Welcome to York University's 49th Annual AGSBS Biology Symposium

Participants and Abstracts

Thursday, May 11th, 2023

Participant List

Symposium Committee Members

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Keynote Speakers

Dr. Anna Banerji, O.Ont., MD, MPH, FRCPC, DTM&H CTropMed
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Poster Judges

Dr. Jean-Paul V. Paluzzi, Ph.D
Dr. Patricia L. Lakin-Thomas, Ph.D
Dr. Mark Bayfield, Ph.D
Dr. Robert G. Tsushima, Ph.D
Dr. Nikola Kovinich, Ph.D.
Dr. Bridget Stutchbury, Ph.D

Career Workshop Speakers

Dr. Chun Chih Chen, Ph.D
Dr. Anthony Choo, Ph.D

Photography

Sehaj Raina

Student Talk Presenters

Shaina Jaff
Adriana Pagnani Primucci
Jennifer Porat
Rebecca Whiley
Nicholas Bragagnolo
Paula Quaglietta

Student Poster Presenters

Fatemeh Soheii
Sydney Steiman
Megan George
Aisha Abdul Rahiman
Sai Sowndarya Sundararaman
Sahib Singh Madahar
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Milad Falahat Chian
Taylor Cargill
Lina Rademacher
Shaina Jaff

Student Talk Presentations

Session 1

Student Talk Presenter #1

Name: Jennifer Porat
Program: Ph.D. Biology, York University
Field: Molecular Biology
PI: Dr. Mark Bayfield

The fission yeast methylphosphate capping enzyme Bmc1/Bin3 promotes 2'-O-methylation of U6 and pre-mRNA splicing

The spliceosomal RNA U6 undergoes numerous processing and post-transcriptional modification steps before incorporation into the spliceosome. Here, we identify a new U6-containing complex in fission yeast that shares components with the telomerase holoenzyme, including the 5' phospho-methyltransferase Bmc1. This complex promotes 2'-O-methylation of U6 and influences formation of the U4/U6 di-snRNP, and cells lacking Bmc1 show splicing defects at inefficiently spliced introns at elevated temperatures. Our results reveal a novel complex of proteins and RNA that cooperate to ensure splicing fidelity.

Student Talk Presenter #2

Name: Shaina Jaff
Program: M.Sc. Biology, York University
Field: Cell and Molecular Biology
PI: Dr. Michael Scheid

Gene Mapping and Effect of Doxorubicin on ICF-related proteins HELLS and CDCA7 and NHEJ associated protein Ku80 Immunodeficiency

Centromeric instability and facial abnormalities (ICF) syndrome, is a rare recessive disease characterized by growth and cognitive delays as well as recurrent life-threatening infections in childhood and is caused by mutations in methylation associated proteins HELLS and CDCA7. Epigenetic DNA methylation by DNMT's (DNA methyl transferases) regulates winding of chromatin to promote DSB repair by either NHEJ (nonhomologous end joining) or HR (homologous recombination). CDCA7 recruits HELLS to chromatin to form a bipartite nucleosome-remodeling complex that allows for CG methylation by DNMT3b and subsequent DSB repair, facilitated by NHEJ associated protein complex Ku80/70. Our lab has previously discovered that the phosphor-adapter protein, 14-3-3, binds with CDCA7 at T163 and when phosphorylated by Akt, this interaction relocates CDCA7 to the cytoplasm. Our lab is exploring the interaction of HELLS and CDCA7 and has demonstrated that this interaction is independent of 14-3-3 association. Further, we have identified an N-terminal region of CDCA7 as critical for

CDCA7's interaction with HELLS. We have also been able to show how Ku80 interaction is doubly enhanced when this specific N-terminal region is deleted, and this interaction is fourfold enhanced when 14-3-3 is prevented from binding at the T163 site. Continuing work will explore how interaction Ku80/70 complex with CDCA7 impacts DNA repair via doxorubicin functional assays visualized using western blot techniques, and could provide insight on potential therapeutic targets for ICF and associated cancers.

Student Talk Presenter #3

Name: Rebecca Whiley
Program: Ph.D. Biophysics, York University
Field: Sensory Neuroscience
PI: Dr. Christopher Bergevin (Sensory Biophysics Lab)

Convergent Otoacoustic Tuning Estimates in Anole Lizards

Rebecca Whiley,[1] and Christopher Bergevin,[2]

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2) Department of Physics and Astronomy, York University, Toronto, Ontario, Canada

The ear is an active detector, using energy to improve its function by enhancing its ability to detect sounds (sensitivity) and selectively differentiate between frequencies (tuning). Because of the work done by its active mechanism, the ear produces faint sounds called otoacoustic emissions (OAEs). OAEs can arise without external stimulation (spontaneous emissions, SOAEs) or in response to acoustic stimuli. For example, stimulus-frequency emissions (SFOAEs) occur at the stimulating frequency, like an echo. OAEs exhibit correlations with behavioural and electrophysiological measures of hearing and have established clinical applications. However, inconsistent relationships between OAEs and other measurements restrict their clinical utility for characterising tuning. In humans, there are disagreements between psychoacoustic estimates, SOAE suppression-tuning curves (STCs), and SFOAE phase-gradient delays (N_{sf}), with the latter overestimating tuning sharpness. The mismatch between STCs and N_{sf} is unexpected since these emissions are predicted to originate from the same sources. Complications may stem from the nonlinear, stimulus-level dependency of N_{sf}, raising questions about the appropriate stimulus level for comparisons. Additionally, potential relationships could be obscured by comparisons across different datasets since emissions are unique to an individual. To reconcile these uncertainties and elucidate the relationship between otoacoustic tuning estimates, we examined correlations between SOAE- and SFOAE-derived estimates in individual green anole lizards (*Anolis carolinensis*). Specifically, we characterised the level-dependence of N_{sf} across frequencies and extracted SOAE "interaction" tuning curves (ITCs) measured simultaneously. This technique allowed us to quantify estimates from each ear using the same stimuli. We also used SOAE inter-peak spacing to calculate N_{SOAE}, providing a stimulus-independent metric for reference. Results demonstrate that accounting for the level-dependence of emissions and individual variations is important for obtaining convergent otoacoustic tuning estimates.

