Northeastern Illinois University

The Student Center for Science Engagement
Seventh Annual Research Symposium

Featuring student presentations

Biology, Chemistry, Computer Science, Earth Science,
Mathematics, Physics, and Psychology

September 18, 2015

Northeastern
Illinois
University

The Student Center for Science Engagement
Seventh Annual Research Symposium

Friday, September 18, 2015
Northeastern Illinois University
Chicago, Illinois

Marcelo Sztainberg, Ph.D.
Associate Dean
College of Arts and Sciences

Joel Olfelt, Ph.D.
Director, SCSE
Professor, Biology

Sylvia Atsalis, Ph.D.
Coordinator, SCSE

Paloma Vargas, Ph.D.
Life Sciences Advisor, SCSE

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Cindy Voisine, Ph.D., Assistant Professor, Biology

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SYMPOSIUM SCHEDULE

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Village Square, Student Union (Poster Presentations)

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Poster Set-up

9:00-9:10 A.M.
Opening Remarks

9:15 A.M.-12:04 P.M.
Oral Presentations

12:15-1:00 P.M.
Break

1:00-2:30 P.M.
Luncheon
Keynote Speakers
Beth Corrigan and Lindsay Darling
Morton Arboretum
The Impact of Urban Forestry in the Chicago Region

2:30 Raffle

2:30-5:00 P.M.
Poster Presentations
Coffee and Dessert
Village Square

Golden Eagles: 4:00-5:00 P.M.
Summer research student roundtable (optional)

ASSOCIATE DEAN'S MESSAGE

Congratulations! Today you are making all of us feel very proud. Making a research presentation is not an easy task. It involves plenty of work, persistence, commitment and passion.

While today represents a culminating moment, we hope that this is just one more step towards your larger academic goals. Take a minute to reflect on how this past summer helped you and your vision of becoming a scientist, be it in an academic, corporate, or not-for-profit environment.

This is a moment to thank your faculty mentors, your advisors and the staff of the Student Center for Science Engagement. These individuals showed, yet again, their commitment to our mission as a College and are counting on each of you to carry on with your success stories.

We are looking forward to seeing you back as a student, or alum. We hope you will continue your research path, presenting and representing us at different venues. Go ahead and make us proud!

For the College of Arts and Sciences,

Marcelo Sztainberg
Acting Dean

DIRECTOR'S MESSAGE

It is my pleasure to welcome you all to the Seventh Annual Research Symposium of the Student Center for Science Engagement (SCSE)! Over the past summer, the SCSE facilitated and coordinated the research experiences of over 60 students at NEIU and partner institutions. This annual symposium serves to inform the NEIU community of the research carried out by this committed group of students, under the guidance of their faculty advisors. The Student Center for Science Engagement supported the research projects of over 46 students and 22 faculty on the NEIU campus. Sixteen students worked alongside as volunteers on these projects. The center also supported student groups working on research projects off-campus at the Field Museum. As our students share their discoveries with you today, you will have the opportunity to see first-hand just what they have achieved this summer. These achievements would not be possible without the mentorship provided by their faculty advisors, the leadership of the SCSE executive board, the support from the College of Arts and Sciences and the Office of Academic Affairs, and the participation of the broader NEIU community. The dedication of the staff at the SCSE ensured that the students and faculty had the infrastructure they needed for research. I thank all these individuals for their dedication to contributing to an environment at NEIU that makes such research experiences not merely possible but also rewarding for our students.

My congratulations to all the participants!

Joel Olfelt, Director, Student Center for Science Engagement

Coordinator's Message

Greetings to all summer research participants and to all symposium guests!

Many of you have heard me say that *the desire to succeed and the relentless drive to reach one's full potential are key to achieving professional excellence*. To our pleasure, we noticed these qualities in you, our summer research students. But, although desire, drive, and potential are part of a solid foundation from which to springboard to success, they are not enough. Learning new lab and field skills, keeping a lab book of accomplishments, working on research team, networking with other professionals, asking questions, writing abstracts, designing posters, learning how to fail, learning how to leverage your successes-these are concrete real life experiences that give power to the internal drive, that fuel the potential. That is essentially what you did this summer. By learning real skills and gaining experience, you make the dream into reality and turn the potential into fact. We at the SCSE are proud to be part of that experience with you and for you. Your success gives us fuel to work for even better programming, develop even more resources and to further improve our advising. We thank you for the privilege of being part of your lives as you navigate these first stages of your professional dreams.

Sylvia Atsalis, PhD
Coordinator, Student Center for Science Engagement

Message from the SCSE Advisors

We very much enjoyed getting to know you and working with you this summer. Do not hesitate to contact us for help with your professional development. Best wishes as you progress through your academic paths.

Tomekia Simeon, PhD
Physical Sciences Advisor

Paloma Vargas, PhD
Life Sciences Advisor

STUDENT CENTER FOR SCIENCE ENGAGEMENT

MISSION AND GOALS

The mission of the SCSE is to significantly improve recruitment, retention and graduation rates for students in STEM disciplines, with an emphasis on minority, low-income, and first generation students. The goals of the SCSE are being achieved by enhancing academic support and mentoring through advising, faculty-student research projects, and peer mentoring, providing professional development opportunities to students through internships, networking opportunities, connections with leaders in STEM industries and academic institutions, career exploration in STEM fields and the development of programming focused on reaching minority, low-income and first generation students. The SCSE is proud to serve NEIU and support future student success in the sciences.

ORAL PRESENTATIONS

9:15 A.M.-12:04 P.M.

Golden Eagles

9:15-9:28- ALL IS ONE OR ONE IS ALL: AN EVOLUTIONARY MYSTERY OF THE BROWN VINE SNAKE (*Oxybelis aeneus*). Anthony Carmona[1], Alma Mendoza[1], John Murphy[2], Sarah A. Orlofske[1] and Robert C. Jadin[1]. Department of Biology[1], Northeastern Illinois University, Chicago, IL. Department of Zoology[2], The Field Museum, Chicago, IL

9:28-9:41- SWIMMING IN DISEASE: PARASITE DIVERSITY DRIVEN BY WATER QUALITY. Jason Block, Alejandra Villegas, Ryan Borchert, Robert C. Jadin, Sarah A. Orlofske**.** Department of Biology, Northeastern Illinois University, Chicago, IL

9:41-9:54- HYBRIDIZATION OF *TYPHA LATIFOLIA* AND *TYPHA ANGUSTIFOLIA* ACROSS THE US MIDWEST. Sarah Whidden, Joel Olfelt, and Pamela Geddes. Department of Biology, Northeastern Illinois University, Chicago, IL

9:54-10:07- OPTIMIZATION OF A DDPH ASSAY TO DETERMINE ANTIOXIDANT ACTIVITY IN DROSOPHILA**.** Janet Garcia, Barbara Rokita, and Elyse Bolterstein**.** Department of Biology, Northeastern Illinois University, Chicago, IL

10:07-10:20- ORGANISMAL AND NEURONAL HEALTH DECLINES IN *C. elegans* EXPRESSING TAR DNA-BINDING PROTEIN. Kirsten Knapton, Zelene Figueroa, Jason Garcia, Cindy Voisine. Department of Biology Northeastern Illinois University, Chicago, IL

10:20-10:33- INVESTIGATION OF FLUORESCAMINE AND DABCYL AS A NEW FRET DONOR-QUENCHER PAIR FOR PROTEASE ACTIVITY ANALYSIS. Krista Lotesto and Jing Su. Department of Chemistry, Northeastern Illinois University, Chicago, IL

10:33-10:46- EXPLORING THE ENTRY CAPABILITIES OF H5N1 INFLUENZA IN THE ABSENCE OF SIALIC ACID BINDING IN HEMAGGLUTININ. Brenna Dooley and Emily Rumschlag-Booms. Department of Biology Northeastern Illinois University, Chicago, IL

10:46-10:59- THE INTEGRATION, MODULATION AND HIERARCHICAL CONTROL OF CENTRAL NERVOUS SYSTEM AROUSAL AND RESPIRATION IN THE PREYING MANTIS. Emily Fioramonti[1], Veronica Skital[1], Greg Prete[1], Salim Patel[1], Bart van Alphen[2], Aaron Schirmer[1], Frederick Prete[1]. Department of Biology, Northeastern Illinois University[1], Chicago, IL, Department of Neurobiology, Northwestern University[2], Evanston, IL

10:59-11:12- STABILITY STUDY OF LI-ION BATTERY CATHODE MATERIALS. Giovanni Monterroso and Chandana Meegoda. Department of Chemistry, Northeastern Illinois University, Chicago, IL

11:12-11:25- DETERMINING RELIABILITY OF EXISTING GRAVITATIONAL WAVEFORMS IN PARAMETER ESTIMATION FOR BINARY BLACK HOLES. Cesar Bustos[1,2], Ben Sandeen[2], Shriram Chennakesavalu[2], Tyson Littenberg[2], Ben Farr[3], and Vicky Kalogera[2]. Department of Physics, Northeastern Illinois University[1], Chicago, IL, Center for Interdisciplinary Exploration and Research in Astrophysics, Northwestern University[2], Evanston, IL, Enrico Fermi Institute, University of Chicago[3], Chicago, IL

