MONTANA ACADEMY OF SCIENCES

2019 ANNUAL MEETING

April 5-6, 2019
Student Union, Montana Tech
Butte, Montana

Chrissie Carpenter, President, Montana Academy of Sciences
James N. Barron, Executive Director, Montana Academy of Sciences

INTRODUCTION

The Montana Academy of Sciences (MAS) was incorporated on the 20th day of March, 1961, as a non-profit, educational organization. The objectives of the Montana Academy of Sciences are to encourage interest and participation in the sciences and to promote public understanding of science and its contribution to society. The Academy accomplishes its objectives by conducting meetings of those interested in sciences and the education of scientists, by publishing contributions to scientific knowledge, by supporting research, by making awards to recognize accomplishments in science, by administering gifts and contributions to accomplish these aims, by assigning and cooperating with affiliated and other organizations with similar objectives, and by engaging in such other activities as deemed necessary to accomplish its objectives.

We held our 2019 Annual Meeting at Montana Tech in Butte, MT. on April 5 and 6. Over 90 registrants participated, viewing 24 contributed oral presentations and 27 poster presentations over the day and a half meeting. We present the abstracts from our meeting here so that the readers of the Intermountain Journal of Sciences can see the quality and types of science supported by MAS. Please mark your calendars for our next meeting, Saturday, April 4, 2020 in Butte. Finally, the Board of Directors of MAS would like to thank the sponsors of our 2019 Annual Meeting:

Dr. John Cech, President, Carroll College, Helena
Dr. Beverly Hartline, Vice Chancellor for Research, Montana Technological University, Butte
The Department of Biological and Physical Sciences, Montana State University, Billings
College of Humanities and Sciences, University of Montana, Missoula
Dr. Matt Redinger, Provost, University of Providence, Great Falls

PRESENTATION ABSTRACTS

***Indicates Presenter**

COMPARING THE HABITAT CONNECTIVITY OF AMERICAN MARTEN AND FISHER IN THE NORTHERN ROCKY MOUNTAINS, USA

Rex Koenig*, Hellgate High School, Missoula, MT

The connectivity of a species is the ability of its individuals to move, and importantly, to move between populations. This project predicts and compares the connectivity of American marten (*Martes americana*), as well as fisher (*Pekania pennanti*) in western Montana and northern Idaho, to determine the presence of wildlife corridors that facilitate the connectivity of both. MaxEnt was used to construct a niche-model for American marten using marten location data coupled with environmental covariates (topography, precipitation, snow, temperature, vegetation). Based on the assumption that identified areas of use also serve to facilitate connectivity, this niche model was transformed into a resistance surface. Connectivity models were then derived from this. This same process was followed using a published niche-model for fisher. Assuming that both fisher and marten might travel between areas of the highest quality habitat, connectivity nodes were located randomly within areas of high quality habitat and Circuitscape was used to infer connectivity paths. To compare these connectivity maps they were then quantiled into ten grading on the value of connectivity, and added together for a total quantile value of twenty. Areas with the top two quantiles of connectivity were define as mutual connectivity. This study identified seven mutual wildlife corridors for these two species, and three areas of high mutual use. These findings may not only advise land management regarding how to better preserve the connectivities of American marten and fisher, but also the connectivities of other similar species.

FAILURE TO DETECT ANTI-VIRAL ACTIVITY BY PROKARYOTIC ARGONAUTE PROTEINS

Paul B.G. van Erp*, Microbiology and Immunology, Montana State University, Bozeman
Tanner Wiegand, Microbiology and Immunology, Montana State University, Bozeman
Royce A. Wilkinson, Microbiology and Immunology, Montana State University, Bozeman
Dominick Faith, Microbiology and Immunology, Montana State University, Bozeman
Blake Wiedenheft, Microbiology and Immunology, Montana State University, Bozeman

Argonaute (Ago) proteins are present in all three domains of life and are involved in nucleic acid guided silencing and interference pathways. The well-studied Eukaryotic Argonautes (eAgo) form the catalytic core of the RNA interference (RNAi) pathway that is involved in gene silencing, transposon silencing and antiviral defense. Limited research on Prokaryotic Argonautes (pAgo) suggests these proteins are involved in defense against foreign genetic elements such as plasmids. pAgos have been hypothesized to defend against bacteriophage, however no direct evidence has been found so far. Here, we report the failure to detect antiviral defense mediated by pAgos against various Escherichia coli bacteriophages. We overexpressed 8 phylogenetically diverse prokaryotic Argonaute proteins in Escherichia coli BL21 (DE3) and challenged them with 7 bacteriophages spanning the Myo-, Sipho-, and Podoviridae families. No antiviral activity was detected that could be attributed towards the pAgo proteins. However, up to 100,000-fold reduction in viral infectivity was observed for 2 phages that correlated with plasmid-based protein expression. The mechanism through which this antiviral activity is mediated is unknown and subject for future study.

LIGAND-CONTROLLED CHEMODIVERGENT SUZUKI CROSS COUPLING USING PALLADIUM-N-HETEROCYCLIC CARBENE CATALYSTS.

Emily Reeves*, Chemistry & Biochemistry, Montana State University, Bozeman.
Sharon Neufeldt, Chemistry & Biochemistry, Montana State University, Bozeman

The successful synthesis of complicated organic molecules such as pharmaceuticals, agrochemicals, and organic materials requires an extensive toolbox of synthetic strategies for constructing carbon-carbon bonds. Problems can arise, however, when a molecule contains multiple functional groups that are reactive toward the same transformations. For example, both aryl halides and aryl triflates can undergo palladium-catalyzed Suzuki cross-coupling in the presence of arylboronic acids. Control of selectivity between these two electrophilic sites using different Pd-phosphine catalysts has been described previously, but the scope of such methodology is severely limited. In this presentation, we describe the discovery of an orthogonal pair of Pd-N-heterocyclic carbene (Pd-NHC) catalysts for chemodivergent cross-coupling of aryl chlorides and aryl triflates with phenylboronic acids and demonstrate the synthetic utility of these catalysts with diverse boronic acids and substrates. The mild conditions used in these reactions allows for high functional group tolerance with respect to both substrates and boronic acids. We additionally present experimental and computational evidence that the origin of selectivity using Pd-NHC catalysts is dissimilar to the mechanism of selectivity control using Pd- phosphine catalysts.

IDENTIFICATION OF CELLULOLYTIC HOT SPRING ORGANISMS THROUGH BIOORTHOGONAL LABELING

Nicholas J. Reichart*, Chemistry and Biochemistry, Montana State University, Bozeman
Zackary Jay, Chemistry and Biochemistry, Montana State University, Bozeman
Viola Krukenberg, Chemistry and Biochemistry, Montana State University, Bozeman
Rachel Spietz, Chemistry and Biochemistry, Montana State University, Bozeman
Roland Hatzenpichler, Chemistry and Biochemistry, Montana State University, Bozeman

Bioprocessing of cellulose from plant waste into ethanol has been a focus of the renewable energy field for several decades. The recent developments of genome sequencing technologies have reinvigorated the topic. Identification of genes and the potential to degrade cellulose has been the major outcome thus far. High-throughput techniques to link taxonomy and in situ function of the organisms responsible for these processes have, however, been lacking. Bioorthogonal non-canonical amino acid tagging is a nondestructive method to fluorescently label active, protein-synthesizing cells that can later be separated from a community using fluorescent activated cell sorting (BONCAT-FACS). Biomass collected from a Yellowstone National Park hot spring was incubated with four cellulose substrates to identify organisms that were preferentially active in the presence, but not the absence of cellulose substrates. A short timeframe (2 weeks) bioorthogonal labeling incubation and a longer enrichment (6 weeks) incubation were compared for differences in community composition to highlight the competition of an incubation that is typically missed with enrichment schemes. Over 14 days of incubation the community began to shift to a simplified population comprised of Aquificae, Deinococcus-Thermus, or Chloroflexi. However, at early time points, the active community was comprised by a multitude of uncultured and cultured organisms including Fervidibacteria, Aigarchaeota, or Thermotogae which were eventually outcompeted by dominating organisms in the later time points. BONCAT-FACS outlines a novel approach of using single-cell bioorthogonal labeling to profile a microbial community’s activity regarding biotechnology industry interest.