Session 2

Student Talk Presenter #1

Name: Nicholas Bragagnolo
Program: Ph.D. Chemistry, York University
Field: Structural Biology
PI: Dr. Gerald Audette

Structural Studies of the Conjugative Entry Exclusion Protein TraG
By: Nicholas Bragagnolo and Gerald F. Audette York University, funded by NSERC

The R100 plasmid is representative of F-like conjugative type IV secretion systems for the transmission of mobile DNA elements in gram-negative bacteria, serving as a major contributor to antibiotic resistance. The TraG protein of F-like systems consists of a membrane-bound N-terminal domain and a periplasmic C-terminal domain, denoted TraG*. TraG* is essential in preventing redundant DNA transfer through a process termed entry exclusion. In the donor cell it interacts with TraN to facilitate mating pair stabilisation, however if a mating pore forms between bacteria with identical plasmids, TraG* interacts with its cognate TraS in the inner membrane of the recipient bacterium to prevent redundant donor-donor conjugation. Structural studies of TraG* from the R100 plasmid have revealed the presence of a dynamic region between the N- and C-terminal domains of TraG; thermofluor, circular dichroism, collision induced unfolding mass spectrometry and SEC-MALS-SAXS experiments showed N-terminal truncation mutants displayed higher stability and less disordered content relative to full-length TraG*. The 45 N-terminal residues of TraG* are hypothesized to serve as a flexible linker between the two independently functioning domains. These studies guide further crystallisation trials to elucidate a high-resolution structure of TraG* and determine the mechanism of the TraG-TraS interaction.

Student Talk Presenter #2

Name: Adriana Pagnani
Program: Ph.D. Biology, York University
Field: Stem Cell Biology
PI: Dr. Terry Sachlos (Stem Cell Engineering Lab)

Engineering an in vitro vascular niche for hematopoietic stem cell fate regulation

Haematopoietic stem and progenitor cells (HSPCs) are crucial to the curative treatment of a variety of cancers and autoimmune diseases. However, their rapid differentiation and exhaustion within 72 hours ex vivo poses a barrier to efficient treatment. Here, we have developed a culture method that mimics that of the in vivo haematopoietic vascular niche in order to extend viability and maintain multipotency of HSPCs. The two-factor approach combined the paracrine support

of endothelial cells as well as the structural and chemical support of an engineered two-dimensional scaffold comprised of several extracellular matrix (ECM) components. Scaffold co-culture was found to be superior to scaffold-only culture or conditioned media in maintaining HSPC viability and function over 7 days, and one multi-combinatorial scaffold was found to upregulate mRNA levels of genes related to HSPC maintenance and function in endothelial cells. Continued development of the culture system and understanding of the molecular pathways at play can lead to improved patient outcomes after transplantation.

Talk Presenter #3

Name: Paula Quaglietta
Program: M.Sc. Medical Science, University of Toronto
Field: Cancer/Pediatric Cancer
PI: Dr. David Malkin and Dr. Reto Baertschiger, The Hospital for Sick Children

Rhabdomyosarcoma-derived extracellular vesicles contain clinical characteristic-specific protein expression patterns

Paula R. Quaglietta[1,2], Ashby Kissoondoyal[1], Ann Gong[1], Ethan Malkin[3], Lisandro Luques[1], David Malkin[1,2,4], Reto M. Baertschiger[1,2,5]

1 Genetics and Genome Biology Program, The Hospital for Sick Children (SickKids), ON, Canada; **2** Institute of Medical Science, The University of Toronto, ON, Canada; **3** Princess Margaret Cancer Centre, ON, Canada; **4** Division of Haematology/Oncology, SickKids, ON, Canada; **5** Department of Thoracic and General Surgery, SickKids, ON, Canada

Rhabdomyosarcoma is the most common pediatric soft tissue sarcoma. Current diagnostic methods involve imaging and tissue biopsy for staging, histology, and *PAX3/7-FOXO1* gene fusion status assessment. There are presently no serum biomarkers for rhabdomyosarcoma diagnosis or surveillance. Novel approaches and identification of biomarkers are warranted for minimally invasive diagnostic/surveillance techniques. Liquid biopsies, a minimally invasive diagnostic/surveillance approach, utilize biological fluids to detect tumour-derived entities. Extracellular vesicles (EVs), critical mediators of intercellular communication and the pathophysiology of tumorigenesis, are an ideal liquid biopsy analyte.This study aimed to characterize the proteome of rhabdomyosarcoma-derived EVs and identify proteomic signatures for future use as minimally invasive liquid biopsy diagnostic and surveillance techniques. We hypothesized that rhabdomyosarcoma-derived EV protein expression was associated with tumoral clinical characteristics, such as histological subtype fusion status, and cancer stage.EVs were isolated from cell culture conditioned media by differential ultracentrifugation from four rhabdomyosarcoma cell lines (RH4, RH18, RH30, RD), each in triplicate, and from 16 biobanked rhabdomyosarcoma patient plasma samples using ExoQuick Ultra. Liquid chromatography-tandem mass spectrometry identified and quantified EV protein cargo for differential expression analysis. We identified 1,183 total proteins in our rhabdomyosarcoma-derived EVs. We also identified protein patterns correlating with PAX3/7-FOXO1 fusion status, histological subtype and *TP53* mutation status. Associations

between unique protein cargo of rhabdomyosarcoma EVs and clinical rhabdomyosarcoma characteristics suggest a potential liquid biopsy method for diagnosis or surveillance. Validation of these expression patterns in human plasma samples is necessary to establish this new technology as an effective liquid biopsy for pediatric rhabdomyosarcoma.

Student Poster Presentations

Poster Presenter #1

Name: Fatemeh Soheili
Program: Ph.D. Biology, York University
Field: Cellular and Molecular Biology, Bioengineering
PI: Dr. Ebrahim Ghafar-Zadeh Lab (BIOSA)

Toward oral neutrophil as a biomarker for the development of new biosensing technology for periodontal disease detection

Periodontal diseases are inflammatory conditions affecting the immune system that, if left untreated, leads to tissue degeneration, loss and, at high levels, death. It has a negative relationship with a variety of diseases. The rising prevalence of periodontal disease allowed the creation of diagnostic tests that could detect active disease, track its progression, and analyze its response to therapy. Neutrophils are immune cells that react quickly to changes in the body. They are a large immune cell population in blood and saliva, which may serve as a diagnostic factor for oral disease severity because the mouth is a microenvironment, and it contains migrated neutrophils from circulation. Monitoring the presence and quantity of neutrophils in the oral environment can have significant implications for assessing the severity of the clinical periodontal disease. Additionally, it presents an opportunity for non-invasive screening using oral fluid as an alternative to blood. However, currently, no assay exists for detecting oral neutrophils for diagnostic purposes. Therefore, the goal of this research project is to develop a novel method for the early detection of periodontal diseases. In this research, we isolate, detect, and count saliva-derived neutrophils with a novel method relying on the adhesion property of oral neutrophils which can be used as a point of care. In the future, we may detect periodontal diseases in the early stage. Keywords: Periodontal Disease, Periodontitis, biomarkers, Neutrophil, Screening tools

