allocentric condition experiment tested 60 subjects (30 women) ages 18-25 and examined their ability to find a hidden target located relative to constant environmental room cues. Results revealed that men outperformed women on this task. In the egocentric condition experiment, 60 subjects (28 women) were directed to find a target location that remained consistent with respect to their body axis and starting position in the experiment. Women outperformed men in the egocentric condition experiment. In the neutral condition, the target was located in the center of the board and could be found using either egocentric or allocentric strategy, which resulted in no sex differences. Our results suggest that when a spatial task requires competition between two sources of information, an egocentric strategy appears more prominent in women whereas an allocentric strategy appears more prominent in males. Future work may use fMRI to see if sex differences in spatial navigation will correlate to differences in functional connectivity.

Stabilized Liposomes transdermal patch for loaded antioxidants skin therapy

Yeonkyeong Lee and Samuel M Mugo
MacEwan University, Physical Sciences Department

As the largest organ in the body, skin acts a protective barrier insulating other organs from physical, chemical or biological damage. Skin aging triggered by sun's ultraviolet rays, and pollution decrease its protective barrier and it's physiological functional properties. The research hunt is on by cosmetic industry and dermatologist for effective therapeutic technologies to slow and reverse skin aging. Some modern skin antiaging therapy include the radiofrequency technology that work on the basis of thermal energy application onto the skin, believed to induce dermal and epidermal remodeling, which triggers regeneration.[1,2] This is an expensive, public inaccessible therapeutic technology, and as such an economical approach remain the use of anti-aging skin care products with functional compounds called antioxidants, which protects the skin from free radical oxidative processes that induce skin aging. Numerous antioxidants exist, —e.g. retinol, algae oil, and lecithin, — however there remains a challenge for optimal transdermal delivery of these compounds the epidermis to afford effective skin protection. In addition, antioxidants are environmentally unstable, and lose their potency with exposure. As such, approach to mitigate both the instability and as a delivery vehicle is the use of liposome technology. Liposome is a (nano) or microsphere with an aqueous center pocket (houses the anti-aging agent) and a lipid exterior, a dual structure that affords skin penetration.[3,4]

As a proof concept, we have developed polyhydroxylated fatty acid (polyol) liposome and used it to encapsulate a model antiaging agent. The polylol liposomes was compared with lecithin based liposomes for controlled release on the anti-aging agent. Towards a fabrication of a dermatologist usable device, we have demonstrated a prototype voltage responsive biobased transdermal patch impregnated with antioxidant loaded liposomes, with controlled release of the antiaging agent triggered by disruption of the liposomes by a mild voltage application. Our presentation, will showcase the developed prototype.



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Investigating the function of snR30 during ribosome biogenesis

Timothy Vos, Erin Kelly, and Ute Kothe
University of Lethbridge, Department of Chemistry and Biochemistry

snR30 is an essential and atypical H/ACA box guide RNA conserved across all eukaryotes. In general, the H/ACA ribonucleic protein (RNP) complex is formed by Cbf5, Gar1, Nop10, and Nhp2 associating with an H/ACA guide RNA. This complex is typically involved in the conversion of uridine to pseudouridine. The snR30 RNP, however, is essential for processing of precursor ribosomal RNA (rRNA) at three sites. These cleavages are required for production of mature 18S rRNA which is necessary for ribosome biogenesis. snR30 differs from other H/ACA guide RNAs in that the binding of the target RNA occurs in the lower half of the unpaired pocket within the terminal hairpin compared to traditional H/ACA RNAs. Additional proteins including Utp23, Utp24, Rrp7, Rok1, and others interact either with snR30 or snR30-interacting proteins.

This project aims at reconstituting and characterizing a purified snR30 RNP complex to study the most critical function of H/ACA RNPs during ribosome biogenesis. The H/ACA core protein complex Cbf5-Nop10-Gar1 was purified using glutathione- and Nickel-sepharose chromatography. Synthesis and purification of RNA was achieved through a series of different techniques. First, purified yeast genomic DNA was used for the amplification of snR30 and 35S rRNA. Sequences were cloned into a plasmid. Next, PCR products of these sequences were used as templates in *in vitro* transcription to generate RNA. Finally, short target RNA comprising a fragment of rRNA was purified using anion exchange chromatography while snR30 was purified by size exclusion chromatography. The target RNA was fluorescently labeled with a fluorescein dye at the oxidized 3' end. With these components, it now becomes possible to study how snR30 interacts with the H/ACA proteins and how the snR30 RNP complex binds to and dissociates from target RNA, e.g by determining the affinity for rRNA.

Examining Correlates and Consequences of Implicit Theories of Social Anxiety

Kyla Doherty and Andrew Howell, PhD
MacEwan University

A small but growing literature concerns the application of implicit theories (i.e., incremental and entity mindsets regarding the stability or malleability of attributes, respectively) to disorders and their symptoms. Implicit theories of social anxiety were explored through a cross-sectional study (*N* = 274 undergraduate participants) examined correlations among implicit theories of social anxiety and social anxiety symptoms, emotional regulation, help-seeking, and behavioural engagement. As predicted, incremental mindsets were correlated withlower social anxiety, greater use of emotional reappraisal, more help-seeking behaviour, greater behavioural activation and less behavioural inhibition. In a regression analysis, incremental mindsets predicted social anxiety symptoms above and beyond the remaining variables. Overall, the current findings warrant additional research of implicit theories of social anxiety, in clinical populations with social anxiety disorder to determine if the found correlates will be replicated and exacerbated within a clinical population.

Synthesis and Applications of Iron Nanoparticles Toward Environmental Remediation

Youssef Wahba, Dr. Liza Abraham, Dr. Chris Wang
Ambrose University, Department of Biology

The applications of iron nanoparticles are numerous, ranging from drug delivery to wastewater treatment. We followed a number of different methods for synthesizing magnetic and nonmagnetic iron nanoparticles. A couple of the nanoparticles were characterized using a Scanning Electron Microscope (SEM). Furthermore, we tested the different nanoparticles using a Fenton-like system, through which it was determined that iron nanoparticles were the most effective, as catalysts, when prepared using sodium borohydride. The degradation of Methylene Blue, using the sodium borohydride synthesized iron nanoparticles, was monitored via Ultraviolet-Visible (UV) spectroscopy, as well as Thin Layer Chromatography (TLC).

Poster Abstracts

Abstracts are listed by group and poster number with the presenter underlined (where needed).

GROUP A | 1:00-1:54 PM

Mental tug of war: How does grasping and language affect each other?

Clarissa Beke, Nicole van Rootselaar, Claudia Gonzalez
University of Lethbridge

Previous studies have found an association between hand motor actions and speech function. The objective of this study was to investigate if verbal fluency tasks (word production) can affect grasping behaviour. We reasoned that the type of word would influence grasping behaviour differentially. Specifically, we hypothesized that when compared to nouns, the generation of verbs would interfere more with grasping because previous research has shown activation in primary motor cortex during verb comprehension. We recruited left- (n=15) and right-handers (n=24) to participate in this study. Each participant was asked to perform a grasping task (LEGO building task), and a word fluency task both separately and simultaneously. The word fluency tasks consisted of noun and verb generation. Our results showed that overall, the number of times participants incorrectly grasped a block (place errors) while simultaneously producing verbs predicted the number of verbs produced while building; the more place errors made, the fewer verbs produced. This was not the case when producing nouns. To conclude, speech production, specifically of verbs interfere with manual action.

Metabolomic Analysis of Prenatal Maternal Stress Effects on Offspring as a Result of the 2011 Queensland Flood

Rebecca R. McHugh[1, 2], Naveenjyote S. Boora[1,2], Gabrielle Simcock[3,5], Sue Kildea[3,4], Marie-Paule Austin[6], David P. Laplante[7], Suzanne King[7,8], Gerlinde A.S. Metz[2], and Tony Montina[1]
[1]University of Lethbridge, Department of Chemistry and Biochemistry; [2]University of Lethbridge, Department of Neuroscience; [3]University of Queensland, Midwifery Research Unit, Mater Research Institute; [4]University of Queensland, School of Nursing, Midwifery and Social Work; [5]University of Queensland, School of Psychology; [6]University of New South Wales; [7]Douglas Mental Health University Institute; [8]McGill University, Department of Psychiatry

INTRODUCTION: It is widely acknowledged that the health outcomes of offspring are directly linked to the health of their mother during pregnancy. The impacts of pre-natal maternal stress (PNMS) can cascade as development of the offspring continues, and are linked to negative health outcomes.

OBJECTIVE: Our goal was to determine the metabolomic differences in offspring who were exposed *in utero* to the 2011 Queensland Flood in relation to the mother's level of subjective distress and objective hardship.

METHODS: Ninety urine samples were obtained from 51 male and 39 female 4-year-old offspring. Metabolomic profiles were acquired using a 700 MHz Bruker Avance III HD NMR spectrometer and subsequently binned. Partial Least Squares-Discriminant Analysis (PLS-DA) was used to identify differences in high vs. low composite subjective distress and high vs. low objective hardship in metabolic profiles, in both male and female groups. Metabolites leading to significant group separation were identified using both Variable Importance Analysis based on random Variable Combination (VIAVC) and a Mann-Whitney U test. Metabolanalyst software was used for metabolite sets enrichment analysis of altered metabolites, and to identify potential biochemical pathways and disease pathologies in the offspring.

RESULTS: Group separation was observed between high and low levels of both objective hardship and composite subjective distress groups, in both males and females. Several metabolites were detected as being either up- or down-regulated, thus contributing to the observed separation, including creatinine and formate.

CONCLUSIONS: The metabolites identified as significantly altered have been associated with several negative health outcomes. Creatinine down-regulation has been associated with dysfunction in Krebs cycle thus potentially disturbing energy metabolism and contributing to psychiatric illness. Formate up-regulation has been linked to oxidative stress and correlated to metabolic dysfunction in genes relating to neurodegenerative diseases. Understanding the biological pathways affected by exposure to PNMS allows for an improved approach to patient treatment.

Synthesis of Sunscreen Dendrimer

Benny Rana, Yelizabeta Dmitriev, & Ahsan Ayub
Mount Royal University, Chemistry Department

Longevity and effectiveness of sunscreens and other UV-protectant lotions have been studied and researched for upwards of 90 years. Sunscreen lotions have been linked with prevention of a number of genetic mutations that may lead to skin cancers. The effectiveness of sunscreens is generally measured as Sun-protection Factor (SPF), which describes the minimal time that a sunscreen product can provide protection. Despite many advances in the field most sunscreens fail to deliver their claimed SPF protection. This is normally a result of human error; either in the amount applied, or the process of application. The focus of this research has been to investigate the use of second-generation dendrimers to increase the quantity of active sunscreen molecules present after application. Dendrimers, with their highly manipulatable physical and chemical properties, enable us to increase the "stickiness" of a sunscreen. This experiment focuses on finding optimal conditions to form a second-generation sunscreen dendrimer, and to test whether the sunscreen will retain its protective function in this context.

Regulating gene expression through targeted RNA modification

Keara Cheredaryk, Dominic Czekay, and Ute Kothe
University of Lethbridge, Alberta RNA Research and Training Institute (ARRTI), Department of Chemistry and Biochemistry

Pseudouridylation refers to the isomerization of uridine to pseudouridine in RNA and is catalyzed by enzymes known as pseudouridine synthases. In eukaryotes, pseudouridylation of rRNA is primarily directed by a complex of proteins and a box H/ACA guide RNA. The guide RNA specifies a target by forming transient base pair interactions on either side of the target uridine, although other standalone pseudouridine synthases may employ different targeting mechanisms.

With this project, we aim to modify naturally occurring guide RNAs to allow for specific targeting in a location different from the original. Pseudouridylation of a premature stop codon in mRNA results in translational readthrough and production of a functional protein. Here, we utilize the CUP1 gene from baker's yeast as a model gene to be targeted by pseudouridylation that enables survival in the presence of high copper concentrations.

First, we have generated and purified two guide RNAs never previously worked with in our lab to test their effectiveness at targeting a specific uridine. Also, the proteins associating with these H/ACA guide RNAs have been expressed and purified for biochemical investigations. Second, a premature stop codon was introduced at the ninth codon of the CUP1 gene (Q9UAA). As a control to mimic the presence of a pseudouridylated stop codon, we have generated the mutants cup1p(Q9S) and cup1p(Q9T) mimicking readthrough of the premature stop codon and tested their ability to chelate copper *in vivo*. Interestingly, these experiments revealed that not all premature stop codons can be rescued by pseudouridylation. Current work focuses on the insertion of test sequences harboring premature termination codons upstream of CUP1. These test sequences are predicted to be targeted by known pseudouridine synthases.