ECOSYSTEM ENGINEERING BY NET-SPINNING CADDISFLIES IN ROCKY MOUNTAIN STREAMS

Benjamin B. Tumolo*, Ecology, Montana State University, Bozeman
Lindsey K. Albertson, Ecology, Montana State University, Bozeman
Molly McLaughlin, San Francisco state university, San Francisco, CA
Zachary Maguire, Ecology, Montana State University, Bozeman
Wyatt F. Cross, Ecology, Montana State University, Bozeman
Melinda D. Daniels, Stroud Water Research Center, Avondale
Leonard S. Sklar, Geography, Planning and Environment, Concordia, Montreal

Ecosystem engineering is a ubiquitous process by which organisms modify physical habitat characteristics and influence patterns of biological organization. Often, modification of physical environments by ecosystem engineers can facilitate other organisms by creating habitats for species that would otherwise be absent. Despite the potentially wide reaching consequences of facilitation through ecosystem engineering, many facets remain poorly understood in stream ecosystems. Here we present a synthesis of ecosystem engineering by hydropsychid caddisflies (***Hydropsychidae***) and describe how they affect stream macroinvertebrate communities. Hydropsychid caddisflies are a globally distributed group of net-spinning insects that live in stream gravel beds and have high abundances across western Montana. Hydropsychid caddisflies act as ecosystem engineers because their silk structures alter sediment transport conditions and local flow patterns of streambeds. Using lab experiments and field surveys, we show that ecosystem engineering by caddisflies changes physical templates of streambeds and influences other members of the macroinvertebrate community. We found that caddisfly nets increase the shear stress required to initiate gravel movement for gravels up to 70 mm. Additionally, we found that caddisfly silk structures substantially alter local flow at the streambed surface by reducing velocity by 70%. Furthermore, we have found that the presence of net-spinning caddisflies markedly increases local abundances and biomass of other stream macroinvertebrates across environmental gradients. Taken together, these findings indicate that caddisflies impart substantial physical changes to streambed habitats that have ecologically significant consequences for stream macroinvertebrate communities. Our findings indicate that caddisflies influence ecological processes from physical habitats to biological community structure and could act as important controls of Rocky Mountain stream ecosystems

---

ASSESSING THE EFFECTS OF COMPETITION AND SEASONALITY ON STRESS, IMMUNITY AND NUMBER OF SCARS IN DEERMICE

Andreas Eleftheriou *, Wildlife Biology Program, University of Montana, Missoula
Amy Kuenzi, Biology, Montana Tech of the University of Montana, Butte
Angela Luis, Ecosystem and Conservation Sciences, University of Montana, Missoula

Infectious wildlife diseases are becoming more common, causing population declines and species extinctions. Ecological and environmental stressors can influence disease spread in wildlife, through effects on parasite transmissibility (regulated by host immunity), and contact rates. Glucocorticoids (GCs) are hormones that mediate physiological and behavioral responses to stressors, and thus, can influence immunity and behavior in wildlife. Sin Nombre virus (SNV) is carried by deermice (*Peromyscus maniculatus*), and in western Montana grasslands, deermice compete with voles (*Microtus* spp.) and shrews (*Sorex* spp.). Because voles are dominant over deermice, they could increase SNV prevalence in deermice via stress-induced immunosuppression and/or alteration in contact rates, while shrews may have a lesser effect. Our objectives were to investigate whether voles and/or shrews could increase SNV prevalence in deermice through changes in stress, immunity and/or contact rates, and to examine seasonal changes in these same measures. We live-trapped small mammals over 2 years in western Montana grasslands. We evaluated deermice for scar numbers (proxy for contact rates), demography, and body condition scores (BCSs). Deermouse blood was evaluated for white blood cell counts/differentials, and SNV antibodies, and feces for fecal corticosterone metabolites (FCMs) to measure stress (baseline and stress-induced). Using mixed effect regression trees, we found that higher vole density was inconsistently associated with lower BCSs and scar numbers. Higher shrew density was consistently associated with lower stress-induced FCMs, but inconsistently with lower BCSs, and higher scar numbers. Neutrophil: lymphocyte (N:L) ratios were highest in spring/summer, and lowest in fall/winter. Due to low SNV prevalence, we could not evaluate effects on infection. Interspecific competition may influence disease spread via effects on chronic stress (i.e. lower stress-induced FCMs and BCSs), and scar numbers. Higher N:L ratios, suggestive of chronic stress, over spring/summer may provide an ideal time for SNV transmission. Our findings may extend to other diseases

---

Evaluating the Accuracy of Bloodstain Pattern Analysis Using Hemodynamic Properties

Paul Yount*, Forensic Science, University of Providence, Great Falls, MT
Chrissie Carpenter, Chemistry, University of Providence, Great Falls, MT
Mykal Gernaat, Forensic Science, University of Providence, Great Falls, MT
John Baluyut, Chemistry, University of Providence, Great Falls, MT
Jessica Martin, Biology, University of Providence, Great Falls, MT
Meredith Hecker, Mathematics, University of Providence, Great Falls, MT

This comparative survey explores the relationships between the discipline of bloodstain pattern analysis (BPA) and hemodynamic blood properties, such as viscosity and hematocrit. In BPA, forensic scientists study the phase change of blood when in contact with air, but little forensic literature connects blood biomechanics, such as hematocrit levels to BPA. Red blood cell count, or hematocrit, in females (37-48% of blood volume) is slightly lower than males (45-52% of blood volume) from menstrual red cell loss, etc. Strong evidence suggests that erythrocytes influence blood viscosity because of their high concentration (4-6 x 10^6 RBC/mm3 or 40-45% of blood volume in healthy individuals). When whole blood is altered by a disorder/disease or alcohol intake, hematocrit levels can be affected as well. With this knowledge, there is reason to believe that blood viscosity changes with individualistic hematocrit levels. Therefore, it is hypothesized that traditional BPA angle of impact tests can produce inaccurate results. Intravenous blood samples were drawn from 9 volunteers (all women, including 8 with blood disorders/alterations and 1 healthy control) at the University of Providence into collection tubes containing ethylenediaminetetraacetic acid as an anticoagulant. Each sample was tested for viscosity using a Canon-Fenske viscometer and for hematocrit levels using an LW Scientific ZipCombo centrifuge. Finally, each sample was used to make several blood stains at varying degrees of impact (10°, 30°, 60°, and 90°). A MANOVA was used to compare viscosity, hematocrit, and angle of impact variables against each other within the 8 participants. This survey connects hemodynamic properties to angle of impact tests in BPA by significantly showing how bloodstains can be inaccurately misinterpreted. By examining blood viscosity among several individuals, this research assesses the accuracy of BPA by comparing experimental and expected bloodstain angles and creating individualistic standards for future forensic methods.

Generation of a High Throughput Screening System for Small Molecules that can Rescue Axonopathy

Cody Walters*, Biological and Physical Sciences, Montana State University, Billings
David McGee, Biological and Physical Sciences, Montana State University, Billings
Lynn George, Biological and Physical Sciences, Montana State University, Billings
David Butler, Biological and Physical Sciences, Montana State University, Billings

Familial Dysautonomia (FD) is a neurological disease with both developmental and degenerative aspects including axonopathy of peripheral nerves. FD results from a point mutation in the ELP1 gene, causing reduced levels of the corresponding protein that functions in assembling a highly conserved, six-subunit complex known as Elongator. Elongator catalyzes the chemical modification of transfer RNAs needed for the translation of codon-biased transcripts that preferentially use AA- or AG-ending codons. Like FD, axonopathies are a common feature of many other neurological diseases including amyotrophic lateral sclerosis (ALS), and Alzheimer's. Despite their prevalence in neurodegenerative diseases, the discovery of therapeutics for treating axonopathies has been impeded by the difficult and costly nature of culturing primary neurons. Therefore, an experimental model that can withstand the manipulation required for a high throughput small molecule screen is essential for drug discovery. Candida albicans shows a pronounced polarized growth phenotype that is distinct among other yeasts. To determine whether this phenotype is dependent on Elongator, as is polarized growth in neurons, we made a C. *albicans* Elp1 knockout. Importantly, this knockout exhibits a severely compromised growth habit. Our long-term goal is to use this knockout to develop a high throughput screen for small molecules that can rescue normal polarized growth. Molecules that rescue in our yeast model system, will then be tested in vitro for the ability to rescue axon elongation in Elp1 deficient neurons.

A Logistic Regression Implementation of the "ABCD" Method for Identifying Malignant Melanoma

Havilah Neujahr*, Biology and Mathematics, University of Providence, Great Falls, MT
Stephen Muir, Mathematics, University of Providence, Great Falls, MT

This project investigated a way to more accurately assess the probability that a skin mole is malignant or benign using the ABCD classification system used in healthcare. To determine the probability that a mole was malignant or benign, numerical values were calculated for each classification. The numerical value for A (asymmetry) was calculated by drawing an estimated half-way point through the image and then filling in each half with simple geometric shapes whose areas could be easily calculated in Microsoft Word. Once the area of each half was found, the absolute value of the difference between the area of the two halves was the numerical value assigned to A. For B (border irregularity), the perimeter and area of each mole was put into the formula $B=(P)2/(4\pi T)$, where T stands for area. C (color) was estimated on a scale of 1-5, where 1 was light, uniform color distribution and 5 was uneven, splotchy, and dark color distribution. For D (diameter), the archive used (ISIC Archive) to obtain the images had the diameter included in the metadata of each image. In total, 45 training images were used, and 5 different test images were used to cross-validate the results obtained. Both a quadratic logistic regression model and linear logistic regression model were used to see how accurate both models were in predicting the probability that a mole was malignant or benign. The results produced showed that the quadratic model was more accurate than the linear; however, both models had a high rate of accurate predictions. The quadratic model accurately predicted 44 out of 45 of the training data sets and 5 out of 5 of the test data sets. The linear model accurately predicted 41 out of 45 of the training data sets and 4 out of 5 of the test data sets.

