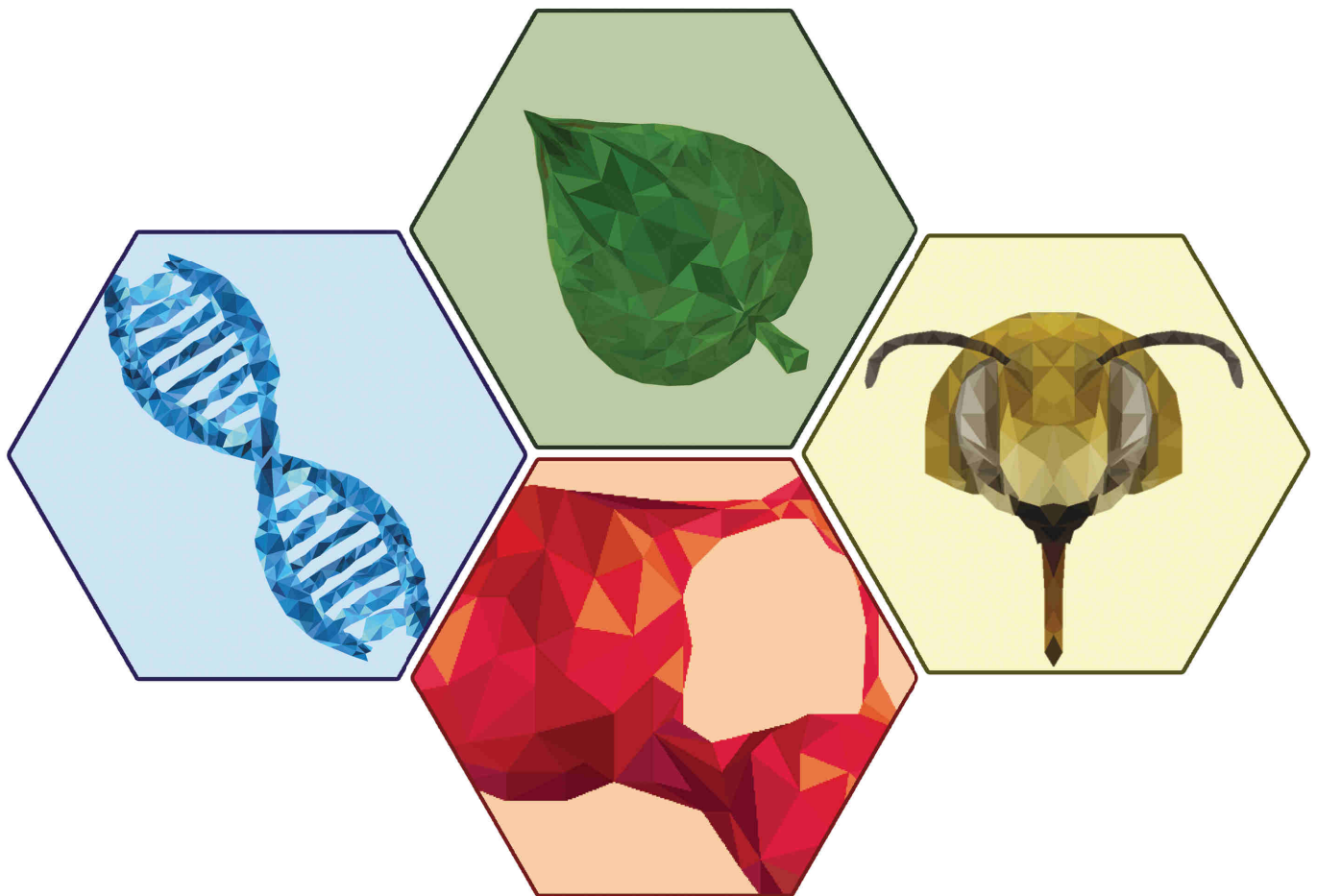


# PUBS

**Prairie University Biology Symposium**



***February 22-24, 2018 - University of Calgary***

**Credits:****Symposium Chairs:**

Kara Vanden Broek, Analisa Lazaro-Côté, Jonathon Lee, Jeremy Morris, Matija Stanic, Scott Seamone, Andrew Thompson

**Biology Graduate Students' Association:**

Danielle Clarke, Haley Glass, Christopher Hooey, Jeremy Morris, Will Murphy, Andrew Thompson

**Media and Graphics:**

Kara Vanden Broek, Alex Perry, Joseph Utomo, Theresa McCaffrey, Will Murphy, Jeremy Morris, Andrew Thompson

**Program Design:**

Will Murphy and Jeremy Morris

**Marketing:**

Kara Vanden Broek, Theresa McCaffrey, Scott Seamone, Natalie Tsao

**Finance and Judge Coordination:**

Jonathon Lee

**Speaker Coordination:**

Andrew Thompson

**Guest Speakers:**

David Suzuki	David Suzuki Foundation
Dr. Anthony Patrick Russell	University of Calgary
Dax Justin	Canadian Explorer and Photographer

**Sponsorship Coordination:**

Kara Vanden Broek, Jeremy Morris, Andrew Thompson

**Workshop Coordination:**

Jessy Bokvist, Oscar Montoya, Will Murphy, Brenna Stanford, Andrew Thompson

**Workshop Presenters:**

Intro to R	Oscar Montoya, Will Murphy, Samuel Robinson
Making Your CV Work for You	Stephanie Warner
Applying Genomics	Jessy Bokvist, Doro Lindtke, Mengmeng Lu
Developing Your Research Proposal	Petra McDougall

**Room Coordination:**

Kara Vanden Broek

**Receptions and Banquet:**

Analisa Lazaro-Côté, Natalie Tsao, Theresa McCaffrey, Matija Stanic

**Session Chairs:**

Danielle Clarke, Analisa Lazaro-Côté, Theresa Marie McCaffrey, Jeremy Morris, Haley Glass, Marwa Thraya, Joseph Utomo, Sean Baek, Mitchell Alberts, Ivette Menendez, Mohsen Ramezanpour, Soham Shah, Andrew Thompson, Jessy Bokvist, Laura Sosa Ponce

**Volunteer Coordinators:**

Analisa Lazaro-Côté

**Volunteers:**

Mitchell Alberts, Sean Baek, Jessy Bokvist, Danielle Clarke, Arminty Clarke, Haydee Mesa Galloso, Haley Glass, Paulette Harrison, Berna-Dean Holland, Christopher Hooey, Claudia Ladisa, Dean Lang, Jennifer Ma, Theresa Marie McCaffrey, Ivette Menendez, Oscar Montoya, Will Murphy, Laura Sosa Ponce, Mohsen Ramezanpour, James Reeve, Soham Shah, Isabella Skuplik, Brenna Stanford, Marwa Thraya, Miguel Torres, Natalie Tsao, Joseph Utomo

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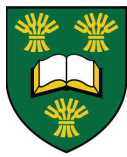
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## **WELCOME**

We welcome you to the 52<sup>nd</sup> Prairie University Biology Symposium! This event brings together undergraduate and graduate students from all backgrounds to present their research, network, and create collaborations and contacts that will last a lifetime. The Committee hopes you'll enjoy our event to the fullest by participating in our skill building workshops, networking at student events, and attending as many presentations by invited speakers and colleagues as possible.

Thank you for Supporting PUBS and we hope you enjoy the University of Calgary.

### **PUBS 2018 Symposium Chairs - February 2018**

Connect with us on Instagram and Twitter (@PUBS2018) using the hashtag #PUBS2018

## SAFETY INFORMATION

The University of Calgary's Campus Security is dedicated to maintaining the campus as a safe and pleasant place to live, work and study. Officers are on duty 24 hours a day, year round, to respond to your security and emergency needs. Closed Circuit Television (CCTV) cameras are strategically located on campus and are monitored by Campus Security 24 hours a day. More information is available at <http://www.ucalgary.ca/security/>.

Campus Security, in partnership with the Students' Union, provides a Safewalk service to any location on campus including the LRT, parking lots, bus zones and campus housing.

Campus Security can be contacted from any of the help phones located around campus or by dialing **403-220-5333**. In the event of a life threatening emergency or crime in progress, please call **9-1-1**.



## REGISTRATION

Guests can pick up their name tags and packages at the registration desk on Thursday February 22nd from 5:00 – 8:00 PM (Science Collaborative Space, ST142), Friday February 23 from 8:00 AM – 2:00 PM (Drummond Hall, BI 192), and Saturday February 24 from 8:30 AM – 12:00 PM (Drummond Hall, BI 192). Please see the maps section for directions and ensure that you wear your name tag throughout the conference.

## INFORMATION FOR PRESENTERS

### ORAL PRESENTATIONS

Each oral presentation is assigned to one of nine sessions occurring in the Biological Sciences building on either Friday February 23 or Saturday February 24 (see schedule for details). To promote interdisciplinary exchange of ideas, each session combines several research areas and avoids segregation by organism or system under study. Each time slot for presenters is 12 minutes of presentation time and 3 minutes of questions. During the question period, the next presenter should come to the front of the room and prepare to begin. We will be maintaining a strict schedule for each time slot to permit movement between concurrent sessions. **Presenters are to bring their presentation on a USB drive and upload their presentation prior to the start of their session.** Session chairs will be in the room 30 minutes before the start of each morning session and 15 minutes before the start of each afternoon session to facilitate the upload. You should have both PDF and PowerPoint copies of your presentation to ensure proper formatting. Use of personal computers to present will not be permitted, unless exceptional circumstances are demonstrated. In such a scenario, you will be responsible for providing your own adapter for VGA or HDMI.

### POSTER PRESENTATIONS

Each poster presentation is assigned to one of two sessions (see schedule). Poster session # 1 will take place from 7:00 – 8:30 PM on Friday February 23, on the 2nd and 3rd floor of the Energy Environmental Experimental Learning building (EEEL; see map). Poster session # 2 will take place from 3:30 – 5:00 PM in the atrium of the Science Theaters building (ST; see map). If your poster was assigned to Friday's session (Poster Session # 1) you can hang it after 1:30 PM on that day. If your poster was assigned to Saturday's session (Poster Session # 2) you can hang it any time after 9:00 AM, but please note that **poster boards will not be supervised during the day.** If you prefer, you may wait to put your poster up until closer to the start of the presentation period. Our only expectation is that your poster is up before the session and judging period officially begins (7:00 PM on Friday, 3:30 PM on Saturday). In order to allow participants to circulate and view other posters, Saturday's session (Poster Session # 2) will be split into two parts: even numbered posters will be judged between 3:30-4:15 PM and odd numbered posters will be judged between 4:15-5:00 PM. Please stand by your poster at the corresponding times so that judges may score your work. Posters must be no larger than 92 cm x 122 cm (3 ft x 4 ft). The included schedule has your poster number - please attach your poster to the corresponding board (pins will be provided).

### THREE MINUTE THESIS

The 3MT competition will occur on Saturday February 24 from 2:15 – 3:30 PM in BI 587. Each time slot is 3 minutes of presentation time followed by a short period for judges to finish scoring. Your presentation must not exceed 3 minutes, and **you will have points deducted from your score for surpassing this time.** Your presentation will start when you first speak/move upon stage. A countdown timer will be visible and you will be given a signal when you have 30 seconds remaining. Your presentation must be spoken word, and cannot be given in song, or poem form. Presenters may display one single slide (no animation or movement of any kind), and will not be able to use any props or additional electronic media during your presentation. If you would prefer, you may also opt to not use a slide at all. All images used on your slide must be your own, or you must have the permission of the owner of the photo(s). The presentation itself must be based on your thesis based research. **Presenters are to bring this slide on a USB drive and upload it to a laptop at our registration desk no later than 10:00 AM on the morning of the competition. Use of personal computers to present will not be permitted under any circumstances.** Presenters are also expected to be in the room 15 minutes before the start of the event for check in and a brief walkthrough of the event itself.

### AWARDS

First, Second, and Third place awards will be given for oral (Sponsored by the University of Lethbridge), poster (Sponsored by the School of Environment and Sustainability at the University of Saskatchewan) and 3-Minute Thesis (Sponsored by IDT) presentations. The winners will be announced during the Banquet on Saturday February 24 at approximately 7:30 PM and posted on the PUBS 2018 website the following day. Winners who are not present to collect their award will be contacted via email to make arrangements. At least two volunteer judges will be present at all oral presentation sessions, and at least two volunteer judges will visit each poster. They will score based on layout/organization, scientific merit, and presentation skills. Symposium chairs are not eligible to win.

## SOCIAL EVENTS

### OPENING RECEPTION

The reception will be held on Thursday February 22 from 7:00 – 10:00 PM in the Science Collaborative Space located within the Science Theaters building (see map). Light refreshments will be provided by EthniCity, and a cash bar will be available. In addition, registered guests will receive one complimentary drink ticket. You may be asked to present your name tag in order to verify registration. *Sponsored by the University Lethbridge*

### LUNCHES & COFFEE BREAKS

Lunch will be provided on Friday (Pizza) and Saturday (Sandwich wraps – *Sponsored by IDT*) in the Science Collaborative Space (see map). Coffee breaks will be held in Drummond Hall (BI 192; see map). These breaks are scheduled for Friday morning and afternoon (*Sponsored by the School of Environment and Sustainability at the University of Saskatchewan*) as well as Saturday morning. Coffee, various teas and light snacks will be provided. Guests are encouraged to bring their own reusable mug. You may be asked to present your name tag in order to verify registration.

### NETWORKING SOCIAL

A networking social event will be held on Friday February 23 from 8:30 – 10:00 PM in The Den and Black Lounge pub located in MacEwan Student Centre (see map). PUBS 2018 will have a reserved table but the pub will be open to the general public. Complimentary drink tickets will not be provided at this event.

### POSTER SESSIONS

Poster session # 1 will be held on Friday February 23 from 7:00 – 8:30 PM on the 2nd and 3rd floor of the Energy Environmental Experimental Learning building (EEEL; see map). Poster session # 2 (*Sponsored by the University of Lethbridge*) will be held on Saturday February 24 from 3:30 – 5:00 PM in the atrium of the Science Theaters building, adjacent to the Science Collaborative Space (ST; see map). Light refreshments will be provided at both sessions, and a cash bar will be available. In addition, registered guests will receive one complimentary drink ticket. We encourage everyone to come out and view the posters and network with colleagues during these sessions.

### BANQUET, AWARDS, & CLOSING CEREMONY

The PUBS 2018 Banquet will be held on Saturday February 24 from 5:30 – 11:00 PM in the Last Defence Lounge located in the MacEwan Student Centre (see map). Following a buffet style dinner, Dax Justin – professional wildlife photographer and Canadian explorer – will regale us with tales of his adventures. After this time, we will announce the Oral, Poster, and Three Minute Thesis Award winners and formally end the symposium with our closing ceremony at 8:00 PM. (*Sponsored by the University of Lethbridge*)

Tickets for the banquet must be purchased separately, either on our website or at the registration desk. Your purchase includes dinner and one complimentary drink ticket.

## TRANSPORTATION AND PARKING

Calgary Transit has several bus lines which provide service to and from the University campus - routes 9, 19, 20, 72, and 73 all stop at the University of Calgary Bus Loop (see map). You can also ride on the light rail transit (also known as the “C-train”) Red Line (Route 201) which traverses the city (Northwest-South), and passes through the University of Calgary LRT station (see map).

A one-time Calgary Transit ticket costs \$3.30 and is valid on all buses and trains (except route 300) within 90 minutes of purchase. Buses accept cash only, and exact change is required. Tickets can be purchased via credit card at C-train stations. Day passes cost \$10.50 and are available at most convenience stores and all C-train stations.

The City of Calgary is also serviced by a number of Taxi companies, as well as Uber. Taxi service to and from the airport costs approximately \$40-\$50, while service to the Downtown Core costs approximately \$20.

From “Hotel Alley” (eg. Comfort Inn & Suites at 2369 Banff Trail NW) the quickest way to the University of Calgary campus is to ride the C-train Red Line one station to the North. If you prefer to walk, the Biological Sciences building is approximately 20 minutes away.

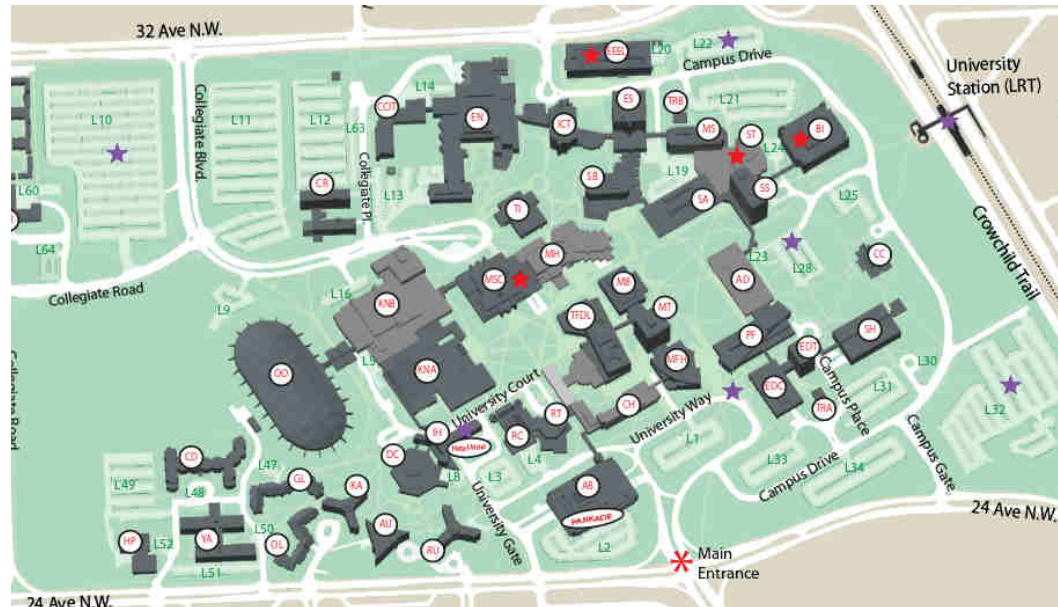
If you are arriving from Calgary International Airport, bus route 300 will take you into the downtown core (\$10.50 charge). From there, you may take a bus or the C-train Red Line (Northbound) to the University of Calgary campus .

We recommend using Google Maps to plan your trips. Alternatively, Calgary Transit also provides an effective trip planner ([www.calgarytransit.com/plan-a-trip](http://www.calgarytransit.com/plan-a-trip))

The University of Calgary campus does not have any free parking, but several paid options exist. On campus, Lots 10 and 32 both charge \$7 per day, or slightly less if you carpool or arrive before 10:30 AM. Campus lots marked as “Public Parking” (eg. Lots 22, 23, 28, etc) charge significantly more, up to \$4 per hour to a daily maximum of \$20. The McMahon Stadium East/West lots (20 minute walk), located across 24 Ave NW, charge \$4 per day.

In the area surrounding campus, you can find several locations to park for free. To the North, across 32 Ave NW, Brentwood Transit Station (10 minute walk) has a large no-cost parking lot. To the East, across Crowchild Trail NW, you can find free parking on select neighbourhood street (10 minute walk) – but pay attention to signage as there are many reserved/tow-away zones!

## UNIVERSITY MAPS



Main Entrance:	University located off Highway 1A
BI:	Biological Sciences
EEEL:	Energy Environmental Experiential Learning Building
ST:	Science Theatres
LRT:	University Train Station
MSC:	MacEwan Student Centre - Food, Coffee, Beer
Hotel Alma:	The University's on campus Hotel
Lot 10	
Lot 22	
Lot 23	
Lot 28	
Lot 32	

Map of Science Theatres





## First Floor of Biological Sciences



## Second Floor of Biological Sciences







## THINGS TO DO IN CALGARY

### PARKS AND RECREATION

Calgary is home to many lovely parks. Prince's Island Park is just a short walk from the Sunnyside train station and is situated along the Bow River. Fish Creek Park is just off the Fish Creek/Lacombe train station and is an excellent place for walking and bird watching. Nose Hill Park, which contains over 11 square kilometers of natural landscape, is a 30 minute walk Northeast of the University of Calgary campus. Other notable attractions include the Calgary Zoo, conveniently located from the Zoo train station, the Telus SPARK Science Center (220 St Georges Dr NE) and the Globe Cinema (617 8 Ave SW).

### WINING, DINING, SHOPPING

If you are taking public transit, the most readily accessible area for dining and shopping is the Downtown Core, which runs between the 8th Street SW and City Hall C-train stations. Travel between the Downtown Core train stations is free of charge! The major mall in that area is the CORE Shopping Centre located just off the 3rd Street SW station. One block south of the Downtown Core, you can visit our high street, known as "Stephen Avenue Walk" (8th Avenue SW). This area has plenty of spots for dining and experiencing the nightlife. Other restaurants and clubs can also be found a couple blocks to the south on 17th Avenue SW. Calgary's largest mall, Chinook Centre (6455 Macleod Trail SW), can be reached by taking the C-train Red line Southbound and getting off at Chinook station. A more detailed listing of attractions in Calgary and the surrounding area is available on our website.

## WORKSHOPS

### Introduction to R

February 22 4:00 - 6:30 PM - BI587

This workshop will provide you with basic skills in using the R programming language. You will learn important differences between R and Excel, how to store and manipulate data, create publication worthy plots, and conduct basic statistical tests. No prior experience needed. Attendees will receive an email with an accompanying R script, example data file, and further instructions for installing R.

### Applying Genomics to Ecological and Evolutionary Research

February 23 12:15 - 1:15 PM - BI211

An introductory level workshop covering the application of genotyping by sequencing (GBS) technologies. Learn the what's and how's of GBS and ways to use this tool for your own research questions. Walk through examples of how GBS has been used in studying speciation, signatures of selection across the genome and for genome wide association studies. *Sponsored by the University of Lethbridge*

### Making your CV and Resume Work for You

February 23 12:15 - 1:15 PM - BI587

Learn the difference between these two documents and strategies to highlight the transferable skills gained from your unique experiences. *Sponsored by IDT*

### Strategies for Developing Research Proposals

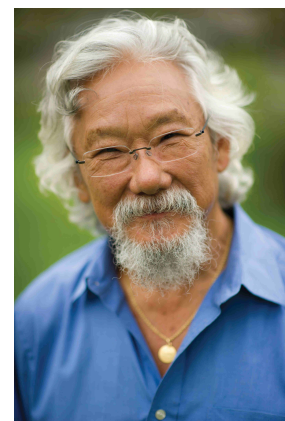
February 24 1:00 - 1:00 PM - BI211

This session provides strategies for developing appropriate research

questions, conceptualizing information surrounding a topic, and selecting a project scope that matches your time frame. While noting differences across disciplines, this workshop discusses strategies students can use to begin the planning and drafting of a research proposal. Key features of the workshop include developing preliminary research questions, creating coherence between parts of the proposal, and revising for errors that prompt confusion or misreading. Please note that this session does not provide information related to preparing proposals for scholarship/ funding applications. *Sponsored by the School of Environment and Sustainability at the University of Saskatchewan*

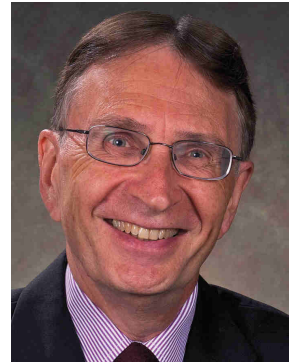
**Keynote Speaker: Dr. David Suzuki***The Challenge of the 21st Century: Setting the Bottomline in the Anthropocene*

Dr. David Suzuki is a scientist, broadcaster, author, and co-founder of the David Suzuki Foundation. He is Companion to the Order of Canada and a recipient of UNESCO's Kalinga Prize for science, the United Nations Environment Program medal, the 2012 Inamori Ethics Prize, the 2009 Right Livelihood Award, and UNEP's Global 500. Dr. Suzuki is Professor Emeritus at the University of British Columbia in Vancouver and holds 29 honorary degrees from universities around the world. He is familiar to television audiences as host of the CBC science and natural history television series *The Nature of Things*, and to radio audiences as the original host of CBC Radio's *Quirks and Quarks*, as well as the acclaimed series *It's a Matter of Survival* and the book *From Naked Ape to Species*. In 1990 he co-founded with Dr. Tara Cullis, The David Suzuki Foundation to "collaborate with Canadians from all walks of life including government and business, to serve our environment and find solutions that will create a sustainable Canada through science-based research, education, and policy work." His written works includes more than 55 books, 19 of them for children. Dr. Suzuki lives with his wife and family in Vancouver, B.C.



**Plenary Speaker: Dr. Anthony Russell***The Sticky Fingers of Geckos:**From Esoteric Backwater to Mainstream Interdisciplinary Science*

Tony Russell completed his Bachelor's degree at the University of Exeter and his PhD at the University of London. Immediately after the completion of his PhD he took up a short teaching appointment at the University of Botswana, Lesotho and Swaziland before beginning his work at the University of Calgary in August 1973. He has authored over 300 peer-reviewed scientific articles, 19 book chapters, and three books. Over his career he has supervised and mentored over 40 graduate students. He has received recognition for his contributions including the NSERC 25 Years of Excellence Award, the Alberta Foundation for Environmental Excellence Award, the University of Calgary Distinguished Faculty Award, and has received the Students' union teaching award for excellence three times. He has been inducted as a member of the Order of the University of Calgary, and is an Alberta Science and Technology Honouree. His field work has taken him to Australia, New Zealand, the Eastern Caribbean, Namibia, and, most recently, Trinidad and Tobago. He served for six years as head of the Department of Biological Sciences, and six years as Associate Dean (Students) of the Faculty of Science. Outside the University he has served as President of the Canadian Society of Zoologists, and President of the International Society of Vertebrate Morphologists.





## Banquet Speaker: Dax Justin

### *Vanishing Vitality*

Dax Justin is a Canadian Explorer, Outdoor Adventure, Landscape Photographer and visual storyteller relentlessly pursuing experiences that will make you feel alive. Based in Calgary, Alberta, the gateway to the Canadian Rockies, Dax's body of photographic work spans outdoor adventure, landscapes, mountain lifestyle and culture yet always retains a human element. Dax collaborates with destinations, adventure companies and travel brands to help tell their stories by producing high-quality visual's rooted in a social narrative that is both creative and immersive. His work aims to deliver a living sense of adventure and vitality to a world-wide online community of over 150,000, expanding brand reach and awareness through social channels and travel networks. Dax works in partnership with Canadian Geographic, Helly Hansen, KEEN Canada, Revo and Edge TV, and is also a public speaker (TEDx) and educator, delivering workshops on smartphone photography and visual storytelling on social media. He is currently working on developing his online course: SmartPhonePRO photography workshop-a complete guide teaching how to capture, process, and share professional-level photos, all from a mobile device. Connect with Dax on social media: @daxjustin and daxjustin.com.





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**CURIOSITY SPARKS DISCOVERY**



"To play a role in the investigative process and help create new knowledge as an undergraduate was an amazing experience, something that likely would not have been available to me at a larger institution."

Jyote Boora | BSc '16

University of  
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# IT'S YOUR TIME TO SHINE

At the University of Lethbridge, everyone has the ability to shine, and we believe it's our job to help make that happen.

Nestled where the Rocky Mountains meet the Alberta prairies, we consistently rank as one of Canada's top undergraduate universities and research institutions. More than that, we are a community of inspiring lights united by one common purpose: You.

Where you learn shapes how you learn, and one of the country's most advanced facilities for transdisciplinary teaching, learning and research is taking shape at uLethbridge. Opening in 2019, our new science and academic building is transforming campus, the Lethbridge skyline and southern Alberta. Here, undergraduate and graduate students alike work alongside researchers from a variety of disciplines to tackle society's most perplexing issues.