11:25-11:38- QUANTIFICATION AND MODELING OF ZEBRAFISH (DANIO RERIO) SHOALING PATTERNS IN RESPONSE TO ENVIRONMENTAL AND PHARMACEUTICAL TREATMENTS. Carly Hall[1,2], Marla Jean Douma[2], Emily Helmke[2], Yesenia Taveras[2], Dr. Shannon Saszik[2]. Department of Mathematics[1], Department of Psychology[2], Northeastern Illinois University, Chicago, IL

11:38-11:51- INFERRING CHANGES THROUGH TIME FROM PALEOLIMNOLOGICAL INDICATORS IN A 6,300-YEAR SEDIMENT CORE FROM VOLO BOG, A *SPHAGNUM* WETLAND. Michael Vujanovic, Naida Zulovic, Omar Morales Luna, and Jennifer E. Slate. Department of Biology, Northeastern Illinois University, Chicago, IL

11:51-12:04- INVESTIGATING POPULATION DEMOGRAPHICS AND GENETIC VARIABILITY IN LEEDY'S ROSEROOT. Alyson Cervantes, Ameer Noureldin, and Joel Olfelt. Department of Biology, Northeastern Illinois University, Chicago, IL

KEYNOTE SPEAKER BIOGRAPHICAL SKETCH

Beth Corrigan

Community Trees Program Specialist
The Morton Arboretum

Beth Corrigan is an ISA (International Society of Arboriculture) Certified Arborist and has been an employee of The Morton Arboretum for 14 years; the last 5 years with the Community Trees Program. She has a Bachelor of Science degree in Industrial Technology and worked as an Industrial Engineer for several pharmaceutical and consumer package goods companies. The experience has provided unique credentials for her approach to community outreach. Beth coordinates daily Community Trees Program operations and outreach for northern Illinois.

The main focus of the Community Trees Program is outreach. Using speaking engagements, training materials, newsletters, website, workshops, collaborative projects and site visits to connect with people, Beth is the liaison between people and the resources they need to preserve, manage and grow the urban forest around them. Outreach audiences include public and private land managers/owners, government entities, homeowner associations, corporate land managers, etc. She is well-versed in urban forestry and advises on tree selection, planting, care and preservation. She provides guidance to enable municipalities to complete tree inventories, management plans, ordinances and urban forestry funding opportunities.

Beth is an advocate for trees in many arenas. She works with neighboring states, in-state partners and NGO’s to advance urban forestry initiatives in Illinois. Beth fulfills the role of secretary and coordinator for the Illinois Urban Forestry Committee, a sub-committee of the Illinois Forestry Development Council and represents Illinois with the national State Urban Forestry Council collaborative, sponsored by Alliance for Community Trees. Beth also coordinates the suburban arm of the Openlands TreeKeeper® program and participates as an instructor.

ABSTRACTS
ORAL PRESENTATIONS

ALL IS ONE OR ONE IS ALL: AN EVOLUTIONARY MYSTERY OF THE BROWN VINE SNAKE (*Oxybelis aeneus*)

Anthony Carmona[1], Alma Mendoza[1], John Murphy[2], Sarah A. Orlofske[1] and Robert C. Jadin[1]
Department of Biology, Northeastern Illinois University[1], Chicago, IL
Department of Zoology, The Field Museum[2], Chicago, IL

Geographic barriers, such as rivers or mountains, play major roles in the formation of new species. When a species is geographically continuous the gene flow among populations leads to a lack of variation. However, when a species' range includes geographic barriers that isolate populations over extending periods, gene flow is interrupted and populations begin to diverge. One model system to study speciation is the Brown Vine Snake (*Oxybelis aeneus*) because of its wide geographic range spanning from the deserts of southern Arizona, through Mexico and Central America, and into South America on the island of Trinidad. Despite numerous geographic barriers (e.g. Sierra Madre Occidental, Isthmus of Tehuantepec, The Panama Canal) across its wide range, the Brown Vine Snake is considered a single species. However, specimens from southern Arizona have several different morphological features from those of Mexico suggesting that there is cryptic diversity and potential new species. In this study, we infer the first molecular phylogeny of the Brown Vine Snake throughout most of its range. In addition, a smaller sampling was conducted for the Green Vine Snake (*Oxybelis fulgidus*) to determine if its evolutionary history was similar across its Central American distribution. Gene fragments at two mitochondrial DNA loci (cyt b and 12S) and one nuclear DNA locus (c-mos) were sequenced for 28 tissues. These sequences were edited and aligned using Geneious R6 6.1.6 and we inferred phylogenies of these taxa along with other members of the Colubrinae subfamily using Mr. Bayes. Our results suggest that the Brown Vine Snake is one continuous species across its range with limited genetic variation among populations. This finding is significant in that this species differs from other lowland, wide ranging snakes, suggesting new ideas about geographic barriers that hinder gene flow in these low dispersing species.

SWIMMING IN DISEASE: PARASITE DIVERSITY DRIVEN BY WATER QUALITY

Jason Block, Alejandra Villegas, Ryan Borchert, Robert C. Jadin, Sarah A. Orlofske
Department of Biology
Northeastern Illinois University, Chicago, IL

Fertilizers used on crops and on urban lawns are running into aquatic habitats disrupting water chemistry (i.e. adding extra nutrients such as phosphorus or nitrogen). This leads to uncontrolled algae growth which can take up any dissolved oxygen in the water. One potential indirect measure of water quality could be the use of snails and their associated parasites. Many parasites of aquatic species have complex life cycles involving several host species leading to the proposal of parasites as indicators of ecosystem health. In this study we examined the relationship between several water quality variables in freshwater wetlands and the parasite diversity within those communities. We sampled freshwater snails at seven different sites in northeastern Illinois and southwestern Wisconsin. We sampled four focal species (*Gyraulus* sp, *Helisoma* sp, *Lymnaea* sp, and *Physa* sp) from each site. Each snail was examined for infective stages of parasites released from the snail or dissected to identify the parasites within the snails. We collected data on water temperature, pH, and dissolved oxygen. Additional tests for phosphorus, nitrate, nitrite, ammonia, turbidity, and hardness were made using a water quality kit on water samples returned to the lab. Our highest phosphorus concentration was 2.75mg/L and highest nitrate was 21.5mg/L both from the same wetland and associated with 8 parasite species. Our findings are important because nutrient pollution could result in uncontrolled algae growth, reducing the dissolved oxygen in that wetland which is detrimental to other species. Parasites could serve as water quality indicators because if no snails survive the organisms that depend on them for resources (i.e. parasites, birds) will also no longer inhabit that wetland; leading to secondary biodiversity loss.

HYBRIDIZATION OF *TYPHA LATIFOLIA* AND *TYPHA ANGUSTIFOLIA* ACROSS THE US MIDWEST

Sarah Whidden, Joel Olfelt, and Pamela Geddes
Department of Biology
Northeastern Illinois University, Chicago, IL

In the Midwestern United States, two plant species: native *Typha latifolia* and exotic *Typha angustifolia* (broad-leaf and narrow-leaf cattail, respectively), hybridize to form *T. x glauca* (F1 hybrid). Fertile F1 hybrids can backcross to either parental species creating advanced-generation hybrids. These hybrid swarms threaten wetlands by forming dense monocultures that out-compete native species and thus lower plant biodiversity. However, relative abundances of F1 and advanced-generation hybrids across the Midwestern United States are still poorly understood given that F1 hybrids were considered sterile until relatively recently. We used 6 previously developed microsatellite loci that discriminate between parent taxa and hybrids to investigate hybridization in 39 populations across 7 Midwestern states (n=178 plant tissue samples). Similar to previous research conducted in a subset of sites within the same region, we found pure native *T. latifolia* to be rare (11% of samples). Additionally, only 5% of samples were pure *T. angustifolia* while 17% were F1 hybrids (*T. x glauca*). Contrary to earlier research that found backcrossed genotypes to be uncommon, 67% of our samples were advanced-generation hybrids (AGH). Within these, 44% were backcrossed to *T. latifolia*, while only 11% were backcrossed to *T. angustifolia*. When molecular data were compared to morphological identification, parental species were correctly identified, but hybrids were underestimated and AGH samples were undetected. Advanced-generation hybrids were most often identified as *T. angustifolia* morphologically, which is comparable to previous studies. These data suggest that the hybrid is replacing both parental species throughout the Midwestern region, and that backcrossing is occurring more often than previously thought. Hybridization appears to have a greater impact on *T. angustifolia*, perhaps due to flowering time phenology. The loss of parental taxa via hybridization could have implications in the management of *Typha* stands as well as possible conservation of the native parental species.

OPTIMIZATION OF A DDPH ASSAY TO DETERMINE ANTIOXIDANT ACTIVITY IN DROSOPHILA

Janet Garcia, Barbara Rokita, and Elyse Bolterstein
Department of Biology
Northeastern Illinois University, Chicago, IL

Reactive oxygen species (ROS), or unstable free radicals, cause DNA damage by scavenging electrons from other molecules to achieve stability. This type of damage can be prevented by a large family of proteins known as the RecQ helicases. Mutations in two of the RecQ helicases, cause Werner's and Bloom syndrome, which are characterized by premature aging (Werner) and elevated risk of cancer/tumors (Bloom). To investigate how ROS may impact aging and tumor formation, we use *Drosophila melanogaster* (fruit flies) that are mutant in BLM and the Drosophila homolog of WRN, WRNexo. Drosophila with WRNexo and BLM mutations, have been shown to have similar phenotypes as Werner and Bloom syndrome patients such as shorter life spans and increased tumor incidence. Preliminary studies in our lab have shown that BLM mutants exhibit higher antioxidant activity which suggests higher levels of oxidative stress/DNA damage. In this study, we worked to optimize an assay that uses the free radical DPPH to determine antioxidant activity of proteins and small molecules. As DPPH is scavenged by antioxidants, the color of the solution turns from purple to yellow, which can be quantified using a spectrophotometer. We first created a standard curve using the powerful antioxidant, ascorbic acid, as a positive control. The resulting standard curve was used to determine the optimal concentration of assay reagents, protein levels, and spectrophotometer methods. We then applied our assay to protein extracts collected from wild type and mutant flies. Our preliminary data suggests that female wild type flies seem to have more antioxidant activity than males. Future studies will investigate antioxidant activity in aged flies where we predict that WRNexo and BLM mutants will exhibit increased antioxidant activity compared to wild type flies.