Ultimately, this experimental system will identify which sequences harboring premature stop codons can be targeted by pseudouridylation to re-activate gene expression. This new system to regulate gene expression has applications in bioengineering and possibly the treatment of inherited diseases resulting from mutations that cause premature stop codons.

Effectiveness of Contact Lens Cleaning Solutions on the Disruption of Biofilms Formed by Different Microorganisms

Bhavjot Garcha
University of Alberta, Augustana Faculty

My objective is to examine biofilm formation of Staphylococcus aureus, Pseudomonas aeruginosa and Candida albicans on contact lenses and to test the effectiveness of different contact lens cleaning solutions to remove or disinfect the biofilms. These particular microorganisms are commonly found as pathogens in ocular tissue. Given the tendency for biofilms to form on contact lenses especially after the lenses are removed from the eye and are saturated with nutrient-rich lipoproteins that "feed" contaminating microorganisms, it is important to undertake simple hygienic measures to ensure biofilm formation is prevented. After biofilms were experimentally formed on daily contact lenses, the lenses were subjected to four different treatment solutions that included a Biotrue™ multipurpose cleaner, an Opti-free™ multipurpose cleaner, a Clear Care™ hydrogen peroxide-based solution or tap water. A second experiment was conducted where the same treatments were tested on rigid gas permeable lenses (RGPs), monthly and extended wear contact lenses. These different solutions were chosen because they have different active ingredients. I anticipate these experiments will provide important information to help inform contact lens users how to best maintain their contact lens cleaning regimens and protect their eyes from infections.

Using 1H NMR Spectroscopy to Compare Urinary Metabolites of Stroke and Spinal Cord Injury Patients Before and After Neurorehabilitation

Elani A. Bykowski[1,3], Jamie N. Petersson[1,3], Zachary R. Wanner[1,3], Chantel T. Debert[2], Gerlinde A. Metz[1], and Tony M. Montina[3]
[1]University of Lethbridge, Department of Neuroscience; [2]University of Calgary, Department of Clinical Neurosciences; [3]University of Lethbridge, Department of Chemistry and Biochemistry

Background: Rehabilitation represents the primary approach to promote long-term functional recovery after neurological injury. There is an urgent need to improve the effectiveness of rehabilitation therapies to optimize the potential for recovery in an individual. Precision medicine approaches using modern 'omics' techniques represent vital prerequisites in stratifying individual patients with neurological injury to their optimal rehabilitation program. Metabolomics research from our laboratory has demonstrated that metabolite levels in urine detected by NMR spectroscopy serve as reliable prognostic markers for neurological injury. This study aims to determine if a proton NMR-based quantitative metabolic profiling approach can identify novel biomarkers in clinically accessible biofluids that are indicative of both the repair processes and treatment efficacy following neurorehabilitation from stroke and spinal cord injury. The main hypotheses of this study are (a) that each of the neurological conditions will yield changes in the metabolic profiles that can be correlated to the extent of recovery of a patient and (b) that biological pathway analysis will provide an insight into the mechanisms behind the repair process. These techniques will provide a greater understanding of the biochemical processes that mediate neural repair in the central nervous system for clinical application.

Methods: Patients with stroke and spinal cord injury ($n \geq 14$ per group and sex) were recruited through the Foothills Medical Centre in Calgary, Alberta. Urine samples were collected from patients within 48-72 hours of injury and again at 6-months post-injury, following neurorehabilitation. A 700MHz Bruker Avance III HD NMR spectrometer located at the Canadian Centre for Behavioural Neuroscience was used to acquire the metabolic profiles of urine samples pre- and post-neurorehabilitation. Multivariate statistical and biomarker analysis tests were used to determine changes in the metabolic fingerprint which can potentially be linked to clinical outcomes.

Impact: Within the rehabilitation field there is an urgent need to generate evidence-based therapies and validate existing ones. Metabolomic analysis will provide a time- and cost- effective method to identify optimal rehabilitation therapies based on an individual's impairments, through translational biomarker discovery. This personalized medicine approach offers a new strategy to evaluate and improve the efficacy of neurorehabilitation strategies for stroke and spinal cord injury patients.

Creating A Fitting Algorithm for Exoplanet Detection

Usman Mohammed
MacEwan University (Research student for Dr. Stefan Cartledge)

The purpose of this project is to create an accurate fitting function for transiting stars. Data from these transiting stars will ultimately be used to identify new exoplanets. It is very apparent that a fitting function that addresses multiple environmental parameters affecting brightness measurements is needed as exoplanet identification can be a cumbersome and time consuming process. Utilising computer code will streamline the process of exoplanet identification and can then allow researchers to focus their energies solely on data collection.

It should be duly noted that in order to collect data from transiting stars; one can use amateur equipment but, for the sake of maximum accuracy; a high powered telescope would be more suitable ("Exoplanet Transit Parameters", 2008). Previous students at MacEwan that collected transiting star data utilised the Athabasca University Robotic Telescope (AURT) ("Defining the Transit Method", 2017). This telescope requires booking periods thus, in order to maximize utility and efficiency; more energy should be spent on data collection and result analysis.

The current state of exoplanet discovery is both innovative and exciting. In fact in February of 2017, a team of astronomers at the University of Liege in Belgium discovered four more Earth-sized exoplanets (bringing the total up to seven) orbiting Trappist-1 which is a star that is classified as an ultracool dwarf ("Astronomers Discover", 2017). Another discovery would be that of Proxima b, the exoplanet that is closest to our solar system ("An Earth-like Atmosphere", 2017). Astronomers are currently debating whether or not Proxima b will be able to sustain life. Thus, it can be shown that exoplanet discovery and analysis yields results and is vital for our understanding of the universe.

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The Effects of Adolescent WIN-55 Exposure: Assessing Changes in Neuroanatomy and Social Behaviour in Rats

Niehaus, C., Burke, C., Gibb, R.
University of Lethbridge

The effect of cannabis on adolescent development is a topical and socially relevant issue, as several states have moved to legalize its use, and with Canada seeming to follow suit. Previous work in this field has found that adolescent exposure to cannabis can lead to deficits in the development of higher-level brain functions like attention and working memory (Ehrenreich et al., 1999). Because of the implication of cannabis exposure on the development of the adolescent brain, particularly regarding executive function skills, we believe studying play will serve as a benchmark from which we can begin to assess these changes. In order to do so, this study utilized WIN-55, a THC analogue and endocannabinoid (CB_1) agonist that elicits comparable effects to those displayed following THC exposure (Schneider and Koch, 2003).

Over the course of this study, animals were exposed to a daily dose of 0.3 mg/kg WIN-55, or a saline control for 10 days during puberty. Dosing encompassed postnatal day (P) 22-32 for females and P32-42 for males. We hypothesized that this dosing paradigm would be sufficient to elicit changes in the behaviour, ultrasonic vocalizations and neuroanatomy of the affected animals. Following the final injection, animals were socially isolated from their cage mate for 24hrs to encourage playful interaction during behavioural testing. The animals were then paired with their cage mate and placed in a dark, soundproof chamber where audio and video were recorded for 10 minutes. This procedure was replicated the following day so as to record a second day of behavioural analysis. Following all behavioural testing the animals were sacrificed and their brains extracted for anatomical analysis. Measures of neuroanatomy included thalamic volume and cortical thickness measurements, which were taken from selected planes of the brain. Stereological analysis was conducted on two frontal regions of the brain, AID and Cg3, which contribute to higher brain functioning. Adolescent play behaviour was recorded over peak-play periods and was analysed to reveal a significant decrease in the number of interactions between affected males. Ultrasonic vocalization analysis also revealed significant decreases in the number of calls exhibited in affected males.

Dilbit toxicity: Behaviour changes in freshwater amphipods.

Melissa Giddy
University of Lethbridge

The Alberta oil sands contain an estimated 167.2 billion barrels of bitumen, a heavy crude oil that comprises the majority of Canada's crude oil production. Unrefined bitumen is extremely viscous compared to conventional oil, which is a fluid at atmospheric pressure and temperature, and therefore must be diluted with natural-gas condensates to create diluted bitumen or 'dilbit', so that it can flow through pipelines. New Canadian dilbit pipelines such as the Enbridge Northern Gateway Pipeline and the Kinder Morgan Trans Mountain Expansion Pipeline will come in close proximity to thousands of freshwater ecosystems. When dilbit is spilled, it will initially float in freshwater, but the added diluents will begin to evaporate and the remaining dilbit will combine with sediments, causing it to sink in freshwater Ongoing research is addressing the toxicity of sediment-bound dilbit to the freshwater amphipod *Hyalella azteca*. In this study, *Hyalella azteca* will be exposed to sediment bound dilbit for 96 hours and the adverse behavioural and physiological effects of dilbit will be assessed. To date, sediment bound dilbit has not been toxicologically studied. This research will address these questions and refine research techniques using dilbit and bitumen products in toxicity research using amphipods and other organisms. Not only that but addressing these issues will lead to better knowledge on how to best lead cleanup efforts in freshwater dilbit spills, saving money, time and possibly preventing environmental devastation as a result of pipeline spills.

Perception of Recreational Opportunities on a Campus to Increase Wellness

Brittni Steeves
University of Lethbridge

Universities strive to enhance the student experience and promote student success. A major contributor to student success is the development of wellness, defined as the state of being in good health, especially as an actively pursued goal. Positive subjective wellness is achieved when individuals actively engage leisure activities to increase wellness. In conjunction with the Lethbridge Campus Ecology Project, the purpose of the study was to investigate undergraduate students' use of campus green space to increase wellness and manage perceived stress. To enhance wellness in practice, it is essential to determine not only what the students want, but also what types of outdoor leisure additions they would use. A survey was generated to explore students' perception of leisure opportunities on campus and investigate what type of outdoor recreation students would use to enhance their wellness. Information gathered from responses will provide insight on what implementations would be utilized to increase greater wellness and reduce stress in students. It is hypothesized that outdoor leisure opportunities will be associated with an increase in subjective student wellness. Additionally, it is expected that females and males will differ significantly in their choices for wellness enhancement strategies.

An analysis of mutational signatures in breast cancer among young women

Nicole Ewert
University of Calgary (under the supervision of Dr. Darren Brenner and Dr. Edwin Wang)

BACKGROUND Approximately 7% of breast cancer cases are diagnosed among women 40 years of age or younger, and over 40% of all cancer diagnoses in this population are breast cancer. In 1969-2012, there was an increasing incidence of breast cancer among young (≤40 years) Canadian women, and in 1995-2006 there was also an increase in incidence of 3% and 1% among European women 20-29 years and 30-39 years respectively. Younger age is related to later stage at diagnosis, and worse outcomes even when controlling for disease stage and other prognostic features. The most aggressive tumour subtypes, human epidermal growth factor receptor 2 positive and triple-negative breast cancer have a higher prevalence among young women. Clinical and molecular differences between tumours diagnosed at different ages motivates study of differences in patterns of mutations at a genomic level. Mutational signatures are patterns in the type and three-nucleotide neighbourhood of somatic single-nucleotide variants across the exome, which may provide insight into the exposures and processes leading to carcinogenesis.

METHODS Clinical and variant call data for 1098 breast cancer patients was taken from The Cancer Genome Atlas. Cases were separated into young (≤40 years) and old (>40 years) age groups, and the mutational load was found for each. The *SomaticSignatures* R package was used to determine the mutational spectrum of one young patient. This package will be used to construct mutational spectra for each age group, then decompose them into mutational signatures.

RESULTS There were 91 and 951 patients in the young and old categories respectively. The young group had a median mutational load of 166.5 mutations, slightly less than the median of 198 in the older group. The mutational spectrum showed a high frequency of TCA>TTA and TCT>TTT variants, which is similar to the previously identified Signature 2, and similarly a high frequency of TCA>TGA and TCT>TGT transitions which resembles Signature 13. These two signatures are commonly found in the same tumour, and are thought to be caused by cytidine deaminase activity of AID/APOBEC proteins.

CONCLUSIONS Patterns in a mutational spectrum suggest that Signatures 2 and 13 may be present in at least one young breast cancer tumour, but this approach should be continued to confirm this hypothesis. Further research should be conducted with a larger sample of young breast cancer patients with known exposures to risk factors.

