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Abstracts for Poster Presentations

Late summer-early fall photosynthesis in cottonwood (*Populus deltoides*)

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Photosynthesis was investigated during late summer and early fall in a population of mature cottonwood (*Populus deltoides*) trees growing on the campus of MSU-Billings in southcentral Montana. Parameters related to photosynthesis were measured in situ with a Licor 6400XT Photosynthesis system. A diurnal fluctuation in assimilation was observed with a peak value of $17.0 \mu\text{M m}^{-2} \text{s}^{-1}$ CO₂ fixed during mid-day. We examined the capacity for assimilation at a PAR of $4000 \mu\text{M m}^{-2} \text{s}^{-1}$ (approx. 200% full sunlight) and observed assimilation values as high as $17.6 \mu\text{M CO}_2 \text{ m}^{-2} \text{s}^{-1}$ with no indication of photoinhibition. *P.deltoides* also responded to high ambient CO₂ ($1600 \mu\text{mol M}^{-1}$) where assimilation increased to $31.5 \mu\text{mol CO}_2 \text{ m}^{-2} \text{s}^{-1}$ under $1000 \mu\text{M m}^{-2} \text{s}^{-1}$ PAR. We used an ACi curve fitting utility to obtain values of $104 \text{ mmol m}^{-2} \text{s}^{-1}$, $117 \text{ mmol m}^{-2} \text{s}^{-1}$ and $8.6 \text{ mmol m}^{-2} \text{s}^{-1}$ for rubisco V_{max}, electron flow rate and triose phosphate utilization, respectively. Transpiration was $0.1\text{-}6.1 \text{ mmol m}^{-2} \text{s}^{-1}$ and correlated with assimilation. Assimilation declined 37% from the earliest measurements on 23Sep to those taken on 15Oct. We conclude that photosynthesis continues in leaves of *P.deltoides* well into autumn despite shorter days and cooler temperatures, but with an adaptive response resulting in less CO₂ fixation. Leaves can photosynthetically fix carbon, presumably stored as reserve carbohydrates well into late fall before the onset of autumnal leaf senescence.

Analysis of human versus machine translation accuracy

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The purpose of this study was to determine whether significant differences exist in Chinese-to-English translation accuracy between moderate to higher-level human translators and commonly employed freely available machine translation tools. A Chinese-to-English language proficiency structure test and a Chinese-to-English phrase and sentence translation test were given to a large sample of machine (n=10) and human translators (n=133) who are native Chinese speakers with at least 15 years of familiarity with the English language. Results demonstrated that native Chinese speakers with this minimum level of English proficiency were significantly better at translating sentences and phrases from Chinese to English, compared to the ten freely available online machine translation applications, which unexpectedly showed a considerable degree of variation in translation accuracy among them. These results indicate that humans with at least a moderate level of exposure to a non-native language make far fewer translation errors compared to machine translation tools. This outcome is understandable, given the unique human ability to take into account subtle linguistic variants, context, and capricious meaning associated with the language and culture of different groups.

Isolation and characterization of an allelochemical from Russian olive, *Elaeagnus angustifolia*.

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Plants excrete compounds that can be beneficial or detrimental to the receiving organism. The detrimental compounds are referred to as allelochemicals and typically inhibit growth, delay germination, and may result in death. Previous unpublished work at Rocky Mountain College has indicated that leaves of the invasive tree species, Russian olive, contain a substance that causes delayed germination and stunted root growth in radish bioassays. The main goal of this study is to extract, isolate, and characterize the compounds causing this delayed germination via bioassays and analytical chemistry techniques. Our current results indicate that extractions of leaves using polar solvents may contain an allelochemical. Future work will include separation of the extract with chromatography and the characterization of the compound. Implications off this research include better infestation management practices and potential applications in agriculture.

Pain Tolerance: Differences According to Sex and Sport

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Objective: Numerous studies have independently examined gender differences in experimental pain, but few have examined the different surfaces of play that may influence an athlete's pain tolerance. The present experiment examined the effects of race, gender, and sport on experimental pain tolerance and threshold.

Methods: Forty (10 female basketball, 10 male basketball, 10 female soccer, 10 male soccer) collegiate athletes were given two pain tolerance tests consisting of a cold water intolerance test (CWIT) and a tourniquet pain test (TPT). The CWIT measured the maximum length of time that each athlete could place his/her hand in an ice cold bucket of water (2°C). The TPT measured the maximum length of time that each athlete could repeatedly squeeze a hand grip dynamometer while blood was occluded from the arm. A series of ANOVA tests determined if there were significant differences in pain tolerances between race, gender, and sport.

