

University of
Waterloo



DEPARTMENT OF BIOLOGY

**GRADUATE STUDENT
SYMPOSIUM**

THURSDAY, APRIL 27, 2017

Table of Contents

Schedule of Speakers	4
List of Sponsors.....	6
The road less traveled – from academia to science writing Jovana Drinjakovic, PhD	7
The photopic negative response in full-field electroretinograms of optic nerve-sectioned young chicks Clement Afari	8
Characterization of Pyruvate Decarboxylase in <i>Sulfolobus</i> species Faisal Alharbi	9
Identifying the toxic organic components within bitumen-influence groundwaters Anthony Bauer	10
Optimizing sensitivity and redundancy: Constructing a multimetric index of ecological health Matthew Bolding	11
Examination of stress-induced heme oxygenase-1 (HO-1) accumulation and function in <i>Xenopus laevis</i> cultured cells James Campbell	12
Lipid content of Atlantic salmon (<i>Salmo salar L.</i>) at West Greenland Audrey Dean	13
Subdural infusion of kynurenic acid causes myelin loss in chicken optic nerves Akshay Gurdita	14
The DNA damage response markers γ H2AX and p53 as potential biomarkers of genotoxic stress in a rainbow trout (<i>Oncorhynchus mykiss</i>) brain cell line Mark Hamilton	15
Acute and chronic effects of multiple stressors on microRNA in zebrafish Heather Ikert	16

Discerning the effects of major energy projects, climate change and distributary flow on lakes of the Athabasca Delta using paleolimnology

Mitchell Kay 17

The effect of isothiocyanates on heme oxygenase-1, heat shock protein and α -tubulin accumulation and localization in *Xenopus* A6 kidney cells

Imran Khamis 18

Assessing the Accuracy of the Community Aquatic Monitoring Program (CAMP) in describing littoral nekton assemblages of estuaries within the southern Gulf of St. Lawrence

Jessica Kidd 19

An occupancy model approach to identifying young-of-year Arctic Grayling habitat in northern mountain streams

Brent Lewis 20

Microbial production of vitamin B₁₂ in soil

Xinda Lu 21

Data mining genomes and metagenomes to uncover botulinum neurotoxin evolution

Michael Mansfield 22

Assessing reasons for changes in the condition of Deception Bay Arctic charr (*Salvelinus alpinus*)

Mackenzie Martyniuk 23

Multi-Stressor Impacts on Fish Energetics: A Comparison between Lab and Field Studies

Hossein Mehdi 24

Scavenging For Bacteria: Identification And Functional Characterization Of Two Rainbow trout (*Oncorhynchus mykiss*) MARCO variants

Sarah Poynter 25

Would You Give a Fish Grapefruit?: The Use of a Fish Intestinal Cell Line to Test Potential Fish Feed Additives

Patrick Pumputis 26

Evaluation of peptide inhibitors on single amyloid molecules and survival to toxic oligomers	
Morgan Robinson	27
The Mammalian Skin Microbiome	
Ashley Ross	28
Combined effects of benzalkonium chloride and UV irradiation on the bovine lens <i>in vitro</i>	
Jordan Rossy	29
An analysis on the role of <i>hindsight</i> in establishing stem cell niches in the developing midgut epithelium of <i>Drosophila melanogaster</i>	
Donya Saghattchi	30
Characterization of CHUP1, a gene potentially involved in chloroplast partitioning in <i>Bienertia sinuspersici</i>	
Dustin Sigurdson	31
Short-term exposure to cadmium and manganese of two members of the <i>Hyalella Azteca</i> cryptic species complex	
Kate Marie Sinclair	32
Expression and Characterization of two <i>Streptococcal</i> zinc metalloproteases, and the novel flagellal protease of <i>C. haemolyticum</i>	
Iain Wallace	33
Reeding the wetland: the effect of invasive <i>P. australis</i> on primary production and decomposition	
Sarah Yuckin	34

Biology Graduate Symposium

Schedule of Speakers

Time	Room	Session 1	Room	Session 2
9:00	QNC 1502	Opening & Welcome – Dr. Hugh Broders & Eric Le Dreff-Kerwin		
		QNC 1502		QNC 2502
		Chair: Quinn Abram		Chair: Matt McLeod
9:45	Akshay Gurdita	Subdural Infusion of Kynurenic Acid causes Myelination Loss in Chicken Optic Nerves	Hossein Mehdi	Multi-Stressor Impacts on Fish Energetics: a Comparison between Lab and Field Studies
10:00	Jordan Rossy	Combined Effects of Benzalkonium Chloride and UV Irradiation on the Bovine Lens <i>in vitro</i>	Heather Ikert	Acute and Chronic Effects of Multiple Stressors on MicroRNA in Zebrafish
10:15	Clement Afari	The Photopic Negative Response in Full-field Electroretinograms of Optic Nerve-sectioned Young Chicks	Mark Hamilton	The DNA Damage Response Markers γ H2AX and p53 as Potential Biomarkers of Genotoxic Stress in a Rainbow Trout (<i>Oncorhynchus mykiss</i>) Brain Cell Line
10:30	Michael Mansfield	Data Mining Genomes and Metagenomes to Uncover Botulinum Neurotoxin Evolution	Patrick Pumputus	Would you Give a Fish Grapefruit? The Use of a Fish Intestinal Cell Line to Test Potential Fish Feed Additives
10:45	QNC Lower Atrium	COFFEE BREAK		
11:00	QNC 1502	KEYNOTE SPEAKER – Dr. Jovana Drinjakovic		
12:00	QNC Lower Atrium	LUNCH		
		QNC 1502		QNC 2502
		Chair: Heather Ikert		Chair: Hossein Mehdi
1:00	Ashley Ross	The Mammalian Skin Microbiome	Mitchell Kay	Discerning the Effects of Major Energy Projects, Climate Change and Distribution Flow on Lakes of the Athabasca Delta using PAleolimnology
1:15	Xinda Lu	Microbial production of vitamin B ₁₂ in soil	Anthony Bauer	Identifying the Toxic Organic Components within Bitumen-Influence Groundwaters
1:30	Faisal Alharbi	Characterization of Pyruvate Decarboxylase in <i>Sulfolobus</i> Species	Sarah Yuckin	Reeding the Wetland: the Effect of Invasive <i>P. australis</i> on Primary Production and Decomposition

