DOES SOCIALITY PREDICT LEARNING ABILITY IN CICHLID FISHES?

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The ability to process and retain information is critical for survival. Highly social animals often have more developed neocortices, as well as improved cognitive skills, and the social brain hypothesis posits that learning capacity (supported by bigger brains) has been selected for in social species as a consequence of the complexities associated with social living. To investigate this, we compared the learning abilities of two closely-related species of cichlid fishes that have divergent social lifestyles. *Neolamprologus pulcher* live in large groups and are highly social, whereas *Telmatochromis temporalis* live in pairs and are less-social. When provided with safe and unsafe shelters, both species learned after only 24 hours to retreat to the safe shelter when startled. However, when learning trials were shortened *N. pulcher* learned to retreat to the safe shelter after only 90 minutes of interaction with the shelters, whereas *T. temporalis* showed no evidence of learning even after 270 minutes of interaction. Interestingly, neither species was able to apply their experience with safe and unsafe shelters in a novel context. Additionally, there was no evidence of social learning in either species, as naïve fish which observed conspecifics interacting with safe and unsafe shelters did not show a preference for safe shelters. Overall, our results suggest that more social species (*N. pulcher*) may have a higher capacity for learning than less-social species (*T. temporalis*). More work (with additional species pairs) is now needed to ascertain whether social living has in fact selected for specialized learning abilities.

Oral Presentation

B: Ecology & Evolution

Observing effect of single base pair and structural variation in the recombinant inbred lines TyJ and RwwJ

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Single nucleotide polymorphisms (SNPs) and copy number variants (CNVs) present across a genome can be attributed to differences in phenotype between two closely related organisms. The mouse (*Mus musculus*) recombinant inbred (RI) lines TyJ and RwwJ, while being used commonly in studies dealing with complex phenotype, have never had an in depth study to observe differences within their SNPs and CNVs and identify any genes affected by the SNP and CNV variation. These RI lines are similar, having the C57BL/6J and DBA/2J inbred mice strains as their parental lines and are both thought to be completely homozygous. By identifying SNP and CNV differences and the genes and phenotypes affected, future researchers could use this information to indicate any genes or phenotypes which are factors in their study. In this study, The Mouse Genotype Diversity Array was used to identify all SNPs and CNVs across these RI lines, allowing data on their characteristics to be obtained. Unexpected heterozygous SNPs were found across the RI line genomes, and for the CNVs present, 71% of TyJ CNVs were recurrent compared to the 74% seen in RwwJ, 63% of all CNVs were inherited with the other 38% arising *de novo*, and 94% of the CNVs present across both RI lines contained genes. In total, 873 genes across the TyJ genome and 1,139 genes across the RwwJ genome were affected by CNVs, providing valuable information to help shape future research with these RI lines.

Oral Presentation

Group A

STRESS-INDUCED EFFECTS OF HTERT OVEREXPRESSION ON CELL VIABILITY AND METABOLISM IN HT22 AND B103 NEURONAL CELL LINES

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Human telomerase reverse transcriptase (hTERT) is the catalytic subunit of the ribonucleoprotein complex telomerase that functions to maintain telomeres at the ends of chromosomes. Apart from this canonical role, hTERT also has telomere-independent roles that improve cellular function such as regulation of glucose transport and the induction of cell signalling pathways. Embedded within the hTERT sequence is a mitochondrial localization sequence which enables shuttling of the protein to the mitochondria following exposure to oxidative stress. In the present work, I examined the effect of overexpressing hTERT on hydrogen peroxide sensitivity in the HT22 neuronal cell line. Ectopic hTERT expression resulted in improved cell viability following exposure to hydrogen-peroxide induced oxidative stress. In addition, transient overexpression of HA-tagged hTERT led to a concurrent decrease in expression and increase in phosphorylation of pyruvate dehydrogenase (PDH); indicative of decreased oxidative phosphorylation. Stable transfection of the B103 neuronal cell line resulted in the generation of two clonal lines stably overexpressing exogenous hTERT-HA. These results suggest that hTERT protects against the degenerative effects of oxidative stress arising from the high level of oxidative phosphorylation within neurons.

Abstract for Oral Presentation

Group A: Cell, Molecular, & Genetics

CONTROL OF DNA DAMAGE REPAIR BY THE EPIDERMAL GROWTH FACTOR RECPETOR

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Cancer cells exhibit heterogeneity in unique morphological and physiological features such as their potential for proliferation and angiogenesis, as well as the proteins they express. This accounts for the different responses of patients as well as of individual cells in a tumor to a single drug therapy. The heterogeneity of cells within a tumor can arise from mutations and alterations in the genome. Mutations to the genome, as well as other problems during replication such as rearrangements and imbalances that the body cannot repair within the cell cycle cause damaged DNA. An example of DNA damage is double strand breaks, which are caused by various cytotoxic drugs such as cisplatin. The epidermal growth factor receptor (EGFR) has often been involved in the pathogenesis of various carcinomas when mutated. EGFR modulates non-homologous end joining, a DNA repair mechanism that repairs double strand breaks. A marker for double-strand breaks is γH2AX, which is an altered histone variant of histone H2A on the DNA core. Using various analytical techniques to measure levels of γH2AX expression in cells exposed to chemotherapeutic drugs with or without EGFR, the role of EGFR on DNA damage repair is observed. The signaling traffic required for EGFR control of DNA damage repair is also examined to determine whether EGFR's proposed modulation of repair is directly due to its translocation to the nucleus, or downstream signals that are activated. These experiments further our understanding of how heterogeneity within cells in a tumor impacts tumor progression and drug response and ultimately provide more individualized therapy for humans.

This abstract is for an oral presentation best fit to be judged by group A (Cell, Molecular, & Genetics).

Effects of Low Temperature and Short Photoperiod on Dehydrin Protein Abundance Across Various Conifer Species

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Dehydrins are a class of proteins that have an important role in plants' responses to various abiotic stresses. A novel 16-kD protein exists in White Pine *(Pinus strobus)* that is involved with the development of cold hardiness and is inducible by low temperature and short photoperiod. This study focused on identifying this 16-kD protein using Western blotting in multiple conifer species field grown in Southern Ontario across November 2017 to February 2018. Similar 16-kD dehydrin proteins were observed to be present in Balsam Fir (*Abies balsamea*), Western Cedar (*Thuja plicata*), White Pine (*Pinus strobus*) and in coastal and interior provenances of Douglas Fir (*Pseudotsuga menziesii*). In all of these cases, the abundance of this protein increased across November to February, which coincides with the development of cold hardiness in these plants. Additionally, a 12-kD dehydrin protein showing the same trend was observed in White Spruce (*Picea glauca*). Lastly, we were able to observe comparable trends from plants grown in controlled environments. This study allows for the aforementioned proteins to be sequenced in the future to better characterise dehydrins.