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## SCHEDULE

## PUBS 2018 Schedule – “At a glance”

Thursday, February 22, 2018		
3:00 – 4:00	McCauley Awards (BI 211)	
4:00 – 6:30	Intro to “R” Workshop (BI 587)	Registration 5:00- 8:00 (Science Collaborative Space – ST 142)
7:00 – 10:00	Opening Reception (Science Collaborative Space – ST 142) <i>Sponsored by the University of Lethbridge</i>	

Friday, February 23, 2018		
8:00	Registration 8:00 - 2:00 (Drummond Hall - BI 192)	
9:00 – 10:30	Oral presentations <i>A1- Microbiology and Bioremediation (BI 211)</i> <i>B1- Cell and Cancer Biology (BI 561)</i> <i>C1- Behaviour and Communication (BI 587)</i> <i>Sponsored by IDT</i>	
10:30 – 10:45	Break (Drummond Hall - BI 192)	
10:45 – 12:00	Oral presentations - <i>Continued</i> <i>A1- Microbiology and Bioremediation (BI 211)</i> <i>B1- Cell and Cancer Biology (BI 561)</i> <i>C1- Behaviour and Communication (BI 587)</i>	
12:00 – 1:30	Lunch (Science Collaborative Space – ST 142)	Workshops 12:15 – 1:15 <b>CV/Résumé</b> – <i>Sponsored by IDT</i> (BI 211) <b>Genomics</b> – <i>Sponsored by the University of Lethbridge</i> (BI 587)
1:30 – 2:45	Oral presentations <i>A2- Physiology &amp; Development (BI 211)</i> <i>B2- Population Biology (BI 561)</i> <i>C2- Conservation Biology &amp; Management (BI 587)</i>	

**Friday, February 23, 2018 - *continued***

2:45 – 3:00	<p>Break (Drummond Hall - BI 192) <i>Sponsored by the School of Environment and Sustainability at the University of Saskatchewan</i></p>
3:00 – 4:00	<p>Oral presentations – <i>Continued</i> <i>A2- Physiology &amp; Development (BI 211)</i> <i>B2- Population Biology (BI 561)</i> <i>C2- Conservation Biology &amp; Management (BI 587)</i></p>
4:30 – 5:00	<p>Registration for Keynote (Energy Environment Experiential Learning (EEL) Atrium)</p>
5:15 – 6:15	<p>Keynote Speaker <b><u>Dr. David Suzuki</u></b> (Energy Environment Experiential Learning (EEL) Atrium)</p>
6:15 – 6:30	<p>Q&amp;A with Dr. David Suzuki (Energy Environment Experiential Learning (EEL) Atrium)</p>
6:30 – 7:30	<p>Book Signing with Dr. David Suzuki (Energy Environment Experiential Learning (EEL) Atrium)</p>
7:00 – 8:30	<p>Poster Session # 1 (Energy Environment Experiential Learning (EEL) Atrium)</p>
8:30 – 10:00	<p>Networking &amp; Social (“The Den” – MacEwan Student Centre)</p>



Saturday, February 24, 2018		
8:30	Registration 8:30 - 12:00 (Drummond Hall - BI 192)	
9:30 – 10:30	Plenary Speaker <b><u>Dr. Anthony Russell</u></b> (EEEL 161) <i>Sponsored by the School of Environment and Sustainability at the University of Saskatchewan</i>	
10:30 – 11:00	Break (Drummond Hall - BI 192)	
11:00 – 12:45	Oral presentations <i>A3- Integrative Cell Biology (BI 211)</i> <i>B3- Specialized Metabolism &amp; Biological Membranes (BI 561)</i> <i>C3- Species Interactions &amp; Dynamics (BI 587)</i>	
12:45 – 2:15	Lunch (Science Collaborative Space – ST 142)	
		Workshop 1:00 – 2:00 <b>Developing a research proposal</b> <i>Sponsored by the School of Environment and Sustainability at the University of Saskatchewan</i> (BI 211)
2:15 – 3:30	3-Minute Thesis Competition (BI 587) <i>Sponsored by the University of Lethbridge</i>	
3:30 – 5:00	Poster Session # 2 (Science Theaters Atrium – “The Zipper”) <i>Sponsored by the University of Lethbridge</i>	
5:30 – 11:00	Banquet & Guest Speaker <b><u>Mr. Dax Justin</u></b> (Last Defence Lounge – MacEwan Student Centre) <i>Sponsored by the University of Lethbridge</i>  Awards Ceremony 8:00	

## Session Schedules

Session A1: Microbiology & Bioremediation		
Session Chairs: Jeremy Morris & Danielle Clake Room: BI 211		
Speaker	Time	Presentation
1	9:00 – 9:15	<b>Damon Brown</b> , <i>University of Calgary</i> Genetic Presence of Multidrug Resistance Efflux Pumps in Response to Biocide Treatment of a Model Microbiologically Influenced Corrosion Community
2	9:15 – 9:30	<b>Felix Nwosu</b> , <i>University of Calgary</i> Co-oxidation of naphthenic acids by methanotrophic bacterial species in Alberta oil sands tailings ponds
3	9:30 – 9:45	<b>Emily Haidl</b> , <i>University of Regina</i> Exploration of human-associated microbial communities using Bayesian Networks
4	9:45 – 10:00	<b>Gurpreet Kharey</b> , <i>University of Calgary</i> BTEX and Alkane Degradation Through Anaerobic Microbial Activity in Contaminated Aquifers in Alberta, Canada
5	10:00 – 10:15	<b>Jenny Nguyen</b> , <i>University of Calgary</i> Does the Prairie Epidemic Strain of <i>Pseudomonas aeruginosa</i> Employ the Type Six Secretion System in Strain Replacement?
6	10:15 – 10:30	<b>Oscar Montoya</b> , <i>University of Calgary</i> Methanogenic and Aerobic Biodegradation of Model Polycyclic Aromatic Compounds Associated with Canadian Oil Sands
	10:30 – 10:45	Break – Refreshments in Drummond Hall (BI 192)
7	10:45 – 11:00	<b>Nadia Monych</b> , <i>University of Calgary</i> Metal Resistance in Dual-Species Biofilms
8	11:00 – 11:15	<b>Jeremy Wong</b> , <i>University of Calgary</i> Identification of Plant Genes Involved in Oil Sands Naphthenic Acid Degradation
9	11:15 – 11:30	<b>Craig Soutar</b> , <i>University of Regina</i> Exploring the contributions of iron-acquisition systems to the evolution of opportunistic human pathogenic bacteria
10	11:30 – 11:45	<b>Natalie Gugala</b> , <i>University of Calgary</i> Bacterial toxicity and resistance originating from the use of metal-based antimicrobials
11	11:45 – 12:00	<b>Austin Nguyen</b> , <i>University of Calgary</i> Carbon Metabolism of <i>Pseudomonas aeruginosa</i> in Cystic Fibrosis

<b>Session B1: Cell &amp; Cancer Biology</b> <b><i>Sponsored by IDT</i></b>		
<b>Session Chairs: Theresa McCaffrey &amp; Marwa Thraya</b> <b>Room: BI 561</b>		
<b>Speaker</b>	<b>Time</b>	<b>Presentation</b>
12	9:00 – 9:15	<b>Colyn Cleland</b> , <i>University of Lethbridge</i> Producing and utilizing myo-inositol phosphate (IP) affinity matrices to identify eukaryotic IP interacting proteins
13	9:15 – 9:30	<b>Adley Mok</b> , <i>University of Calgary</i> Granzyme B is required for Natural Killer cell-mediated antifungal activity
14	9:30 – 9:45	<b>Elina Levchenko</b> , <i>University of Calgary</i> REMPing the knowledge towards the protein translocation pathway: understanding the mechanism of folded proteins transport
15	9:45 – 10:00	<b>Apurva Bhardwaj</b> , <i>University of Winnipeg</i> Unraveling the effect of rapamycin on IGFBP-3 localization
16	10:00 – 10:15	<b>Sibapriya Chaudhuri</b> , <i>University of Calgary</i> Protein phosphatase 2A-B56 controls mitosis by interacting with LXXIXE motif containing proteins
17	10:15 – 10:30	<b>Kareem Hassan</b> , <i>University of Winnipeg</i> Rapamycin Treatment Alters Localization of N-Myristoyltransferase in Breast Cancer Cells
	10:30 – 10:45	Break – Refreshments in Drummond Hall (BI 192)
18	10:45 – 11:00	<b>Mohamed Abo Aoun</b> , <i>University of Winnipeg</i> Diagnosis from a prick: N-Myristoyltransferase expression and sub-cellular localisation in peripheral blood mononuclear cells (PBMC) as a potential screening test for colorectal cancer
19	11:00 – 11:15	<b>Joey Lockhart</b> , <i>University of Calgary</i> Neutrophil Inflammatory Responses to Extracellular Factors and Lipopolysaccharide from Anaerobic Bacterial Biofilms
20	11:15 – 11:30	<b>Dean Reddick</b> , <i>University of Winnipeg</i> Role of N-myristoyltransferase in Endocrine Therapy Resistance in Estrogen Receptor Positive Breast Cancer
21	11:30 – 11:45	<b>Charnae Hubscher</b> , <i>University of Winnipeg</i> Unravelling the Mechanism of Rapamycin and Metformin Mediated Apoptosis in Cancer Cells
22	11:45 – 12:00	<b>Syeda Yousra Irshad</b> , <i>University of Winnipeg</i> Effect of Metformin on Endogenous levels of IGFBP-3 on mammary carcinoma cells



Session C1: Behaviour & Communication		
Session Chairs: Analisa Lazaro-Côté & Haley Glass Room: BI 587		
Speaker	Time	Presentation
23	9:00 – 9:15	<b>Patricia Tomchuk</b> , <i>University of Saskatchewan</i> Habitat selection of black bears ( <i>Ursus americanus</i> ) in Saskatchewan's Boreal Shield
24	9:15 – 9:30	<b>Jillian Kusch</b> , <i>University of Saskatchewan</i> The individual variation of social strategies in a population of Canadian black-tailed prairie dogs ( <i>Cynomys ludovicianus</i> )
25	9:30 – 9:45	<b>Katherine Fedoroff</b> , <i>University of Saskatchewan</i> The effect of sublethal concentrations of Selenium on the antipredator response of fathead minnows to alarm cues
26	9:45 – 10:00	<b>Anthony Leong</b> , <i>University of Winnipeg</i> Human responses to distress cries across species
27	10:00 – 10:15	<b>Trevor Moore</b> , <i>University of Winnipeg</i> Thermoregulatory Energetics of Female Little Brown Bat ( <i>Myotis lucifugus</i> )
28	10:15 – 10:30	<b>Branden Neufeld</b> , <i>University of Saskatchewan</i> This Bed is too Soft: American Black Bear Den Phenology and Site Selection in Saskatchewan's Boreal Shield
	10:30 – 10:45	Break – Refreshments in Drummond Hall (BI 192)
29	10:45 – 11:00	<b>Emmanuel Olarewaju</b> , <i>University of Manitoba</i> MIRROR OF THE MIND: A Functional Analysis of Imitation in Humans
30	11:00 – 11:15	<b>Kevin Bairos-Novak</b> , <i>University of Saskatchewan</i> When to heed the call: how kinship, familiarity, and predation risk affect aquatic prey reliance on chemical disturbance cues
31	11:15 – 11:30	<b>Mikala Epp</b> , <i>University of Manitoba</i> Speaking whale: Investigating the functions of humpback whale non-song calls in the North Atlantic
32	11:30 – 11:45	<b>Alyssa Stulberg</b> , <i>University of Regina</i> The effects of body condition and wing asymmetry on personality of Cape horseshoe bats ( <i>Rhinolophus capensis</i> )
33	11:45 – 12:00	<b>Dale Barks</b> , <i>University of Saskatchewan</i> The Bear Essentials: Home Range and Movement of Boreal Forest Black Bears, With Respect to Hunter Baiting

Session A2: Physiology & Development		
Session Chairs: Joseph Utomo & Ivette Menéndez Perdomo Room: BI 211		
Speaker	Time	Presentation
34	1:30 – 1:45	<b>Marwa Thraya</b> , <i>University of Calgary</i> Stress-mediated rapid effects of cortisol in rainbow trout liver
35	1:45 – 2:00	<b>Abhinandan Kumar</b> , <i>University of Calgary</i> The Opposing Roles of Flavonoids and Reactive oxygen species in Mediating Pollination in Ornamental Kale
36	2:00 – 2:15	<b>Emma Kunkel</b> , <i>University of Winnipeg</i> Free falling or free flying? Activity Thermoregulatory Substitution during Rewarming from Torpor in migratory bats
37	2:15 -2:30	<b>Kelton Braun</b> , <i>University of Saskatchewan</i> Evaluating the use of nectary vascularization and morphology as phylogenetic characteristics in the Asteracean tribe Astereae
38	2:30 – 2:45	<b>Dimitri Desmouts de Lamache</b> , <i>University of Calgary</i> The Use of Antibiotics to Treat Viral infections: Immuno-modulating properties of Tulathromycin in porcine reproductive and respiratory syndrome
	2:45 – 3:00	Break – Refreshments in Drummond Hall (BI 192)
39	3:00 – 3:15	<b>Isabella Hutchison</b> , <i>University of Calgary</i> Young and Defended: Age and Resin Duct Metrics in Lodgepole Pines
40	3:15 – 3:30	<b>Eva Slight-Simcoe</b> , <i>University of Winnipeg</i> Thermogenesis in fish: A potential role for the SERCA pump uncoupling protein, Sarcoplipin, in a whole-body endotherm, the Opah ( <i>Lampris guttatus</i> )
41	3:30 – 3:45	<b>Matija Stanic</b> , <i>University of Calgary</i> Improving Canola productivity through manipulation of shoot branching pathway
42	3:45 – 4:00	

Session B2: Population Biology		
Session Chairs: Mitchel Alberts & Soham Shah Room: BI 561		
Speaker	Time	Presentation
43	1:30 – 1:45	<b>Jori Harrison</b> , <i>University of Calgary</i> What does it mean? Evaluating uncertainty and reliability in environmental DNA interpretation.
44	1:45 – 2:00	<b>Christina Tollett</b> , <i>University of Saskatchewan</i> Genomic Diversity in the Canadian Feral Horse ( <i>Equus ferus caballus</i> )
45	2:00 – 2:15	<b>Chulnatha Diyes</b> , <i>University of Saskatchewan</i> Examination of the life history patterns of the hard tick <i>Haemaphysalis intermedia</i>
46	2:15 -2:30	<b>Julie Colpitts</b> , <i>University of Saskatchewan</i> Inbreeding depression in an island population of feral horses ( <i>Equus ferus caballus</i> ): fine-scale variation and fitness consequences
47	2:30 – 2:45	<b>Adam Watson</b> , <i>University of Calgary</i> Integrating estimates of genetic diversity to inform Burrowing Owl ( <i>Athene cunicularia</i> ) conservation strategies
	2:45 – 3:00	Break – Refreshments in Drummond Hall (BI 192)
48	3:00 – 3:15	<b>Jessy Bokvist</b> , <i>University of Calgary</i> The impact of enriched rearing in captivity: genetic and environmental determinants of Pacific coho salmon ( <i>Oncorhynchus kisutch</i> ) survival phenotypes
49	3:15 – 3:30	<b>Zach Balzer</b> , <i>University of Saskatchewan</i> Morphology of the First Instar Larvae of <i>Stylops</i> sp. (Strepsiptera), which infect <i>Andrena milwaukeensis</i> (Hymenoptera)
50	3:30 – 3:45	
51	3:45 – 4:00	

Session C2: Conservation Biology & Management		
Session Chairs: Sean Baek & Mohsen Ramezanpour Room: BI 587		
Speaker	Time	Presentation
52	1:30 – 1:45	<b>Adam Sprott</b> , <i>University of Regina</i> Spatial Analyses of Canopy Structure of Forests in the Cypress Hills
53	1:45 – 2:00	<b>Bethany Topping</b> , <i>St. Mary's University</i> Bees: The dependence on adequate nutrition for a healthy immune system
54	2:00 – 2:15	<b>Kyle Wilson</b> , <i>University of Calgary</i> Network asymmetry and social-ecological diversity drives collapses of inland fisheries
55	2:15 -2:30	<b>Nicole Dorville</b> , <i>University of Winnipeg</i> Species differences in susceptibility to white-nose syndrome
56	2:30 – 2:45	<b>Robyn Demare</b> , <i>University of Winnipeg</i> Preliminary assessment of the population biology of yellow perch ( <i>Perca flavescens</i> ) in Waterhen Lake, Manitoba
	2:45 – 3:00	Break – Refreshments in Drummond Hall (BI 192)
57	3:00 – 3:15	<b>Danielle Clake</b> , <i>University of Calgary</i> Bumble bees ( <i>Bombus sp.</i> ) in the Alberta Rockies: effects of natural land cover heterogeneity on species richness and abundance
58	3:15 – 3:30	<b>Kendra Gietzen</b> , <i>University of Regina</i> Stress in Walleye during Catch and Release Angling
59	3:30 – 3:45	<b>Andrea Wishart</b> , <i>University of Saskatchewan</i> The "fitness" of a territory: is the reproductive success of a food-caching animal more associated with habitat or individual quality?
60	3:45 – 4:00	<b>Shayna Hamilton</b> , <i>University of Regina</i> Scaling the question of Age vs Size - An examination of yellow perch ( <i>Perca flavescens</i> ) morphology and age in a high-use Saskatchewan Lake

Session A3: Integrative Cell Biology		
Session Chair: Andrew Thompson Room: BI 211		
Speaker	Time	Presentation
61	11:00 -11:15	<b>Charlene Watterston, University of Calgary</b> MicroRNA regulation of BMP signaling and its effects on vascular smooth muscle cells
62	11:15 -11:30	<b>Tom Whitesell, University of Calgary</b> foxc1b as a marker of early vascular smooth muscle cells in zebrafish
63	11:30 – 11:45	<b>Amber Hiebert, University of Manitoba</b> Single fiber studies of muscle growth during development of the Lake Sturgeon ( <i>Acipenser fulvescens</i> )
64	11:45 – 12:00	<b>Anja Ljubojevic, University of Calgary</b> Exploring the interaction between Shox2 and Sonic hedgehog signalling in mouse limb development
65	12:00 – 12:15	<b>Maria Alejandra Castilla Bolanos, University of Regina</b> Effects of glutamate and engineered scaffolds on neural stem cell differentiation
66	12:15 – 12:30	<b>Nabila Bahrami, University of Calgary</b> Identifying differences between pericyte and smooth muscle contraction-relaxation <i>in vivo</i>
67	12:30 – 12:45	<b>Alwyn Go, University of Winnipeg</b> Sterility and differential gene expression in Drosophila interspecies hybrids

Session B3: Specialized Metabolism & Biological Membranes		
Session Chair: Laura Sosa Ponce Room: BI 561		
Speaker	Time	Presentation
68	11:00 -11:15	<b>Ashley Williams</b> , <i>University of Regina</i> Discovery of a natural product antibiotic effective against the multi-drug resistant human pathogen, <i>Acinetobacter baumannii</i>
69	11:15 -11:30	<b>Maria Laura Sosa Ponce</b> , <i>University of Calgary</i> Lysophosphatidylcholine Analogues Alter Yeast Nuclear Envelope Architecture and Function
70	11:30 – 11:45	<b>Connor Hodgins</b> , <i>University of Calgary</i> Natural rubber and sesquiterpene lactones co-accumulate in laticifer but their promoters show differential expression patterns in lettuce.
71	11:45 – 12:00	<b>Weiam Daear</b> , <i>University of Calgary</i> Biophysical studies on the interaction of polymeric nanoparticles with model lung surfactant
72	12:00 – 12:15	<b>Naveen Sorout</b> , <i>University of Regina</i> Investigation of an antibiotic effective against the enteric human pathogens
73	12:15 – 12:30	<b>Mohsen Ramezanpour</b> , <i>University of Calgary</i> Computational Insights into the Drug Release from Endosome for Lipid Nanoparticles Based on Ionizable Cationic Lipids
74	12:30 – 12:45	<b>Robyn Mundle</b> , <i>University of Calgary</i> Lead Interactions Affect the Fluidity and Lateral Organization of Complex Lipid Membranes

**Session C3: Species Interactions & Dynamics**

**Session Chair: Jessy Bokvist**  
**Room: BI 587**

<b>Speaker</b>	<b>Time</b>	<b>Presentation</b>
75	11:00 -11:15	<b>Micky Ahn</b> , <i>University of Lethbridge</i> Consequences of parasitism: Reproduction of a population of male fathead minnows in northern Alberta
76	11:15 -11:30	<b>Jillian Perreaux</b> , <i>Brandon University</i> The mycota of soils associated with snake hibernacula
77	11:30 – 11:45	<b>Ivan Drahun</b> , <i>University of Winnipeg</i> Oviposition site selection by <i>Aedes aegypti</i> and <i>Anopheles gambiae</i> mosquitoes with respect to water with different organic content
78	11:45 – 12:00	<b>Ruth Greuel</b> , <i>University of Saskatchewan</i> Relating stand-level characteristics to ground lichen abundance for estimating availability of boreal caribou forage
79	12:00 – 12:15	<b>Tanvir Shovon</b> , <i>University of Regina</i> Overstory tree composition drives the ecological strategies of understory plant communities
80	12:15 – 12:30	<b>Jessica Thoroughgood</b> , <i>University of Saskatchewan</i> Differentiating species of fleas found on sciurid rodents in Southern Saskatchewan
81	12:30 – 12:45	<b>Sarah Unrau</b> , <i>University of Lethbridge</i> Aggregation of trematode-infected zombie ants on flowers

## Poster session # 1

Friday February 23, 2018

7:00 – 8:30 PM

Energy Environment Experiential Learning (EEL) building

1	<b>Khadija Abdullahi</b> , <i>Concordia University of Edmonton</i> Blue LED irradiation of breast cancer cell line MDA-MB-231: Induction of apoptosis through ROS mediated signalling pathway
2	<b>Casey Carlisle</b> , <i>University of Alberta</i> Sarcomere assembly and maintenance in the zebrafish muscle mutant, herzsclag
3	<b>Adriana Carvalho Natal de Moraes</b> , Instituto de Biofísica Carlos Chagas Filho Cylindrospermopsin Adversely Impacts Zebrafish ( <i>Danio rerio</i> ) Development
4	<b>Chinmayee Das</b> , <i>Univeristy of Calgary</i> Inhibition of cortisol-mediated rapid glucocorticoid receptor translocation triggered by membrane modifications in trout hepatocytes
5	<b>Camila dos Santos Meira</b> , <i>University of Calgary</i> Cathepsin B cysteine protease of <i>L. donovani</i> : role in the modulation of parasitic exosomal proteins
6	<b>Sean Everitt</b> , <i>University of Lethbridge</i> Toxicity of sediment-bound diluted bitumen to <i>Hyaella azteca</i>
7	<b>Erin Faught</b> , <i>University of Calgary</i> The glucocorticoid receptor knockout affects growth and metabolism in zebrafish
8	<b>Odul Karayazi Atici</b> , <i>University of Calgary</i> ATM Is Required for the Prolactin-Induced HSP90-Mediated Increase in Cellular Viability and Clonogenic Growth After DNA Damage
9	<b>Silvia Losada &amp; Adam Mitton</b> , <i>University of Calgary</i> Long-term biomonitoring of macroinvertebrate metrics in the Kananaskis River, Alberta
10	<b>Kiana Matwichuk</b> , <i>University of Victoria</i> Environmental enrichment of Coho salmon ( <i>Oncorhynchus kisutch</i> ) fry reduces boldness in hatchery reared fish
11	<b>Theresa McCaffrey</b> , <i>University of Calgary</i> Blue shark morphology: youth are unstable, adults rocket but don't roll
12	<b>Ivette Menendez-Perdomo</b> , <i>University of Calgary</i> Biochemical characterization of O-methyltransferases involved in BIA biosynthesis in Sacred Lotus
13	<b>Haydee Mesa Galloso</b> , <i>University of Calgary</i> Understanding the pore-forming mechanism of peptides derived from the N-terminus of sticholysin
14	<b>Zachary Nurcombe</b> , <i>University of Calgary</i> The role of Clusterin and its putative Plexina4 receptor in the developing zebrafish brain
15	<b>Christina Ridley</b> , <i>University of Calgary</i> Microbial Ecology of the Subsurface Athabasca Oil Sands
16	<b>Soham Shah</b> , <i>University of Calgary</i> Adverse Health Impacts of Sulfolane Exposure on Zebrafish ( <i>Danio rerio</i> ) Development
17	<b>Lisa Sims</b> , <i>University of Calgary</i> How has hurricane disturbance affected bat communities on the Caribbean island of Dominica?
18	<b>Isabella Skuplik</b> , <i>University of Calgary</i> Characterization of a novel limb-specific enhancer of the human SHOX gene
19	<b>Kevin Sule</b> , <i>University of Calgary</i> Characterization of manganese interaction with lipid membranes
20	<b>Ryleigh-Raye Wolfe</b> , <i>Concordia University of Edmonton</i> Effect of Wildfires on Mobilization of Heavy Metals in Alberta's Peatland Boreal Forest



## Poster session # 2

Saturday February 24, 2018  
3:30 – 5:00 PM  
Science Theaters Atrium – “The Zipper”

Even numbered posters will be judged between 3:30-4:15 and odd numbered posters will be judged between 4:15-5:00.  
Please stand by your poster at these times.

21	<b>Ahmed Abdelaziz, University of Calgary</b> Functional characterization of the Pumilio gene <i>puf4+</i> in <i>Schizosaccharomyces pombe</i>
22	<b>Juwayriya Abdullahi, Concordia University of Edmonton</b> Effect of Ataluren on MYO7A nonsense mutation responsible for Usher syndrome
23	<b>John Alho, University of Calgary</b> Bats Fatalities and Wind Turbines
24	<b>Dilini Atugala, University of Calgary</b> Establishing an in vivo approach to identify interactions between plant RNA-binding proteins and their mRNA targets
25	<b>Sandra Black, University of Calgary</b> A critical review on the “health” of narwhal ( <i>Monodon monoceros</i> ) in a time of anthropogenic and climate changes: Do we know enough?
26	<b>Deborah Buhlers, University of Calgary</b> Characterization of the two ribitol catabolic gene systems on pRleVF39c and d of <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> strain VF39SM
27	<b>Allison Crawford, Concordia University of Edmonton</b> Near-infrared spectroscopic analysis of intact canola seeds for evaluating seed quality
28	<b>Danika Deibert, Concordia University of Edmonton</b> Transcriptome analysis: Synergism with <i>Streptococcus pneumoniae</i> and 1918 pandemic influenza virus
29	<b>Amanda Dickson, University of Calgary</b> The relationship between diet and activity level of black howler monkeys ( <i>Alouatta pigra</i> ) at the Monkey River research site in southern Belize
30	<b>Sheen Dube, University of Winnipeg</b> Bugs on Smart Phones: A Nuisance at the Clinical Point of Care
31	<b>Rasha Etman, University of Calgary</b> The Role of Prolactin in Tumor Progression and Tumor Microenvironment in Response to DNA Damaging Agents
32	<b>Suriakarthiga Ganesan, University of Calgary</b> Metabolic Control of Two Dynamic Pools of Diacylglycerol in Budding Yeast
33	<b>Nayantara Govindraj, University of Calgary</b> Investigating the Role of KAP1 in Mammary Gland Development
34	<b>Emily Harrison &amp; Alixis Hassell, University of Calgary</b> Are Benthic Macroinvertebrates the True Kings and Queens in the Castle?
35	<b>Kasuni Hiniduma Gama Achchi, University of Calgary</b> Regulation of plasmid transfer gene expression in <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> VF39SM
36	<b>Chris Hooey, University of Calgary</b> Global Gene Expression Changes in the Liver of Fathead Minnows Sampled Downstream of Municipal Wastewater Treatment Plants
37	<b>Sydney Huculak, Concordia University of Edmonton</b> The effect of a 6-degree temperature increase on the growth and biomass of the native submerged macrophyte, <i>Myriophyllum sibiricum</i> , in a northern Albertan lake
38	<b>Kirsten Johnsen, University of Saskatchewan</b> Potential Differences in Foraging Behaviors of the Sable Island Horse
39	<b>Aishwarya Khanduja, University of Calgary</b> Serum Levels of Angiogenic Factors in Preeclampsia and the HELLP Syndrome

40	<b>Melissa King</b> , <i>University of Calgary</i> Cellular Metabolomics of DCMA, a Pediatric Mitochondrial Cardiomyopathy
41	<b>Damitha Koswaththa-Muhandiramlage</b> , <i>University of Calgary</i> Comparative genomics of rhizobiophages from western Canada
42	<b>Claudia Ladisa</b> , <i>University of Calgary</i> Metabolic profiling of goldfish liver during early gonadotropic phase
43	<b>Joseph Lafont</b> , <i>University of Saskatchewan</i> Mapping local density to model density-dependent processes on Sable Island
44	<b>Nabiha Mehina &amp; Nicole Jarvis</b> , <i>University of Calgary</i> Are Non-Ribosomal Peptide Synthetase genes of <i>Pseudomonas aeruginosa</i> involved in diketopiperazine production?
45	<b>Erin Miller</b> , <i>University of Calgary</i> Day-roost selection of Alberta bats in an urban setting
46	<b>Christie Miller</b> , <i>University of Lethbridge</i> Effects of early life-stage exposure to tebuconazole on the reproductive physiology of adult zebrafish ( <i>Danio rerio</i> )
47	<b>Adam Moghrabi</b> , <i>Concordia University of Edmonton</i> Factors affecting the recovery of the keystone sea urchin <i>Diadema antillarum</i> in the Caribbean
48	<b>Hamideh P. Fallah</b> , <i>University of Calgary</i> Native isoforms of gonadal GnRH are involved in the paracrine/autocrine control of testicular development and spermatogenesis in Zebrafish ( <i>Danio rerio</i> )
49	<b>Kathlyn Crisanta Piga</b> , <i>University of Calgary</i> Aggregation and Membrane Permeabilization of Modulated Antimicrobial Peptides
50	<b>Trevor Randall</b> , <i>University of Calgary</i> Heat activates c-di-GMP production in bacteria
51	<b>James Reeve</b> , <i>University of Calgary</i> The genetic basis of convergent evolution in four fish species
52	<b>Meredith Shuffler</b> , <i>University of Calgary</i> A strategy for effective predation on a large, dangerous predator, the Atlantic bluefin tuna, <i>Thunnus thynnus</i>
53	<b>Sarah Teillet</b> , <i>University of Winnipeg</i> The influence of temperature and prey availability on the relative activity of insectivorous bats
54	<b>Natalie Tsao</b> , <i>University of Calgary</i> Scaling morphology in Blue Sharks ( <i>Prionace glauca</i> ): The fight against gravity!
55	<b>Joseph Utomo</b> , <i>University of Calgary</i> Creating a synthetic microbial platform for diterpenoids production
56	<b>Xin Wen</b> , <i>University of Calgary</i> A strategy for regulating the stability of specific cellular mRNAs using a novel PUF RNA-binding protein
57	<b>Madeleine Wiebe</b> , <i>Concordia University of Edmonton</i> Genomic analysis of highly expressed <i>Streptococcus pneumoniae</i> genes in a 1918 Influenza and <i>S. pneumoniae</i> coinfection using systems biology and CRISPR technology
58	<b>Jonathon Lee</b> , <i>University of Calgary</i> Mitochondrial Dysfunction in Aging Neurons: the Link Between Plasma Membrane Oxidation and Excitability Decline?
59	<b>XingYu (Amy) Chen</b> , <i>University of Calgary</i> Engineered recombinant E. coli for production of Poly (3-hydroxybutyrate)

**Three Minute Thesis Competition**  
*Sponsored by the University of Lethbridge*

Saturday February 24, 2018  
2:15 – 3:30 PM  
Chair: Andrew Thompson  
Room: BI 587

**XingYu (Amy) Chen**, *University of Calgary*  
Engineered recombinant *E. coli* for production of Poly (3-hydroxybutyrate)

**Damon Brown**, *University of Calgary*  
Genetic Presence of Multidrug Resistance Efflux Pumps in Response to Biocide Treatment of a Model Microbiologically Influenced Corrosion Community

**Emmanuel Olarewaju**, *University of Manitoba*  
MIRROR OF THE MIND: A Functional Analysis of Imitation in Humans

**Anthony Leong**, *University of Winnipeg*  
Human responses to human and non-human cries

**Nandun Wathugala**, *University of Calgary*  
Regulation of Conjugation and Mechanism of Transfer of Plasmid pRleVF39b of *Rhizobium leguminosarum*

**Kathlyn Crisanta Piga**, *University of Calgary*  
Aggregation and Membrane Permeabilization of Modulated Antimicrobial Peptides

**Maria Alejandra Castilla Bolanos**, *University of Regina*  
Effects of glutamate and engineered scaffolds on neural stem cell differentiation

**Adam H. Sprott**, *University of Regina*  
Spatial Analyses of Canopy Structure of Forests in the Cypress Hills

**Kendra Gietzen**, *University of Regina*  
Stress in Walleye during Catch and Release Angling

**Tanvir Ahmed Shovon**, *University of Regina*  
Overstory tree composition drives the ecological strategies of understory plant communities

## ABSTRACTS

## Session A1: Microbiology & Bioremediation

### 1 **Genetic Presence of Multidrug Resistance Efflux Pumps in Response to Biocide Treatment of a Model Microbiologically Influenced Corrosion Community**

Damon Brown\* and Ray J. Turner - *University of Calgary*

Microbiologically influenced corrosion (MIC) in the oil and gas, and pipeline transmission industries is a significant source of internal corrosion damage and loss of product and facilities. Corrosion is caused by surface-associated microbes growing in extracellular matrices known as a biofilm, which are treated with antispectics and surfactants known as biocides. Repetitive treatment of a system with the same biocide will eventually see diminished efficacy, potentially from the horizontal transfer and expression of multidrug resistance efflux pumps (MDREPs). These MDREPs are membrane transporters originally identified for conveying antibiotic resistances, but some have been found to efflux non-specific biocides such as glutaraldehyde or quaternary ammonium compounds. MDREPs are frequently encoded on mobile gene elements and capable of horizontal gene transfer (HGT) which will be monitored in a defined microbial community of fully sequenced organisms, each previously identified in MIC incidents. Based on the annotated genomes, custom primers are designed using multiple sequence alignments of key MDREPs and their abundance tracked using qPCR. The copies of MDREPs will be tracked in relation to 16S rDNA gene counts in mixed cultures to follow HGT events into species without the targeted MDREP in single culture. It is expected that repeated treatments of a biocide will increase the relevant MDREP gene counts with respect to 16S gene counts. In such instances when community diversity is maintained and MDREP gene counts have increased, thus suggesting an increase in resistance to that biocide resulting from HGT events of MDREP genes.

### 2 **Co-oxidation of naphthenic acids by methanotrophic bacterial species in Alberta oil sands tailings ponds**

Felix C. Nwosu\*, Lisa Gieg, and Peter Dunfield - *University of Calgary*

Surface mining of Alberta oil sands has led to the generation of considerable amounts of raw slurry waste deposited into large engineered areas known as tailings ponds. Such waste is contained to promote water recycling and to minimize disposal into the environment due to toxicity concerns. Ubiquitous naphthenic acids (NA) released into the oil sands process-affected water (OSPW) in tailings ponds, have been identified as primary source of acute aquatic toxicity of the waste. The persistence of NA in tailings thus represent a major challenge to the detoxification of OSPW and reclamation of mining impacted areas. To date, microbial attenuation has been proven to be a feasible and cost effective NA bioremediation approach for OSPW. However, the diversity of NA complicates this effort as implicated microorganisms only target a specific or minor subset of NA. As a novel approach, the potential exists for aerobic methanotrophic bacteria to non-specifically biodegrade or biotransform NA. Methanotrophs uniquely utilize methane as sole source of carbon and energy, harboring the promiscuous methane monooxygenase enzyme (MMO) that may transform NA which would thus help to mitigate OSPW toxicity. MMO have been shown to cometabolize a variety of hydrocarbon or organic pollutants by hydroxylating the terminal methyl or sub-terminal alkyl groups of their structure. For our investigation into NA biodegradation in experimental microcosms using indigenous OSPW methanotrophs, we conducted both routine chemical analytics (GC, GC/MS) and molecular (16S rRNA gene sequencing) to profile the active microbial community and quantify NA loss over time. Microcosms with and without an active methane oxidation activity and a sterile control showed very different rates of surrogate NA biodegradation, despite similar microbial community structure. Of all three experimental set ups, systems with active methane oxidation were the most

effective in the complete biodegradation of the tested NA. This preliminary observation, supports the role of methanotrophs in NA degradation and hence can play a role in the detoxification of OSPW. Efforts are ongoing to further elucidate the mechanism of methanotrophic NA bioconversion.

