Abstracts for Poster Presentations

Montana Academy of Sciences Annual Meeting
5:30-9:30 pm, April 11, 2014
Kelly Stewart Room (SUB)

Monitoring the Movement of Transposable Elements in *Chlamydomonas*

Amy Bump, Mark Osterlund.
Department of Biology, Rocky Mountain College, Billings, MT.

Transposable elements (TEs) have been identified in all known organisms. Although they are usually found in the non-coding regions of DNA, TEs do have the ability to move around in the genome. We are specifically interested in a unique type of TE called a Miniature Inverted-repeat Transposable Element (MITE). At the 2013 Montana Academy of Sciences we proposed a method to monitor MITE movement, where we are attempting to block expression of the green fluorescent protein (GFP) in *Chlamydomonas reinhardtii* with the presence of an interfering MITE. Future movement of the MITE will be observable in a simple plate assay due to the acquired fluorescence of the *Chlamydomonas*. Two separate DNA constructs are being created for this assay. In our first construct, a MITE is located between a promoter and the GFP gene. Anticipating leaky expression due to the small size of the MITE, a second construct places the MITE inside the GFP gene. We currently show the successful use of Polymerase Chain Reaction to amplify a Gulliver-like MITE from *Chlamydomonas*, the introduction of specific restriction sites flanking the MITE, and preliminary cloning results.

Measuring growth of *Chlorella vulgaris* in a Semi-solid Media

Erin Burns[1], Mark Osterlund[1]
[1] Biology Department, Rocky Mountain College, Billings, MT.

Through a NASA Hunch grant, in collaboration with Billings Central Catholic High School, we are attempting to grow algae on the International Space Station (ISS). Because liquid cultures are not conducive to the microgravity environment of space, novel growing conditions are necessary to sustain the algae on the ISS. Therefore, we have developed a method of growing algae in a semi-solid agar media. *Chlorella vulgaris* was grown to saturation in liquid TAP media using a 12 hour light / dark cycle. Aliquots of liquid culture were added to autoclaved TAP media containing 1.5% agar that had cooled to 50°C. Following thorough mixing, the algae embedded agar was distributed to a customized container designed to withstand space travel. Using blue and red LED lights, the container was then exposed to 12 hour light / dark conditions. Over the course of 14 days, algal growth was measured daily through a simple

photographic assay. A duplicate experiment will be launched to the ISS in July 2014 to compare algal growth in space relative to algal growth in the lab.

Species Diversity Studies on the Developmental Expression of *Aquaporin 3*

Kelly K. Christensen[1], Christa Merzdorf[2].
[1]Dept. of Microbiology, Montana State University, Bozeman, MT. [2]Dept. of Cell Biology Neuroscience, Montana State University, Bozeman, MT

Neurulation is a developmental process involving the conversion of the flat neural plate into the hollow neural tube, the precursor to the adult nervous system. Failure to close properly results in neural tube defects (NTDs), which are the most prevalent birth defects in today's world. To better understand NTDs, it is crucial to study the role of genes that direct *normal* neural tube closure in model species. *Aquaporin3b* is expressed in the neural folds of *Xenopus laevis*, and when this gene is interfered with, the neural tube closes improperly. The question is whether there is evolutionary conservation of *aqp3* expression in the embryos of other vertebrate species, such as *Xenopus tropicalis,* zebrafish, and chicken *(Gallus gallus domesticus)*. *In situ* hybridization was used to analyze *aqp3* gene expression among the four species at various developmental stages, where the organism-specific anti-sense RNA probes were visualized using anti-digoxygenin antibodies and NBT/ BCIP substrate. All four species demonstrated *aqp3* expression patterns. *Xenopus tropicalis* embryos expressed *aqp3* in the neural folds, in a pattern very similar to *Xenopus laevis*. Zebrafish embryos, expressed *aqp3b* in a broader pattern, possibly throughout the entire neural plate. In chicken embryos, specific determination of *aqp3* expression will require further testing.