ORGANISMAL AND NEURONAL HEALTH DECLINES IN *C. elegans* EXPRESSING TAR DNA-BINDING PROTEIN

Kirsten Knapton, Zelene Figueroa, Jason Garcia, Cindy Voisine
Department of Biology
Northeastern Illinois University, Chicago, IL

Neurodegenerative diseases are common age-related disorders that are characterized by progressive loss of neuronal integrity resulting in defects that significantly impact a patient's quality of life. Neurons affected by Amyotrophic lateral sclerosis (ALS) are characterized by the presence of protein aggregates and studies have suggested an association between the disease state and a disruption in proteostasis. Cellular proteostasis is achieved through the functioning of an evolutionarily conserved quality control system, which ensures that proteins fold properly and minimizes harm done to cells and organisms when proteins misfold. TAR DNA-binding protein, 43 kDa (TDP-43) has been identified as a protein that accumulates and aggregates in the cytoplasm in neurons of patients affected by ALS, and mutations in the gene that encode TDP-43 have been linked to the familial form of the disease. To understand the effects that disturbances in neuronal proteostasis have on organismal lifespan and neuron function, the nematode *C. elegans* was used to generate transgenic animals expressing human TDP-43 fused to a yellow fluorescent protein (YFP) reporter gene in all neurons in the worm. Lifespan assays were conducted and the data indicate that TDP-43 expression is correlated with a reduced life expectancy. To measure neuronal function, we tested the ability of the AWC sensory neuron to detect a chemical attractant and found that TDP-43 expression also resulted in a decrease in chemosensation. To examine the hypothesis that disturbances in proteostasis lead to neuronal dysfunction, two additional transgenic lines carrying extra copies and a mutant form of *hsf-1*, an evolutionarily conserved transcriptional regulator of molecular chaperones, components of the protein folding quality control system, were crossed with TDP-43 expressing animals. Data suggest that the sensory deficit associated with expression of TDP-43 can be modulated by HSF1 activity, suggesting that clearance of protein aggregates may mitigate associated defects.

INVESTIGATION OF FLUORESCAMINE AND DABCYL AS A NEW FRET DONOR-QUENCHER PAIR FOR PROTEASE ACTIVITY ANALYSIS

Krista Lotesto and Jing Su
Department of Chemistry
Northeastern Illinois University, Chicago, IL

Fluorometric assays are used in biomedical applications including disease diagnostics, gene analysis, and pharmaceutical design. Many of these applications are focused on determining the activity of proteases, which are enzymes involved in the cleavage of proteins. One particular method of fluroremetric protease assays relies on the phenomenon known as Förster Resonance Energy Transfer (FRET), where emission of fluorescence by a donor group is initially inhibited by a quencher group in proximity within a protease substrate molecule. Cleavage of the substrate by a protease separates the donor from the quencher, and results in increased emission of fluorescence. Development of donor-quencher pairs, referred to as *probes*, is essential in FRET protease assays. This work aims to investigate the pairing between fluorescamine (donor) and DABCYL (quencher) in such application. Using UV-Vis and fluorescence spectroscopy, we have verified the excitation and emission wavelengths (λ_{ex} 390 nm, λ_{em} 480 nm) for fluorescamine conjugated to amino acids and a peptide substrate for Trypsin protease. Fluorescence emission of fluorescamine-peptide conjugates was quenched by DABCYL (λ_{max} 465 nm) in a concentration-dependent manner. The peptide substrate for trypsin, synthesized by solid phase peptide synthesis to contain the sequence of Ac-Cys-Ala-Arg-Gly-Ala-Lys-NH_2, will be used to include both fluorescamine and DABCYL within distance suitable for FRET. Methods for conjugating fluorescamine and DABCYL to the peptide are currently being tested. The FRET peptide Ac-Cys(DABCYL)-Ala-Arg-Gly-Ala-Lys(fluorescamine)-NH_2 product is expected to be cleaved by trypsin between Arg and Gly, leading to separation between the donor and the quencher and therefor increased fluorescence emitted by fluorescamine at λ_{em} 480 nm. Quantitative analysis of fluorescence emission will be carried out to exam trypsin activity *in vitro.* Our study of fluorescamine and DABCYL as a new donor-quencher pair can shed light on development of cost-effective and flexible FRET-based bioassays.

EXPLORING THE ENTRY CAPABILITIES OF H5N1 INFLUENZA IN THE ABSENCE OF SIALIC ACID BINDING IN HEMAGGLUTININ

Brenna Dooley and Emily Rumschlag-Booms
Department of Biology
Northeastern Illinois University, Chicago, IL

With high mutation rates and increased pathogenicity, influenza has the potential to cross the species barrier, sparking a global pandemic. H5N1 avian influenza has already jumped the species barrier, and although transfer between humans is not currently viable, elevated mutation rates in the influenza envelope protein, hemagglutinin (HA), may trigger sustainable transmission among humans. The only known mechanism for influenza to attach and enter host cells is via the sialic acid (SA) binding region of HA and host cell SA receptors; however, studies suggest that other entry routes may be possible. Therefore, if H5N1 can mediate entry in the absence of the SA binding region, the virus may be using another mechanism or cofactor to enter the cell. Our research is centered on exploring the entry capabilities of H5N1 virus deficient in the SA binding region. Using site-directed mutagenesis, amino acid residues were substituted to alanine, altering the SA binding region of HA. Then, pseudovirus containing the mutated HA or wild type HA was produced and used to infect target cells. Thus far, our data has shown that single amino acid substitutions Glu190A and Ser137A resulted in similar viral entry levels compared to wild type HA. This suggests that H5N1 may be entering cells via another method or with the help of an unidentified cofactor. To further explore the presence of an alternative entry mechanism, viral entry levels will be analyzed using combined mutations (Glu190A, Ser136A, Tyr98A, and Ser228A). Fully understanding H5N1 entry mechanics could help direct antiviral therapeutics and treatments.

THE INTEGRATION, MODULATION AND HIERARCHICAL CONTROL OF CENTRAL NERVOUS SYSTEM AROUSAL AND RESPIRATION IN THE PREYING MANTIS

Emily Fioramonti[1], Veronica Skital[1], Greg Prete[1], Salim Patel[1], Bart van Alphen[2], Aaron Schirmer[1], Frederick Prete[1]
Department of Biology, Northeastern Illinois University[1], Chicago, IL
Department of Neurobiology, Northwestern University[2], Evanston, IL

Physiological processes function synergistically as a constellation of integrated, nested systems shaped by natural selection. Understanding these relationships requires studying sufficiently complex (but tractable) model systems across levels of analysis. We do so using the praying mantis. At the molecular level, we are pursuing the clock gene *Period* (*Per*), a critical constituent of insect molecular circadian clocks which control biological rhythms throughout the organism. We have designed degenerate primers and amplified 400 and 1000 bp putative *Per* fragments from mantis cDNA. Sequencing revealed novel DNA fragments used to design gene-specific primers for use in RACE (Rapid Amplification of cDNA Ends) PCR. At the systems level, we are analyzing the mantis' unique breathing patterns which range from phasic to continuous. We believe that lower-level pattern generators controlling respiratory musculature are modulated by higher-level, cephalic pattern generators and this modulation influences respiratory pattern switching. Video analyses across species, and during rest and activity, have revealed that when breathing is phasic; restrained mantises breathe in bouts lasting approximately 100 sec separated by 50 sec intervals. In quiescent, unrestrained animals, overall bout and interval lengths are doubled. These data support our hypothesized hierarchical model of pattern generator control, and suggest the existence of a lower-level phase-modulated pattern generator operating consistently at a 66% duty cycle. Preliminary data suggest that switching from phasic to continuous breathing is associated with increased activity and/or arousal. Our previously published research has shown that there are oscillations in optic lobe physiology, and whole organism behavior. Hence, respiratory patterns may also oscillate in conjunction with the other patterns that we have discovered. As our research moves across levels of analysis in this model system, we are beginning to understand the integrated functioning of the component, nested systems that give rise to the organism that we know as mantis.