Oral Presentation

Cell, Molecular, & Genetics

CHARACTERIZATION OF DETOXIFICATION CAPABILITY OF 5 TOMATO-ADAPTED SPIDER MITE STRAINS

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Abstract

Agricultural crops are under threat from different abiotic and biotic stresses, the latter includes pests and pathogens. The two-spotted spider mite, *Tetranychus urticae*, is a polyphagous herbivore pest which annually causes yield losses of a variety of field and greenhouse crops. Spider mites have developed mechanisms allowing them to adapt to a large range of host plants as well as to quickly acquire resistance to new acaricides. Two major physiological host-adaptation mechanisms are suppression of plant host defenses and detoxification of plant defense compounds. My research objective is to determine the relative importance of detoxification as an adaptation strategy in five independently tomato-adapted spider mite strains, collected from different field populations across Canada and the US, compared to a non-adapted control strain. I utilized a newly developed kimwipe delivery method using kimwipes soaked in an esterase enzyme inhibitor solution, which allows spider mites to uptake the inhibitor directly. The bioassay methodology resulted in a dose response where increased mortality corresponded with the increased concentration of inhibitor, as expected. Further, enzymatic assay showed a decrease in esterase activity in the different strains of spider mites following inhibitor uptake. Appropriate concentrations of the esterase inhibitor obtained from the kimwipe dose response allowed me to proceed with fecundity assays to determine whether this specific class of enzymes contributes to spider mite adaptation to tomato.

Oral presentation

A: Cell, Molecular, & Genetics

Measuring the Effect of Environmental Stress on Checkpoint Mutant Survival in Relation to Autophagy

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Checkpoints in the cell cycle ensures that only fit cells progress through division without any complications. The replication checkpoint restrains replication fork progression to arrest the cell cycle under replication stress. Without checkpoint proteins, cells cannot arrest and die when exposed to replication stress by hydroxyurea (HU). Autophagy, or "self-eating" allows cells to survive under starvation conditions. The Sabatinos lab has showed that cellular environment alters a cell's response to replication stress and enhances checkpoint mutant survival. The aim of my project was to determine the effects of environment stress on environmental stress on checkpoint progression in fission yeast deficient for both autophagy (*atg8Δ*) and checkpoint components (*cds1Δ, rad3Δ, chk1Δ and mrc1Δ*). I discuss viability assays that were performed to heat- shocked cells. We propose that in determining the relationship between environmental stressors and cell cycle checkpoints, preventable measures can be taken to ensure checkpoint mutant cells do not survive drug treatment.

Oral presentation
Group A: Cell, Molecular, & Genetics

MY ENEMY'S ENEMY: TARGETING *PSEUDOMONAS* BIOFILMS WITH LYTIC PHAGE

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Pseudomonas aeruginosa is a gram-negative pathogen with high antimicrobial resistance. It forms biofilms, multicellular communities that provide further protection from antibiotics and host defenses through production of an extracellular matrix and metabolic heterogeneity. A need for new methods of biofilm eradication led us to explore alternative avenues. Bacteriophages, or phages, are host-specific viruses that are a potential way to tackle antibiotic resistant infections. We hypothesize that a phage or phage cocktail can disperse *P. aeruginosa* biofilms. First, we initiated collection and characterization of a library of *P. aeruginosa* specific phages. Most *P. aeruginosa* phages use lipopolysaccharides or type IV pili as receptors. To identify pilus specific phages, we compared their ability to infect and lyse a representative array of *P. aeruginosa* strains. In this preliminary screen, 149 phages were tested for a broad host range and strong lysis, of which two phages, Lindberg 68 and Ib2, were identified. Furthermore, 181 complementary pairs of phages have been identified that, when combined, should lyse strains expressing all 5 pilin variants. We are investigating the efficacy of the chosen phages against static *P. aeruginosa* biofilms with the end goal of optimizing a phage cocktail. To date, these experiments demonstrate the lysis ability of phage across a range of *P. aeruginosa* hosts. Furthermore, we show the combinatorial potential of a phage library. These results support the hypothesis that bacteriophages are an effective tool for tackling *P. aeruginosa*. Future studies will investigate the applicability of bacteriophages against *P. aeruginosa* biofilms in an *in vivo* infection model.

Oral Presentation

Group A: Cell, Molecular, and Genetics

THE DEVELOPMENT OF A METHOD TO DETECT NEURONAL APOPTOSIS IN SONGBIRDS (*PASSERI*)

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Stress is part of life and it affects our everyday lives. Increased stress will cause glucocorticoids, such as corticosterone (CORT) to increase in the bloodstream. Stress can be detrimental to many organisms, it can alter their physiology and behavioral traits. Stress can also be experienced by birds. Increased CORT can cause the programmed death (apoptosis) in neurons, including in songbird brain regions such as HVC. My research will investigate different methods of detecting neuronal apoptosis in zebra finches (*Taeniopygia guttata*) due to this increase in corticosterone. In a prior study, 28 birds were randomly assigned into four conditions; socially housed vehicle implants, socially housed CORT implants, isolate housed vehicle implants and isolate housed CORT implants. The birds that were housed in the isolate condition were housed individually whereas the birds in the social housing condition were housed with 3-4 birds. Birds in the CORT condition received an implant which contained CORT. In my study, cells that undergo apoptosis will be detected. Apoptotic cells will be detected using terminal deoxynucleotidyl transferase (TdT) dUTP Nick-End Labeling (TUNEL) staining. My research thus involves developing methods to use TUNEL labelling in songbirds and comparing them to other apoptotic markers.

Oral Presentation

A: Cell, Molecular, & Genetics

IMMUNE STIMULI INDUCE LYSOSOMAL REMODELING AND ADAPTATION IN PRIMARY MURINE PHAGOCYTIC CELLS

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Lysosomes are dynamic organelles residing within eukaryotic cells that degrade macromolecules retrieved from phagocytic, endocytic and autophagic pathways. These organelles contain over 50 acid hydrolases that digest and process macromolecules and exogenous antigens. Moreover, lysosomes are predominantly characterized by a dense, punctate morphology with a diameter of approximately 0.5-1 μm, however lysosomes can undergo adaptation and form elongated tubular networks. Lysosome tubulation and remodelling occurs when immune cells, such as macrophages and dendritic cells, are exposed to phorbol 12-myristate 13-acetate or the bacterial component, lipopolysaccharides (LPS). Lysosome tubules have implications in enhancing fluid-phase uptake, phagosome maturation and antigen presentation, via the major histocompatibility complex class II (MHCII), to lymphocytes. Similarly, other immunostimulatory molecules such as vaccine adjuvants or other synthetic products boost immunity through lymphocyte activation. This study aims to investigate and characterize the effects of two immune stimulants on their ability to remodel the lysosome population in bone marrow-derived dendritic cells (BMDCs) and macrophages (BMDMs). The objective of this study was to create a dose-response curve in order to determine the optimal concentration of stimulants A and B that induces lysosomal remodeling and to determine if they enhance fluid phase uptake in activated cells. Preliminary data suggests that stimulating BMDCs and BMDMs with 50 ng/mL of stimulant A and 10 μg/mL of stimulant B induces optimal lysosomal remodeling and adaptation. Furthermore, stimulation with the optimal concentration enhances the uptake of the fluid phase marker, Lucifer yellow. Since stimulants A and B are shown to induce lysosome adaptation, this work may provide insight into the roles of this lysosomal remodeling in the immune-enhancing effects of these agents.

