

**Friday, April 5, 2019: Big Butte/Highlands Room**

## **POSTER PRESENTATIONS**

*(Alphabetical by Title)*

*\*Indicates Presenting Author*

**A REVIEW ON PROPHYLAXIS TREATMENTS FOR CHRONIC LYMPHOCYTIC LEUKEMIA INFECTIONS** *Diana Gonzalez Vazquez \**, *Biology and Chemistry, University of Providence, Great Falls*

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, The 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

*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. bacilliformis*, 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

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*

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 (2018 Graduate Grant Awardee)*

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 Feuerstein\*, Biology, 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 XENOPUS LAEVIS EMBRYOS?**

*Dean Ricker\*, Chemical Engineering, Montana State University, Bozeman (2018 Undergraduate Grant Awardee)*

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 *Xenopus laevis* (African clawed frog) 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*

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 CO<sub>2</sub> incubator set at 37 °C. 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,  $\bar{x} = 9.8\%$  growth (SD = 15.705). After the treat was given,  $\bar{x} = 10.023\%$  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 POECILIA RETICULATA**

*Sarah Gallup\*, MSU-Billings, Billings*

*Poecilia reticulata* (commonly known as guppies) 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 (Fig. 1). 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 Technological University, 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<sup>-</sup> 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 (Fig 1).

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 Lacey\**, Ecology, Montana State University, Bozeman

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, MSU-Billings, 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 pneumoniae*, *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**

*Chelsea Coons \**, *Biological and Physical Sciences, MSU 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, 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**

*Zachary Maguire\**, *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 caddisfly larvae, leaving the retreat structure intact. We made velocity measurements with acoustic doppler velocimetry 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*

Honey bees 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.", "Honey bees, hemocyte, virus, immune response

## **PRODUCTION OF POLY-N-ACETYLGLUCOSAMINE BY THE LYME DISEASE SPIROCHETE *Borrelia burgdorferi***

*Adam Drobish\**, *Biological Sciences, University of Montana, Missoula (2018 Graduate Grant Awardee)*

## **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*

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**

*Sarah Gallup\*, Biological and Physical Sciences, MSU 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.", "AQP2, collecting duct, ELP1, kidney disease

### **“THAT’S NOT COMING OFF OF THERE”; AN EXPLORATION OF LIGAND LIABILITY IN CARBON TETRACHLORIDE DECHLORINATION TECHNOLOGIES**

*James Unzaga and Devin Williams, Chemistry, MSU-Billings, 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: CO<sub>2</sub> and Cl<sup>-</sup>. 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 quantitate the phosphorus covalency of a series of PR<sub>3</sub> transition metal ligands [Cu(PDTC)L] (L= PPh<sub>3</sub>, and PCy<sub>3</sub>). 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*

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/m<sup>2</sup> 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 (*LITHOBATES LUTEIVENTRIS*) TO CHYTRIDIOMYCOSIS**

*Delaney Burrows \**, Carroll College, Helena

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**

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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 ( $\delta_{1}^{2}\text{H}$ ) 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**

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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 *Zic1* in 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. McGe

### **ZIC TRANSCRIPTION FACTORS THAT INFLUENCE CONVERGENT EXTENSION**

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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 will also analyze zic1,4, and 5 for convergent extension regulation.