STABILITY STUDY OF LI-ION BATTERY CATHODE MATERIALS

Giovanni Monterroso and Chandana Meegoda
Department of Chemistry
Northeastern Illinois University, Chicago, IL

Lithium ion batteries have been successfully used by many industries such as consumer electronics, motorized vehicles and recently for military and aerospace applications. In spite of their widespread use, Li-ion batteries suffer from having flammable electrolyte materials, which can sometimes even lead to explosions. Therefore, it is important to study the stability of these batteries. Cathode materials play an important role on the electrochemical performance of the batteries and $LiFePO_4$ is widely used as a cathode material in view of its large theoretical capacity (170 $mAhg^{-1}$). However, low electronic conductivity and ionic conduction are major drawbacks of this material. In this study, we examined the stability of $LiMPO_4$ (M=Fe, Co, and Ni) cathode materials under different acidic, basic, and temperature conditions. FTIR spectroscopy was mainly used for the stability study and the spectra show a dominant band for the stretching and bending modes of the PO_4^{3-} polyanions. It was found out that both $LiFePO_4$ and $LiCoPO_4$ are stable even at 200 °C. Under acidic conditions $LiCoPO_4$ seems more stable than $LiFePO_4$ and $LiNiPO_4$. In order to better understand the stability and structure of these materials, $LiMPO_4$ (M=Fe, Co, Ni, Mn and Cu) was synthesized using sol gel synthesis and microwave synthesis. As compared to sol gel method, microwave synthesis needs shorter time. The study has shown that some cathode materials are more stable than others. This indicates that the stability of Li-Ion battery cathode materials is connected to which metal is being used in $LiMPO_4$.

DETERMINING RELIABILITY OF EXISTING GRAVITATIONAL WAVEFORMS IN PARAMETER ESTIMATION FOR BINARY BLACK HOLES

Cesar Bustos[1,2], Ben Sandeen[2], Shriram Chennakesavalu[2], Tyson Littenberg[2], Ben Farr[3], and Vicky Kalogera[2]
Department of Physics, Northeastern Illinois University[1], Chicago, IL
Center for Interdisciplinary Exploration and Research in Astrophysics, Northwestern University[2], Evanston, IL
Enrico Fermi Institute, University of Chicago[3], Chicago, IL

Gravitational Waves (GWs) were predicted by Einstein's Theory of General Relativity as ripples in space-time that propagate outward from a source. Strong GW sources consist of compact binary systems such as Binary Neutron Stars (BNS) or Binary Black Holes (BBHs) that experience orbital shrinkage (inspiral) and eventual merger. Indirect evidence for the existence of GWs has been obtained through radio pulsar studies in BNS systems. A study of BBHs and other compact objects has limitations in the electromagnetic spectrum, therefore direct detections of GWs will open a new window into their nature. The effort targeting direct GWs detection is anchored on the development of a detector known as Advanced LIGO (Laser Interferometer Gravitational Wave Observation). Although detecting GW sources represents an anticipated breakthrough in physics, making GW astrophysics a reality critically relies on our ability to determine and measure the physical parameters associated with GW sources. We use Markov Chain Monte Carlo (MCMC) simulations on high-performance computing clusters for parameter estimation on high dimensional spaces (GW sources - 15 parameters). The quality of GW parameter estimation greatly depends on having the best possible knowledge of the expected waveform. Unfortunately, BBH GW production is very complex and our best waveforms are not valid across the full parameter space. With large-scale simulations we examine quantitatively the limitations of these waveforms in terms of extracting the astrophysical properties of BBH GW sources. We find that current waveforms are inadequate for BBH of unequal masses and demonstrate that improved waveforms are critically needed.

QUANTIFICATION AND MODELING OF ZEBRAFISH (DANIO RERIO) SHOALING PATTERNS IN RESPONSE TO ENVIRONMENTAL AND PHARMACEUTICAL TREATMENTS

Carly Hall[1,2], Marla Jean Douma[2], Emily Helmke[2], Yesenia Taveras[2], Dr. Shannon Saszik[2]
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The collective motion of Zebrafish (*Danio rerio*) has been a subject of interest for neuroscientists and behavioral scientists in recent years. Zebrafish are an excellent model to study complex social behavior mechanisms due to their highly social nature, genetic conservation, and neural pathways analogous to humans. The purpose of this research was to quantify shoaling behavior in zebrafish after two treatments; environmental (number of fish, novel tank size of 18 X 18cm, volume of 300mL) and pharmaceutical (200μM MPTP). MPTP alters dopamine signals in neurological pathways involved in complex social behaviors. Adult zebrafish were randomly selected from different housing tanks in the lab and placed in groups of 3 or 5 zebrafish (3F and 5F). The 3F and 5F groups were placed into control or MPTP treatment conditions. Shoaling behavior was observed and recorded for two minutes in a novel tank. Videos were recorded and swim behavior was analyzed using Virtual Dub and ImageJ. The manual tracking plugin in ImageJ was used to measure velocity and distance. Microsoft Excel was used to calculate average velocity, total distance traveled, nearest neighbor distance for each fish, and shoal size. SPSS was used for statistical analysis. Analysis of the average velocity and the total distance traveled demonstrated that neither the environmental nor the pharmaceutical treatment had an impact on the motor function of the zebrafish. SPSS analysis is expected to show significant differences between the MPTP and control groups. Shoal size fluctuated sinusoidally. The fluctuations in shoal size were analyzed using the FFT. Results were used to build a model to assess the behavior of the MPTP groups. The improvement of behavioral quantification methods will facilitate research and lead to the development of a potential mathematical model that can be used to study shoaling, other types of social behaviors, and interactions between zebrafish.

INFERRING CHANGES THROUGH TIME FROM PALEOLIMNOLOGICAL INDICATORS IN A 6,300-YEAR SEDIMENT CORE FROM VOLO BOG, A *SPHAGNUM* WETLAND

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As Illinois's only quaking bog, Volo Bog is unique due to the naturally acidic water caused by a floating mat of *Sphagnum* moss. To determine how Volo Bog may have developed, we analyzed sediment deposited in the bog over time. We collected an 8.5-m core of sediment underlying the bog, which radiocarbon dating revealed spanned the past 6300 years. We determined percent organic content through loss-on-ignition, in which we dried the sediment and then burned off organics at 550°C. We also examined the abundance of microscopic remains of chrysophyte and diatom algae that thrive in acidic conditions. Percent organic matter was consistently high (75-93%) above 7-m, but decreased to <53% below 7.5-m. Acidophilic diatoms (e.g. *Eunotia*) and ten morphotypes of chrysophyte cysts were identified. The increase in percent organic content at around 7-m depth may indicate when the *Sphagnum* moss began to appear. Additionally, the high preservation of chrysophyte cysts and acidophilic diatoms suggest that they may be used to determine if acidity changed when the mat of *Sphagnum* moss developed.

INVESTIGATING POPULATION DEMOGRAPHICS AND GENETIC VARIABILITY IN LEEDY'S ROSEROOT

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Data on the demographics and genetic variability of populations are useful for the purposes of monitoring the viability of populations and making management decisions. Leedy's roseroot (*Rhodiola integrifolia ssp. leedyi*) is a rare and endangered species with a total of seven populations in Minnesota, New York, and South Dakota. Its close relative, *R. integrifolia* ssp. *integrifolia* is widespread in North America and is useful for comparison with Leedy's roseroot populations. Because data on the genetic variability and demographics of rare and endangered plants are useful to wildlife managers and can give insights into the evolution and population dynamics of small natural populations, we are investigating the demographic and genetic characteristics of the Minnesota and New York Leedy's roseroot populations and their western relatives using both traditional botanical, and molecular genetic tools. We censused the four Minnesota populations by making visual counts of the total number of individuals at each population, and we recorded the size and reproductive status of 16 to 36 permanently marked individuals at three of the Minnesota populations. To investigate the genetic variability of the populations, we tested 11 microsatellite marker regions that were developed for Asian *Rhodiola* species for their utility in the Leedy's roseroot populations and in 34 *R. integrifolia* ssp. *integrifolia* individuals. The estimated census sizes of the populations ranged from 197 to 882 plants, and their effective to actual population size ratios as estimated using traditional botanical data ranged from 0.22 to 0.63. Four of the 11 microsatellite regions reliably give amplification product, and so far we have successfully genotyped 49 individuals for three of the four reliable microsatellite regions. We will continue genotyping individuals from the populations and will analyze our molecular genetic data to estimate the levels of genetic variability and effective population sizes.

POSTER PRESENTATIONS

SNAIL SUPER-SPREADERS: DETERMINING THE KEY FACTOR BEHIND PARASITE INFECTION

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Parasites are fundamental components of biodiversity, with an estimated 30 to 50 percent of all known animal species being parasitic. Various human diseases, like Schistosomiasis, are caused by parasites and inflict widespread illness. Thus, understanding the environmental and ecological parameters that impact parasitic infections is critical for addressing human and wildlife diseases. In this study, we examined parasite communities of freshwater snails in a variety of wetland ecosystems to determine the relationship between parasitic infections and food web structure. Freshwater snails are critical hosts in parasite life cycles and are prey to various organisms, making them useful models to study in food web interactions and disease ecology. Our study focuses on the number of particular parasites in a single snail (intensity) and proportion of snails infected with a particular parasite (prevalence). We examined four independent variables representing independent hypotheses explaining variation in intensity and prevalence: food web connectivity, snail density, snail occupancy among wetlands, and snail body size. Seven sites were surveyed for biodiversity and snail populations from May to August 2015. Snails were collected and examined in the lab for parasite infections. We found an extensive range for parasite intensity, uninfected to 2074 parasites in an individual snail, and a prevalence range of 0% to 98% of snails infected with a particular parasite life stage. Body size ranged from 1.97 mm to 44.69 mm; density ranged from 0 to 45.7 snails per square meter; occupancy ranged from 5 to 10 individual snail species out of 14 total site visits. To measure food web properties, we will construct a network model and derive metrics to test in generalized linear models with our other factors. These results will reveal important insights behind factors driving parasite infection patterns and further develop an understanding of how parasites influence the dynamics of the ecosystem.

