

Program in Ecology Student Research Symposium

February, 16th 2018

Berry Biodiversity Conservation Center,
University of Wyoming, Laramie Wyoming

#SymPiEsium2018

Oral and Poster Presentation Abstracts



Schedule Overview

Friday, February 16th	
12:20pm–12:50 pm	Opening Remarks: Dr. Gary Beauvais , Director of the Wyoming Natural Diversity Database; Dr. Merav Ben-David , outgoing Director of PiE
12:50 pm–1:45 pm	Keynote Talk: "The role of adaptation in speciation: a comparative, integrative perspective" by Dr. Rebecca Safran ; Associate Professor in Ecology and Evolutionary Biology at the University of Colorado, Boulder
1:45 pm–2:00 pm	Break
2:00 pm–3:15 pm	Session 1: Student Speakers Lisa Barrett, Gabe Barrile, Courtney Duchardt, Kristina Harkins, and Chloe Mattilio
3:15 pm–3:30 pm	Break
3:30 pm–4:45 pm	Session 2: Student Speakers Libby Megna, Elizabeth Traver, Rebecca Upjohn, Rebecca Wilcox, and Megan Wilson
4:45 pm–5:00 pm	Closing Remarks: Dr. Mark Clementz , incoming Director of PiE
5:00 pm–6:00 pm	Poster session Gordon Custer, Jimena Golcher-Benavides, Michele Larson, Liana Lynch, Hilary Madinger, Bryan Maitland, Kennan Oyen, Jessica Rick, and Lauren Stanton
6:00 pm–7:00 pm	Dinner
7:00 pm	Awards for best student talk and poster
7:30pm	Silent auction closes

Keynote Speaker: Rebecca Safran

Our guest keynote speaker, Dr. Rebecca Safran, is currently an Associate Professor in the Department of Ecology and Evolutionary Biology at the University of Colorado, Boulder. Her research focuses on the interactions between phenotype and behavior and how these shape patterns of variation, using barn swallow populations as her main study system. Dr. Safran's innovative work also examines the role of sexual selection in adaptation and reproductive isolation.

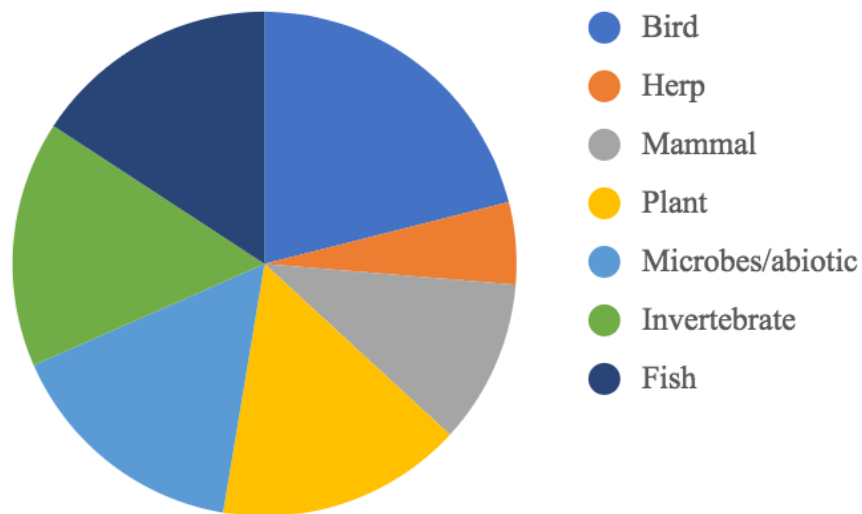
About PiE and the symposium

The Program in Ecology (PiE) is an interdepartmental cross-college doctoral program that provides advanced, integrated training in the science of ecology. PiE is the largest interdisciplinary PhD program at the University of Wyoming that includes 42 faculty, 21 affiliates, 45 current students and 39 alumni.

Departments with faculty in PiE (* indicates student(s) presenting today)

Botany*
Ecosystem Science and Management*
Haub School of Environment and Natural Resources
Geography and Recreation
Geology and Geophysics
Mathematics
Molecular Biology
Philosophy
Plant Sciences*
Veterinary Sciences
Zoology and Physiology*