	QNC 1502		QNC 2502	
	Chair: Heather Ikert		Chair: Hossein Mehdi	
1:45	Iain Wallace	Expression and Characterization of two <i>Streptococcal</i> zinc metalloproteases, and the novel flagellar protease of <i>C. haemolyticum</i>	Jessica Kidd	Assessing the Accuracy of the Community Aquatic Monitoring Program (CAMP) in Describing Littoral Nekton Assemblages of Estuaries within the Southern Gulf of St. Lawrence
2:00	Sarah Poynter	Identification and Functional Characterization of two Rainbow Trout (<i>Oncorhynchus mykiss</i>) MARCO Variants	Matthew Bolding	Optimizing sensitivity and redundancy: Constructing a multimetric index of ecological health
2:15	QNC Lower Atrium	COFFEE BREAK		
	QNC 1502		QNC 2502	
	Chair: Shawna Semple		Chair: Sarah Yuckin	
2:30	James Campbell	Examination of stress-induced heme oxygenase-1 (HO-1) accumulation and function in <i>Xenopus laevis</i> cultured cells	Audrey Dean	Lipid Content of Atlantic Salmon (<i>Salmo salar</i> L.) at West Greenland
2:45	Imran Khamis	The effect of isothiocyanates on heme oxygenase-1, heat shock protein and α -tubulin accumulation and localization in <i>Xenopus</i> A6 kidney cells	Mackenzie Martyniuk	Assessing Reasons for Changes in the Condition of Deception Bay Arctic Charr (<i>Salvelinus alpinus</i>)
3:00	Morgan Robinson	Evaluation of Peptide Inhibitors on Single Amyloid Molecules and Survival to Toxic Oligomers	Kate Sinclair	Short-term Exposure to Cadmium and Manganese of Two Members of the <i>Hyalella Azteca</i> Cryptic Species Complex
3:15	Donya Saghatchi	An analysis on the role of <i>hindsight</i> in establishing stem cell niches in the developing midgut epithelium of <i>Drosophila melanogaster</i>	Brent Lewis	An Occupancy Model Approach to Identify Young-of-year Arctic Grayling Habitat in Northern Mountain Streams
3:30	Dustin Sigurdson	Characterization of CHUP1, a Gene Potentially Involved in Chloroplast Partitioning in <i>Bienertia sinuspersici</i>		
3:45	QNC 1502	CLOSING REMARKS – Dr. Kirsten Muller & Eric Le Dreff-Kerwin		
4:00	Grad House	POST-SYMPOSIUM SOCIAL		

Biology Graduate Symposium
List of Sponsors

A special thank you to the following sponsors:

Department of Biology
University of Waterloo

ThermoFisher
S C I E N T I F I C

VWR ®
We Enable Science

Keynote Address:

The road less traveled – from academia to science writing

**Jovana Drinjakovic, PhD
Writer at the Donnelly Centre
University of Toronto**

There are many ways to contribute to science beyond tinkering in a lab (or in the field!) and science writing is one of them. Compelling storytellers help deepen an understanding of science among the public, whose unwavering support is key for any future progress.

My own foray into science writing was unplanned and happened when I realized, after a decade of academic research, that my heart was no longer in it. And to my great surprise, I found out that writing about science is just as fun as doing it! These days I write about some of the most exciting biomedical discoveries at the University of Toronto, but the skill set is the same whether you're writing for a university or a scientific journal, or about genetics or ecology.

One thing I learned during my career detour - you never know where life will take you and don't worry if you don't yet have a plan. And for those of you who do have a plan, be prepared to change it.

The photopic negative response in full-field electroretinograms of optic nerve-sectioned young chicks

Clement Afari

Supervisors: Daphne McCulloch and Vivian Choh

Authors: Afari, Clement¹; McCulloch, Daphne L.¹; Gurdita, Akshay¹; Choh, Vivian¹

Institution: 1. School of Optometry and Vision Science, University of Waterloo, Waterloo, ON, Canada.

Purpose: The photopic negative response (PhNR) is known to reflect the functions of retinal ganglion cells (RGCs) in mammals but its origin in non-mammalian species is not established. Optic nerve section leads to RGC dysfunction. PhNRs are a component of electroretinograms (ERGs), which objectively assess retinal functions in response to flashes of light. This study was undertaken to determine whether the PhNR from optic nerve-sectioned young White Leghorn (*Gallus gallus domesticus*) chicks reflects RGC functions and to describe the nature of PhNRs across time.

Methods: Full-field photopic ERGs were recorded bilaterally from hatchling chicks (N = 4) before optic nerve section (ONS) on one eye and sham surgery on the fellow control eye. ERGs were recorded again on 3, 5 and 7 days post-ONS. Stimuli were 4 ms red ($\lambda = 650$ nm) flashes from 0.3 to 8 cd·s/m² on rod suppressing blue ($\lambda = 462$ nm) background (30 cd/m²). The a-wave, b-wave and PhNR components of the ERG were measured

Results: ERGs were clearly recordable from all eyes showing the expected luminance-response functions, with saturation at 3 cd·s/m². At all luminance levels, PhNR amplitudes for control eyes (63.77 ± 4.81 μ V) were similar ($p = 0.16$) to those of ONS eyes (54.49 ± 4.09 μ V). The a-wave and b-wave amplitudes were also not different between the eyes for all time points and luminance levels ($p = 0.31$). Differences in ERG amplitudes with maturation were not significant ($p \geq 0.14$).

Conclusions: Although the PhNR of the ERG is diminished in conditions affecting RGC function in mammalian models, this component did not appear to be affected by retinal dysfunction in the chick. Vascular ocular anatomy may be a reason for the differences between species.

Characterization of Pyruvate Decarboxylase in *Sulfolobus* species

Faisal Alharbi

Supervisor: Kesen Ma

Pyruvate decarboxylase (PDC) contains thiamine pyrophosphate and responses for the non-oxidative decarboxylation of pyruvate to acetaldehyde in many mesophilic organisms. Bifunctional PDC/POR enzymes have been purified and characterized from several hyperthermophilic organisms. These enzymes convert the non-oxidative and oxidative decarboxylation of pyruvate to acetaldehyde and acetyl-CoA respectively. Pyruvate ferredoxin oxidoreductase (POR) has been previously purified and characterized from the hyperthermophilic archaeon such as *Sulfolobus solfataricus* and *Sulfolobus acidocaldarius*, microorganisms that grow optimally at 80°C. Most of PORs from hyperthermophiles are oxygen sensitive; however, PORs from *Sulfolobus* are not oxygen sensitive, which is a great advantage to work with. It is anticipated that its PDC activity would not be oxygen-sensitive. If this would be the case, it would be the most thermal stable PDC. *S. acidocaldarius* and *S. solfataricus*, will be used for the proposed study. The PDC/POR activity of both will be determined by measuring the production of acetaldehyde and measuring the pyruvate-dependent reduction of methyl viologen, and the PDC/POR enzyme will be purified using a Fast Performance Liquid Chromatography (FPLC) system. In addition, the biochemical and biophysical properties will be characterized. The study is on-going and preliminary results will be presented.