WHAT IS THE BEST WAY TO LEARN COMPLEX CONCEPTS?

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Can gesture production index adult learning of a complex science concept? Experimentation reveals neural and behavioral connections between speech-plus-gesture production and comprehension of math and science concepts. Research has shown that linguistic information is processed by the left hemisphere, while spatial information is processed by the right. Advanced learning requires neural activation of both linguistic and spatial regions and use of hands indexes activation of hemispheres. We found that college students vary in hand usage when gesturing during explanations of stereoisomers. We hypothesized that hand usage in novice learners might be an indicator of complex understanding; specifically, two-hand usage (indicating involvement of both hemispheres) when describing stereoisomers indexes *readiness to learn*. A pretest-instruction-posttest design, tested whether use of hands when gesturing in the pretest influenced the learning of stereoisomers. For the pre- and posttest, 49 college students were asked to create structures of a 6 stereoisomer molecules. Instruction designed to activate spatial representations of stereoisomers included 3 types: (1) *Imagination* asked the participant to create a mental picture of the molecule, (2) *Gesture* asked the participant to create hand movements to create pictures of molecules and (3) *Modeling*, asked the participant to create a 3-D model of the molecule. Learning was increased from the pre-to the posttest in correct depictions of stereoisomer molecules. Preliminary results support our hypothesis and *Gesture* and *Imagination* instruction yielded the greatest learning for those who used both hands when gesturing during pretest explanations.

FRESHWATER SPONGES AS PALEOLIMNOLOGICAL INDICATORS IN VOLO BOG

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Volo Bog Nature Preserve has one of northeastern Illinois's most unique wetlands, containing naturally acidic water with pH ranging from 5.7-6.2. The wetland originated as a kettle lake and is now ringed by a floating mat of Sphagnum moss. To investigate how the wetland developed, we collected an 8.5-m sediment core and analyzed siliceous spicules of sponges preserved in the sediment. Three types of spicules (skeletal support structures) were well preserved throughout the sediment core. Megascleres (large supportive structures) were most common, but microscleres (smaller structures), and gemmoscleres (spicules coating reproductive cell masses), which can be used to identify species, were also present. *Anheteromeyenia ryderi* and *Spongilla lacustris* were present at all sediment depths analyzed. *A. ryderi* is an indicator of acidic water, suggesting that the wetland was acidic throughout the entire ~6300 years spanned by the sediment core. In continuing research, spicules of *A. ryderi* and *S. lacustris* will be quantified, to determine if relative abundances change over time. Sponge spicules are thicker and thus more resistant to dissolution than are diatoms, allowing sponge spicules to be used as paleolimnological indicators when diatoms are absent.

PROTEOGLYCAN REGULATION OF CHONDROCYTE DIFFERENTIATION

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Proteoglycans are glycoproteins involved in both differentiation and proliferation of cells in development. Specifically, chondroitin sulfate proteoglycans (CSPGs), in particular aggrecan, are critical for proper limb growth plate development in vertebrates. During limb development bones are formed from cartilage anlagen produce by chondrocytes progressing through stages of differentiation. Aggrecan-deficient and reduced-sulfation mutant models have been used to examine the involvement of CSPGs in establishing and modulating signaling pathways during skeletal development. Chick and mouse models lacking aggrecan, show both premature death and extreme dwarfism due to accelerated chondrocyte differentiation in the growth plate. To study how CSPGs in the extracellular matrix influence chondrocyte differentiation we established a tissue culture system from primary chick chondrocytes and modified their extracellular matrix by enzymatic digestion (chondroitinase and hyaluronidase treatment) or biosynthetic modification (sodium chlorate and β-xyloside treatment). Using qPCR, we showed that changes in CSPGs by digestion with chondroitinase or reduction of sulfation by chlorate treatment increased levels of collagen 10A1 mRNA, a marker of chondrocyte hypertrophy, and enhanced matrix production as indicated by increases in Sox9, collagen 2A1 and aggrecan mRNA levels. We confirm these changes in cellular morphology and by mRNA in situ hybridization studies. Thus, our tissue culture system's outcomes are consistent with the observations in animal models in which changes in aggrecan matrix induce an acceleration of chondrocyte differentiation. This tissue culture system will be pivotal in understanding the changes in signaling pathways that lead to the increase rate of differentiation and ultimately to the chondrodysplasias associated with these animal models.

EXPRESSION OF AGGREGATION-PRONE PROTEINS ASSOCIATED WITH HUNTINGTON'S AND LOU GEHRIG'S DISEASE REDUCE CAENORHABDITIS ELEGANS ADULT LIFESPAN

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Multiple neurodegenerative diseases such as Alzheimer's disease (AD), Huntington's disease (HD) and Amyotrophic Lateral Sclerosis (ALS) begin during adulthood and progress rapidly leading to fatality. Research in disease pathology indicates that proteins associated with these diseases tend to aggregate, which could lead to neuronal dysfunction. For example, in HD, the huntingtin protein contains an expansion in the glutamine tract (polyQ), producing toxic abnormal protein folds leading to neurodegeneration. Similarly, individuals with ALS carry mutations in a gene called TDP-43, which is also prone to aggregation. Therefore, it is hypothesized that the expression of these disease-associated proteins will not only affect neuronal function but also affect organismal health. To test this hypothesis, I am using two nematode, *C. elegans,* models that express either of the aggregation prone proteins associated with HD and ALS, respectively. To monitor the effects of the expression of polyQ and TDP-43 on organismal health, I measured the adult lifespan of these two disease models compared to wild type animals. Lifespan assays were performed by examining populations of worms for each model daily until all animals expired. Preliminary data suggests that animals expressing polyQ or TDP-43 have a shorter median lifespan compared to wild type animals. The data suggest that expression of aggregation prone disease proteins triggers a decline in neuronal function that results in a shorter lifespan. Our studies using *C. elegans* models will continue to enhance our understanding of the relationship between aggregation prone proteins and neurodegenerative diseases.

ROLE OF FOLIC ACID IN THE DEVELOPMENT OF JAW AND SKULL OF ICR MICE – SIZE DOES MATTER

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Folic acid is a water-soluble, B vitamin that is important in cell production, mutation development and gene expression during embryogenesis. An increase in folic acid during pregnancy can prevent the frequency of Neural Tube Defects, or NTD's, such as cleft lip and palate, Anencephaly and Spina Bifida. Excessive levels of folic acid during embryo development has been shown to contribute to other developmental defects such as asthma, allergies, tumor growth, and high gestational age birth weight. The purpose of this research is to show that folic acid will have a varying effect on the formation of the mandibles between the different treatment groups. The mice in this study were exposed to varying doses of folic acid while they were embryos. When they mice reached adulthood, they were sacrificed, tissue removed from the bones, the mandibles were compared for size and shape differences. Three-dimensional models of the mandibles were created using a Laser Design, Inc. RPS-120 Probe at 0.01 mm interpoint distances. The 3D models were edited using Geomagic Studios, 2012. The coordinate points outlining major anatomical points were collected using Landmark Editor. Landmark points were analyzed using principle components analysis to examine shape differences across the treatment groups. Our results indicate that there are significant dosage-dependent differences in size and morphology. Previous analysis of the craniums of these same mice, showed variations, also dosage-dependent, in the shape of the craniums of the different dosage groups. This showed us that during skull formation, the folic acid has a different effect on the mandible vs the effect on the entire skull.

THE EFFECTS OF OXYGEN ON GROWTH AND SIZE IN MODERN BENTHIC FORAMINIFERA FROM THE SANTA MONICA BASIN

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The ocean is a diverse environment. Although areas of the ocean might be considered too harsh for life, almost no environment is uninhabited. We hypothesized that benthic foraminifera living in anoxic waters will have reduced test volume with fewer chamber numbers than those living in more oxygenated waters. The Santa Monica Basin (SMB), located off southern California, is an oxygen minimum zone where we can study the body size response of foraminifera to changes in oxygen availability. Meiofauna that live between seafloor sediment, such as benthic foraminifera, often dominate anoxic environments that are devoid of macrofauna such as gastropods and bivalves. Anoxic environments are unable to support macrofauna because there is not enough oxygen to meet the high metabolic demand of larger organisms. Oxygen is essential for metabolic reactions and the size of an organism correlates positively with metabolic demand. Organism size is expected to respond to changes in oxygen concentrations. Foraminifera are single-celled organisms occurring in most marine environments that are sensitive to environmental change making them ideal for investigating their size response to oxygen conditions. We collected four species of rotaliid foraminifera from core tops at 11 locations in SMB: *Bolivina argentea*, *B. spissa*, *Loxostomum pseudobeyrichi*, and *Uvigerina peregrina*. We grouped sites based on their oxygen levels into low-oxygen, suboxic, dysoxic, and anoxic conditions. Contrary to our hypothesis, *U. peregrina* shows a negative correlation between test volume and oxygen concentration while *L. pseudobeyrichi* and *B. spissa* show little variation in test volume between sites. Only *B. argentea* exhibits a positive correlation between test volume and oxygen concentration. Our results show that foraminiferal species have unique morphological responses to variations in oxygen. Although oxygen is an important energy source, additional variables, such as ecological interactions or food availability, might be influencing the individual species trends observed in the SMB.