Results: Based on the results, there are no differences in pain tolerance when comparing sport; however, there is a significance difference ($p < 0.05$) in pain tolerance when comparing race and gender. The CWIT shows that white females have a significantly higher pain tolerance than non-white females; however, there is no significant data that shows that white males have a higher pain tolerance than non-white males.

Conclusion: This data is beneficial for physicians, trainers, coaches, etc. because they now know to treat injuries of both males and females of indoor and outdoor sports equally because sport has no effect on pain tolerance.

Measuring Algal Growth in Agar for use on the International Space Station

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Through a NASA Hunch grant, we are attempting to grow algae in a semi-solid agar media for oxygen production on the International Space Station (ISS). Novel growing conditions are necessary to sustain algal cultures in the microgravity environment of space. The results show that algae can be grown on earth, embedded in agar, with a uniform growth pattern. A 3% agar growth media is cooled to 47°C and inoculated using a saturated liquid culture. The inoculated agar is poured into impact-resistant Nalgene® containers. Once solidified, the agar is exposed to near-IR (infrared) and near-UV (ultraviolet) lights for 13 hour light / 11 hour dark cycles. Within a Nanoracks one unit aluminum box, we are able to fit 3 Nalgene® containers, two of which have algae and one does not. An exact duplicate of this experiment will be launched to the ISS in July 2015 to compare algal growth in microgravity with algal growth in the lab. The long-term goal of this project addresses the use of algae to produce oxygen from carbon dioxide on the ISS.

An Entomological Study of the Transfer of Melatonin, Nicotine, and Zeranol from Tissue to Maggot

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Throughout daily life humans consume substances that are metabolized by the body and eventually secreted. When death occurs metabolism stops and substances are trapped inside the body for a limited amount of time. If the body is left out, eventually flies and other bugs will make their way to it and lay eggs. When the eggs hatch, maggots begin to eat the tissue of the body. Since the tissue contains the consumed substances they should be transferred to the maggots. This is important in forensics because any substances that have dissipated from the tissue of the body may still be found in the maggots. If the maggots are collected they can be analyzed to determine what substances they contain. Knowing what can and cannot be transferred is important, as well as knowledge of how long it will take different substances to dissipate from the body. To imitate dead human tissue, skinned pig muscle was soaked in solutions of melatonin, nicotine, and zeranol (an animal steroid). Maggots were introduced and allowed to feed on the tissue for 72 hours. Samples of maggots were collected every 12 hours, as well as a sample of tissue at the beginning and end of the experiment. All samples were digested in nitric acid. Analysis on the GC-MS of each sample was compared to standards to identify the substances they contained.

Mycobacterium tuberculosis Resistance to PZA

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The aim of this project is to understand the mechanism of horizontal gene transfer and, more specifically, how resistance arises via mutations in *Mycobacterium tuberculosis* (TB). In particular, its resistance to the drug Pyrazinamide (PZA) will be examined. I will conduct two phases of this research. The first will be to observe horizontal gene transfer in everyday bacteria. The second phase will be to insert the mutant *pncA* gene that confers PZA resistance to a competent, non-virulent bacteria, *E. coli*, and study the rate of transfer in PZA-resistant TB. By doing this, it will be possible to better understand the mechanisms by which PZA-resistant bacteria transfer resistance and learn more about the mutations of this disease.

Spatiotemporal variation in grassland biomass and forage quality across the Upper Yellowstone River Basin

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Spatial and temporal heterogeneity in the abundance of high quality forage is known to play an important role in migratory ungulate ecology. While many studies have documented how variations in the timing of start of growth and land use affect the availability of high quality forage across temperate landscapes, few studies have quantified how the abundance of high quality forage varies across these gradients. In this study we quantified how aboveground biomass, crude protein, and digestibility varied throughout the growing season in (1) grasslands that start growth early, mid, and late in the season and (2) in irrigated agriculture, private grasslands, and public grasslands and then used these estimates to (3) assess how the seasonal abundance of high quality forage differed in these start of season and land use classes in the Upper Yellowstone River Basin. We found that grasslands that start growth late in the season had up to 150% greater aboveground biomass, 20% greater crude protein, and 15% greater digestibility at its seasonal peak than grasslands that start growth mid and early in the season. Irrigated agriculture had up to 500% greater aboveground biomass, 90% greater crude protein, and 10% greater digestibility at its seasonal peak than private and public grasslands. Overall, the abundance of high quality forage was greater in the late start of season and irrigated agriculture grasslands. Understanding these landscape-scale variations in the abundance of high quality forage may provide important information for migratory ungulate research and management.