### **3 Exploration of human-associated microbial communities using Bayesian Networks**

Emily Haidl\*, John Stavrinides and Cory Butz - *University of Regina*

Humans are populated by communities of microbes that have been shown to have a great impact on human health; they help guard against pathogens, aide in digestion and play a large role in our metabolism. Many studies have advanced our understanding of the human microbiome by isolating small but informative fragments of DNA (often the 16s rRNA sequences) from different regions on the human body. These studies have resulted in a large repository of publicly available data, much of which is accessible at MG-RAST, which to date represents well over 3000 studies of human microbiomes. While valid analysis has been conducted on human microbiome data, there is currently no way to utilize all of the information available to uncover more about relationships in the human microbiome. Bayesian Networks (BNs) are ideally suited to describe human microbiome data because they can illustrate relationships from large datasets in a compact and simplified manner. My research has resulted in the development of an exploratory BN that describes the relationships of the 15 most relatively abundant microbial genera in the human microbiome. The development of my preliminary BN provides an instrumental foundation for the construction of a larger, more comprehensive BN that will generate a deeper understanding of the relationships between human-associated microbes, and human health.

### **4 BTEX and Alkane Degradation Through Anaerobic Microbial Activity in Contaminated Aquifers in Alberta, Canada**

Gurpreet S. Kharey\* and Lisa Gieg – *University of Calgary*

Over time, underground gasoline storage tanks below gasoline stations can begin to degrade, slowly releasing gasoline into the environment. The persistence of hydrocarbons in the environment can be long lasting, expensive, and hazardous issue. Compounds of concern in gasoline and diesel include short chain alkanes (hexane, octane, nonane, etc.), and aromatics (benzene, toluene, ethylbenzene, and xylene (BTEX)), which pose hazards to human and environmental health. To reduce the economic and environmental cost to remove these compounds, bioremediation via microorganisms that use hydrocarbons as a source of carbon, ultimately producing non-toxic compounds, is being heavily explored. In such hydrocarbon spills, oxygen is rapidly depleted, thus anaerobic organisms dominate. The main mechanism of anaerobic hydrocarbon degradation is via fumarate addition enzymes, alkylsuccinate synthase (ASS; alkanes) and benzylsuccinate synthase (BSS; monoaromatics), which produce unique ‘signature metabolites’. The presence of these genes and produced ‘signature metabolites’ are used as biomarkers to accurately detect anaerobic hydrocarbon degradation. Nutrients can be added to stimulate microbial activity (biostimulation) to increase hydrocarbon degradation. However, to increase efficiency as much as possible, they must be tailored to the diets of the native microorganism community. In this research, we are studying the feasibility of bioremediation using biostimulation in two hydrocarbon contaminated sites in Alberta. By monitoring the microbial community, quantifying the ass and bss genes, and quantifying produced ‘signature metabolites’ under different nutrient conditions, biostimulation can be tailored for each site for maximum hydrocarbon biodegradation efficiency.

## **5 Does the Prairie Epidemic Strain of *Pseudomonas aeruginosa* Employ the Type Six Secretion System in Strain Replacement?**

Jenny Nguyen\*, Jessica Duong, Michael D. Parkins and Douglas G. Storey – *University of Calgary*

*Pseudomonas aeruginosa* is an opportunistic bacterial pathogen that has been associated with chronic lung infections and accelerated clinical decline in cystic fibrosis patients. Recently, a local epidemic strain called the Prairie Epidemic Strain (PES), has been found to replace other unique non-epidemic strains of *P. aeruginosa* in the CF lungs, leading to the investigation of the mechanisms in which PES achieves strain replacement. We focused on the type six secretion system (T6SS) and hypothesized that PES utilizes the T6SS to competitively kill other *P. aeruginosa* isolates in the lung to displace them.

In vitro cell-to-cell killing assays were performed to observe the competitive ability of a PES isolate against other bacterial species in order to determine whether the T6SS was functional. Moreover, the competitive ability of PES was assessed against the lab strain PAO1 and a non-epidemic unique *P. aeruginosa* isolate. We found that PES competes similarly to PAO1 in that both isolates could kill competing bacteria, which suggests that the T6SS may be functional in PES. However, PES was unable to kill the unique non-epidemic CF isolate. An *in vivo* *Drosophila melanogaster* infection model was used to investigate the role of the T6SS in strain replacement. These assays differed from the cell-to-cell killing assays since PES was the dominant isolate in vivo and was able to compete with the non-epidemic CF isolate in a fly model. Furthermore, the sooner the flies were coinfecting with PES, the better PES was able to compete against the unique isolate.

## **6 Methanogenic and Aerobic Biodegradation of Model Polycyclic Aromatic Compounds Associated with Canadian Oil Sands**

Oscar Montoya\* - *University of Calgary*

Polycyclic aromatic compounds (PACs) are ubiquitous molecules that can be of high importance to remediate due to their potential negative health and environmental effects. The present study used Canadian Oil Sands-derived microbial consortia established methanogenically or aerobically and amended with phenanthrene, dibenzothiophene (DBT), or 2,6-dimethylnaphthalene (2,6-diMN) as sole carbon and energy sources under three salinities. Methane formation was statistically higher in PAC-amended treatments relative to unamended controls under brackish conditions. A fumarate addition metabolite was tentatively detected in incubations amended with 2,6-diMN. DBT was degraded with concomitant methane formation, the first report of this metabolism. 16S rRNA gene sequencing revealed the dominance of methanogens and known PACs degraders. Genus *Smithella* was only detected in DBT-amended incubations in relatively high abundances suggesting its role in DBT degradation anaerobically. Aerobic degradation of PHEN and 2,6-diMN was also observed. Time-course experiments showed faster PHEN degradation under saline conditions and that the microbial communities were dominated by *Janibacter* sp, which was also isolated. This research shows that microbial communities from bitumen-impacted environments have the natural ability to degrade PACs, with potential applications in bioremediation.



## 7 **Metal Resistance in Dual-Species Biofilms**

Nadia Monych\* - *University of Calgary*

Biofilms may be thought of as one of the more common physiological states of bacteria in nature. Microorganisms adhered to a surface surrounded by an extracellular polymeric substance with higher antimicrobial resistance compared to planktonic bacteria may be classified as a biofilm. Many sources of acute and chronic bacterial infections can be linked to formation and maturation of a biofilm either in wounds or in-dwelling medical devices. In most cases antibiotics have very little efficacy against biofilms, which gives rise to a need for different types of antimicrobials. Metal antimicrobials are being used more commonly in clinical and environmental settings and display an increased level of efficacy towards single species biofilms. However, when bacteria grow together as a dual species biofilm, similar to what occurs in nature, there is a much greater resistance to antimicrobials, including metals. By determining the cause of this phenomenon, it may be possible to prevent this increase in resistance. *Pseudomonas aeruginosa* and *Staphylococcus aureus* are two of the most common bacteria that populate infections. They also display increased resistance to metals when grown together as opposed to either grown as a single species biofilm. Previously, it was suggested that compounds secreted by *S. aureus* might help increase *P. aeruginosa*'s resistance to metals. Through exploration of various culturing conditions and separation of secreted compounds by *S. aureus* under these conditions it will be possible to identify the compound responsible for this resistance.

## 8 **Identification of Plant Genes Involved in Oil Sands Naphthenic Acid Degradation**

Jeremy Wong\* and Douglas Muench - *University of Calgary*

Surface mining of bitumen in the Northern Alberta oil sands requires vast quantities of water. Due to its toxicity, the resulting oil sands process affected water (OSPW) is stored in tailings ponds. Naphthenic acids (NAs) are a family of aliphatic and alicyclic carboxylic acids found in the acid-extractable organic (AEO) fraction of OSPW, and are toxic to a variety of living organisms. Plants can degrade a range of organic compounds and thus can potentially remediate OSPW through sequestration or metabolism of NAs. Little is known about a plant's ability to metabolize NAs or the genes that may be involved in NA remediation. In an attempt to identify these plant genes, we developed a forward genetic screen using the model plant, *Arabidopsis thaliana*. Over 20,000 activation-tagged lines of *Arabidopsis* were screened on NA-containing agar plates. Activated genes that are involved in NA sequestration or degradation would lead to an NA tolerant phenotype, allowing the plants to grow on NA-containing plates. Several mutants that tolerate NAs have been identified, and TAIL-PCR is being used to identify the activated genes. The identification of NA metabolizing genes in *Arabidopsis* would allow us to screen genotypes of native plants, such as willow, that exhibit naturally high levels of expression of these genes. These selected plants could be implemented as part of an NA remediation strategy.

## 9 **Exploring the contributions of iron-acquisition systems to the evolution of opportunistic human pathogenic bacteria**

Craig D Soutar\* and John Stavrinos - *University of Regina*

Iron is an important limiting micronutrient for many microorganisms. To aid iron acquisition, many bacterial species produce small molecules, known as siderophores, which have high iron affinity. Siderophores are also used by various pathogens to facilitate iron acquisition from a host, including humans. The enterobacterial genus *Pantoea* is composed of many species groups having diverse life histories, both free-living and host-associating, with some species causing

opportunistic infections in humans. We presently know little about the role siderophore-mediated iron acquisition strategies might play in host colonization or human infection. The objective of this research was to investigate the distribution and evolution of siderophore gene clusters in *Pantoea* to improve understanding of niche-specialization, host-association, and opportunism. Complete and draft genomes of plant, environmental and clinical isolates of *Pantoea* were analyzed using antiSMASH to identify siderophore biosynthetic gene clusters. Biosynthetic gene clusters for three siderophores, desferrioxamine, aerobactin and enterobactin, were found to be widely distributed. Phylogenetic analysis of these clusters revealed a complex evolutionary history that involved multiple transfer events between *Pantoea* and relative genera. The enterobactin cluster was present in the common ancestor of all *Pantoea* with evidence of three independent loss events in different species. The aerobactin and desferrioxamine clusters both contain strong evidence suggesting horizontal acquisition from other members of the Enterobacteriaceae. The gain and loss of siderophore biosynthetic clusters from different species groups has important implications for understanding adaptation, niche-specialization and host-association in this highly diversified bacterial group.

#### **10 Bacterial toxicity and resistance originating from the use of metal-based antimicrobials**

Natalie Gugala\* - *University of Calgary*

In the last several decades, consumers have seen a rise in the use of metals as antimicrobials as a means of controlling infectious diseases. Studies have documented the pronounced efficacy and performance of metal ions in conjugation with medical devices, other healthcare associated tools, and even consumer products. Despite this, the precise mechanisms by which metals kill bacterial cells are still unknown. Recently, our group has demonstrated that different metals – and even different formulations of the same metal, such as silver – display variable efficacy, thereby drawing on the suggestion that metals may have distinct modes of toxicity and resistance that hide among generalized mechanisms. To warrant insight, we undertook a robotic chemical genetic screen of an ordered mutant library of *Escherichia coli*, called the Keio collection, against metals ions, including Ag, Cu and Ga. Using the Keio strains we have generated a list of genes involved in metal toxicity and resistance, and have performed several analyses on each collection using Ecocyc, among other programs. In short, using this information we hope to generate comparison between different metals, in what way they poison bacteria and how bacteria are able to resist these threats.

#### **11 Carbon Metabolism of *Pseudomonas aeruginosa* in Cystic Fibrosis**

Austin Nguyen\* - *University of Calgary*

The cystic fibrosis (CF) airway is a nutritionally rich environment that allows opportunistic pathogens, such as the bacterium *Pseudomonas aeruginosa*, to establish chronic infections. This unique long-term selection promotes certain traits and adaptations in *P. aeruginosa* carbon metabolism. Examples of such traits are gluconate production which is thought to promote iron uptake and the widespread reliance by clinical isolates on external sources of amino acids. These carbon metabolic traits have not been investigated in a diverse clinical *P. aeruginosa* population. Using high-resolution mass spectrometry (LC-MS) and nuclear magnetic resonance spectroscopy (NMR), we analyzed the metabolism of a panel of clinical *P. aeruginosa* isolates (n = 90) in rich and minimal media. Glucose was unexpectedly taken up by most clinical isolates, contrary to conventional thought regarding carbon catabolite repression (CCR). Retrospective analysis shows that *P. aeruginosa* stoichiometrically converts glucose to gluconate. While other studies have linked gluconate production to virulence, these results suggest that this process is instead driven

by redox and energy demands. Furthermore, there was preferential uptake of amino acids involved in the tricarboxylic acid (TCA) cycle and nitrogen metabolism by clinical isolates. Upon metabolic analysis of expectorated patient samples (n = 36), most of the *P. aeruginosa* preferred amino acids were found in low concentrations compared to other amino acids. Our data show that fitness and energy optimization is a major selective force shaping *P. aeruginosa* carbon metabolism in CF.

## Session B1: Cell & Cancer Biology

### 12 Producing and utilizing myo-inositol phosphate (IP) affinity matrices to identify eukaryotic IP interacting proteins

Colyn P. Cleland\* and Steven C. Mosimann - *University of Lethbridge*

Myo-inositol phosphates (IPs) are a family of compounds that are ubiquitous within eukaryotes and archaea, with many of the IPs compounds being bio-active. To date, there has been no systematic study of eukaryotic proteins that interact with IPs, even though proteins with high affinity for various IPs have been identified. In order to advance and provide further insight into the network of proteins that directly interact with IPs in vivo, we have immobilized myo-inositol-1,2,3,4,5,6-hexakisphosphate (InsP6), a representative IP, on an agarose resin coated with diaminodipropylamine (DADPA). The resulting InsP6 affinity resin allows us to selectively retain proteins in cell lysates that interact with InsP6. Ultimately, proteins specifically bound to our resin will be subject LC MS/MS and provide a means for systematically identifying proteins that interact with InsP6. This same method can and will be utilized to generate affinity resins with a range of IPs produced in our laboratory and allow us to generate interaction networks for the family of IPs in a variety of eukaryotic cell types.

### 13 Granzyme B is required for Natural Killer cell-mediated antifungal activity

Adley Mok\* , Shushun Li , Richard Xiang and Christopher H. Mody - *University of Calgary*

Natural Killer cells play an important role in antimicrobial host defense by binding directly to and killing fungal pathogens; however, the cytolytic mechanisms used to kill extracellular pathogens are incompletely understood. Previous studies showed that NK cells require perforin-containing granules to kill the fungal pathogen *Cryptococcus neoformans*, which is the most common cause of fungal meningitis. Since granzyme B promotes oxidative killing of intracellular Mycobacteria and disrupts bacterial metabolic and biosynthetic pathways during intracellular infection, we asked whether granzyme B has a role in direct, extracellular anti-fungal activity of NK cells. We used YT cells, an NK cell line, to examine the role of granzyme B in NK cell cytotoxicity against *C. neoformans*. We found that YT cells express granzyme B by western blot and kill *C. neoformans*. After YT cells were cultured with *C. neoformans*, increased levels of perforin and granzyme B were observed in the culture medium, indicating release during killing. To determine whether granzyme B was required for NK cell cytotoxicity against *C. neoformans*, we used siRNA to knock down granzyme B, and treated YT cells with z-aad-cmk and dichloroisocoumarin, which have different mechanisms of inhibiting granzyme B. These approaches diminished the anti-fungal effect of NK cells in a dose-dependent manner. Collectively, these results reveal that granzyme B and perforin are both required and play an important role in the NK cell cytotoxicity against extracellular *C. neoformans*.

**14 REMPing the knowledge towards the protein translocation pathway: understanding the mechanism of folded proteins transport**

Elina Levchenko\* and Raymond J. Turner - *University of Calgary*

Currently, two translocation systems across the cytoplasmic membrane in bacteria are known: Sec and Tat, where the first moves unfolded proteins and the second deals with fully folded substrates which all bear a “twin arginine” motif with a consensus sequence S/TRRXFLK. Considerable efforts were made to understand the structure of proteins that comprise the channel and proteins that assist in folding and targeting towards it. However, there is still a gap in knowledge regarding the steps involved. The purpose of the following project is to better comprehend the sequence of events between the synthesis of the protein and the export event. Utilizing our model system of Dimethyl sulfoxide reductase in *E. coli* we are exploring the pathway of protein folding from the ribosome to the Tat system. The enzyme is comprised of three proteins; two of those (DmsA and DmsB) have to be assisted by a DmsD chaperone and transported across the membrane. Our lab proposed the steps required for maturation and showed that there were interactions between the substrate DmsA, which contains the Tat targeting leader sequence, Tat system components (TatABC) and the chaperone DmsD. The goal here is to study the order of events during the docking of DmsA onto the TatB and potential involvement of DmsD in the process. Through protein chromatography approaches combined with biophysical methods of Isothermal Titration Calorimetry (ITC), and differential scanning fluorometry (DSF) early results confirm a triad of interaction between DmsD::TatB::DmsAleader.

**15 Unraveling the effect of rapamycin on IGFBP-3 localization**

Apurva Bhardwaj\* and Shailly Varma Shrivastav - *University of Winnipeg*

Insulin-like growth factor binding protein-3 (IGFBP-3), one of the six members of the IGFBP family, is a key protein in the insulin-like growth factor (IGF) pathway that not only plays an important endocrine role but is also being studied for several other roles that are anticipated to be critical in cellular processes. IGFBP-3 functions both in the extracellular and intracellular compartments along with other proteins and regulates cellular functions such as cell growth, survival and apoptosis. Several studies support the role of IGFBP-3 in mediating both the IGF-dependent as well as IGF-independent effects. From the extracellular compartment IGFBP-3 is transported across the plasma membrane and can also translocate into the nucleus in mammalian cancer cell lines. The involvement of nuclear IGFBP-3 in transcriptional regulation, DNA damage and induction of apoptosis support its role in cancer progression. Rapamycin is an inhibitor of mammalian target of rapamycin (mTOR), which is a ser/thr kinase and is known to regulate various metabolic processes. Rapamycin is under clinical trial for the treatment of various types of cancer including head and neck cancer and breast cancer. The role of rapamycin on the regulation of IGFBP-3 and its translocation into the nucleus is unknown. We treated mammalian breast cancer, MCF-7 cells with rapamycin at different time points, isolated the nuclear and cytoplasmic fractions and determined the IGFBP-3 levels using Western blot analyses. As hypothesized, rapamycin treatment increased the translocation of IGFBP-3 in the nucleus. The overarching goal of our research is to determine if localisation of IGFBP-3 can be used as a diagnostic marker for better prognosis and treatment regimen of cancer.

**16 Protein phosphatase 2A-B56 controls mitosis by interacting with LXXIXE motif containing proteins**

Sibapriya Chaudhuri\* and Greg Moorhead - *University of Calgary*

Mitosis, like many other cellular processes, is tightly regulated by several protein phosphorylation events. PP2A-B56 is an important mitotic protein phosphatase which contributes to the fidelity of the process of sister chromatid segregation during mitosis by dephosphorylating certain outer kinetochore proteins and thereby stabilizing attachments between sister chromatids and the microtubules of mitotic spindle. Recent proteomic studies show that PP2A-B56 recognizes a short linear motif LXXIXE on its interactors. We hypothesize that LXXIXE is a general consensus motif for recruitment of PP2A-B56, particularly during mitosis, and that additional proteins utilize this recruitment sequence. We speculate that recruitment of PP2A-B56 is regulated by the phosphorylation status of this motif and this in turn plays an important role in controlling the progression of the cell cycle. Our preliminary results show a putative LXXIXE motif is present in more than 100 mitotic regulators and several of them interact with PP2A-B56 in a phosphorylation dependent and isoform dependent manner. Further understanding of how interactions between the target proteins and PP2A-B56 affect mitotic progression and/or mitotic exit will provide valuable insight about the mechanisms of specific recruitment and mitotic functions of PP2A-B56.

**17 Rapamycin Treatment Alters Localization of N-Myristoyltransferase in Breast Cancer Cells**

Kareem Hassan\* - *University of Winnipeg*

Breast cancer affects one in eight women in Canada. Breast cancer is classified based on the presence or absence of estrogen receptor (ER), progesterone receptor (PR) and/or human epidermal growth factor receptor 2 (HER2 neu). Treatment modalities are based on the receptor status. About 70% of breast cancer patients are ER-positive and hence undergo hormonal treatment. Selective ER modulators (SERM) such as tamoxifen are the first line of endocrine treatment of breast cancer with proven efficacy in metastatic breast cancer and chemoprevention. Despite the expression of ER $\alpha$ , some patients develop tamoxifen resistance and 50% present de novo tamoxifen resistance. Targets such as N-Myristoyltransferase 1 (NMT) and NMT 2, proteins located in the cytoplasm, are of interest in breast cancer cell therapy since they lie upstream of numerous oncogenic pathways. Rapamycin is a macrolide that inhibits mTOR. The overall goal of this study is to inhibit mTOR by rapamycin in ER positive breast cancer cells and investigate its effect on NMT expression and localization. Our preliminary data indicate that rapamycin treatment resulted in translocation of NMT1 in the nucleus. Further study is in progress to investigate the mechanism of NMT1 translocation to the nucleus.

**18 Diagnosis from a prick: N-Myristoyltransferase expression and sub-cellular localisation in peripheral blood mononuclear cells (PBMC) as a potential screening test for colorectal cancer**

Mohamed Abo Aoun\*, Jenny Rathinagopal, Shibby Kuriakose and Anuraag Shrivastav - *University of Winnipeg*

Colorectal cancer (CRC) is the second most common cause of cancer-related deaths in North America. When caught in its early stages, CRC is one of the most curable types of cancer. Unfortunately, most patients do not get diagnosed until they reach advanced stages. Currently available screening programs for CRC cause a great deal of discomfort to the population, which is reflected by the low levels of compliance. The development of less-invasive screening programs



would allow for earlier detection of CRC, potentially decreasing the mortality rates associated with it. *N*-myristoyltransferase exists in two isoforms in mammals (NMT1 and NMT2). NMT has been proposed as a potential marker for cancers. Blood samples obtained from CRC patients and controls were used to isolate peripheral blood mononuclear cells (PBMCs). The PBMCs were fixed on cytospin slides, which will be sent to Cancer Care Manitoba for immunohistochemical staining (IHS) for NMT1 and NMT2. The slides will then be marked for sub-cellular localisation and expression of the enzymes. In addition to the IHS, ELISA and Q-PCR will also be employed to test for the presence of the aforementioned antigens. Statistical analysis will compare results obtained from controls to CRC patients in hope of developing a less-invasive screening program.

## **19 Neutrophil Inflammatory Responses to Extracellular Factors and Lipopolysaccharide from Anaerobic Bacterial Biofilms**

Joey Lockhart\*, Stefanie Anderson, Douglas Storey, Howard Ceri, Andre Buret and Douglas Moreck - *University of Calgary*

Background: Chronic bacterial infections and associated inflammation have a dramatic impact in veterinary and human medicine. Bacterial biofilms are a major cause of the persistent inflammation observed in chronic infections and nearly 80% of all infections involve biofilm formation. Host immune cells such as neutrophils have difficulty resolving biofilm-related infections, which can lead to tissue damage and chronic inflammation. The respective neutrophil responses to biofilms remains incompletely understood, particularly in the context of mixed bacterial infections. Aims: To generate mixed species bacterial biofilms composed of the two opportunistic pathogens *Fusobacterium necrophorum* and *Porphyromonas levii*, and to evaluate neutrophil responses to bacterial-origin components from extracellular fractions (ECFs) of both biofilms and planktonic cells. Results: Bovine neutrophils exposed to ECFs of mixed-species planktonic bacteria showed an elevated oxidative response compared to neutrophils exposed to ECFs of biofilms. Biofilm bacteria produced substantially more lipopolysaccharide (LPS) than planktonic cells under these experimental conditions. Depletion of LPS significantly reduced neutrophil oxidative response to planktonic bacteria. Oxidative responses to LPS-depleted biofilm fractions and LPS-depleted planktonic cell fractions were similar. Conclusions: The limited neutrophil response to biofilms in this study supports the reduced ability of the innate immune system to eradicate biofilm-associated infections. LPS and the presence of other extracellular, immune-modifying molecules in the bacterial media appear to be important in adversely affecting neutrophil function and the potential clearance of biofilm. Understanding these responses may lead to the development of effective, non-antibiotic therapies for biofilm-mediated infections, decreasing our reliance on antibiotics in veterinary and human medicine.

## **20 Role of *N*-myristoyltransferase in Endocrine Therapy Resistance in Estrogen Receptor Positive Breast Cancer**

Dean Reddick\*, Shiby Kuriakose, David Datzwik, and Anuraag Shrivastav - *University of Winnipeg*

Tamoxifen is a very effective drug for the treatment of Estrogen receptor positive (ER+) breast cancers. However, approximately 50% of all patients taking the drug develop a resistance. There are reports suggesting involvement of PI3K/mTOR pathway in endocrine therapy resistance in ER+ positive breast cancer. However, the mechanism by which resistance is developed remains poorly understood. Research has shown that *N*-myristoyltransferase (NMT) interactions with mTOR may be involved with resistance development. In humans, NMT exists in two isoforms-

NMT1 and NMT2. The overarching goal of my research is to determine potential sites in NMT2 that are phosphorylation substrate of mTOR and study whether NMT2 phosphorylation has any role in resistance development. Using bioinformatics tools putative phosphorylation sites in NMT2 have been identified. These putative sites were mutated to alanine (phospho dead) or glutamic acid (phospho mimic) by site directed mutagenesis. In order to determine the expression and localization of NMT2, GFP fusion was performed. Various NMT2 mutants along with wild type (wt) NMT2-GFP plasmids were prepared and sequenced. The NMT2-GFP plasmids were expressed in ER+ breast cancer cells and the efficiency of transfection varied with mutants and wt. The phospho mimics showed slower growth suggesting the role of NMT2 in cell proliferation. Future studies are directed towards treating ER+ breast cancer cells expressing NMT2-GFP wt or mutants with tamoxifen and investigate whether phosphorylation site(s) confers resistance to treatment.

## **21 Unravelling the Mechanism of Rapamycin and Metformin Mediated Apoptosis in Cancer Cells**

Charnae Hubscher\*, Apurva Bhardwaj and Shailly Varma Shrivastav - *University of Winnipeg*

Observations that rapamycin and metformin have antiproliferative activity have generated interest in possible clinical applications of these drugs as potential anti-cancer agents. Mammalian target of rapamycin (mTOR) is a multiprotein complex that exists as two complexes mTORC1 and mTORC2. Rapamycin directly inhibits mTORC1, whereas, metformin is an indirect inhibitor of mTORC1 that functions either through the inhibition of tuberous sclerosis complex (TSC) 1/2, a GTPase that cleaves GTP-Rheb required for the activation of mTORC1 or through the phosphorylation of IRS-1 at Ser789, a site reported to be a downregulator of phosphatidylinositol-3 kinase (PI-3K) pathway. The aim of this study was to unravel the mechanism of rapamycin and metformin in inducing cell death. The various apoptotic proteins activated by the inhibition of the Akt/PI3K pathway were studied using Western blot analysis on human oral squamous carcinoma Cal-27 and human prostate cancer cells PC-3 treated with rapamycin and/or metformin, with interest in caspase activation and phosphorylation patterns of mTOR and Akt at both Ser473 and Thr308 residue. Treatment with rapamycin resulted in increased phosphorylation of p-Akt at both Ser473 and Thr308 residues, whereas, mTOR activity was inhibited. There was no expression of cleaved caspase-3 in Cal-27 or PC-3 cells. Interestingly, cleaved caspase-9 was observed in PC-3 cells but not in Cal-27. This has led to the idea that the phosphorylation patterns of Akt and mTOR are consistent in both cell lines upon treatment with rapamycin and metformin but that caspases are regulated differently in squamous cell carcinoma compared to prostatic adenocarcinoma.

## **22 Effect of Metformin on Endogenous levels of IGFBP-3 on mammary carcinoma cells**

Syeda Yousra Irshad\*, Apurva Bhardwaj and Shailly Varma Shrivastav - *University of Winnipeg*

In Canada, 1 in every 9 women is expected to develop breast cancer in their lifetime and 26% of the all cancers diagnosed are breast cancer. Insulin-like growth factors (IGF, IGF-1 and IGF-2) are important mitogen peptides, which promote cell growth. IGFs are transported as a ternary complex comprising of IGF, IGF binding proteins (IGFBP) and acid labile subunit. There are six isoforms of IGFBPs of which IGFBP-3 is the most abundant isoform. Increased serum levels of IGF-1, and decreased levels of its binding protein is linked to increased risk of developing breast cancer. A recent study demonstrated that metformin treatment to non-diabetic, breast cancer women resulted in increased serum IGFBP-3. Metformin is an indirect inhibitor of mammalian target of rapamycin (mTOR), a serine /threonine kinase that regulates various metabolic processes



like cell proliferation, apoptosis, etc. Our aim was to investigate the effects of metformin on the endogenous levels of IGFBP-3 in estrogen receptor positive breast cancer cells (MCF7 cells). As expected metformin treatment resulted in decrease in the active form of mTOR (phosphorylated at Serine 2448). We report here for the first time that metformin treatment to MCF7 cells for 24h resulted in increase in the endogenous IGFBP-3 levels. We plan on performing a time-dependent metformin treatment to determine the optimal time required to increase IGFBP-3 levels. The overarching goal of the study is to investigate the regulation of IGFBP-3 levels upon metformin treatment.

## Session C1: Behaviour & Communication

### 23 **Habitat selection of black bears (*Ursus americanus*) in Saskatchewan's Boreal Shield** Patricia Tomchuk\* and Phil McLoughlin - *University of Saskatchewan*

Habitat selection is the behavioural process by which individuals use a non-random set of available resources. Studies of habitat selection are designed to answer fundamental ecological questions as they reveal priorities in resources needed for survival and reproduction. Boreal woodland caribou (*Rangifer tarandus caribou*) are listed as Threatened on Schedule 1 of the Canada Species at Risk Act. Their decline has been driven largely by anthropogenic impacts. In Saskatchewan's Boreal Shield, woodland caribou exist in conditions with low anthropogenic impacts, high fire, and few invasive species. Wolves (*Canis lupus*) are key predators of adult caribou but black bears (*Ursus americanus*) may be effective predators of caribou calves. I intend to use resource selection functions (RSFs) to model habitat selection of collared black bears, wolves, and caribou in Saskatchewan's Boreal Shield. From these data, I will test the predator facilitation hypothesis in relation to caribou. If predator facilitation plays a role in caribou habitat selection during calving season, then selection patterns of black bears and caribou should show greater overlap as caribou choose calving sites away from wolves. My objectives are to: (i) provide novel information on black bear ecology in Saskatchewan's Boreal Shield; (ii) provide baseline data to which black bear-caribou interactions in more disturbed areas can be compared; and (iii) determine the extent to which black bears play a role in limiting caribou populations through predation. Overall, these results will inform management decisions regarding black bears and uncover potentially important factors relevant to conservation of woodland caribou in Saskatchewan.

### 24 **The individual variation of social strategies in a population of Canadian black-tailed prairie dogs (*Cynomys ludovicianus*)** Jillian M Kusch\* and Jeffrey E Lane - *University of Saskatchewan*

Most research in social systems has focused on population-level costs and benefits, with less attention paid to variable costs and benefits to the individual. Social network analysis (SNA) provides a tool to interpret behavioural interactions between individuals of a population. Previous studies have suggested that large numbers of social connections may contribute to higher survival, foraging success, and reproductive success. These studies primarily use measurements of contact (often proximity) that ignore the likely importance of detailed social behaviours in estimates of sociality benefits and also the temporal variation in these behaviours. Black-tailed prairie dogs live in highly social colonies and display an elaborate range of social behaviours. I hypothesized that prairie dog behaviours will vary to best increase their individual fitness (reproductive success and survival). I constructed a social network of members of a

prairie dog colony from southern Saskatchewan through behavioural observation and examined components of life history and fitness (body condition, reproductive status) of each prairie dog in the network. I compared sociality between two seasons that greatly differed in their importance for reproductive success, and life history traits at both time points. Social interactions during the reproductive season were more intense and more frequent, but this was variable between ages and sexes of individuals. By focusing on a study species with diverse and easily observed social interactions, this research should both improve our understanding of the utility of SNA for wild populations and provide insight into the ecological consequences of natural individual variation in sociality in black-tailed prairie dogs.