Structure-Activity-Relationship of anti-tumor agents that target Quadruplex DNA Stabilization

Nathan S. Duncan[1], Howard D. Beall[1], Nicholas R. Natale[1]*.
[1]Department of Biomedical and Pharmaceutical Sciences, The University of Montana, 32 Campus Drive, Missoula, MT 59812.

Genomic DNA, which is organized around double-stranded B-form DNA, is both durable and flexible enough to store and pass on genetic information. Once freed from the associations of an extended complimentary sequence, single stranded DNA and RNA can adopt a vast array of other stable secondary structure motifs, such as stem-loop, pseudo-knots, and tetra-loops, ideal for its involvement in other biological settings other than as a store of genetic information. Guanine-rich nucleic acids can fold into distinctive four-stranded conformers found in telomeric DNA repeats (i.e. TTAGGG), also known as G-quadruplexes (G4), as well as in sequences in the promoter and other regulatory regions of genes, especially those involved in cellular proliferation. Small molecules that induce the formation of, and/or selectively bind to, G-quadruplex

structures are of interest for development as potential therapeutic agents, particularly in the anticancer therapeutic area. To date, quarfloxin is the only G-quadruplex ligand that has progressed to clinical evaluation. Novel 10-substituted anthracene ether double tails (AIMs) derivatives were synthesized and will be presented. They have recently been evaluated for biological activity and cytotoxicity against SNB-19 CNS glioblastoma cells. The synthesis, characterization, biological studies, and future directions will be presented.

Gene Expression of Skeletal Muscle of Red Face Hereford Steers

Bailey Engle, Jennifer Thomson, Jane Ann Boles.
Dept. of Animal Science, Montana State Universtity,
Bozeman, MT.

The objective of this study was to evaluate the relationship between quality grade and genetic growth patterns on meat tenderness. The research sought to elucidate the effect of stage of growth on tenderness. Evaluation of loin samples from 16 different Hereford steers with different growth patterns were collected and allowed to age for 1, 3, 7, 14, and 21 days postmortem and frozen. Tenderness was measured on cooked steaks after each postmortem aging time. Tenderness was evaluated using Warner-Bratzler shear. Muscle samples were taken after death and RNA was extracted from these samples to evaluate which genes were being turned on in the muscle at time of harvest. After harvest, carcasses were quality graded by an experienced grader. Grading of carcasses resulted in six carcasses grading Choice and five carcasses each for Select and Standard. Standard carcasses were significantly lighter, less fat with smaller loin muscle area than the Select and Choice carcasses. Suggesting the steers yielding Standard carcasses were not at the same growth phase as the steers yielding Choice or Select carcasses. Shear force measurements unexpectedly indicated that there was no difference in the tenderness of steaks from Choice and Standard carcasses, while steaks from Select carcasses were significantly less tender. Meat quality and tenderness are two of the most important traits for beef production, and ongoing research will be required in order to gain a better understanding of the genetic and molecular basis of these traits, and how selection and growth interact in these economically significant characteristics.

Identifying a Hydrogen Production Assay for Microorganisms Using a Metal Catalyst and a Chemical Oxidizer

Jessica Hayes, Gereint Sis and Mark Osterlund.
Biology Department, Rocky Mountain College, 1511 Poly Drive, Billings, MT 59102.
jessica.hayes@rocky.edu.

Many microorganisms produce an enzyme called hydrogenase that can combine hydrogen ions (H^+) to make trace amounts of hydrogen gas (H_2). Currently, there is not a sensitive assay available to quickly and efficiently detect hydrogen production by microorganisms. Our research is focused on developing such an assay, specifically using a mixture of a catalyst, a chemical oxidizer, and colorimetric detection system. We

are currently exploring reactions that use platinum as a catalyst in combination with various oxidizing agents. The expectation is that H_2 interacting with the platinum will dissociate into hydrogen atoms. The oxidizer will then release H^+ ions into solution, ultimately lowering pH levels. By testing different oxidizers in combination with platinum nanoparticles, we have identified three potential candidates. One of the oxidizers that proved most useful is potassium ferricyanide ($K_3[Fe(CN)_6]$), which changes from light yellow to dark green after being exposed to hydrogen gas.