Poster Presenter #2

Name: Sydney Steiman
Program: M.Sc. Biology, York University
Field: Cell and Molecular Biology
PI: Dr. John C. McDermott

Expanding our knowledge of the role of MEF2 during myogenesis using innovative biochemical approaches

Understanding novel protein interactions during myogenesis, the embryonic and adult stages of muscle development, in tandem with emerging biochemical approaches allows researchers to take innovative approaches to expand our knowledge. Myogenesis is a complex multistage developmental process that requires stringent control of both genetic transcription, translation, and protein interaction to ensure proper muscle formation. A key transcriptional switch highly

involved in the conversion of myoblasts, proliferative cells, in a mature multinucleated myotube during repair or stress, is Myocyte Enhancer Factor 2, MEF2. MEF2 proteins are regulators for satellite cells, quiescent cells in skeletal muscle that become active under stress conditions, as well as maintaining cardiomyocyte populations that are not able to divide in adulthood. MEF2 and its interacting partners have been implicated in many diseases including cardiac hypertrophy. To investigate the role of this vital protein we employed various biochemical approaches including a GFP-Nanobody trap using nanobodies and conjugated beads tandem with LC/MS-MS, bimolecular functional complemental (BIFC), EYFP fusion proteins for liquid-liquid phase separation, and GBP-lamin B1 anchoring assays. A combination of all of these assays has allowed for the characterization of novel protein-protein interactions between MEF2 and other key factors during myogenesis that can play a larger role in both the development and maintenance of striated muscle.

Poster Presenter #3

Name: Megan George
Program: Undergraduate Thesis, York University
Field: Urban Ecology
PI: Dr. Sandra Rehan

Rapid urbanization - understanding the effects of land use on bee body size, abundance and foraging efforts

Urbanization continues to impact biodiversity, including bees primarily because of the growth of urbanized areas and the changes in land-use types. The impact of urbanization on wild bee populations is still uncertain, as evidenced by the conflicting accounts of the variety of bee species and functional traits found in urban landscapes. In order to explore this existing controversy, we examined whether three urbanization levels (low, medium and high) influence the abundance, foraging efforts and body size of five wild bee species. We observed all five wild bee species to be highly abundant in low and medium-intensity sites. In addition, Agapostemon sericeus displayed a male-bias sex ratio in the highest-intensity site. Based on wing wear, a proxy used for foraging effort, we observed the highest wing wear in male Eucera pruinosa at the lowest intensity level and the highest wing wear in male Ceratina calcarata at the medium-intensity sites. Based on body size, male E. pruinosa bees were largest in the medium-intensity sites and female C. calcarata were largest in the highest-intensity sites. Our results indicate that wild bee species can obtain adequate resources for food and nesting in moderate to highly urbanized sites. Furthermore, based on our discovery of increased bee abundance in low to medium-urbanization sites, we propose the preservation of varying degrees of urbanization levels in densely populated cities could have a more favourable effect on the conservation of wild bee species.

Poster Presenter #4

Name: Aisha Abdul Rahiman
Program: M.Sc. Biology, York University
Field: Developmental Neuroscience
PI: Dr. Dorota Anna Crawford

Maternal exposure to prostaglandin E2 affects hippocampal synaptic plasticity in mice offspring – a link to autism spectrum disorders

Prostaglandin E2 (PGE2) is a lipid signaling molecule involved in early healthy brain development. Exposure to environmental risk factors such as air pollutants, infections, inflammation or drugs such as acetaminophen during early pregnancy impact PGE2 levels and have all been linked to Autism Spectrum Disorders (ASDs). Our previous studies show that maternal exposure to PGE2 and the lack of the PGE2 producing enzyme Cyclooxygenase-2 (COX2) results in sex-specific abnormal dendritic arborization, cell soma size, branch length, and looping within the cerebellum and ASD-like behaviors including motor deficits and anxiety in mice offspring. In this study, we investigate sex-dependent effects of prenatal PGE2 exposure on hippocampal electrophysiology in the C57bl/6 mice offspring at postnatal day 90-100. We measured long-term potentiation (LTP), paired-pulse facilitation (PPF) and input/output (I/O) responses and the expression of glutamate receptor components NMDA subunit 2A (GluN2A), AMPA subunit GluR1 and beta-actin. We found that PGE2 exposure decreased LTP in males and I/O responses in females at higher stimulation intensities with no effect on PPF. PGE2 also increased the expression of GluN2A in males with no effect on GluR1 or beta-actin. Overall, our data suggests that prenatal PGE2 exposure disrupts innate sex differences by reducing LTP maintenance in males, while impairing basal synaptic transmission in females. Interestingly, upregulated expression of GluN2A observed in PGE2 males may reflect a homeostatic compensatory response to impaired synaptic plasticity, suggesting that in utero exposure to PGE2 shifts both physiological responses to neural activity, and the complement of NMDARs required for learning and memory which are functions implicated in ASD.

Poster Presenter #5

Name: Svati Balaji and Jacquelina DaSilva
Program: Undergraduate Thesis, York University
Field: Biology (Science) Education
PI: Dr. Tamara Kelly

Complexity genetics - determining levels of genetic deterministic thinking of undergraduate Biology students.

The way that genetics has been traditionally taught (i.e., with a focus on Mendelian genetics) can reinforce ideas of genetic determinism; the belief that phenotypes are mostly unaffected by environmental factors and instead, are largely influenced by genetic contributions (Carver et al.,

2017). This can reinforce the assumption that individuals of one race are very similar to one another and distinct from people of another race. Repeated exposure to this traditional view will affect students' perceptions of human biological variation thereby causing students to endorse the idea that racial differences are determined by genetics (Donovan, 2017). Students who learn from a genetics curriculum that talks about racial biological disparities may be less likely to work cooperatively with peers who identify differently from themselves which might have detrimental effects on one's sense of belonging and learning experience within the classroom. Our undergraduate honours thesis conducted focus groups to determine the levels of genetic determinism within undergraduate biology students. We also conducted interviews to validate a survey that is currently used to monitor changes in deterministic thinking in students enrolled in an introductory Genetics course at York University. The purpose of validating this survey tool is to better inform whether the survey questions are being interpreted as intended. This research can better inform future modifications to course content to ensure that a more authentic approach to genetics is being put forth, improving the learning experience for students and by connection, their sense of belonging within the classroom.