Metabolomic Profiling of Biomarkers Indicative of Ancestral and Lifetime Adversity in a Two-Hit Stress Model

Prachi Sanghavi[1], Joshua Heynen[1], Keiko J.K. McCreary[1], Tony Montina[2] and Gerlinde A.S. Metz[1]
[1]University of Lethbridge, Department of Neuroscience; [2]University of Lethbridge, Department of Chemistry and Biochemistry

Introduction: Chronic prenatal maternal stress (PNMS) can have adverse effects on the developing fetus and lifetime health. The effects depend on the number of stressors individuals are exposed to. Over-activation of the mother's stress response also potentially triggers epigenetic marks that can be transmitted to several generations of offspring. To date, very little research has focused on how exposure to ancestral PNMS affects an individual's response to both chronic and acute stress throughout their lifetime.

The purpose of this study was to investigate if exposure to ancestral PNMS puts an individual at an evolutionary advantage or disadvantage with respect to their altered stress response. This study utilized a rat model of ancestral PNMS to explore the response of the metabolome to both acute and chronic stress.

Methods: Forty-eight male rats from the third filial generation were derived from three different lineages: (1) a transgenerational PNMS lineage where only the F0 mother was exposed to stress; (2) a multigenerational PNMS lineage where the mother from each generation was exposed to stress; and (3) a control lineage where there was no experimental stress exposure. Each of these groups were split in two; an acute stress group and a chronic stress group. Plasma was collected from each animal, processed to extract the water-soluble metabolites, added to NMR buffer, and pipetted into NMR tubes. NMR spectra were acquired and the data underwent a data reduction step (binning), normalization, scaling, and both univariate and multivariate statistical testing. These tests identified spectral peaks from metabolites that had been significantly altered across comparison groups. Chemometric software was utilized to determine the identity of altered metabolites and pathway topology analysis was performed.

Results: Multivariate and univariate statistical tests indicated that exposure to chronic stress in ancestrally stressed rats creates significant alteration in the metabolomic profile when compared to control animals. No differences were observed in the case of acute stress.

Conclusions: Our results support the hypothesis that ancestral and lifetime stress cumulatively affect the metabolome. A subset of metabolites can potentially act as biomarkers of stress during pregnancy. This procedure may aid in the development of new predictive and diagnostic strategies in precision medicine approaches.

Modelling Variations in Solar Irradiance

Kirsti Long[1]
[1]MacEwan University, Department of Physical Sciences

The sun is the main source of energy for the Earth, and governs most atmospheric, biological, and environmental processes. Due to fluctuating composition, thickness, and pollution, solar radiation can be scattered or absorbed in the atmosphere affecting the amount received by Earth's surface as these interactions vary. Solar irradiance is the total amount of radiation reaching Earth's surface, in watts per square meter, from the sun. Irradiance can be measured with a pyranometer, and is governed by the solar constant, atmospheric thickness, atmospheric composition, and beam dilution. In this project we have modeled the solar irradiance expected from a plane-parallel atmosphere to determine the sensitivity of the PYR-BTA Vernier Pyranometer to variations in atmospheric transparency with the intent to quantify pollution levels in urban areas. We used the solar irradiance data captured from MacEwan University to model the partial solar eclipse of August 21, 2017.

The role of eukaryotic initiation factor 5B (eIF5B) in cell cycle regulation

Kamiko Bressler, Divya Sharma, Dr. Nehal Thakor
University of Lethbridge, Department of Chemistry and Biochemistry

Gene expression is critically regulated at the transcriptional, translational, and post-translational levels. Dysregulation and altered mechanisms of translational control have significant consequences in processes including cell growth, cell death, cell proliferation, and maturation. Initiation is the rate-limiting step of translation, which is inhibited under physiological stress conditions. During the integrated stress response, the α subunit of eukaryotic initiation factor 2 (eIF2) is phosphorylated. This phosphorylation attenuates general translation, by preventing the reformation of the necessary ternary complex. Despite the attenuation of general translation, certain mRNAs containing upstream open reading frames (uORFs) are favorably translated during this condition. uORFs are mRNA elements with a start codon in the 5' UTR that is out-of-frame with the main coding sequence. Bioinformatic studies have shown 49% of human transcripts to contain uORFs.

Preliminary data suggests that the depletion of eIF5B parallels the effects of phosphorylation of eIF2α. eIF5B depletion has been observed to inhibit global translation, while enhancing the translation of certain uORF-containing mRNAs. The Thakor lab has shown the protein p27 to be upregulated when eIF5B is knocked down in U343 (human glioblastoma multiforme) cells. As p27 is a cyclin-dependent kinase inhibitor (CKI), which controls cell progression from the G1 to S phase, this suggests a significant role for eIF5B in the cell cycle. However, eIF5B depletion has been observed to not have significant effects on the cyclin-dependent kinase inhibitor: p21. Further, PI staining and flow cytometric analysis have demonstrated that eIF5B does not have any significant effects on the cell cycle. This data suggests that eIF5B has a significant role in the regulation of p27, but does not contribute to cell cycle regulation.

The effects of molecular crowding on the kinetics and small molecule inhibition of alkaline phosphatase

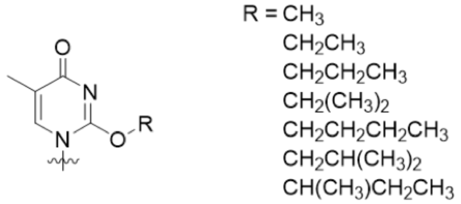
Michael Cordara, Kyle Poffenroth and John K. Chik
Mount Royal University, Department of Chemistry and Physics

Enzymes have adapted to function in complex environments crowded with many other solutes. To get a better understanding of *in vivo* crowding, we used polyethylene glycol (MW 8000) and dextran (MW 6000) as *in vitro* crowding agents and observed their effects both the kinetics of alkaline phosphatase-catalyzed para-nitrophenyl phosphate hydrolysis and the inhibition of this reaction by competitive and uncompetitive inhibitors. Reaction kinetics were followed using UV-visible spectrometry and the initial rate was analyzed using Michaelis-Menten kinetics to arrive at an apparent V_{max} and K_m for each reaction condition. We observed that polyethylene glycol increased V_{max} while a similar amount of dextran strongly reduced V_{max}. Crowding by these agents also significantly altered the effectiveness of small-molecule inhibitors and suggests that the action of drugs can be different going from "bench" research to "bedside" application.

Computer Modeling of the Hydrogen-bonded Dimers Between O2-alkylthymine and the Canonical DNA Bases

Dylan J. Nikkel, Priya Bhutani, Katie A. Wilson and Stacey D. Wetmore*
University of Lethbridge

Alkylation of the DNA bases is induced by a variety of exogenous sources, including tobacco smoke, atmospheric halocarbons, chemotherapeutic drugs, and contaminants within certain foods, as well as endogenous sources, such as S-adenosylmethionine (SAM). If not repaired before DNA replication takes place, this damage typically stalls a standard DNA polymerase and replication instead occurs through translesion synthesis (TLS). Although TLSpolymerases have more flexible active sites and can bypass the damaged site, the TLS process is error-prone, and can lead to changes in the selective Watson-Crick (WC) pairing observed in undamaged DNA. These mutations can lead to diseases, such as cancer. The present study investigates the effects of alkylation at the O_2 site of thymine (T), including the effects of increasing the alkyl chain size (see below), on the structures of dimers formed with the canonical DNA bases. Alkylation alters the WC face of T, leading to a high frequency of mutations during DNA replication. However, previously reported experimental data indicates that the types and frequencies of mutations depend on the size and degree of branching of the alkyl chain. Using density functional theory (DFT) and molecular dynamics (MD) simulations, the structural properties of potential mispairs formed upon DNA alkylation are characterized. This work provides the first structural insight to rationalize the experimentally observed mutations, and provides the foundation for future modeling that will consider the interactions between damaged DNA and TLS polymerases.



The extraction of undecaprenol from sumac leaves

Luke Vanderwekken, Dr. Leah Martin-Vissche
The King's University

Bacterial cells are fortified by an outer layer of peptidoglycan and lipid II is the key precursor molecule in the biosynthesis of peptidoglycan. Lipid II is comprised of several units: a disaccharide moiety, a pentapeptide, and a C55 undecaprenyl chain, which attaches to the disaccharide via a pyrophosphate linker. Since lipid II plays a key role in providing structure and integrity to bacterial cells, it is an attractive target for the development of novel antimicrobial agents. Such studies require the ability to synthesize lipid II and its analogues. However, one of the limitations to synthesizing lipid II is the preparation of the C55 lipid chain. While this molecule is difficult to synthesize, its immediate precursor, undecaprenol (C55-OH) can be extracted from sumac leaves. In this project, we describe the isolation of undecaprenol from the leaves of the sumac tree (*Rhus typhina*) and its purification by HPLC. At the conclusion of the procedure, roughly 20 mg of undecaprenol was collected. Two major results of the project are presented: first, the development of a simple method to extract this important compound from an abundant and renewable source; and second, the observation of the instability of undecaprenol.

Nucleotide Specificity Analysis in Universally Conserved NTPases

Daniel Rocca, Dr. Binod Pageni, Dr. Senthilkumar Kailasam, Harland Brandon, Dr. H.J. Wieden
University of Lethbridge

P-loop GTPases and related ATPases play important roles in many cellular processes. These processes include translation, motility and ribosome biogenesis. P-loop NTPases often serve to regulate these processes by acting as "molecular switches" that change between active NTP-bound states and inactive NDP-bound states (1,2). The YchF subfamily of the Obg family of P-loop GTPases is characterized based on its homology to bacterial YchF (1). This subfamily is notable because it differentially binds and hydrolyzes ATP and/or GTP based on small changes to the G4 motif, or "nucleotide differentiation motif". This motif varies between protiens and it has been shown that changes to its sequence affect the nucleotide specifity of the protein(1). Most protiens of the YchF family have not been characterized as ATPases or GTPases. To this end we intend to characterize the nucleotide binding and hydrolysis activity the G4 motif of multiple YchF protiens. Characterizing the G4 motifs will help to predict the nucleotide specificity of the protiens as a whole. An understanding of how changes to the G4 motif affect nucleotide binding is important for building understanding of ATPase/GTPase activity. This will be useful in the development of synthetic purine binding proteins and the examination of other similar proteins. Examination of the changes to the G4 motif in YchF homologues in multiple organisms will also help to develop an understanding of what evolutionary pressures cause the unusual variation in substrate for these proteins. Previously created Escherichia coli (*E. coli*) BL21-DE3 cells containing pET28a plasmids coding for YchF G4 variants were used to analyze the purine binding and hydrolysis properties. These G4 varriants consist of *E. coli* YchF with a G4 motif altered to match a different YchF homologue. Protien variants were analyzed using fluorescence titration and multiple turnover NTPase assays. Data were analyzed and used to determine differences in the binding and hydrolysis of purine nucleotide phosphates for each G4 motif variant. Analysis showed that each variant displayed differential binding and hydrolysis of purine phosphates. Furthermore the variant based on a previously characterized YchF homologue (OsYchF) showed dual ATPase and GTPase activity matching the original protein (3).

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Analysis of Aspartame and its Degradation Using HPLC-MS/MS

Nicholas Wawryk[1], Lindsay Blackstock[2] and Xing-Fang Li[2]
[1]The King's University; [2]University of Alberta, Division of Analytical and Environmental Toxicology, Department of Laboratory Medicine and Pathology

Disinfectants (e.g. chlorine) are used to inactivate pathogens, such as E. coli, in drinking water in order to prevent the transmission of waterborne disease. Unfortunately, disinfection by-products (DBPs) are formed when natural organic matter, present in raw water, reacts with the disinfectant. Many disinfection by-products are regulated in finished drinking water by Health Canada. However, these regulated DBPs do not explain the observed risk of developing bladder cancer. Halobenzoquinones (HBQs) are an emerging class of drinking water disinfection by-products (DBPs) detected frequently in Canadian tap water with an in vitro cytotoxicity up to 1000 times greater than regulated DBPs. Preliminary investigations show that aromatic amino acids, such as phenylalanine, act as HBQ precursors under disinfection conditions. Phenylalanine is a building block of aspartame (APM), a common artificial sweetener. Drinking water treatment processes can remove portions of natural organic matter, present in raw water that may act as HBQ precursors. However residual chlorine, present in tap water, may react with organic matter used in food and drink preparation, potentially forming HBQs in situ, prior to consumption. The main objective for this project is to investigate locally available foodstuffs containing APM that are prepared with tap water such as instant drink mixes and packaged sweeteners. Next, the concentration of APM, and its degradation products, in the prepared foodstuff will be determined. APM, and its degradation products, will be separated from the food matrix using high performance liquid chromatography (HPLC) and then detected with mass spectrometry (MS). Though a method was successfully developed, aspartame's degradation products, phenylalanine (PHE) and 5-benzyl-3,6-dioxo-2-piperazieacetic acid (DKP), the leading precursors for HBQs, were found to be below quantification limits in all samples. Regardless, this project provides a foundation for future studies regarding in-situ formation of HBQs.