APOMORPHINE, ANXIETY, AGGRESSION, OH MY!
DOPAMINERGIC MANIPULATION WITH APOMORPHINE AND MPTP USING A ZEBRAFISH MODEL

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Dopamine (DA) is a neurotransmitter that plays an important role in regulating complex social behaviors. This research seeks to understand how aggression is controlled by dopamine using a zebrafish (*Danio rerio*) model. Increased levels of dopamine have been shown to elicit aggressive behavior. Apomorphine (APO) is a dopamine agonist that affects motor function and induces aggression in rodent models. MPTP is a neurotoxin which causes apoptosis in dopaminergic neurons. Both were used to manipulate dopaminergic systems. This research hypothesizes that administration of APO will increase DA levels, which in turn increases aggression. Adult zebrafish were randomly selected and assigned to 1 of 4 groups: [control, MPTP (200 μM), MPTP/APO (200/150 μM), and APO (150 μM)], and dosed for two minutes. Behavior was recorded with a USB camera in groups of 3 or 5 fish in 300 mL of water in a novel tank. Behavior was defined using modified definitions of aggression in the Comprehensive Catalog of Zebrafish Behavior. Aggression in individuals was measured by calculating total distance swam (cm) and average velocity (cm/sec). Aggression directed at shoal mates was measured by calculating nearest neighbor distance (cm) and shoal area (cm^2). Results showed that all dosed fish swam greater total distances and had a higher average velocity than the control fish, which may be indicative of anxiety rather than aggression. The dosed fish also maintained larger distances between neighbors when compared with control fish, which further indicates anxiety. The effects of APO on zebrafish vary from those seen in the rodent model, implicating varying brain structures and their functional role in behavior across species. Manipulation of the dopaminergic system may help to better understand the connection between complex biological mechanisms and behaviors, such as aggression and anxiety, as well as better understand human social systems and their neurophysiological basis.

ELECTROCHEMICAL ETCHING TECHNIQUE OF PLATINUM-IRIDIUM TIPS FOR SCANNING TUNNELING MICROSCOPY

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The scanning tunneling microscope (STM) allows researchers to investigate atomic structure and properties of nanomaterials. Through the quantum tunneling effect a charge is transferred between the surface of the nanomaterial and the platinum-iridium (Pt-Ir) tip. The production of Pt-Ir tips by electrochemical etching (ECE) has been developed as an alternative technique, to achieve enhanced scanned images of samples, in contrast to the standard mechanical method (SMM). The sharpness apex structure is an essential feature during scanning in order to provide reliable data. We generated a control group of tips by the SMM technique and another group by the ECE technique to investigate the resolution effectiveness in scanning of graphite. The etching of the tips was produced using an auto-variable transformer running a 30 V AC in a 1.5 M $CaCl_2$ solution. The scanning of the graphite surface was conducted at 7x7 nm image width, 0.2 seconds time/line, 256 points/line and 0.05 V for tip voltage. The apparatus developed for the etching technique uses a laser, radial/angle circle and a standard level tool to achieve accuracy of the wire depth during etching. ECE etched tips displayed consistent image resolution, and the sharpness of the tip apex was generally uniform. Further, we investigate the following parameters: resistance (Ohms) of different types of solutions, reproducibility of the technique, waste reduction, depth of tip etching using a laser and cost efficiency based on materials.

A COMPARATIVE MODEL: EFFECTS OF FOLIC ACID ON NEURAL TUBE DEVELOPMENT IN MICE AND ZEBRAFISH

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In the United States, distributions of birth defects vary among ethnic groups. Among Hispanics the most common birth defects are anencephaly, spina bifida, cephalocele, gastroschisis and Down's syndrome. Among non-Hispanic or African-American mothers, prevalent defects are listed as Tetralogy of Fallot, lower limb reduction defects and Trisomy 18. In this investigation, we compared neural tube-derived birth defects in mice and zebrafish using varying dosages of folic acid and methyltrexate. Both models provide clues to further our understanding of modulatory changes involved in neural tube defects. Folic acid treatments in mice were compared to zebrafish hatch rates, and survival data of both treatment and control groups. Outbred zebrafish embryos were collected within 1 hour of spawn, during the segmentation period. Embryos were treated with folic acid (FA) and methyltrexate (MTX) (200μM) at 1-3 hours post-fertilization (hpf). At 48 hpf, (Pharyngula period) embryos were washed and housed in 20 ml of parent water, kept at 28-30°C from the hatching period (48-72 hpf) through larval stages of development. Daily living counts were recorded and fry displaying defects were identified, isolated in individual beakers and categorized by defect type. For spawn groups, photographs of each individual (n=100) were taken on three sampling occasions; days 2, 10 and 21 post fertilization (dpf). Fish with defective phenotypes were photographed daily. Defects were grouped and analyzed by relative time of visibility, somite region, orientation and touch-response. Survival, photo and motor-reflex data were used to compare fish defects to those identified in mice from previous trials. Predictable and visually identifiable ranges of time and developmental characteristics exist for zebrafish embryonic development, making survival data and defect types useful parameters in analyzing neural tube defects, furthering our understanding of species differences in neural tube birth defects.

USING *C. ELEGANS* AS A MODEL FOR AMYOTROPHIC LATERAL SCLEROSIS TO STUDY THE RELATIONSHIP BETWEEN TDP-43 AGGREGATION AND NEURONAL DYSFUNCTION

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Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease that primarily affects motor neurons, leading to rapid progressive paralysis and death. Approximately 10 % of ALS cases are inherited and mutations in the gene that **encodes the** Tar DNA-binding protein (TDP43) are linked to 3% of these familial cases. **TDP-43 is a DNA/RNA binding protein that is** normally found in the nucleus. However, TDP-43 has been found to aggregate in the cytoplasm of motor neurons of ALS patients. It is unclear whether TDP-4**3 aggregation is a** cause or a consequence of neuronal dysfunction in ALS patients. To begin to test the relationship between aggregation and disease, we have developed *C. elegans* transgenic lines expressing wild type or mutant forms of TDP-43. After propagating a population of young adults for each transgenic line, I generated protein lysates and centrifuged the samples to separate soluble and aggregated forms of TDP-43. SDS PAGE followed by western analysis is underway to quantify the level of TDP-43 protein aggregation in both the wild type and mutant strains. I anticipate that mutant forms of TDP-43 will aggregate more than wild type TDP-43. Furthermore, I anticipate that aggregation of TDP-43 will increase as the worms age, recapitulating the progressive pathology associated with this disease.

INVESTIGATING THE PRESENCE OF A SECONDARY RECEPTOR IN AVIAN INFLUENZA H5N1

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Avian Influenza viruses are highly pathogenic bird viruses that have the ability to cause disease in humans by crossing the species barrier and continue to pose threats to human health. H5N1 avian influenza is a prime example. H5N1 emerged in 1997 in Hong Kong, China and reemerged in 2003 with nearly 650 human cases reported from 15 countries. To cross the species barrier and infect a host cell, the viral surface protein hemagglutinin (HA) must be able to utilize the appropriate host cell receptor(s). Currently, the only known receptor for influenza is sialic acid, however, recent research suggests the presence of a secondary receptor; cells with an abundance of sialic acid are not susceptible to H5N1 entry. To study the presence of a secondary receptor, single and combination residues (G135A, S137A, E190A, L194A) in the sialic acid binding domain were targeted and mutated to disrupt the interaction of HA with its the sialic acid receptor. Virus was produced containing either wild type HA or mutant HA containing sialic acid binding domain substitutions and then used to infect target cells. Findings indicate that mutant HA and wild type HA has comparable levels of viral entry to host cells, suggesting the presence of a secondary receptor that HA is using to enter host cell. Confirming and identifying the presence of a secondary receptor could open the door for future therapeutic developments.

FIRST PRINCIPLES COMPUTATIONAL INVESTIGATIONS OF THE INTERACTIONS OF GRAPHENE WITH ATOMS AND MOLECULES

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Efficient storage of hydrogen molecules is a problem of interest in the advancement of hydrogen fuel cell technology. Research on the potential of graphene as a substrate for hydrogen storage has shown promising results. In this study, we investigate the lowest energy arrangements of atomic and molecular adsorbates (H, H_2) and the interaction of noble metals (Pt, Au, Ag) with graphene. We use the first-principles method of density functional theory (DFT) under the generalized gradient approximation (GGA) on finite models of graphene to examine the interaction of atomic and molecular hydrogen and noble metals with graphene. Contracted Gaussian type orbitals with all-electron double zeta basis sets (D95, DGTZVP) for the carbon and hydrogen atoms, and the Stuttgart-Dresden effective core potentials (ECP) and the associated basis for the noble metal atoms were used to calculate the energy of different structural configurations of graphene and surface adsorbates. We used a series of expanding graphene models of sheets and rings to examine trends in how different geometries and system sizes play a role in the interaction of graphene with adsorbates, and to identify the energetically favorable configurations. Our data shows that platinum and gold interact slightly with graphene. Furthermore, the adsorbed platinum forms a complex with molecular hydrogen, and shows promise as an intermediary for hydrogen storage on graphene.