Online Professional Learning Networks

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As technological advancements are made in the social media world, more people are connecting for professional development this way. This study served as an update to a 2011 study conducted by Dr. Hilary Risser. The previous study established a base network of teachers that used blogs to communicate educational practices. The purpose of this investigation is to analyze the differences, similarities, and benefits of online versus face-to-face communication. Interviews with multiple math and science teachers were conducted first with an online survey, and followed up via Skype. Their blogs were examined to identify connections between these teachers so that a new network of communication could be established. Preliminary results show that since 2011, networks have grown. Moving forward, the contents of each blog will be assessed. One future goal is that the conclusion of this study could lead to better equipped online social media for education professionals to grow.

An Investigation of the Common Loon, (*Gavia immer*), on Spencer Lake and Blanchard Lake, Montana: Identifying Populations of Banded and Non-Banded Birds of the Common Loon.

Spencer Hale

Montana Tech- Undergraduate Research Program

Common Loon (*Gavia immer*) studies were conducted between May and August, 2014 at known loon territories in the Whitefish, Montana area. Data were collected on nesting pairs at Spencer Lake and Blanchard Lake, both of which are a few miles of Whitefish. Loon pairs were observed and behaviors recorded as well as leg-band identifications, foraging habits, territorial behaviors, chick stages, and nesting success. The study covered 46 hours of observational study. Based on prior data provided by the Montana Common Loon Working Group and the Flathead National Forest Service, it is possible to identify pairs that are returning to the same locations and remaining with the same breeding pair. This summer research provided valuable data including identification of nesting pairs on both Blanchard and Spencer Lake, adult band data from both of these lakes, and both lakes had chick hatch dates allowing for a comparison between both lakes of study noting their differences as possible causes for differing nest success and hatch dates between Spencer Lake and Blanchard Lake.

In-vitro Reconstitution of Sulfite Reductase from *Pseudomonas aeruginosa*

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Recent work has established a link between a ferredoxin:NAD(P)H oxidoreductase (FprA) and sulfite assimilation in members of the genus *Pseudomonas*. This suggested that FprA is a component of a novel sulfite reductase enzyme. That hypothesis is consistent with the fact that only one component of the well-characterized *E. coli* a8 β 4 sulfite reductase has been identified in *Pseudomonas* genomes; i.e the β siroheme subunit CysI is present but not the α flavoprotein subunit CysJ. This led to the hypothesis that FprA is a component of a novel sulfite reductase enzyme. Our aim is to test that hypothesis by in-vitro reconstitution using the purified proteins CysI and FprA. We have successfully overexpressed and purified FprA from *Pseudomonas aeruginosa*. The strategy for production of purified CysI has been complicated by the requirement for concomitant expression of CysG (siroheme synthase). We are also investigating the possibility that a downstream, overlapping reading frame (PA1837) may also be necessary for functional CysI production.

Forensic Application of Larvae Analysis to Detect Chemicals In Muscle Tissue

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Past events cannot be observed, that is where forensic toxicology comes into play regarding the detection of toxic amounts of chemicals. This is useful in the forensic science field because it allows death investigators to deduce if the body at the scene had been under the influence of any chemicals before death. The purpose of this research is to determine if maggots can uptake trace amounts of chemicals from muscle and to determine if this uptake can be detected and quantified. This research will specifically examine the toxicology of three common chemicals (alcohol, caffeine, and penicillin) as absorbed by fetal pig muscle. To do such, fetal pig thighs were removed and skinned then placed in individual solutions of alcohol, caffeine, or penicillin to soak for 24 hours. Once all the liquid was removed, maggots were placed on the muscle. Samples of maggots were collected every 12 hours for a total of 72 hours. The maggots were then frozen and later placed in a nitric acid digestion to create a liquid solution that was later analyzed using the GC-MS.

Biochemical and functional characterization of a potential 2', 3'-cyclic-nucleotide 3'-phosphodiesterase (CNPase) found in tumorigenic fish retroviruses

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Tumorigenic retroviruses cause seasonal cancer in fish. Many of these retroviruses contain an interesting unknown gene of cellular origin. Computational programs predict that this gene encodes a CNPase (2',3'-Cyclic-nucleotide 3'-phosphodiesterase). In mammals, the natural function of CNPase is unknown. The purpose of the experiment is to isolate and characterize the potential viral CNPase. Utilizing a vector from zebrafish endogenous retrovirus (ZFERV), the potential CNPase genetic sequence will be isolated and analyzed. Thereafter, the potential CNPase protein will be expressed and purified, and characterization will include enzymatic activity assays, inhibition activity studies, and NMR studies. Future studies involve functional characterization of the potential CNPase, including binding and transformation studies. Potential CNPase is predicted to function as an oncogene that promotes tumorigenesis in fish. Exploring this potential CNPase may aide in the treatment of affected fish as well as provide insight into the function of this enzyme in humans.