**25      The effect of sublethal concentrations of Selenium on the antipredator response of fathead minnows to alarm cues**

Katherine Fedoroff \*, Phil Anderson and Maud Ferrari - *University of Saskatchewan*

Injured conspecific cues, also known as alarm cues, are a crucial source of predation-related information for aquatic prey. By their nature, these cues represent a reliable indicator of risk known to mediate most antipredator responses, such as alteration in behaviour, morphology or life-history, the development of defended phenotypes and the facilitation of the learned recognition of novel predators. Prey species unable to use these cues suffer increased mortality. A number of aquatic pollutants interfere with the ability of prey to detect and respond to these cues, either via a chemical interference with the cues themselves, or by impairing the ability of prey to properly respond to these cues. While selenium is a trace element required for life, it is also a contaminant of concern because of its ability to rapidly bioaccumulate in animal tissues, leading to population failure with little warning. Our goal was to determine if sublethal concentration of selenium could affect the ability of fathead minnows *Pimephales promelas* to detect alarm cues. We exposed minnows to a selenium-enriched diet for 70 days prior to testing, and tested the ability of Se-contaminated or control fish to respond to alarm cues derived from Se-contaminated or control donors.

**26      Human responses to distress cries across species**

Anthony Leong\*, Mary E. Timonin, Susan Lingle and Cora Romanow - *University of Winnipeg*

Infant cries elicit a robust protective response from caregivers across a wide array of species. The sensitivity of caregivers to cries is crucial to the mammalian infant's survival. This research aims to better understand mechanisms underlying both the cry and the caregiver response, and to explore the possibility that these mechanisms are shared across species. We presented a series of human and non-human cries to human participants and measured their emotional responses via survey. Results showed that participants felt a "desire to help" both human and non-human individuals. This finding provides further evidence for shared evolutionary mechanisms of caregiver responses across species.

**27      Thermoregulatory Energetics of Female Little Brown Bat (*Myotis lucifugus*)**

Trevor Moore\* - *University of Winnipeg*

White-nose syndrome (WNS) is a leading cause in the reduction of little brown bat (*Myotis lucifugus*) populations across North America. During winter WNS causes many bats to arouse and use fat reserves at an accelerated rate, resulting in increased mortality. Survivors often emerge during spring with reduced body conditions. Often this results in female bats being

unable to gestate their young and the resorption of the embryo. My research is focused on the thermoregulatory energetics of WNS surviving pregnant and lactating female little brown bats specifically during critical spring and summer seasons of the bats' annual cycle. Artificially heated roosts in the bats' thermoneutral range would remove the stress of thermoregulation. Allowing bats to allocate more energy to gestation and recovery from WNS, and possible transfer of hereditary 'survival' traits to offspring. We examined thermoregulatory data collected from June and July 2017, at two maternity colony sites in north western Ontario. These data were collected via pulse-interval radio transmitters attached to the dorsal side of the bats. Currently results are still preliminary. If the data support my hypothesis it would show how bats are regulating their temperatures during and after their pregnancies. Showing when the bats may be most active, and when they use torpor during this time. It also allows us some insight into what types of roosts or microclimates these bats are selecting when they come back to these maternity colonies. This would provide information to be used in conservation and wildlife management, as well as providing an alternative means of aiding recovering bat populations.

**28      This Bed is too Soft: American Black Bear Den Phenology and Site Selection in Saskatchewan's Boreal Shield**

Branden Neufeld\*, Dale Barks, Patricia Tomchuk, and Phil McLoughlin - *University of Saskatchewan*

Bears likely evolved denning behaviour to avoid unsuitable weather and periods of food scarcity during winter. The project examines American black bear denning phenology and site selection as part of a larger woodland caribou project which studies the population ecology and habitat selection of caribou, wolves, and black bears in the Saskatchewan boreal shield. This project includes the first studies of black bears in Saskatchewan. In the spring seasons of 2016 and 2017, 27 bears were captured and fitted with GPS-tracking collars. Using the data from surviving bears (2016 - N=1, 2017 - N=13), I assessed the database of location fixes during the denning period. Den locations were determined using clusters of positions from September through October before signals ceased. Dens averaged 422 m from a water body and 14.7 km from a roadway. Subadult bears (age 2-4 years) were more likely to den in the periphery of their home range, while adults ( $\geq 5$  years) were more likely to den centrally. The first half of this study examines the phenology of den construction and denning date. The second analysis is constructing a resource selection function for ecological variables crucial for den site selection. Initial analysis indicates that bears prefer young to mid coniferous, over mature coniferous patches while avoiding deciduous and more open ground. Analysis of denning behaviour offers insight about crucial habitat for black bears in Saskatchewan while showing proximity to calving grounds of the threatened woodland caribou, a known prey of black bears.

**29      MIRROR OF THE MIND: A Functional Analysis of Imitation in Humans**

Emmanuel Olarewaju\*, James Hare and Jason Leboe-McGowan - *University of Manitoba*

A significant gap exists in our scientific knowledge of the underlying cognitive, perceptual, and mechanistic factors that guide and direct movements during imitation. To examine these factors, I formulated a quantitative procedure that analyzes the perception-action relations inherent in imitation. Accordingly, when imitation is reliant only upon visual cues with paired subjects oriented face-to-face, the action-initiator and action-imitator are behaviourally linked, due to their reliance on two variables: (1) relative body orientation and (2) anatomical location imitated. Consequently, I established two states of imitation: (1) ipsilateral imitation (mirroring) and (2) contralateral imitation (matching). The results from 65 pairs of subjects revealed that mirroring

was less cognitively taxing than matching, and thus was generated more rapidly and with greater efficacy. Consistent with ideomotor theory, this pattern emerged in both the action-initiator and the action-imitator. Due to the stability of this pattern, the link between physical actions and mental perceptions can be expressed using the binary code employed in the instruction architecture of computer systems. With this in mind, the development of a computational model (i.e., simulation) of the scaling and dynamic properties of imitation are plausible. Furthermore, this same method could be employed to characterize neural activity during imitation, thus revealing how social interactions contribute to the development of the brain.

**30      When to heed the call: how kinship, familiarity, and predation risk affect aquatic prey reliance on chemical disturbance cues**

Bairos-Novak KR\*, Crane AL, Chivers DP and Ferrari MCO - *University of Saskatchewan*

Prey can acquire information about predators by eavesdropping on conspecific cues, but these cues are not always reliable. In aquatic systems, disturbance cues are a pulse of urea or ammonia that is commonly released by prey while fleeing a predator, with nearby individuals displaying antipredator responses after detecting these cues. Here, we sought to test whether disturbance cues might function as an antipredator signal in wood frog tadpoles, *Lithobates sylvaticus*. Using a series of experiments, we assessed how relatedness and familiarity with individuals releasing the cues affects the antipredator response of a receiver, and whether background risk levels for the cue releaser and receiver play a role. Tadpoles responded similarly to the disturbance cues of related and unrelated individuals, suggesting that related individuals did not provide more reliable information. Counter to expectation, tadpoles exposed to disturbance cues from unfamiliar individuals displayed a fright response, whereas disturbance cues from familiar individuals were ignored, possibly because these cues became unreliable after being detected repeatedly in the absence of a true threat. When we manipulated background predation risk, we observed that high-risk receivers, but not low-risk receivers, responded to disturbance cues from low-risk donors. In contrast, disturbance cues from high-risk donors elicited a fright response in both high- and low-risk receivers. Taken together, these experiments provide strong evidence that tadpoles detect variation in disturbance cues and may be capable of modulating their disturbance cues as antipredator signals.

**31      Speaking whale: Investigating the functions of humpback whale non-song calls in the North Atlantic**

Mikala Epp\* and Gail Davoren - *University of Manitoba*

Signals, in various forms, are necessary for animals to interact with each other and their environment in situations related to survival and gene propagation. Humpback whales (*Megaptera novaeangliae*) are a highly vocal species that produce both songs and non-song calls. The original objective of this study was to characterize and categorize the non-song calls made by humpback whales on their foraging grounds on the northeast coast of Newfoundland, Canada, using passive acoustic monitoring in order to create a catalogue of calls for this region and contribute to a global catalogue. Recordings from both a marine recorder with a hydrophone as well as animal borne tags were examined aurally and visually and calls were described with a selected of parameters related to duration, frequency and entropy. The calls from the Newfoundland region were classified using 24 variables, and both a principal components analysis (PCA) and a Ward's dendrogram, which resulted in the identification of nine call groups. While the PCA indicated that the calls fall along a continuum, examination of the groups from the dendrogram and call type descriptions from the literature show some distinct calls

types, some of which seem to occur in multiple regions. My continued work will look further into the call characteristics and how they compare to other regions as well as involve the deployment of more animal borne tags to investigate individual call rate and behavioural links.

**32 The effects of body condition and wing asymmetry on personality of Cape horseshoe bats (*Rhinolophus capensis*)**

Alyssa Stulberg\* - *University of Regina*

Animal personality, or consistent individual differences in behaviour across time, has been studied in a variety of taxa and has implications for overall fitness of individuals; however, only a handful of studies have attempted to describe the personality of bats. With over 1200 species, bats provide the potential for understanding dynamics of personality in a variety of phylogenetic and ecological contexts. Currently, the effects of morphological differences on personality in bats are poorly understood. Thus the primary objective of my study was to test the hypothesis that body condition and fluctuating wing asymmetry influence intraspecific differences in bat personality. We captured 27 adult Cape horseshoe bats (*Rhinolophus capensis*) in a cave within the Table Farm Farmstead, South Africa. We assessed personality by recording ten-minute trials in a modified hole-board test, then scored the videos for a range of behaviours including latency to enter the chamber (60 seconds as a maximum), frequency of flight attempts, time spent echolocating, time spent crawling (locomotion), latency to head dip into chamber holes, frequency of head dips into chamber holes, and frequency of line crossing. We found no effect of body condition or wing asymmetry on personality scores. These results indicate that personality is independent of morphological variation in this species.

**32 The Bear Essentials: Home Range and Movement of Boreal Forest Black Bears, With Respect to Hunter Baiting**

Dale Barks\*, Branden Neufeld, Patricia Tomchuk and Phil McLoughlin - *University of Saskatchewan*

Life for most creatures must balance foraging, mating, and predator avoidance. Consequently, many animals establish “home ranges,” generally containing all necessary components for survival and reproduction. I examined variations in seasonal home range size and movement rates of boreal forest black bears (*Ursus americanus*), particularly in relation to spring hunter-baits. Previous studies indicate that baiting reduces home range size and increases bear-density, but no studies have been performed on Saskatchewan black bears and few on the lasting impacts of discontinued bait-sites. In 2016-2017, we GPS collared twenty-seven (n=27) black bears in Saskatchewan’s Boreal Shield region and monitored daily movement. From May 30-June 30, these bears were exposed to hunter-baits. Seasonal home ranges and movement rates were subsequently analyzed. If baiting reduces bear movement, we expect smaller home ranges and higher local bear density in the baiting period, compared to the post-baiting period. Our study found some of the largest home ranges reported in literature, with dispersing males having the largest average home ranges in each season, at an average annual range of 1933.99 km<sup>2</sup>; adult males had the second largest with an annual average of 316.50 km<sup>2</sup>, and females had the smallest home ranges of 79.79 km<sup>2</sup>. High food abundance at baits caused bears to alter their spring home ranges and tolerate greater density of competitors, but bear activity around baits declined rapidly post-baiting. Looking forward, this study will give insight into overlap of black bears with, and their impact on, Saskatchewan’s threatened woodland caribou (*Rangifer tarandus caribou*).



**34 Stress-mediated rapid effects of cortisol in rainbow trout liver**

Marwa Thraya\* and Mathilakath M. Vijayan - *University of Calgary*

Glucocorticoids are steroid hormones critical in the regulation of wide-spread cellular processes for stress adaptation. Cortisol, the primary glucocorticoid in teleost fishes, exerts physiological effects through genomic and nongenomic signalling pathways. Unlike the genomic response, which is characterized by activation of the classical glucocorticoid receptor (GR), the nongenomic effects are rapid (seconds to minutes) and involve changes to second-messenger signalling cascades independent of transcription and translation. However, reports on the nongenomic cortisol actions in fish are few and the receptor(s) that mediate these rapid effects remain poorly characterized. Studies thus far have shown that cortisol treatment in rainbow trout (*Oncorhynchus mykiss*) hepatocytes rapidly altered membrane fluidity and topography and this corresponded to a rapid phosphorylation of substrate proteins. In this same species, cortisol induced reactive-oxygen species (ROS) in skeletal myotubules, an effect that was blocked by the GR antagonist, RU486, indicating that this rapid response involves GR-mediated signalling. In this study, we exposed rainbow trout to an acute stressor and sampled livers 30 minutes and 4 hours post-stressor exposure. Our results show a significant reduction in ROS production and glutathione within 30 minutes in vivo in trout liver. Also, treatment of the liver in vitro with RU486 did not abolish this effect of cortisol, suggesting a GR-independent mechanism of rapid action in trout. Altogether, our findings highlight that cortisol may rapidly activate distinct signalling pathways in target tissues during stress adaptation, but the mechanism remains to be elucidated.

**35 The Opposing Roles of Flavonoids and Reactive oxygen species in Mediating Pollination in Ornamental Kale**

Abhinandan Kumar\* - *University of Calgary*

Self-incompatibility (SI) in hermaphroditic angiosperms is a complex mechanism of mate selection/rejection during sexual reproduction. The landing of a self-pollen on the stigma of the Brassicaceae family (kale, canola, cabbage) triggers a haplotype-specific rejection of the pollen caused by a ligand-receptor (SCR/SRK) mediated intracellular signaling cascade. Except for a few identified downstream targets, knowledge of proteins involved during this response and their temporal regulation has remained elusive. Here we report 107 differentially expressed proteins (DEPs) in the developing stigma (Stage 1- Stage 5) of kale using 2D-DIGE and MALDI-TOF-TOF MS/MS. From the analysis of these DEPs, we have identified a progressive downregulation of the flavonoid-related proteins with concomitant upregulation in the levels of reactive oxygen species (ROS). In-vivo confocal imaging of the ROS levels in the stigmas using DCFH2-DA revealed an increase in ROS during stigma maturity. Our ROS quenching studies indicate that ROS accumulation is not required during SI response while it was necessary for successful pollination to occur. Supplementing mature stigmas before flower opening, with the flavonoid, kaempferol, mimicked the ROS quenching studies suggesting flavonoids could influence ROS levels in the stigmas. Interestingly, kaempferol treatment led to breaking down of SI response in mature stigmas suggesting an accumulation of flavonoids could prevent the full manifestation of SI response in mature flowers. These findings suggest that ROS and flavonoid pathways play distinct and overlapping functions during compatibility and SI responses in kale have likely coevolved as an outcome of selective pressure to maintain vigor while avoiding unfavorable interactions at the stigmatic surface.

**36 Free falling or free flying? Activity Thermoregulatory Substitution during Rewarming from Torpor in migratory bats**

Emma L. Kunkel\* and Craig K. R. Wilils - *University of Winnipeg*

Many bats reduce body temperature (Tb) and enter torpor to conserve energy. Torpid bats use shivering and non-shivering thermogenesis to rewarm to normal Tb but both processes are expensive. During winter, some non-flying mammals substitute heat generated during activity (e.g., while foraging) for thermoregulatory heat production and this can reduce energetic costs of activity. However, the importance of activity-thermoregulatory substitution during rewarming from torpor is not understood. If bats can fly at Tbs below normothermia, the cost of rewarming before departing roosts at dusk could be offset by some of the energy required to commute to foraging areas. We tested two predictions of this hypothesis using silver-haired bats (*Lasionycteris noctivagans*) and eastern red bats (*Lasiurus borealis*): 1) Bats are capable of flight at Tb below normothermia; and 2) Opportunities to fly increase rates of rewarming and, therefore, reduce energetic costs. We captured 70 silver-haired and 18 red bats in southeastern Manitoba, Canada. We housed bats for 12 hours in a temperature-controlled cabinet at 8°C to induce torpor. Half the bats of each species were then allowed to warm passively while the other half were dropped from a height of 1.5m onto a well-padded floor to induce flight. We allowed bats in the flight group to attempt flight every 2 minutes and measured Tb every 2 minutes for both groups. Consistent with our first prediction, bats were capable of flight at Tb as low as 25°C. Our results have implications for understanding how bats minimize energetic costs and maintain energy balance.

**37 Evaluating the use of nectary vascularization and morphology as phylogenetic characteristics in the Asteracean tribe Astereae**

Kelton Braun\* and Art Davis - *University of Saskatchewan*

Nectar, the sweet substance many insects and other animals feed upon when visiting flowers, is secreted by structures known as nectaries. These relatively poorly studied structures occur in almost all of the 25,000 species of the sunflower family (Asteraceae). Within this family, floral nectaries are most frequently of the annular type, forming a ring of tissue surrounding the base of the style, filling the space between the style and the corolla tube. Because the nectaries are located deep within the corolla tube, photosynthesis by these cryptic glands presumably is almost negligible, such that rather than producing carbohydrates locally, sugars must be supplied to the nectaries through vascular tissue originating from elsewhere in the capitulum. The vascularization of nectaries in many genera throughout the North American clade of Astereae (a large tribe within Asteraceae) is being investigated using both resin and paraffin wax sectioning, whereas the general nectary morphology is being examined using scanning electron microscopy. Floral nectaries potentially hold important information regarding phylogenetic relationships between species. The data obtained from this research will be analysed to determine if both nectary vascularization and morphology can be utilized as characters to advance our phylogenetic understanding within this clade and, if successful, extrapolated to other groups within this largest dicot family.



**38 The Use of Antibiotics to Treat Viral infections: Immuno-modulating properties of Tulathromycin in porcine reproductive and respiratory syndrome**

Dimitri Desmonts de Lamache\*, Moges R., Feener T.D., Muench G.P., McKenna N., Yates R. M. and Buret A.G. - *University of Calgary*

Porcine reproductive and respiratory syndrome virus (PRRSV) is a positive-strand RNA virus that grows in alveolar macrophages and causes acute pneumonia in pigs. Due to its high antigenic variability, and poorly understood immunopathogenesis, there is currently no treatment to control PRRSV infections. The common occurrence of PRRSV infection with bacterial infections as well as its inflammatory driven pathobiology raises the question of the value of antibiotics for the treatment of the disease it causes. Tulathromycin, a macrolide antibiotic has been shown to exhibit potent anti-inflammatory and immunomodulatory actions. We hypothesize that these may attenuate the detrimental effects of PRRSV in porcine macrophages. To assess the effect of Tulathromycin on PRRSV-infected macrophages activation and functions, cytokine and (IL-8 and IL-10) reactive oxygen species (ROS) production assays were performed. Phagocytic properties were measured using zymosan particles or opsonized latex beads. Cell death ELISA, Annexin V immunostaining and lactate dehydrogenase assay were used to evaluate the effects of Tulathromycin on PRRSV-induced necrosis and apoptosis. In this study we show that Tulathromycin, a macrolide used for the treatment and prevention of respiratory disease in pigs and cattle, attenuates macrophage-driven inflammatory response induced by PRRSV, restores PRRSV-induced phagocytic impairment, and inhibits cell necrosis. Together, these data demonstrate the potential clinical benefits of Tulathromycin in the context of PRRSV-induced pneumonia through the modulation of a viral-induced macrophage-driven inflammation. Such findings will help characterize novel mechanism through which an anti-microbial agent may deliver clinical benefits in the context of a viral infection.

**39 Young and Defended: Age and Resin Duct Metrics in Lodgepole Pines**

Isabella Hutchison\* and Mary Reid - *University of Calgary*

In coniferous trees, resin is a primary defence that is stored in ducts throughout the tree. Older trees are believed to be more vulnerable to pest attack because fewer carbon resources are available to be allocated to resin and defensive processes, while younger trees may invest more in defensive metrics due to life history demands. If tree age is a main determinant in resource allocation to defence, then a decrease in defensive traits such as increased resin duct size and density should be observed between old and young stands, regardless of tree size. Large trees are also expected to have lower defensive traits, as bigger trees have to allocate carbon resources to growth over a larger area. If tree size is the main factor in influencing defensive traits, then larger trees should have lower resin characteristics than smaller trees, across stands of all ages. To distinguish between tree age, size, resin parameters, we studied 96 lodgepole pines in old (>80 years) and young (40-50 years) forest stands, selected to represent different sizes. Young trees had higher resin duct density in phloem than older trees of similar sizes, and duct size increased with tree size. Over the most recent growth, younger trees had more and larger xylem ducts, than older trees of a similar size. Resin production demonstrated no clear trend across tree age. Overall, younger trees are more defended by resin duct metrics. Other explanations for these trends could be how competition for resources changes between old and young forests.

**40 Thermogenesis in fish: A potential role for the SERCA pump uncoupling protein, Sarcoplipin, in a whole-body endotherm, the Opah (*Lampris guttatus*)**

Eva Slight-Simcoe\* and Jens Franck - *University of Winnipeg*

Sarcoplipin (SLN), is a small transmembrane protein located within the sarcoplasmic reticulum proximal to the sarco(endo)plasmic reticulum calcium ATPase (SERCA) pump in myocytes. Although SLN is known to modulate the activity of SERCA, the nature of this influence varies among species and tissue type. In mammals, SLN facilitates a mechanism of non-shivering thermogenesis (NST) by uncoupling calcium transport from ATPase activity in SERCA. However, little is known about the role of SLN in fish tissues. Certain species of fish exhibit endothermy, the ability to maintain body temperature above ambient water temperature. Opah (*Lampris guttatus*), a mesopelagic teleost fish, demonstrates whole-body endothermy, distinguishing it from regional endotherms such as lamnid sharks and billfishes, whose endothermic capacities are localized to specific tissues. The sln gene has been annotated in the genomes of several species of teleost fish, however, it has not yet been annotated in the opah. The purpose of this study is first to confirm the expression of sln in opah, and second to determine if sln is differentially or overexpressed in opah thermogenic muscle tissues, specifically in the deep red pectoral tissues that have been implicated as the primary source of metabolic heat. This will be tested through confirming the presence of sln transcripts in opah followed by an analysis of relative expression levels among different tissue types via quantitative polymerase chain reaction (qPCR) using opah sln-specific primers.

**41 Improving Canola productivity through manipulation of shoot branching pathway**

Matija Stanic\* and Marcus Samuel - *University of Calgary*

Plant architecture development is a highly plastic event and is the outcome of a complex interaction between environmental stimuli and genotype. In crops, proper plant architecture is critical for production of biomass and yield. Manipulation of architecture, such as promoting increased branching, would allow for yield improvements without increase in arable lands. In higher plants, the shoot system (above-ground tissues) is organized in a modular fashion consisting of nodes, internodes, axillary buds, and leaves, with the axillary buds representing dormant clusters of meristematic cells (equivalent to stem cells) located at the base of leaves. Upon proper stimuli, these buds are able to break dormancy and enter a developmental stage whereby they can produce a new shoot (branch). Several hormonal regulators are involved in this process which can be manipulated to yield variable branching phenotypes. My research focuses on the genetic manipulation of *B. napus* (Canola) for the purpose of increasing branching and yield via interfering with the Strigolactone pathway; strigolactones are known inhibitors of shoot branching. Canola being the most significant cash crop in Canada, creating varieties with increased branching could lead to considerably improved yields and contribute to the economy.

## Session B2: Population Biology

### 43 What does it mean? Evaluating uncertainty and reliability in environmental DNA interpretation

Jori Harrison\* - *University of Calgary*

The use of environmental DNA (eDNA) metabarcoding to describe aquatic biodiversity is a rapidly emerging technique, but the robustness of the application for both species detection and quantification has not been well characterized. This study aims to develop an eDNA assay capable of distinguishing closely related salmonid species and to test predictions about the presence of eDNA in a replicated large-scale semi-naturalized system. Novel eDNA primers, capable of distinguishing between Brook trout (*Salvelinus fontinalis*), Rainbow Trout (*Oncorhynchus mykiss*), and Cutthroat Trout (*Oncorhynchus clarkii*) salmonid species were developed and a controlled winter experiment was conducted at the Advancing Canadian Wastewater Assets (ACWA)'s experimental research streams. This facility contains 12 naturalized streams 320 meters in length, with inflow from a common headwater pond. Fish species were caged at the start of each stream at varying biomass levels. Water samples were collected from the start, middle, and end of each stream and filtered to collect DNA. Sampling was repeated three times, and DNA from the filters was sequenced with an Illumina NextSeq. All species were reliably detected, however the quantity of DNA obtained showed high variation unrelated to biomass. To our knowledge, this is the first eDNA experiment under a controlled, replicated design within a semi-natural system and should advance our understanding of this promising ecological application.

### 44 Genomic Diversity in the Canadian Feral Horse (*Equus ferus caballus*)

Christina Tollett\*, Philip McLoughlin and Jocelyn Poissant - *University of Saskatchewan*

Investigating the genomic diversity of feral horse (*Equus ferus caballus*) populations in Canada can provide researchers with an important framework for genetic conservation and improve the understanding of the evolution of unique populations. This study aims to assess broad patterns of genetic diversity in the Sable Island and Alberta Foothills feral horses characterizing the horse populations relative to well-defined breeds and discerning their origins. We utilized equine SNP microarrays (Illumina equineSNP74 BeadChip) to genotype samples from two Canadian feral horse populations and integrated the samples with samples from well-defined origins. Our analyses support the inferences that Sable Island is the most unique and inbred population being greatly diverged from even its closest relative, the Mongolian horse. These results suggest that the population is a result of the high impact of evolutionary forces. The Alberta Foothills feral horse population was determined to be the product of great admixture with a strong relationship to draft breeds. Higher than anticipated inbreeding levels suggest the presence of breeding groups across the Alberta landscape. The results of this study offer government agencies an essential and objective decision-making platform regarding the conservation of feral horse populations in Canada.

### 45 Examination of the life history patterns of the hard tick *Haemaphysalis intermedia*

Chulnatha Diyes\* and R S Rajakaruna - *University of Saskatchewan*

The three-host tick, *Haemaphysalis intermedia*, is of significant veterinary importance in Sri Lanka and India because of the pathogens (Bhanja virus, Nairobi sheep disease virus, and Ganjam virus) it transmits to cattle and poultry. In this study, we determined the life history

patterns of a Sri Lankan population of *H. intermedia* in the laboratory using albino rabbits as hosts. Female ticks that had fed on cattle in the field were transferred to the laboratory and maintained at 28 °C and 80% RH to lay eggs. The results of our study revealed that female ticks had an average pre-oviposition period of 11.1 days. They took on average 9.0 days to complete oviposition and produced 683.5 ( $\pm 271.8$ ) eggs. Larger females produced significantly more eggs than smaller females (Pearson correlation;  $r = 0.7$ ,  $p < 0.05$ ). Incubation times declined as temperatures increased. In addition, larvae took 3.4 ( $\pm 0.9$ ) days to feed on rabbits and 8.4 ( $\pm 1.1$ ) days to moult to the nymph stage, while nymphs took 4.9 ( $\pm 0.7$ ) days to feed on hosts and 10.5 ( $\pm 1.5$ ) days to moult to the adult stage. Adult ticks did not successfully feed or mate on rabbits. The duration of the life cycle was estimated to range from 149–476 days. Although the life history of the Sri Lankan population *H. intermedia* shared similarities with the Indian population of this species, it more closely resembled that of morphologically similar *Haemaphysalis bispinosa* that occurs in the oriental region.

**46 Inbreeding depression in an island population of feral horses (*Equus ferus caballus*): fine-scale variation and fitness consequences**

Julie Colpitts\*, Philip McLoughlin and Jocelyn Poissant - *University of Saskatchewan*

Understanding the degree of inbreeding depression present in small, isolated wildlife populations is crucial to elucidating their genetic health, adaptability and potential for successful management. Inbreeding depression occurs when closely related individuals mate, having negative impacts on both survival and reproductive output through a variety of avenues, but its role in island populations is often unclear. The feral horses (*Equus ferus caballus*) of Sable Island National Park Reserve, Nova Scotia, Canada have existed as a small ( $N \approx 200$ –550) unmanaged herd with little human interference for approximately 200 years. Previous work has shown that genetic diversity is generally low within the population, and varies from one end of the long thin island to the other. However, the degree of inbreeding depression and its fitness correlates remain poorly understood in this system. In this study we investigated inbreeding depression in this population by contrasting genome-wide inbreeding metrics estimated using ~40000 single nucleotide polymorphisms with several fitness-related traits including body condition, parasite load and reproductive success. In addition, as the island is characterized by an important gradient in horse habitat quality (access to preferred forage and fresh water) which affects both horse density and behavioural traits, it presents an opportunity to test for spatial variation in inbreeding depression. This study provides useful insight into the genetic viability and adaptive potential of the Sable Island horses which may inform future management practices, and contributes to the ongoing discussion regarding genetic diversity and viability as it relates to island processes.

**47 Integrating estimates of genetic diversity to inform Burrowing Owl (*Athene cunicularia*) conservation strategies**

Adam J. Watson\*, Laura Burns, Alexandra L.M. Froese, Stephen D. Petersen and Sean M. Rogers - *University of Calgary*

Burrowing Owls are listed both federally and provincially as Endangered throughout their Canadian range due to population declines and periods of extirpation from some provinces. Three provinces have established captive breeding and reintroduction programs often with little to no information on relatedness of founding owls. The objective of this study is to estimate genetic diversity changes across five years in the Manitoba Burrowing Owl Recovery Program (MBORP) in order to inform conservation and reintroduction strategies. DNA has been isolated

from blood samples (N = 90) and 16 microsatellite loci will be genotyped to estimate inbreeding (Fis) levels across five generations. These data will also be used to estimate genetic population structure in association with the putative source populations of the captive owls. Analyses suggest that these loci are polymorphic, and with the full suite of genotypes this will inform the MBORP breeding and reintroduction program.

**48 The impact of enriched rearing in captivity: genetic and environmental determinants of Pacific coho salmon (*Oncorhynchus kisutch*) survival phenotypes**

Jessy Bokvist\* and Sean Rogers - *University of Calgary*

Understanding the underlying mechanisms through which captive rearing influences phenotypic development and survival is crucial to the management of cultivated species and their potential impact on wild counterparts. Pacific coho salmon (*Oncorhynchus kisutch*) are one of the most susceptible salmonids to domestication in hatcheries, showing a lower fitness in the wild as compared to natural-origin coho. High mortality rates in released hatchery coho have prompted management practices that include rearing juveniles in enriched environments to imitate wild conditions, a method shown to mitigate development of deleterious domestic traits. Yet, the genetic and environmental determinants of survival phenotypes in association with such practices remain unknown. In this study we worked with Canada's largest hatchery (the Nitinat River Hatchery) to produce 250 F1 full-sib crosses coho (2013 and 2014 cohorts) reared under controlled enrichment treatments. Replicate cohorts will be compared across millions of single nucleotide polymorphisms to quantify genetic variation underlying differential phenotypes. Likewise, environmental influences on phenotypes will be explored genome-wide via comparison of methylation patterns. The integration of genomic and epigenetic mechanisms is fundamental to a better understanding and implementation of salmon enhancement practices.