Monitoring Algae Growth in the Nanoracks Enclosure on the International Space Station

Kobi Hudson, Tucker Downs.
Rocky Mountain College, Billings, MT.

One major challenge with long term manned space flight is that human beings consume O2 and produce CO2, yet in microgravity environments there are few sustainable solutions for converting CO2 back into O2. Algae are seemingly an ideal candidate for such a conversion; on earth algae grow quickly and are responsible for significant CO2 remediation. However, algae normally grow in liquid media, and, in general, liquids are problematic in microgravity environments. The Algal Growth And Remediation (AGAR) experiment hypothesizes that *Chlorella Vulgaris* grown in agar can produce O2 from CO2 in a microgravity environment.
We have received permission for a 2kg autonomous experiment on the International Space Station (ISS) in a 10x10x15cm slot in a NanoRacks enclosure that uses no more than 0.5a of power at 5V. We hope to confirm growth in the chamber by measuring the change in optical density, the color of reflected/absorbed light from the chamber and the ratio of gases in the (closed) chamber. This research describes the engineering task of designing an appropriate sensor and recording package that can operate under these constraints, while surviving the 11g of vibrations that the experiment will be exposed to in the flight up to the ISS. If the hypothesis is confirmed, it could lead to a significant breakthrough in O2 production in microgravity environments.

Two-Hybrid Analysis of GPM1 and TSA1

Rochelle Johnson, Joy Goffena, and Kurt A. Toenjes
Montana State University - Billings

Candida albicans is an opportunistic and commensal fungal pathogen commonly found within humans. The cell growth of *C. albicans* is either yeast or filamentous/hyphal. It is not understood how the switch to filamentous growth is made as well as its' role within cell growth and morphogenesis. Ubiquitin F-Box proteins, CDC4 and GRR1, play a role in both cell growth and cell morphogenesis. These proteins are found within the SCF complex which acts during the E3 stage of ubiquitation. The SCF complex contains an ubiquitin protein ligase that catalyzes the ubiquitation of proteins destined for proteasomal degradation. CDC4 and GRR1 role in the complex is to direct potential

protein targets to the ubiquitin ligase. Using 2D-Difference Gel Electrophoresis GPM1 was elevated in CDC4 mutant compared to budded and hyphal cells, while TSA1 had two isoforms that were found to be elevated in CDC4 mutant compared to yeast and hyphal cells and other multiple isoforms that were decreased in CDC4 mutant. GMP1 and TSA1 are hypothesized to be potential target proteins of CDC4 and/or GRR1. GMP1 is a phosphoglycerate mutase in glycolysis and gluconeogenesis. TSA1 is a thioredoxin peroxidase that helps with chaperoning proteins under oxidative stress and required for telomere length maintenance. Testing interaction of GMP1 and TSA1 to the F-Box proteins through a two-hybrid approach will give a better understanding as to whether they are "bonafide" target proteins. GPM1 had minimal growth interaction with CDC4 and GRR1. The interaction of TSA1 with CDC4 and GRR1 is still in process.

Estimating Population Density of the White-Tailed Jackrabbit *Lepus townsendii* in Select Central Montana Agricultural Fields

David Kemp and Nate Bickford
Biology Department
University of Great Falls
1301 20th St S.
Great Falls, MT 59405

Historically, the white-tailed jackrabbit *Lepus townsendii* was a prominent mammal of the plains and shrub-steppe regions of North America. However, agriculture and human sprawl appears to have decreased the hare's numbers throughout most of its native range, although little evidence exists to support this claim outside of observations and comparison from historical records. Establishing a baseline population estimate for two agricultural areas in Central Montana was the focus of this study and provided data to expound observations of the hare's reduced presence. Using nighttime spotlight line transect sampling during early winter and early spring seasons over the course of two years, a preliminary population estimate of was established for 2 strata using multiple computations and program DISTANCE 6.0. Sampling revealed distinct variation between populations, with 0.002 hares per ha (DISTANCE 6.0) for stratum 1 and 0.00 hares per ha (DISTANCE 6.0) for stratum 2, respectively. As a significant prey item for several species of concern in the state of Montana, including the golden eagle *Aquila chrysaetos* and swift fox *Vulpes velox*, the white-tailed jackrabbit may be an important aspect of management to be considered when evaluating the status of sensitive species in Montana that prey on the hare.