Identification of potential targets of the Grr1p SCF ubiquitin ligase in fungi

Elizabeth Mullins, Joy Goffena, Kurt A. Toenjes, David K. Butler

The opportunistic human pathogen *Candida albicans* causes both superficial and life-threatening systemic infections and is a leading cause of fungal disease in immunocompromised individuals. *C. albicans* can grow in different cell shapes, or morphologies, including yeast-like cells and a variety of filamentous forms, such as true hyphae and pseudohyphae. Yeast, hyphae and pseudohyphae have been observed at the sites of *Candida* infection and there is strong evidence that morphogenesis, the transition between yeast and filamentous growth forms, is essential for

virulence. Several studies have implicated ubiquitin-dependent proteolysis in the regulation of morphogenesis, yet the mechanism by which this pathway does so is largely unknown. Previously, we have shown that deletion of the GRR1 gene results in the constitutive formation of filamentous growth forms. The Grr1 protein is a component of an SCF ubiquitin ligase system that selectively targets proteins for degradation. Thus, the loss of Grr1-mediated proteolysis presumably leads to the aberrant accumulation, and inappropriate activity, of a protein or proteins that induce filamentous growth. The spectrum of proteins targeted for degradation by Grr1 is not known. The goal of this project is to identify Grr1 targets in *Saccharomyces cerevisiae*, an experimentally tractable model system for pathogenic fungi. We are using a novel proteomics-based approach to isolate and characterize proteins that are ubiquitinated in a Grr1-dependent fashion. The successful identification of Grr1p targets will be important for developing a working model of the pathways involved in the yeast to filamentous growth transition in pathogenic fungi.

Analysis of *tacA* overexpression on phenotypic characteristics of *Sinorhizobium meliloti*

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Sinorhizobium meliloti is a nitrogen-fixing bacterium that forms a symbiosis with legumes. These bacteria colonize plant roots within nodules and undergo a novel cell cycle as a symbiont. Free-living in soil, it undergoes asymmetrical cell division with one round of DNA replication per cell cycle. We are interested in identifying cell cycle regulators and understanding their function during free-living growth and symbiosis. We hypothesize that TacA is a cell cycle regulator since deletion of the TacA ortholog in *Caulobacter crescentus* shows morphology, motility, and cell membrane defects. To test this, we examined IPTG-induced overexpression of *tacA* for exopolysaccharide, membrane, and motility defects. Our results show low IPTG levels decrease motility of wild type and $\Delta cbrA$ strains. Surprisingly, higher amounts of IPTG restore motility to each strain's original level. Additionally, *tacA* overexpression causes a membrane defect in WT that is similar to $\Delta cbrA$, while *tacA* does not appear to regulate exopolysaccharide production. In conclusion, *tacA* overexpression has several cell cycle phenotypes, which makes it a good candidate for further investigation. *S. meliloti* is an important model organism, not only for its potential to replace synthetic nitrogen fertilizers, but also because it is related to bacteria that cause brucellosis and plant tumors.

The role of ZIC1 in cranial suture formation

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The *zic1* gene plays an important role in embryonic development, in part by regulating the expression of many other genes including the engrailed gene. Previous investigators have reported that abnormal engrailed expression shifts the location of cranial suture formation and affects gene expression in the developing sutures (Deckelbaum et al. 2012). Such defects may cause a premature fusion of cranial sutures, leading to a serious birth defect known as craniosynostosis. Dr. Andrew Wilkie (Oxford University) has found that mutations in the human ZIC1 gene cause craniosynostosis. He hypothesizes that the engrailed gene is abnormally regulated in patients with these ZIC1 mutations. In collaboration with the Wilkie lab, we are testing this hypothesis by injecting RNA derived from the human ZIC1 mutants into *Xenopus* frog embryos. The goal of our experiments is to observe whether the mutated human ZIC1 genes affect the expression of the engrailed gene in frog embryos, which we were able to show by in situ hybridization. The degree of abnormality of engrailed expression caused by the various human ZIC1 mutations corresponds to the severity of the patients' phenotypes. These findings provide a better understanding of the molecular mechanisms underlying craniosynostosis and suggest possible gene regulatory pathways.