Due to a potential patent the names of the immune stimuli in this study cannot be disclosed.

Oral presentation

A: Cell, Molecular & Genetics

BREAK AND ENTER: Investigating the expression of mitophagy and autophagy related genes during diapause in Colorado potato beetles

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During diapause, Colorado potato beetles (CPB) suppress their metabolic rate and show a depletion of mitochondria in their flight muscle. It is unknown whether the fate of mitochondrial loss in CPB is driven by general autophagy, selective mitophagy or a reduction in mitochondrial biosynthesis. If autophagy or mitophagy was driving decreased mitochondrial abundance, we predicted there would be increased mRNA expression of autophagy- and mitophagy-related genes. However, if mitochondrial depletion was driven by a decrease in mitochondria turnover, we predicted there would be an increase in the mRNA expression of genes associated with mitochondrial biosynthesis. To determine the underlying mechanism of mitochondrial depletion, we quantified mRNA expression levels of *mTOR*, *FOXO*, *ATG5*, *PINK1*, *Parkin*, *NRF1* and *PGC1α* using reverse-transcription quantitative PCR (RT-qPCR) in CPB reared under normal conditions and exposed to diapause-inducing conditions for three, six and nine weeks. There was a significant reduction in the expression of *ATG5* (autophagy related 5) when CPB were exposed to diapause inducing conditions. There was also increased expression of *Parkin* in CPB exposed to diapause inducing conditions for nine weeks relative to six weeks. The expression of *Atg5* is necessary for autophagosome formation during autophagy and mitophagy and Parkin tags damaged mitochondria for ubiquitylation. These findings suggest an alternate hypothesis: during diapause in CPB mitochondria are tagged for degradation but not removed.

Oral presentation
A. Cell, Molecular & Genetics

EFFICACY OF REACTIVE OXYGEN SPECIES ON LYSOSOMAL DYNAMICS

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Lysosomes are membrane-bound organelles that play a vital role in degrading molecules and microbes in various cells and including during immune response. This allows lysosomes to recycle molecular components, organelles and other microbes. Lysosomes play a role in cellular homeostasis, plasma membrane repair, and metabolic signaling. Dysfunctional lysosomes induce various disorders related to waste accumulation. These disorders are regarded as Lysosomal Storage Disorders resulting in enlarged and defective lysosomes, possibly induced by defections in microtubules which facilitate fusion and fission events of lysosomes. This may be due to the inhibition of PIKfyve, a kinase functioning in the PIK pathway and inhibited by apilimod. A mechanism that may mediate this process and leads to the reduction of enlarged lysosomes are Reactive Oxygen Species (ROS) agents such as H_2O_2 and the drug rotenone. ROS can be induced by external sources such as pollutants and radiation or naturally produced upon mechanisms such as endocytosis undertaken by macrophages in the body through NADPH Oxidase (NOX enzymes), where it is used as an antimicrobial. The primary goal of this study is to determine the effects of ROS agents on the dynamics of lysosomes and microtubule dynamics. Using immunocytochemistry assays, our data indicate an increase in the number lysosomes, while a decrease in the average lysosomal volume with the use of ROS agents compared to ampilimod removal. This study can offer solutions in determining effects on ROS activity on cytoskeletal structures that may affect lysosome dynamics, which may have implications in therapies for lysosomal storage disorders.

Oral Presentation
Cell, Molecular & Genetics

The Significance of Transcription Factor Binding Motifs in Transcriptional Regulation in Embryonic Stem Cells

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In the human genome, genes make up only about 2% of the DNA sequence. The remaining 98% is non-coding and our understanding of the function of most of this non-coding DNA is limited. Transcriptional regulatory networks maintain cell states and are controlled by transcription factors (TFs) that bind to short sequence motifs in non-coding DNA regulatory elements; however, it is not clear how many TF motifs are necessary for regulatory element activity in embryonic stem cells. We hypothesize that modifying weak TF binding motifs in regulatory elements with weak enhancer activity would increase enhancer activity. Using a weak enhancer downstream of Sall1 we modified weak SOX2::OCT4, SMAD3, TCFCP2L1, and ESRRB binding sites to the stronger consensus binding sites. Using a dual luciferase reporter assay in embryonic stem cells, we show that the enhancer activity of this region increased as additional TF consensus binding sites were modified. Overall, this result shows that TF binding motifs play an important role in determining the strength of enhancers and that individual TFs function in a combinatorial manner to increase transcriptional output. This approach will allow us to identify enhancers elements in the human genome increasing our understanding of how our genome functions.

Oral presentation

I would like to be judged on A: Cell, Molecular, & Genetics

EXPOSURE OF THE COPEPOD *TIGRIOPUS CALIFORNICUS* TO DIFFERENT LEVELS OF HYDROGEN PEROXIDE AND ITS EFFECT ON ALTERNATIVE OXIDASE PROTEIN LEVELS

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Copepods are small aquatic crustaceans and an important food source for various organisms. Our study focuses on the copepod *Tigriopus californicus,* which experience significant fluctuations in temperature, salinity, predation, and oxygen levels. Hydrogen peroxide $(\mathrm{H_2O_2})$ has been used in several studies to examine its toxicity in copepods. However, insufficient studies have been conducted to determine the impact of $\mathrm{H_2O_2}$ on the alternative oxidase (AOX) of copepods. The AOX is part of the electron transport chain, and it is found in the mitochondria of all plants, however, recently AOX has been discovered in some animals. It catalyzes the oxidation of ubiquinol and cyanide-resistant reduction of O_2 to H_2O through the bypassing of Complexes III and IV. The AOX pathway is considered energetically wasteful because it does not pump protons across the inner mitochondrial membrane, decreasing ATP production. However, the AOX pathway is beneficial as it allows organisms to survive in the presence of unfavourable conditions. The purpose of our study was to determine whether $\mathrm{H_2O_2}$ would cause oxidative stress and affect the concentration of AOX in *T. californicus.* Preliminary results indicate that prolonged exposure and a concentration greater than 0.3% of $\mathrm{H_2O_2}$ leads to higher mortality. The swimming behaviour of the copepods appeared to be slower and bubbles were observed when exposed to 0.1%, 0.2%, and 0.3% of $\mathrm{H_2O_2}$. Further investigation is required to determine the impact of $\mathrm{H_2O_2}$ on *AOX* at the aforementioned concentrations.