Rainbow trout (Oncorhynchus mykiss) chemosensory detection ability for copper nanoparticles

Justin Sharpe, Parastoo Razmara, Dr. Greg Pyle
University of Lethbridge, Pyle Lab

Metal nanoparticles (NP) have become increasingly prevalent in aquatic environments that receive effluents containing metal nanoparticles. Copper NPs are of specific interest for this study and have exhibited toxic effects for many different organisms. This study aims to identify if rainbow trout (Oncorhynchus mykiss) can detect copper NPs at first exposure to IC_{20} concentrations and what their response will be in a flow-through choice maze. A statistically significant avoidance response to copper NPs was observed. These findings indicate that rainbow trout can detect and avoid copper NPs at IC_{20} concentrations upon first exposure.

Consequences of 1,3-butadiene DNA adducts – R,R-N^6,N^6-DHB-dA and R,S-1,N^6-γ-HMHP-dA – on DNA base pairing

Cynthia Fonderson, Ryan Kung and Stacey Wetmore

University of Lethbridge, Department of Chemistry and Biochemistry

DNA is the hereditary material in humans and almost all other organisms. Unfortunately, upon exposure to carcinogenic species and other compounds, our DNA can be damaged in a variety of ways. An example of DNA damage includes the formation of bulky nucleobase addition products (adducts), which may give rise to cancer. This poster focuses on adducts formed upon exposure to 1,3-butadiene – a human carcinogen that has been associated with an increased incidence of leukemia (cancer of the blood cells). Sources of 1,3-butadiene exposure include automobile exhaust and tobacco smoke, as well as polluted water and air at or near chemical, plastic or rubber facilities. In order to understand the consequences of DNA exposure to 1,2,3,4-diepoxybutane – a metabolite of 1,3-butadiene – this study examines the hydrogen-bonding properties of two adenine (dA) adducts formed upon addition of a bulky moiety to the N6 position, namely the R,R-N^6,N^6-DHB-dA and R,S-1,N^6-γ-HMHP-dA adducts. Previous studies have shown that human translesion DNA polymerases η and κ preferentially incorporated A, C, G or T opposite R,R-N^6,N^6-DHB-dA, and A, G or T opposite R,S-1,N^6-γ-HMHP-dA. This study seeks to explain the observed mutagenicity of these adducts and is the first step in determining the effect of these adducts on the DNA duplex.

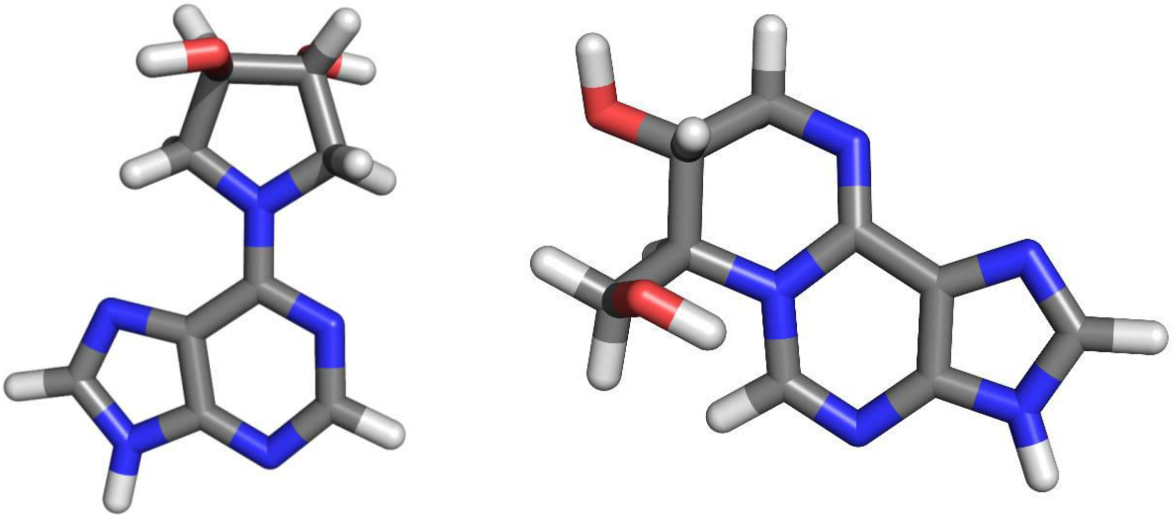


Figure 1. 1,3-butadiene adducts *R,R*-N^6,N^6-DHB-dA (left) and *R,S*-1,N^6-γ-HMHP-dA (right)

Identifying Biomarkers for Assessing an Athlete's Readiness to Return to Play Following a Sport-Related Concussion Using ^{1}H NMR Spectroscopy

Marrissa S. Buchan[3], Zachary R. Wanner[1,3], Mashal Fida[1], Chantel T. Debert[2], Gerlinde A. Metz[1], and Tony M. Montina[3]
[1]University of Lethbridge, Department of Chemistry & Biochemistry; [2]University of Lethbridge, Department of Neuroscience; [3]University of Lethbridge, Faculty of Health Sciences, Public Health Program

Background: Sport-related concussion (SRC) is a very common form of mild traumatic brain injury (mTBI). Presently, there is no official assessment used to objectively diagnose SRC and to prognosticate recovery of patients. Several tools have been developed to aid in these aspects, however, due to issues such as restricted specificity, cost and validity, the use of these assessment tools is limited and remains highly subjective. Metabolomics provides a quantitative measurement of the metabolites within a living organism and can be used to measure the metabolic response of an organism to different stimuli. Thus, urinary metabolites that have been altered as a result of an SRC provide a potential avenue for biomarker discovery as it relates to diagnosis and recovery.

Hypothesis: The ^{1}H NMR spectroscopy detected urinary metabolome of athletes will reflect changes in the brain caused by both SRC and the recovery process.

Methods: Samples were obtained from athletes at the beginning of the season, within 72 hours after injury and following medical clearance to return to play. Urine samples were prepared with NMR buffer, centrifuged, the supernatant was pipetted into 5mm NMR tubes. These samples were then analyzed using a 700 MHz Bruker Avance III HD NMR spectrometer. Multivariate statistical analyses were applied to spectral data obtained to determine if there was a significant distinction between baseline, post-SRC and asymptomatic samples. Permutation and cross-validation testing were applied to all Partial Least Squares Discriminant Analysis (PLS-DA) tests for each comparison to ensure the validity of the results. Metabolites that contributed to the observed differences between the metabolomic profiles were identified using Chemometric software.

Results: Statistical data analyses revealed several metabolites that were significantly altered between groups. The identified metabolites were then correlated to biochemical pathways using pathway topology analysis.

Conclusion: This work shows that ^{1}H-NMR based metabolomics is a powerful platform for conducting sport-related concussion analysis. Understanding the lasting metabolic changes that persist even after an athlete has returned to play is key for monitoring individuals following SRC and ultimately preventing cumulative and permanent brain damage.

I hear, therefore I perceive: Effects of speech accent on perception of physicians

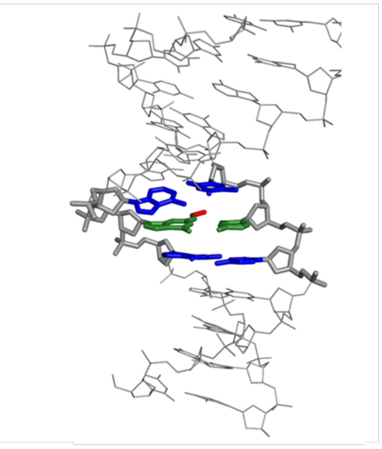
Chin Lorelei C. Baquiran & Elena Nicoladis
University of Alberta

People sometimes assume that a person who speaks with a foreign accent possesses negative traits and personality characteristics. The purpose of this study is to test if doctors who speak with a foreign accent are perceived as less competent than doctors who speak with a standard accent. We asked both Canadian and Chinese Canadian undergraduates to rate the competence of a doctor with either a standard Canadian accent or a Chinese accent. The doctor was delivering either good or bad news about the patient's cholesterol levels or cancer. Previous research has shown that when reminded of death, participants favour in-group members (Solomon, Greenberg, & Pyszczynski, 1991). We therefore predicted that the Chinese-accented doctor is more likely to be judged positively by Chinese Canadian participants when given bad news about cancer. Similarly, the standard-accented doctor is more likely to be favourably perceived by Canadian participants in the same condition. The initial results suggest that, as predicted, the accent affects participants' judgments of the doctors' competence.

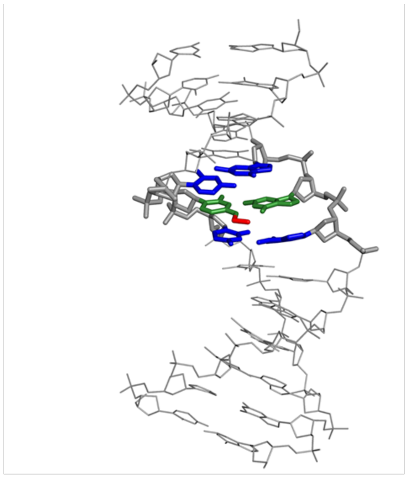
Effects of Formaldehyde on DNA: A Molecular Dynamics Study of Formaldehyde Adducts

Josh L. Garden, Katie A. Wilson, and Stacey D. Wetmore
University of Lethbridge, Department of Chemistry and Biochemistry

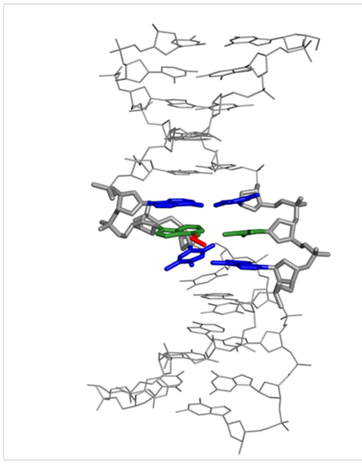
Formaldehyde is a known carcinogen, which damages and mutates DNA in the cells of mammals. Acute and chronic exposure to formaldehyde may occur in both occupational settings (e.g., embalmers) and from several household products (e.g., insulation, particle boards, and carpeting). Upon human exposure to formaldehyde, several DNA adducts may be formed, including those with the amino groups of guanine (denoted CH_2OH-N2-G), cytosine (CH_2OH-N4-C), and adenine (CH_2OH-N6-A). Each of these adducts consists of a methoxy moiety linked to the exocyclic amino group of the respective DNA nucleobase. The methoxy moiety can interfere with several noncovalent interactions within a DNA helix, including Watson-Crick hydrogen bonding, Hoogsteen hydrogen bonding, and stacking interactions between neighboring DNA nucleobases. These interactions are essential to the normal function of DNA and their disruption could lead to mutations when DNA is copied, which in turn lead to health effects such as cancer. Although insight into the implications on formaldehyde adducts are currently lacking from experimental studies, computational chemistry can be used to predict the effects of the methoxy moiety on the nucleobase interactions and the mutagenicity of these adducts. In the current study, molecular dynamics (MD) simulations, along with advanced structural analysis and energy calculations, were used to study the preferred conformations of the nucleobase within damaged DNA, and thereby characterize the structural impacts of this damage. Using this analysis, key insight was gained into the mutagenicity of the CH_2OH adducts and the data obtained can be used to direct future biochemical studies of the harmful effects of these lesions.



CH_2OH-N2-G



CH_2OH-N4-C



CH_2OH-N6-C

Examining Correlates and Consequences of Implicit Theories of Social Anxiety

Kyla Doherty and Andrew Howell, PhD
MacEwan University

A small but growing literature concerns the application of implicit theories (i.e., incremental and entity mindsets regarding the stability or malleability of attributes, respectively) to disorders and their symptoms. Implicit theories of social anxiety were explored through a cross-sectional study (*N* = 274 undergraduate participants) examined correlations among implicit theories of social anxiety and social anxiety symptoms, emotional regulation, help-seeking, and behavioural engagement. As predicted, incremental mindsets were correlated with lower social anxiety, greater use of emotional reappraisal, more help-seeking behaviour, greater behavioural activation and less behavioural inhibition. In a regression analysis, incremental mindsets predicted social anxiety symptoms above and beyond the remaining variables. Overall, the current findings warrant additional research of implicit theories of social anxiety, in clinical populations with social anxiety disorder to determine if the found correlates will be replicated and exacerbated within a clinical population.