Creating Genetic Profiles of MITEs in *Chlamydomonas reinhardtii* Using Electrophoresis

Keenan N. Kruger[1] and Mark T. Osterlund[1]
[1]Rocky Mountain College

Miniature Inverted-repeat Transposable Elements (MITEs) are small pieces of DNA known to move within a host's genome. The goal of this project is to develop an assay that creates a profile of MITE distribution within an organism. The organism we are using is *Chlamydomonas reinhardtii* because it contains multiple copies of an active MITE called Gulliver-like. The designed assay requires digesting *Chlamydomonas* genomic DNA with restriction enzymes that do not cut within the Gulliver-like MITE. Digested DNA is then ligated into circularized DNA fragments, some of which should contain MITEs. Polymerase Chain Reaction (PCR) will be performed with primers that hybridize within the MITE sequence, but face outward toward the flanking DNA. PCR should amplify the entire circularized DNA fragment, generating a product whose length is determined by the location of restriction sites flanking the MITE. Multiple PCR fragments should be generated with a single PCR reaction because the same primers should bind to several highly conserved MITEs. Those PCR products can be observed simultaneously through gel electrophoresis with the reproducible combination of bands on the gel representing a genetic profile of Gulliver-like MITEs in *Chlamydomonas.*

Using Spectroscopy for the Early Detection of *Borrelia burgdorferi* Transformants Plated by Limiting Dilution

Dustin Marchant and Todd Marchant
Department of Biology, University of Montana-Western, Dillon, MT.

Borrelia burgdorferi, the causative agent of Lyme disease, is cultured using Barbour, Stoenner, Kelly (BSK) Medium. The detection of cell growth in the liquid medium is facilitated by a pH indicator (Penol Red) that changes color from red to yellow as the pH of the medium changes from 7.6 to 6.8. The change in pH is due to the lactic acid produced as the bacteria ferment sugars. The selection of genetic transformants of *B. burgdorferi* occurs in this same medium. After electroporation, cells are diluted in BSK medium containing the appropriate antibiotic(s) and aliquots of this cell suspension are placed in 96-well plates. The outgrowth of transformants is indicated by color change, which is detected by holding the plates up to a white light source and simply looking. Due to the doubling time of *B. burgdorferi* (8-24 hrs) and limits of the human eye, it can take several days before transformants can be detected (10 21 days is normal). Using a microplate reader to increase the sensitivity of this screening and detect transformants earlier seems logical; however, to our knowledge, this has yet to be done. Therefore, individual wells of 96-well plates were inoculated with BSK medium containing 200 µg/ml kanamycin, 50 µg/ml streptomycin and increasing concentrations of *B. burgdorferi* cells (strain A3-LS-OPK). Daily absorbance readings at a variety of wavelengths were obtained using a Spectra Max Plus 384 microplate reader (Molecular Devices) and analyzed for correlations with cell number using Soft Max Pro 5.2 sofware (Molecular Devices).

Effects of forage availability and temperature on reproductive traits in *Blaberus atropos*

Richelle Marquess, E. Bryson, T. Pegar, J.N. Barron
Department of Biological and Physical Sciences, Montana State University - Billings, Billings, MT.