Slicing up the PiE (Symposium) 2018



ORAL PRESENTATIONS

TIME	2:00	Personality and problem solving in zebra finches
		<u>Lisa Barrett</u> ¹ and Sarah Benson-Amram ¹ ¹ Program in Ecology and Department of Zoology & Physiology, University of Wyoming
		<p>Abstract</p> <p>Individual differences in how animals respond to their physical and social environments represent a new and exciting area of research within the field of behavioral ecology. Animal personality, defined as individual behavioral responses that are stable over time or context, is pervasive across the animal kingdom and has substantial effects on fitness. Personality may also interact with other traits, such as cognition, to impact how animals respond to and solve novel problems. For example, bolder individuals may learn to solve a novel task more quickly than shy individuals. Previous studies have shown an effect of both personality and cognition on mate choice and reproductive success. Zebra finches (<i>Taeniopygia guttata</i>) are a model species for studies of personality, cognition, and mate choice, yet we lack an understanding about how personality and cognition interact in this species. We present preliminary results of 40 birds' performances on personality and problem-solving assessments. We investigate whether there is evidence of repeatable individual differences in personality assessments, examine sex differences in personality and cognitive abilities, and identify which personality traits influence performance on problem-solving tasks. We conclude by describing the next phase of this research, which will investigate performance of dissimilar and similar personality pair bonds of zebra finches on cognitive tasks requiring coordination of pair members.</p>
TIME	2:15	Habitat use and body temperature influence boreal toad disease risk in western Wyoming
		<u>Gabe Barrile</u> ¹ , Anna D. Chalfoun ² , and Annika Walters ² ¹ Wyoming Cooperative Fish and Wildlife Research Unit, Department of Zoology and Physiology, University of Wyoming ² US Geological Survey, Wyoming Cooperative Fish and Wildlife Research Unit, Department of Zoology and Physiology, University of Wyoming
		<p>Abstract</p> <p>Emerging infectious diseases pose a significant threat to global biodiversity. <i>Batrachochytrium dendrobatidis</i> (Bd), an emerging fungal pathogen primarily affecting amphibians, is of particular concern because it has caused severe population declines and several extinctions in amphibian populations worldwide. Prior research has stressed the importance of host body temperature and environmental conditions on Bd prevalence; however, it remains unclear how host behavior (e.g., habitat use) influences body temperature, ultimately affecting Bd growth. To better understand the link between amphibian behavior, host thermal biology, and disease risk, we examined the influence of individual habitat use and body temperature on Bd infection rates in boreal toads (<i>Anaxyrus boreas boreas</i>). In the summer months of 2015 and 2016, we used radio-telemetry to study the habitat use of adult boreal toads (n=100) on the Bridger-Teton National Forest in western Wyoming. In a subset of toads (n=42), we recorded body temperature during each tracking event and swabbed each individual for Bd on five separate occasions to develop a disease history through time. Warmer body temperatures significantly decreased the probability of Bd infection,</p>

particularly when body temperatures exceeded 25°C. Toads that used habitats with low shrub cover and high sedge cover had significantly higher body temperatures and these habitats were associated with a lower probability of Bd infection. We demonstrate that individual habitat use can influence disease risk, with strong support that body temperature acts as the mechanism to lower infection probability. Identifying habitats that lower disease risk will provide valuable information to several agencies working to improve management of boreal toad populations in Wyoming. More broadly, by developing a better understanding of how habitat influences body temperature and ultimately amphibian-Bd interactions, our results will help inform amphibian conservation worldwide.

TIME 2:30 “Digging in” to the importance of prairie dogs for breeding mountain plover habitat on a grassland-sagebrush ecotone

Courtney J. Duchardt^{1,2}, Jeffrey L. Beck^{1,2}, and David J. Augustine³

¹Program in Ecology, University of Wyoming

²Department of Ecosystem Science and Management, University of Wyoming

³Rangeland Resources Research Unit, USDA-ARS

Abstract

Black-tailed prairie dogs (*Cynomys ludovicianus*) are “ecosystem engineers”, clipping vegetation to maintain the short, sparse habitat structure required by many wildlife species in North America. One such species is the mountain plover (*Charadrius montanus*), a shortgrass bird declining throughout its range. Although mountain plovers will use many different habitats if adequate bare ground is available (e.g., recent burns, early-season croplands), along the wetter eastern edge of its range it is partially restricted to prairie dog colonies. This is the case in the Thunder Basin National Grassland (TBNG), located on the ecotone between the Great Plains and sagebrush steppe. The TBNG contains some of the largest prairie dog colonies remaining, providing a unique opportunity to examine how plovers respond to the size, shape and vegetation cover within colonies. We examined densities, nest-site use and nest success of mountain plovers across a range of colony sizes in the TBNG from 2015-2017. Observations of plovers were restricted to black-tailed prairie dog colonies, confirming their reliance on prairie dogs.

Abundance and distribution of plover nests varied across prairie dog colony sizes and ages, but plovers did not preferentially nest in very large colonies. This information is especially pertinent given the grassland must also provide undisturbed sagebrush for species like the greater sage-grouse (*Centrocercus urophasianus*), and adequate forage for livestock grazing.