Abstract for Oral Presentation
I would like to be judged in category C: Physiology & Toxicology

LIVE-AND-DIE: A TALE OF JUMPING GENE EVOLUTION

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Mobile elements, commonly called “jumping genes,” are genetic elements capable of inserting into new locations in the genome. Although mobile elements used to be viewed as genome parasites, they are now known to play important roles in genome evolution and gene function. LINE1 (L1) sequences are mobile elements that are capable of encoding the molecular machinery for “jumping” or transposing DNA sequences. All other active transposons in the primate genomes rely on L1s to encode proteins for their transposition. However, an evolutionary model of intact L1 propagation and retention in the genome has not been proposed.

Using a bioinformatics approach, we performed an unbiased statistical analysis to determine 1) biochemical requirements of intact L1s, 2) mode of evolution of intact L1s, and 3) *cis*-preference of intact L1s on a genome-wide scale.

Based on the analysis, we established that intact L1s evolve through a “Live-and-Die” model. Under this model, L1s that are capable of encoding proteins may produce many new copies of themselves while “alive” in a cis-preference fashion. Over evolutionary time, the original L1 acquires random, inactivating mutations to lose coding capacity and “dies”. Thus, each new generation of intact L1s quickly acquire the responsibility to produce transposition molecular machinery for the entire genome.

Interestingly, the human genome has a much higher number of intact L1s than all other primates examined. This suggests that humans, of all primates, have the greatest potential to further evolve due to mobile elements or “jumping genes”.

Oral presentation
A: Cell, Molecular, & Genetics

COMPARISON OF THE EXTENT AND NATURE OF STRUCTURAL VARIATION IN THE GENOMES OF LABORATORY MICE AND WILD CAUGHT MICE

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Copy number variants (CNVs) are large deletions or amplifications of genomic segments, that may contain genes, and may provide a selective advantage in a certain environment. Wild-caught and classical inbred mice have been used as models in human disease study, and are both affected by CNVs. CNVs have been implicated in many diseases, including cancer and schizophrenia. Yet, CNVs in one of the most valued model organisms in genetic research, the mouse, have not fully been characterized. The current study investigates differences in CNVs of mice of different environments. Using publicly available data from the mouse diversity genotyping array, 2067 and 996 CNVs were identified in 105 classical inbred and 37 wild-caught mice, respectively. There were several observed differences in CNVs between classical inbred and wild-caught mice: wild-caught mice had a higher proportion of unique CNV events and loss CNV events, and a lower proportion of genic CNV events. As determined by gene ontology analysis, classical inbred mice have CNVs affecting genes enriched in pathways involved in DNA organization, immunity, and development, whereas wild-caught mice have CNVs affecting genes enriched in pathways involved in sensory perception, splicing, and metabolism. The cohorts studied differ in mate selection, food access, diversity of environment, and breeding scheme, and their different CNV profiles may reflect these differences. The differences in CNV profiles between laboratory and natural environmental conditions are suggestive of adaptation to the different environments but require experimental testing to confirm.

Oral presentation, group A

PLASTID GENOME SEQUENCE ASSEMBLY AND ANNOTATION OF A PARASITE SPECIES *CUSCUTA AFRICANA*

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Parasitic plants acquire most or all of their nutrients from a host organism, instead of independently synthesizing these nutrients as is done by autotrophs. *Cuscuta* (otherwise known as dodders) is a genus of ~200 species of parasitic plants in the family Convolvulaceae. *Cuscuta* is comprised of four subgenera: *Cuscuta, Monogynella, Grammica,* and *Pachystigma*. All members of *Cucusta* are parasites to some degree, ranging from hemi-parasitic to fully parasitic, and lacking photosynthetic ability entirely. Prior studies of plastid genomes displayed significant variations in content that may be related to this photosynthetic spectrum. The goal of this project was to assemble and annotate the plastid genome of *Cuscuta africana* from the subgenus *Pachystigma.* The genome was assembled using a sequence assembly pipeline beginning from raw sequence data composed of 126 base pair long reads. This data was trimmed after assigning a PHRED score threshold for quality testing, and then assembled into contigs using de novo assembly. The contigs were examined and selected for plastid content based on a variety of characteristics, and then concatenated into a circular sequence of DNA. The assembled genome was then annotated by comparing it to a reference species to identify genes and other marker features on the plastid. In the future, this study will allow for comparisons to be done between the *C. africana* genome to the genomes of species within *Cuscuta,* as well as other photosynthetic species, to search for differences and similarities that might exist, and the biological impacts of these differences, if any.

ORAL PRESENTATION
B: Ecology & Evolution

USING GENOMICS TO INVESTIGATE TWO STRAINS OF *PSEUDANABAENA SP.* (CYANOBACTERIA) ISOLATED FROM A BLOOM IN AN OLIGOTROPHIC LAKE.

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Pseudanabaena is a poorly known genus of filamentous cyanobacteria that is often responsible for freshwater cyanobacterial blooms. Two strains of *Pseudanabaena*, one red and the other green, were cultivated from a 2014 bloom in Dickson Lake found at Algonquin Park, Ontario - an oligotrophic lake where blooms have not been historically known. To investigate the biology of these strains in contributing to the Lake Dickson bloom, a genomics approach was used. Contigs representing the genomes of the two strains have been assembled resulting in genome sizes of 5.26 and 5.21 Mbp with 4,417 and 4,695 genes annotated for the green and red strains, respectively. The genetic data indicate that these strains are two distinct, but closely related *Pseudanabaena* species, and the green strain is even more similar to a previously sequenced *Pseudanabaena* strain isolated from Switzerland. We investigated the potential for these strains to inhabit different light environments by examining genes responsible for pigment synthesis and complementary chromatic adaptation (through which cyanobacteria can modulate the composition of their pigments). The green strain was missing phycoerythrin synthesis genes, explaining their green colour, but both red and green strains had homologues for regulatory genes of complementary chromatic adaptation even though physiological tests indicated that they could not perform this function. This suggests that these regulatory genes have other functions related to photosynthesis or light sensing. The information from these genomes will be used alongside physiological investigations to further understand the recent emergence of cyanobacterial blooms in oligotrophic lakes.