CHARACTERIZATION OF RED LIGHT PHOTORECEPTORS DERIVED FROM STIGMATELLA AURANTIACA USING ATOMIC FORCE MICROSCOPY

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Bacteriophytochromes (BphPs) are photoreceptors that play a key role in the growth and development of photosynthetic and non-photosynthetic bacteria. BphP's contain a chromophore called biliverdin, an open-chain tetrapyrrole, which undergoes a cis/trans- isomerization upon the absorption of red light or far-red light of the electromagnetic spectrum. The purpose of this interdisciplinary research project is to characterize non-photosynthetic *Stigmatella aurantiaca* bacteriophytochrome SaBphP2 (P2) using Atomic Force Microscopy (AFM). While sacrificing the resolution X-ray crystallography and Nuclear Magnetic Resonance (NMR) affords, AFM has several advantages over these existing methods to analyze BphP structure and function. First, intact Bphps are notoriously challenging to crystallize, due to their size, particularly in their light-adapted states whereas protein single crystals are not required for AFM analysis. Secondly, AFM can be performed in aqueous solution which enables the photoreceptor to remain in a more native environment. Therefore, we have employed the Peak Force Quantitative Nanomechanical Property Mapping (PF- QNM) imaging mode to collect over thirty images of the photosensory module and the fully intact protein which also includes a signaling effector domain. Dimensional analyses of these images will be directly compared to existing X-ray crystallographic data on similar BphPs. Preliminary results indicate that as a result of the hydration of the protein and tip convolution, the protein appears larger in the picture produced by AFM than what would be expected using X-ray crystallography. However, the individual domains of the photoreceptor are clearly identified. The future goal is to study how the structure of both the photosensory module and the intact P2 molecule changes upon exposure to different light conditions.

UNDERSTANDING THE RELATIONSHIP BETWEEN AGGREGATION-PRONE PROTEINS AND NEUROTOXICITY BY ASSESSING SENSORY NEURONAL FUNCTION IN C. ELEGANS

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Proteostasis, or protein homeostasis, is critical to cellular health because this intricate network maintains proteome integrity by ensuring proper folding of proteins, which all cells must perform. In many of the age-related neurodegenerative diseases, misfolded proteins are found in large clumps. The accumulation of a disease protein in large aggregates may lead to a disruption in proteostasis that further affects neuronal function. Both polyglutamine protein expansions (polyQ) and transactive DNA binding protein 43 kD (TDP-43) are aggregation-prone proteins that are associated with Huntington's disease and Amyotrophic lateral sclerosis (ALS) respectively. Previous studies show a correlation in length-dependent polyQ expansions with neurotoxicity. It has also been well established that expression of TDP-43 leads to deficiency in motor neuron function. In this study we investigate whether the disruption of proteostasis inducing neurotoxicity is a common pathogenic feature or exclusive to a specific neuronal subtype. We performed chemosensory assays on the bilateral Amphid Wing "C" (AWC) olfactory neurons, which can sense volatile odorants that act as chemical attractants in *C. elegans*. Taking advantage of the chemosensation capability of the animal, we evaluated the sensory neuronal function by examining the chemotaxis behavior in two transgenic lines expressing aggregation-prone proteins (TDP-43 and polyQ) compared to wild type animals. Our data show that experimental groups could not detect the chemical attractant as well as the control group. This lowered chemosensation response suggests impairment of AWC neurons. Our finding on the deficit in sensory neuronal function in animals with both disease-related proteins indicates that aggregation may trigger neurotoxicity in multiple neuronal subtypes. These observations of non-exclusive cell type neurotoxicity suggest a common mechanism, the disruption of proteostasis.

A SELECTIVE CAPTURE/RELEASE APROACH TO SIMPLIFY METABOLIC STUDY OF PEPTIDE DRUGS

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Drug metabolism is defined as the biochemical modification of molecular structures by enzymatic systems in living organisms. Further understanding of drug metabolism can provide guidelines for the optimization of drug structures and properties. Isolating drug metabolites from complex biological mixtures, such as the blood and urea, is challenging when attempting to identify specific structural modifications. Currently, such isolation processes are labor-intensive and time-consuming. This work aims to develop a straightforward method for separating drug metabolites from complex biological samples, allowing purified metabolites to be readily analyzed by mass spectrometry. A drug molecule is designed to attach to a biotin group, which can selectively bind to a neutravidin-coated solid surface and be separated from the initial biological complex through rinsing of the surface. Incubation of the surface-bound drug-biotin conjugate with a solution containing free biotin molecules releases the conjugates. This approach avoids the tedious separation process in conventional drug metabolism studies. As proof of concept, the enzymatic cleavage of a synthetic peptide-biotin conjugate, biotin-Gly-Trp-Lys-Gly-NH_2, by the protease Trypsin was used to demonstrate this selective capture /release approach *in vitro*. Mixing the conjugate and Trypsin resulted in peptide cleavage producing a biotin-Glys-Trp-Lys-OH as the modified structure. All biotin-containing molecules, including modified and unmodified peptide conjugates, were captured onto the solid surface and subsequently released and characterized by electrospray ionization mass spectrometry. Experimental conditions for releasing peptide-biotin conjugates and sample enrichment prior to MS analysis have been developed to achieve desirable detection sensitivity. We believe this selective capture/release method for drug metabolite isolation is widely applicable to the metabolic study of various peptide drugs.

AN ISLAND OF MAROONED SERPENTS: ASSESSING EVOLUTIONARY DISTINCTION AND EDEMISM OF TRINIDAD SNAKES

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Discovering endemic (geographically restricted) island species is important for both conservation and evolutionary studies. Islands are natural experiments of evolutionary processes in which populations become isolated from the mainland by geographic barriers resulting in different species over time (allopatric speciation). Trinidad is one of the most biologically diverse and largest islands in the Caribbean, separated from the South American mainland by the narrow (~7 miles) but geographically significant Columbus Channel. While Trinidad has several endemic species, the majority of species are currently considered as synonymous to mainland taxa. Very few studies, however, have assessed the genetic distinctiveness of Trinidad species. Snakes tend to have low dispersal abilities making them excellent models to study the effect of geographic barriers on gene flow and speciation. Therefore, we applied molecular phylogenetics to six snake species (both venomous and nonvenomous) to determine whether any were endemic to the island of Trinidad and assess whether biogeographic barriers, such as the Columbus Channel, promotes allopatric speciation. Four mitochondrial gene fragments (12S, 16S, cytochrome b, and NADH dehydrogenase subunit 4) were used to create a Bayesian phylogenetic tree. We found that the Bushmaster (*Lachesis muta*), Tiger Ratsnake (*Spilotes pullatus*), and Common bird snake (*Phrynonax polylepis*) were genetically similar to their conspecifics from South America and did not represent new species. However, we identified a lineage of Lancehead (*Bothrops* spp.) that is a distinct sister species to mainland *Bothrops atrox.* This lineage likely represents an undescribed species endemic to the island of Trinidad. We also found that our *Liophis* and *Chironius* taxa are distinct from mainland snakes but may represent previously described species. Our detection of endemic evolutionary lineages may allow conservation biologists to propose protection of both the snakes and their habitat and allow for the creation of more effective anti-venoms.

LIGAND FUNCTIONALIZATION OF IRON CARBIDE MAGNETIC NANOPARTICLES FOR BIOMEDICAL APPLICATIONS

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Alternating magnetic fields can heat magnetic nanoparticles through magnetophoresis. Magnetic hyperthermia is the biomedical treatment that applies such phenomena to eliminate multicellular complexes like cancerous tumors. Monodisperse iron carbide magnetic nanoparticles (FeC MNPs) magnetic properties are comparable to those of bulk iron and are of interest in such applications because iron has excellent magnetization and carbon distribution can be modulated for magnetic anisotropy tuning. However, FeC MNPs are water insoluble which had to be confronted before successful introduction into biosystems. To address the problem, specialized ligands were designed to promote hyrdophilicity and biocompatibility of FeC MNPs. Modification included functionalization with a tetraethylene glycol for its hydration shell, a long chain akyl group to maintain molecular stability, an amide bond to strengthen the molecule, and a catechol for FeC MNP ligation. A series of reaction mechanisms were executed to produce desirable ligands. Mass Spectrometry (MS), Dynamic Light Scattering (DLS), and Transmission Electron Microscopy (TEM) techniques were used in ligand and FeC MNP characterization. The synthesized ligands were found to successfully increase both hydrophilicity and biocompatibility of FeC MNPs.

EVALUATING A DROSOPHILA MODEL SYSTEM TO DETERMINE PROTEIN INTERACTIONS WITH WERNER EXONUCLEASE

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Everyday our DNA is subjected to damage, which if not repaired properly, can lead to mutations that cause aging and cancer. In humans, deficiencies in the DNA repair proteins, Werner (WRN) and Bloom (Blm), are associated with Werner syndrome and Bloom syndrome, which are diseases characterized by accelerated aging and high susceptibility to cancer, respectively. Previously, we've shown that flies mutant in Blm and the *Drosophila* homolog of WRN, WRNexo, have hatching defects and are sensitive to the fork-stalling drug hydroxyurea, suggesting that these proteins interact when responding to stress during DNA replication. Currently, we are investigating a possible physical interaction between WRNexo and Blm. We designed a transgenic WRNexo mutant in which WRNexo is fused to green florescent protein (GFP) and have confirmed by western blot that the WRNexo-GFP fusion protein is expressed. Next, we will determine if the WRNexo-GFP fusion protein is functional by testing hatching frequency and hydroxyurea sensitivity. We predict that the WRNexo-GFP fusion protein will be functional in these flies and they will not exhibit defects associated with WRNexo deletion mutants. We will then use antibodies specific to GFP in a co-immunoprecipitation assay to "pull down" the WRNexo-GFP fusion protein along with any other proteins that are attached to it. Finally, we will use mass spectrometry analysis of the protein complex to identify bound proteins. We predict that Blm will be bound to WRNexo. Demonstrating the physical interactions of these proteins will yield further insights into the molecular bases of aging and cancer predisposition.