LIGAND K-EDGE STUDY OF M(PDTC)L COMPLEXES

Alexander Fryett*, Biological and Physical Science, Montana State University, Billings
Kyle Pickens, Biological and Physical Science, Montana State University, Billings
Siana Wiles, Biological and Physical Science, Montana State University, Billings
Dr. Matt Queen, Biological and Physical Science, Montana State University, Billings

Carbon tetrachloride is a known carcinogen that can cause cancer related illnesses when it is dechlorinated by Cytochrome P450, located in the human liver. Environmental reduction of carbon tetrachloride can produce lesser chlorinated intermediates, such as the trichloromethyl radical, which is harmful to living organisms. [Cu(PDTC)L]- has shown to be able to dechlorinate carbon tetrachloride so that it will produce CO2 and chloride, which are environmentally safe compared to lesser chlorinated intermediates. The mechanism between [Cu(PDTC)L]- and carbon tetrachloride is poorly understood. This study links the dechlorination reactivity of a series of [M(PDTC)L]- complexes (L = Cl-, CN-, and PPh3 and M = Cu and Ni) to the individual electronic structures of each complex by using sulfur k-edge. We find that reactivity of a given [Cu(PDTC)L]- species is linked to the lability of L in a given solvent rather than to the relative covalency of the M-S bond in each species.

ELECTRICAL PROPERTIES OF CARBON NANOFLUIDS

Isaac Gilfeather*, Mechanical Engineering, Montana Tech, Butte

Electrically conductive inks have wide applications in wearable electronics, sensors, and inkjet printed circuits. The goal of this project was to make quantitative measurements on the electrical properties of aqueous suspensions of carbon nanomaterials. To create the electrically conductive ink, Sodium Dodecyl Sulfate (SDS) was used to stabilize the MWNTs in solution. Coats of ink were applied to standard printer paper to measure the sheet resistance of the ink using a Signatone S-302 4-point probe. The resistivity of the ink was determined with an apparatus that I designed and built, it used a series of inter-locking vinyl tubes and solid copper rods as the electrodes. An Agilent 3458A 81/2 Digital Multimeter was used to capture a resistance measurement which was then used along with the dimensions of the vinyl tubes to calculate the resistivity of the ink. By measuring the resistivity of a 5 wt% sample of saltwater and then comparing it to the values found in a table, it was concluded that the apparatus was accurate within a reasonable margin of error.

CHICKEN TAIL VERTEBRAL FUSION SHEDS LIGHT ON A HUMAN BACKBONE DISEASE

Kevin Surya*, Honors College, Montana State University, Bozeman
Dana J. Rashid, Cell Biology and Neuroscience, Montana State University, Bozeman
Susan C. Chapman, Biological Sciences, Clemson University, Clemson, SC.

Ankylosing spondylitis (AS) is an inflammatory disease that causes vertebral fusion, affecting approximately 0.6% of the U.S. population. Genome-wide association studies have shown that over 90% of AS patients harbor the HLA-B27 allele, which is associated with the histocompatibility complex. Still, underlying cellular mechanisms of AS are little understood, and a trigger has not been identified. Since AS mechanisms are difficult to study in humans, we require a suitable animal model. The chicken naturally fuses four of its last tail vertebrae during post-hatching growth, forming a compound bone called the pygostyle.

As part of this fusion process, cartilaginous intervertebral discs remodel to become bone, and the nuclei pulposi at the centers of the discs completely degrade. How do chicken discs mineralize and does this phenomenon follow a similar path as human AS? We have observed several analogous features between chicken and AS vertebral fusion, including tissue bands bridging fusing vertebrae and fat deposits at the base of fusing vertebrae. Also, we observe an infiltration of neutrophil-like cells, suggesting that chicken vertebral fusion, like in AS, involves the immune system. Histology stains indicate that mineralization is present, but osteoid and osteoclasts are absent; fusion does not occur by endochondral ossification. We hypothesize this phenomenon represents the unusual transchondral ossification, where chondrocytes transform into osteoblasts. Currently, we're testing for cell death using TUNEL assays. Cell deaths would suggest that chondrocytes are dying not transforming. A possible trigger scenario involves transdifferentiation of disc chondrocytes into osteoblasts. Dying notochordal cells may cause the release of Complement 3 which facilitates transchondral ossification by recruiting neutrophil cells and promotes transdifferentiation of chondrocytes to osteoblasts. Finally, this study provides insights into AS mechanisms and elevates the chicken as an animal model.

Design, Build and Testing of Resonant Air Compressor

Grace Ostermiller*, Mechanical Engineering, Montana Tech, Butte
Emily Maynard , Mechanical Engineering, Montana Tech, Butte
Dr. Peter Lucon, Mechanical Engineering, Montana tech, Butte

Mechanical resonance of a system is achieved when the oscillation amplitude of a system is maximized and the resultant velocity and input force are in phase. In theory, a vacuum pump running at resonance should be more efficient when compared to an off-the-shelf air compressor. The focus of this project was to build a resonant compressor, obtain efficiency values from that compressor, and compare those values to that of an off-the-shelf compressor. An off-the-shelf air compressor was tested by pulling a vacuum of a bell jar while collecting data for every 100 mmHg of vacuum that was pulled to the vacuum pressure of 400 mmHg. The values collected were the current, voltage, power, and time it took to reach each vacuum value. In building the resonant air compressor various pieces were printed using 3D printing technology, machining various parts out of steel, and purchasing steel springs. In the design of the new compressor, the piston and valving from the off-the-shelf compressor were used. A copper wire was coiled around a 3D printed bobbin and the compressor was assembled. Alternating current was sent through the copper wire and the current, voltage, and power values were all collected during the same vacuum test as previously defined. These values were then compared to the values collected from the off-the-shelf air compressor.

Zic Transcription Factors that Influence Convergent Extension

Jocelyn Waggoner*, Cell Biology and Neuroscience, Montana State Univeristy, Bozeman

My research is focused on a specific time frame during embryonic development called gastrulation, in which intricate cell movements give rise to the ectoderm, mesoderm and endoderm layers of the embryo. The mesoderm layer undergoes movements called convergent extension, which allow cells to intercalate and move inside the embryo. The Zic family of zinc-finger proteins have a crucial role in gastrulation and neurulation. Based on findings from our lab (K. See and Merzdorf, in preparation) and others (Cast et al., 2012), I hypothesize that zic genes are required for convergent extension during gastrulation. Since there are 5 different, but very similar, zic genes, I will test each of these genes for a role in convergent extension during gastrulation. A knockdown method for each of the 5 zic genes in embryos of the model organism Xenopus laevis will be combined with a method called Keller Explants to allow analysis of convergent extension. In my experiments, I have ruled out zic 2 as a regulator of convergent extension. My current hypothesis is that zic3 is the most likely candidate because of its known roles in neural tube formation and other reasons I will explain below. I am also analyzing zic1,4 and 5 for convergent extension regulation

---

IS TIME RESOLVED INFRARED RADIOMETRY AN ALTERNATIVE OF POSITRON ANNIHILATION LIFETIME SPECTROSCOPY FOR DEFECT DETECTION IN METALS: AN EXPERIMENTAL APPROACH AND A MODEL DEVELOPMENT

Md Salah Uddin*, Material Science & Engineering Program, Montana Technological Univ., Butte
Brahmananda Pramanik, Mechanical Engineering, Montana Technological University, Butte

Time resolved infrared radiometry (TRIR) and positron annihilation lifetime spectroscopy (PALS) are both defect detection methods used in different materials for more than 40 years. Interestingly, both of the methods are similar in many ways, such as non-invasive testing procedures and follow a decay scheme. Both of the methods are successfully applied to metals, polymers, and composites materials. However, the methods are different in application mechanism and principle. TRIR is a thermography technique that measures temperature decay with time of the investigated material whereas PALS uses positronium decay with time of the tested material. In PALS, two-state trapping model is mostly used. Two state trapping model is a positronium trapping model used to describe positron diffusion inside the material. According to the trapping model, high energy positron beam is emitted from radioactive nuclei, diffused into the material, and trapped in a defect caused emissions of comparatively lower energy γ (gamma) rays. We develop a model to describe the similarity between time resolved infrared radiometry and positron annihilation lifetime spectroscopy. In the model, we describe the heat transfer and diffusion mechanism in the investigated material in time resolved infrared radiometry. The model also describes an experimental development for time resolved infrared radiometry research.

STUDENT ENGAGEMENT WHILE ESTABLISHING CLASSROOM MATHEMATICAL PRACTICES

Emmanuel Barton Odro*, Mathematics, Montana State University, Bozeman
Derek Andrew Williams, Mathematics, Montana State University, Bozeman

There is a significant connection between student engagement and performance achievement. Klem and Connell write, "student engagement has been found to be one of the most robust predictors of student achievement and behavior in school, a conclusion which holds regardless of whether students come from families that are relatively advantaged or disadvantaged economically or socially" (2004, p. 5). However, student engagement is complex, and currently relationships to outcomes such as mathematical understanding and learning are elusive (Fredricks, Blumenfeld, & Paris, 2004; Middleton, Jansen, & Goldin, 2017). This study investigated student engagement while learning through use of an app that collected student engagement reported by participants during a classroom teaching experiment. This paper discusses preliminary results on students' engagement in the process of learning. Though not anticipated, we observed differences between male and female students' engagement while working in mixed-pairs worthy of investigation. In particular, we observed differences between male and female students' engagement while working in

mixed-pairs surrounding important mathematical contributions from female partners. Female students described situations in which they perceived of male partners overlooking valuable contributions towards completing tasks, resulting in dips in engagement. With, regards to data collection, the app and survey effectively gathered information on student engagement, which was triangulated by students' descriptions in recall interviews.