Identifying the toxic organic components within bitumen-influence groundwaters

Anthony Bauer

Supervisor: George Dixon

Surface and in-situ mining operations in the region surrounding Ft. McMurray, AB are employed for extraction of bitumen from oil sands deposits. The by-products of are stored in large tailings ponds, and have been accumulating for decades with increases in oil sands extraction. Investigations have identified the presence of oil sands process-affected water (OSPW) in nearby groundwater due to tailings seepage. However, these same groundwater systems often flow through bitumen deposits, potentially mobilizing water-soluble bitumen components leading to natural bitumen inputs to the Athabasca River watershed. The present study assessed the toxicity of isolated groundwater soluble organic fractions through exposure to two freshwater fish; fathead minnow (*Pimephales promelas*) and Japanese medaka (*Oryzias latipes*), and invertebrates; *D. magna*, *H. azteca*, and a freshwater mussel. Two samples suspected of influence by natural bitumen sources alone, and two samples suspected of influence by anthropogenic and natural bitumen sources (>100 L each), were fractionated using a preparative solid phase extraction methodology. For each sample, this protocol produced three fractions of the soluble organics separated using differences in polarity. Both fish bioassays exhibited differences in toxicological responses between fractions within sites, and also between sites. Generally, the fish bioassays results were very similar but distinct from invertebrate bioassays conducted in parallel. Coupled with high resolution chemical characterization data, this study will aid in guiding future comprehensive fractionation studies intent on better elucidating the bioactive components within bitumen-influenced waters. The present study is important for the development of water quality criteria in future water monitoring programs in the Athabasca region.

Optimizing sensitivity and redundancy: Constructing a multimetric index of ecological health

Matthew Bolding

Supervisor: Rebecca Rooney

To implement their new wetland policy, the Government of Alberta has called for development of an assessment tool to provide reliable, valid assessments of wetland condition. Multimetric indices (MMIs) are commonly used to assess the ecological integrity of aquatic ecosystems. MMIs work by combining measurement of several metrics that collectively describe the condition of a representative biological assemblage (e.g. vascular plants). Under the traditional MMI development protocol, candidate metrics are considered individually regarding their sensitivity to disturbance. A set of non-redundant metrics is selected from the list of sensitive metrics such that collinearity is minimized. This process is informed by expert judgement in terms of which combination of metrics will optimize the balance of sensitivity and redundancy. Yet, setting thresholds for redundancy presents a challenge, as any metric sensitive to disturbance will be correlated with any other sensitive metric when they are measured in the same suite of wetlands. A novel approach to the dilemma of identifying what metrics to include from the pool of sensitive candidates involves generating a large number of permutations of MMIs comprising randomly selected metrics and testing these MMIs in a model competition framework to identify the best whole MMI. This is in contrast with the traditional approach of identifying the best individual, non-redundant metrics and combining these to make a final MMI. We applied both approaches to develop MMIs for prairie potholes in Alberta using wetland vascular plants from a pool of 55 candidate metrics. Permutations involved generating 50,000 MMIs with either 4, 6, or 8 metrics and identifying the best MMI using AICc values. We then compared these best MMIs with the MMI developed following the traditional approach, testing the MMIs with an independent validation dataset. We conclude that the best randomly generated MMI was more strongly predictive of wetland condition than the MMI produced following the traditional method. We recommend that future MMI development follow a permutation approach focused on competing whole MMIs rather than developing an MMI metric-by-metric, informed by expert judgement.

Examination of stress-induced heme oxygenase-1 (HO-1) accumulation and function in *Xenopus laevis* cultured cells

James Campbell

Supervisor: John Heikkila

Heme oxygenase-1 (HO-1) is a stress-inducible enzyme that catalyzes the rate-limiting step in the heme degradation pathway. Studies in mammalian systems determined that HO-1 promoted cell survival by inhibiting apoptosis and reducing oxidative damage in cells exposed to heavy metal toxicants. Furthermore, various inducers of HO-1 including hemin and baicalein, a plant flavonoid, are being investigated for their cytoprotective properties. While most of the knowledge regarding HO-1 synthesis and function has been derived from mammals, less is known about this stress-inducible protein in poikilothermic vertebrates including fish and amphibians. The aim of the present study is to investigate the stress-induced accumulation of HO-1 and its potential cytoprotective effects in A6 kidney epithelial cells derived from the aquatic frog, *Xenopus laevis*. Treatment of A6 cells with cadmium chloride, hemin or baicalein determined that HO-1 levels accumulated in a concentration- and time-dependent manner. While cadmium treatment also induced the accumulation of the heat shock proteins (HSPs), HSP70 and HSP30, their accumulation was not detectable in cells treated with baicalein or hemin. Pretreatment of cells with actinomycin D or cycloheximide (inhibitors of transcription and translation, respectively) abolished stressor-dependent HO-1 accumulation denoting its *de novo* synthesis. Since stress-induced HO-1 accumulation can occur in response to oxidative stress, reactive oxygen species (ROS) production was measured using a fluorescent probe in A6 cells. Putative ROS generation by these stressors was compared to cells treated with a known ROS inducer, namely, buthionine sulfoximine (BSO), an inhibitor of glutathione synthesis. While cadmium chloride treatment resulted in increased production of ROS, treatment of A6 cells with hemin or baicalein did not. This suggested that hemin- and baicalein-induced accumulation of HO-1 in A6 cells was largely independent of ROS generation. Given that hemin and baicalein treatment induced HO-1 accumulation without enhancing ROS levels, future studies will examine if their pretreatment in A6 cells can ameliorate the harmful effects of cadmium exposure. Additional information on the cytoprotective role of HO-1 is of vital importance given that aquatic poikilothermic vertebrates are sentinel species for environmental contaminants. (Supported by NSERC)

Lipid content of Atlantic salmon (*Salmo salar* L.) at West Greenland

Audrey Dean

Supervisor: Michael Power

Lipids in Atlantic salmon (*Salmo salar*) serve as important energy reserves to sustain the fish on its migration from their summer feeding grounds to their natal streams to spawn and are critical determinants of spawning success. To date, very few studies have examined the marine phase of Atlantic salmon life history. Given that feeding and the acquisition of lipids are critical components of the marine life history of Atlantic salmon, this study seeks to examine the lipid content of summer feeding Atlantic salmon captured at West Greenland to determine: 1) the spatial and temporal variation in lipid content; 2) the relationship between diet and lipid content; 3) the relationship between growth and lipid content; and, 4) the relationship between migration distance to West Greenland and lipid content. We expect to find that Atlantic salmon collected from higher latitude locations in Greenland will have greater lipid content. We expect that Atlantic salmon consuming capelin will have the highest lipid content. We expect that there will be a negative correlation between somatic growth and lipid storage and between migration distance and lipid storage.