THE INFLUENCE OF FLORAL-VISITOR ANATOMY ON POLLEN REMOVAL FROM THE COMMON MILKWEED *ASCLEPIAS SYRIACA*

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Flowering plants use vectors, such as wind or animals, to move pollen between plants. From a plant's perspective, it is important that the vector fits well with its flowers, so that its pollen movement and reproduction are efficient. In this study, we investigated the relationship between insect visitor anatomy and pollen removal from the flowers of *Asclepias syriaca* (Common Milkweed). In the summers of 2014 and 2015, we collected insects after they visited the flowers of *A. syriaca* plants, which were located on the campus of Northeastern Illinois University, and preserved the insects in a freezer for further analysis. In the lab we quantified the amount of pollen each visitor carried along with the size of various insect anatomical features, such as body length, intertegular length, and tibia diameter. We collected a total of 501 insects, 323 in 2014 and 178 in 2015. We collected fewer visitors in 2015 because fewer insects were flying, perhaps because the early summer months were both colder and wetter than average. Tibia diameter and body size were strong predictors of the quantity of pollen carried by a visitor. A visitor was more likely to carry pollen when its tibia diameter was similar in size to *Apis mellifera*'s (Western Honey Bee) tibia diameter, and a visitor had a bigger pollen load if it had a larger body size. Large pollen loads are known to negatively influence pollinator foraging, and the bigger visitors in our population may carry more pollen because they can physically compensate for the negative effects of pollen load on foraging. Studying *A. syriaca*'s pollination system helps to conserve it and organisms, such as the declining *Danaus plexippus* (Monarch Butterfly), which rely on it as a host.

HOW GENDER EFFECTS THE WAY STUDENTS LEARN COMPLEX CONCEPTS

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Research shows that genders differ in cognitive strengths that impact learning. Past research has relives that males conceptualize information spatially more than females and, show an advantage when it comes to learning math and science concepts. Previous research has also shown that students also perform better academically when their gender matches their teachers'. Is this gender effect being driven by compatible modes of thinking between same sex teachers and students or by social expectation in gender bias. To test what role gender congruence plays we held instruction constant across the sex of instructors. Using a pretest-instruction-posttest design, we tested whether gender of the teacher and the student influenced the learning of stereoisomers. For the pre- and posttest, 57 college students were asked to create structures of a 6 stereoisomer molecules. Instruction designed to activate spatial representations of stereoisomers included 3 types: (1) *Imagination* asks the participant to create a mental picture of the molecule, (2) *Gesture* asks the participant to create hand movements to create pictures of molecules and (3) *Modeling*, asks the participant to create a 3-D model of the molecule. Learning was a change from the pre- to posttest in accurate depictions of stereoisomers. Preliminary results reveal that males were unaffected by teacher gender and more likely to learn from the Model instruction. Females were more likely to learn with Gesture instruction and this was enhanced when the teacher was female. Implications for the role gender plays in instruction of complex spatial concepts is discussed.

THE IMPACT OF *ASCLEPIAS SYRACA* (COMMON MILKWEED) FLOWER PIGMENTATION ON FLORAL-VISITOR BEHAVIOR AND POLLINATION

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The large decline of *Asclepias syriaca* (Common milkweed) that has occurred over the last decade in the Midwest can be attributed to many environmental factors, including habitat fragmentation and loss of native pollinators. Therefore, investigating milkweed pollination is essential for understanding its reproductive success and developing conservation plans. Flower pigmentation is a floral trait known to influence various aspects of pollination, including which types of organisms visit flowers and visitor behavior. While previous studies indicate that flower pigmentation influences the amount of pollen removed and deposited in milkweed, no study has quantified how flower pigmentation influences the behavior of visitors and pollen transport. In this study, we investigated the influence of *A. syriaca* flower pigmentation on visitor behavior and pollen movement. To do this, we quantified the behavior of visitors to the flowers of *A. syriaca* plants located in the Swamp White Oak Savanna on the campus of Northeastern Illinois University in Chicago, IL. We then collected flowers from the visited plants to measure pigment (anthocyanin) concentration as well as pollen deposition and removal. After counting the number of pollinia removed and inserted per flower (total of 600 flowers), our results indicate that the number of visitors decreased as pigment concentration increased, and that there was a positive relationship between the number of visitors and the amount of pollen deposited and removed. The higher visitation rate and pollen movement for low pigment flowers may be due to their greater abundance in our population than high pigment flowers. These results are consistent with previous studies that found bumblebees have a distinct preference for flowers with lower pigment concentrations. Further data collection would allow for us to see if this distinct pollinator preference is due to pollinator constancy or perhaps another type of pollinator specialization.

DETERMINING THE ABILITY OF H5N1 INFLUENZA TO MEDIATE ENTRY IN THE ABSENCE OF A FUNCTIONAL HEMAGGLUTININ SIALIC ACID BINDING POCKET

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H5N1 Avian Influenza Virus, more commonly known as “bird flu”, is a highly pathogenic strain of influenza. Since 1997, there have been 650 individuals infected with bird flu with a mortality rate of over 60%. Though direct transmission to humans is possible, sustained human-to-human transmission has not been seen. However, a strengthened interaction between the viral protein, hemagglutinin (HA), and its host cell receptor, sialic acid (SA), may lead to sustained transmission. This strengthened viral-host cell interaction is predicted to spark a pandemic. It has been proposed that a pandemic could also be sparked by an increase in influenza’s use of an unknown co-receptor in humans. Previous studies have suggested the presence of a co-receptor in other strains of influenza, where infection is still possible without the utilization of SA as traditionally seen. To further explore the presence of an H5N1 co-receptor, this study aimed to disrupt the traditional viral attachment mechanism between HA and SA. To disrupt the interaction, site-directed mutagenesis was used to create alanine substitutions at Glycine135, Serine136, and Tyrosine98 in the sialic acid binding domain of HA. These amino acid residues were chosen due to their stability so as to minimize conformational changes. If the HA-SA interaction is blocked and viral entry is comparable to wild-type, this further suggests that influenza entry may be mediated by an additional co-receptor. Identification of a co-receptor could then be applied more broadly to other strains of influenza as well as in the development of novel therapeutic approaches in treating influenza.

MISSING LINKS: THE IMPORTANCE OF PARASITES IN FOOD WEBS

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Food webs are graphical depictions that allow us to see the interactions, connectivity, and relationships between the variety of species in a community. Parasites, however, have long been excluded from food webs, leading to depictions that are missing an integral part of the overall community structure. Species commonly used by parasites as hosts can be found in food webs, but the effects of infection and coinfection on species interactions are lost without their inclusion. Here, we explore the roles of singly infected and co-infected snails in their respective communities. We predict that taking varying levels of infection into account (no infection, single infection, and coinfection), will show varying number of links and levels of complexity in a food web. We conducted a biodiversity survey of urban and suburban wetlands to explore a range of different food webs. Four snail species were sampled at each site: *Gyraulus* sp., *Helisoma* sp., *Lymnaea* sp*., and Physa* sp. Standardized net sweeping was used to take an unbiased survey of the different species in the community. Snails were returned to the lab and examined to determine the parasite diversity and infection status. These were shed, held overnight to determine the presence of trematode cercariae. Following standard protocol, non-shedding snails were crushed to determine trematode infection. It is expected that food webs with coinfected hosts will show more complex community interactions. Our observations show the importance of parasite connectivity in food webs when investigating the effects of transmission dynamics and have implications for understanding biodiversity loss and disease emergence.

DIGITIZATION OF COLLECTION HELPS SCIENTISTS TRACK BIODIVERSITY CHANGES OF THE WORLD'S ECOSYSTEMS

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Herbaria play an important role for scientists studying plant distributions as they can contribute significantly to determining and tracking ecosystem biodiversity. While herbaria in many institutions around the world contain millions of specimens, access is a major problem. Actual physical records allow only a limited amount of accessibility to researchers worldwide. Digitizing collections is an important step towards increasing accessibility to both experts and the public. Recent digitization efforts in the Botanical Collections at The Field Museum include collaborations on a variety of projects with dozens of research institutions both nationally and globally. Having online accessible data from multiple institutions will allow researchers to visualize global changes in distribution patterns of plants and may even correlate them with environmental changes over time. A massive amount of work, however, is required in order for collections to become digitized such as: repackaging, barcoding, labeling, photographing, and uploading. To date, we have uploaded over 4 million specimens to various portals with many more still to go. The information is pooled into a larger collective web accessible database that will track species ranges over the last 150 years and allow researchers the ability to look at specific species' worldwide movements. Here we present our group's digitization efforts on three separate projects similarly aimed at studying the impact of climate change and cataloguing species diversity- the Algae Portal, the Bryophyte Portal, and the Microplants Project.

ABOUT THE STUDENT CENTER FOR SCIENCE ENGAGEMENT (SCSE)

The Student Center for Science Engagement (SCSE) is a resource to help students succeed at NEIU and in their future careers in the sciences. We serve all students interested in the sciences, and we support the following departments and programs: Biology, Chemistry, Physics, Earth Science, Environmental Science, Computer Science, Mathematics, and Psychology.

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Evening hours:
Tuesdays 5PM - 6PM (Physical Sciences) and Thursdays 5PM – 6PM (Life Sciences)

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