Characterization of Engineered Protein Switches Using Intramolecular Disulfide Bridges

Gemmill, Darren, Girodat, Dylan, Wieden, Hans-Joachim
University of Lethbridge, Alberta RNA Research and Training Institute (ARRTI), Department of Chemistry and Biochemistry

Protein engineering is the process of developing proteins that can perform functions that often are novel and do not occur in nature. Development of proteins with new properties is critical for a wide range of biotechnology applications including new metabolic pathways, biosensors, and molecular scaffolds. Engineered proteins are frequently used in the food industry, medicine, nanobiotechnology, and environmental applications. One of the limits of protein engineering is the lack of ability to rationally design molecular switches. Here we report on the development of a molecular switch which utilizes cysteine disulfide bridges.

Our model system for the development of a designer molecular switch is the translation elongation factor (EF) G. EF-G stimulates translocation of tRNA through the ribosome, a process that requires a conformational change in EF-G. We have developed and implemented a Molecular Dynamics simulation pipeline to design 3 EF-G variants (G163C-T650C, P121C-K675C, and T125C-S679C) with disulfide bridges that limit the conformational changes of EF-G to specific functional states. To assess correct folding of these conformationally restricted EF-G variants, we have used circular dichroism and determined key enzymatic properties such as nucleotide binding and GTP hydrolysis rates for these EF-G variants.

The reported data validates the ability of our Molecular Dynamics pipeline to rationally design novel molecular switches.

Development of culture medium for high density micropropagation of potato plants *in vitro*

Andrea Gelene Abenoja and Dmytro Yevtushenko
University of Lethbridge, Department of Biological Sciences

All commercial seed potatoes start off as small plantlets grown in tissue culture, and *in vitro* clonal micropropagation is the only way to ensure a constant supply of certified virus-free plants. Selecting the correct culture medium is one of the most important steps in developing a useful protocol for successful growth and propagation of plant species *in vitro*. In Alberta, all commercial tissue culture labs rely on the classic Murashige and Skoog (MS) medium to clonally propagate potato plants *in vitro*. Although MS composition is widely used as a standard growth medium, the nutrients it supplies may not be optimal for plant growth on an industrial scale. To meet the growers' demand for seed potatoes, commercial producers have to grow plants at 4–10 times higher densities than those in research laboratories. The resulting plants are often of poor quality and exhibit reduced survival rate after being transferred to the greenhouse, thereby causing serious economic losses for the industry. Hence, the composition of MS medium likely requires major modifications to improve its efficiency for commercial use, particularly when potato plants are grown in culture vessels at high density and suboptimal culture conditions. The aim of this study was to evaluate the effects of additional MS nutrients on shoot quality and to determine the most critical culture medium components for improved plant growth response in potato. A factorial approach was used to test combinations of five nutrient factors: 1) NH_4NO_3, 2) KNO_3, 3) mesos ($CaCl_2$, KH_2PO_4 and $MgSO_4$), 4) micronutrients (B, Cu, Co, I, Mn, Mo, Zn, Fe), and 5) source of carbohydrates. Each factor varied over a range of concentrations, added to MS medium. In total, 25 medium compositions were tested. The effects of these treatments on plant quality, such as shoot length, leaf size and color, were determined. An increase of mesos and micronutrients to concentrations four times higher than in the original MS medium was found to be the most significant factor associated with plant quality, multiplication and shoot length in all plants. This optimized growth medium can be used to produce higher quality potato plants *in vitro*.

Group D | 2:00-2:54 PM

The Octagon Navigation Task Reveals Sex Differences in Spatial Ability

Kate Chua
University of Lethbridge

The Morris Water Maze (MWM) is commonly used in research for investigating spatial cognition and hippocampal-dependent learning in nonhuman animals. One of the most consistent findings in the literature is the male advantage in spatial ability. Usually, the MWM is adapted as a virtual reality for testing in humans. In our lab, we constructed a real-world navigation task and found that by default, men implemented an allocentric strategy whereas women adopted an egocentric strategy when finding the target location. Based on these findings, the present study designed a table-top version of the MWM. The goal of each subject is to locate a hidden target by navigating on an octagonal board using different spatial navigation strategies. The allocentric condition experiment tested 60 subjects (30 women) ages 18-25 and examined their ability to find a hidden target located relative to constant environmental room cues. Results revealed that men outperformed women on this task. In the egocentric condition experiment, 60 subjects (28 women) were directed to find a target location that remained consistent with respect to their body axis and starting position in the experiment. Women outperformed men in the egocentric condition experiment. In the neutral condition, the target was located in the center of the board and could be found using either egocentric or allocentric strategy, which resulted in no sex differences. Our results suggest that when a spatial task requires competition between two sources of information, an egocentric strategy appears more prominent in women whereas an allocentric strategy appears more prominent in males. Future work may use fMRI to see if sex differences in spatial navigation will correlate to differences in functional connectivity.

Using cortical thickness and elevated plus maze as a means to assess brain and behaviour in adolescent rodents: Paternal preconception nicotine exposure and enriched housing

Amatto, L., Harker, A., Kolb, B., Gibb, R.
University of Lethbrige, Dr. Robbin Gibb's Lab

The effect of maternal experience on the prenatal environment is well researched, however, comprehensive examination of father experience is lacking. This project aims to gain insight into paternal nicotine exposure and complex housing on offspring brain and behaviour. In this study, four experimental groups were used; nicotine enriched, nicotine pair housed, control enriched and control pair housed. Male Long Evans rats were either kept in pair houses or enriched in complex housing at P45 for 96 days and administered the appropriate solution (nicotine/control) during the last 48 days. Rats were then immediately mated with female Long Evan rats following cessation of enrichment and treatment administration. Offspring were then born to the mothers, never coming into contact with the fathers. A subset of the offspring were perfused on P21 for anatomical analysis while the remaining underwent behavioral testing on P36 and were subsequently perfused. Cortical thickness measurements were completed on the animals perfused at P21 and elevated plus maze (EPM) behavioral task - a measure of anxiety - was conducted on the remaining animals at P36. An increased amount of time spent in the closed arms of the EPM is used as a measure of anxiety in these rodents. Nicotine pair housed males as well as control enriched males were found to have significantly thicker cortexes. However, when these treatments were combined in the nicotine enrichment males, this observed thickness in the cortex seemed to be nullified as the cortex thickness was now comparable to the control pair housed males. Male and female offspring of enriched fathers and male offspring of nicotine exposed fathers spent significantly more time in the closed arms of the EPM, thus being considered more anxious than the controls.

Development and Characterization of Calcium Sensors for In vivo Neuronal Activity Imaging

Abhi Aggarwal
University of Alberta

Genetically-Encoded Fluorescent Calcium Indicators for Optical Imaging (GECOs), that modulate their fluorescence intensity in response to changes in calcium ion concentration, are powerful tools for the investigation of cell biology. These fluorescent indicators are vital when it comes to cellular imaging because they allow the non-invasive study of cells, tissues, and sub-cellular structures at a detail that was previously not possible. The focus of this project is engineering a new GECO that exhibits favourable characteristics, such as increased brightness and a higher fold change. To develop this new GECO, we started from mNeonGreen, the brightest monomeric fluorescent protein currently available. An initial prototype construct was made using rational design, following the precedent of the GCaMP series of indicators. This construct was further improved using directed protein evolution with colony-based screening of libraries of randomly generated variants. We observe the brightness of promising new variants and perform tests to see how new mutations have affected the brightness and the fold change of the variant. After many rounds of screening, our latest variant of mNeonGreen-GECO exhibits a Ca2+-dependent change of eight. When compared to the original construct, this indicator appears significantly brighter with higher contrast between Ca2+-bound and Ca2+-free states. Directed evolution is ongoing and we expect to produce a fluorescent indicator that will be used for in vivo imaging of intracellular Ca2+ dynamics. We will further image its calcium dynamics directly in Zebrafish and compare our variants with mNeonGreen fluorescent protein and the GCaMP series. Using mNeonGreen, we hope to create a calcium indicator that researchers can use to investigate the physiological activity of organs, understand the signaling patterns within tissues, and use to study the various disease states which may lead to the development of new therapies.

Modification of the Stripe Rust Resistance Gene Yr10 in Triticum aestivum

Kaden Fujita[1], Michele Frick[2] and André Laroche[2]
[1]University of Lethbridge; [2]Agriculture & Agri-Food Canada

Stripe rust is a disease in *Triticum aestivum* (bread wheat) that is caused by the fungal pathogen *Puccinia striiformis*. The pathogen has evolved to defeat an R gene in *T. aestivum* known as the *Yr10* gene. The *Yr10* gene was found to encode an evolutionary-conserved sequence known as the CC-NBS-LRR. This conserved sequence was found to be involved in producing resistance to various pathogens. Within this sequence the coiled coil (CC) and leucine rich repeat (LRR) domains are thought to be important to the protein's function. This project made use of PCR overlap-extension mutagenesis to mutagenize the CC and LRR domains in an attempt to create modified constructs of the *Yr10* gene. PCR reactions gave fragments of the expected sizes which were then assembled into the pANIC6D vector to be used in transformation. Transformation of the vector with inserted sequences into *Escherichia coli* will be done to confirm the successful insertion of the fragments. There is hope that in the future the modified constructs could be transformed into wheat.

Metabolomic Profiling of Gestational Diabetes Mellitus: A 1H-NMR Based Approach

Caylin Chadwick[1,2], Mariya Markovina[2], Hannah Scott[1,2], Brenda Leung[3], Gerlinde Metz[2], & Tony Montina[1]
[1]University of Lethbridge, Department of Chemistry & Biochemistry; [2]University of Lethbridge, Department of Neuroscience; [3]University of Lethbridge, Faculty of Health Sciences, Public Health Program

Introduction: Gestational diabetes mellitus (GDM) has been shown to increase the occurrence of pregnancy complications, including preeclampsia, preterm births, caesarean sections, intrauterine growth retardation, and neonatal intensive care unit admissions. Current tests for diagnosing GDM and pre-diabetic states in pregnancy are time-consuming and often unreliable. Our main objective was to characterize any metabolomic differences in the urine of women with GDM and healthy pregnant controls to identify diagnostic and predictive biomarkers.

Methods: Urine samples from the second trimester of pregnancy from 33 women with GDM and 34 age-, income-, and education-matched healthy controls were obtained from the Alberta Pregnancy Outcomes and Nutrition (APrON) cohort. Proton nuclear magnetic resonance (^{1}H-NMR) data was acquired using a 700 MHz spectrometer and subsequently binned for data analysis. Group separation was evaluated using principle component analysis (PCA) and partial least square discriminant analysis (PLS-DA). Variable importance analysis based on random variable combination (VIAVC) and Mann-Whitney testing were used to determine which metabolites were significantly altered across the comparison groups. Lastly, pathway analysis was carried out to determine which biological pathways were potentially altered by these metabolites.

Results: The analyses revealed group separation between the metabolomic profiles of pregnant women diagnosed with GDM and health pregnant controls. Several significantly altered metabolites, along with some potentially altered biological pathways, were identified across the comparison groups.

Conclusions: These results demonstrate the potential for ^{1}H-NMR and metabolomics to diagnose pregnant woman with, or assess their risk for developing, GDM. Furthermore, the subset of metabolites identified as significantly altered provides potential biomarkers that can be correlated with pregnancy outcomes in order to identify women at high risk of negative pregnancy outcomes.