Subdural infusion of kynurenic acid causes myelin loss in chicken optic nerves

Akshay Gurdita

Supervisor: Vivian Choh

Purpose: Kynurenic acid (KYNA) is a neuro-active metabolite of tryptophan present in the central nervous system. Previous work revealed that prolonged subdural infusion of high levels of KYNA reduced the numbers of myelin sheaths in the rat spinal cord without inducing an inflammatory response. We hypothesize that a similar infusion of KYNA induces myelin loss in the optic nerves of chickens.

Methods: Seven day old *gallus gallus domesticus* chickens were randomly selected for infusion of 50 mM KYNA (n = 4) or phosphate buffered saline (PBS; n = 3), at a rate of 0.5 mL/hr into the optic nerve. After 7 days of infusion, birds were sacrificed by cardiac perfusion. A third group of age-matched birds received no treatment (n = 4) and served as negative controls. Electron micrographs were collected and the percentage of myelinated axons were calculated. A one-way ANOVA was used to determine differences between the groups.

Results: KYNA-infused nerves exhibited widespread loss of myelin sheaths associated with astrogliosis and without inflammatory infiltration of the nerve. PBS-infused nerves exhibited slight localised loss of myelin sheaths while all the nerves in the negative control birds had no changes. Preliminary data for the implanted nerves from each group indicated that the percent of myelinated axons in KYNA-infused chicks (mean \pm sd: 22.4% \pm 14%) were lower than the PBS-infused (72.8% \pm 11.0%; p = 0.0004) and negative control birds (90.0% \pm 4.10; p = 0.0008). The percent of myelinated axons in PBS-infused birds, were slightly reduced compared to negative control birds (p = 0.0401).

Conclusions: Subdural infusion of 50 mM KYNA for 7 days induces myelin loss without inflammatory infiltration in the chicken optic nerve. PBS-infused birds also showed a slight loss of myelination, likely due to the surgical procedure. Our model of subdural infusion of KYNA may be useful for illuminating mechanisms of oligodendrocyte function and myelination in the optic nerve.

The DNA damage response markers γ H2AX and p53 as potential biomarkers of genotoxic stress in a rainbow trout (*Oncorhynchus mykiss*) brain cell line

Mark Hamilton

Supervisor: Bernard Duncker and Niels Bols

Environmental contamination due to by-products and waste from industrial activities is a growing universal concern, especially regarding the impact on water and the aquaculture industry. Conventional tests to diagnose genotoxicity in fish include the comet assay and the quantification of micronuclei; however, these techniques are tedious and uninformative as to the nature of DNA damage occurring and the resulting gene response of the organism. Biomarkers are continually being identified and characterized for use in affected fish species. This study involves surveying the activity of two biomarkers involved in the DNA damage response - the phosphorylated histone variant γ H2AX, a marker of double-stranded breaks, and the tumour suppressor protein p53 – in a brain cell line derived from rainbow trout named RTbrain-W1. Using Western blotting, we show that both are robustly inducible within 4h in non-lethal acute exposures of bleocin, a radiomimetic drug, and testing with methyl methanesulfonate (MMS), a DNA adduct forming agent, induces γ H2AX after 12h and leads to p53 destabilization. Treatment with non-model genotoxicants 2-mercaptobenzothiazole (2-MBTH) and 4-nitroquinoline-N-oxide (4-NQO), leads to abrupt downregulation of p53, and subtle inductions of both biomarkers, respectively. Taken together, these data highlight the potential of p53 and γ H2AX as biomarkers in diagnosing various genotoxic effects to rainbow trout *in vitro*.

Acute and chronic effects of multiple stressors on microRNA in zebrafish

Heather Ikert

Supervisor: Paul Craig

As the human population increases, increased anthropogenic stress is placed on the environment. Venlafaxine (VFX) is an antidepressant found downstream of wastewater treatment plants, at 1 µg/L. Also, increased water temperature and decreased oxygen content have been observed as a result of human activity. A multi-stressor approach was used to understand the cumulative effects of different stressors on zebrafish. Specifically, the effects of VFX, increased temperature, and decreased oxygen on microRNA (miRNA) levels in adult zebrafish were studied to determine sub-lethal, epigenetic effects. Adult zebrafish were exposed to control (27°C, 100% O₂, 0 µg/L VFX) or stressed (32°C, 50% O₂, 1 µg/L VFX) treatments for 24 hours or 21 days. Liver, gonad, and muscle tissues were removed, RNA was extracted, and RT-qPCR was performed on specific miRNA related to proteins that respond to hypoxia, heat stress, and contaminants. This comparison between times of exposure showed differences between initial and acclimated responses. Due to the conserved nature of miRNA, this will improve our understanding of the effects that environmental stressors have on epigenetic regulation.

Discerning the effects of major energy projects, climate change and distributary flow on lakes of the Athabasca Delta using paleolimnology

Mitchell Kay

Supervisor: Roland Hall

The Peace-Athabasca Delta (PAD) in northern Alberta is the world's largest boreal freshwater delta. The majority of the PAD lies within the borders of Wood Buffalo National Park, which is Canada's largest national park and one of Canada's UNESCO World Heritage Sites. Ecological health of the abundant lakes and wetlands is largely dependent on periodic river floodwaters and is closely tied to shifting hydrologic conditions. These lakes and wetlands provide important natural resources for the nearby indigenous communities and habitats for a variety of biota. Concern has been growing over potential effects of major energy projects (WAC Bennett and Site C dams on the Peace River, oil sands development on the Athabasca River) and climate change on lakes in the delta. In the southern Athabasca sector of the delta, prior paleolimnological analyses at three lakes identified that hydrological conditions are strongly influenced by recent changes in distributary flow and other research determined that river sediment metal concentrations are within the range of natural variability. Yet, uncertainty remains regarding the extrapolation of these results over space and time, given the hydrologically dynamic and complex nature of the Athabasca Delta. Consequently, sediment cores were collected in summer of 2015 and 2016 from 10 lakes spanning the upstream and downstream portions of the Athabasca Delta using a hammer gravity corer, and sectioned into 1-cm intervals (~2-5yr resolution). Sub-samples from each interval are being analyzed for chronological, physical, and geochemical variables, diatom algae, and concentrations of metals to reconstruct past hydroecological conditions and metal deposition for the past >100 years. Preliminary results appear to confirm that recent geomorphic changes, which have altered the flow-path of the Athabasca River and its distributaries within the delta, have had a profound influence on sediment composition. In recent decades, Athabasca River flow has become diverted away from the Athabasca Delta, the traditional territory of the Athabasca Chipewyan First Nation, and northward towards Mamawi Lake and the Peace River. The timing of the changes identifies the natural river avulsion in 1982, known as the Embarras Breakthrough, as the main cause of the changes, not the 1968 construction of the WAC Bennett Dam as has been widely believed. Ongoing analyses will continue to refine paleohydrological reconstructions and establish baseline sediment metals concentrations required to assess for evidence of pollution from upstream oil sands development.