CREATING A RECIPROCATIONG AIR COMPRESSOR USING A SINGLE DEGREE OF FREEDOM SPRING MASS DAMPER RESONANT SYSTEM

Emily Maynard*, Mechanical Engineering, Montana Technological University, Butte

Theoretically, a reciprocating air compressor should work with a single degree of freedom spring mass damper resonant (1D-SMD) design. The following steps were used to demonstrate how the system could be applied to an air compressor. Once a mathematical model was created, the calculated results determined the parameters for the solid model using SolidWorks. The model included a design that was based around an off-the-shelf air compressor. These parts were either 3d printed, ordered or machined and assembled. Finally, the system was tested as an air compressor. Several design iterations were performed to improve the system. The application of this project resulted in a newly built air compressor, which suggests this is an efficient way to compress air.

DEVELOPMENT OF A UAS-BASED ELECTROMAGNETIC INDUCTION SENSOR FOR SUBSURFACE CONDUCTIVITY MAPPING

Andrew Wilson*, Geophysical Engineering, Montana Technological University, Butte
Xiaobing Zhou, Geophysical Engineering, Montana Technological University, Butte

The Electromagnetic Induction (EMI) method is a popular and favorable geophysical technique for shallow subsurface exploration because of its high-quality, rapid data acquisition of subsurface conductivity or resistivity. However, EMI based instruments are generally ground-based. Our research aimed to investigate the practical application of an airborne EMI sensor that does not require direct contact with the ground. The objective for our project was to measure the inductive response of a conductive subsurface, and locate anomalously high subsurface zone in conductivity. To address our objective, we designed and constructed a lightweight EMI sensor for an unmanned aircraft system (UAS) based on the principles of EM induction and EM sounding. We successfully tested the instrument by measuring the secondary field response from a metal-cased Unexploded Ordinances (UXO) during its high conductivity. The innovative design and construction of our EMI sensor is original and has shown to be a practical approach for use with an UAS. The EMI sensor consists of a signal wave generator, a power amplifier, concentric transmitter and a receiver coils, and a microcontroller-based data collection and storage system. The microcontroller code for the data collection and storage system was developed in the open-source Arduino Software, Integrated Development Environment (IDE). EMI sensors operate using a transmitter coil to generate a primary magnetic field that penetrates into the subsurface and induces eddy currents in conductive subsurface Earth materials. A secondary magnetic field generated by the eddy current induced in the conductive Earth material will pass through the receiver coil, and generating an electromotive force (emf). By measuring the emf induced in the receiver, we can approximate the conductivity of Earth material.

Sin Nombre Virus Prevalence in Deer Mice Captured in Ranch Buildings in Southeastern Montana

Kelsey Schmidt*, Biological Sciences, Montana Tech, Butte

Sin Nombre Virus (SNV) is a type of Hantavirus that is carried by deer mice (*Peromyscus maniculatus*). When SNV is transmitted to humans it causes a serious, sometimes fatal, illness known as Hantavirus Pulmonary Syndrome (HPS). Most HPS cases are linked to SNV exposure in peridomestic environments, particularly human dwellings and out-buildings such as garages, sheds, or barns. While many studies have examined SNV prevalence and transmission in natural environments, little work has been done in peridomestic environments. The objectives of my study were to determine the prevalence of SNV in deer mice found in the outbuildings of my family's ranch south of Hardin, MT. I used Sherman live traps to capture mice in around ranch buildings for 3 nights each month beginning in August 2018 and continuing until February 2019. Captured mice were ear tagged with sequentially numbered metal fingerling tags and a blood samples were collected. Blood samples were tested for antibodies reactive with SNV recombinant nucleocapsid protein by an enzyme-linked immunosorbent assay (ELISA). During the course of my study I collected 31 blood samples from 25 different mice captured in ranch buildings. The majority of mice I captured were females (64%) and capture were highest in December. None of the mice I captured tested positive for SNV antibodies.

Science Education Exploration

Terachelle Gregory*, Biology Department, Montana Tech, Butte
Arlene Alvarado, Institute for Educational Opportunities, Montana Tech, Butte
Abby Peltomaa, Institute for Educational Opportunities/Biology, Montana Tech, Butte

What inspires college-bound people to enter science-related majors? This question is critical to understanding the complex issue of getting more people to go into STEM fields in order for the USA to remain competitive and to advance our economy and society. The objectives of this study was to: explore what variables have influenced undergraduate student's decision to select a science-related major at Montana Tech; gain an understanding of students' attitudes toward K-12 education; examine the influences from K-12 teachers; and explore the level of external support to choose a science major. I hypothesized that studying these influences, along with prior research, would lead to a greater understanding of students who selected a science major as well as reveal ideas of how to support and recruit a diverse group of students for these majors. My research indicates that over half of our responders felt that their K-12 education prepared them for college and that their favorite subject influenced their chosen major. A new understanding could lead to improved techniques in science education in the Montana school systems, including high school and elementary, to engage and interest the students.

Metagenomic VS 16S DNA Sequencing for Identifying Bacterial Populations

Luke Stout*, Software Engineering, Montana Tech, Butte
Marisa Pedulla, PhD, Biological Science, Montana Tech, Butte

Next Generation Sequencing (NGS) technology has launched immense growth of DNA sequence databases, paving the way to better categorize the genetic diversity of the biosphere. Bioinformaticians curate and analyze this massive amount of DNA sequence data for applications that range from science and medicine to forensics and commercial ancestry services. The DNA sequences provided by NGS can be analyzed to profile bacterial communities within environmental niches. Experimental approaches for assessing these communities vary widely between labs. Our goal was to compare two common methods to test for cohesion between these approaches' results. We obtained DNA sequences from both metagenomic ("shotgun") and bacterial 16S gene sequencing for five DNA samples (two soil and three human microbiome). We developed a custom software pipeline in conjunction with the program BLAST, processed hundreds of thousands of DNA sequence reads produced by each sequencing method (metagenomic or 16S) and, for each sample, compared the two resulting bacterial profiles. For all five samples, community taxonomic profiles produced from the two methods were distinctly different. Explanations for these disparities may include sampling bias in databases or the reliability of the 16S gene as a species identifier. These results highlight the importance of establishing a common methodology to accurately infer bacterial communities from DNA sequence data.

COMPARISON OF WORDS AND PHRASES USED FOR CATEGORIES IN RISK ASSESSMENT MATRICES

Haley Hansen*, Occupational Safety & Health, Montana Tech, Butte

Occupational safety has moved from a rule-based practice to a progression making use of risk assessments. A core assessment tool in risk assessment is a risk matrix consisting of two or three categories for assessing a hazard. This project addressed the words and used to define the categories of severity, likelihood and exposure frequency. We identified from literature 16 words for each category and created a 16-page paper survey to obtain numerical ratings of all of the words. After obtaining Institutional Review Board approval, we surveyed senior engineering design courses and an OSH senior course. These courses were selected because the students are likely to be involved in risk assessments during their career. Respondents rated each word on a 100-point rating scale. An initial quality check was performed to identify respondents who made reasonable efforts and understanding to provide a genuine rating. Data from the selected booklets were used to determine the mean and standard deviation of each word. The last phase of the analysis involved Montana Tech Occupational Safety and Health faculty with professional credentials to identify recommended word sets. We had 82 qualified survey results. The faulty meeting resulted in recommended sets of ordered words of 3, 4, 5 and 6 word-sets for severity, likelihood and exposure. For example, an exposure category we recommend a 4-word categorization of very frequent, frequent, infrequent and very infrequent with mean values of 85, 72, 23, and 15, respectively.

POSTER ABSTRACTS

A REVIEW ON PROPHYLAXIS TREATMENTS FOR CHRONIC LYMPHOCYTIC LEUKEMIA INFECTIONS

Diana Gonzalez Vazquez*, Biology and Chemistry, University of Providence, Great Falls, MT

Chronic Lymphocytic Leukemia (CLL) is a type of cancer of the blood and bone marrow that degrades the immune system of a person. This is due to the uncontrolled white blood cell (lymphocyte) growth. The disruption of lymphocyte growth affects the response to pathogens, leading to a disruption in the immune system. Patients with CLL are prone to infections due to their immunodeficiency. As of 2019, there have been 20, 720 new cases of CLL in the United States and approximately 3,930 deaths. Recent studies have analyzed infection prevention

methods to increase survival rates for people with CLL. Intravenous Immunoglobulin Prophylaxis (IVIG) has been demonstrated to elevate levels of immunoglobulins, which are as the first line of defense against pathogens. The IVIG entails extracting antibody proteins from the plasma of a healthy donor and injecting those antibodies into a CLL patient. Another treatment for this infection is the antimicrobial drug Fludarabine Prophylaxis (FAMP). FAMP reduces the growth of lymphocytes in the blood system which allows for the immune system to produce regular amounts of immunoglobulins necessary to prevent infections. This review compares the biochemistry of IVIG and FAMP as treatments for infections in patients with CLL and indicates that IVIG is a more effective treatment than FAMP.