Poster Presenter #6

Name: Arghavan Sammak Moghaddam
Program: Undergraduate Thesis, York University
Field: Biomedical Science
PI: Dr. Patricia Lakin-Thomas Lab

The Effect of Glucose and Arginine on TOR pathway and Circadian rhythm of Neurospora crassa

Circadian rhythms are normally generated using a transcription-translation feedback loop. To control cellular growth, division, autophagy, and stress responses, the TOR (Target of Rapamycin) pathway is a highly conserved cellular route in eukaryotes. It monitors nutritional and stress signals from both external and intracellular sources. In yeast and mammals, it is known that this cellular process responds to amino acids or carbon resources. In the filamentous fungus, Neurospora crassa, the TOR pathway has importance in nutrient sensing and growth as well as in controlling circadian rhythmicity. Previous work established that S6 phosphorylation (an assay for TOR activity) is rhythmic in Neurospora. It was hypothesized that the addition of arginine and glucose will induce the TOR pathway and result in changes in the circadian rhythm as well. Using immunodetection of S6-P and phase observation, it was determined that arginine does not change the TOR pathway while glucose can increase the activity. Preliminary results from phase experiments indicate effects of glucose not arginine. Overall, these results showed new knowledge about the TOR pathway in Neurospora crassa and potential interactions between TOR and circadian rhythms.

Poster Presenter #7

Name: Sai Sowndarya Sundararaman
Program: Ph.D. Biology, York University
Field: Antimicrobial Resistance
PI: Dr. Dasantila Golemi-Kotra

Elucidating the molecular mechanism of Staphylococcus aureus response to cell wall damage

Staphylococcus aureus is a major pathogen that causes a series of infections in humans. The first line of defense against invading pathogens in humans is produced by Antimicrobial Peptides(AMP). AMPs are cationic in nature, enabling their binding to the bacterial membrane through electrostatic attraction. S. aureus has developed resistance mechanisms against these AMPs. Bacteria can recognize these signals with the help of two-component systems (TCS). TCSs play a role in antibiotic resistance in many bacteria including S. aureus. TCS has a sensor kinase that senses the signal and undergoes autophosphorylation at a histidine residue and a response regulator which regulates the expression of genes needed for resistance. S. aureus resistance to glycopeptide antibiotics has been linked to the GraSR two-component system. GraSR requires the help of an ABC transporter, VraFG, as a co-sensor and an auxiliary protein GraX for the signal transduction mechanism. GraR is known to regulate genes dltABCD and mprF in response to AMPs, by adding a positive charge to the cell surface of bacteria. However, the complete mechanism of this system is not yet understood and this report mainly focuses on understanding the molecular mechanism of the GraSR system.

Poster Presenter #8

Name: Julia Arrigo
Program: M.Sc. Biology, York University
Field: Virology
PI: Dr. Andrew White

Investigating regulatory RNA structures in the PLRV viral RNA genome.

Potato leafroll virus (PLRV) is a positive-sense single-stranded RNA plant virus in the genus Polerovirus (family Solemoviridae). Comparative analysis of polerovirus genomes revealed three conserved structural elements: (i) a subgenomic mRNA (sg mRNA) promoter element, (ii) a RNA structure (termed xrRNA) resistant to the 5-to-3 exoribonuclease Xrn digestion, and (iii) a downstream stem loop (dSL), possibly involved in regulating translation of a viral protein, p3a. The potential roles of these structures in regulating viral transcription and translation were investigated using various assays including, plant cell infections, in vitro yeast Xrn degradation assays, and in vitro translation in a wheat germ extract system. The results showed that (i) ectopic expression of the sg mRNA promoter element failed to generate sg mRNA in plant cell infections, (ii) disruption of the xrRNA structure abolishes production of a virally-derived

degradation product in vitro Xrn assays, and (iii) the dSL does not alter p3a translation in in vitro translation assays. Collectively, the results indicate that the sg mRNA promoter element is not modular and cannot be moved from its natural viral context, the xrRNA structure is active for blocking Xrn activity in vitro, and the dSL is not involved in regulating translation of p3a in in vitro assays. Future work will investigate the sg mRNA promoter in its natural context, and the possible roles of xrRNA and dSL will be examined further in infected plant cells.

Poster Presenter #9

Name: Aleeza Qayyum
Program: Undergraduate Thesis, York University
Field: Biochemistry
PI: Dr. Derek Wilson

A Structural Analysis and in vitro Synthesis Optimization of Hyperphosphorylated Amyloidogenic Tau

Tau is a microtubule-associated protein that plays a critical role in stabilizing microtubules in neurons. In certain biological conditions, Tau can undergo modifications, including hyperphosphorylation by glycogen synthase kinase 3β (GSK3β). This leads to the formation of abnormal aggregates that are toxic to neurons, resulting in neurological diseases known as Tauopathies, with Alzheimer’s disease being the most recognized. With an estimated 152 million cases of Alzheimer's worldwide by 2050, it is essential to develop strategies to halt the progression of Tauopathies. In this study, we optimized the in vitro synthesis of phosphorylated Tau (pTau) using various techniques and parameters. The optimization of in vitro pTau expression is crucial in developing treatments for neurodegenerative disorders. We utilized Time-Resolved ElectroSpray Ionization Hydrogen-Deuterium Exchange Mass Spectrometry (TRESI-HDX-MS) to investigate the structural behavior of hyperphosphorylated Tau. This labelling technique allows analysis of the conformational dynamics and structural changes of proteins. Our results indicate that when Tau is hyperphosphorylated, there is a global increase in deuterium uptake, and six notable peptides, including the regions that bind to the microtubule, show significant deuterium uptake. These findings provide insight into how pathogenic hyperphosphorylated Tau behaves and will be useful in understanding the mechanisms that lead to Tauopathies. In conclusion, our study offers a novel approach to optimize the in vitro synthesis of pTau and provides new insights into the structural behavior of hyperphosphorylated Tau. Our findings contribute to better understanding the pathogenic dynamics associated with Tau and will aid in developing new therapeutic strategies for Tauopathies.