**49 Morphology of the First Instar Larvae of *Stylops* sp. (Strepsiptera), which infect *Andrena milwaukeeensis* (Hymenoptera)**

Zach Balzer\* and Arthur Davis - *University of Saskatchewan*

Strepsiptera is an order of endoparasitic insects with an extremely unique life cycle. The life cycle includes mobile adult males as well as permanently endoparasitic females. Once the pair has mated the male dies and the female stays within her host to develop the offspring. The female gives viviparous birth, and the larvae leave their mother to try to find a new host. Species of Strepsiptera belonging to *Stylops* infect numerous species of *Andrena* bees. *Andrena* are ground nesting bees, so for the *Stylops* larvae to find an immature host it must get into an adult bee's nest. To do this, larvae need to hitch a ride on an adult bee and travel with it back to its nest. Certain morphological adaptations aid strepsipteran larvae in this journey, and these traits were examined using SEM. The head possesses sensory setae and olfactory pits, used for detecting a host and perceiving the environment. Oar-like tarsi were observed on the pro- and mesothoracic legs, and could help with staying on a flying host. The metathoracic tarsi are cylindrical, before widening at the tip, and are probably only for locomotion. The entire body, except the head, is covered in spinules of various lengths. These spinules may get caught on the compound hairs of its phoretic bee host, allowing the larvae to stay attached during the bee's flight. At the end of the abdomen are a pair of caudal filaments which dilate at the tip, but which are not believed to be used in a springing fashion by *Stylops* species.



## Session C2: Conservation Biology & Management

### 52 Spatial Analyses of Canopy Structure of Forests in the Cypress Hills

Adam H. Sprott\*, Tanvir Ahmed Shovon and Mark Vanderwel - *University of Regina*

Healthy forests are complex ecosystems that depend upon the interactions of many organisms in response to many factors. Consequently, biologists require an accurate method to frequently survey field sites to understand how forest communities are affected by seasonal and long-term phenomenon. Using data captured from unmanned aerial vehicles (UAVs or drones) it is now possible to rapidly, affordably, and repeatedly create geo-referenced spatial reconstructions of real-world environments. This presents the opportunity to extract canopy characteristics of a large number of individual trees over vast areas that can be used to develop scaling relationships to predict tree above-ground biomass and develop tree species niche models that are related to site-specific gradients such as elevation, aspect, and moisture availability. Due to rapid change in elevation from the broader prairie landscape, the forests of the Cypress Hills present an interesting opportunity to develop 3D visualizations of tree species response to a range of environmental conditions at a local level. Furthermore, when ground-truthed observations from soil, plant, lichen, and wildlife surveys are overlaid on top of the virtual surfaces it can be seen how canopy structure influences multiple functional layers within the forest community. Subsequently, when drone surveys are repeated across a large and/or remote landscape it may be possible to predict key sites of ecological services from the canopy surface at low cost and with low disturbance. Such techniques may have profound impacts on how we manage and restore our forests in response to changing climates and evolving anthropogenic demands.

### 53 Bees: The dependence on adequate nutrition for a healthy immune system

Bethany Topping\* and Mary-Anne McLean - *St. Mary's University*

It has been revealed that individual bees have the ability to choose food types that contain specific nutrients based on what is lacking in the overall food collection of a bee colony. Alternatively, humans depend on bees to pollinate our crops and other flowering plants. There is a great industry in honey bee farming, however the introduction of pathogens, pests and pesticides has been prompted by poor apiarian management practices. Additionally, apiarian bees can face periods of starvation, such as in the occurrence of severe weather, or when crop yield is scarce. However, the idea that pathogens, pests and pesticides are causing the death of colonies leads to a common thread. Not unlike other animals, a resilient immune system for bees is associated with a balanced and healthy diet. Pollen is the source for amino acids, which are the indispensable primary building blocks to all living things. It is important to consider the implications that our current agricultural practices impose on the pollen supply to bees: the richness of bee species is directly correlated to the richness of plant species. However the increase in anthropogenic development – urban sprawl and agricultural practices – has caused great reduction in nutrition quality and diversity for bees, therefore has influenced the lack of richness of bee species. Therefore, if the diversity of plants were increased through permacultural practices, urban greening or shifting from our highly manicured lawns into a more natural, native wildflower lawn setting, then perhaps we really could save the bees.

#### 54 **Network asymmetry and social-ecological diversity drives collapses of inland fisheries**

Kyle Wilson\* - *University of Calgary*

Spatially-structured recreational fisheries are complex adaptive social-ecological systems. Macro-scale patterns, like the distribution of overfished populations, can emerge from local-scale interactions between fish and people which occurs across space and time. There is thus a need to understand how these macro-scale patterns emerge to help guide management. We present a generalizable and stochastic social-ecological model that varies (1) the spatial-configuration of a recreational fishery, (2) fish population production, and (3) heterogeneity in angler preferences for site-attributes. We then modelled different combinations of these processes (e.g., angler heterogeneity versus homogeneity, or patchy versus diffuse distribution of a lake-to-town network) to test how changes in these processes drive macro-scale patterns in the fishery, like angling effort and fish population collapses. Our general findings corroborate expectations of the systematic depletion of fish populations adjacent to towns. Individual fish populations exhibit wide boom-bust cycles due to site-switching behavior of catch-oriented anglers, however the aggregate fishery (i.e., the landscape-scale) is more stable than these individual populations. Diverse and asynchronous fish population dynamics tended to provide a mechanism for this stability. Heterogeneity in angler preferences tended to increase the risk of collapse, but this depended on the preferences for catch-attributes in the angler population. Results of our theoretical model have general implications for spatially-oriented management, with different scale-dependent patterns emerging from different combinations of spatial, social, and ecological processes.

#### 55 **Species differences in susceptibility to white-nose syndrome**

Nicole A. S.-Y Dorville\*, Emma L. Kunkel, Ana M. Breit, Kaleigh J. Norquay, Yvonne A. Dzal, Quinn E. Fletcher, and Craig K. R. Willis - *University of Winnipeg*

Wildlife pathogens can cause population declines and extinctions, and understanding species differences in susceptibility is important for conservation. White-nose syndrome (WNS), caused by the fungus *Pseudogymnoascus destructans* (Pd), is a skin disease devastating populations of North American hibernating bats. Two of nine species WNS-impacted (i.e., little brown bats, *Myotis lucifugus*; and big brown bats, *Eptesicus fuscus*) both hibernate in conditions favouring Pd growth. However, little brown bats have faced significantly steeper declines. Three competing hypotheses could explain this species difference in WNS impacts: i) Big brown bats are behaviourally resistant to WNS; (ii) physiologically resistant to WNS; or (iii) tolerant to WNS. In this context, physiological and behavioural resistance, and tolerance are determined by their levels of morbidity and disease severity respectively. We tested these hypotheses using an inoculation-challenge experiment. We housed Pd-inoculated and sham-inoculated groups of both species in separate cages within temperature and humidity-controlled incubators to maintain hibernation conditions. There was no difference in survival between species on the timescale of our experiment but, Pd-infected big brown bats had significantly higher intensities of Pd infection after 60 days, despite receiving identical inoculation doses as little brown bats. This is consistent with the hypothesis that reduced impacts of WNS on big brown bats relative to other species reflects tolerance rather than physiological or behavioural resistance. Although big brown bats appear tolerant of high Pd loads, management actions that reduce loads for this species could still be important for conservation by reducing potential inter-species transmission within and between hibernacula.



**56 Preliminary assessment of the population biology of yellow perch (*Perca flavescens*) in Waterhen Lake, Manitoba**

Robyn Demare\* - *University of Winnipeg*

Ecocertification of fisheries has become increasingly important in recent years in fisheries management. It is based upon a third party audit to ensure that a fishery adheres to sustainable fishing practices. An essential prerequisite for such an audit is a stock assessment of the proposed population for harvest. Here I report preliminary findings on the population biology of a yellow perch (*Perca flavescens*) in from Waterhen Lake, Manitoba. Gill-net sampling of the population was conducted on Waterhen Lake in the fall of 2017 using mesh sizes ranging from 38 mm to 102 mm in 6 mm to 12 mm increments. Total length and mass of each fish was measured; its sex and whether it was reproductively mature was assessed. Opercular bones and otolith were taken for age assessment. The maximum age observed in the sample of 130 perch was 5 years. Males reached 100% reproductive maturity at age 2; females matured later, with 63% (12 of 19) percent reaching maturity at age 2, and 100% (n=23) mature at age 3. The natural rate of mortality in the population was estimated at 60.0%, which is at the high end of observed mortality rates for other yellow perch populations. Perch in this population appeared to mature early and died quickly compared to other yellow perch populations.

**57 Bumble bees (*Bombus* sp.) in the Alberta Rockies: effects of natural land cover heterogeneity on species richness and abundance**

Danielle Clake\*, Paul Galpern and Sean Rogers - *University of Calgary*

Land use change can result in both habitat loss and fragmentation. While negative impacts of habitat loss on biodiversity are ubiquitous, many studies have suggested a positive impact of habitat fragmentation when considered independently of habitat loss. While this trend appears to be consistent across many different species and biomes, the mechanisms behind it are not well understood. We examine whether the positive impact of landscape fragmentation extends to naturally heterogeneous mountain landscapes where humans have historically had minimal impacts on land use and land cover. To do this we have sampled bumble bees (*Bombus* sp.) across protected areas in the Rocky Mountains of Alberta and adjacent foothills. Samples were collected continuously over a six week period at 40 sites spanning roughly 10,000 square km. Sites were selected to minimize correlations between land cover composition (total area of a given land cover type) and configuration (the shape and arrangement of land cover patches). We collected over 20 different species of bumble bees with a range of roughly 0 – 12 species per site. We investigate predictions about the relative influence of land cover composition and configuration on bumble bee abundance and species richness, and test for positive impacts of land cover fragmentation on bumble bee communities. By focusing on inherently heterogeneous mountain habitats we can better understand the influence of landscape heterogeneity on organisms when it is independent from human influence. This will provide important background knowledge when evaluating the impacts of anthropogenic landscape changes, including habitat loss and fragmentation.

**58 Stress in Walleye during Catch and Release Angling**

Kendra Gietzen\* and Richard Manzon - *University of Regina*

Catch and release angling has been shown to induce physiological stress responses in Walleye. This study aims to examine the relationships between external stress indices and physiological measures of stress in Walleye caught during catch and release tournaments in Saskatchewan.

Working with Saskatchewan anglers and tournament organizers, I will sample their catch to evaluate the effects of angling duration, air exposure, live-well conditions and stress mitigation methods on stress at capture and during recovery. By linking quantifiable measures of stress such as cortisol and lactate concentrations to Walleye performance, my research aims to provide information on which practices minimize stress during catch and release tournaments, maximizing the health of Walleye when they are released. With these measures of physiological stress we can evaluate condition, recovery and mitigation procedures. Collectively, this data will provide fisheries managers with much needed information to evaluate guidelines for anglers and tournaments for reducing the impact on Walleye populations.

**59 The "fitness" of a territory: is the reproductive success of a food-caching animal more associated with habitat or individual quality?**

Andrea E Wishart\*, Stan Boutin, Andrew G McAdam, Benjamin J Dantzer, Murray M Humphries and Jeffrey E Lane - *University of Saskatchewan*

Reproductive success is typically considered to be a trait of the individual. However, habitat quality is also frequently correlated with reproductive success, making it difficult to disentangle the two influences, particularly for species with high site fidelity (e.g., territorial animals). The effects of territory quality may be masked for animals that create long-term food caches to buffer against periods of environmental food shortages. In heterogeneous environments with high inter-annual variation in food abundance, a territory that is high quality in terms of food production one year may not be high quality in subsequent years. Discerning between individual and territory quality in such systems requires multiple years of reproductive success data for different individuals on the same territory as well as data for the same individual in different territories. We have monitored a fully-censused population of North American red squirrels (*Tamiasciurus hudsonicus*) in the southwest Yukon for 30 years through the Kluane Red Squirrel Project. Here, squirrels cache cones of white spruce (*Picea glauca*) in centralized larder-hoards ("middens") that they actively defend year-round, allowing us to quantify the cached resources available to individual squirrels. In addition to inter-annual fluctuations, white spruce shows individual variation in cone production within years, creating heterogeneity in habitat quality for squirrels. Using annual measures for cone production across our study area and reproductive success of individuals, we identify whether long-term habitat quality influences reproductive success in squirrels and determine whether individual quality may interact with territory quality through food-caching.

**60 Scaling the question of Age vs Size - An examination of yellow perch (*Perca flavescens*) morphology and age in a high-use Saskatchewan Lake**

Shayna Hamilton\* and Chris Somers - *University of Regina*

Yellow perch (*Perca flavescens*) are one of the most important fish species for recreational angling in Canada. To properly manage perch populations it is important to know the sizes fish first become susceptible to angling and harvest. Perhaps more important is quantifying the age of fish being removed from a system to determine how long it takes to replace a target-sized fish. In Saskatchewan, yellow perch are one of the most commonly caught species, especially during the winter fishery. My project will measure a variety of metrics such as length, mass, body depth, and age of yellow perch from Buffalo Pound Lake, and potentially other sites in southern Saskatchewan. Buffalo Pound Lake is accessible to two urban centres, is shallow enough to avoid barotrauma, and is known as a 'hot spot' for perch. The aim is to use size and age cohorts to quantify the youngest fish susceptible to angling and the average age of fish targeted for

harvest (>25 cm). Fish aging will be determined by collecting scales non-invasively so the fish may be Floy-tagged and released as part of an on-going mark-recapture program. The fish will be caught by the research team or by involving citizen scientist anglers. In this presentation, I will provide an overview of my yellow perch research and my progress to date.

### Session A3: Integrative Cell Biology

#### 61 **MicroRNA regulation of BMP signaling and its effects on vascular smooth muscle cells**

Charlene Watterston\*, Lei Zeng\*, Abidemi Onobadejo and Sarah J Childs - *University of Calgary*

Background: Vascular smooth muscle cells (vSMC) support the endothelial lining of blood vessels. vSMCs can switch their phenotype from contractile (differentiated) to synthetic (undifferentiated). Synthetic vSMCs cannot properly support blood vessels; the effects of which can lead to uncontrolled bleeding (hemorrhage). BMP signalling can act as a molecular switch between differentiation states.

Purpose: microRNA26 (miR26) targets smad1 downstream of BMP signaling in vitro. We use the zebrafish model to ask whether miR26 also controls vSMC differentiation in vivo via modulating BMP signalling.

Results: We find that miR26 is expressed around brain blood vessels and loss of miR26 leads to alterations in the vSMC marker genes *pdgfr $\beta$*  and *acta2*. We show that knockdown of miR26 leads to brain hemorrhage and that Smad1 is upregulated. Concomitantly overexpression of miR26 leads to decreased Smad1. Double knockdown of miR26 and Smad1 reduces hemorrhage. Finally, overexpression of Smad1 in wild type fish leads to hemorrhage, linking Smad1 directly to vascular stability. BMP plays a role in vSMC differentiation as inhibition of the BMP receptor leads to a reduction in *acta2*-positive vSMC cell number in wild type embryos. Knockdown of *mir26* leads to increased pSmad1/5/8 suggesting increased activation of the BMP pathway. However, inhibiting BMP signalling combined with miR26 knockdown does not reduce vSMC number suggesting that miR26 functions downstream of active BMP signalling to promote vSMC differentiation.

Conclusion: Together this data suggests that miR26 mediates vascular stabilization via targeting of Smad1, promoting smooth muscle differentiation.

#### 62 **foxc1b as a marker of early vascular smooth muscle cells in zebrafish**

Tom Whitesell\*, Ryu JR, Workentine M, Lawson N and Childs SJ - *University of Calgary*

We are interested in the morphological and molecular processes that determine how early vascular mural cells (smooth muscle cells and pericytes) are recruited to, and stabilize, nascent blood vessels. We find one of the earliest smooth muscle markers is the transcription factor *foxc1b*. Cells expressing *foxc1b*:EGFP associate with the endothelium and colocalize with smooth muscle in early development through to adulthood. Expression of *foxc1b* around vessels occurs earlier than currently studied smooth muscle markers, and can be used to study smooth muscle differentiation. We examined differences in mural cell marker expression, which vary with anatomical location, vessel diameter, and age. We have employed fluorescence-activated cell sorting and RNA-Seq to explore the transcriptomes of the different mural cell populations and have determined there are distinct gene expression signatures. Taken together, our data and gene expression signatures define different populations of vascular mural cells.

**63 Single fiber studies of muscle growth during development of the Lake Sturgeon (*Acipenser fulvescens*)**

Amber Hiebert\* and Judy E Anderson - *University of Manitoba*

The Lake Sturgeon (*Acipenser fulvescens*) continues to grow throughout life, though the process by which muscle stem cells, called satellite cells (SCs) contribute to formation of fibers in the myotome is largely unknown in this endangered fish. Since muscle function and growth are critical to survival, it is important to understand the functional basis of fiber growth, and how SCs provide daughter cells that fuse into fibers in myotome development and regeneration. The hypotheses are that during aging: the cell cycle of SCs lengthens, the ratio of SCs to myonuclei decreases, and myonuclear domain increases. This experiment used the single fiber model and a pulse-chase design in which exposure to bromodeoxyuridine (BrdU) labeled S-phase for the final 2 hr in culture. Myofibers were isolated from 20-40 fish per age (1-6 months post-hatch). After fiber culture for 24 hours, fibers were fixed and stained for BrdU or Pax7 (expressed by myogenic stem cells) with colour detection. The number of positive nuclei was counted per fiber in 8-20 fibers per dish. Preliminary data shows a significant decrease in the ratio of SCs to myonuclei as the fish age ( $p < 0.05$ ) without an apparent change in cell cycle duration. This investigation adds to our understanding of SC contributions to myofiber growth in the developing Lake Sturgeon and results will be a new foundation for future research on the role of environmental influences on muscle in Lake Sturgeon.

**64 Exploring the interaction between Shox2 and Sonic hedgehog signalling in mouse limb development**

Anja Ljubojevic\*, Samuel Abassah-Oppong and John Cobb - *University of Calgary*

Short-stature homeobox (Shox) genes encode for proteins that mediate the proper formation of limbs during embryonic development. SHOX gene deficiencies in humans result in shortening of bones in the middle limb segment, specifically the radius/ulna and tibia/fibula, and have been implicated in several disorders. In mice, a related gene, Shox2, is used to study the role of these genes, since mice with a disruption of Shox2 in the limbs develop skeletal abnormalities similar to the human phenotype; however, these mice exhibit extreme shortening of the proximal bones of the limbs – the humerus and femur. Despite the critical roles these genes play in development, how Shox2 fits into the gene regulatory network governing the formation of limbs and which pathways it interacts with remains largely unknown. The hedgehog pathway has long been established to play a key role in patterning the limb during early development. The ligand of this pathway, Sonic hedgehog (Shh), is known to be essential for the correct development of the distal segment of the limb, the future fingers and toes; however, its influence on the long bones of the limb has not been well characterized. We have set up crosses to generate mouse embryos, which lack functional copies of Shox2 and Shh genes in the limbs, in order to study how these genes interact. Our results indicate that the loss of Shh rescues the truncations observed in proximal limbs of Shox2 mutant embryos, providing evidence that Shh plays a role in humerus length.

**65 Effects of glutamate and engineered scaffolds on neural stem cell differentiation**

Maria Alejandra Castilla Bolanos\* and Josef Buttigieg - *University of Regina*

Spinal cord injury (SCI) causes significant impairment in motor function and decrease in quality of life. In Canada, each year, there are over 4,259 new SCIs. Due to the large incidence and

negative effects on the Canadian healthcare system, there is significant interest in developing techniques that reverse the severity of injury. While there is the inherent ability for the spinal cord to repair itself, there is little regeneration of tissue post injury. While it is not clear as to why there is the impairment of self-regeneration capacity, there is intensive research exploring the use of stem cells and artificial scaffolds that can provide support for transplanted stem cells. In comparison to 2D cell cultures, 3D scaffolds enhance viability, proliferation and stem cell differentiation into neurons and oligodendrocytes (OLs). Here we present the development of 3D cultures by the integration of neural progenitor cells (NPCs) in extracellular matrix scaffolds. In addition to assessing the physiological responses of NPCs in scaffolds, we will also be investigating the effects of neurotransmitters e.g. glutamate, in the differentiation of NPCs. Recent evidence suggests that extra-synaptic glutamate release helps guide NPCs to differentiate into OLs *in vitro*. Hence, this neurotransmitter would not only promote neuron communication at the synapse, but also may play a key role in neural stem cells differentiation. Testing the effect of glutamate in neural stem cells into scaffolds could develop a better understanding of stem cell differentiation and lead to therapies that could be used to replace lost tissue in SCI.

**66 Identifying differences between pericyte and smooth muscle contraction-relaxation *in vivo***  
Nabila Bahrami\* and Sarah Childs - *University of Calgary*

Compromised blood flow to the brain results in cerebral small vessel disease; an umbrella term for any pathological condition affecting the small vessels of the brain, (small arteries, arterioles, capillaries and venules) and leading to flow deficiencies. Currently, there are conflicting reports in the literature regarding the mural cell type (pericytes or vascular smooth muscle cells (vSMCs)) responsible for blood flow regulation in the brain. While traditionally vSMCs have been thought to regulate cerebral blood flow, some propose that pericytes rather than vSMCs are the primarily mural cells responsible for cerebral blood flow regulation. Here, we identify how mural cells regulate cerebral blood flow *in vivo* using the zebrafish model. Using live imaging, we determined that pericytes and vSMCs are usually present on different sized vessels. We also identified some vessels that are covered by both types of cells, which we have called the transition zone. We applied vasodilating and contracting drugs and measured the *in vivo* response to these agents. Early on in development, the vSMC-covered vessels and transition zone vessels both dilate in response to a vasodilating agent. However, later on in development, the pericyte-covered vessels, the smaller vessels, also begin to actively respond to vasodilating and vasoconstricting agents. Our results suggest that pericytes and vSMCs both contribute to vascular contractility and dilation during development, and there are differences in their activity at different developmental stages.

**67 Sterility and differential gene expression in *Drosophila* interspecies hybrid**  
Alwyn Go\*, Doaa Alhazmi and Alberto Civetta - *University of Winnipeg*

The *Drosophila pseudoobscura pseudoobscura* and *Drosophila pseudoobscura bogotana* subspecies pair show incomplete reproductive isolation and exhibit unidirectional hybrid male sterility. Comparison of gene expression in hybrids relative to parental species allows the identification of misregulated genes. Misregulation can be driven by incompatibilities present in the hybrid genome (i.e. fast male regulatory divergence) but the availability of both sterile and fertile F1 hybrid progenies allows the identification of gene misregulation likely linked to sterility. An alternative explanation for the misregulation of gene expression unique to sterile F1 hybrids is incompatibilities present in the hybrid genome. Specifically, X-autosomal, mitochondrial-nuclear, and cytoplasmic-nuclear incompatibilities. These incompatibilities can be



tested by using different backcross designs. Male hybrid sterility in this subspecies pair is due to incompatibilities between the *bogotana* X-chromosome and the 2nd and 3rd *pseudoobscura* autosome. A major hybrid male sterility locus (ovd) found within the *pseudoobscura* X-chromosome is linked to the visible marker *sepia*. Introgression (IG) lines will be used to introduce the sterility locus from *pseudoobscura* into the *bogotana* X-chromosome, eliminating the incompatibilities between the X-chromosome and autosomes, restoring fertility. Genes uniquely misregulated in sterile IG lines are possible targets of the ovd protein. Previous genome-wide expression analysis identified cell adhesion as one of the larger classes of uniquely misregulated genes in the sterile F1 hybrids. My project focuses on genes related to cell adhesion and is aimed at discerning whether the previously detected misregulation in sterile F1 male hybrids is in fact linked to sterility or driven by genomic incompatibilities.

### Session B3: Specialized Metabolism & Biological Membranes

#### 68 **Discovery of a natural product antibiotic effective against the multi-drug resistant human pathogen, *Acinetobacter baumannii***

Ashley N. Williams\* and John Stavrinos - *University of Regina*

Multi-drug resistant human pathogens are a serious worldwide healthcare concern, spurring the need to identify new therapeutics to address evolving bacterial diseases. *Acinetobacter baumannii* is one such pathogen deemed a top threat by the World Health Organization in 2017. *A. baumannii* infections readily spread within hospital settings, especially in areas of war and natural disaster. Many isolates are resistant to one or more last-line antibiotics, while a few isolates are resistant to all available treatment options. The objective of this research is to identify and characterize an antibiotic effective against *A. baumannii*. Members of the bacterial group, Pantoea, produce a variety of compounds with antimicrobial activity. To identify an antibiotic effective to treat *A. baumannii*, a collection of over 100 Pantoea isolates was surveyed for antibiotic activity, and an antibiotic-producing strain was identified. The antibiotic biosynthetic genes were identified by creating and sequencing Pantoea mutants no longer producing the antibiotic, indicating that the mutations were in genes necessary for antibiotic production. Once identified, the antibiotic genes were overexpressed to produce the antibiotic in large quantities, which can be isolated from bacterial supernatants and analyzed with spectroscopic methods to determine the chemical structure. A survey of the spectrum of activity showed the antibiotic to be effective against several multi-drug resistant *A. baumannii* isolates and a variety of Gram-negative pathogens, including *Pseudomonas aeruginosa* and several members of Enterobacteriaceae. In an age of antibiotic resistance, the identification of new antibiotics and sources is of critical importance.

#### 69 **Lysophosphatidylcholine Analogues Alter Yeast Nuclear Envelope Architecture and Function** Maria Laura Sosa Ponce\*, Jennifer A. Cobb and Vanina Zarembek - *University of Calgary*

The lysophosphatidylcholine analog edelfosine is an anticancer lipid drug that targets cellular membranes. Therefore, it is alleged that in contrast to other chemotherapeutic agents edelfosine does not impact DNA. Despite this claim, a genetic screen in *Saccharomyces cerevisiae* found that lack of silent information regulator (Sir) proteins, alleviated the toxic effect of edelfosine. Since Sir proteins are key architects and regulators of the genome, we decided to investigate if this unusual connection with edelfosine could be related to a potential effect of the



lysophosphatidylcholine analog on the nuclear envelope (NE) structure and function. Indeed, we found that edelfosine alters NE morphology, leading to an abnormal elongation of the membrane. Since it is known that Sir proteins mediate tethering of subtelomeric chromatin to the NE, we investigated if this was affected by treatment of wild type cells with the drug. Results from chromatin immunoprecipitation of Sir4 showed a significant reduction in the association of the protein with telomeres when cells were treated with edelfosine. Current evidence also supports alterations of telomere clustering in the presence of the lysophosphatidylcholine analogue. Therefore, our results suggest that edelfosine alters NE morphology and function. We speculate that mislocalization of Sir proteins in the nucleus probably results in abnormal silencing of genes that may be implicated in pathways that confer resistance to this lysophosphatidylcholine analog.

**70 Natural rubber and sesquiterpene lactones co-accumulate in laticifer but their promoters show differential expression patterns in lettuce**

Connor L. HODGINS\*, Elysabeth REAVELL-ROY, Moonhyuk KWON, Eun-Joo KWON and Dae-Kyun RO - *University of Calgary*

Lettuce (*Lactuca sativa*) accumulates two distinct terpenoid products, natural rubber (NR) and sesquiterpene lactones (STL), in specialized laticifer cells. Although the biosynthesis of NR and STLs has been partially elucidated, it remains unknown how the transcription of their metabolic genes, which share the precursor isopentenyl diphosphate (IPP), is regulated at the cellular level. To investigate the transcriptional regulation of the biosynthetic NR and STL genes, promoters of cis-Prenyltransferase Binding Protein isoform 2 (LsCBP2) and germacrene A synthase (LsGAS) were isolated from lettuce genomic DNA. Their cellular specific expression patterns were examined in transgenic lettuce plants by expressing beta-glucuronidase (GUS) transcriptionally fused to either the LsCBP2 or LsGAS promoter. Both transgenic lines showed specific GUS-staining patterns along the vasculature. However, fluorescent assays using isolated latex showed the latex from LsCBP2-GUS lines had three-orders of magnitude higher levels of GUS activity than those from LsGAS-GUS. Quantitative PCR data showed exclusive expression of LsCBP2 in latex while LsGAS showed higher expression in whole stem compared to latex. Sectioning of the GUS-stained transgenic lettuce plants demonstrated that the LsCBP2 promoter drives expression in latex, whereas the LsGAS promoter displayed strong expression in the parenchymal cells surrounding the laticifer. These results suggest that transcription of LsGAS and LsCBP occur in different cell-types in lettuce, even though their metabolic products, NR and STL, co-accumulate in laticifers. This metabolic compartmentalization helps to explain how copious amounts of two different terpenoids co-accumulate in a single cell-type and further indicates the presence STL-trafficking from parenchyma cells to laticifer cells.

**71 Biophysical studies on the interaction of polymeric nanoparticles with model lung surfactant** Weiam Daear\* and Elmar J. Prenner - *University of Calgary*

The pulmonary route offers many advantages for drug delivery such as the high surface area of the lungs and the close proximity to the blood circulation. The air-blood barrier of the lungs is around 500 nm thick. In the lungs, the first mode of drug/particle interaction is a monolayer of 90% lipids and 10% proteins known as the lung surfactant (LS). One of the main roles of the LS is to reduce the surface tension experienced in the lungs during breathing cycles in order to prevent lung collapse. From the perspective of pulmonary drug delivery, the LS is the first point of interaction for the drug carriers. With the advancements of nanomedicine, nanoparticles (NPs) became highly relevant as novel drug delivery systems. In particular, there is a great scientific

interest for the use of biodegradable NPs for the pulmonary delivery route. The objective of our work is to develop a biomimetic model of the LS and study the effects upon interaction with NPs. Therefore, we focus on understanding the mechanism of interaction between biodegradable polymeric NPs with the biomimetic model of the LS and test whether the stability and lateral architecture of LS is affected. These measurements are done by using Langmuir monolayers at the air-water interface and imaged using Brewster angle microscopy. This work is significant because it helps understand the mechanism of NP-LS interaction and will provide an in-vitro screening approach to assess nanotoxicology.

## 72 Investigation of an antibiotic effective against the enteric human pathogens

Naveen Sorout\* and John Stavrinides - *University of Regina*

Increasing numbers of antibiotic resistant human pathogens have become a major concern for human health. The Gram-negative members of the Enterobacteriaceae constitute a group of high risk pathogens that have been deemed serious threats by the World Health Organization.

*Cronobacter* and *Enterobacter* are two such pathogens that inhabit hospital settings where they are known to cause a wide variety of infections in both healthy and immunocompromised individuals. The magnitude of risk these pathogens pose combined with their drug resistant nature requires that we identify new antibiotics that can target them.

A survey of over one hundred strains of the bacterial group *Pantoea* identified one strain of *Pantoea agglomerans* that produces at least one natural product having antimicrobial activity against both *Enterobacter* and *Cronobacter*. This project aims to evaluate the spectrum of activity of this natural product, identify the genes that are responsible for its production, and eventually determine its structure. To identify the biosynthetic genes, mutants of the antibiotic-producing strain were created using a transposon. The transposon jumps into the genome, which disrupts genes randomly. Those that lose the ability to produce the antibiotic were considered candidates since it was likely the transposon had jumped into the genes responsible for antibiotic production. Approximately 3000 mutants were evaluated for their ability to produce the antibiotic, yielding 16 candidate mutants. The genes bordering the transposon in the 16 candidates were amplified using inverse PCR, sequenced and identified by comparing them to the available DNA databases. Several of the disrupted genes appear to be clustered in one region of the genome, possibly indicating the position of the antibiotic cluster. The information on the gene cluster will help us to understand how the antibiotic is being produced at a molecular level and will allow us to manipulate the system to produce it at an industrial scale. This study aims to provide an additional antibiotic for use against the multi-drug resistant human pathogens of the Enterobacteriaceae.

## 73 Computational Insights into the Drug Release from Endosome for Lipid Nanoparticles Based on Ionizable Cationic Lipids

Mohsen Ramezanzpour\*, Miranda L. Schmidt, Iulia Bodnariuc, Bashe Y.M. Bashe, Jenifer L. Thewalt and D. Peter Tieleman - *University of Calgary*

Lipid nanoparticles (LNPs) based on ionizable cationic lipids are currently the leading systems for siRNA delivery in liver disease, with a major limitation limited release efficacy in the cytoplasm. An ionizable cationic lipid (e.g. Dlin-Kc2-Dma also known as XTC2) with an apparent pKa of ca. 6.8 is known to be of a critical importance in gene delivery efficiency, especially in the drug release stage. In this study, we investigated both the structure and dynamics of binary lipid mixtures composed of POPC and XTC2 lipids using molecular dynamics simulation, deuterium NMR, and SAXS experiments. Simulations strongly suggested

that the neutral XTC2 lipid is hydrophobic enough to be confined to the POPC bilayer hydrophobic core, a finding which was further supported by the SAXS experiments. Moreover, adding a small amount of XTC2 lipids to POPC bilayers was shown to induce chain order in POPC lipids. These findings might explain why the XTC2 lipids have more limited interactions with the negatively charged lipids of endosome than expected. Lack of enough lipid-lipid interactions might cause delay in the lamellar-to-inverted hexagonal phase transition, a phase transition required for drug release, as the early endosome matures into late endosome stage, resulting in a low release.