The ability to be phenotypically plastic to salient environmental cues should increase organisms' fitness. One area of plasticity that should be directly tied to fitness is reproductive allocation. We investigated how variable environments (temperature and forage availability) influenced reproductive allocation in the arthropod *Blaberus atropos* (a Neotropical cockroach). Roaches were purchased from a commercial dealer, and reared until a sufficient number of adult females were produced. Adult females were then placed into one of four treatment groups: high temp/high food; high temp/low food; low temp/high food; low temp/low food. Second and third litters produced while on the treatment conditions were analyzed for: inter-litter interval; offspring number, mean offspring size, and relative clutch mass (RCM the mass of the litter divided by the mass of the post-parturient female). Results indicate that high temperature decreased inter-litter interval significantly, and resulted in smaller litters produced at lower RCM. Forage availability had less of an effect, but by the third litter females from the high forage level showed larger litters and larger postparturient mass. Neither treatment influenced mean offspring size. These results are consistent with predictions from reproductive investment theory.

Prey Densities in Goshawk Nesting Territories

Ryan Martin and Nate Bickford
University of Great Falls

There is some question of nest being abandoned in the Lewis and Clark National Forest due to lack of prey in nest and hunting areas because of over hunting. The lack of prey could be a reason nest sites are abandoned for a few years before being reused. Prey abundance is an important habitat attribute. The potential Prey for goshawks will include bird species in the size range between grouse and woodpeckers, also squirrels, rabbits, and other small mammals.

Availability of goshawk prey may be strongly influenced by forest management practices. More than any other activity these practices will likely determine the long-term persistence of the species. The mechanisms of food limitations are difficult to identify and understand their effects on the populations. To truly manage Eastern Montana Forest for Goshawk population we need to understand the possible effects of food limitations. The change of abundance of certain prey species can dramatically affect goshawk nesting success and consequently the potential use of the nest area in the next year.

For the last two years we have been study prey abundance in Goshawk nesting habitat in Lewis and Clark National Forest

Walleye Larval Distribution in the Missouri River

McKenzie Leonard and Nate Bickford

One of the many fish species that is most interested in the Missouri River is the Walleye, and more particular walleye larvae. The walleye larvae are of interest because not much research has been done on their larvae stage. Also walleye have the ability to impact trout populations so understanding walleye distribution is key knowledge for trout management. Montana FWP want to know where the walleye larvae are located in the Missouri River and if they are flowing over dams. To get an estimate of the walleye larvae population five sites were tested two days a week at various times looking to see how many walleye were coming over the dam. From the five sites it was concluded that not a lot of walleye were coming over the dams, a total of five fish were collected the summer of 2012. From those results it was indicated that more information could be gained because the five fish came from one dam in particular. That dam was Holter, so FWP wanted to look more closely at Holter Dam to see if the numbers varied. The summer of 2013 there were 15 walleye larvae collected. From the information gained it can be indicated that the number of walleye larvae collected did not vary between the two year studies.

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

Elizabeth Mullins, Joy Goffena, David K. Butler, Kurt A. Toenjes
Department of Biological & Physical Sciences
Montana State University-Billings
Billings, Montana

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.

Mutations abrogating siderophore transport in *Pseudomonas aeruginosa*

Shauna Newton, Angela Glassing, and Tom Lewis.
Dept. of Biological and Physical Sciences, Montana State University, Billings, MT

Iron is an essential nutrient for most organisms. In response to limiting iron availability, many microorganisms and plants produce *siderophores*, low molecular weight, excreted molecules with high binding affinity for ferric iron and which allow transport of iron into cells via specific receptors on cell surfaces. Siderophore production is a highly regulated process; in order to minimize the wasteful production of those diffusible, excreted products, bacteria have evolved regulatory systems that allow maximal production only when material is returned to the producing cells. This has been termed signaling. Characterized siderophore signaling processes depend on specific receptors that are also involved in transport of iron:siderophore complexes across the cell envelope. We have observed signaling by the siderophore PDTC (pyridine dithiocarboxylic acid) in mutant strains of the bacterium *Pseudomonas putida* lacking specific PDTC:iron receptors. This work is aimed at determining whether unrecognized receptors are responsible for that signaling, or whether it represents a unique, receptor-independent mode of signaling. We have used the bacterium *Pseudomonas aeruginosa*, an opportunistic human pathogen with well-characterized siderophore transport and signaling systems, as a surrogate host for *P. putida* genes. Our methods are aimed at reconstituting signaling by PDTC in *P.aeruginosa,* a bacterium which does not produce PDTC. In order to test whether conventional, receptor-dependent signaling explains PDTC signaling, we have constructed *P. aeruginosa* mutants lacking TonB energy-transducing proteins necessary for known siderophore transport systems in *P. aeruginosa*. Data presented will include description of those constructs and tests of their ability to respond to purified siderophores using transcriptional reporters.