Oral Presentation, A: Cell, Molecular & Genetics

THE DISTRIBUTION OF ESSENTIAL FATTY ACIDS THROUGH TROPHIC LEVELS IN A SOUTHERN ONTARIO POND

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Aquatic trophic levels classify organism based on their location in food webs. Food webs exhibit the flow of energy that is constantly cycled within a system. Essential fatty acids flow through these food webs and are important indicators of health in ecology. Specifically, eicosapentaenoic acid (EPA; 20:5n-3) and docosahexaenoic acid (DHA; 22:6n-3) are important due to their ability to promote growth and reproduction in aquatic organisms. The distribution of EPA and DHA was profiled from a pond in Whitby Ontario by the collection of aquatic organisms across trophic levels. Primary producers were represented by biofilm, pelagic phytoplankton and macrophytes. Primary consumers included zooplankton and macroinvertebrates. Secondary consumers consisted of aquatic insect larvae, tadpoles and fish species. The effect of light and age in *Chara spp.* was also investigated to determine the range of EPA and DHA concentrations in freshwater aquatic vegetation. Lipid extractions were performed using the Folch method and analysis using gas chromatography - FID. Macrophyte age had no significant difference on concentrations of EPA, DHA, and total fatty acids. In one location new macrophyte age had higher total lipid content. Preliminary tests have shown top trophic levels have higher concentrations of EPA, DHA, and total lipid content. This research aims to quantify the concentrations of essential fatty acids in a single freshwater food web to further provide framework (form and function) of ponds in the ecologically important Oak Ridges Moraine area.

Oral Presentation
B: Ecology & Evolution

THE EFFECTS OF ANTHROPOGENIC NOISE ON FORAGING BEHAVIOUR IN BLACK BULLHEAD (*AMEIURUS MELAS*)

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Anthropogenic noise in aquatic ecosystems is on the rise, but the effects it has on the behaviour and survival of freshwater fish is not well studied. Here, we observe the affects of noise on the foraging behaviour of black bullhead (*Ameiurus melas*), a common species in the Laurentian Great Lakes with known hearing specializations. Fish were exposed to either white noise, boat noise, environmental sounds or a quiet control and monitored for their reaction to the presence of food. We measured their behaviours by quantifying the number of foraging attacks made in each treatment on an array of well secured worms. Fish exposed to the playback of boat noise and white noise attacked less often and spent more time engaged in erratic swimming behaviours. When presented with no noise or environmental noise playbacks, the fish swam with more normalcy and were more likely to forage on the worms provided. Here we demonstrate that fish exposed to anthropogenic noise are impacted in terms of foraging efficiency and swimming behaviour which could have implications on fitness and ultimately survival.

Oral presentation

B: Ecology & Evolution

SEASONAL CHANGES IN THE BRAIN SIZE OF THE COLD-WATER PREDATOR, LAKE TROUT, *SALVELINUS NAMAYCUSH*

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Lake Trout, *Salvelinus namaycush*, are a cold-water, highly mobile predator that forage across multiple habitat types. Spatially complex foraging has previously been linked with high cognitive demands which is reflected in the enlargement of brain regions. However, no study to date has explored whether the brain size of Trout is seasonally plastic. Research on the relationship between brain size and behaviour has been done predominantly in the Summer rendering their behaviour during the Fall unknown. The present study measured seasonal changes in the total brain size and size of individual brain regions of Trout sampled during the Summer and Fall. We anticipated that during the Summer, Trout should have, relative to total brain size, larger optic tecta, olfactory bulbs and cerebellum – lobes that are at work in complex, visual foraging behaviors during brighter days and peak metabolism. A decrease in each of these lobes relative to total brain size was expected during the Fall due to the need to conserve energy and decrease metabolism as temperatures drop. Trout were sampled in the Summer and Fall, decapitated and brains were extracted. Volumes of whole brains and brain lobes were calculated. Olfactory bulbs, optic tecta and the cerebellum were larger in the Summer as predicted, indicating high use of vision and smell-oriented foraging coupled with enhanced swim and muscle control. The cerebrum, responsible for parental behaviour and sexual reproduction, was larger in the Fall which may be connected to the spawning of Trout during the Fall. Based on these findings, seasonal plasticity in the size of individual brain regions combined with knowledge of their preassigned functions may provide valuable information about the connection between cognition and response to changes in environmental conditions in Lake Trout.

Oral presentation
Ecology and Evolution

PREDATOR/PREY RATIOS OF TERRESTRIAL MAMMALS IN AFRICA

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The predator/prey dynamics in Africa were examined and ratios were developed to detect any patterns between the number of terrestrial mammalian predators and the number of terrestrial mammalian prey species within one biome. Each biome in Africa was examined and a review of literature was done to determine the number or terrestrial mammalian predators and prey within each biome. From these lists, ratios were developed and each biome was compared statistically. It was determined that orders Insectivora, Chiroptera, and megafauna were not a part of any terrestrial mammalian predator/prey system and no biomes consisted of the same composition of species. When compared to Northern Hemisphere ratios, the ratios for African biomes were smaller which deviated from the previous idea of an ideal ratio that could be applied to all biomes. In warmer climates, mammals are smaller and evolution occurs faster, resulting in a higher number of diverse species. Predators in Africa are able to hunt a larger range of prey as there are more mammal species that have a lesser mass and are therefore more opportunistic when it comes to prey selection. Due to warmer climates having more species richness, a more diverse range of species, and large amount of smaller mammals, there was no pattern observed for predator/prey ratios of terrestrial mammals in Africa.

Oral Presentation

Ecology and Evolution

WOLVERINE (*Gulo gulo*) DIET IN THE YUKON TERRITORY, CANADA

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A predator hunts, kills, and eats other organisms as a source of energy; failure to obtain such energy is as unforgiving as the failure to avoid a predator. Understanding the foraging ecology of the wolverine (*Gulo gulo*) is a challenge requiring long term and detailed observations, as they are a long-lived and wide-ranging generalist scavenger. In this study, we analyzed the Yukon Territory wolverine's diet by observing the stomach contents of wolverines trapped in the 2015 and 2017 trapping seasons. These were donated by Canadian trappers from across the Yukon Territory. This data was added to data taken from twelve-consecutive years of study on the stomach contents of wolverine carcasses performed by members of Dr. Robitaille's lab at Laurentian University. Diet richness, frequency of prey species occurrence, and volumes for each prey type were analyzed for each stomach. We found that snowshoe hare (*Lepus americanus*) and moose (*Alces alces*) were the most frequently consumed species in the wolverine's diet, contributing the most to the proportion of total volume in both the years 2015 and 2017. Plant material was also frequently occurring in the wolverine's diet for both years though in fragments only. Previous studies into wolverine diet have shown that the wolverine's reproduction is closely linked to food abundance. By analyzing diet, we are able to customize conservation efforts and manage wolverine populations affected by trapping in the Yukon Territory.