**74 Lead Interactions Affect the Fluidity and Lateral Organization of Complex Lipid Membranes** Robyn L. Mundle\* and Elmar J. Prenner - *University of Calgary*

Lead poisoning is an ongoing health issue due to its utilization throughout the 20th century and continued prevalence in consumer goods, soil, and the biosphere. Humans regularly consume lead through contaminated sources of water or lead dust particles. Once the toxic metal reaches circulation, cellular membranes are one of the primary points of contact, particularly red blood cells. The purpose of this study is to investigate the interactions of lead with lipids, the main constituent of membranes, as these effects remain largely unknown. Previous studies observed Pb(II) to adhere to both surfaces of the bilayer and disturb lamellar organization by inducing considerable disorder at the polar regions of external and internal leaflets. Biomimetic model membranes and Langmuir monolayers are used with a defined size, concentration, and lipid composition with varying metal to lipid ratios. Lipid classes were screened as potential targets for lead by comparing head group structures and acyl chain lengths and saturation levels. Under physiological conditions, lead exhibits 93.1% positively charged species: PbCl<sup>+</sup>, PbOH<sup>+</sup>, and Pb<sup>2+</sup>, suggesting localized lead-lipid binding interactions to negatively charged lipid head group regions. In this study we will address some of the largest differences in the binding of Pb amongst lipids of different backbone and head group architectures.

### Session C3: Species Interactions & Dynamics

**75 Consequences of parasitism: Reproduction of a population of male fathead minnows in northern Alberta**

Sangwook (Micky) Ahn\*, Jason Schleppe and Cameron Goater - *University of Lethbridge*

Parasites have the potential to reduce the fitness of their hosts. But the extent to which that potential is realized in natural host populations is rarely assessed. We investigated correlates of breeding success of male fathead minnows (*Pimephales promelas*) in a population in north-central Alberta. Morphological characteristics and parasite burdens were analyzed using GLMs between males that successfully entered the breeding population (breeders) and those that were unable to enter the breeding population (non-breeders). Breeding males that were collected during their defense of a nest harboured fewer numbers of the larvae of 3 different trematode parasites found in the brains, livers, and skin, respectively, compared to non-breeding males. Overall, mean abundance of the 3 larval trematodes were 18-49% lower in breeding males than non-breeding males. The results of our logistic regression analyses indicated that the abundances of two of these trematodes, as well as body condition, were significant in predicting the breeding status of male minnows. Differences in parasite abundances in males could not be explained by differences in host size or by differences in parasite transmission into the two male types. These

results support the idea that exposure to a suite of common larval trematodes influence a male minnows' ability to obtain or defend a nest.

**76 The mycota of soils associated with snake hibernacula**

Jillian D. Perreaux\*, Jasmine R. Scantlebury and Wendy A. Untereiner - *Brandon University*

Areas surrounding the dens and hibernacula of animals are often littered with keratin-rich debris (e.g., feathers, hair, skin) but few studies have examined the diversity and distribution of keratin-degrading fungi in these habitats. Most keratin-degrading fungi belong to the Onygenales (Phylum Ascomycota), an order that includes the most important fungal pathogens of vertebrates. To test the hypothesis that larger numbers and a greater diversity of Onygenales would be found near snake hibernacula, we inventoried the fungi associated with snake dens at the Narcisse Wildlife Management Area. This management area, 130 km north of Winnipeg, MB, is the location of numerous subterranean caverns estimated to house tens of thousands of red-sided garter snakes. Fungi from soils collected at the entrances of dens and non-den sites were isolated using suspension plating and direct plating of fresh and dried soils on a variety of media. Isolates were sub-cultured and identified based on cultural and micro-morphological characteristics. This study yielded over 3,500 fungal isolates. The most abundant fungi were species of *Beauveria*, *Geomyces*, and taxa identified as *acremonium*-like. *Paecilomyces* and *Penicillium* were dominant in non-den soils. Den-specific taxa included members of the ascomycete genera *Arthroderma* and *Chrysosporium* (Onygenaceae). Fresh soils yielded greater numbers of isolates than air-dried soils as well as a higher diversity of Onygenaceae. All isolates of den-specific species tested to date are keratinase positive.

**77 Oviposition site selection by *Aedes aegypti* and *Anopheles gambiae* mosquitoes with respect to water with different organic content**

Ivan Drahun\* - *University of Winnipeg*

*Aedes aegypti* and *Anopheles gambiae* mosquitoes are established vectors of several pathogens - *Ae. aegypti* transmit many arboviruses, whereas, *An. gambiae* are primary vectors of malaria parasites in Africa. *Ae. aegypti* and *An. gambiae* are highly attracted to humans and their domestic environment, making them effective vectors of the pathogens they transmit. Mosquitoes primarily use olfaction to find suitable blood hosts, nectar and oviposition sites. Based on unpublished observation of oviposition bias by *Culex restuans* toward water used by horses for drinking, the oviposition behavior of *Ae. aegypti* and *An. gambiae* mosquitoes was examined using water from horse troughs, hay infusions, and from *Ae. aegypti* and *An. gambiae* laboratory rearing trays. Here, we show that neither *Ae. aegypti* nor *An. gambiae* are attracted to water used by horses for drinking, yet each species has a distinct oviposition bias towards water containing different organic content. While *Ae. aegypti* showed a strong bias towards *Ae. aegypti* rearing water and even stronger bias towards *An. gambiae* rearing water; *An. gambiae* displayed a significant deterrence from *Ae. aegypti* rearing water. We also showed that highly concentrated, hay-infused water not only deterred females from laying eggs but seemed to attract them as a site for defecation. The attractiveness of larval rearing water and repellency of fecally-contaminated water could have potential in a "push/pull" approach to pest control. Understanding odour-mediated orientation behaviour can inform mosquito repellent design to reduce mosquito-human contact rate, or for attractant design to lure mosquitoes into traps for study, and potential control.

**78 Relating stand-level characteristics to ground lichen abundance for estimating availability of boreal caribou forage**

Ruth J. Greuel\*, Jill F. Johnstone and Philip D McLoughlin - *University of Saskatchewan*

Boreal caribou (*Rangifer tarandus caribou*), a threatened species in Canada, rely on the availability of ground-dwelling lichens, principally several *Cladonia spp.* that exist in the boreal forest. Traditionally, forest inventory data-gathering protocols do not account in detail for cryptic vegetation, such as lichens; focusing instead on easily-detected vascular plant species. The challenge, as it relates to caribou critical habitat determination, is to otherwise determine the availability of forage lichens. Boosted regression trees (BRTs) have become a useful tool for ecologists in the past decade. Boosted regression trees are a type of machine learning in which a series of simple decision stumps are built, each following from the residuals of the previous one. This method is particularly suitable when the system in question is very complex (as in much of ecology), as it searches out patterns without building from *a priori* hypotheses, and allows for interactions. I used forest variables and lichen abundance data collected from 312 sites across northern Saskatchewan to determine the drivers of lichen abundance and typical characteristics of forest stands that support high quantities of lichen. Stand age, density of trees, dominant tree species and geographic location are among the best predictors of lichen abundance, with stand age being the most important factor. Stands with moderate tree density, areas far north, and stands older than 50 years had the highest lichen abundance. Areas dominated by jack pine were modelled separately as they showed rapid lichen regeneration after fire.

**79 Overstory tree composition drives the ecological strategies of understory plant communities**

Tanvir Ahmed Shovon\*, Fidji Gendron, Mary Vetter, Danaë Rozendaal and Mark Vanderwel - *University of Regina*

Ecological strategies for resource use determine how individual species persist within a local community. Plant species are generally considered to have either resource acquisitive and conservation strategies, as reflected by suites of functional traits. Plant communities in resource poor and resource rich environments are dominated by species with conservative traits and acquisitive traits, respectively. Most studies examine ecological strategies along a single resource gradient, but complex dynamics may emerge when multiple resources are considered. How multiple resources affect the ecological strategies of understory vegetation in boreal forest is poorly understood. This study focuses the role of light and water availability on the ecological strategies of understory vegetation in cypress hills forest, an outlier of boreal forest ecosystem. Here we show the ecological strategies of understory vegetation is mainly driven by overstory vegetation. With the increase of conifers, understory vegetation becomes more dominated by resource conservative species. Light and water do affect the ecological strategies of understory species under trembling aspen canopy- fast growing species dominate the resource rich areas and slow growing species dominate resource poor areas. However, these two limiting resources have no impact on the ecological strategies of the understory communities in conifer stands. Conifer tree litter reportedly decrease soil nutrient availability and pH, thus creates poor resource condition which allows species mainly with resource conservative strategies to dominate. Climate change driven drought are increasing the tree mortality rate of trembling aspen in North America, which can in turn affect the understory plant communities with resource acquisitive strategies.



**80 Differentiating species of fleas found on sciurid rodents in Southern Saskatchewan**

Jessica Thoroughgood\* and Neil Chilton - *University of Saskatchewan*

Fleas are vectors of a multitude of bacterial pathogens that are transmitted to vertebrate hosts. However, little is known about fleas and their associated bacteria in Saskatchewan. Some flea species, (e.g. *Oropsylla rupestris*) are known vectors of *Yersinia pestis*, the causative agent of plague; however, not all species are capable of transmitting this bacterium. Traditionally, fleas are identified based on morphological characteristics including genitalia shape and structure, distribution and/or presence of setae, spines and ctenidia. This is achieved through microscopic examination after chemically clearing the internal structures of individual fleas. Clearing the internal structures prevents DNA studies of the fleas and their associated bacteria. In this study, fleas parasitizing sciurid rodents (Richardson's ground squirrels [*Uroditellus richardsonii*], thirteen-lined ground squirrels [*Ictidomys tridecemlineatus*], and black-tailed prairie dogs [*Cynomys ludovicianus*]) from Southern Saskatchewan were identified using PCR-based techniques including DNA-sequencing and single stranded conformation polymorphism (SSCP) analysis on the nuclear 28S rRNA gene. These molecular techniques allowed us to detect sequence variations between different flea specimens. Once fleas are identified they can be screened for four genera of bacteria (*Bartonella*, *Francisella*, *Rickettsia*, and *Wolbachia*) using similar PCR-based techniques. This study will provide insight into the diversity of fleas parasitizing sciurid rodents and associated bacteria in Southern Saskatchewan.

**81 Aggregation of trematode-infected zombie ants on flowers**

Sarah Unrau\* and Cameron Goater - *University of Lethbridge*

Larvae of the trematode *Dicrocoelium dendriticum* are iconic host manipulators. These parasites invade their ant hosts' brain, altering their normal behaviour and causing them to attach with their mandibles to flowers during the cool hours of the day. We observe thousands of ants infected with *D. dendriticum* larvae attached to flowers in Cypress Hills Park in Southern Alberta. In this region, attachment facilitates the transmission of larvae into grazing elk, deer, and beef cattle. Results from our field surveys indicate that individual ants are highly aggregated on available flowers. Thus, whereas many available flowers have no attached ants, and some have a single ant, more than 50% have between 2-35 ants attached to individual petals. To test potential mechanisms leading to observed patterns of ant aggregation on flowers, we designed laboratory choice experiments involving infected ants and cut flowers. In an initial experiment, infected ants were offered a choice of a flower with an infected ant attached to it, and a control flower. More than 90% of individuals chose the flower with the infected ant. In a follow-up experiment, ants were offered the same choice, but the attached ant had been removed. Infected ants chose more often the flower that had contained an infected ant. These results indicate that infected ants may communicate their infection status to other infected ants, potentially through the use of pheromone trails.



**1 Blue LED irradiation of breast cancer cell line MDA-MB-231: Induction of apoptosis through ROS mediated signalling pathway**

Khadija Abdullahi\* and Deborah Hemmerling - *Concordia University of Edmonton*

Breast cancer is one of the most common cancers and is responsible for millions of deaths globally every year. Triple negative breast cancers are very difficult to treat because of their lack of estrogen, progesterone and human epidermal growth factor receptors. As such, these cancers are unresponsive to conventional hormonal therapies and are most commonly treated by means of neo-adjuvant and adjuvant chemotherapy. Previous studies show that blue LED's, due to a spectrum of wavelengths, possess anti-microbial, anti-inflammatory, apoptotic and anti-proliferative properties. Due to these properties, they have been used in treating acne and neonatal jaundice. In this experiment, we aim to study the effects of different wavelengths and exposure times of Blue LED on cancer cells, mainly to examine if an apoptotic process is indicated as well as understand phototherapy mechanisms in treatment of triple negative breast cancers. In this study, we irradiate MDA-MB-231 cells with Blue LED at wavelengths of 400nm, 450nm and 480nm at durations of 1hr, 3hr, 6hr and 24hr in order to induce apoptosis. The cells are irradiated and then exposed to alamarBlue viability reagent. Metabolic activity is visualized by alamarBlue viability reagent and is measured by absorbance spectrophotometry.

**2 Sarcomere assembly and maintenance in the zebrafish muscle mutant, herzs Schlag**

Casey Carlisle\*, Kendal Prill and David Pilgrim - *University of Alberta*

The precise organization and alignment of muscle proteins into its smallest functional unit, the sarcomere, is essential for muscle function. In skeletal muscle, failures in this process can lead to a variety of incurable muscle diseases (myopathies), many of which are fatal. A limiting factor in developing cures for myopathies lies in our lack of understanding of how the sarcomere assembles normally. Zebrafish make an appropriate model system to study muscle development due to their ability to survive with myopathies that are fatal in other organisms, and many zebrafish with defects in this process are available for study. One such mutant, herzs Schlag, shows disorganized muscle myosin due to a mutation in the protein Titin a. However, the early stages of muscle assembly appear normal, and we propose that the disorganized myosin may be a consequence of contraction induced damage. We hypothesize that the Titin a mutation interrupts a sarcomere bracing function of titin. Supporting this hypothesis, chemically paralyzed herzs Schlag mutants devoid of skeletal muscle contractions show reduced sarcomere damage. Furthermore, we propose that the herzs Schlag mutation exacerbates muscle atrophy, primarily in slow twitch muscle, which is supported by transmission electron microscopy and preliminary western blot data. By screening through various protein quality control factors, we aim to uncover the mechanism controlling this selective protein turnover and highlight potential targets for myopathy therapies.

**3 Cylindrospermopsin Adversely Impacts Zebrafish (*Danio rerio*) Development**

Adriana C N Moraes \*, Soham Shah, Valéria F Magalhães and Hamid R Habibi - *Instituto de Biofísica Carlos Chagas Filho*

Cyanobacteria are known to produce a variety of toxic compounds known as cyanotoxins which threaten both human and environmental health by contaminating drinking water and

aquatic ecosystems. Growing evidence indicates cyanotoxins act as developmental toxins, inhibiting or impairing several pathways of vertebrate development. Among them, cylindrospermopsin (CYN) is a 415 Da alkaloid produced by a range of cyanobacteria. Due to the widespread presence of cyanobacteria around the world, CYN is found in numerous locations and elevated CYN concentrations have been reported in algal blooms from very low concentrations to 8000 µg/L. Previous studies have described CYN as a protein synthesis inhibitor and capable of damaging several organs in mammals. However, little is known about its toxicity in aquatic vertebrates. This study aims to characterize the adverse developmental effects of CYN using zebrafish (*Danio rerio*) larvae as a model organism. A wide range of CYN concentrations (0 - 2000 µg/L) were assessed using a morphometric approach for various growth (condition factor, eye volume) and developmental abnormalities (yolk and pericardial edemas, hemorrhaging, spinal malformations, touch reflex, and swim bladder malformation), alongside survival and hatching. The results demonstrate that CYN exposure causes changes in development such as decreased growth and, increased developmental abnormalities in zebrafish larvae with threshold of 100 µg/L. These results provide novel evidence in a vertebrate model organism that exposure to CYN results in multiple adverse actions and adversely affects the development of zebrafish.

#### **4 Inhibition of cortisol-mediated rapid glucocorticoid receptor translocation triggered by membrane modifications in trout hepatocytes**

Chinmayee Das and Mathilakth Vijayan - *Univeristy of Calgary*

Cortisol rapidly activates cell signalling in trout hepatocytes; however, the mechanisms are far from clear. In our present study we tested the hypothesis that rapid intracellular glucocorticoid receptor (GR) translocation is inhibited by membrane alterations and this inhibition may be dependent on changes to intracellular calcium levels in trout hepatocytes. GR distribution in hepatocytes was confirmed by immunofluorescence labeling with antibody specific to trout GR. There was a rapid translocation of GR to the cell periphery within minutes after cortisol addition, and this GR translocation was dependent on extracellular calcium. However, this rapid GR translocation in response to cortisol was hindered by changes in membrane properties. We also showed that membrane modifications affect intracellular calcium levels using ratiometric imaging. Overall, changes in intracellular calcium levels due to membrane alterations may be linked to the inhibition of GR translocation, leading to the proposal that cortisol-mediated membrane alterations may play a role in the GR dynamics in trout hepatocytes. Acknowledgements: This study was supported by the Natural Sciences and Engineering Research Council of Canada Discovery Grant to MMV.

#### **5 Cathepsin B cysteine protease of *L. donovani*: role in the modulation of parasitic exosomal proteins**

Camila dos Santos Meira\* and Lashitew Gedamu - *University of Calgary*

*Leishmania donovani* is an intracellular parasite that causes visceral leishmaniasis, a chronic disease with no effective treatment. Cathepsin B cysteine protease (CatB) is a *Leishmania* virulence factor and its disruption induces proteome remodeling in *L. donovani*, affecting proteins secreted into exosomes, vesicles involved in intercellular communication. Our hypothesis is that CatB-modulated exosomal proteins might be associated with *L. donovani* pathogenesis. Thus, we aimed to assess the proteomic profile of *L. donovani* exosomes using wild type (WT), CatB knockout (KO) and episomally complemented CatB knockout (CM)

parasites. We have observed previously described morphological features of exosomes by transmission electron microscopy and nanotracking system. Using LC-MS/MS, we identified a total of 787 proteins, 51% of which were shared among WT, KO and CM exosomes. We also observed Elongation Factor (EF)-1 $\alpha$ , heat shock and antioxidant components of *Leishmania* among the most abundant proteins in each group. We have further validated by immunoblotting the exosome-based secretion of Peroxidoxin (Pxn)-4, CatB and EF-1 $\alpha$ . Our preliminary analyses indicate that *L. donovani* WT, KO and CM parasites produce and release bona fide exosomes. We observed that the expression of Pxn4 and EF-1 $\alpha$  were downregulated in KO exosomes, which is consistent with the decreased expression of these proteins in *L. donovani* KO parasites. Overall, these findings suggest that CatB modulates the expression of exosomal proteins that are associated with *L. donovani* pathogenesis. Understanding the effect of CatB on exosomal proteins will assist in the development of new approaches for the treatment of leishmaniasis.

## 6 Toxicity of sediment-bound diluted bitumen to *Hyaella Azteca*

Sean L. Everitt\*, Steve B. Wiseman and Greg G. Pyle - *University of Lethbridge*

The Alberta oil sands contain greater than 165 billion barrels of bitumen, a heavy form of crude oil that makes up the majority of Canadian crude oil production. Proposed pipelines stemming from Alberta will increase the volume of bitumen being transported in close proximity to freshwater ecosystems. Compared to conventional oil, bitumen has a much greater viscosity and density, and therefore it must be diluted with natural gas condensates, forming a mixture known as diluted bitumen or 'dilbit', so that it can be transported through pipelines. Because dilbit differs chemically and physically from conventional crude oils, its toxicity and behaviour in aquatic systems is likely to be different from conventional oils. When dilbit is spilled into an aquatic environment, the diluents will evaporate rapidly and what is left behind will combine with sediment in the water and sink. To date, toxicity of sediment-bound dilbit has not been characterized. Ongoing research is addressing this knowledge gap by characterizing effects of exposure to sediment-bound dilbit on the health of freshwater amphipods (*Hyaella azteca*). Results from this research will provide insight to how dilbit affects aquatic organisms physiologically and behaviourally, while comparing the toxicity to that of conventional oils. Ultimately, this research is an important step towards developing spill-management guidelines that can be implemented in future spills.

## 7 The glucocorticoid receptor knockout affects growth and metabolism in zebrafish

Erin Faught and Matt Vijayan - *University of Calgary*

Cortisol, the primary glucocorticoid in teleost fishes, signals primarily through the glucocorticoid (GR) and mineralocorticoid (MR) receptors. Previous work has established that cortisol-GR signalling is important not only in the vertebrate stress response, but for programming proper development and growth trajectories. While it is known that cortisol has a negative impact on growth, the extent to which cortisol-GR signalling plays a role in growth programming is unclear. We tested the hypothesis that elevated cortisol content decreases growth, and this involves GR-mediated energy partitioning. Using CRISPR/Cas9, we first generated homozygous GR knockout [GR -/-] zebrafish which were viable and phenotypically indistinguishable from wild type [GR +/+]. Physiologically, [GR -/-] had high cortisol levels and they were unable to elicit a cortisol response to stress. By 15 days post-fertilization (dpf) there was no difference in body mass between the [GR -/-] and [GR +/+], while excess cortisol stimulation of the wild type zebrafish led to a reduced body mass.

These results clearly establish that the early growth reduction due to cortisol stimulation requires a functional GR. GR knockout led to higher body mass in juveniles and adults at 3 and 9 months, respectively, and this corresponded with altered body mass index and proximal composition. However, despite the higher body mass, adult [GR -/-] ate significantly less food compared to the [GR +/+], suggesting differences in nutrient energy homeostasis. Overall, our results indicate for the first time that cortisol-GR signalling is key regulator of developmental growth in zebrafish, and this may involve increased energy substrate repartitioning.

## **8 ATM Is Required for the Prolactin-Induced HSP90-Mediated Increase in Cellular Viability and Clonogenic Growth After DNA Damage**

Odul Karayazi Atici\* - *University of Calgary*

Prolactin (PRL) acts as survival factor for breast cancer cells, but the PRL signalling pathway and the mechanism are unknown. We previously identified that heat shock protein 90 $\alpha$  (HSP90 $\alpha$ ) is a prolactin-Janus kinase-2 (JAK2)-signal transducer and activator of transcription-5 (STAT5) regulated gene in breast cancer cells and HSP90 has a role in PRL-induced viability in response to DNA damage. The ataxia-telangiectasia mutated (ATM) protein plays a critical role in the cellular response to double-strand DNA damage. Here we showed that PRL increased the viability of breast cancer cells to DNA damaging chemotherapeutics. Two different HSP90 inhibitors, 17AAG and BIIB021, abrogated the effect of PRL, indicating the mechanism of enhanced viability involves the master cancer chaperone HSP90. The inhibitors also led to a decrease in JAK2, ATM and phospho-ATM protein levels. Inhibition of JAK2 and ATM, with specific inhibitors (G6 and KU55933, respectively), abrogated PRL-enhanced viability, suggesting the involvement of each, as well as the crosstalk of ATM with the PRL pathway in the context of DNA damage. Drug synergism was detected between the ATM inhibitor (KU55933) and doxorubicin and between the HSP90 inhibitor (BIIB021) and doxorubicin. Short interfering RNA directed against ATM prevented the PRL-mediated increase in cell survival in both two- and three-dimensional collagen gel cultures, and in clonogenic cell survival, after doxorubicin treatment. Our results indicate that ATM contributes to the PRL-JAK2-STAT5-HSP90 pathway in mediating cellular resistance to DNA-damaging agents.

## **9 Long-term biomonitoring of macroinvertebrate metrics in the Kananaskis River, Alberta**

Tobin Benedict, Silvia Losada\*, Adam Mitton\* and Mary Reid - *University of Calgary*

Biodiversity monitoring is a tool that has been used to assess the environmental impacts of both human activities and natural events. Macroinvertebrate metrics have been well established as effective bioindicators of water quality. Long-term studies provide a robust understanding of the natural fluctuations in ecosystem processes that take place over time. Macroinvertebrate biodiversity data has been collected in Kananaskis river annually over a span of 17 years by University of Calgary students. Over this time frame there has been two major flooding events in the Kananaskis River. The macroinvertebrates orders of interest are Ephemeroptera, Plecoptera, and Trichoptera, which make up the EPT community. These invertebrates are often used together as a bioindicator community, as they are sensitive to pollutants. Thus, this study aims to examine the effects of the flooding events on macroinvertebrate metrics as a measure of water quality. Community diversity and abundance of EPT organisms will be measured in order to observe their response to a variety

of physical and chemical parameters, which are expected to be altered by the flooding events. We expect to discover significant differences in macroinvertebrate metrics, particularly diversity and abundance, in the years before and after the flooding events.

**10 Environmental enrichment of Coho salmon (*Oncorhynchus kisutch*) fry reduces boldness in hatchery reared fish**

Kiana Matwichuk\* - *University of Victoria*

Habitat enrichment can potentially impact the behaviour caused by the domestication of fishes reared in hatchery environments. Salmon reared in tanks with no environmental enrichment appear to have a reduced survival rate and are generally maladapted to the wild post-release, which reduces the effectiveness of conservation programs. This study compares the foraging behaviour of Coho salmon fry (*Oncorhynchus kisutch*) reared in traditional hatchery environments, to those reared in enriched tanks with added environmental complexity. Coho from Nitinat Hatchery, British Columbia were recorded using high speed camera and digitized with ImageJ to record time to peak gape (TTPG), attack velocity, and attack range as proxies for boldness of five individuals from each rearing condition. No differences were found between the TTPG or attack velocity of the rearing conditions, but the attack range was greater in traditionally reared Coho when compared to the enriched group. The difference in attack ranges suggests greater boldness in Coho raised with no environmental enrichment. Fish with increased boldness may readily expose themselves to predators, which may decrease survival rates of hatchery salmon and ultimately have an impact on hatchery return rates.

**11 Blue shark morphology: youth are unstable, adults rocket but don't roll**

Theresa M. McCaffrey\*, Natalie K. Tsao, Scott G. Seamone and Douglas A. Syme - *University of Calgary*

Many adult sharks are apex predators that cruise at high speeds while searching for prey, whereby the tendency to roll and pitch are less desirable. Adult sharks would thus benefit from high static stability in the form of relatively short fins and large moments of inertia when required to turn. Conversely, when smaller, juveniles face higher risks of predation and likely require enhanced maneuverability, and would thus benefit from high dynamic stability in the form of relatively long fins and small turning inertia compared to their larger counterparts. As such, we hypothesize that sharks grow in a geometrically similar fashion (isometry), like magnifying an image, such that fins get smaller and moment of inertia larger relative to mass as they grow. Dorsal and lateral images of blue sharks (*Prionace glauca*) of various masses (26.3-144.8 kg) were analyzed for changes in area and span of the dorsal, caudal and pectoral fins, and moment of inertia of the body for roll, yaw and pitch. Pectoral fin span and area scaled with a slope less than 1 relative to body mass, while moments of inertia scaled with a slope greater than 1, which suggest that as mass increases, pectoral fins are relatively smaller and moments of inertia are larger. This indicates that larger bodied sharks are more statically stable promoting economical, high speed cruising in pursuit of prey, while smaller sharks are more dynamically stable, promoting maneuverability for defense against predation.



**12 Biochemical characterization of *O*-methyltransferases involved in BIA biosynthesis in Sacred Lotus**

Ivette M Menéndez Perdomo\* and Peter J Facchini - *University of Calgary*

The opioid analgesics morphine and codeine are recognized as “essential medicines” by the World Health Organization. These highly demanded pharmaceuticals belong to a class of plant metabolites known as benzyloquinoline alkaloids (BIAs) and are exclusively obtained by opium poppy farming. Attempts to BIAs engineered biosynthesis are hampered by the presence of chiral centers that leads to the formation of racemic mixtures (R and S conformers), whereas the available enzymes only process the S conformers into the desired products. The discovery of novel enzymes capable of processing the R conformers will overcome current industry challenges for their large-scale production. In this regard, the aquatic plant sacred lotus (*Nelumbo nucifera*) presents a significant number of R BIAs and therefore, it constitutes a reservoir of enzymes specific for these R conformers. The goal of this research is the biochemical characterization of sacred lotus *O*-methyltransferases, crucial enzymes on BIAs common biosynthetic pathway. Through a combination of phylogenetic analysis, gene amplification and cloning, protein heterologous expression and purification, and in vitro enzymatic assays, two catalytically active *O*-methyltransferases (OMT1 and OMT5) were detected in *N. nucifera*. Preliminary substrate range experiments suggest that OMT1 is capable to accept the R conformers and the enzyme kinetics is currently under investigation. Future perspectives are to validate the physiological role of the identified enzymes through functional genomics approaches. The improvement of current bioengineered platforms will be highly significant to Canada, which stands the second-highest level of prescription opioid analgesics use worldwide.

**13 Understanding the pore-forming mechanism of peptides derived from the *N*-terminus of sticholysin**

Haydee Mesa-Galloso\*, Uris Ros, Pedro A. Valiente and D. Peter Tieleman - *University of Calgary*

Actinoporins are pore-forming toxins found in sea anemones that bind and oligomerize in membranes, leading to cell swelling, impairment of ionic gradients and, eventually, to cell death. These proteins when encapsulated into liposomes as an adjuvant, can induce a robust and specific CTL immune response. Therefore, they can be used in the design of vaccines capable of forming pores and cross plasma and endosomal membranes to enhance immune response in anti-cancer treatments. Sticholysin I and II (StI and StII) are actinoporins produced by the Caribbean sea anemone *Stichodactyla helianthus*. Despite their high sequence identity (93%), these actinoporins exhibit differences in hemolytic activity that could be related to those found in their N-termini. StII1-30 and StI1-31 are peptides spanning the first thirty (StII) or thirty-one (StI) N-terminal amino acid residues of StII and StI respectively. Experimental evidence obtained by fluorescence and permeability assays suggest that StII1-30 is more active than StI1-31 in cells. However, the molecular determinants that explain this difference in functional activity are still unknown. Here, we used molecular dynamics (MD) simulations to characterize the mechanism of pore formation by StII1-30 and the effect of membrane curvature on its permeabilizing activity. The effect of StII1-30 aggregation and binding to membranes was compared with its StI1-31 counterpart. Our data shows that, the higher hydrophobicity of StII1-30 facilitates not only its partition into the membrane hydrophobic core but also peptide oligomerization. Our results show an integrated picture of cell membrane pore formation by these StII and StI derived peptides.



**14      The role of Clusterin and its putative Plexina4 receptor in the developing zebrafish brain**

Zachary Nurcombe\*, Carrie Hehr and Sarah McFarlane - *University of Calgary*

Two proteins have been found to be associated with Alzheimer's disease; Plexina4, a transmembrane protein involved in development and axon guidance of the central nervous system (CNS), and; Clusterin, a secreted heat-shock protein with many biological roles, including as a regulator of apoptosis. In Alzheimer's disease, Plexina4 is downregulated, while Clusterin exhibits increased expression. A recent study showed that Plexina4 is a receptor for Clusterin in the adult nervous system, and that this interaction may promote neuronal survival. This study uses zebrafish embryos to determine if Clusterin and Plexina4 interact to promote neuronal survival in the developing CNS. We found by using RNA in situ hybridization that clusterin is expressed in the floorplate of the hindbrain by 36 hours post-fertilization, with plexina4 expressed in bilateral cell clusters on either side of this expression domain. These data support the idea that Clusterin acts as a ligand for Plexina4 in the embryonic zebrafish hindbrain. In zebrafish, we are manipulating Clusterin and/or Plexina4 function by injections of antisense morpholino oligonucleotides to mediate protein knock-down or mRNA for gain-of-function, as well as with genetic loss of plexina4. We are assaying neuronal survival in brain development, with a particular focus on ventral hindbrain. If the interaction between Clusterin and Plexina4 promotes neuronal survival in the developmental context, the results could shed light on the role of Clusterin and Plexina4 in Alzheimer's disease.