The effect of isothiocyanates on heme oxygenase-1, heat shock protein and α -tubulin accumulation and localization in *Xenopus* A6 kidney cells

Imran Khamis

Supervisor: John Heikkila

Numerous studies have elucidated the health promoting properties of organosulfur compounds derived from cruciferous vegetables known as isothiocyanates (ITCs). As electrophiles, the impact of ITCs at the molecular level is profound, with the ability to directly bind and modify thiol-containing compounds such as glutathione and cellular protein, including tubulin. In the present study, I examined the effect of 10 μ M benzyl isothiocyanate (BITC), 5 μ M phenethyl isothiocyanate (PEITC) and 20 μ M sulforaphane (SFN) on stress protein (heme oxygenase-1 [HO-1] and heat shock proteins [HSP70 and 30]) accumulation and localization in A6 kidney epithelial cells derived from the frog, *Xenopus laevis*. Immunoblot analysis revealed that treatment with each of the 3 ITCs for 12 h at 22 °C induced the accumulation of HO-1 and HSP70 while HSP30 was only observed in cells treated with BITC at 30 °C. Interestingly, the addition of BITC to A6 cells enhanced the presence of aggregated protein as determined by immunocytochemistry. Furthermore, pretreatment of cells with BITC reduced the formation of MG132-induced aggresome-like structures. Since the formation of aggresomes involves their movement along microtubules, it was possible that BITC may disrupt this process. Immunoblot analysis revealed significant decreases in the relative levels of tubulin following BITC or PEITC treatment while SFN had a lesser effect. Immunocytochemical analysis determined that BITC induced the collapse and fragmenting of the microtubule cytoskeleton while PEITC and SFN treatment of A6 cells had a lesser effect. Finally, BITC and PEITC treatments performed at 30 °C greatly enhanced microtubule disruption. Since a great deal of the molecular and cellular research with *Xenopus* is applicable to humans, an increase in our knowledge of the effects of ITCs is of importance given their potential role as therapeutic compounds in the treatment of cancer, neurodegenerative diseases and bacterial and viral infections (Supported by NSERC).

Assessing the Accuracy of the Community Aquatic Monitoring Program (CAMP) in describing littoral nekton assemblages of estuaries within the southern Gulf of St. Lawrence

Jessica Kidd

Supervisors: Simon Courtenay² and Mark Servos¹

¹Canadian Rivers Institute and Department of Biology, University of Waterloo, Waterloo ON

²Canadian Rivers Institute and School of Environment, Resources and Sustainability, University of Waterloo, Waterloo ON

The Community Aquatic Monitoring Program (CAMP) is a community-based monitoring program that involves local stakeholders to monitor estuaries and bays in the southern Gulf of St. Lawrence. Implemented in 2003, CAMP continues to be administered by Fisheries and Oceans Canada (DFO) in collaboration with the Southern Gulf of St. Lawrence Coalition on Sustainability (Coalition-SGSL). Data are collected annually from up to 35 sites, and include counts of nearshore fish, shrimp, and crabs (i.e., nekton) along with measures of aquatic vegetation, water quality and sediment. The CAMP dataset has potential to inform decision-makers on the relationship between the health of an estuary and its nekton assemblages. However, concerns have been raised regarding the CAMP station selection method, as the majority of station locations were selected to provide easy road access for volunteers. The objective of this study was to assess the ability of CAMP to provide a measure of littoral nekton that represents the overall littoral nekton community of the estuary. The sampling design of CAMP was tested by comparing it to a sampling program that applied a stratified random design. In the summer of 2016, ten estuaries were sampled using CAMP methodology and a boat to access stations. Twelve stations were sampled within each estuary with six stations located where CAMP samples, and another six stations randomly located and stratified among the upper, middle, and lower estuary. Differences between the nekton community data were assessed using a cluster analysis, non-metric Multidimensional Scaling (nMDS) ordination, and permutational MANOVA (PERMANOVA). Significant differences were not detected. The results indicate the application of CAMP is not limited by station selection bias. Furthermore, programs designed to accommodate volunteers can produce comparable data to scientific studies. Analysis of the entire CAMP dataset is needed to determine how it can be used to inform decision-makers.

An occupancy model approach to identifying young-of-year Arctic Grayling habitat in northern mountain streams

Brent Lewis

Supervisor: Heidi Swanson

An improved understanding of the distribution and habitat requirements for mountain stream populations of Arctic Grayling (*Thymallus arcticus*) is necessary to assess their vulnerability to environmental stressors, establish thresholds for development activities, and evaluate population distribution trends over time. As developmental activities reach deeper into remote mountain environments in Canada's north, populations of Arctic Grayling may be used as an indicator of changes in freshwater health. Life stage-specific habitat use may be a particularly sensitive indicator of environmental change, but baseline data is lacking, especially for young-of year (YOY) Arctic Grayling. Occupancy based survey methods were used in the Little Nahanni River watershed in 2015 to quantify Arctic Grayling occupancy across the landscape. Data on a suite of associated habitat variables were also collected to explain YOY occupancy and to relate to detection efficiency during field surveys; detection efficiency is an often-neglected aspect of field sampling that affects species-habitat relationships. Occupancy modelling has revealed that stream temperature and percent coarse woody debris best explain YOY occupancy in the Little Nahanni River. Factors affecting the detection efficiency of our surveys included percent boulder substrate and percent riffle. By accounting for imperfect detection, my research helps to better quantify habitat that is important for a sensitive life stage of Arctic Grayling and create baseline distribution data for future monitoring efforts. Similar occupancy methods can be used by industry and regulatory organizations to increase standardization and efficiency of sampling in remote areas, and assess changes in Arctic Grayling distribution that may reflect changes in water quality and stream features.