A SMALL RNA THAT REGULATES PYRIMIDINE AND METHIONINE METABOLISM IS NECESSARY FOR ESTABLISHING COXIELLA BURNETII'S INTRACELLULAR NICHE DURING EARLY STAGES OF INFECTION

Shaun Wachter*, Department of Biological Sciences, University of Montana, Missoula
Matteo Bonazzi, CNRS, Université de Montpellier, France
Kyle Shifflett, Department of Biological Sciences, University of Montana, Missoula
Abraham S. Moses, Department of Biology and Center for Life in Extreme Environments, Portland State University, Portland
Rahul Raghavan, Department of Biology and Center for Life in Extreme Environments, Portland State University, Portland
Michael F. Minnick, Department of Biological Sciences, University of Montana, Missoula

Coxiella burnetii is an obligate intracellular gammaproteobacterium and zoonotic agent of Q fever in humans. We previously identified 15 small RNAs (sRNAs) in C. burnetii with differential expression in the large and small cell developmental forms grown axenically and in infected host cells. Here, we describe the function of one of these sRNAs, termed Coxiella burnetii small RNA 12 (CbsR12). CbsR12 is highly expressed in both large- and small-cell variants in vitro, and is the dominant non-tRNA/rRNA/tmRNA transcript in both morphotypes during mammalian tissue culture infection. Through a combination of in vitro and in vivo assays, we have identified several targets of CbsR12. Of these, we have confirmed that CbsR12 binds to and upregulates translation of carA transcripts coding for carbamoyl phosphate synthetase A; an enzyme that catalyzes the first step of pyrimidine biosynthesis. In addition, Cbsr12 binds and downregulates translation of metK transcripts coding for S-adenosyl methionine (SAM) synthase, an essential component of the methionine cycle. Furthermore, we have established that CbsR12 is necessary for full expansion of Coxiella-containing vacuoles (CCVs) and is linked to growth rate in a dose-dependent manner in the early phase of infection of Vero and THP-1 cell lines. This is the first characterization of a trans-acting sRNA of C. burnetii and the first description of a bacterial sRNA that regulates carA and metK expression. This study also illustrates the utility of transposon insertion mutants in elucidating Coxiella's sRNAs and the importance of sRNA regulation in establishment of the intracellular CCV niche.

BARTONELLA BACILLIFORMIS HFQ REGULATES SMALL RNAS

Kyle Shifflett*, Division of Biological Sciences, The University of Montana, Missoula
Linda D. Hicks, Division of Biological Sciences, The University of Montana, Missoula
Shaun Wachter, Division of Biological Sciences, The University of Montana, Missoula
Michael F. Minnick, Department of Biological Sciences, University of Montana, Missoula

Bartonella bacilliformis is a facultative bacterial intracellular pathogen of the human circulatory system, causing Carrion's disease. B. bacilliformis is transmitted between human

hosts by a sand-fly vector, two markedly distinct backgrounds. As such, it presumably requires a high degree of regulation at the genomic level. Hfq, a common RNA-binding protein of bacteria, is present in B. bacilliforms, and likely plays a key role in post-transcriptional regulation. Hfq is involved in regulating many processes by choreographing small RNA (sRNA) binding to mRNA targets for transcriptional regulation via specific base pairing interactions. To better understand the role of Hfq in B. bacilliformis, the hfq gene was cloned into an expression plasmid to generate a His-tagged Hfq fusion protein. The plasmid was then used to transform E. coli, which was then induced with IPTG, to produce high quantities of the Hfq protein. The cells were lysed and the Hfq protein was purified by affinity chromatography using a NiNTA column with His tag specificity. Recombinant Hfq was used to generate rabbit polyclonal anti-Hfq antibodies, and specificity was verified by western blots. The anti-Hfq antibody will be utilized to co-immunoprecipitate Hfq and its sRNA / mRNA targets from B. bacilliformis lysates. The resulting RNAs will then be used to construct a cDNA library, which in turn will be deep sequenced to generate a list of RNAs that interact with Hfq. Results will directly inform us of the genes that are regulated by Hfq in this potentially life-threatening pathogen.

BIOINFORMATIC ANALYSIS OF THE FLATHEAD LAKE MONSTER BACTERIOPHAGE

Jake Plagenz*, Biochemistry, Carroll College, Helena, MT
Dr. Dan Gretch, Biochemistry, Carroll College, Helena, MT

The Flathead Lake Monster (FLM) bacteriophage was noted to have an abnormally-long tail upon its discovery. Once its genome was sequenced, this research sought out to identify the 117 FLM gene products using the BLASTp sequence alignment algorithm. This resulted in the discovery of five genes that are considered to be novel to the FLM. A specific gene within the FLM genome called the tape measure gene (TMG) was further analyzed once it was identified based on homology with other phages. Previous literature has suggested that a longer TMG can manifest itself as a longer bacteriophage tail length. This observation led to the hypothesis that a long tail length should yield a correspondingly-long TMG within the FLM. The bioinformatic investigation involved comparing the FLM tail length and FLM tape measure gene length to other phages. The results found that the FLM does not have an abnormally long TMG when compared to how long its tail is, indicating that the FLM is an anomaly when compared to other phages. Future examination of phage mosaicism may yield more information as to why the FLM tail length is abnormally long.

CANCER RISK DUE TO CUMULATION DIAGNOSTIC RADIATION

Abi Oliver*, Biology, University of Providence, Great Falls, MT

The computed tomography (CT) scan is the best imaging tool in emergency situations. The use of CT scanning has increased drastically in the last few decades due to its helical capability. Advantages of helical CT scans include dramatically shorter examination times, improvement in vascular visibility, and enhancement of the outline of parenchymal organs. Helical scans also permit retrospective reconstruction of three-dimensional structures. Cancer risk related to ionizing radiation from CT scans increases as the cumulative radiation dose increases. While a typical CT scan delivers 10 millisieverts (mSv) of ionizing radiation, a single dose of 100 mSv can lead to solid organ cancer or leukemia. Because children have a higher cell turnover rate, they are more susceptible to developing radiation-induced cancers. We found that brain CT scans have similar carcinogenic potential in men and women, whereas, abdominopelvic CT scans are more likely to induce cancers in women. Body mass

index (BMI) also influences radiation-induced cancer risk, because a higher dose of radiation is needed to penetrate a more massive body.

COORDINATED REGULATION OF STEM CELL PROLIFERATION AND DIFFERENTIATION BY RNA-BINDING PROTEINS COOPERATING WITH CCR4-NOT DEADENYLASE COMPLEX IN *C. ELEGANS*

Xiaobo Wang*, DBS, University of Montana, Missoula
Mary Ellenbecker, DBS, University of Montana, Missoula
Ben Hickey, DBS, University of Montana, Missoula
Nicholas Day, DBS, University of Montana, Missoula
Ella Baumgarten, DBS, University of Montana, Missoula
Ekaterina Voronina, DBS, University of Montana, Missoula

Uncovering molecular mechanisms regulating the balance of stem cell proliferation and differentiation can help us understand the causative factors for ageing, cancer and various degenerative disorders. Pumilio and FBF (PUF) family RNA-binding proteins are highly conserved regulators of stem cell development. We are investigating how PUF proteins regulate proliferation and differentiation of stem cells using C. elegans as a model organism. FBF-1 and FBF-2, two PUF family proteins in C. elegans, are required for maintaining germline stem cells by translational repression of their target mRNAs (Crittenden et al., 2002). FBF-1 and FBF-2 are very similar in primary sequence and share target mRNAs (Prasad et al., 2016, Kershner et al., 2010 and Porter et al., 2018), but we found that they have differential effects on target mRNAs and maintained stem cell numbers. Our findings suggest that FBF-1 may destabilize target mRNAs while FBF-2 may protect targets from degradation; FBF-1 may slow stem cell proliferation and differentiation whereas FBF-2 may promote stem cell proliferation and differentiation in coordinate fashion. Additionally, we found that FBF-1 activity in stem cells requires CCR4-NOT deadenylase machinery that shortens poly (A) tail of mRNA leading to mRNA instability. By contrast, FBF-2 activity in stem cells shows less dependence on CCR4-NOT, which is related to FBF-2 interaction with its specific cofactor, DLC-1. We propose that FBF-1, but not FBF-2, interacts with CCR4-NOT complex in stem cells. We are going to test this hypothesis by performing proximity ligation assay. In conclusion, our study uncovered mechanisms of PUF proteins controlling stem cell proliferation and differentiation through differential cooperation with CCR4-NOT deadenylase machinery.

DETECTION OF TETRACAPSULOIDES BRYOSALMONAE IN THE BEAVERHEAD RIVER USING ENVIRONMENTAL DNA ANALYSIS

Colter A. Feuerstein*, Department of Biology, The University of Montana Western, Dillon
Michael A. Gilbert, Department of Biology, The University of Montana Western, Dillon

Tetracapsuloides bryosalmonae is a Myxozoan parasite that causes proliferative kidney disease (PKD) in Salmonid fish. An outbreak of PKD in the Yellowstone River in 2016 resulted in a significant kill of mountain whitefish (*Prosopium williamsoni*); however, the exact reason for this outbreak remains unclear. Researchers first suspected a recent introduction of the parasite, but the analysis of samples collected from the Yellowstone prior to 2016 revealed that the parasite was present before to this event. This led to the hypothesis that environmental conditions may have exacerbated the effects of infection leading to increased mortality. To obtain more insight into the effects of environmental conditions it would be helpful to compare the spatial and temporal distribution of T. bryosalmonae in the

Yellowstone to other rivers where the parasite is known to occur. This comparison should include other freestone rivers with environmental conditions similar to the Yellowstone, as well as tailwaters with different parameters. We thought the Big Hole and Beaverhead rivers might be suitable for this purpose. The parasite was detected in the Big Hole in 2016, but there is no documented occurrence of the parasite in the Beaverhead. Therefore, we collected eDNA samples from five locations on the Beaverhead river in May, August and September and tested them by PCR using primers specific for T. bryosalmonae 18S rDNA. We detected parasite DNA at one of the five locations in two of the three samples collected from that location. To our knowledge, this is the first report of T. bryosalmonae in the Beaverhead River and it indicates that the Beaverhead may be suitable for a long-term study examining the spatial and temporal distribution of T. bryosalmonae. In addition, the positive samples will provide another source of parasite DNA from Montana that can be used in comparative genetic studies.