**15      Microbial Ecology of the Subsurface Athabasca Oil Sands**

Christina Ridley\* - *University of Calgary*

Little is known about the microbial ecology of the subsurface Athabasca oil sands in Northern Alberta, Canada. Progressive biodegradation of low molecular weight hydrocarbons by indigenous subsurface microbes has enriched the concentration of high molecular weight hydrocarbons, cumulatively known as bitumen. Furthermore, this environment is characterized by low microbial biomass due to limited nutrient availability and restricted access to water. Recent advances in DNA isolation protocols and increasingly sensitive sequencing methods have allowed for an in-depth investigation into the microbial ecology of this unique subsurface environmental niche. The microbial community composition was studied using core samples (n=62) that were retrieved from 2 sites within the Athabasca oil sands at depths between 220 and 320 meters below the surface. The majority of the microbial communities were dominated by aerobic taxa, such as *Pseudomonas* and *Acinetobacter*; however, a large proportion of anaerobic taxa, including *Methanoculleus*, *Desulfomicrobium* and *Thauera*, were observed in one core sample. Although the in-situ temperature of the bitumen-containing subsurface is low (8-10°C), high fractions of the potentially thermophilic taxon, *Thermus*, was observed in two core samples. These studies provide insight into the indigenous microbial ecology of the subsurface oil sands environment.

**16      Adverse Health Impacts of Sulfolane Exposure on Zebrafish (*Danio rerio*) Development**

Soham Shah\*, Gopal Achari and Hamid R. Habibi - *University of Calgary*

Sulfolane, a polar, aprotic solvent initially developed to increase refining efficiency in the oil and gas industry, has now spread to multiple applications / industries. With increased global

utilization and with over 150 sulfolane production sites worldwide, some operating under no environmental regulations, sulfolane has been introduced into the environment through problems with storage, leaks, spills, and leeching from disposal sites. Sulfolane has been detected by chemical analysis in groundwater and creeks around the world including Alberta, Canada (800mgL<sup>-1</sup>) and Louisiana, USA (2900mgL<sup>-1</sup>). Previous research on terrestrial vertebrates has demonstrated some health impacts following sulfolane exposure, however, relatively limited information is available on the adverse impacts of sulfolane on aquatic organisms. This study focuses on the effect of sulfolane exposure on early development of zebrafish larvae as model organisms, using a morphometric, behavioral and molecular approach. A wide range of doses (0 - 5000 mgL<sup>-1</sup>) were tested and various growth, morphometric and behavioral parameters were quantified. Negative impact trends for growth and morphometric abnormalities were observed in doses higher than 800 mgL<sup>-1</sup> and significant differences from control were observed in doses higher than 3000 mgL<sup>-1</sup> of sulfolane. Using the behavioral approach, changes in activity levels were observed in doses higher than 200 mgL<sup>-1</sup> and utilizing the molecular approach showed changes in transcript abundances of certain genes in doses higher than 1 mgL<sup>-1</sup>. These results provide novel information on adverse effects of sulfolane in aquatic vertebrate species and provide a framework for better understanding of health risks associated with environmental levels of sulfolane in fish and other vertebrates.

**17      How has hurricane disturbance affected bat communities on the Caribbean island of Dominica?**

Lisa Sims\* - *University of Calgary*

Understanding species' responses to hurricane disturbance can help us predict future impacts and aid in conservation actions which will become progressively more important with climate change. On 17 September 2017 Hurricane Maria, a category 5 storm, made landfall on the small island of Dominica causing substantial damage to the vegetation. This presents a unique opportunity to assess the hurricane's impact on bat community structure and composition in the Caribbean. My study will measure changes in diversity, relative abundance, reproductive rate, body condition, and habitat use using pre-hurricane data I collected during mist netting surveys in 2016 and 2017, and post-hurricane data (to be collected in 2018). I will conduct mist netting surveys post-hurricane in pre-hurricane plot locations following the same survey protocols. I caught nine species of bats (756 individuals) comprising four families across 33 sites in the two years prior to the hurricane, with reproductive individuals documented for all species. My study is on-going and further results will be presented once post-hurricane data have been collected.

**18      Characterization of a novel limb-specific enhancer of the human SHOX gene**

Isabella Skuplik\* - *University of Calgary*

Limb abnormalities caused by disruption of the human short-stature homeobox (SHOX) gene and its surrounding regions are quite common, affecting up to 1:1000 individuals. Deficiencies in SHOX gene function cause shortening of the middle limb segment (zeugopod), and are associated with several short-stature syndromes including Léri-Weill dyschondrosteosis (LWD) and Langer syndrome. Importantly, more than one-third of patients with LWD do not have mutations within the SHOX gene, but have deletions that remove non-coding sequences far downstream of the gene. These deletions are thought to remove an enhancer element(s) required to activate SHOX limb expression. Our lab recently

identified a limb enhancer within the SHOX downstream region that drove the expression of a lacZ reporter gene in the zeugopod of transgenic mice. We hypothesize that this enhancer likely functions as the main regulatory input required to activate SHOX limb expression. Using a combination of luciferase assays in mouse limb primary cells and transgenic mice to screen fragments for enhancer activity, we are further narrowing down the core enhancer sequence and identifying the transcription factors that bind within this region to regulate SHOX expression. Preliminary data suggests that most of the enhancer activity is located within a 563bp region, with inputs from adjacent sequences to create a zeugopod-specific domain of SHOX expression. This research will ultimately contribute to a greater understanding of enhancer regulation within the context of human disease and may assist in the screening of LWD patients without SHOX coding mutations.

## **19 Characterization of manganese interaction with lipid membranes**

Kevin Sule\* and Elmar J Prenner - *University of Calgary*

Understanding the mechanisms of metal toxicity is important, as it is an ongoing global public health concern. Despite its essentiality, long-term overexposure of the trace metal manganese (Mn) can result in a permanent neurological disorder that shares similar symptoms with Parkinson's Disease (PD), known as Manganism. Its interactions with lipid membranes are an important area to consider since the first point of contact of this metal is with the cellular membrane in living cells. The focus of this work is to investigate the interactions of Manganese (Mn<sup>2+</sup>) with lipid model systems. Biophysical techniques, such as fluorescence spectroscopy and Dynamic light scattering, were used to characterize the interactions of manganese with lipid model systems. For fluorescence spectroscopy, the dye laurdan was used, which display shifts in its emission spectrum depending on the phase properties of the lipid membrane. These shifts are quantified by calculating for Generalized polarization (Gp), and plotted as a function of temperature, to obtain a Gp curve and assess metal-induced changes in membrane fluidity. Additionally, Dynamic light scattering was used to assess any metal-induced size changes. Phospholipids containing a net negative charge on its headgroup showed strong interactions with Mn and are the preferred targets. This work provides good insight into the interaction of Mn with lipid model system since effects on the membrane can have consequences for the cell.

## **20 Effect of Wildfires on Mobilization of Heavy Metals in Alberta's Peatland Boreal Forest**

Ryleigh-Raye Wolfe\* - *Concordia University of Edmonton*

Numerous studies in Europe and the US have found increased metal concentrations in soils after forest fires, however further research in Canada's peatland ecosystem is required. There is significance in studying the movement of these harmful substances in peatlands because they are an important pathway to aquatic ecosystems. Highly mobile dissolved toxic compounds within ash and soil can be transported to nearby water sources through erosion and storm run-off. This can directly affect water quality, threatening the health of humans and other organisms. We conducted a field study near Fort McMurray, Alberta that represents a snapshot of pre- and post-fire metal movement between vegetation and the soil. Two sampling fields were selected based on the following controls: common vegetation, soil type, uniform topography, and similar microclimate condition; thus allowing for an accurate representation of metal mobilization in a forested peatland before and after the 2016 Horse River Fire. From each the burned and unburned peatland, 25 soil samples from the surface and 25 soil samples from the 10 cm subsurface were collected. The soil samples were air

dried and stored. Metal analysis is currently underway; concentration of dissolved heavy metals (Cd, Cu, Fe, Mn, Pb) in each soil sample are being measured using Atomic Absorption Spectroscopy. Statistical analyses will be conducted for testing the difference in heavy metal content between the burned and unburned peatlands.

## Poster session # 2

- 21 Functional characterization of the Pumilio gene *puf4+* in *Schizosaccharomyces pombe***  
Ahmed Abdelaziz\*, Darren Henry and Gordon Chua -*University of Calgary*

The Puf family of RNA-binding proteins consists of highly-conserved posttranscriptional regulators present throughout eukaryotes. Puf proteins recognize their target mRNAs through a conserved Pumilio homology domain (Pum-HD) at the 3'-untranslated region usually at a site containing a 5'-UGUA-3' core sequence. The consequence of Puf binding can result in posttranscriptional regulation of target mRNAs through stability, translational initiation or intracellular localization. In the fission yeast *Schizosaccharomyces pombe*, there are seven nonessential genes that encode for classical Puf proteins. The biological function and mRNA targets of these *puf+* genes have not been elucidated. The single deletion of almost all these genes does not exhibit an obvious cell phenotype in rich media while their systematic overexpression results in the majority displaying an aberrant phenotype. Here, we focus on the functional analysis of the previously-uncharacterized *puf4+* gene in *S. pombe*. Deletion of the *puf4+* gene revealed slightly shorter cells compared with the wild type while overexpression of the *puf4+* gene caused cell elongation indicating a cell cycle defect, and a subset of cells exhibiting an irregular shape. Loss of *puf4+* resulted in hypersensitivity to hydroxyurea suggesting a potential role in DNA replication. We have identified putative mRNA targets potentially degraded by Puf4 using transcriptome profiling of *puf4* deletion and overexpression strains and RNA-immunoprecipitation protein-microarray (RIP-Chip) analysis of an endogenous TAP-tagged *puf4* strain. By integration of the functional genomic data with drug-sensitivity assays and bioinformatics, we were able to predict four potential mRNA targets of Puf4. We are currently carrying out several experiments to validate these putative target mRNAs of Puf4.

- 22 Effect of Ataluren on MYO7A nonsense mutation responsible for Usher syndrome**  
Juwayriya Abdullahi\* and Mariola Janowicz - *Concordia University of Edmonton*

In-frame nonsense mutation is responsible for a majority of genetic diseases present today. Premature termination codon (PTC), also known as nonsense mutation causes an abrupt stop by introducing the presence of one of three stop codons UAG, UAA, and UGA. This is caused by changing a single point alteration in the DNA to the messenger RNA transcript. These stop codons cause a premature and abrupt termination of translation. The earlier the mutation occurs in the gene, the more truncated the protein becomes. This leads to defective function of the protein as well as multiple disabilities. Nonsense mutations present in MYO7A are responsible for Usher syndrome type I, the most severe version of Usher syndrome. It is categorized by sensorineural hearing loss and retinitis pigmentosa. Certain aminoglycosides and pharmaceutical drugs such as Ataluren, can induce the functionality and addition of an amino acid, thus continuing translation and producing a complete and functional protein by having the ribosomes read through a premature stop codon in mRNA. In

this experiment, we will compare for the first time the relative efficacies of the oxadiazole Ataluren in restoring the nonsense mutation in the USH1B gene, which encodes the protein myosin VIIA. We will be treating primary Usher fibroblast cell lines with Ataluren. The results will be analyzed using immunofluorescence microscopy to localize our protein and allow us to observe the expression of potentially restored truncated proteins using fluorescent dyes.

## **23 Bats Fatalities and Wind Turbines**

John Alho\* - *University of Calgary*

Wind power is an important part of the energy transition away from fossil fuels. Unfortunately, many bats are killed each year due to collisions with wind turbines. It is unclear as to why bats collide with wind turbines, although there is some evidence that bats may be attracted to wind turbines. This project explores one possible contribution to why bats are colliding with wind turbines: magnetic fields created by wind turbines. Some species of bats such as the big brown bat (*Eptesicus fuscus*) and the Chinese noctule (*Nyctalus plancyi*) have been shown to respond to changes in the magnetic field. Bats may navigate using a magnetic compass or through use of magnetic signposts in which subtle changes in the field are used to trigger changes in direction. This project explores whether the magnetic field of a wind turbine would be strong enough to interfere with bat navigation.

## **24 Establishing an *in vivo* approach to identify interactions between plant RNA-binding proteins and their mRNA targets**

Dilini Atugala\* and Doug Muench - *University of Calgary*

RNA binding proteins (RBPs) have a central role in post-transcriptional regulation of gene expression. A recently developed “mRNA interactome” method has increased our confidence toward the identification of RNA targets of RBPs. This method involves *in vivo* UV crosslinking RBPs to their authentic mRNA targets, thereby resulting in covalently bound interactions. Here we discuss the purification of the plant RNA-binding interactome from *Arabidopsis* cell cultures, leaves and roots. Similar to other model organisms, the plant RNA interactome consists of a large proportion of proteins with non-classical and unknown RNA binding domains. We present validation data for these domain categorized RBPs (classical, non-classical and unknown). We have followed the UV crosslinking step by immunoprecipitation of RBPs of interest using specific antibodies and are in the process of identifying their target RNAs using deep sequencing of bound RNAs. Further, we are determining the functional role of these specific RBP-RNA interactions in plants that are exposed to environmental stresses, such as toxins, cold, heat shock and nutrient deficiency. This research approach has provided us with a valuable tool to identify authentic RNA targets of interesting RBPs, and expands our understanding of the functional roles of RBPs in gene expression in plant cells.



**25 A critical review on the “health” of narwhal (*Monodon monoceros*) in a time of anthropogenic and climate changes: Do we know enough?**

Sandra R. Black\*, Susan J. Kutz, Robert M.R. Barclay and Alessandro Massolo - *University of Calgary*

Narwhals are highly specialized small arctic whales of great cultural and economic significance. These apex predators now exist in a rapidly changing marine landscape as ice patterns shift and ice cover decreases, shipping traffic increases, commercial fisheries are developed, water warms, food webs and phenology change and more southerly species move north. From the past 50 years there exists a good breadth of literature on narwhals covering general biology, populations and habitat use, diet, toxicology, predation, management and health. Despite this there is little data to support predictions narwhal population trends, and even the extent to which narwhal depend on ice is unknown. We systematically review the published literature on narwhals and assess 264 articles for information pertinent to health of individual animals or populations. Critical review was undertaken of articles which presented novel data, or a review of previous work, and where the data and findings were pertinent to one or more of the following identified key ecological factors: Health and Disease, Predation, Hunting and Management, Environmental Toxicants, Disturbance, Climate Change, Habitat Loss and Fragmentation, Food Web Alterations. The value of the available data was measured against several variables: the time and spatial scale of the data, the design of the study, whether opportunistic or experimental, the gender and ages of animals included and the size of the data set, number of research subjects or events. Results are presented in tabular and graphic format. Finally, we analysed each ecological factor to identify gaps in our knowledge of the current and future health of narwhal, and present these as a guide to ranking priorities of future narwhal health research.

**26 Characterization of the two ribitol catabolic gene systems on pRleVF39c and d of *Rhizobium leguminosarum* bv. *viciae* strain VF39SM**

Deborah L. Buhlers and Michael F. Hynes - *University of Calgary*

*R. leguminosarum* bv. *viciae* belongs to the Rhizobia, a group of soil bacteria that enter a symbiotic relationship with legume crop plants such as peas, beans and lentils, fixing nitrogen for the host plant, resulting in increased crop yields. Biovar *viciae* strain VF39SM has six plasmids, pRleVF39a to f, which contain genes involved in the uptake and catabolism of many different carbon sources, including glycerol, erythritol and ribitol. Previous research on the role of glycerol and erythritol catabolism on nodulation competitiveness of *R. leguminosarum* bv. *viciae* strain VF39SM demonstrated that these genes are important in plant colonization. Strain VF39SM has two non-orthologous systems of ribitol catabolic genes located on plasmids pRleVF39c and d. The goal of this research was to establish the role of these ribitol catabolic genes in nodulation competitiveness, as well as to investigate the gene regulation and operon arrangements. Insertional and deletion mutants of key ribitol catabolic and transport genes on each plasmid were not able to grow on ribitol. Promoter fusions constructed using *gusA* as a reporter gene were used to show that both sets of catabolic genes were induced by ribitol and seed exudates. Nodulation competition assays using wild-type, single and double ribitol catabolic gene mutants demonstrate decreased competitiveness of the double mutant on lentils but not peas.



- 27     **Near-infrared spectroscopic analysis of intact canola seeds for evaluating seed quality**  
Allison Crawford\* - *Concordia University of Edmonton*

Canola (*Brassica napus*) is an important crop in Canada. The development of a high-speed, non-destructive, and reliable instrumental method to evaluate quality of canola seeds is of major interest to growers, processors and oilseed breeders. Near Infrared Spectroscopy (NIRS) has shown to be a promising method toward that end. Previous investigations have shown a good agreement between the reference data and NIRS predicted values for quality of canola seed. These calibrations were specific to the growing locations and environmental conditions under which the seed was grown. This study examines the attributes of the near infrared reflectance spectra of intact seed of canola grown in Alberta. NIRS reflectance measurements were taken for various samples with different percentage of foreign material, moisture, as well as oil content.

- 28     **Transcriptome analysis: Synergism with *Streptococcus pneumoniae* and 1918 pandemic influenza virus**

Danika M. Deibert\*, Madeleine C. Wiebe, Jade Roy-Spencer, Deborah Hemmerling, and Kathie-Ann Walters - *Concordia University of Edmonton*

This study delves further into the synergy of co-infection between the 1918 pandemic influenza virus and *Streptococcus pneumoniae*. Most mortality seen in this outbreak was due to the secondary bacterial infection. Transcriptome data was derived by comparing single agent infection *S. pneumoniae* with the transcriptome from *S. pneumoniae* in a co-infected lung. This data revealed that the co-infecting *S. pneumoniae* had a different transcriptional profile then when it infected alone. This study examines the preferentially upregulated transcripts of what appears to be novel genes, specifically to determine if those genes contribute to virulence. These genes were analyzed and mapped using BLAST programs. Once the uncharacterized genes were located, adjacent characterized genes with known proteins were examined for their respective function. If the function is related to pathogenicity, the assumption is that the neighbouring uncharacterized gene has a similar function. The goal is to establish uncharacterized genes that could be related to the pathogenicity of the bacteria and subsequent synergism.

- 29     **The relationship between diet and activity level of black howler monkeys (*Alouatta pigra*) at the Monkey River research site in southern Belize**

Amanda Dickson\* - *University of Calgary*

Diet has been shown to impact behavior in many species of primates (1,2). Howler monkeys are considered the most folivorous new world monkeys (3), meeting their energy requirements through the consumption of leaves and fermentative digestion (4). The howler's highly folivorous diet has been used to explain their inactive lifestyle (5). However, past research mainly examined mantled howlers (*Alouatta palliata*) (6, 7, 8, 9, 10, 11). Recent studies on black howler monkeys (*Alouatta pigra*) reveal that black howlers have a varied diet, including large quantities of high-energy fruit (12, 13, 14), though they still conform to the traditional inactive lifestyle seen in other howler species (5). Therefore, the precise relationship between the role of diet and activity level in howler monkeys is unknown. Here I show that black howlers at the Monkey River research site in southern Belize are opportunistic frugivores, and exhibit an inactive lifestyle. This research demonstrates that howler monkeys are largely inactive regardless of variations in diet, suggesting that diet may

not have a large impact on behavior in all species of primates. I anticipate this study will lead to further research on diet and activity levels in howler monkeys as well as in other primate species. Future studies could examine the nutritional composition of the variety of foods that howler monkeys eat to determine the relationship between consumption of specific nutrients and behavior. This research would shed light on the importance of food traits other than energy-density on the activity level of primates.

**30 Bugs on Smart Phones: A Nuisance at the Clinical Point of Care**

Sheen Dube\*, Shibby Kuriakose and Anuraag Shrivastav - *University of Winnipeg*

The onset and progression of cancer is invariably associated with a depression in the host's immune response regardless of the location or aetiology of the tumour. Therefore, it becomes highly important to manage infections in cancer hospitals. To investigate whether smart phones of health care workers in a cancer hospital in Winnipeg carry bacteria, we conducted a pilot study that included 20 health care workers. Their smart phones were swabbed with sterile swabs before and after cleaning the smart phones with disinfectant wipes. The swabs were then transferred onto a petri dish containing agar bacterial growth medium. The plates were incubated at 37°C for 48h. Any growth in the petri dishes was noted and gram staining was performed to identify the morphology of the bacteria. The results indicated that out of 20 smart phones swabbed, 12 showed bacterial growth. Phones that were positive for bacterial growth showed mixed colonies of bacteria. Colonies displayed gram-positive cocci in clusters and chains, gram-positive bacilli, gram negative bacilli and large gram positive cocci similar to that of *canadia* sp. Furthermore, 9 out of 12 smart phones displayed growth of gram positive bacteria. The remaining smart phones were gram negative. Interestingly, 11 out of 12 smart phones, after being cleaned with disinfectant wipes, showed no bacterial growth. However, one phone showed persistent growth of bacteria despite cleaning with disinfectant wipes. A follow up study is warranted with larger sample size to sub-classify the bacteria found on smart phones and determine their pathogenicity. This study is highly significant as the results indicate that a simple measure of using disinfectant wipes can kill bacteria.

**31 The Role of Prolactin in Tumor Progression and Tumor Microenvironment in Response to DNA Damaging Agents**

Rasha S. Etman\*, Ödül Karayazi Atici and Carrie S. Shemanko - *University of Calgary*

Prolactin (PRL) decreases apoptosis and acts as a survival factor for breast cancer cells. In our in vitro experiments we demonstrated that PRL increased the viability of breast cancer cells to DNA-damaging chemotherapeutics and ATM contributes to the PRL-JAK2-STAT5-HSP90 pathway in mediating cellular resistance to DNA-damaging agents. In order to investigate the role of autocrine PRL in tumor progression in response to DNA damage, we used a novel model of breast cancer recurrence. Breast cancer cells were treated with DNA damaging agent doxorubicin in the cell culture, in the presence or absence of PRL, and the cells were injected into mammary fat pad of immune deficient SCID mice. Interestingly, in orthotopic xenograft studies, autocrine prolactin from human breast cancer cells increased the tumor latency of doxorubicin induced DNA damaged cells in SCID mice compared to untreated or prolactin or doxorubicin alone. We hypothesize that this is in part due to the cross-talk of the prolactin and DNA damage response pathways that may be affecting the tumor microenvironment. In order to test our hypothesis, we are currently investigating the attraction of natural killer (NK) cells to DNA-damaged breast cancer cells in the presence or

absence of prolactin. Our study will provide a unique experimental approach to understand the role of PRL in tumor progression and tumor microenvironment in a cross-talk with DNA damage repair pathway.

**32 Metabolic Control of Two Dynamic Pools of Diacylglycerol in Budding Yeast**  
**Suriakarthiga Ganesan\*** - *University of Calgary*

The location of lipids and their distributions across cellular membranes have critical biological consequences, particularly for lipids involved in cellular signaling. In this study, diacylglycerol pools were monitored in budding yeast under conditions where lipid homeostasis was altered. Two predominant pools of diacylglycerol were visualized using the C1 domain of mammalian PKC $\delta$  fused to GFP. One pool was associated with vacuolar membranes and the other localized to sites of polarized growth. Upon growth resumption, diacylglycerol pools appeared more dynamic than those of phosphatidic acid and phosphatidylserine. During this period, diacylglycerol enriched puncta and vacuolar rings experienced constant morphological changes with clusters of lipid droplets closely attached. Lack of conversion of diacylglycerol to phosphatidate by Dgk1 led to the accumulation of diacylglycerol in a vacuolar associated compartment. Diacylglycerol distribution was strongly affected in cells lacking the phosphatidylserine synthase Cho1/Pss1. Supplementation of lysophosphatidylserine to cho1 cells did not correct mislocalization of DAG, pointing to a role for phosphatidylserine synthesis and traffic in the establishment of cellular diacylglycerol pools.

**33 Investigating the Role of KAP1 in Mammary Gland Development**

Nayantara Govindrajan\*, Negar Heidari, Sharmin Chowdhury, Carrie Shemanko -  
*University of Calgary*

KRAB domain-associated protein 1 (KAP1) is a multi-functional nuclear protein which, in part, acts as a transcriptional co repressor by binding to the conserved KRAB repression domain present on many transcription factors, helping regulate the genes necessary for cell survival and differentiation. The purpose of this study is to explore the potential role of KAP1 in mammary gland development. In order to do so, we will compare all stages of mammary gland development between Mouse Mammary Tumor Virus (MMTV)Cre mice having KAP1 knocked out of their mammary glands using a cre-lox system and control littermates. Morphometric analysis of mammary gland whole mounts from pubertal and pregnant developmental stages was performed using ImageJ. The parameters under consideration were mammary gland area and length; and branching complexity and decay, using Sholl analysis. Preliminary evidence suggests that mammary glands from pregnant knockout mice displayed greater branching decay, i.e the extent of branching decreased more rapidly with distance from origin as compared to the control mice. Mammary gland development is a complex process regulated by several transcription factors. Our work will help identify KAP1's role in the mammary gland development, and potentially the other factors and pathways involved in each stage.

**34      Are Benthic Macroinvertebrates the True Kings and Queens in the Castle?**

Alixis Hassell\*, Emily Harrison\*, Dr. Mindi Summers and John Swann - *University of Calgary*

Castle Wildland Provincial Park and the newly established Castle Provincial Park support some of the most biodiverse ecosystems within Alberta. These parks connect major Rocky Mountain wildlife corridors and are important headwaters for the South Saskatchewan River Basin. Stream and river quality are important for both animal and downstream human use. Benthic macroinvertebrates, particularly Ephemeroptera, Plecoptera, and Trichoptera (EPT), play important roles in the foodweb of a healthy aquatic ecosystem, and are also used as biological indicators in freshwater monitoring programs. Identification of these specimens can be difficult and the level of identification necessary to gain an accurate measure of stream health is debated. To investigate EPT diversity in the Castle Parks, we sampled and identified benthic macroinvertebrates from seven different sites within tributaries of the Castle River. Biodiversity indices were calculated for different levels of taxonomic classification and compared using data on habitat parameters (e.g., flow rate, pH, and temperature). We also created a table-style identification key to assist in future work in this area and other freshwater communities in Alberta. Together, these efforts provide baseline macroinvertebrate biodiversity data for a newly established park and resources and recommendations for future biodiversity studies.

**35      Regulation of plasmid transfer gene expression in *Rhizobium leguminosarum* bv. *viciae* VF39SM**

Kasuni M. Hemananda\* and Michael F. Hynes - *University of Calgary*

The agriculturally important bacterium *Rhizobium leguminosarum* normally contains 2-8 large plasmids in addition to a single circular chromosome. Plasmids can be horizontally transferred between bacteria using a process called conjugation. Four conjugation systems (Types I to IV) have been so far identified that can mediate horizontal transfer of rhizobial plasmids. The most recently discovered type of system, type IVa, on plasmid pRleVF39b of strain VF39, is unusual due to the presence of a truncated relaxase gene (traA), and a gene encoding a negative transcriptional regulator (trbR) belonging to the Xenobiotic response element (Xre) family. The annotated coupling protein, TraG, located between the trbN operon and the relaxase gene, traA, was hypothesized to function in plasmid transfer. Past experiments revealed that TrbR protein represses the genes from trbN to traA and trbR promoter is not subject to autoregulation by TrbR. To investigate the role of traG gene in plasmid transfer, marked and unmarked deletions in traG gene were constructed. The transfer frequency of traG marked and unmarked mutants, from *Rhizobium* to *Agrobacterium* recipients, exhibited 10<sup>-4</sup> and 10<sup>-5</sup> reductions compared to wild type VF39SM. The functionality of the trbR gene cloned in expression vector pSRKGm was determined prior to production and purification of TrbR protein. Wild type VF39 and trbR mutant containing pSRKGm expressing trbR, induced with IPTG, were used to confirm that the cloned trbR gene in pSRKGm retained function as repressor of tra and trb genes.

**36      Global Gene Expression Changes in the Liver of Fathead Minnows Sampled Downstream of Municipal Wastewater Treatment Plants**

Chris Hooley\* and Mathilakath M. Vijayan - *University of Calgary*

Municipal wastewater effluent (MWWE) is always a hot topic of concern regarding human and ecosystem health. The growing concern over new emerging contaminants such as pharmaceuticals and personal care products being released into local waterways, and what their collective impacts could be, requires further examination. This research aims to discover what molecular responses are being exhibited at the organismal level to MWWE exposure using the fish species the fathead minnow (*Pimephales promelas*). A sample population of approximately 350 fathead minnows was exposed to MWWE at various sites upstream and downstream from three effluent discharge outlets. A total of five sites were chosen, two upstream reference sites and three downstream exposure sites. Each downstream site was set at various incremental distances from the MWWE discharge pipes. At the end of the 26-day exposure period an assortment of fathead minnows was dissected at the riverside with the collected tissues flash frozen in a liquid nitrogen chamber, while the remaining fathead minnows were brought back to the lab for breeding. The fathead minnow liver molecular responses were analyzed upon RNA extraction using transcriptomics and bioinformatics technologies. The determination of differentially expressed genes between each of the exposure sites compared to the upstream reference sites displays the molecular responses of the fathead minnows to MWWE. Ultimately 43 differentially expressed genes were found in the fathead minnow liver transcriptomics results, with the exposure site closest to the effluent discharge showing the greatest impact. These findings can inform risk assessments and contamination monitoring.

**37      The effect of a 6-degree temperature increase on the growth and biomass of the native submerged macrophyte, *Myriophyllum sibiricum*, in a northern Albertan lake**

Sydney Huculak\* - *Concordia University of Edmonton*

Macrophytes play a structuring role in lake ecosystems by creating crucial habitat for many zooplankton and fish species in the littoral zone of the lake. Therefore, changes in the abundance or biomass of macrophytes can alter community-level dynamics. Previous research has shown that macrophytes growth response to increases in temperature is species specific. However, there is a severe lack of research focused on the relation between climate change and native macrophytes in Alberta. This study focuses on the effect of climate change on the growth and biomass of a native macrophyte species in a northern Alberta lake in an attempt to address this unexplored area of research. A 6-degree temperature treatment was used to simulate an extreme climate change scenario in Alberta. *Myriophyllum sibiricum* and lake water were sampled from Lac La Nonne, Alberta. The filtered lake water and native macrophyte were used to create 10 1L microcosms stored in environmental chambers. Growth, water quality parameters, and chlorophyll a are currently being measured biweekly for a 4-month period. After the measurement period is complete, final biomass measurements will be recorded and analyzed. It has been hypothesized that the 6-degree temperature treatment will have a negative effect on the macrophytes causing a reduction in growth and overall biomass. Preliminary results show that the 6-degree temperature treatment is significantly affecting the growth of the macrophyte, with reduced growth observed in the treatment microcosms. These results suggest that Alberta lakes could see changes in macrophyte growth under an extreme climate change scenario.



**38 Potential Differences in Foraging Behaviors of the Sable Island Horse**

Kirsten Johnsen\*, Philip McLoughlin and Daniel Fortin - *University of Saskatchewan*

The Sable Island Horse provides a unique opportunity to study how various constraints can affect time budgets and foraging behaviors without the confounding factors of predation and interspecific competition. In the west, where there are permanent ponds, the horses do not spend as much time acquiring water as their eastern counterparts who must dig wells in order to drink. I aim to test if there are different foraging strategies that stem from this main difference in their time budgets. There are also differences in parasite loads on the island and I am interested in studying how this constraint can affect foraging behaviors within the main differences that may be caused by the water source that the horse frequents. I will test these ideas by estimating net energy intake with the assumption that more energy translates to greater success as horses with more fat tend to be more fit than horses with less fat. Energy intake will be estimated by measuring bite rate in different areas as well as the average vegetation quality by community. Energy losses will be estimated by considering the metabolizable energy available from each community and losses due to performing different activities in their time budgets. Then differences in net energy intake between groups will be tested using generalized linear models while accounting for variability between individuals as Sable Island has a long running census program that has information on each horse on the island.