Determining Coliform and *E. coli* Levels in Pryor Creek

Melinda Obritschkewitsch, Jordyn Eastlick, Shelby Burton, Cristi Hunnes
Rocky Mountain College, Billings, MT

On the Crow Reservation in Southeastern Montana, water quality is a significant concern. Their creeks and rivers serve as sources of water for drinking, agricultural use, sweat lodges and other traditional uses, and recreation. This project focused on the water quality of Pryor Creek near the town of Pryor, MT on the Crow Reservation. There is concern about the impact of the sewage lagoon, located next to the creek, agriculture, and septic systems on the creek. The primary purpose of this project is to monitor coliform and *E. coli* levels in the creek upstream, in the vicinity, and downstream of the sewage lagoon, and in the sacred springs at Plenty Coup State

Park. *E. coli* is indicative of fecal contamination. Secondarily, antibiotic resistance of *E. coli* isolated from the creek is of interest.

Water samples are collected from Pryor Creek every two to three weeks. Samples are kept on ice and taken to the lab at Rocky Mountain College for immediate analysis. The samples are analyzed for coliform and *E. coli* concentrations using the Colilert® Most Probable Number methodology. Periodically, bacteria from water samples are isolated and used in Kirby-Bauer antibiotic susceptibility studies.

Significant coliform and *E. coli* levels have been found. Sites near the sewage lagoon have not proven to be the most contaminated areas. Antibiotic susceptibility tests have been initiated, with tetracycline and streptomycin resistance being observed in some isolates.

Assessing Genetic Diversity Between Bighorn Sheep Populations in the Bitterroot Valley, Montana

Roxy Rademacher, Allison Neils-LeMoine
Classroom Without Walls, Corvallis High School, Corvallis, MT

Genetic diversity is a key component in determining a healthy population (Gutierrez-Espeleta et al, 2000). Low genetic diversity as a result of geographic isolation is a common cause of inbreeding depression, a detrimental phenomenon to populations (Keller and Waller, 2002). Two *O. canadensis* subpopulations in the Bitterroot Valley, Montana are separated by a river, and state highway. Through non invasive sampling methods, we isolated mitochondrial DNA from each subpopulation to run statistical testing on six known *O. canadensis* microsatellite loci. Using the Excel add on GenAlEx, we ran tests to determine F Statistics (inbreeding coefficients), allele frequencies, and allelic patterns across the populations. 47 different alleles were present between the two sub-populations, with a maximum frequency of 0.804 (allele 118). The inbreeding coefficient (F_{IS}) was 0.376, suggesting a reduced level of observed heterozygotes. The fixation index (F_{ST}) was 0.049, indicating little genetic differentiation among each subpopulation. The overall fixation index (F_{IT}) was 0.407. Ultimately, from these results, we have concluded that there is a greater level of genetic differentiation between the two subpopulations than among each subpopulation. Each subpopulation also shows a decreased level of heterozygosity. A reduced level of genetic differentiation among a population coupled with an increased homozygosity can suggest a heightened risk of inbreeding, and therefore inbreeding depression. While these are preliminary results, further study is suggested to provide definitive management implications.

Feasibility, Impact, and Economic Viability of Operating Missoula Aquifer Groundwater Heat Pumps at the Former Champion Sawmill site, Missoula, Montana.