Does Aquaporin 3B Affect the Number and Characteristics of Calcium Waves in the Neural Plate of African Clawed Frog Embryos?

Dean Ricker*, Chemical Engineering, Montana State University, Bozeman
Christa Merzdorf, CBN, Montana State University, Bozeman
Jen Forecki, CBN, Montana State University, Bozeman

Early in the development of the nervous system, vertebrate embryos undergo neural tube closure. During this process, the cells in the dorsal part of an embryo, the neural plate, constrict on their outward facing side (apical constriction) to form a tube. The Merzdorf lab has found that expression of the Aquaporin 3b (Aqp3b) protein in African clawed frog (*Xenopus laevis*) embryos is critical for neural tube closure, specifically for apical constriction of the cells of the neural plate. While aqp3b is only expressed in a well-defined line along the outer edge of each side of the neural plate, it affects a pan-neural plate process. Thus, the question my study attempts to answer is how Aqp3b signals to the rest of the neural plate. A likely candidate for the signal is calcium, a common intercellular and cellular signal. I hypothesize that the neural plate in embryos with inhibited Aqp3b expression will have fewer calcium waves and/or calcium waves with different characteristics. To test this hypothesis, the number and characteristics of calcium activity will be compared between control embryos and embryos that have been inhibited from expressing Aqp3b. This is accomplished by injecting a morpholino oligonucleotide, which inhibits Aqp3b expression, and GCaMP6, which is fluorescent in the presence of calcium, into frog embryos at the four-cell stage. I then collect time lapses of calcium activity that occurs during neural tube closure and analyze them for differences in the length, period, intensity, etc. of calcium signaling events using a variety of software. As my project continues, I will continue to collect data and begin to draw a conclusion on it.

Effectiveness of Teeth Cleaning Treats on Dogs Oral Hygiene

Katherine Chandler, Biology, University of Providence, Great Falls, MT

Domestic dogs can transfer bacteria from their mouth to the mouth of a human, the most common being bacteria that cause gingivitis and periodontitis. Even though most humans will not receive any medical consequences from this bacteria, problems may arise if that human has a reduced immune system. The purpose of this experiment was to determine the effectiveness of oral hygiene treats in reducing bacterial growth in domestic dog mouths (*Canis lupus familiaris*). The saliva samples were taken from dogs at Associated Veterinary Services (AVS), the University of Providence (UP), and the Great Falls Animal Shelter (GFAS), located in Great Falls, Montana. Information such as age, breed, weight, health, food consumption, and oral care for each dog was recorded. There were 30 dogs sampled. A cheek swab was taken from each dog immediately before the canine received an oral hygiene treat and 5 minutes after treat administration. Canine saliva samples were placed on agar plates. Before the samples were placed on the agar plates, each agar plate was divided in half and labeled “before treat” and “after treat”. The samples were then incubated for 7 days in a CO2 incubator set at 37 ºC. After 3, 5, and 7 days, the plates were examined. The preliminary results cannot identify what kinds of bacteria were growing. On day 7, before the treat was given, xÌ = 9.8% growth (SD = 15.705). After the treat was given, xÌ = 10.023% growth (SD = 17.284). The results suggest that there is no difference in the amount of growth between the Before and the After (F = 0.250, P = 0.619, df = 1, 53). The results indicate the oral hygiene treats were ineffective in the short amount of time the treats were given, but further studies are necessary.

Effects of Familiarity on Mate Selection in Guppies

Sarah Gallup*, Biological Sciences, Montana State University, Billings
Lea Henderson, Biological Sciences, Montana State University, Billings
Carl Castles, Biological Sciences, Montana State University, Billings

Guppies (*Poecilia reticulata*) are freshwater fish commonly used in behavioral research. Originating from South America, this species can be purchased locally in the United States. We investigated the effect of familiarity on female mate selection. Our research consisted of individual female guppies each paired with two male guppies, from separate schools of fish, which were bred at MSUB. Preceding each experiment, one female was familiarized with one male in a divided fish tank. Uniform experiments were then conducted by placing a female guppy in a sectioned fish tank with the familiar male and a second unfamiliar male. Both males were placed on either side of the female. Following each trial, the individual female would be familiarized with the male that was not familiarized in the previous trial. Results were concluded by calculating time intervals that a female guppy spent near either male guppy or in the middle of the experimental fish tank. To record live behavior, with least amount of stress, a video recorder was used to record the guppies. To show effects of familiarization on female guppy choosiness, familiarizations were alternated monthly between a selected pair of males and one female. In these data there is a trial that suggests female mate preference may be influenced by familiarity.

Enhanced Reductive Defluorination of 6:2 Fluorotelomer Alcohol using Bio-Electrochemical Systems

Ashton Cummings*, Environmental Engineering, Montana Tech, Butte
Raul Tenorio, Civil and Environmental Engineering, Colorado School of Mines, Golden
Daqian Jiang, Environmental Engineering, Montana Tech, Butte

Current research on the biological degradation of poly- and perfluorinated alkyl substances (PFASs) is still challenged by two limitations:

1) Poor feasibility: successful biodegradation is limited to a small number of perfluoroalkyl acid precursors such as fluorotelomer alcohols (FTOHs);
2) Lack of means to precisely study the mechanism: conventional biological methods can

only create an anaerobic (vs. aerobic) environment, which cannot pinpoint whether the mechanism is oxidative or reductive.

This study uses Bio-Electrochemical Systems (BES) to precisely accomplish and enhance reductive PFAS degradation. BES is a platform technology where bacteria directly exchange electrons with solid electrodes to catalyze biochemical reactions. It has great potential for studying and enhancing PFAS degradation because it can:

1) Enhance bio-reactions by utilizing electric power;

2) Precisely separate oxidation and reduction reactions given the fuel-cell-like setup.

This study monitored the reductive defluorination of 6:2 fluorotelomer alcohol (6:2 FTOH) for over two months in BES. The results indicated that BES significantly increased (p-value<0.05) the rate of F- release under -0.55V poised potentials (vs. AgCl), and decreased the accumulation of 6:2 fluorotelomer carboxylic acid (6:2 FTCA), an intermediate degradation product. This study was the first time that reductive PFAS bio-degradation was precisely achieved, and the first report of successful BES-driven PFAS degradation. The findings provided the proof of concept needed to further explore whether enhanced defluorination can be accomplished with BES on more recalcitrant PFAS classes (e.g., perfluoroalkyl acids), and develop a new remediation technology.

Examining the Relationship Between Injury and Dominance in the Alpha Female Wolves of Yellowstone National Park

Claire E.B. Lacey*, Fish and Wildlife Ecology and Management, Montana State University, Bozeman
Doug W. Smith, Yellowstone National Park Wolf Restoration Project, National Park Service, Mammoth
Rick McIntyre, Yellowstone National Park Wolf Restoration Project, National Park Service, Silver Gate

The social dynamics of wolf packs have been heavily studied, and nowhere as extensively as in Yellowstone National Park (YNP) since the reintroduction of gray wolves in 1995. The objective of this study is to gather data on the impact of injury of alpha female wolves in Yellowstone, specifically the effect of injury on their dominant status. Injury is a serious threat to wild wolves in the park, who may sustain several injuries during their average lifespan of 5 years. Female wolves may only have a few litters of pups in their lifetime, and the alpha female is the primary breeder in a pack. There have been multiple documented cases of alpha females sustaining injuries and subsequently losing their status to another related female. We collected observational data on four established wolf packs in the Northern Range of YNP, focusing primarily on wolves 907F and 969F, two sisters who alternated as dominant females of the Junction Butte Pack from 2017 to 2019. We also analyzed observational data on wolves 870F and 970F, a second pair of sisters who alternated as dominant females of the same pack from 2012 to 2015. The results of this project will add to our understanding of the long-term impacts of injury in alpha females on pack dynamics. Understanding this issue is a key component of wolf conservation in the Greater Yellowstone Ecosystem.