Microbial production of vitamin B₁₂ in soil

Xinda Lu

Supervisor: Josh Neufeld

Xinda Lu¹, Katherine R. Heal², Anitra E. Ingalls², Andrew C. Doxey¹, Josh D. Neufeld¹

¹Department of Biology, University of Waterloo, Waterloo, ON, Canada

²School of Oceanography, University of Washington, Seattle, WA, USA

Vitamin B₁₂ (cobalamin) is the most structurally complex vitamin, requiring approximately 30 enzymatic steps for its synthesis. Despite the availability of genomes from cultivated cobalamin producers, microorganisms that produce cobalamin *in situ* are poorly characterized, especially in terrestrial environments. Given the necessity of cobalamin for microbial growth, and the fact that soil contains enormous microbial diversity, it is important to elucidate the production and consumption of cobalamin in terrestrial environments. We analyzed 156 global soil metagenomes from wide variety of terrestrial biomes, within which three representative sets of *cob/cbi* genes (coding enzymes for corrin ring biosynthesis, final synthesis, and lower ligand synthesis and activation) were surveyed to identify cobalamin producers, using profile Hidden Markov models (HMMs). The dominant cobalamin-producing taxa include members of the *Proteobacteria*, *Actinobacteria*, *Firmicutes*, and *Thaumarcheota*, but the relative abundance of cobalamin-producing genes affiliated with these phyla varied across samples. The overall cobalamin production potential relative to the community size was $9.8 \pm 4.0\%$, based on a comparison of cobalamin synthesis genes and a reference housekeeping gene (*rpoB*). The dominant microorganisms for different steps of cobalamin synthesis varied. For example, *Proteobacteria* were dominant for all biosynthesis steps, but contributed to bottom ligand synthesis disproportionately. In addition to surveying for genomic potential, we also measured four different forms of cobalamin (Ado-, CN-, Me- and OH-) in water-extractable and whole soil samples. OH-B₁₂ was the dominant form of cobalamin in the analyzed soils, although CN-B₁₂, an inactivated form of cobalamin was detected in several soils at relatively high concentrations, at times exceeding the OH-B₁₂ concentration. The concentrations of cobalamin varied among different soils, accumulating as high as ~ 6.7 pmol g⁻¹ dry soil, indicating soil is not a cobalamin-oligotrophic environment. The water-extractable portion of the cobalamin concentration contributed only a small percentage of the total cobalamin measured, suggesting only a small fraction of biosynthesized cobalamin is being exuded. The concentration of the lower ligand of cobalamin was up to 2 orders of magnitude higher than cobalamin, indicating a possible cooperation among cohorts that produce different parts of cobalamin molecule, supporting the genomic analyses. Our results showed taxonomic affiliations with *in situ* microbial cobalamin production in soil, and accurately demonstrated the presence of different forms of terrestrial cobalamin. The variation of cobalamin-producing gene abundances in different steps within cobalamin producers, together with the presence of *btuB* gene in species unlikely to produce cobalamin, suggests that cobalamin and its precursors and degradation products may serve as molecules that regulate interactions among soil microorganisms.

Data mining genomes and metagenomes to uncover botulinum neurotoxin evolution

Michael Mansfield

Supervisor: Andrew Doxey

Little is known about the evolutionary origins of the botulinum neurotoxin (BoNT), which is an important agent of foodborne illness. In order to elucidate the relationships between BoNTs and other protein families, we performed a large-scale search of publically available microbial genomes and metagenomes. Further, we created the first vertebrate carrion metagenome, an environment known to harbour *Clostridium botulinum*, and which may contain clues needed to understand the origins of the BoNT family. In this work, we present new BoNT homologs with links to several other important toxin families, as well as a new model of neurotoxin evolution. We also present the evidence for the vertebrate carrion environment as an important reservoir of unexplored phylogenetic and functional novelty.

Assessing reasons for changes in the condition of Deception Bay Arctic charr (*Salvelinus alpinus*)

Mackenzie Martyniuk

Supervisor: Michael Power

The Raglan Mine has offered a sport fishing program for employees for almost 20 years, and since 2004, biological data collected through this program, as well as environmental monitoring data, have documented a decline in the somatic condition of Deception Bay Arctic charr (*Salvelinus alpinus*). This has prompted the local Hunting, Fishing, and Trapping Coordinating Committee (HFTCC) to authorize the necessary scientific research to assess the Arctic charr populations of Deception Bay and River. To address this request: (1) a comparative statistical analysis of available Arctic charr biological data from the Nunavik region will be performed to determine if a similar region wide pattern of declining condition exists, and (2) a series of within and between site assessments of condition will be completed to link observed changes to seasonal and/or environmental factors. Muscle, liver, and water samples collected from Deception Bay, the Red Dog River (reference site near Aupaluk, Québec), and Deception River headwater lakes Duquet and François-Malherbe will be analyzed for As, Cd, Cr, Cu, Hg, Ni, Pb, and Zn concentrations. Dorsal muscle tissue will also be used for the determination of stable isotope composition ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$). Thus the project will address possible reasons for the declines in the average somatic condition of Deception River Arctic charr, which are of critical importance to local communities.

Multi-Stressor Impacts on Fish Energetics: A Comparison between Lab and Field Studies

Hossein Mehdi

Supervisor: Paul Craig

Aquatic organisms face numerous stressors simultaneously in their environments. While each of these stressors pose great threats to aquatic life, studying each stressor individually is not sufficient, as these stressors are not independent, but work cumulatively and synergistically to alter aquatic ecosystems. The objective of this study was to compare and contrast the impacts of multi-stressors under lab and field conditions using two fish species, zebrafish (*Danio rerio*) and rainbow darters (*Etheostoma caeruleum*). Under lab conditions, the study examined the impacts of chronic exposure to environmentally relevant concentrations of venlafaxine, an antidepressant pharmaceutical contaminant found abundantly in wastewater treatment plant effluents, in combination to elevated water temperatures on zebrafish. Under field conditions, rainbow darters were collected from two sites, upstream and downstream of a wastewater treatment plant, which served as control and contaminated sites respectively. Muscle tissue was sampled from both lab and field species to measure enzyme activity of major metabolic enzymes and metabolites involved in regulating energetics in fishes. Circulating levels of stress hormone, cortisol, were measured from holding water of fishes. Oxygen consumption was measured using respirometers to assess the effects of stressors on standard metabolic rate, active metabolic rate, and aerobic scope, all of which can be used as ecological performance indicators. The results of this study will contribute to the recognized importance of including multi-stressor approach assessments to make predictions regarding the impact of stressors on fish health and abundance.