Poster Presenter #10

Name: Taylor Cargill
Program: Undergraduate Thesis, York University
Field: RNA Biology
PI: Dr. Mark Bayfield

Assaying RNA chaperone activity and protein-RNA interactions for Trm1 and other candidates in vitro

Recent research in the past decade has characterized novel tRNA chaperone activities in a variety of bacterial tRNA modification enzymes, which were previously thought to only modify tRNAs but are now known to also play an important role in promoting proper tRNA folding. These discoveries have sparked increasing investigation into the potential RNA chaperone activities of eukaryotic tRNA modification enzymes involved in the tRNA maturation process. Trm1 is a tRNA methyltransferase enzyme that makes a m22G26 modification on tRNA molecules to help increase their stability and promote correct folding. It is currently unknown whether, and by what mechanism, Trm1 is able to act as a tRNA chaperone. This thesis project outlines the experimental process by which a series of in vitro molecular beacon-based assays were conducted to investigate the RNA binding and folding ability of wildtype Trm1 and its catalytically-inactive mutant, Trm1 D201A. Based on our results, we showed that wildtype and catalytically-inactive Trm1 both have comparable binding affinities for an RNA substrate that mimics the D-arm of tRNA, suggesting that Trm1 may possess a function outside its known catalytic activity. Further, we also demonstrated that wildtype and catalytically-inactive Trm1 are capable of promoting proper folding of RNA hairpins in a FRET assay, indicating that Trm1 is likely a dual-function protein with genuine RNA chaperone activity.

Poster Presenter #11

Name: Fatema Nakhuda
Program: M.Sc. Biology, York University
Field: Molecular and Cellular Neuroscience
PI: Dr. George Zoidl

The Synaptic Symphony: Examining the Role of Panx1 in Maintaining Neuronal Communication and Memory Formation Presting
Author(s): Fatema Nakhuda (fatema28@my.yorku.ca) Supervisor: Dr Georg R Zoidl (gzoidl@yorku.ca) Affiliations: Department of Biology, York University & Centre for Vision Research, York University, Toronto, ON MSJ 1P3, Canada

We are our memories. Our existence and behavior are direct representations of what we learn and remember. On a molecular level, memory is the result of changes in gene expression and new protein synthesis, leading to long-lasting connections between neurons. Many proteins aid in continuous communication between neurons. In this study, we explore the role of Pannexin1

(Panx1), a protein that forms electrical synapses. Previous studies in our lab have shown that panx1 knockout mice have decreased learning responses compared to the wild type, suggesting that panx1 might modulate pre- and postsynaptic activities. We tested the roles of two zebrafish Panx1 ohnologs, Panx1a and Panx1b, using a behavioral paradigm to quantify the short-term and long-term memory responses of 6-day-old larvae (6dpf). We compared the behavioral phenotypes of wild type and knockout zebrafish and assessed molecular changes. We found that the ablation of Panx1a altered the ability to habituate to light stimuli, while the ablation of Panx1b had no effect on the ability of 6 dpf larvae to habituate. Qualitative real-time PCR analysis demonstrated the differential expression of genes involved in synaptic plasticity, providing evidence for biomarkers for habituation. In a zebrafish model for seizures, we compared transcriptomic changes for IEGs between genotypes in vivo using click chemistry to label newly synthesized RNA. Specific brain regions were identified that were activated during seizures. The preliminary findings of this research support the potential role(s) of Panx1 in maintaining synaptic plasticity during a simple learning task.

Poster Presenter #12

Name: Sahib Singh Madahar
Program: M.Sc. Biology, York University
Field: Cellular and Molecular Biology (Immunology)
PI: Dr. Ali Abdul-Sater

SINGLE AMINO ACID MUTATION IN TRAF1 REDUCES INFLAMMATION AND CAN PROTECT MICE FROM LPS-INDUCED SEPSIS

Rheumatoid arthritis (RA) is a chronic autoimmune disease characterized by persistent and abnormal inflammation leading to the destruction of cartilage and bone. This disease affects approximately 1.2% of Canadians aged 16 years and older, with a higher incidence and prevalence in females compared to males. Recent studies show that the tumour necrosis factor receptor associated factor 1 (TRAF1) has a dichotomous role in the immune system, making it an excellent candidate to target in the development of RA therapies. Our lab has recently identified a single amino acid mutation in TRAF1 in human monocyte cells which can reduce their inflammatory responses when stimulated with lipopolysaccharide (LPS). To this end, we have generated a knock-in mouse model to determine whether these results translate to a mouse model with the same mutation in TRAF1. This mutation selectively targets TRAF1 to limit lymphocyte activation while reducing the production of pro-inflammatory cytokines in macrophages. Protection from LPS-induced sepsis is measured by subjecting mice to a lethal dose of LPS and performing survival curves. Mice are subjected to a sublethal dose of LPS to measure inflammatory cytokine production from the serum using the LEGENDplex immunoassay. Primary bone marrow derived macrophages are treated with LPS for in-vitro experiments. These experiments include techniques such as real-time quantitative polymerase chain reaction (RT-qPCR), western blot and flow cytometry to measure levels of TRAF1, NF-κB activity (IκBα, p-IκBα, p50, and p65) and pro-inflammatory genes (TNF, IFN-, IL-1, and IL-6).

Preliminary results indicate that the knock-in mouse model exhibits a reduced inflammatory response to LPS.

Poster Presenter #13

Name: Britney Remnant
Program: Undergraduate Thesis, York University
Field: Molecular Biology
PI: Dr. Mark Bayfield

Mlp1 functions through protein and RNA complexes during non-coding RNA biogenesis in Tetrahymena thermophila

La proteins are conserved RNA binding proteins that function in the biogenesis pre- transfer RNAs (pre-tRNA) and small nuclear RNAs (snRNAs). La-dependent pre-tRNA processing is highly conserved in eukaryotes: the RNA recognition motif-1 (RRM1) works with the La motif to bind 3'-uridylate trailers and protect them from degradation. The La protein, Mlp1, in Tetrahymena thermophila lacks the conserved RRM1 and binds pre-tRNAs with lower affinity and specificity than human La, suggesting an alternative pre-tRNA 3'-end protection mechanism. Previous work identified candidate Mlp1-associated proteins that we hypothesize may be involved in pre-tRNA processing. These proteins were purified, and interactions were confirmed by in vitro GST-pulldown assays. Mlp1 protein complexes did not restore traditional La associated pre-tRNA 3' end protection from 3' exonucleases in vitro. However, Mlp1 expressed individually with protein candidates Serine/Threonine Kinase, Tgp1 and Tgp3 in Schizosaccharomyces pombe stabilized a distinct Mlp1 associated pre-tRNA intermediate species, implicating these complexes in an uncharacterized pre-tRNA processing mechanism. Additionally, ribonucleoprotein immunoprecipitation coupled to RNA sequencing identified that Mlp1 associates with mature snRNAs. We characterize Mlp1 binding to the U6 and U1 snRNAs through a uridylate independent mechanism in which Mlp1 amino acids in a defined short basic region 226-250 seem to be an important binding determinant. This work characterizes novel features of Mlp1 protein and RNA complexes and has potential to highlight the variability existing across eukaryotic species.