**39 Serum Levels of Angiogenic Factors in Preeclampsia and the HELLP Syndrome**

Aishwarya Khanduja\* and Kamran Yusuf - *University of Calgary*

Introduction: Preeclampsia is a major cause of maternal and neonatal morbidity and mortality worldwide. A severe form of preeclampsia is the HELLP (Hemolysis, Elevated Liver enzymes, and Low Platelets) syndrome. Angiogenic factors play a key role in the pathogenesis of preeclampsia. It is unknown if the differences in levels of these factors exist in preeclampsia and HELLP. Objective: To estimate levels of angiogenic factors in HELLP and preeclampsia. Methods: Pregnant mothers were recruited from the Obstetrics Department at Foothills Medical Centre with preeclampsia mothers (n=40) and HELLP syndrome (n=35). Exclusion criteria included chronic hypertension, gestational hypertension, cardiovascular, renal, or endocrine disease and mothers in labour. Placental Growth Factor (PlGF), soluble Vascular Endothelial Growth Factor Receptor (VEGFR) 1 and soluble VEGFR2 were assessed by enzyme-linked immunosorbent assays (ELISA). The Mann-WhitneyU test and chi-squared tests were used for statistical analysis as appropriate. P-value of <0.05 was considered significant. Results & Conclusions: The prospective study is ongoing and the preliminary results suggest the growth factors: VEGFR-1, and VEGFR-2 are expected to be present in higher levels in HELLP mothers than preeclamptic mothers, and vice-versa for the growth factor PlGF. The Mann-WhitneyU test was used for continuous variables and chi-squared test for categorical variables. P-value of <0.05 was considered statistical. Ultimately, 1. Compared with mothers with preeclampsia, we found lower levels of Placental growth factor (PlGF) in mothers with HELLP syndrome. 2. Placental growth factor levels may be used for early detection of HELLP in preeclamptic mothers.



**40 Cellular Metabolomics of DCMA, a Pediatric Mitochondrial Cardiomyopathy**  
Melissa King\*, Ian Lewis and Steven Greenway - *University of Calgary*

Dilated cardiomyopathy with ataxia (DCMA) syndrome is caused by a mutation in the essential but poorly understood DNAJC19 gene, which encodes a protein unique to the inner mitochondrial membrane (IMM). The IMM is mainly composed of cardiolipin, a phospholipid with a unique structure that stabilizes and allows for the efficiency of the electron transport chain (ETC). A previous study suggested that DNAJC19 modifies and matures cardiolipin, and so mutations in this gene causes downstream implications from inefficient energy production on central carbon metabolism. Normally, cells utilize energy from carbon sources through electron transfers into the ETC. In DCMA, I hypothesize that abnormal cardiolipin reduces the efficiency of the ETC and has downstream implications causing the DCMA clinical outcomes such as an enlarged and weakened heart. The aim of this project is to identify metabolic deficiencies to characterize DCMA syndrome using an in-vitro model of human dermal fibroblasts, and test potential therapeutics for this disease. Cellular metabolites are specifically quantified using high resolution mass spectrometry. Preliminary studies in this project have shown that DCMA cells secrete a higher lactate to pyruvate ratio than healthy cells, which is indicative of mitochondrial metabolic disruption due to the inability to efficiently utilize energy stored in central carbon metabolites. One promising therapy, the heart medication digoxin, improves cardiac function and I theorize that this is due to effects on metabolic function. Using the fibroblasts model system, the therapeutic effects of digoxin on mitochondrial metabolism and its effectiveness as a treatment for DCMA will be determined.

**41 Comparative genomics of rhizobiophages from western Canada**  
K.M. Damitha Gunathilake\*, Anupama P. Halmillawewa, Marcela Restrepo-Córdoba, Benjamin J. Perry, Christopher K. Yost and Michael F. Hynes - *University of Calgary*

Rhizobiophages are viruses that infect rhizobia, which are nitrogen-fixing root nodule bacteria. We have isolated a large collection of rhizobiophages that infect *Rhizobium leguminosarum*, *Mesorhizobium loti*, and *R. gallicum*. Complete genome sequences have been produced for six of them, including *M. loti* phage Cp1R7ANS-C2. Five of the completed genomes are available in NCBI: L338C (KF614509), P106B (KF977490), PPF1 (KJ746502), P10VF (KM199770) and Lo5R7ANS (KM199771). The completed genome of *M. loti* phage Cp1R7ANS-C2 is available but has not been submitted to NCBI. Five additional draft genomes are available for four *R. leguminosarum* phages: P9VFCl, AF3, V1VF A, L338G and for one *M. loti* phage: Cp1R7A-A1. The majority of the phage isolates in the collection have genomes modified to resist many common restriction enzymes. Phages such as P10VF, L338G, AF3, and P9VFCl encode many genes with hypothetical proteins. BLAST and phylogenetic analyses indicated that Rhizobium phage P10VF shows significant similarities and phylogenetic relationship to *Sinorhizobium meliloti* Phage ΦM9 for which the complete genome is now available. Although isolated from different geographic locations, from soils planted with different legumes, and being isolated using different strains, draft genomes of phages P9VFCl, AF3 and V1VF A also shows genomic similarities and phylogenetic relationship to P10VF as indicated by the phylogenetic analyses with amino acid sequences of putative terminases and capsid proteins. Mesorhizobium phages Cp1R7AS-C2 and Lo5R7ANS (Podoviridae) have similar genome arrangements and sizes, and share some properties with T7-like phages. Mesorhizobium phage Cp1R7A-A1 has a much larger genome with no strong similarities to anything so far sequenced.

**42 Metabolic profiling of goldfish liver during early gonadotropic phase**

Ladisa Claudia\*, Ma Yifei and Hamid R Habibi - *University of Calgary*

Many species, from mammals to fish, are seasonal breeders, and show distinct reproductive (gonadotropic phase) and growth (somatotrophic phase) phases during seasonal cycle. The main concept is that when an animal is reproducing it cannot energetically sustain active growth, and vice-versa. This energetic shift is particularly important in oviparous animals such as fishes, amphibians and reptiles that require significant metabolic energy investment to develop their ovaries and testes. Control of reproduction and growth is multifactorial, and involves hormonally-induced changes in gonadal development, circulating hormones and metabolism during the reproductive and growth cycles. The main objective of this study is to investigate changes in the metabolic pathways in the liver in order to energetically sustain the physiological processes related to reproduction. To investigate the phenotype metabolism, we use goldfish as experimental model organism. We used metabolomics approach and measured the concentrations of metabolites by LC-MS. The results obtained from the analysis of liver samples of male goldfish during early gametogenesis show that GnRH (Gonadotropin-releasing hormone) and GnIH (Gonadotropin-inhibitory hormone) are involved in the regulation of liver metabolism. Treatments with GnRH and GnIH resulted in significant shift in metabolic profile that involves changes in lipid, protein and carbohydrates metabolism in the goldfish liver. The findings provide a framework for better understanding of the hormonally induced changes in metabolism to energetically sustain reproduction in fish and other oviparous species undergoing seasonal cycle.

**43 Mapping local density to model density-dependent processes on Sable Island**

Joseph Lafont\*, Urvee, Jocelyn Poissant and Phil McLoughlin - *University of Saskatchewan*

The horses of Sable Island National Park Reserve, Nova Scotia are a unique and naturalized population. This provides an opportunity to study ecology and microevolution of a large ungulate in an island setting. My project is based on a continued study (since 2007) of the life histories of all horses on Sable Island ( $n = 489$  in 2016). Using the mapping software, ArcGIS, I will develop heatmaps of density at various scales based on an individual's movement across the island. Specifically, I will address how individual horses experience annual density from an individual's point of view (e.g. horses within 2000m, 4000m, 8000m). Using the data created from these maps, generalized linear models will be created to see how strongly density at scale  $x$  predicts trait data collected for individuals. For example, I expect that, due to the life cycle of strongyle nematodes (dioecious, obligatory parasites), fecal egg counts (FECs) collected annually for each horse will show a positive correlation with its exposure to local density. All classes of horses, based on age and sex, as well as the size of the bands (social group), will be considered in building my models. The project will yield important information on potential mechanisms of density dependence in isolated populations, particularly where predation is absent.

**44 Are Non-Ribosomal Peptide Synthetase genes of *Pseudomonas aeruginosa* involved in diketopiperazine production?**

Nicole M Jervis\*, Nabiha M Mehina\*, Karinn Crain, Joe Harrison and Douglas G Storey - *University of Calgary*

We have found that some *Pseudomonas aeruginosa* isolates from cystic fibrosis (CF) patients produce diketopiperazines (DKPs). DKPs are organic molecules synthesized by non-ribosomal peptide synthetases (NRPS) that have been shown to have inhibitory effects on growth or quorum sensing in other bacterial species growing in the same CF lung environment. The prototypical *P. aeruginosa* lab strain PAO1 produces DKPs: cyclo ala-val, cyclo pro-val, cyclo leu-pro, and cyclo phe-pro as identified through the use of gas chromatography-mass spectrometry (GC-MS). The objective of this study was to characterize the specific NRPS genes that are involved in DKP synthesis by *Pseudomonas aeruginosa* PAO1. In this study, single knock-out mutants of hypothetical NRPS genes were generated using two-step allelic exchange mutagenesis. GC-MS was then used to identify and quantify DKPs produced by the 3 mutant strains. In comparison to the wild-type strain, PAO1, mutant  $\Delta$ PA2402 showed to have a significant decrease in cyclo phe-pro production, whereas  $\Delta$ PA3327 was observed to have a significantly decreased production in cyclo pro-val and cyclo leu-pro. Overall, the results indicate that the production of DKPs may be specific to certain NRPS genes. However, the results also showed none of the mutants to have a total loss in DKP production, possibly indicating genetic redundancy within the PAO1 genome. Future work will provide a greater understanding of DKP production and its antagonistic properties against other bacterial species.

**45 Day-roost selection of Alberta bats in an urban setting**

Erin Miller\* - *University of Calgary*

Alberta bats roost in old trees during the summer. The compounding effects of deforestation and urbanization have reduced roosting opportunities and some bat species' ranges now encroach into urban areas. Two species consistently occupy artificial roosts; the little brown bat (*Myotis lucifugus*) and the big brown bat (*Eptesicus fuscus*). The processes involved in roost selection in forests are similar to those for urban roosts: microclimate, distance to food and water sources, and predator and parasite avoidance are some of the key factors. I studied roost selection by bats using bat boxes in Southern Alberta. Based on the thermoregulatory needs of female reproductive bats, I predicted that the characteristics that would create a warmer microclimate would positively correlate with successful occupation (dark exterior colour, low shade, South aspect, etc.). I also predicted that more protected bat boxes would increase the rate of occupation (tall with close tree cover and water source). In Summer 2017, I collected data on measurable and observational variables for forty-five bat boxes. To determine the occupation status of the boxes, at least three exit counts were performed at each. Initial results show that some box designs were never occupied whereas almost half of standard styles were occupied. Some bat boxes reached temperatures well above the limits tolerated by bats. Ongoing analyses form part of my honours research. Providing effective artificial roosts for bats is particularly important given the eventual arrival of white-nose syndrome (a disease killing millions of bats) in Alberta.

**46      Effects of early life-stage exposure to tebuconazole on the reproductive physiology of adult zebrafish (*Danio rerio*)**

Christie Miller\* and Steve Wiseman - *University of Lethbridge*

Tebuconazole is a fungicide used in agriculture to control pathogenic fungi by inhibiting the enzyme, 14 $\alpha$ -demethylase, which is critical for maintaining cell membrane fluidity and function. However, it has been shown that tebuconazole can have endocrine disrupting effects on nontarget species through inhibition of aromatase, which catalyzes conversion of testosterone to 17 $\beta$ -estradiol, which is the terminal step in the sex hormone steroidogenesis pathway. Disruption of this reaction alters concentrations of hormones that are critical for reproduction by adults and development of early life-stages, including development of the brain and gonads. Tebuconazole is ranked 11th in Alberta pesticide sales by active ingredient. Concentrations of tebuconazole in surface waters have been quantified at levels capable of causing physiological effects in fishes. The objectives of this research are to 1) determine whether pulse exposures of early life-stages of the model teleost fish, Zebrafish (*Danio rerio*), to tebuconazole affects the reproductive capacity of adults, 2) determine the effects of re-exposure to tebuconazole on reproductive capacity of adult fish exposed to tebuconazole during early life-stages, and 3) to determine the molecular and biochemical mechanisms of any persistent effects of exposure to tebuconazole during early life-stages. These objectives will be addressed through assays at two timepoints in the zebrafish life: early life-stage (1-hour post-fertilization – 24-hours post-hatch) and sexual maturity (3 – 4 months of age). Embryos used in the early life-stage assay will be raised to sexual maturity in order to assess persistent effects on reproductive capacity.

**47      Factors affecting the recovery of the keystone sea urchin *Diadema antillarum* in the Caribbean**

Adam Moghrabi\*, Sheri Dalton, Saskia Van Dongen, Max Bodmer and Dan Exton - *Concordia University of Edmonton*

In the Caribbean, sea urchins are a prominent herbivore and play a vital role in removing macroalgae from the surface of the coral reefs, keeping the benthic community healthy due to correlations seen of sea urchin density and reef complexity. The most productive of the sea urchins in the Caribbean is the long-spined sea urchin, *Diadema antillarum*. In 1983 *D. antillarum* faced a massive die-off due to an unknown pathogen, facilitating a phase-shift from coral dominated reefs to algae-dominated reefs. In this experiment we analyze the relationship of *Diadema* density, predator and competitor density, macroalgal cover, coral cover, and complexity of the reef system. This is done by comparing these factors between two sites in Honduras; in Utila, which has been shown to be representative of the majority of the Caribbean (low urchin density, low coral cover, and high macroalgal cover), and the Banco Capiro off-shore reef system in Tela Bay. The Banco Capiro reef has shown to be uniquely healthy compared to the majority of the Caribbean (low macroalgal cover, high coral cover) while maintaining a high *Diadema* density. Using Principle Component Analysis (PCA), we intend to draw correlations between important factors that allows the sustainment of a healthy reef system and *Diadema* presence.

**48 Native isoforms of gonadal GnRH are involved in the paracrine/autocrine control of testicular development and spermatogenesis in Zebrafish (*Danio rerio*)**

Hamideh P. Fallah and Hamid R. Habibi - *University of Calgary*

It is well established that the control of testicular development is multifactorial, and involves a number of hypophysial, peripheral and gonadal hormones. Hypothalamic GnRH (Gonadotropin-Releasing Hormone) is one of the key peptides involved in the multifactorial control of spermatogenesis. However, the paracrine/ autocrine role of GnRH native isoforms (sGnRH and cGnRH-II) and their complex interaction with hypophysial and peripheral hormones in the testis is poorly understood. Here we investigated the potential role of the two isoforms of GnRH peptides including salmon GnRH (GnRH3) and chicken GnRH-II (GnRH2) in the paracrine/ autocrine control of spermatogenesis in zebrafish. QPCR, FACScan cell cycle analysis with Propidium Iodide (PI) as well as morphometric histological analysis were used as experimental approaches to investigate direct actions of GnRH isoforms on cultured testis in vitro. Our results provide novel information on the transcription abundance of these two isoforms in the testis and it also shows the effect of GnRH peptides on the basal and gonadotropin (GtH)-induced control of testicular development. The present study demonstrates both inhibitory and stimulatory effects of GnRH2 and GnRH3 on spermatogonial proliferation and differentiation in adult zebrafish. Treatment with both GnRH isoforms was found to significantly alter production of postmeiotic haploid cell populations after treatment for 7 days, in vitro. Measurement of the secretion of testosterone level by ELISA and co-treatment of tissue with an androgen receptor antagonist (Flutamide) demonstrated that the effects of GnRH is androgen-dependent. This finding suggests that GnRH local peptides are important components of the complex multifactorial system that regulate testicular development and function in adult zebrafish.

**49 Aggregation and Membrane Permeabilization of Modulated Antimicrobial Peptides**

Mauricio Arias, Kathlyn Crisanta Piga\* and Hans J. Vogel - *University of Calgary*

Antimicrobial peptides (AMPs) are part of the immune system that protect a host from pathogenic bacteria. They are variable in length, amino acid composition and secondary structure and adopt a membrane-bound amphipathic conformation. They are currently seen as an alternative to antibiotics. While it is known that AMPs protect against bacteria by disrupting the integrity of the membrane, experimental conditions prove to significantly affect peptide structure, such as high peptide concentration, pH, and ionic strength, resulting in peptide oligomerization or aggregation. The research project aims to examine peptide aggregation and structure at various experimental conditions using nuclear magnetic resonance (NMR) spectroscopy and circular dichroism (CD) spectroscopy. Various peptides, wild-type and mutated, known in literature for their alpha-helical structure upon binding to bacterial membranes were examined for a change in secondary structure and hydrodynamic radius. Calcein leakage studies were also conducted to determine the ability of AMPs to permeabilize model membranes such as large unilamellar vesicles. CD spectroscopy studies suggest that peptides at normal physiological conditions have random secondary structure, whereas denaturing conditions result in a general alpha helical structure. From calcein leakage studies, mutated versions of Tritrpticin were used for examining their ability to permeabilize large unilamellar vesicles containing choline head groups, POPC, and 1:1 ratio of choline and serine head groups, PCPS. Tritrp1 had a greater percent leakage than Tritrp2. NMR studies showed that the peptides have a hydrodynamic radius in the range of 2-3A, although more experiments are being conducted to ascertain peptide aggregation.



**50 Heat activates c-di-GMP production in bacteria**

Trevor E. Randall\*, Henrik Almblad, Jacquelyn D. Rich, Fanny Liu, Katherine Leblanc, Ryan Groves, Nicolas Fournier, Tara M. L. Winstone, Ian Lewis, Justin MacCallum, Bryan G. Yipp and Joe J. Harrison - *University of Calgary*

Stimulus perception via signal transduction pathways is essential for all life, allowing organisms to regulate their internal processes to suit the conditions of the external environment. Environmental stimuli are often transduced into physiological responses through the production of a second messenger, which can regulate many protein targets simultaneously. The second messenger cyclic diguanylate (c-di-GMP) in the model bacterium *Pseudomonas aeruginosa* regulates biofilm formation, which may be key for survival in a host. C-di-GMP is produced by a variety of intercellular diguanylate cyclases (DGCs). However, the stimuli of DGC activation are in many cases unknown. Here we identify a thermosensing diguanylate cyclase (tdcA) that enables *P. aeruginosa* to increase biofilm formation as temperature rises from 25 to 37 °C. Recombinant TdcA displays thermostatted activity: it is inactive at 25 °C, but displays linearly increasing activity between 28 and 42 °C, allowing for large c-di-GMP changes over a narrow temperature range. Heat-sensing is mediated via a Per-Arnt-SIM type III (PAS\_3) domain, a widespread domain with a previously undescribed function. In infection models, a functional tdcA allele in *P. aeruginosa* allowed for acute virulence factor production to be attenuated in waxworms, and mediated the expression of c-di-GMP-regulated extracellular polysaccharides that were essential for innate immune suppression in a mouse model. Finally, bioinformatics analyses indicate that tdcA orthologues may be widespread in environmental and pathogenic bacteria. We propose that tdcA exemplifies a new class of thermosensing enzymes, allowing for the rapid change of cellular c-di-GMP over a narrow but physiologically relevant range of temperatures.

**51 The genetic basis of convergent evolution in four fish species**

James Reeve\* - *University of Calgary*

For centuries naturalists have observed that different organisms converge upon similar solutions to meet matching environmental challenges. On the phenotypic level convergent evolution is understood well, but we have only just begun exploring its genetic basis. There are two hypotheses for the genetic basis of convergent evolution; either many different genes can develop the same phenotype, or due to constraints one gene repeatedly is behind the same phenotypes. I intend to test these hypothesis by screening and comparing the whole genome of four different fish species to find the genes each species use to adapt to the effects of latitude. I have collected 50 fish from two populations per species. I am currently extracting DNA from each fish. Afterwards, the DNA within a population will be pooled together for next generation sequencing. The sequenced reads will be processed via standard bioinformatic pipelines, to identify single nucleotide polymorphisms (SNPs). The fixation index (FST) will then be calculated for each SNP between populations within a species. These scores will be used to identify regions of the genome with the strongest association to the environment. I will then align the sequences of these regions to identify any matching sequences in other species. By contrasting these regions among the species, I will determine if convergent evolution extend to the genes used for local adaptation.



**52      A strategy for effective predation on a large, dangerous predator, the Atlantic bluefin tuna, *Thunnus thynnus***

Meredith Shuffler\*, Scott Seamone and Douglas Syme - *University of Calgary*

The Atlantic bluefin tuna (*Thunnus thynnus*) is a fish of massive size and speed, capable of reaching masses up to 900 kg and speeds of 81 km/hr. Although it is a significant source of caloric energy, the high momentum with which it can travel makes predation dangerous, especially for animals like the blue shark (*Prionace glauca*) which may be smaller than it. To explore the potential predation strategies of predators hunting bluefin tuna, we considered tuna body dimension – mass relationships in conjunction with gape size – mass relationships of a model predator species, the blue shark (*Prionace glauca*). Using these relationships, we showed that a tuna's caudal peduncle is the narrowest point on the animal and shows comparatively little variation with change in body mass. On even the largest tuna, the caudal peduncle is smaller than the gape size of small sharks, suggesting that even the smallest sharks can successfully attack very large tuna at this point. Our results indicate that the presence of the narrow caudal peduncle in tuna is essential to the success of smaller predators such as the blue shark. Not only is the caudal peduncle a viable attack site, but a successful attack here can effectively immobilize the tail, significantly reducing prey speed and making subsequent attacks less dangerous to the predator.

**53      The influence of temperature and prey availability on the relative activity of insectivorous bats**

Sarah Y Teillet\* and Craig K.R. Willis - *University of Winnipeg*

The extent to which ambient temperature ( $T_a$ ) and food availability have impacted the behaviour of animals has been a longstanding area of study for ecologists. The activity of animals, particularly the populations of insectivorous bats, is thought to be influenced by  $T_a$  and food availability. I tested the hypothesis that insect abundance and bat activity is positively correlated with  $T_a$ , but that the strongest predictor of bat activity is the availability of insect prey. I used recordings of echolocation calls, and point light surveys to test the hypothesis that  $T_a$  and insect abundance influence the relative activity of insectivorous bats in riparian woodland in central Canada. Echolocation calls of bats native to Manitoba and number of insects spotted were recorded during 30-second trials on three consecutive nights in July 2017. I predicted that bat activity is positively correlated with insect abundance and  $T_a$ . I found positive correlations between these variables but the strongest predictor of bat activity was insect abundance. I suggest that insectivorous bats are more active during nights with a greater abundance of prey and a warmer temperature in order to maximize nutrient intake per unit energy expenditure. This demonstrates the use of foraging strategy in insectivorous bats.

**54      Scaling morphology in Blue Sharks (*Prionace glauca*): The fight against gravity!**

Natalie K. Tsao\*, Theresa M. McCaffrey, Scott G. Seamone, Douglas A. Syme - *University of Calgary*

Sharks are negatively buoyant, and thrust from their heterocercal tail is suggested to also pitch their noses downward when swimming. They resist sinking through hydrostatic lift generated from the liver, which is less dense than water, and hydrodynamic lift generated as water moves around the head and pectoral fins. If sharks grow isometrically, like magnifying a picture, then larger sharks will have less span and area of these lifting surfaces relative to

mass and become more prone to sinking. We thus hypothesize that sharks will exhibit growth of fins that is disproportionate to increases in size of the shark (i.e. not isometric) to maintain adequate lifting forces when swimming. We analyzed images of dorsal and lateral views of blue sharks (*Prionace glauca*) to assess changes with growth in head area, upper body volume (proportional to liver volume), pectoral and caudal fin dorsal lobe area and span. In contrast to expectations, head area, pectoral and caudal fin dorsal lobe area and span scaled isometrically with mass, indicating less lift relative to increasing mass. Upper body (liver) volume increased more than body mass, indicating increased buoyancy relative to increasing mass. Thus, larger sharks achieve relatively less hydrodynamic lift (fins and head) but more hydrostatic lift (liver) when compared to small sharks. Further, in larger sharks we propose there is reduced downward pitching of the nose because area and span of the caudal fin is proportionally less compared to mass, allowing larger sharks to remain buoyant.

## 55 **Creating a synthetic microbial platform for diterpenoids production**

Joseph Utomo\* - *University of Calgary*

Diterpenoid is a subclass of terpenoid superfamily, all of which are synthesized from a simple precursor isopentenyl diphosphate (IPP). Diterpenoids possess 20-carbon backbones, and their direct precursor is C20 geranylgeranyl diphosphate (GGPP). Many pharmaceuticals and nutraceuticals belong to diterpenoids, and a number of the biosynthetic genes for medically important diterpenoids, such as taxol, have been identified in recent years. However, practical tools to aid the bulk production of diterpenoids are still lacking, hindering the research on diterpenoids metabolisms. To achieve a versatile microbial platform to produce various diterpenoids, we chose yeast (*Saccharomyces cerevisiae*) for metabolic modifications with an aim to produce diterpenoids taxol precursor, taxadiene. Taxadiene synthase (TmTDS) cDNA was isolated from *Taxus media* (Anglojap yew), and its expression in yeast showed a nano-gram scale of taxadiene in L-culture. Naturally yeast does not have any GGPP-derived metabolites, and its GGPP synthase is primarily used to produce a minute quantity of GGPP for protein prenylations. Therefore, to increase the level of GGPP in yeast, we built and used an IPP-producing plasmid encoding 4 genes in the mevalonate pathway (called IPP-plasmid) and also overexpressed yeast GGPP synthase. Incorporating IPP-plasmid and yeast GGPP synthase overexpression in the base strain (i.e., overexpressing TmTDS alone) resulted in 212-fold increase of taxadiene. We are currently testing GGPP synthases from different organisms (bacterium, algae, and plant) and altering yeast genome by a CRISPR genome-editing tool to further improve taxadiene production in yeast.

## 56 **A strategy for regulating the stability of specific cellular mRNAs using a novel PUF RNA-binding protein**

Xin Wen and Douglas Muench - *University of Calgary*

RNA-binding proteins have an important role in the regulation of post-transcriptional gene expression. The Puf family of RNA-binding proteins recognize their target RNAs in a sequence specific manner using their Pumilio Homology Domain, and RNA-binding domain. An *Arabidopsis* Puf protein, APUM23, is able to specifically recognize an 11-nucleotide RNA sequence, compared to the 8-nucleotide target sequence of most Puf proteins studied to date. Previous research showed that by fusing an artificial site-specific RNA endonuclease to classical Puf proteins, specific cellular RNAs can be targeted and cleaved. Additionally, by altering the three amino acids of the tripartite recognition motif in a Puf repeat, the specificity of a Puf protein can be altered. Therefore, in our research, we fused a non-specific

ribonuclease (the PIN-domain) to two Arabidopsis Puf proteins (APUM23 and APUM2) to determine if the PIN RNase can specifically cleave its target mRNA when expressed in plant epidermal cells. To perform the expression in vivo, APUM-PIN constructs were co-expressed with their target sequence located in the 3' UTR of an mRNA encoding a fluorescent protein. The expression of the fluorescent protein was observed visually by epifluorescence microscopy, and quantitatively by western blot. Different combinations of APUM-PIN proteins and mRNA targets are compared to determine whether APUM23 proteins can specifically target mRNAs in vivo.

- 57 Genomic analysis of highly expressed *Streptococcus pneumoniae* genes in a 1918 Influenza and *S. pneumoniae* coinfection using systems biology and CRISPR technology**  
 Madeleine C. Wiebe\*, Danika M. Deibert, Jade C. Roy-Spencer, Deborah Hemmerling and Kathie-Anne Walters - *Concordia University of Edmonton*

Nearly 50 million people died during the 1918 Spanish influenza pandemic. However, there is evidence that the main cause of mortality was a secondary infection of *Streptococcus pneumoniae*. Post-mortem samples of 1918 human tissue reveal mass thrombosis and inflammation of the lungs. When the coinfection was simulated in mice by Walters *et al.*, similar lung pathology was observed, which was significantly more pronounced than pathologies seen in mice solely infected with *S. pneumoniae* (2016). There was also preliminary evidence of a dysfunctional immune response during the coinfection, including an over-calling to neutrophils. A number of highly expressed bacterial genes were identified for significant days of the coinfection and these expression levels are not seen in *S. pneumoniae* infections alone. Thus, this study will examine the relationships and mechanisms between the viral and bacterial infections, using the previous research and results of Walters *et al.* (2016). In Phase 1, bioinformatics was conducted on the upregulated and uncharacterized bacterial genes to determine potential roles in pathology. Data was collected to support the hypothesized roles of elements of interest. Phase 2 will consist of researching procedures and techniques to knockout sequences of interest and successfully transform bacterial strains. Techniques under consideration include the CRISPR/Cas 9 system. This project will continue later in 2018 with transformation of strains and eventual reproduction of the Walters experiment to determine if genes of interest have a specific role in the coinfection.

- 58 Mitochondrial Dysfunction in Aging Neurons: the Link Between Plasma Membrane Oxidation and Excitability Decline?**  
 Jonathon R. Lee\*, Keenan A. Boughton, Petra M. Hermann, Douglas A. Syme and Willem C. Wildering - *University of Calgary*

Age-related neuronal excitability decline may arise from accumulating free radical damage of the plasma membrane, known as lipid peroxidation. This can be repaired at great metabolic cost. The required energy is produced by mitochondria - organelles that acquire functional deficits that may cause them to over-produce free radicals during aging. While mitochondria are thus seen as perpetrators in age-related oxidative stress, it is possible that they are instead victims of an oxidative shift originating in the plasma membrane. Here, we show in *Lymnaea stagnalis* that, as with the age-related decline in neuronal excitability, changes in mitochondrial activity also coincide with lipid peroxidation of the plasma membrane. Moreover, involvement of the membrane repair enzyme phospholipase A (PLA2) suggests that fatty acids may be important in this neuronal aging process.

**59      Engineered recombinant *E. coli* for production of Poly (3-hydroxybutyrate)**

XingYu Chen, Alina Kunitskaya, Kaitlin Schaaf, Harry Wilton-Clark, Michaela Olsakova, Patricia Lim, Preetha Gopalakrishnan, Syeda Atika Ibrahim, Jacob Grainger, Maliyat Anika Noor, Lalit Bharadwaj, Alexandra Ivanova, Zi Fei Wang, Bilal Sher, David Feehan, Rachelle Varga and Mayi Arcellana-Panlilio- *University of Calgary*

Space exploration has inspired scientists and engineers to find innovative and efficient solutions to various problems. The current focus for space exploration is on sending humans to study Mars and to answer questions that have puzzled scientists for a long time. However, two major challenges need to be solved before pioneering Mars are as follows: 1) Difficulty transporting materials to Mars due to the long mission duration, high transportation costs, and difficulties anticipating the material needs on Mars. 2) Lack of waste management processes to recycle waste in long duration space missions. To address these two problems, our project called Astroplastic aims to genetically engineer *Escherichia coli* that can use chemical components of solid human waste to produce polymer granules called Poly (3-hydroxybutyrate) (PHB), which could be used for 3D printing useful items for astronauts. PHB granules are produced by bacteria (such as *Ralstonia eutropha* and *Pseudomonas aeruginosa*) for carbon and energy storage. We have engineered recombinant *Escherichia coli* to utilize genes from native PHB-producing bacteria. These genes code for enzymes in PHB production as well as genes used in the glycolysis and fatty acid  $\beta$ -oxidation pathways, which break down sugars and lipids, respectively. In addition, we aim to design a continuous PHB production process in which lysis of cells is not required for extraction of the polymers. To achieve this, we have also engineered recombinant *E. coli* to utilize genes in its natural type I secretion system. These genes include phasin which electrostatically interacts with PHB, and membrane transporters which will co-transport PHB out of the cell. We thus hope to optimize a sustainable and continuous PHB production system with these bacteria, which will address the problems of transportation costs and waste management for future space missions.