Scavenging For Bacteria: Identification And Functional Characterization Of Two Rainbow trout (*Oncorhynchus mykiss*) MARCO variants

Sarah Poynter

Supervisors: Brian Dixon and Stephanie DeWitte-Orr

SARAH J. POYNTER, Andrea Monjo, Gabi Micheli, and Stephanie J. DeWitte-Orr

Class A scavenger receptors (SR-As) are a family of key innate immune receptors, which bind to a wide range of polyanionic ligands including bacterial components and nucleic acids. Macrophage receptor with collagenous structure (MARCO) is a SR-A that has been studied in mammals largely for its role in binding bacteria. To date there is little information about SRAs in fish, and what ligands specific SR-A family members bind remains largely unknown. In this present study two novel rainbow trout MARCO transcripts have been identified and their sequence and putative protein domains have been analyzed. While there is only moderate sequence similarity to mammalian MARCO sequences there are notable protein domain similarities and MARCO-1 and MARCO-2 cluster with MARCO sequences from other species more closely than other fish scavenger receptors. When overexpressed in CHSE-214, a cell line that lacks functional scavenger receptors, rainbow trout MARCO is able to bind gram-positive, and gram-negative bacteria (of both mammalian and aquatic sources). MARCO did not show any binding to the yeast cell wall component zymosan or to dsRNA. When the MARCO sequences were mutated to remove a domain necessary for bacterial binding in mammals, the scavenger receptor cysteine-rich domain, MARCO no longer bound bacteria. This is the first time rainbow trout MARCO sequences have been identified, and the first in-depth study exploring a rainbow trout class A scavenger receptor ligand binding profile. This study provides novel insight into the role of rainbow trout MARCO variants in bacterial innate immunity.

Would You Give a Fish Grapefruit?: The Use of a Fish Intestinal Cell Line to Test Potential Fish Feed Additives

Patrick Pumputis

Supervisors: Niels Bols and Vivian Dayeh

P.G. PUMPUTIS¹, V.R. Dayeh¹, L.E.J. Lee² and N.C. Bols¹.

¹University of Waterloo, Department of Biology, Waterloo, ON N2L 3G1, CANADA and

²University of the Fraser Valley, Department of Biology, Abbotsford, V2S 7M8, CANADA.

Identifying feed additives to promote fish health can have beneficial impacts on the aquaculture industry. Rising water temperatures resulting from global warming are a hurdle to overcome in the industry. Fish more frequently subjected to intense heat stress have lower reproductive rates and higher mortality. Dietary modulations provide the means to mitigate these unwanted effects. However, *in vivo* studies are difficult, time consuming, and expensive. Here we demonstrate *in vitro* assays that can identify potential feed additives in a quick and relatively cheap manner. RTgutGC, a rainbow trout intestinal epithelial cell line, was used as a model to study the effects of various potential feed additives. One component of interest was naringenin, a plant secondary metabolite found in grapefruits with antioxidant, anti-inflammatory, and anti-carcinogenic properties. With our assays, naringenin morphologically helped the cells survive heat stress, increased barrier functions, and promoted peripheral actin arrangements. Naringenin's actin modulating effects decreased lamellipodia and filopodia structure formation and thus migratory capabilities. Naringenin appears to exert protective effects for barrier maintenance, possibly through actin modulation. The lack of cell migration when treated with naringenin suggest that it promotes a type of "cellular anchoring" by possibly altering signaling pathways when considering proper actin arrangement plays a large role in cellular migration. At low concentrations naringenin could be a useful feed additive to promote barrier integrity.

Evaluation of peptide inhibitors on single amyloid molecules and survival to toxic oligomers

Morgan Robinson

Supervisors: Zoya Leonenko

Alzheimer's disease (AD) is potentially the single greatest age related challenge facing our society today. A key component in AD is the amyloid-beta protein which aggregates to form toxic oligomers that bind to and damages neurons, disrupting synaptic plasticity and eventually resulting in major atrophy of brain regions important for memory and learning, this results in cognitive decline and memory loss. Prevention of toxic oligomer formation may prove to be effective in ameliorating the pathology associated with amyloid-beta, as such peptide based inhibitors designed to prevent self association of amyloid monomers and the toxic cascade of AD have been developed. Evaluation of these inhibitors to prevent dimerization and thus aggregation as well as the ability of inhibitors to prevent toxicity of amyloid-beta on neuronal cell lines is presented here. These SG inhibitor drugs are effective at preventing monomer-monomer interactions as measured using single molecule platform via atomic force spectroscopy and that SG inhibitors show some evidence to suggest that they improve cell viability of neurons exposed to amyloid-beta.

The Mammalian Skin Microbiome

Ashley Ross

Supervisor: Josh Neufeld

Characterization of the microorganisms on skin is essential for understanding how a host evolves in association with its microbial symbionts, modeling immune system development, diagnosing illnesses, and exploring the origins and etiology of disease. Although many studies have characterized the human microbiome, far less is known about the skin microbiome of non-human mammals. The objective of this research was to create a baseline skin microbiome dataset for the Mammalia class, testing the effects of species, location, hygiene, body region, and biological sex. The back, torso, and inner thigh regions of 187 non-human mammals and 20 human participants were collected to include representatives from 38 species and 10 mammalian orders. Animals were collected from local farms, zoos, households, and the wild. All samples were amplified using the V3-V4 16S rRNA gene region and sequenced using a MiSeq (Illumina). Human skin was significantly less diverse than all other mammalian orders according to Shannon indices (6.54 versus 3.96, $p < 0.001$). The factor most strongly associated with community variation for all samples was whether the host was a human (PERMANOVA, $F = 37.8$, $p < 0.001$; Figure 2). By analyzing all samples together, random forest modelling identified that human and animal samples could be distinguished correctly $98.5 \pm 1.2\%$ of the time. This study represents the largest mammalian skin microbiome project to date and is the first study to elucidate the skin microbiota for 32 distinct species. Additionally, these findings are the first to demonstrate that human skin is distinct, not only distinct from other Primates, but from all 10 mammalian orders sampled. Baseline data on the mammalian skin microbiome is crucial to make informed decisions for veterinarian research and conservation strategies, as well as providing implications for mammalian evolutionary history.