Poster Presenter #14

Name: Pooja Upadhayay
Program: Ph.D. Biology, York University
Field: Ecology
PI: Dr. Valerie Schoof

The effects of gastrointestinal parasites on fecal glucocorticoids and behaviours in vervet monkeys (Chlorocebus pygerythrus)
Relationships between parasites, host physiology and behaviours are complex and variable. Several studies have shown that parasites can influence host hormonal microenvironment and

behaviour through so called “sickness behaviours” such as increased resting and foraging, and decreased movement and social grooming. In contrast, other studies found no association between host parasitism, hormones, and behaviour. Using a parasite removal experiment, we examined the effects of gastrointestinal parasites on the fecal glucocorticoid metabolites (fGC) and behaviours in vervet monkeys (Chlorocebus pygerythrus) at Lake Nabugabo, Uganda in summer 2014. The study period had three phases: pre-deworming (June), dewormed with ivermectin (July), and re-infection (August-December), during which parasitological, hormonal, and behavioural data were collected from adult and subadult male and female vervet monkeys (N = 19). To contextualize our results and control for possible seasonal variation in behaviour across summer, we compared behaviour during the 2014 experimental period to the same months in the following year. We used LMM and GLMM with fGC and proportion of behaviour scans as outcomes and maximum parasite species richness, months, and sex as fixed effects, and individual ID as a random effect. Mean fGC varied significantly across months for females with or without infants, but not for males. There was no significant mean fGC decrease after deworming treatment, but compared to the pre-deworming phase, there was a significant increase following natural re-infection. Moving, resting, and grooming differed significantly across months during the experimental period, with a significant negative correlation between feeding and mean fGC levels ($r = -0.26$, $p < 0.05$). Finally, no significant changes were found in feeding, moving, resting, grooming between the study period and the following year. Despite behavioural variation during the experimental study period, we cannot conclude that behavioural changes are due to parasitism rather than other seasonal variation. However, fGC increased following re-infection, which is consistent with parasitism being costly for hosts. It is possible that host physiological response to parasitism is sufficient to limit the need for “sickness behaviours”, but we cannot exclude the possibility that fGC variation is tied to seasonal variation rather than the parasitism as we lack hormone data for other years for comparison. Keywords: Gastrointestinal parasites, deworming experiment, fecal glucocorticoid metabolites, hormones, behaviour, primates.

Poster Presenter #15

Name: Sarah Houshangi-Tabrizi
Program: M.Sc. Health, York University
Field: Vision Neuroscience
PI: Dr. George Zoidl

Panx1b Modulates the Luminance Response and Direction of Locomotion in the Zebrafish

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In the zebrafish retina there are two isoforms of Pannexin1(Panx1), Panx1a and Panx1b, that forms weakly voltage gated ATP channels involved in cell-signalling cascades downstream of the adrenergic, purinergic, NMDA receptors, and transient receptor potential vanilloid. Panx1a channels are localized in the horizontal cell layer of the outer retina and via an ATP/pH-dependent pathway, it regulates and detects light decrement. Panx1b is localized in the horizontal cell layer and ganglion cell layer. In this study, we investigated how the expression of Panx1b channels in the inner retina and ganglion cell layer regulates visually guided behavior in the 6-day post fertilization larvae. We generated knockout fish lines using TALEN technology for Panx1a and Panx1b. This was followed by RNA-seq analysis, real-time PCR, and optic flow behavioral testing. The Panx1b fish lines exhibited an abrupt luminance response in the retina and the larvae had problem navigating through the leftward motion in low light conditions. We concluded that Panx1b is a modulator of the circadian rhythm, and this suggested that Panx1b can be involved in forming non-image processes in the inner retina. Moreover, we saw that Panx1b channels are associated with the final retinal output of luminance, and it is involved in motion detection.

Poster Presenter #16

Name: Sejal Dave
Program: M.Sc. Biology, York University
Field: Animal Physiology
PI: Dr. Raymond Kwong

Plastics are widely used, but they are extremely difficult to degrade. Instead, it breaks into smaller pieces known as microplastics (MP), which are particles smaller than 5mm. The extent of microplastic (MP) pollution is unknown in the Great Lakes and this is concerning because they make up 20% of the world's freshwater. To characterize MP characteristics in freshwater bioindicators can be used; this is a species whose reactions can assess the current ecological impact of a pollutant in environments. For example, researchers can measure the accumulation of a pollutant in a bioindicator's body, and this concentration should reflect environmental concentrations. Daphnia (*Daphnia magna*) and zebra mussels (*Dreissena polymorpha*) are commonly used in MP ecotoxicity studies because they are filter feeders, and so they are easily exposed to MP. However, it is undetermined whether they are good bioindicators of MP because they may be able to select between food and non-food particles, and so they may not give an accurate representation of environmental MP. My objective is to determine whether the organisms display selectivity during uptake between MP and food. Specifically, I will conduct exposure studies in daphnia and zebra mussels and evaluate the bioaccumulation, filtration rates, and elimination of polyethylene microspheres.

Poster Presenter #17

Name: Bakhtiyar Taghizada
Program: Ph.D. Biology, York University
Field: Epigenetics, Molecular Biology
PI: Dr. Peter Cheung

Genomic and biochemical characterization of ubiquitylated histone H2A.Z

H2A.Z is an essential histone variant with multitude of functional implications in all DNA templated processes including transcription, replication, DNA damage and homologous recombination. Evidence supports its roles in both transcriptional activation and repression. This divergence in function is partly attributed to its post translational modifications (PTMs); acetylated H2A.Z is considered an active chromatin mark, while its ubiquitylation is associated with transcriptional repression. Unlike H2A.Z acetylation, due to lack of reagents and antibodies specific to ubiquitylated H2A.Z (H2A.Zub), elucidation of its function through immunoprecipitation has not been possible. To circumvent this problem, we designed a simple transient expression system - ubiquitylation dependent self-biotinylation (UDSB), where ubiquitylation of H2A.Z leads to its subsequent self-biotinylation, allowing its purification by streptavidin conjugated beads. Using this method, we performed mono-nucleosome immunoprecipitation and analyzed H2A.Zub associated DNA by sequencing and its interacting protein partners by mass spectrometry. Here I present genome-wide distribution of H2A.Zub and its association with several major chromatin marks. I also present our preliminary mass spectrometry data on H2A.Zub protein interactors. Overall, this research provides direct evidence for long standing chromatin interactions of H2A.Zub and reveals its novel associations on both genomic and biochemical levels.