- **Oral presentation B: Ecology & Evolution**

DOES PREDATION AFFECT THE ELECTRIC ORGAN DISCHARGE AND BODY SHAPE IN THE WEAKLY ELECTRIC FISH, *BRACHYHYPOPOMUS OCCIDENTALIS*?

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Brachyhypopomus occidentalis is a fresh-water pulse-type electric knifefish. The biology of this species is relatively unknown, which offers a great research opportunity. This study investigated whether the electric organ discharge (EOD) used for intraspecific communication and interspecies recognition, as well as the general fish body shape varies among sites. Fish were sampled in 2014 and 2015 at eight different locations in Panama. EODs were recorded using pre-determined protocols. Photographs of each fish were taken for landmark-based geometrical morphometric analyses to quantify body shape. Using the fish photo records, sites were categorized as having high or low predation rates. Preliminary results show significant variation in fish body length and somatic mass, as well as EODs were found among sampling sites (P<0.0001). Interestingly, EODs displayed a significant variation based on predation rate in each site (P=0.005). Additionally, variation in body length, somatic mass and EODs were found to be significant among gender (P<0.0001, P<0.0001, P=0.041, respectively). Even though Principal Component 1 (PC1) values for geometrical morphometrics explained 72.7% of the variation in body shape among individuals, no significant variation was found among sampling sites. However, PC1 values varied significantly based on gender (P=0.004). These results establish a trend of the effect of predator presence on an individual's communication pattern and its natural geometrical morphometry with respect to gender in different sites. These results can be used to further research in order better understand the species biology.

Oral Presentation
B. Ecology and Evolution

ROOT ASSOCIATED FUNGI FOUND IN NEW BRUNSWICK CAVES AND MINES

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Discovery of white-nose syndrome in bats has brought attention to the lack of understanding of cave mycology. Although fungal-root interactions are fundamental to tree health and terrestrial ecosystem functioning, no research has been conducted on the fungal associates of roots in caves. The fungal community composition of roots found in mines and caves of New Brunswick, Canada was assessed by Illumina sequencing of PCR amplicons produced from root-extracted DNA by three primer sets. One primer set targets the D1 variable region of the large ribosomal subunit (D1 LSU) DNA of Basidiomycota, Glomeromycota, and plants. Another set targets this region in Ascomycota. The last primer set targets the internal transcribed spacer 2 (ITS2) region of all fungi. Successful amplification of 34 root samples using each of the three primer sets has been achieved. Analyses of Illumina sequencing output for D1 LSU-BG, D1 LSU-A, and ITS2 amplicons resulted in 79, 89, and 103 OTUs, respectively. Phylogenetic analysis of OTUs and their corresponding BLAST matches has resulted in the effective identification of tree roots and their fungal associates. Multivariate analyses of root fungal communities are ongoing. Data collected will be used to identify and catalog the presence and distribution of distinct fungal and plant species within the caves to improve our understanding of this ecosystem. Use of three primer sets should detect a wider variety of fungal species than any one primer set, offering a more accurate view of root-associated fungi in cave habitats.

Oral Presentation

Section B: Ecology & Evolution

MINING THE CLONES: IMPROVING THE PHYLOGENETIC INFORMATION FROM A SET OF CLONES OF SOIL-DERIVED FUNGAL rDNA

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Abstract

Lynch and Thorn (2006) PCR-amplified basidiomycetes from soil using primers to the small and large ribosomal subunit, and reported on the identities and phylogenetic placement of 409 clones obtained based on their partial LSU sequences. The adjacent, highly informative internal transcribed spacer (ITS) region, which these clones also contain, has since been designated as the "universal barcode" for Fungi. The purpose of this study is to obtain ITS sequence data from a selection of these clones to improve the resolution of their identifications and phylogenetic placement. I focused on clones representing 6 groups of mushroom fungi (Agaricomycetes): the Entolomaceae and allies; Hygrophoraceae-Pluteaceae; Clavariaceae; hymenochaetoid clade; gomphoid-phalloid/russuloid/thelephoroid clades; and the bolete clade. PCR-amplification and bidirectional Sanger sequencing of the ITS region is continuing, and ITS sequences already obtained have been assembled with the corresponding previously published LSU region of each clone. Each region (ITS1, ITS2, LSU) of each clone will be used in BLAST searches for matching reference sequences. BLAST matches and phylogenetic analyses of clones and reference sequences will be used to identify unknown clones and increase the clarity of the phylogenetic relationships among them. The data obtained will also be valuable as a source of contiguous ITS1-ITS2-LSU reference sequences for metagenomic studies, which typically retrieve only one of these regions.

Oral Presentation

ECOLOGY AND EVOLUTION

THE PERSISTANCE OF TRANSPLANTED *SACCHAROMYCES CEREVISIAE* IN THE WILD

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Saccharomyces paradoxus, the wild sister species of *Saccharomyces cerevisiae*, has been shown to persist yearly, around the bases of oak trees in Southern Ontario. Literature suggests that our locality may be too cold to support *S. cerevisiae,* which often is associated with fruits rather than tree bark and soil. The goal of my research was to determine whether or not transplanted, genetically marked strains of *S. cerevisiae*, would persist along with *S. paradoxus* in Southern Ontario. To mark strains of *S. cerevisiae*, spontaneous mutations of His- phenotype and Ura- phenotype, which confers resistance to 5-Fluoroorotic acid (5-FOA), were used. Three oak trees, each with three sites, were chosen for transplantation; Approximately 10^{10} cells suspended in 100 mL of water were introduced to the soil surface. For each tree, one site consisted of *S. cerevisiae*, another of *S. paradoxus*, and the third site was an equal mix of *S. cerevisiae* to *S. paradoxus*. The nine sites were sampled weekly for six weeks in the fall. The soil was suspended in water and plated on 5-FOA medium to calculate the number of yeast colony forming units per gram of soil (CFU/g). No other soil microorganisms grew on this medium. Although there was a gradual decrease in abundance for *S. paradoxus* and *S. cerevisiae*, all transplanted strains were able to persist. *S. cerevisiae* showed no deficit in persistence relative to *S. paradoxus*. All sites will be re-sampled in the spring to determine if *S. cerevisiae* was able to persist throughout the winter months.