Gram-Positive Bacterial Inhibition by a Potential Antimicrobial Small Molecule

Aaron Sharp*, Science, Montana State University, Billings
Kurt Toenjes, Science, Montana State University, Billings

With the advent of antimicrobial molecules in the mid nineteenth century countless people were saved from life threatening infections. With decades of use, antimicrobials put enormous selective pressure on targeted pathogens resulting in resistances forming in many common microbes. These resistant strains of pathogens result in over two million illnesses, 23,000 deaths every year, and billions of dollars in medical expenses. This represents a need to research new molecules that have antimicrobial properties to combat the rise of resistance and prevent undue suffering to those afflicted. A small molecule is under investigation now that displays promising antimicrobial properties in preliminary studies against Candida species and many pathogenic gram-positive bacteria. The gram-positive bacteria that are inhibited by this small molecule at include Staphylococcus aureus, Streptococcus pneumonia, Listeria monocytogenes, Staphylococcus epidermidis, Streptococcus pyogenes, Bacillus cereus and Clostridium difficile. Research is currently focused on S. aureus and C. difficile with disk assays performed on both and plate assays performed on S. aureus to narrow down the minimum inhibitory concentration. C. difficile has a zone of inhibition of 9mm, while S. aureus has zone of inhibition at 10mm. The plate assay for S. aureus has shown a minimum inhibitory concentration to be between 150-100 uM of the small molecule, though further studies are needed. Plans are being made to find the mechanism of action of the small molecule by using mutant strains of S. aureus.

INVESTIGATING THE BINDING OF BH3I-1 DERIVATIVES TO ANTI-APOPTOTIC BCL-2 PROTEINS

Kyler Pawlowski*, Biological and Physical Science, Montana State University - Billings, Billings
Joy Goffena, Biological and Physical Science, Montana State University - Billings, Billings
Dr. Kurt Toenjes, Biology and Physical Sciences, Montana State University - Billings, Billings

Candida albicans is a leading cause of superficial and life threatening fungal disease. The ability to grow as filamentous cells is an important virulence trait for this fungus. Thus, molecules that block filamentous growth may form the basis for a novel approach to controlling infections by *C. albicans*. We have characterized a small molecule called BH3I-1 that specifically inhibits filamentous growth, but not yeast-form growth. BH3I-1 is not likely to be a good candidate for an anti-fungal drug, as it targets human Bcl-2 proteins and has the potential to induce apoptosis in human cells. The goal of our project is to identify structural derivatives of BH3I-1 that retain anti-fungal activity, but not Bcl-2 binding activity.

KNOCKOUT OF ELP3 GENE IN CANDIDA ALBICANS

David McGee*, Biological and Physical Sciences, MSU, BILLINGS
Cody Walters, Biological and Physical Sciences, MSU, BILLINGS
Joy Goffena, Biological and Physical Sciences, MSU, BILLINGS
Lynn George, Biological and Physical Sciences, MSU, BILLINGS
David Butler, Biological and Physical Sciences, MSU, BILLINGS

Familial Dysautonomia (FD) is a devastating neurodegenerative childhood disease characterized by diminished polarized growth of autonomic neurons. FD results from a mutation in the ELP1 gene and reduced levels of the corresponding protein ELP1, a scaffolding protein that assembles a multi-subunit complex called Elongator. Elongator functions in the modification of tRNAs that mediate efficient translation of AA- and AG-ending codons. The Elongator complex also includes the ELP3 protein, a catalytic subunit of the complex. We are using hyphal growth in the fungus Candida albicans to model the role of Elongator in polarized growth. In this study C. albicans was genetically modified to knockout the ELP3 gene. As with the ELP1 gene, the absence of the ELP3 is expected to eliminate Elongator function. We have found that knocking out ELP3 mitigates the polarized growth of hyphal filaments under certain growth conditions.

LEGACY EFFECTS OF ABANDONED INSECT ECOSYSTEM ENGINEERING STRUCTURES ON MONTANA STREAM HYDRAULICS

Benjamin Tumolo*, Ecology, Montana State University, Bozeman
Lindsey Albertson, Ecology, Montana State University, Bozeman

Habitat modifications from ecosystem engineering can have profound legacy effects on ecological processes and communities. Our research identifies a hydraulic effect stemming from net-spinning caddisfly (*Hydropsychidae*) retreat structures that are ubiquitous in Montana stream ecosystems and describes the longevity of this effect over ecologically relevant timescales. We used a laboratory experiment to investigate how caddisfly net and retreat structures built in Montana streams influence fluid dynamics at local spatial scales over a two month time period after simulating abandonment by removing the caddisly larvae, leaving the retreat structure intact. We made velocity measurements with accoustic doppler velocimetery around caddisfly silk structures to test how hydropsychid caddisflies influence flow velocity and if any changes to flow velocity are maintained after the structure is abandoned by its caddisfly. We found that caddisfly silk nets reduce flow downstream of the structure by 85% and upstream of the structure by 17%. We also found that caddisfly silk structures without their caddisfly present can persist for over 60 days, suggesting ecologically significant legacy effects of these biotic structures on near bed hydraulics. The legacy of these local changes to hydrology may provide important refugia for less flow-tolerant benthic macroinvertebrate taxa and especially to those with rapid life histories and high turnover rates. Future work could address variation in the magnitude and duration in biotic engineering effects among different silk-producing species, densities of the structures through space or time, and decay rates of the silk structures at different flows that span those observed in Montana streams.

NATURAL INFECTION IN HONEY BEE HEMOCYTES

Verena Lawrence*, Microbiology and Immunology, Montana State University, Bozeman
Alexander McMenamin, Microbiology, Montana State University, Bozeman

Honey bees (*Apis* spp.)act as the primary pollinators of plants including fruit, nut, and vegetable crops. Since 2006, however, viral and other pathogens have caused honey bee colony losses averaging 33% annually (Lee et al, 2015). In an effort to better understand how the immune system of honey bees works, especially honey bee antiviral responses, I am investigating natural infection in honey bee larvae and in isolated hemocytes, which are macrophage-like immune cells. It was discovered that fruit fly hemocytes remained uninfected in virus-infected larvae, since hemocytes are important in mediating antiviral responses (Tassetto et al., 2017). The goal of this research project was to determine if these cells may also remain free of viruses in otherwise infected honey bee larvae and, thus, play an important role in honey bee antiviral defense. RNA was extracted separately from larval carcasses and hemocytes and cDNA was made, which was then screened for eight different honey bee viruses to determine the presence of viruses in the hemocytes and in the cells that make up the carcass. I found that in naturally infected larvae, hemocytes are generally uninfected. Of 39 larvae, 13 had natural infections. Three of the eight viruses were responsible for these infections. Of these 13 infected larvae, the hemocytes of only one larva was infected with the same virus that had infected the larva. Further experimentation will include testing hemocytes and carcasses from a larger sample of naturally infected larvae and from adult honey bees that will be injected with flock house virus. This will help determine if adult honey bee hemocytes are similarly resistant to viruses as larval hemocytes. Should hemocytes remain uninfected in otherwise infected larvae or adult bees, they may be a useful model for studying infection and the resulting antiviral response in honey bees at a cellular level.

STUDY OF AN ATOMIC COMPRESSIVE MATERIAL BEHAVIOR AT HIGH STRAIN RATE COMPRESSION IN A SIMPLE ALUMINUM SYSTEM

Md Salah Uddin*, Material Science and Engineering Program, Montana Technological University, Butte
Brahmananda Pramanik, Mechanical Engineering, Montana Technological University, Butte

Aluminum alloys are one of the structural materials with novel properties for building functional parts. Aluminum alloys are light metal alloys which have high demand in aerospace and automotive industries. In structural applications, functional parts are designed for over a broad range of strain rates and temperatures. A numerical simulation was performed to characterize an aluminum (Al) system at high strain rate uniaxial compressive loading conditions. We deformed the Al system at room temperature to higher temperatures with zero pressure. Al has face-centered cubic structure and we use four thousand atoms in periodic boundary conditions to perform the analysis. We used a modified embedded atom method, a widely used atomic level semi-empirical model for metals and impurities, for many-body interatomic potentials for monoatomic metal. We found characteristic material behavior for the Al system at different temperature at high strain rate compressive loading.

STUDYING CODON BIAS AND KIDNEY DYSFUNCTION IN A MOUSE MODEL FOR FAMILIAL DYSAUTONOMIA (POSTER)

Sarah Gallup*, Biological Sciences, Montana State University-Billings, Billings
Aurora Krebs*, Biological Sciences, Montana State University-Billings, Billings
Lynn George, Biological Sciences, Montana State University-Billings, Billings

Familial dysautonomia (FD) is a debilitating disease primarily known for its damage to the peripheral nervous system. However, kidney failure is the most common cause of death in FD patients. FD results from a mutation in the ELP1 gene, which is part of the 6-subunit complex, Elongator. It is known that some genes preferentially use specific synonymous codons, and Elongator is essential for translating genes that are enriched in either AA- or AG-ending synonymous codons. It has been assumed that kidney disease in FD results from irregular blood pressure and compromised innervation of kidney vasculature. However, here we show that ELP1 is robustly expressed in the kidney collecting duct, suggesting that it may play a direct role in kidney function and therefore the dysfunction in FD. To investigate this hypothesis, we made a mouse model where ELP1 is selectively ablated in the kidney collecting duct. Our data indicate an essential role for ELP1 in normal kidney function. These data suggest that compromised ELP1 levels in the kidneys of FD patients may be a contributing factor to chronic kidney disease. Our ongoing work focuses on identifying kidney-specific, codon-biased genes that are misregulated in the absence of Elongator and thus contribute to kidney dysfunction.