An aerial inventory of rock glaciers in the Southern Alberta Rocky Mountains

Mishélle Scott[1], Mark F.A. Furze[1], Nancy K. McKeown[1], Steven Pawley[2], Dan Utting[2]
[1]MacEwan University, Department of Physical Sciences; [2]Alberta Geological Survey, Edmonton

Rock glaciers are large lobes of rocky debris commonly found within alpine permafrost in the Alberta Rocky Mountains. Alpine permafrost is of significant scientific interest as it encompasses a large area and exhibits unique responses to climate change. Rock glacier falls from these increasingly unstable mountain slopes can represent significant geohazards, which makes mapping the spatial distribution of these features and classifying their morphology important. They can also be used to identify and understand past climatic change in these alpine regions, with relict (fossilized) rock glaciers indicating a past climate formerly able to create and support these features. Although a common feature within the Alberta Rocky Mountains, information on rock glacier characteristics and distribution within this region is rather limited. The inventory is based on the aerial classification of rock glaciers using high-resolution satellite imagery available through Google Earth and in ArcMap, a geospatial processing program. Geospatial mapping and remote sensing techniques were used for the quantitative and spatial analysis of these features to create an inventory that classifies, quantifies, and characterizes the rock glaciers within this region. Classification of talus-derived and glacier-derived rock glaciers was done using morphological characteristics as the

elemental method for identification. Digital Elevation Models (DEM) and optical satellite imagery were used to quantify various attributes such as shape, state, slope, aspect, and elevation. A digital database with the findings from this research will be made publically available for future research through the Alberta Geological Survey.

Development of a Cell-Free Synthetic Biology Platform

Josh Friesen
University of Lethbridge

Cell-free systems allow for a reliable and consistent expression of recombinant proteins outside of a living cell, bypassing issues with genetic regulation and cellular noise (Hodgman and Jewett, 2012). Such systems are advantageous over cell-based synthetic biology due to the capability of tolerating toxins normally detrimental to the cell, increased freedom of design, reduced risk for biocontamination, and a rapid design-build-test cycle. Emerging as a new platform for synthetic biology, cell-free systems have shown potential for use in a variety of applications, including biofuel production, biomanufacturing, health and medicine. However, current cell-free systems are inaccessible due to their high cost or incredibly laborious lab work required to reproduce them. The goal of this work is to develop a completely customizable and accessible cell-free system composed of 38 proteins required for transcription and translation. Each protein is designed with a hexa-histidine tag on the N or C terminus to allow for easy nickel-sepharose purification. Protein overexpression and purification is verified using sodium dodecyl sulfate polyacrylamide electrophoresis (SDS-PAGE), and all 38 proteins are reconstituted to form a function cell-free system. 8 proteins have currently been successfully overexpressed and confirmed by SDS-PAGE.

To simplify the process, multiple proteins are purified at once by combining cell pellets from multiple overexpressions and purifying them on a single nickel-sepharose column. The concentrations of purified proteins will be determined using mass spectroscopy. Preliminary results include successful multi-protein purification of four proteins (Release Factor 3, Histidine Synthetase, Tryptophan Synthetase and Ribosome Recycling Factor) on a single nickel-sepharose column, subsequently verified by SDS-PAGE. Future goals for this work include complete overexpression and purification of all 38 proteins, followed by functional validation. Ultimately, this work will provide a safe and customizable cell-free system for protein production.

REFERENCE
Hodgman, C.E. and M.C. Jewett, Cell-Free Synthetic Biology: Thinking Outside the Cell.
Metabolic Engineering, 2012. 14(3): p. 261-269.

Mathematical Modelling of a Measles Outbreak in Pre-vaccine England and Wales

Murdoch McKinnon[1], Michael Wendlandt[1], Ashok Krishnamurthy, PhD[2], Loren Cobb, PhD[3]
[1]Mount Royal University, Department of Earth and Environmental Sciences; [2]Mount Royal University, Department of Mathematics and Computing;
[3]University of Colorado, Department of Mathematical and Statistical Sciences

We present a spatial variant of the time series susceptible-infectious-recovered (TSIR) stochastic population-based model to capture the spatial transmission dynamics of a measles outbreak across the landscape of England and Wales during the pre-vaccine era. Specifically, we explore how the basic dynamical features of a measles outbreak with a seasonal forcing of transmission acts as a major driver of a long-term epidemic behavior.

We use a 20-year pre-vaccination era biweekly time series data (births by year and incidence of measles for the years 1944-1966) from 60 towns and cities in England and Wales to capture the spatial spread of measles.

In England and Wales prior to vaccination, measles was endemic in large cities, but in smaller cities disease fadeout occurred. Reappearance of the disease would then occur only after a case was imported from a surrounding city where measles was endemic. To capture spatio-temporal dynamics, multi-city models must be developed, but these models can become very large requiring more memory and processing power than a single computer can deliver.

Rather than represent the population as a linked set of cities, we represent the population as a gridded map. Each grid cell can transmit infectious disease to its neighbors, with probabilities that decline exponentially with distance. We present a stochastic spatial model with six compartments. We call this the kids-susceptible-infectious-recovered-adults-dead (KSIRAD) model.

From the simulation, we recover spatiotemporal maps of the incidence of the infection. We compare simulated time-series graphs with real data compiled by Grenfell and others. Our future work includes testing of our spatial model for measles outbreaks reported in the modern era, for example, in conflict affected areas of the Republic of the Niger in Western Africa in 2016. Socioeconomic disparities in a country like Niger presents significant challenges to reporting and real-time tracking of human infectious diseases.

Modifying the Stripe Rust Resistance Gene Yr10 in Wheat (Triticum aestivum L.) by PCR Mutagenesis

Darren Van Essen[1], Michele Frick[2], André Laroche[2]
[1]University of Lethbridge; [2]Agriculture and Agri-Food Canada

Stripe rust is a disease in cereal crops caused by the fungal pathogen *Puccinia striiformis* which can have devastating effects on crop yields. Cereal plants have unique resistance (R) genes which code for resistance (R) proteins with coiled coil (CC), nucleotide binding site (NBS), and leucine rich repeat (LRR) domains. The CC and LRR domains are thought to be particularly important for protein function/interaction in the resistance response. The *Yr10* gene is a stripe rust resistance gene in *Triticum aestivum* that codes for a unique CC-NBS-LRR sequence but no longer confers resistance to some races of rust. Previous studies indicate that by mutagenizing the DNA sequences that code for the CC and LRR domains it is possible to change the R protein's sequence, and possibly the interaction during the resistance response[3]. Thus, the defeated R genes can confer resistance once again when mutagenized in these regions.

This study used PCR mutagenesis (by overlap extension) to mutagenize the *Yr10* gene in the regions encoding the CC and LRR domains. Primers were designed to amplify *Yr10* such that products contained mutated sequence as extensions, available for overlap. The amplifications were the expected size, indicted primers were successful. The PCR products containing the mutagenized sequences of *Yr10* were then assembled with the pANIC 6D vector to be used in further experiments involving the transformation of wheat crops to test resistance.

Group E | 2:00-2:54 PM

Investigating the Interaction Between DDX17 and The Rift Valley Fever Virus 3' Terminal Region Using a Nano-scale Structural Approach

Simmone D'souza[1], Tyler Mrozowich[1], Justin Vigar[1], Hans-Joachim Wieden[1], Trushar R. Patel[1,2,3]
[1]University of Lethbridge, Alberta RNA Research and Training Institute, Department of Chemistry and Biochemistry; [2]University of Alberta, DiscoveryLAB, Faculty of Medicine & Dentistry; [3]University of Calgary, Department of Microbiology, Immunology & Infectious Diseases, Cumming School of Medicine

Rift Valley Fever (RVF) is a currently an untreatable disease that affects both humans and livestock in sub-Saharan Africa. This disease is viral in origin and the Rift Valley Fever virus (RVFV) is transmitted primarily through mosquito vectors Aedes and Culex. RVFV is a part of the *Bunyaviridae* family, and the genus *Phlebovirus*. Recent studies have indicated that RVFV interacts with the human DEAD-box RNA helicase protein DDX17. There is minimal research on the specific interactions between this host protein and the viral RNA, although DDX17 has been shown to inhibit RVFV replication. The DDX17 helicase performs a critical role in viral replication, and we are trying to dissect the specific role by which it inhibits RVFV replication. In addition, we are also studying two regions of the RVFV which forms a stem-loop structure that is proposed to interact with DDX17. Using selective 2'-hydroxy acylation analyzed by primer extension (SHAPE) and small-angle x-ray scattering (SAXS) techniques we aim to gain both secondary and 3-dimensional structural information. To identify specific domains of DDX17 that interact with both viral constructs, we require a highly pure preparation of full-length DDX17 and its truncated domains. Thus, the primary objective of my project is to establish protocols for large scale preparation of full-length and individual domains of DDX17 to identify a specific domain of DDX17 that interacts with the RVFV RNA using Electrophoretic mobility shift assays (EMSA) and study interactions using microscale thermophoresis (MST).

Single-dose UV-C irradiation induces the formation of gamma-H2AX foci in the human cell line (MCF7) that are not resolved after 2 and 24 hours of recovery as determined by immunofluorescence microscopy

Taylor[1], K., Johnson[1], H., Saleh[1], M., & Tuescher[2], J.
[1]University of Lethbridge, Department of Biological Science, Research Internship Program; [2]University of Lethbridge, Department of Biological Science, The Natural Product and Cancer Cell Laboratories

The integrity of the genome is of utmost importance for proper functioning existence of all living systems. Genotoxic insults, such as UV-C radiation, may exert adverse effects on genomic integrity. Cells have developed a number of highly conserved repair mechanism to counteract the variety of mutagenic and cytotoxic DNA lesions induced by genotoxic agents. Phosphorylation of gamma-histone H2AX is a known DNA-repair signaling response to double-stranded breaks (DSBs); however, the formation of DSB by UV-C radiation is reported to be rare. We sought to determine whether a single dose of UV-C radiation (0.31 J/cm^2, 254nm) can induce the formation of gamma-H2AX foci in the human cell line (MCF7) and determine the amount of DNA damage present after a recovery period of two and 24 hours by immunofluorescence microscopy. We also exposed cells to 50 nM of camptothecin (CPT), a

DNA damaging agent, as a positive control. We found that similar to CPT, human cells exposed to UV-C radiation (0.31 J/cm^2) showed upregulated gamma-H2AX foci at both 2 h and 24 h after the genotoxic insult. Cells exposed to this single dose showed significantly higher gamma-H2AX from non-treated cells and the extent of DNA damage remained the same between 2 and 24 h. Our results indicate that UV-C radiation is capable of inducing the formation of the DSB signaling foci gamma-H2AX and that cells are unable to repair the genotoxic insult within 24 h of recovery. This further indicates that human cell line (MCF7) may require longer than 24 hours to noticeably repair the extent of DNA damage induced by (0.31 J/cm^2) of UV-C light.

Identification and Alignment of Human and Mouse SNPs in the *DMD* Gene using a Bioinfomatical Approach

Lindsay Muller
Concordia University of Edmonton

Muscular dystrophy (MD) is a fatal, muscle wasting disease affecting individuals who have acquired a mutation in their dystrophin (*DMD*) gene. Some of these mutations are a single nucleotide alteration. Dystrophin is a vital part of a protein complex in skeletal and cardiac muscle tissue. The gene is the largest in the human genome, spanning 79 exons on the X chromosome. MD is X linked dominant, targeting mostly males that are affected by the one of the two most common forms, Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD). Both DMD and BMD result from single nucleotide polymorphisms (SNPs). To date, there is no cure for the disease. Of the identified SNP mutations, the phenotype for many has not yet been characterized. To this end, identifying conserved regions between humans and mice would allow for further characterization of these SNPs, as dystrophinin in mice is functionally analogous. Therefore, I hypothesize that some of the human SNPs in *DMD* are conserved in mouse DMD. Using a bioinformatical approach, I collected various SNP mutations, and using Ensemble, I then aligned the genes. Of the exons examined, 212 SNPs were identified, 17 of which were on exon 57. Furthermore, many of the human SNPs align with mouse *DMD* gene SNPs. This study will allow for further characterization of the *DMD* SNPs, as well as serve as a platform for future *in vivo* studies, opening opportunities to possible gene therapies for individuals with muscular dystrophy.