Oral Presentation
Group B: Ecology and Evolution

MUTATIONAL DIVERSIFICATION OF *SACCHAROMYCES PARADOXUS*

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Genetic diversity of yeasts eg. the wild yeast *Saccharomyces paradoxus* and its domesticated sister species *S. cerevisiae* has been documented on global and long-term temporal scales. I investigated the genetic diversification and population genomics of *S. paradoxus* over a very small spatial scale. S. *paradoxus* strains were collected this year from various microsites around the base of one oak tree, to answer the two main questions: 1) How much and what kind genetic variation is seen in this population of *S. paradoxus*? 2) How has this population's genetic variation changed over a time scale of three years? Eighteen strains of *paradoxus* were collected from microsites in 2014, 2015 and 2016. Whole genome data was used to find single nucleotide polymorphisms (SNPs) in the 2016 strains. The variant loci were analyzed in the strains from previous years to assess when the variance emerged. Variant calling revealed 42 SNPs. These SNP sites were clustered in several small patches within the genome and were heterozygous in the majority of the strains; in some strains, these patches showed loss of heterozygosity (LOH), becoming haploid. LOH was likely due to gene conversion events. The LOHs in 2016 were not seen in previous years, indicating that these events are novel. Growth curves showed that no strains grew differently than the others. My results indicate that genetic variability within this population is low, and that SNPs have mostly happened due to LOH events.

ORAL PRESENTATION

B: Ecology and Evolution

MITOCHONDRIAL MULTILOCUS GENOTYPE ANALYSIS REVEALS LOW GENETIC VARIABILITY BETWEEN GLOBAL POPULATIONS WITHIN THE MATSUTAKE MUSHROOM SPECIES COMPLEX

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Matsutake mushrooms are ectomycorrhizal fungi that grow around the northern hemisphere and play a crucial role in nutrient cycling and improving plant health within temperate ecosystems. These edible mushrooms also have high economic value in Japan. DNA barcoding, based on sequences of the nuclear internal transcribed spacer (ITS), divide matsutake mushrooms from different geographical regions into several species: *Tricholoma matsutake* (Asia), *T. anatolicum* (Mediterranean), *T. magnivelare* (Eastern North America), *T. murrillianum* (Western North America) and *T. mesoamericanum* (Mexico). Together, these species constitute the matsutake species complex. This project examined the phylogeography of matsutake mushrooms through a multilocus genotype analysis to gain a more complete understanding of the global distribution and evolutionary history of these organisms. ITS sequences and four mitochondrial loci were examined for 100 matsutake samples collected from North America, Europe and Asia. Overall, low genetic variability was observed among the mitochondrial loci of samples from different geographical populations. Phylogeographical and population structure analyses have important implications for conservation.

Oral Presentation
B: Ecology & Evolution

THE EVOLUTIONARY SIGNIFICANCE OF MATING PLUGS IN REPRODUCTIVE BEHAVIOUR OF CAENORHABDITIS NEMATODES

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In species where individuals mate multiply sexual selection can act to exaggerate or eliminate traits to enhance successful fertilization after insemination. For instance, larger sperm have the ability to displace the sperm of competitors, and hence increase the number of offspring that a male sires. However, males in some species use mate guarding strategies, such as copulatory plugs, to prevent females from re-mating. Previous research on *Caenorhabditis* found an inverse relationship among species in the size of sperm and the size of plug, which could indicate that there exists a trade-off between the two. However, despite the common occurrence of plugging behavior across the *Caenorhabditis* phylogeny, the exact function of the copulatory plugs has not been conclusively demonstrated. I aim to understand the function of the copulatory plugs in *Caenorhabditis macrosperma* by performing controlled mating assays and visualizing gamete transfer, using mitochondrial dyes and fluorescent microscopy. Preliminary results suggest that females with copulatory plugs deposited in their vulva are less likely to receive sperm from the second male, compared to the non-plugged females. This suggests that copulatory plugs might benefit males, by assuring paternity. Smaller plugs deposited by strains with sperm gigantism appear to be less effective barriers to subsequent mating attempts by males, which is consistent with the trade-off hypothesis. Future work involves testing potential benefits of plugs to the females, by quantifying sperm retention rates in plugged and non-plugged females. The results of these experiments shed light on evolution by sexual selection and sexual conflict in *Caenorhabditis* nematodes.

Oral Presentation

B: Ecology and Evolution

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Effects of elevated temperature and CO_2 levels on ectomycorrhizal interactions in *Populus x. canadensis* roots

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The implications of climate change for mycorrhizal interactions are not well understood. Elevated CO_2 may increase photosynthetic activity and elevated temperature may increase enzyme activity, allowing for extra carbon to be allocated to mycorrhizal symbionts, possibly increasing mycorrhizal symbiosis with climate change. The objective of my research project is to investigate how elevated temperatures and CO_2 levels will affect the frequency and structure of the mutualistic symbiosis of ectomycorrhizal fungi, specifically between *Populus x canadensis* and the fungus *Paxillus involutus*. Seedlings were grown under six different climatic treatments of temperature and CO_2 concentration combinations, with half inoculated with *P. involutus*. Temperature conditions included ambient temperature (AT), ambient +4 ˚C (4T) or ambient +8˚C (8T) temperatures. CO_2 concentration conditions were either ambient (AC, 400 ppm) or elevated (EC, 750 ppm). All plant tissues were harvested to assess biomass allocation and proportion of mycorrhizal roots to nonmycorrhizal roots was recorded. Roots were cross-sectioned and observed with interference contrast microscopy to examine differences in mycorrhizal interaction with climate change treatments. Preliminary results show elevated root biomass and higher frequency of mycorrhizal colonization in elevated temperature and CO_2 (4TEC, 8TEC) treatments compared to other treatments. Elevated mycorrhizal colonization in these treatments may be a result of elevated biomass as opposed to direct climate change effects. Analysis of micrographs will reveal possible structural differences with climate change. It is important that we investigate how climate change will affect mycorrhiza as they are integral part of forest ecosystems.

Oral presentation

GROUP C: Physiology & Toxicology

A calorimetric method for measuring ice content of the freeze-tolerant cricket *Gryllus veletis*

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Freeze tolerant insects survive ice formation in their bodies. Fall-acclimated *G. veletis* nymphs are freeze-tolerant (FT). The nymphs survive freezing at temperatures above their lower lethal temperature (-12 °C) and for durations shorter than their lethal time (7 days). Summer-acclimated *G. veletis* do not survive freezing, i.e. are freeze-sensitive (FS). The cause of death in FS insects, and in FT crickets frozen beyond their lethal limits is poorly understood. Ice content increases in frozen insects both with time and a decrease in temperature. I therefore hypothesize that exceeding a critical ice content causes mortality. I designed and constructed a calorimeter with which I measured *G. veletis* ice content. I compared the proportion of body water that froze in both FT and FS *G. veletis* at -8 °C, and -16 °C, and at different time points (2 h, 18 h, 2 weeks) during the freezing process. Measured ice content was highly variable; the percent body water frozen in FT and FS crickets at -8 °C was 54.9 ± 56.9 % and 76.7 ± 19.4 %, respectively. The mean ice content did not increase in FT *G. veletis* when frozen for longer than 7 d (lethal time), or when frozen below their -12 °C (lower lethal temperature) as compared to FT crickets frozen at -8 °C for 18 h. I systematically tested the precision of parameters involved in my calculation of ice content to check accuracy of the calorimeter. I determined that measurement error accumulation may have masked differences between treatment groups.