D. Louise Spencer.
Department of Geosciences, The University of Montana, Missoula, MT.

The use of geothermal energy for sustainable heating and cooling is becoming an important option to consider in large residential and commercial developments. Projects are feasible when groundwater yield and temperatures provide for both cooling and heating opportunities. The multi-component analysis includes collecting, compiling and analyzing hydrogeological data, evaluating potential groundwater development logistics and costs, and assessing potential savings and alternatives to the use of heat pumps in proposed structures. I have compiled information about the hydrogeological setting from existing documents and literature and identified data gaps. I am using a 10-shallow-monitoring well network where I have hand measured water level and temperature profile data. I have installed pressure transducers in 6 wells to monitoring water level and temperature changes seasonally. Aquifer properties have been derived from previous studies. Extraction and injection well designs will be completed and installation costs and operations will be determined using local construction estimates. I will obtain building specifications, including heating and cooling requirements of the development and perform an economic analysis. It is anticipated that building heating and cooling at this site will be both physically and economically viable.

Bio-Vegetation Survey of the MacDonald Gold Prospect, Lewis and Clark County, MT

Scott Thielman
Simms High School, Simms, MT

There are many ways to prospect for gold. These methods include panning, rock chip sampling, soil samples, stream sediment samples, water samples, and vegetation samples. Rock sampling is useful when the ore body is exposed. Vegetation surveys are useful when the ore body is buried beneath overburden or blind. The purpose of this research is to determine if bio-vegetation surveys can be used to detect a blind gold deposit. Samples were collected from stems and needles of Ponderosa Pine trees over mineralized and unmineralized areas. They were analyzed for gold and selected pathfinders. Gold increased in both stems and needles from unmineralized to mineralized areas. Pathfinders such as silver and thallium had mixed results. Gold is the best indicator for a blind deposit using stems or needles from Ponderosa Pine trees.

Cost Benefit of Cattle on Public Lands

Marilyn Wright, Sonja Bickford, and Nate Bickford

The United States Forest Reserves were originally established to protect the country's

timberlands and watershed (USFS, 2013) with the goal of preserving some of the most beautiful and unique habitats across the states. Despite this ardent dedication to the natural world and its preservation as well as commitment to American citizens, nearly half of all National Forest land, around 90 million acres across 34 states, has been divided into grazing allotments for domestic livestock (Thompson, 2004). Though the Forest Service states a primary objective of the range management program is, "To manage range vegetation to protect basic soil and water resources, provide for ecological diversity, improve or maintain environmental quality, and meet public needs for interrelated resources use (USFS, 2013)," they have failed to meet this objective and thus have contributed to the degradation of the ecological integrity of the National Forest nationwide shown through extensive research on rivers, riparian zones, forest vegetation, and wildlife. By examining the effects of domesticated ungulates on these important areas, it is possible to quantify the damage, making the devastation more real and tangible to the general public. A cost benefit analysis was prepared to demonstrate the problem associated with the unsustainable practice of turning protected lands into grazing plots. By examining the numbers, it is evident that domestic ungulate grazing is causing far more harm overall than it is worth.

Translational regulation by codon usage bias in the human disease familial dysautonomia.

Avery E. Hanson[1], Lynn George[1], and Frances Lefcort[2]
[1]Department of Biology, Montana State University-Billings, Billings, MT 59101
[2]Department of Cell Biology and Neuroscience, Montana State University, Bozeman, MT 59717

Familial dysautonomia (FD) is a devastating human disease affecting the peripheral nervous system. The disease is characterized by the severe depletion of neurons in both the sympathetic and dorsal root ganglia, in part due to aberrations in cell-cycle progression. The molecular origin of FD is a mutation in the gene encoding the protein IKAP, a subunit of the "Elongator" complex, which plays a pivotal role in tRNA modification and the translation of functionally related families of genes. In yeast, genes required for mitotic progression have been shown to be Elongator dependent. Using a murine model for FD, our goal is to demonstrate a role for IKAP in the translation of these same cell-cycle progression genes in mammalian neurons and glia.