"THAT'S NOT COMING OFF OF THERE"; AN EXPLORATION OF LIGAND LABILITY IN CARBON TETRACHLORIDE DECHLORINATION TECHNOLOGIES

James Unzaga*, Chemistry, Monrana State University, Billings
Devin Williams, Chemistry, Monrana State University, Billings
Kyle Pickens, Chemistry, Monrana State University, Billings
Alex Fryett, Chemistry, Monrana State University, Billings
Matt Queen, Chemistry, Monrana State University, Billings

Carbon Tetrachloride (CT) is a carcinogenic industrial solvent, and known environmental contaminant. The Department of Energy's Hanford Site has been identified as a Superfund

Site. CT, is just one of the many environmental concerns. Environmentally CT dechlorinates in a stepwise manner forming lesser chlorinated intermediate complexes that pose a health threat to humans. [Cu(PDTC)L] is a small coordination compound capable of dechlorinating CT into less harmless decomposition products: CO2 and Cl-. In this study we draw a correlation between the dechlorination kinetics of CT of [Cu(PDTC)L] and the ligand liability of the L ligand. We use P K-edge X-Ray Absorption Spectroscopy to quanititate the phosphorus covalency of a series of PR_3 transition metal ligands [Cu(PDTC)L] (L= PPh_3, and PCy_3). Our results show that there is no correlation between the covalent character of Cu-P bonds and the kinetics of dechlorination. Instead, we propose that the correlation has a greater correlation with the solubility of a ligand in a given solvent system.

The Effects of Surfactants in Glyphosate-Based Herbicides on the Spotted Salamander

Grace Ibsen*, Chemistry, University of Providence, Great Falls, MT
Chrissie Carpenter, Chemistry, University of Providence, Great Falls, MT
Jessica Martin, Biology, University of Providence, Great Fall, MT
Roberta Newbury, Biology, University of Providence, Great Falls, MT

Salamander populations have been declining worldwide. There are many reasons that are thought to be contributing to this decline, one being the use of agricultural herbicides. Glyphosate-based herbicides are one of the most commonly used herbicides worldwide and their use is continuing to increase. Originally it was thought that glyphosate was the toxic ingredient causing declines in amphibian populations; however, studies are indicating that the surfactants used in these herbicides are what is responsible for the toxicity. The purpose of this study is to evaluate the toxicity (48 h) of a silicon-based surfactant on the spotted salamander (*Ambystoma maculatum*) compared to the surfactant in Glystar Plus®. The two experimental groups will be exposed to a solution containing 41% glyphosate with varying concentrations of a silicon based non-ionic surfactant at 14% and 28% respectively at an application rate of 0.35 mL/m2 added to Glystar Original®. Toxicity will be evaluated by comparing length, girth, weight, liver somatic index, and physical appearances.

The Influence of Antimicrobial Peptides, Cutaneous Microbial Communities and Water Quality on the Susceptibility of Columbia Spotted Frogs To Chytridiomycosis

Delaney Burrows*, Carroll College, Helena, MT
Brandon Sheafor, Carroll College, Helena, MT
Emma Esposito, Carroll College, Helena, MT
Bob Pearhill, Carroll College, Helena, MT
Kyle Strode, Carroll College, Helena, MT
Eric Sullivan, Carroll College, Helena, MT
Andy Loudon, Cleveland Metroparks Zoo, OH
Kevin Minbiole, Villanova University, Radnor Township, PA

Chytridiomycosis is a potentially deadly skin disease found in amphibian populations all over the world. Chytridiomycosis is caused by the fungus *Batrachochytrium dendrobatidis* (Bd) that grows on the skin of amphibians. The fungus can cause a disruption in the homeostatic functions of the amphibian skin and can lead to death. The relationship between an amphibian's antimicrobial skin secretions, cutaneous microbial communities and environmental water quality can affect their resistance and susceptibility to Bd infection.

Columbia spotted frogs (*Lithobates luteiventris*) are native to western Montana and have been affected by chytridiomycosis. Three lakes known to be positive for Bd were used as collection sites where a total of ten frogs were caught on three different occasions throughout the summer for a total of 90 collected samples. Each frog was swabbed for bacterial and fungal samples and placed in a solution that would collect antimicrobial peptides secreted from the frogs' skin. Water samples were collected at each site and analyses were performed to assess various parameters. Early results suggest that AMPs may affect the relative abundance of an important anti-fungal bacteria (*Rhizobacta*) which influenced Bd status. The goal of the ongoing research is to determine what parameters of environmental conditions, antimicrobial skin secretions, and cutaneous microbial communities allow Columbia spotted frogs to be resistant to chytridiomycosis in order to better predict and treat future outbreaks.

The Relationship Between Deuterium Excess and Uranium Groundwater Concentrations in Whitehall, Montana

Daniel P. Wight*, Environmental Sciences, The University of Montana Western, Dillon
Eric M. Dyreson, Mathematics, The University of Montana Western, Dillon

Uranium can become elevated in the environment and pose a human health risk to water resources. Therefore, it is important to understand the origin, transport and concentration of uranium in the environment. With this study we propose that deuterium (δ(_1^2)H) excess may be a viable way to understand uranium groundwater contamination that is mainly derived from the surface. We collected 23 water samples and compiled data from a study done by the United States Geological Survey (USGS) within the area of Whitehall, MT. With a linear regression we show that there is a significant relationship between deuterium excess and uranium water concentrations for our data (t_19= -3.015,p=0.0071,R^2=0.32). We also showed that there is a significant linear relationship between uranium water concentrations and nitrate water concentrations for our data (t_19= 2.573,p=0.0192,R^2=0.27). In addition we showed that there is a significant linear relationship between calcium carbonate and uranium groundwater concentrations for the compiled USGS data (t_66= 6.295,p=2.846e^(-8),R^2=0.38). The results of a Wilcoxon rank sum test showed that wells close to ponds have a significantly higher median uranium concentration for our data added to the USGS data (WRS_8,12,W=111.5,p=0.033778). With this relationship we may infer that an influx of uranium into the aquifer originates at the surface most likely from the Boulder Batholith. These results are also consistent with a model that involves insoluble uranium being transported in suspension and settling out in ponds where an influx of nitrates and/or carbonates react to produce higher concentrations of water-soluble forms of uranium. We suggest that the relationship found between uranium concentration and deuterium excess in water samples may be related to the higher rates of evaporation in ponds. Thus, in this specific hydrologic environment of valley ponds close to the Boulder Batholith source, deuterium excess may serve to help predict levels of uranium concentration.

XFEB, a Direct Target of ZIC1, is Involved in Neural Crest Development

Lillian Ball*, Cell Biology and Neuroscience, Montana State University, Bozeman
Haley Cox*, Cell Biology & Neuroscience, Chemistry and Biochemistry, Montana State University, Bozeman
Jennifer Forecki, Cell Biology and Neuroscience, Montana State University, Bozeman
Christa Merzdorf, Cell Biology and Neuroscience, Montana State University, Bozeman

During early embryonic development, neural crest cells give rise to the peripheral nervous system, melanocytes, bone and craniofacial cartilage. A network of signaling and transcription factors regulate early neural crest development, including Zic1, Pax3, Gbx2, and Xfeb.

Combinations of Zic1 plus Pax3 and Gbx2 plus Pax3 are able to induce ectopic neural crest development. We hypothesized that Xfeb also contributes to neural crest development, as it is present in the same region at the correct time. Besides being a direct downstream target of the transcription factor Zic1, Xfeb was also identified as a potential neural crest gene induced by Zic1in genomic screens. We hypothesize that pax3, Xfeb, gbx2 and zic1 are all part of a gene regulatory network controlling neural crest development. To investigate these relationships, we overexpressed the Xfeb gene using Xfeb sense RNA and inhibited Xfeb expression with morpholino oligonucleotides (MO). We used in situ hybridization to visualize neural crest induction by staining for slug RNA expression, a known neural crest marker. Our results show that embryos injected with Xfeb sense RNA expanded slug expression while those injected with Xfeb MO diminished slug expression. In further experiments, we injected embryos with pax3 sense RNA without and with Xfeb MO. Injection with pax3 sense RNA alone expanded slug expression, while embryos injected with pax3 sense RNA plus Xfeb MO showed a decrease in slug expression. This suggests that Xfeb acts downstream of Pax3 in the neural crest gene regulation network. Our next step will be to determine if upregulation of gbx2 or zic1 will rescue neural crest development in the absence of Xfeb. This research will contribute to our understanding of gene regulatory networks, and how these contribute to early neural crest development.

Zic Transcription Factors that Influence Convergent Extension

Jocelyn Waggoner, Cell Biology and Neuroscience, Montana State Univeristy, Bozeman

My research is focused on a specific time frame during embryonic development called gastrulation, in which intricate cell movements give rise to the ectoderm, mesoderm and endoderm layers of the embryo. The mesoderm layer undergoes movements called convergent extension, which allow cells to intercalate and move inside the embryo. The Zic family of zinc-finger proteins have a crucial role in gastrulation and neurulation. Based on findings from our lab (K. See and Merzdorf, in preparation) and others (Cast et al., 2012), I hypothesize that zic genes are required for convergent extension during gastrulation. Since there are 5 different, but very similar, zic genes, I will test each of these genes for a role in convergent extension during gastrulation. A knockdown method for each of the 5 zic genes in embryos of the model organism *Xenopus laevis* will be combined with a method called Keller Explants to allow analysis of convergent extension. In my experiments, I have ruled out zic 2 as a regulator of convergent extension. My current hypothesis is that zic3 is the most likely candidate because of its known roles in neural tube formation and other reasons I will explain below. I am also analyzing zic1,4, and 5 for convergent extension regulation.