Oral presentation, Group C

COLD COMFORTS: LONG TERM COLD EXPOSURE PROLONGS MEMORY IN COMMON POND SNAIL, *LYMNAEA STAGNALIS*

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Cold blocks formation and potentially promotes retention of long-term memory (LTM) in ectotherms, likely by stopping or slowing gene activation and protein synthesis. Forgetting is an active process that can be blocked by the cold. The pond snail, *Lymnaea stagnalis*, is a model system for studying memory that overwinters at approximately 4°C. The established inter-neuronal network of *L. stagnalis* respiration has been used to identify neuronal changes in response to operant conditioning. Snails are easily conditioned to avoid aerial respiration. This study determined if snails can keep and create new LTM before, in, and after cold similar to temperatures of its natural winter environment. We hypothesized that cold blocks LTM formation, by slowing physiological processes involved in memory consolidation. Additionally, we hypothesized that cold enhances LTM retention by inhibiting the active process of forgetting. We studied *L. stagnalis* ability to form and retain LTM in response to one-hour 4°C cold-shock and two-week 4°C acclimation. We exposed snails to KCl solution upon first aerial respiration attempt, to operantly condition them to stop aerial respiration. Snails learned when the duration of aerial respiration was significantly less one day after operant conditioning than one day before. Cold-shocked snails did not form new LTM but retained LTM consolidated before cold-shock. Further, acclimated snails formed LTM at 4°C, and snails kept at 4°C retained LTM for two weeks; which is longer then when kept at room temperature. We demonstrated acute cold exposure has more negative effects than long term cold exposure on LTM in *L. stagnalis*.

Oral Presentation, Group C: Physiology and Toxicology

THE EFFECTS OF GUT-ASSOCIATED YEASTS ON *DROSOPHILA MELANOGASTER* WATER BALANCE

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ABSTRACT

Most studies about gut microbiota-host relationship focus on bacteria resulting in gut-associated yeasts being less understood, despite improving some *Drosophila melanogaster* physiological traits. As some insects can survive desiccation better with their microbiota intact than when axenic (microbe-free), the effects of three yeasts (*Pichia kluyveri*, *Lachancea kluyveri*, and *Saccharomyces cerevisiae*) on fly water balance was investigated. I hypothesized that yeasts determine *D. melanogaster* survival under desiccation, and that yeasts affect adult desiccation resistance differently when inoculated as adults versus throughout development. I compared survival time, initial water content (IWC), water content at death (WCD), and water loss rate (WLR) under desiccating conditions between axenic and gnotobiotic (colonized by select microbes) adult flies. I also measure if those factors differed upon inoculating flies with yeasts as adults and upon rearing flies with yeasts until adulthood. I observed no differences in desiccation survival time between axenic and adult-inoculated gnotobiotic flies, despite *S. cerevisiae*-flies having significant differences in IWC and WLR. *L. kluyveri*- and *S. cerevisiae*-reared flies survived for significantly shorter times under desiccating conditions and had significantly higher IWCs and WLRs. Desiccation survival time did not differ between *P. kluyveri*-reared and axenic flies. Thus yeasts may hinder fly desiccation survival, indicating that while gut-associated yeasts are beneficial to some physiological processes they might not be essential to all. Additionally, yeasts affect host physiology differently depending on time of inoculation indicating that there might be a specific window for acquiring microbiota effects. Lastly, these effects on fly desiccation resistance may be yeast species-specific.

Abstract for: Oral Presentation
Preferred group: C) Physiology & Toxicology

THE EFFECT OF LEPTIN ON MIGRATORY RESTLESSNESS AND BODY COMPOSITION IN WHITE-THROATED SPARROWS (*ZONOTRICHIA ALBICOLLIS)*

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Bird migration is an energetic feat that requires changes in behaviour, morphology, and physiology to complete. Often, the likelihood of a bird leaving a site to migrate depends on fuel accumulation. This fuel is primarily fat. Leptin is the master energy balance regulating hormone in mammalian and non-mammalian species. Leptin signals fat levels to the brain and consequently influences behaviour involving energy expenditure. In birds, however, leptin's existence and function have been debated for decades. As evidence for avian leptin's existence accumulates, it becomes important to understand its function. The object of this experiment was to determine if leptin influences migratory behaviour and body composition. We did this by injecting white-throated sparrows (*Zonotrichia albicollis)* daily with leptin and monitoring their migratory restlessness; a quantification of the likelihood a bird will migrate. Considering leptin's role in signaling fat levels to the brain in other species, we hypothesized that leptin has a similar role in birds and will influence migratory restlessness intensity. We also hypothesized injecting birds with leptin will affect how much fat a bird has. We expected migratory restlessness intensity to increase, and fat levels to decrease in response to leptin compared to control birds. Our results on body composition contradict our hypothesis; leptin did not decrease body fat. Rather, there was a trend indicating the opposite. We urge future research to investigate if avian leptin acts as part of a positive feedback loop. Migratory restlessness results will be discussed.

Oral Presentation, Group C: Physiology and Toxicology

Word Count: 240

THE EFFECTS OF HYPOXIA ON PILOCARPINE INDUCED HYPERKINESIA PLANARIA

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Status epilepticus (SE) is a seizure lasting more than 30 minutes, or multiple seizures without regaining consciousness between them. Studies have shown that near-death experiences involving hypoxia created electrical alterations in the temporal region of the brain. We examined the effects of an acute hypoxic incident in planaria exposed to Pilocarpine in a model similar to that of vertebrate SE. Pilocarpine is a muscarinic acetylcholine receptor agonist capable of creating seizure related brain damage. To create a hypoxic episode, we used carbonated water. Planaria were exposed to one of four conditions then observed to record their open field behaviour. The behaviours of interest were C-shape, corkscrew, grids crossed, whips and odd. The four conditions were: water, Pilocarpine, carbonated water and Pilocarpine followed by carbonated water. Planaria were trained to transverse a T-maze which contained both a box with and without a light. The dark box was the target arm, planaria exhibit negative photo-taxis, therefore avoid light. On each day of training, two runs of three, 210 second trials per planaria were conducted. After training, planaria were exposed to a condition and tested for memory retention in the T-maze in absence of the negative stimulus. We anticipate that the exposure to the combination of Pilocarpine followed by carbonated water will decrease the number of hyperkinetic movements and improve retention in a T-maze learning paradigm as compared to Pilocarpine alone. This research will lead to future research, for example testing carbonated water as an effective alternative to current antiepileptic drugs.

Oral presentation
Physiology & Toxicology