The Effect of Varying Doses of UVC Radiation on the Viability of Human Cancer Cells

Nadia Hand, Andrea DeGroot, Jan Tuescher
University of Lethbridge

UVC radiation has the ability to damage DNA in cells. This causes the cell to either arrest division or undergo apoptosis. In this study we observed the effects of increasing doses of UVC radiation on the division rates and viability of cells from the human cancer cell line MCF7. We hypothesized that at a certain dose the cells would no longer be able to repair DNA and apoptosis would be induced. Furthermore, we hypothesized that the division rate would decrease as the dose of UVC increased. Cells were irradiated at either, 0 mJ/cm^2 (negative control), 0.31 mJ/cm^2, 1.55 mJ/cm^2, 4.65 mJ/cm^2, 9.3 mJ/cm^2, 18.6 mJ/cm^2, 37.2 mJ/cm^2, or 74.4 mJ/cm^2. 48 hours after irradiation, a Trypan Blue viability assay was performed to determine the percentage of dead cells at each dose. To compare division rates, the total number of cells in each treatment was taken as a percentage of the total number of non-treated cells. The IC50 for apoptosis was found to be 21.25 mJ/cm^2. Our results showed that the total number of cells decreased significantly between 0 mJ/cm^2, and 4.65 mJ/cm^2. At concentrations above 4.65 mJ/cm^2, the total number of cells remained constant. Suggesting that this is the point in which cells may have stopped growing. In contrast, the percentage of dead cells did not differ between the nontreated cells and those treated with UVC doses up to 9.3 mJ/cm^2, but was significantly higher at doses above 18.6 mJ/cm^2. The point at which the percentage of dead cells begins to increase significantly and where division rates plateau is relatively close, thus, we infer that this the point in which cells stopped trying to repair their DNA and instead began to undergo apoptosis. As we hypothesized, at a high enough dose, the DNA in cells would become irreparable and the cells would die. Because all cells above this dose show significant death, the observation is consistent with our hypothesis.

Quantification of Tissue Specific Expression of ABC type B transporters in *Eschscholzia californica*

Jonathan Roveredo, Perpetua Uzuegbu, and David Bird
Mount Royal University

Adenosine triphosphate (ATP)-binding cassette (ABC) transporters are a diverse superfamily of transmembrane proteins found in all eukaryotes. These proteins couple the hydrolysis of ATP to the transport of a wide variety of substrates across cellular membranes. In plants, ABC type B (ABCB) transporters have been shown to be involved in the transport of both growth regulators (auxin) and secondary metabolites. Plant secondary metabolism refers to the vast array of small molecules being produced, but not directly required for plant growth and development. However, secondary metabolites have been shown to play important roles in plant defense, such as in deterring herbivory or resistance to pathogens. It has been shown that transport between cell types is necessary in the biosynthesis of many of these metabolites and that ABC transporters play a necessary role in this trafficking. *Eschscholzia californica*, or the California poppy, accumulates alkaloids within specialized cells within roots. Our lab previously identified *EcABCB1*, a transporter involved in the transport of these alkaloids. In this project, using the recently-released draft genome of *E. californica*, we have identified seven additional putative ABCB transporters (ABCB2-7). Using quantitative polymerase chain reaction (qPCR), we will quantify their expression profiles in a tissue-specific manner. These results will then be used to draw inferences of the function of each candidate gene, based on comparative analysis of expression profiles of ABCB homologs in *Arabidopsis thaliana*. Preliminary data shows that *EcABCB1* is expressed in both roots and stems, whereas EcABCB2 is expressed ubiquitously across all tissues. This may indicate that *EcABCB2* may be involved in the transport a growth factor such as auxin, which is a metabolite necessary for growth across all organs. In order to obtain a better understanding of the biochemistry of plants and the synthesis of their alkaloids, the transporters required for this synthesis must be characterized.

Analysis of Potential Anti-Cancer Effects of Cannabinol and Cannabidiol using HCC1806 and HEK293 Cell Lines

Marina Galatonov, Dongping Li, Nuanying Zhong & Igor Kovalchuk
University of Lethbridge, Department of Biological Sciences

Humans produce endocannabinoids that act as neuromodulators in the endocannabinoid system. They bind to Gαi protein-coupled cannabinoid receptors to control the release of many neurotransmitters. Cannabinoids receptor 1 (CB1) mediates psychoactive effects through its location mostly in the central nervous system while Cannabinoid receptor 2 (CB2) regulates various immune responses through its location in peripheral tissues. The endocannabinoid system has been used as a molecular target by research to treat diseases such as multiple sclerosis, cardiovascular disorders, obesity and inflammatory pain. Thus, the endocannabinoid system is a potential molecular target to treat cancer. With the proposed legalization of recreational marijuana and with growing number of patients using cannabis for medicinal purpose, there is an urgent need to provide data on potential medicinal value of cannabis and cannabinoids.

The *Cannabis Sativa* plant naturally synthesizes numerous different cannabinoids of which (CBN) and cannabidiol (CBD) have promising properties in cancer treatment. CBD is a phytocannabinoid known for its anticonvulsant and anti-nausea properties. Previous research suggests that CBD can target breast cancer cells while preserving normal cells. CBN is another phytocannabinoid with anti-inflammatory properties that can potentially aid to reduce inflammation resulting from cancer. This study aims to determine if CBN and CBD have an effect on cancer cells and normal cells. We hypothesize that we may observe an increase in apoptosis of cancer cells treated with the two compounds but no effect or perhaps even a slight increase in normal cell growth. Preliminary data in lab suggests that these compounds have anti-cancer properties and we want to solidify this evidence through repetition of the experiment. Various concentrations of CBN and CBD were administered separately to HCC1806 breast cancer cells and HEK293 normal human kidney cells for 24 hours before conducting apoptosis and cell cycle assays to determine if the cannabinoids had induced cell death or affected proliferation.

Foraminifera: a tool for elucidating past and recent climate change in marine Arctic Canada

Rabecca Thiessen[1], Anna J. Pieńkowski[1], Mark F.A. Furze[1], Alix G. Cage[2], Alexandre Caouette[1], Sina Coates[1]
[1]MacEwan University, Department of Physical Sciences; [2]Keele University, School of Geography, Geology and the Environment

Over the past decades, polar regions such as the Canadian Arctic Archipelago have experienced pronounced changes associated with climate warming (e.g., decreased sea ice extent and thickness). Such relatively recent environmental shifts have motivated research regarding past climate variability to understand how polar marine environments respond to changing conditions, for example glacial to interglacial transitions. This presentation outlines ongoing research that is part of a larger project (funded by ArcticNet and NSERC) focussed on the palaeoclimatology, palaeoceanography and deglacial histories of the Canadian Arctic Archipelago. In particular, the use of foraminifera (benthics and planktonics) is highlighted as a proxy for reconstructing past environmental conditions via assemblage and geochemical ($\delta^{13}C$ and $\delta^{18}O$) analyses, including water temperatures, sea ice conditions, and ecosystem productivity, in the eastern (Lancaster Sound/Baffin Bay) and western (M'Clure Strait) entrances to the historical Northwest Passage. To allow for accurate interpretations of past environments, ongoing work also focusses on foraminiferal distribution in surface (modern) sediments in relation to measured oceanographic parameters (temperature, salinity, sea ice) as a baseline for paleo-interpretations. Preliminary results from foraminiferal surface sediment calibrations, along with the taxonomic issues associated with some important indicator taxa will be discussed.

Implementation of a new method to identify *Verticillium* isolates affecting potato cultivars in Alberta

Jesse J. G. Holbein, Anne-Sophie Tillault, and Dmytro P. Yevtushenko
University of Lethbridge, Department of Biological Sciences

Potato (*Solanum tuberosum* L.) is the most important non-cereal crop in the world, with 300 million tons produced every year. Despite its economic importance, potato plants are susceptible to numerous diseases caused by fungi, bacteria, and viruses, that lead to tremendous financial losses for the industry. A common potato disease called Verticillium wilt, or potato early dying, is caused by fungi from the genus *Verticillium*. The two species that affect potato cultivars in Alberta are *V. dahliae* and *V. albo-atrum*. These soil-borne fungi affect xylem tissues preventing water intake causing dehydration in plants. This results in necrosis of the tissues and thus, leads to early plant mortality. Unfortunately, once a crop has developed disease symptoms, there is little that can be done to prevent harvest losses that year. This is why a fast and reliable method for early detection of the fungi is necessary.

Traditionally, fungal identification is performed by observing morphological characteristics of mycelia on solid media with a microscope; however, it is time consuming, requires specialized skill set, and species identification can only be achieved by genome sequencing. We are currently implementing a new method developed by Inderbitzin et al. (2013) to identify the species of *Verticillium* isolates by detecting the presence of species-specific nucleotide sequences[1]. After extracting fungal DNA, a polymerization chain reaction (PCR) is conducted with species-specific primers for both *V. dahlia* and *V. albo-atrum*. By visualizing the presence of an amplified fragment on agarose gel, it is possible to determine the *Verticillium* species.

We are testing and optimizing this method on eight non-identified pure *Verticillium* cultures isolated from fields in Alberta to determine their species. We are also working on the isolation of new *Vertcillium* cultures from seven potato plant samples collected during the past growing season across Southern Alberta that showed symptoms of Verticillium wilt. This will allow us to build a collection of *Verticillium* isolates for future genetic analysis. Overall, this new method will be a very powerful tool to detect the presence of *Verticillium* fungi in soil and plants before the emergence of any disease symptoms, which allows potato grower to control this disease in a timely manner preventing harvest losses.

[1] Inderbitzin P, Davis RM, Bostock RM, Subbarao KV (2013) Identification and Differentiation of Verticillium Species and V. longisporum Lineages by Simplex and Multiplex PCR Assays. PLoS ONE 8:e65990

Synergistic Effects of Ancestral Stress and Aging on Anxiety-like Behaviours

Natasha Patel, Mirela Ambeskovic, Jamshid Faraji, Gerlinde A.S Metz
University of Lethbridge

Exposure to adverse environments such as prenatal stress early in life is associated with anxiety-like behaviours in adulthood, which is potentially further exacerbated by aging. Recent studies have indicated that ancestral prenatal stress can propagate across generations to alter emotional wellbeing of unexposed offspring. Here we investigated if exposure to prenatal stress in the great-grandmother (transgenerational stress), or exposure across four consecutive generations (multigenerational stress) can alter anxiety-like behaviours in male and female fourth (F4) generation offspring. Anxiety-like behaviours were evaluated by means of the elevated plus maze in both males and females across three different groups: transgenerational stress (SNNN), multigenerational stress (SSSS), and non-stressed controls (NNNN). Both sexes were evaluated at the age of 12 months (middle age) and 18 months (old age). Our results demonstrate that aging and ancestral stress synergistically heightened anxiety-like behaviour, especially in males. Interestingly, the highest levels of anxiety-like behaviours were observed in transgenerationally stressed offspring of both ages. Overall, these results indicate that males are more sensitive to ancestral stress and more likely to respond by developing anxiety-like behaviours. Thus, ancestral stress and aging may synergistically alter mental health outcomes particularly in males.

Group F | 2:00-2:54 PM

Detecting chemical modifications of Ribonucleic Acid

Anileen Pageni, Sarah Schultz, Dr. Ute Kothe
University of Lethbridge, Alberta RNA Research and Training Institute (ARRTI), Department of Chemistry and Biochemistry

Transfer Ribonucleic acid (tRNA) is one of the highly chemically modified RNA in the cell, and the isomerization of uridine to pseudouridine (Ψ) is the most abundant RNA modification found in all domains of life. Although the function of RNA modification is not yet fully understood, the chemical

changes in RNA have been implicated in cellular fitness and development of genetic diseases. For example, the bacterial proteins TruA and RluA are both pseudouridine synthases which catalyze the isomerization of uridine to pseudouridine. TruA is capable of modifying several nearby sites in tRNAs while RluA modifies different RNAs at positions with a shared sequence and structure. These modifications are conserved in all forms of life, but little is known about their function.

The objective of this research project was to modify tRNA using modification enzymes and to establish a method to detect multiple RNA modifications at once using High Performance Liquid Chromatography (HPLC). Using a reverse phase chromatography column will allow to separate samples based on hydrophobicity. On one side, tRNA was successfully *in vitro* transcribed, purified and digested into nucleosides, which were then separated using the HPLC column. On the other side, TruA and RluA wild-type proteins were successfully overexpressed and purified, in order to prepare modified tRNA. In the future, this system will enable us to detect and quantify the presence of pseudouridine as well as other chemical modifications in any type of RNA. This tool will thereby greatly advance research in the Kothe lab to understand the mechanisms and functions of RNA modifications.