Combined effects of benzalkonium chloride and UV irradiation on the bovine lens *in vitro*

Jordan Rossy

Supervisor: Jake Sivak

Purpose: Exposure to ocular preservatives and ultraviolet (UV) irradiation have been associated with cataract formation. The purpose of this study was to evaluate the effects produced by consecutive exposure to BAK and UV irradiation on *in vitro* lens optical quality.

Methods: The study evaluated and compared the effects of three treatments on the bovine lens: (1) BAK (2) UV irradiation (3) BAK and UV irradiation (n=5). Control lenses were exposed to phosphate buffered saline (PBS) solution. For condition 1, lenses were exposed to BAK solutions (0.01%, 0.005%, and 0.001%) for 10 min. For condition 2, lenses were exposed to UV (280-400 nm) irradiation for 1.5 h. The measured irradiance was 1132.411 $\mu\text{W}\cdot\text{cm}^{-2}\cdot\text{nm}^{-1}$. For lenses in group 3 receiving both treatments, the lenses were exposed first to a BAK solution and then UV irradiation. The optical quality of the lenses was evaluated using a laser scanning instrument on day 0, day 2, day 7, day 14, day 16, day 18, and day 20 following exposure.

Results: The optical quality for lenses exposed to BAK was significantly reduced after day 7. The damage produced by exposure to BAK resulted in an increase in back vertex distance (BVD) variability. Treatment with BAK appeared to follow a dose-dependent model of damage. Similarly, lenses exposed to UV irradiation had increased BVD variability indicating reduced optical quality beyond day 7. For group 3, exposure to BAK and UV irradiation also produced reduced optical quality following day 7. However, there was no significant difference between the damage resulting from single or combined exposures to UV and BAK.

Conclusion: Exposure to either BAK or UV, or BAK and UV produces damage to the bovine lens after 7 days. However, combined exposure of BAK and UV did not produce significantly more damage than BAK exposure alone.

An analysis on the role of *hindsight* in establishing stem cell niches in the developing midgut epithelium of *Drosophila melanogaster*

Donya Saghattchi

Supervisor: Bruce Reed

The larval *Drosophila* midgut includes undifferentiated multipotent cells known as the Adult Midgut Precursors (AMPs). The AMPs give rise to three cell types found in the adult midgut epithelium: the intestinal stem cells (ISCs), the secretory enteroendocrine cells (EEs), and the absorptive enterocytes (ECs). During the late larval stages, AMPs produce a specialized cell type called the peripheral cell (PC), which encapsulates the AMPs and functions as a transient stem cell niche that is required to prevent premature AMP differentiation. AMPs communicate with PCs via the Notch signaling pathway. The gene *hindsight* (*hnt*) encodes a transcription factor that has been identified as a downstream target of Notch signalling in certain contexts. *hnt* is expressed throughout the larval midgut, and is expressed in the mature larval ECs as well as the AMPs and PCs. The expression of *hnt* within the PCs is elevated with respect to the AMPs but the role of *hnt* in the specification or differentiation of PCs has not been explored. Using a mosaic analysis approach, I show that *hindsight* expression is required for PC differentiation.

Characterization of CHUP1, a gene potentially involved in chloroplast partitioning in *Bienertia sinuspersici*

Dustin Sigurdson

Supervisor: Simon Chuong

Bienertia sinuspersici is one of four known terrestrial plant species capable of performing C4 photosynthesis without Kranz anatomy. These single-cell C4 species achieve the spatial and functional separation of carboxylation and decarboxylation reactions by compartmentation of organelles and photosynthetic enzymes in distinct cytoplasmic regions of individual chlorenchyma cells. While expression of photosynthetic enzymes has been studied extensively during development at the cellular level, little is known about the processes responsible for the unique organelle partitioning in *B. sinuspersici*. To further investigate the mechanisms underlying the intracellular compartmentation of organelles in *B. sinuspersici*, we characterized a potential candidate gene, chloroplast unusual positioning 1 (CHUP1), known for its role in chloroplast movement. In *Arabidopsis thaliana*, CHUP1 is required for normal chloroplast movement and relocation.

Short-term exposure to cadmium and manganese of two members of the *Hyaella Azteca* cryptic species complex

Kate Marie Sinclair

Supervisors: Jonathan Witt and George Dixon

Hyaella azteca is a freshwater amphipod crustacean broadly distributed across North America and has been used extensively in toxicity tests for over 25 years. Due to morphological similarities, *H. azteca* was considered a single species until recent molecular studies identified 85 different species. Toxicity tests using this amphipod have historically been conducted under the assumption of a single species, and only more recent studies have begun to investigate the effect of interspecific variability on results. This thesis explores exposure to cadmium and manganese of the two *Hyaella* species commonly used in Canadian and American laboratories. The responses considered are mortality, growth inhibition, bioaccumulation, uptake, and depuration kinetics. Previous work has shown that these two species differ in their short- and long-term responses to nickel and copper. Results from this study will contribute to the understanding of sensitivity differences among members within the *Hyaella* cryptic species complex.

Expression and Characterization of two *Streptococcal* zinc metalloproteases, and the novel flagellal protease of *C. haemolyticum*

Iain Wallace

Supervisor: Todd Holyoak

Zinc metalloproteases are a broad and ubiquitous class of enzymes. Among potentially pathogenic bacteria looking to subvert, evade or gain nourishment from the host, such enzymes provide appropriate functionality for survival and establishing infections. My work seeks to characterize biochemically, and ultimately structurally, the human IgA1 protease of *S. pneumoniae*, zinc metalloprotease C of *S. suis*, and the novel flagellal protease FliA(H) of *C. haemolyticum*.

Reeding the wetland: the effect of invasive *P. australis* on primary production and decomposition

Sarah Yuckin

Supervisor: Rebecca Rooney

A non-native lineage of *Phragmites australis* is replacing wetland vegetation communities in Long Point Peninsula on Lake Erie. Invasive *P. australis* is most commonly replacing rare meadow and cattail marshes. My research focuses on how primary production and decomposition rates in invaded *P. australis*, emergent cattail, and meadow marshes differ. To look at the effect of invasion on primary production, I examined above- and belowground standing crop biomass in invaded *P. australis* and uninvaded meadow and cattail marshes. I also measured decomposition rates, comparing rates for plant tissues produced by invasive *P. australis*, *Typha spp.* and *Calamagrostis canadensis*. Using a litter transplant experiment I was able to partition the effect of litter source from the effect of invasion on edaphic conditions. Carbon cycling may be altered in invaded wetlands if net primary production and decomposition rates are affected by *P. australis* invasion. Next summer, I will examine the efficacy of restoration and control efforts in returning primary production and decomposition rates to rates found in uninvaded marshes in this region.