A Bioassay of Montana Grassland Plant Resistance to Catechin: An Exudate of Spotted knapweed, *Centaurea maculosa*

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Centaurea maculosa, or Spotted knapweed, is considered an invasive species in the Western United States, including Montana. It has established sizeable populations and displaced native plant communities through what is believed to be a result of the plant's exudate, catechin. Catechin is an allelochemical documented to have phytotoxic, antimicrobial, and chelating properties. Current methods of remediation (biological, mechanical, and chemical) have demonstrated limited degrees of success. It is hypothesized that the degree of resistance to catechin of neighboring plant species determines the degree of knapweed invasiveness. The goal of this research is to test Montana native grassland species for resistance to catechin. Assembling a bioassay on agar plates, Montana grassland seeds will be grown in the presence and absence of catechin. The degree of resistance for each respective grassland species will be assessed through percent germination, root length, and shoot length. In identifying a Montana native grassland species with catechin resistance, the species could provide potential means of remediation and prevention.

Riverine dissolved organic matter decomposition and dynamics

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Aquatic and terrestrial ecosystems are intimately linked through the transfer of energy and materials. A common example of ecosystem linkage is the input of terrestrial dissolved organic matter (DOM) to rivers and streams. DOM can play a variety of roles in stream ecosystem function by fueling local food webs, influencing trophic state, and affecting the dissolved nutrient availability. Microorganisms utilize, transform, and produce DOM during microbial metabolism, a relationship that links microbes to DOM quality and quantity. Chemical and physical properties are known to vary with DOM source, and thus the type of terrestrial input may dictate how DOM is processed in a stream. Using laboratory microcosms, and added terrestrial organic matter substrates, we carried out a leaching experiment over forty-five days. We employed a suite of complementary techniques to determine the effect of leaching DOM sources on microorganisms, DOM processing, and ecosystem function. Microbial community composition changed from the original stream water inoculum and depended on DOM source. Cell abundances for all DOM sources spiked after two days, after which abundances dropped and remained relatively steady until the end of the experiment. DOM concentrations decreased exponentially with the maximum amount of carbon utilization taking place within the first five days. The DOM fluorescent signature, initially influenced by amino acid-like fluorescence shifts to more humic-like character over the course of the experiment, indicating DOM humification over time. Our results showcase the advantages of interdisciplinary tools to elucidate the connection of microbial processing, DOM chemistry, and ecosystem function.

Rescuing Convergent Extension After Inhibition of an Aquaporin

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Much is known about the function of aquaporins within individual cells. Aquaporins are membrane protein channels that are permeable to water and a subset, the aquaglyceroporins, are also permeable to glycerol. Little research has been conducted on how they contribute to larger processes such as gastrulation. Gastrulation organizes embryos into germ layers, which will later form different body tissues. Convergent extension cell movements are critical for driving gastrulation. During convergent extension, cells fold into the embryo at the dorsal lip of the blastopore and then merge to help form the long body axis. An aquaglyceroporin, aqp3b, is expressed during convergent extension. When it is inhibited using a morpholino oligonucleotide, convergent extension does not occur properly. Since this process is difficult to manipulate in whole embryos, I explant and culture the dorsal lip of the blastopore region of embryos, which then undergoes convergent extension by growing long and narrow protrusions. When aqp3b is inhibited, these protrusions do not develop. My project focuses on rescuing the convergent extension defects caused by inhibiting. If rescue methods are successful, explants will form a long

and narrow protrusion as observed in control embryos. For these experiments, 4-cell embryos are injected into the dorsal blastomeres and explants are cut at early gastrula stage. So far, I have achieved 25-35% convergent extension in control explants. I plan to achieve 80% convergent extension and will then begin the rescue experiments.

Sequencing and Characterization of Canine Viral Genomes

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Some viruses, like canine parvoviruses, are known to infect both human and canine hosts. Currently there is a significant lack of information about canine viruses, as a result there is no conclusive way to evaluate whether a virus is capable of cross species infection. Another problem that stems from this lack of information is that screening for viruses in sick canines is rarely practiced and instead antibiotics are almost exclusively the choice remedy. Improper use of antibiotics will not stop viral infection and may create antibiotic resistance as well as cause further discomfort to sick dogs. The goal of this research project is to isolate and sequence viral strains, to drastically improve the genome databases for other scientists to use, and conduct phylogenetic analysis to characterize found viruses. To accomplish these goals, fecal samples will be taken from sick and healthy canines noting in detail any symptoms the dog is exhibiting. The viral DNA/RNA is extracted and purified using a specially designed kit. After extraction the viral DNA/RNA is amplified and the products are sequenced. The newly sequenced viruses will be compared to each other as well as known strains to aid in characterizing their type. Using the information that corresponds to each sample, characterized viruses will be correlated to symptoms found in canines. By expanding the known information about viruses, it may be used later to determine more viruses that infect both human and canine hosts as well as a way to better diagnose sick dogs.