Potential sulfate sources for the Paskapoo aquifer of Alberta

Hugh Alvarez and Jenni Scott
Mount Royal University, Earth and Environmental Sciences

The Paskapoo aquifer of Alberta is one of the most significant sources of groundwater for domestic and industrial use in the entire province. However, there are pronounced levels of sulfate in the southern part of the aquifer between Red Deer and Calgary, above the 500 mg/L drinking safety limit advised by Environment Canada. The focus of this study is to examine the potential origins of this sulfate from three primary sources: (1) self-sourced from the Paskapoo Formation, deposited ~60 million years ago; (2) overlying Cordilleran till; and (3) and overlying Laurentian till. Oxidation of sulphide minerals from Laurentide till is the primary source of sulfate based on findings from published research. The Cordilleran till has not been examined as a sulfate source to the same extent. This study used three methods to determine whether Cordilleran till had any potential to add sulfate to the Paskapoo aquifer. A geochemical test utilizing X-Ray Fluorescence (XRF) determined sulfur content in rock samples from several potential source formations of Cordilleran till. Next, we immersed two grain-sizes of sediment (10 grams) from each formation into distilled water (40 ml) and reacted the sample with barium chloride to determine if and how much sulfate each formation could generate. Finally, a GIS map was constructed using flow directions of the Cordilleran and Laurentide Ice sheets, and the outcrop distribution of bedrock formations. This was used to determine whether each formation had the potential to be integrated as till material and subsequently deposited over the Paskapoo. This study found that several of the tested formations from the Cordillera had sizeable levels of sulfate and were capable of producing sulfate when immersed in water. Although sulfur did have the potential to be integrated into Cordilleran till, the flow direction of the Laurentide glacier ultimately restricted placement of Cordilleran till over the Paskapoo aquifer and may have limited the western input of sulfate into the aquifer. However, regional groundwater flow could potentially transport the sulfate to other aquifers due to the regional dip of Tertiary and uppermost Cretaceous strata. This study presents a multidisciplinary approach involving GIS, geochemistry, geology, and hydrogeology to determine potential sources of groundwater contamination.

Eukaryotic Initiation factor 5B (eIF5B) provides glioblastoma multiforme with resistance towards apoptotic agents

Keiran Vanden Dungen, Joseph Ross, Nehal Thakor
University of Lethbridge, Department of Chemistry and Biochemistry

Eukaryotic initiation factors (eIFs) are proteins involved in the general process of mRNA translation. However, under conditions of physiological stress, alternative methods of translation initiation are often activated and relied upon to continue translation of a subset of mRNAs. Specific eIFs such as eIF5B have been shown to use cap-independent mechanisms to promote the production of anti-apoptotic proteins, such as X-linked inhibitor of apoptosis protein (XIAP). In the present study, we have explored if eIF5B provides resistance to glioblastoma multiforme (GBM) cells towards apoptotic agents. Using siRNA, we depleted eIF5B from various GBM cells and treated them with agents that promote apoptosis. In order to activate intrinsic apoptosis pathway we treated these cells with genotoxic agents such as doxorubicin (DXR), and temozolomide (TMZ). Moreover, we treated GBM cells with tumor necrosis factor alpha (TNFα), and/or TNF-related apoptosis-inducing ligand (TRAIL) to activate extrinsic apoptosis pathway. The depletion of eIF5B did not sensitize GBM cells to DXR or TMZ. However, further viability assays showed that knockdown of eIF5B sensitized U343 cells to TRAIL or TRAIL + TNFα. Further, the combination of TRAIL + SMAC-mimetic compounds (SMC) showed statistically significant decreases in cell viability when eIF5B was depleted. So far, six different glioblastoma cell lines have been assessed for this effect, and further studies are underway to observe the effects of eIF5B depletion on cell viability of various cancer and non-cancer cells. Our preliminary data suggest that eIF5B enhances cell survival of GBM cells and could represent a potentially important therapeutic target.

Light Pollution: An Aerial Perspective

Ryan Hofer, Phil Langill
University of Calgary, Astrophysical Observatory

Artificial Sky glow is a growing obstacle for both the public to enjoy the night sky, and Astronomers to make accurate measurements of the universe around us. Given Calgary's expanding urban geography and population, light pollution and resulting sky glow has continued make the stars less accessible. In this first aerial light pollution observation in Canada, this study will give quantifiable resolution to which areas of the SW quadrant of Calgary and area surrounding the Rothney Astrophysical Observatory create Sky Glow. Measuring Sky glow from above and below the plane using a sky quality meter, giving results in magnitudes per square arcseconds, and further instruments on the bottom giving photon counts from ground sources via digital CCD and a wide lens optics. Resulting in measurements of Sky Glow from above and tying them with sources from below to see if there is a correlation. Further using this data, we will explore the impact of urban development on our night sky.

Investigation of myo-inositol Phosphates on Human Cells by Phenotypic Cell-Based Assays

Maya Degrood, Jan Tuescher, Steven Mosimann, Roy M. Golsteyn
University of Lethbridge

Myo-inositol phosphates (IPs) are a large family of compounds that are ubiquitous in eukaryotes. They are involved in many critical cellular functions, from signal transduction to DNA repair in eukaryotes. *Myo*-inositol hexa*kis*phosphate (InsP_6), commonly known as phytic acid, is the most abundant cellular IP and previous studies have suggested that exogenous InsP_6 has anti-proliferative effects on multiple cancer cell lines. By contrast, derivatives of InsP_6 with lower phosphate number, such as *myo*-inositol (1,2,4,5,6)-penta*kis*phosphate (InsP_5), have not been studied due to their costly preparation. Here we investigated the effects of InsP_6 and InsP_5 on the human bone osteosarcoma cell line, U2OS, by phenotypic assays. After 48 h after treatment with either InsP_6 and InsP_5 at 15 or 50 μM, cells display a striking vacuole formation, as observed by light microscopy. By staining with acridine orange and observing by fluorescence microscopy, the vacuolated cells showed acidic vesicle accumulation, indicative of increased autophagy. By staining with the non-permeant fluorescent dye Lucifer yellow and fluorescence microscopy we observed that vacuolated cells showed higher levels of the fluorescent dye, indicative of endocytosis, than non-treated cells. Vacuoles observed by phase contrast microscopy are frequently stained with Lucifer yellow and acridine orange. These findings suggest that InsP_5 and InsP_6 affect endocytosis, which subsequently leads to increased lysosomal degradation the engulfed material. Understanding the effects of IPs on human cells is important in understanding inositol signalling pathways and may lead to the discovery of novel anticancer compounds.

Maternal Preconception Nicotine and Enriched Housing: The Effects on Offspring Anxiety Behaviour

Leora Hiar
University of Lethbridge

A mother's environment can affect her offspring even before conception. Both positive factors, such as an enriched environment, and negative factors, such as drug use, have the potential to shape offspring development. The influence of psychoactive drugs is especially concerning because of the role they play in modulating important survival instincts, such as anxiety; therefore, strategies to counteract the changes induced by drug use are of particular interest. One possible way to counteract the transgenerational effects of drugs may be through enriching the maternal environment, which has been previously shown to attenuate the effects of nicotine. Enriched environments have huge beneficial effects on individuals, and hopefully these benefits can be passed down to offspring as a protective factor. In this experiment, female rats received moderate levels of nicotine in their drinking water (15mg/L sweetened with 1% sucralose) while being housed in either standard lab conditions or an enriched environment. The rats undergoing enriched housing were placed in a larger cage with multiple levels, more cage mates, and a rotation of stimulating objects. Control females received water sweetened with 1% sucralose while living in either environment. The offspring underwent behavioural testing in adolescence and adulthood to look for changes in elevated plus maze behaviours, a test that measure anxiety-like behaviours. Cortical thickness and thalamic size were also examined to look for effects on brain morphology. The results showed significant effects of preconception nicotine and enriched housing in the anxiety-like behaviours of the offspring in both adolescence and adulthood, dependent on sex. Results suggest that maternal preconception nicotine use lowers the amount of anxiety present in offspring. When the mothers are kept in enriched housing, however, the anxiety levels in the nicotine cohort return to levels near that of the control group. These results have important implications in the ability of the offspring to survive their environment, as differences in anxiety levels affect the survival strategies used by the offspring. Additionally, the return to control levels in the offspring whose mothers lived in an enriched environment does in fact suggest that maternal enrichment acts as a protective factor against preconception nicotine use. These results are not surprising as nicotinic acetylcholine receptors play a major role in the modulation of anxiety pathways, evidenced by both increases and decreases in anxiety due to nicotine use.

Identification of Conserved Proteins in *Nocardia brasiliensis* and other Actinomycetoma causative agents using a Bioinformatic approach

Brynne Gourlay
Concordia University of Edmonton

Mycetoma, a neglected tropical disease, is caused by a multitude of different microorganisms. This condition may be caused by both bacterial and fungal species, with the bacterial species suggested to spread more quickly through the body. Often untreated due to lack of medical access, amputation is ultimately a commonly relied upon resolution to avoid further complications in patients. *Nocardia brasiliensis*, although a rare pathogen, is the main culprit of actinomycetoma (bacterial-caused mycetoma). This underreported disease has not been fully explored. Currently, actinomycetoma has no preventative measures. Given the difficult patient accessibility of medical care, an effective, practical, pre-emptive approach is worth exploring. One such measure is the implementation of a broad-spectrum vaccine aimed at most, even all, mycetoma causative bacterial agents by targeting a conserved motif. I hypothesize that at least one *Nocardia brasiliensis* encoded protein is conserved amongst other actinomycetoma bacteria. Using a bioinformatical approach, identified *Nocardia brasiliensis* proteins were used to search for homologs in other potential mycetoma-causative agents. Three key DNA replication proteins have been identified as potential candidates. Interestingly, homologs were identified in other *Nocardia* species, as well as *Rhodococcus*, *Actinobacteria*, and *Corynebacteriales* species. Furthermore, nucleotide sequences encoded by the three most common causative agents of mycetoma were compared. From these analyses, the 16S ribosom was identified as partially conserved amongst them. These identified elements can now serve as a platform for future studies exploring them as a potential vaccine candidate.

The Wellness Value of Campus Landscapes

Sydnie Erlendson
University of Lethbridge

As part of the Campus Ecology Project at the University of Lethbridge, a twenty question online survey was administered to 265 students in Psychology 1000 or select Psychology 2000 level courses, who attend the campus. The students answered anonymously, and provided insight into their interactions with different plant and animal species that exist on the University of Lethbridge campus. This 10-20 minute survey gathered information about how landscapes and ecology affect and improve an individual's experience on campus. The survey also attempted to gain insight about how individuals feel about allocating funds towards ecology on campus, and the protection of potentially endangered species. Lastly, students were given the opportunity to indicate any ways in which they felt that the University of Lethbridge campus could better promote wellness for it's visitors.

Sprouting behavior of potato seed tubers (cv. Russet Burbank) after the application of different plant growth regulators

Garrett Rockafellow, Florian Dieker, Dmytro Yevtushenko
University of Lethbridge, Department of Biological Sciences

Key words: seed potato, growth regulator, dormancy, sprouting, physiological age, *Solanum tuberosum L.*

The yield of a potato crop is strongly influenced by the physiological age of potato tubers at planting. Physiological age can be defined as the stage of development of a seed tuber, which changes progressively by increasing chronological age and is modified by growth history and storage conditions (Struik & Wiersema, 1999). It is often characterized as the sprouting potential of seed. It is hard to overstate the importance of physiological age of seed potatoes to the potato industry: it strongly affects emergence of sprouts, number of stems per plant, number of tubers per stem, tuber-size distribution and tuber yield of the progeny crop (Van der Zaag & Van Loon, 1987; Van Ittersum, 1992; Struik & Wiersema, 1999; Struik, 2007). Thus, understanding the mechanisms of physiological aging and the ability to control it is crucial to maximizing crop yield and quality. Previous studies on physiological age of seed potato have been focused on environmental factors, such as relative humidity, temperature, photoperiod, and diffuse light (Struik & Wiersema, 1999; Struik *et al.*, 2006). Tuber respiration appears to be a pacemaker of aging: the longer the respiration rate remains high, the older the seed tubers will be (Blauer *et al.*, 2013). In addition, research has shown that plant growth regulators such as abscisic acid (ABA), ethylene, indole-3-acetic acid (IAA), cytokinins and gibberellins play a role in the control of tuber dormancy and subsequent sprout growth (Suttle, 2007). Up to date, there is still a strong need for further research to better understand their role and the effect on the physiological age (Suttle, 2004; Suttle, 2007; Kloostermann & Bachem, 2014; Wohlleb *et al.*, 2014).

In this study, different growth regulators such as Gibberellic Acid, ABA, Auxin, Cytokinin and 2.4-D were applied to the meristematic tissue of the seed tuber at three different concentrations (2.5, 5, 10 ppm) and stored at two different temperatures (5, 12°C). Afterwards, the break of dormancy and the sprouting behaviour were observed. At the time of writing, the study was not completed and thus no results can be presented at this time. The findings of this study will give indications for further research to develop new methods to control physiological age.

Notes

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