Poster Presenter #18

Name: Meghan Osborne
Program: M.Sc. Biology, York University
Field: Structural Biology
PI: Dr. Philip Johnson

"The Analysis of the Affinity and Stability of Modification of the Glucose-Binding and Cocaine-Binding Aptamers"

Aptamers are selected to bind to their ligands, usually with high affinity and selectivity for their targets. Due to this aptamers can be used as sensing molecules in several different biosensor applications. Previously published research by the Stojanovic group selected an aptamer to bind glucose, but not any structurally related carbohydrates. The Kd of this aptamer-ligand interaction is only 10mM, which is much lower than the nM affinities seen in other aptamer-ligand systems. This is of physiological relevance as the blood glucose concentration usually falls between 4 mM to 11 mM, meaning it can be used in possible in vivo applications. Glucose is a difficult molecule to select an aptamer for as there are no strong epitopes present

of glucose for DNA bases to interact with. NMR spectroscopy is suited to study weaker aptamer-ligand interactions such as these due to the greater concentrations required for NMR relative to other methods. 1H NMR spectroscopy was used to investigate the affinity, specificity, and stability of the wild-type glucose aptamer, and to try and engineer an aptamer variant with a stronger affinity for glucose than the wild-type aptamer that could be useful for future biosensing applications. The stability of high affinity glucose binding modifications will be studied using differential scanning calorimetry (DSC) similar to an analysis performed on the cocaine-binding aptamer. The cocaine-binding aptamer is a DNA aptamer selected to bind cocaine and is composed of three stems constructed around a three-way junction with 2 A-G mismatches at the centre. DSC is being used to investigate the thermostability of the cocaine-binding aptamer as a function of how many base pairs are in stem one. The length of stem one can change how tightly the aptamer binds a ligand, and how well defined the free state of the aptamer is. This was done with the hope of determining which stem one variant is the most thermodynamically stable.

Poster Presenter #19

Name: Jie Lin
Program: Ph.D. Biology, York University
Field: System Biology, Biochemistry
PI: Dr. Nik Kovinich

Identifying missing glyceollin transcription factors in soybean (Glycine max L. Merr)

Plants have evolved defenses in response to pathogen attack, including the generation of different kinds of reactive oxygen species, expressing pathogenesis-related proteins, and biosynthesizing antimicrobial metabolites called phytoalexins. Glyceollins are phytoalexins from soybean (Glycine max L. Merr), and they play a pivotal role in providing defense against pathogens such as Phytophthora sojae. Besides their importance in agriculture, glyceollins have potential applications in medicine because of their impressive pharmaceutical activities in human cell lines. Thus, it is quite urgent to understand the regulation of glyceollin biosynthesis and identify the relevant transcription factors (TFs) that could be manipulated to enhance glyceollin biosynthesis. According to our previous research, two TFs, GmMYB29A2 and GmNAC42-1, were found to regulate glyceollin biosynthesis genes in response to the wall glucan elicitor (WGE) from P. sojae. These two TFs activated different glyceollin genes with and without WGE treatment. However, overexpressing either GmNAC42-1 or GmMYB29A2 in the absence of WGE failed to completely activate glyceollin biosynthesis, suggesting that additional TFs may be required to complete this function.

Poster Presenter #20

Name: Sihat Salam
Program: M.Sc. Biology, York University
Field: Cellular and Molecular Biology
PI: Dr. Peter Cheung

Examining the epigenetic impact of CBP/p300 inhibition on the upregulation of proto-oncogenic immediate early genes via crosstalk between histone H3 acetylation and phosphorylation response

Post-translational histone-tail modifications result in the epigenetic regulation of gene expression. Of these modifications, histone H3 acetylation of lysine residues and phosphorylation of serine residues directly remodel the chromatin towards a loosened euchromatin state by decreasing the DNA-protein affinity within the nucleosome. Of the variants of H3, K27M mutation in H3.3 poses major risks in genomic integrity, leading to alteration of cellular functions and progression of malignant paediatric glioblastoma. Previous work has established that H3 phosphorylation is induced via the MAPK pathway as a response to stress or growth factor stimulation, which in turn, facilitates H3 acetylation and transcriptional activation of immediate early genes (IEGs). Recently, our lab found that Anisomycin-induced H3 phosphorylation response was completely abolished by chemical inhibitors of the histone acetyltransferase CBP (CBPi). To further investigate this finding, we tested whether enhancing histone acetylation via Trichostatin A prior to CBPi could rescue the Anisomycin-induced H3 phosphorylation response. Western blot analysis was carried out with the use of antibodies against serine phosphorylation and lysine acetylation under said conditions. To test whether the previous findings are due to upstream interactions between CBP/p300 and MAPK pathway, further Western blot analysis involved antibodies against activated kinases in the pathway under similar conditions. RT-qPCR analysis of proto-oncogenic IEGs, such as cJUN, cFOS, cMYC, and EGR1 under said treatment conditions. Thus, the data and results of this study could be used to develop future pharmaceutical drugs against cancer pertaining to CBP inhibition.

Poster Presenter #21

Name: Shaina Jaff
Program: M.Sc. Biology, York University
Field: Cell and Molecular Biology
PI: Dr. Michael Scheid

Gene Mapping and Effect of Doxorubicin on ICF-related proteins HELLS and CDCA7 and NHEJ associated protein Ku80 Immunodeficiency

Centromeric instability and facial abnormalities (ICF) syndrome, is a rare recessive disease characterized by growth and cognitive delays as well as recurrent life-threatening infections in

childhood and is caused by mutations in methylation associated proteins HELLS and CDCA7. Epigenetic DNA methylation by DNMT's (DNA methyl transferases) regulates winding of chromatin to promote DSB repair by either NHEJ (nonhomologous end joining) or HR (homologous recombination). CDCA7 recruits HELLS to chromatin to form a bipartite nucleosome-remodeling complex that allows for CG methylation by DNMT3b and subsequent DSB repair, facilitated by NHEJ associated protein complex Ku80/70. Our lab has previously discovered that the phosphor-adapter protein, 14-3-3, binds with CDCA7 at T163 and when phosphorylated by Akt, this interaction relocates CDCA7 to the cytoplasm. Our lab is exploring the interaction of HELLS and CDCA7 and has demonstrated that this interaction is independent of 14-3-3 association. Further, we have identified an N-terminal region of CDCA7 as critical for CDCA7's interaction with HELLS. We have also been able to show how Ku80 interaction is doubly enhanced when this specific N-terminal region is deleted, and this interaction is fourfold enhanced when 14-3-3 is prevented from binding at the T163 site. Continuing work will explore how interaction Ku80/70 complex with CDCA7 impacts DNA repair via doxorubicin functional assays visualized using western blot techniques, and could provide insight on potential therapeutic targets for ICF and associated cancers.

Poster Presenter #22

Name: Milad Falahat Chian
Program: Ph.D. Biology, York University
Field: Cell and Molecular Biology
PI: Dr. Terry Sachlos

Antibody-free Fluorescence Barcoding of AML cells for Deconvolution of Biological Response to Therapeutic Agents using High Throughput Flow Cytometry

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Drugs demonstrate varying biological responses between human patients ranging from responders to non-responders. A high-throughput cellular barcoding technique for simultaneously testing drug response on multiple patient samples can facilitate deconvolution of biological response variation and promote biomarker and patient stratification. Fluorescent protein reporters have been used for long-term cell-tracing experiments; however, these systems inherently transform primary cells which can perturb biological responses. Therefore, the development of an antibody-free, broad emission colour spectrum barcoding system is powerful tool for analyzing variations in biological responses. Here we show the use of carbocyanine lipophilic cell membrane dyes, DiD, DiI, and DiO (far-red, red, and green emission, respectively) to barcode human myeloid leukemia cells (HL60) as a method to simultaneously deconvolute biological responses using volumetric flow cytometry. Utilization of these lipophilic stains not only provides strong, uniformly stained cells but also allows for parallel measurements in biological populations under the same experimental environments. These 3

lipophilic stains permitted barcoding of 8 separate cell populations while minimizing cytotoxicity. This technique can be used to test the biological response of anti-leukemic stem cells agents by simultaneously barcoding patient leukemia and healthy blood stem cells and analyzing for selective anti-leukemic toxicity while sparing blood stem cell populations. Importantly, this method ensures that cell surface markers remain free and untouched by antibodies, thereby permitting investigations which probe receptors of therapeutic. These investigations can permit deeper insight into cell signaling pathways to aid in the development of biomarker and patient stratification for safer and more effective drug treatments.

Poster Presenter #23

Name: Lina Rademacher
Program: M.Sc. Biology, York University
Field: Ecology and Evolution
PI: Dr. Valerie Schoof

Using fecal samples to determine female reproductive status in wild vervet monkeys

Females practice mate choice as a reproductive strategy to maximize fitness. However, male reproductive strategies may limit females' ability to exercise mate preferences. To combat male strategies, females of some species have evolved concealed ovulation (lacking external ovulation signals) to aid in practicing mate choice. Concealed ovulation also makes it difficult for researchers to observe mate choice in relation to female reproductive status, necessitating other methods to detect ovulation. Vervet monkeys (Chlorocebus pygerythrus) are a good species to study female choice in, as they mate with multiple males and have concealed ovulation. Previous studies on female reproduction in wild vervets have used urine to monitor female reproduction by quantifying progesterone (P) and estradiol (E2) levels. However, feces may present a more convenient collection method, and has been successfully utilized to detect ovulatory periods in other primates. To test this method in wild vervets, fecal samples were collected opportunistically from reproductive-age female vervets (N=12) at Lake Nabugabo, Uganda from April – August 2022. Fecal samples were analyzed using commercial enzyme immunoassay kits for progesterone and 17β estradiol, with successful preliminary results in detection of variation in P and E2 levels. These results will be compared with behavioural data to gain insight into variations of female behaviour and mate preferences across reproductive states.

Poster Presenter #24

Name: Maryam Zarean Adarmanabadi
Program: Ph.D. Biology, York University
Field: Environmental Toxicology
PI: Dr. Raymond Kwong and Prof. Satinder K. Brar

The co-occurrence and interaction of microplastics and antibiotic resistance in aquatic ecosystems: An emerging health threat

The wide distribution and potential environmental risks of microplastics (MPs), defined as plastic particles < 5 mm, have received increasing scientific concerns globally. MPs can act as an emerging hotspot for the growth of distinct microbial biofilm—known as the plastisphere—that is phylogenetically different from the biofilm growing on other natural particles and surrounding environment. Recent research has suggested that plastisphere may contain a variety of pathogens, bacterial cells, antibiotic resistant genes (ARGs), and mobile genetic elements (MGEs). The packed bacterial cells in the plastisphere may provide favourable conditions for horizontal gene transfer (HGT). Additionally, trace concentrations of antibiotics can be adsorbed onto MP surfaces, thus influencing the microbial composition through selective enrichment of antibiotic resistant bacteria. Therefore, the plastisphere may have the potential to influence the microbiome of the water ecosystems by increasing HGT and supporting diverse bacterial species . For these reasons and since no study has yet determined the co-occurrence of MPs and antibiotic resistance in Canadian freshwaters, we use the Lake Ontario as a study area, to investigate the abundance patterns of antibiotics and ARGs, and profile of bacterial communities in biofilm on MPs compared to surrounding aquatic ecosystems, which promoted the understanding of the co-pollution properties

Career Workshop

Dr. Anthony Choo
Ph.D., University of British Columbia
Confocal Sales Specialist, Leica Microsystems

After completion of his postdoctoral training in Traumatic Brain Injury at the University of Pennsylvania in, Dr. Choo began his first role as a Principal Scientist at PsychoGenics Inc. There, he took on the role of Project Director of Neurotrauma Research in Post-Traumatic Stress Disorder (PTSD) development. Currently, Dr. Choo works as a Confocal Sales Specialist at Leica-Microsystems and offers Confocal Training in the GTA, including here at York University! Come join Dr. Anthony Choo at the AGSBS Symposium as he discusses his transition from Academia to the Biotech Industry and his navigation through the industry.

Dr. Chun Chih Chen
Ph.D., York University
Organizational and Human Development, University of Waterloo

Making the transition from academia to industry can be a daunting experience. No matter your career stage, it is rarely a simple or unemotional decision. Come join us at the AGSBS Symposium and Dr. Chun Chih Chen (Ph.D., Biology, York University) from Organizational and Human Development at the University of Waterloo as we discuss strategies to facilitate this career transition. In this 30-minutes workshop, we will discuss approaches for:

- navigating job listings,
- advertising yourself and,
- understanding the onboarding process.

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