TIME 2:45 It’s a trap: approaches for detecting rare small mammals

Kristina Harkins¹, Merav Ben-David¹, Doug Keinath²

¹Department of Zoology and Physiology, University of Wyoming, Laramie, WY 82071

²U. S. Fish and Wildlife Service, Cheyenne, WY 82009

Abstract

Many species of small mammals are considered rare largely because they are difficult to detect on the landscape. Such species will therefore require specific survey methods to optimize their detection. Most studies of small mammals follow a similar protocol that includes trapping a relatively small area with Sherman live traps and using a peanut-butter- oat mix for bait. As part

of a larger study focused on delineation of the distribution of rare pocket mice (*Perognathus spp.*) across Wyoming, we tested a new protocol designed to maximize the capture success of these small mammals. We also determined trap and bait preferences of different species. We used three trap types: Sherman, Havahart, and Longworth set at 25m intervals along four transects of 20 stations each. We baited each station with one of three different bait types in an alternate fashion: peanut butter and oat mix, three-way horse feed with molasses, and roasted bird seed. We found that overall selection was highest for Havaharts baited with either peanut butter or bird seed, while Shermans baited with horse feed were avoided by all species. Havaharts were the preferred trap for the species that had the highest capture rates including deer mice (*Perognathus maniculatus*), Ord's kangaroo rats (*Dipodomys ordii*), harvest mice (*Reithrodontomys spp.*), olive-backed pocket mice (*Perognathus fasciatus*), voles (*Microtus spp.* and *Lemmiscus curtatus*), least chipmunks (*Tamias minimus*), thirteen-lined ground squirrels (*Ictidomys tridecemlineatus*), and northern grasshopper mice (*Onchomys leucogaster*). Bait preference significantly varied by species with pocket mice exhibiting strong selection for bird seed. Detection of pocket mice was greatly increased in traps baited with bird seed bait rather than peanut butter. These results can be used to develop species-specific capture protocols for future studies.

TIME 3:00 **Untapped potential: forest site factors and sap sweetness in birches**

Chloe M. Mattilio^{1,2} and Dr. Celia A. Evans²

¹Program in Ecology & Plant Science Department, University of Wyoming

²S-STEM Program, Paul Smith's College

Abstract

Two birch species (*Betula papyrifera* and *Betula allegheniensis*), the two most commonly tapped birches in North America, were tapped at two sites of different fertility in the Northern Adirondacks to examine the relationship between site factors and sap quality. Sites were described by their soil base cation content, soil pH, and community structure while sap was analyzed for nutrients and sugar content. Forty sap samples were collected in the spring of 2016 and forty soil samples were collected in the fall of 2016 to determine some site characteristics that may indicate higher quality birch sap. Sap samples were analyzed using an inductively coupled plasma spectrophotometer (ICP) and a Brix refractometer. Soil samples were analyzed using ICP, as well as a pH meter. Differences in sample tree DBH, soil nutrient content, and sap sweetness were found between the two sites. Paper birch sap was found to have higher levels of Ca, K, and Mg in the sap, while yellow birch had higher levels of sap Na. There was no significant difference in sweetness (Brix) between the two species. Sap sweetness, however, was correlated with sample tree DBH, soil pH, soil Ca content, and soil Na content. Recommendations for improving birch sap quality for sugarbush managers and landowners are to select paper birch over yellow birch, to carefully consider, and ideally test soil fertility before choosing tap trees.

TIME	3:30	Genome-wide patterns of divergence in <i>Passerina</i> and <i>Cyanocompsa</i> buntings
		<u>Libby Megna</u> ¹ , Matthew D. Carling ¹ ¹ Program in Ecology and Department of Zoology and Physiology, University of Wyoming
		<p>Abstract</p> <p>Recently, genomic datasets have been harnessed to elucidate the underlying genetic architecture of speciation and thus can illuminate important evolutionary processes. Here, we take a novel approach to correlate patterns of genome-wide divergence with degree of reproductive isolation among three closely related species pairs within Cardinalidae (Aves: Passeriformes). These species pairs represent varying degrees of reproductive isolation (hybridizing vs. non-hybridizing) and different geographic relationships (allopatric vs. sympatric). Our study provides empirical data to inform theory of genome-wide divergence by making comparisons of 1) different geographic outcomes of speciation, and 2) different levels of reproductive isolation upon secondary contact. We first generated a reference genome for <i>Passerina amoena</i>. Our sequencing generated ~760 million reads; the resultant assembly is 0.92 Gb with a contig N50 of 62.7 kb. We will align whole-genome resequencing data (~1.5 billion reads) from 56 individuals of <i>P. amoena</i>, <i>P. cyanea</i>, <i>P. ciris</i>, <i>P. versicolor</i>, <i>Cyanocompsa parcellina</i>, and <i>C. brissonii</i> to this reference. <i>P. amoena</i> and <i>P. cyanea</i> hybridize extensively in the Great Plains, while <i>P. ciris</i> and <i>P. versicolor</i> do not hybridize despite sympatry in Texas and Mexico. The <i>Cyanocompsa</i> species are completely allopatric. We will quantify patterns of genome-wide divergence for these species pairs and identify specific genomic divergence patterns associated with degree of reproductive isolation by comparing among species pairs. For example, comparing the location of divergence peaks between the hybridizing, sympatric species pair to those between the non-hybridizing, sympatric species pair will allow us to investigate how gene flow impacts patterns of genome-wide divergence.</p>

TIME	3:45	Soil properties and microbial activity in newly-formed soils at the retreating Dinwoody Glacier, WY
		<u>Elizabeth Traver</u> ¹ , Linda van Diepen ¹ , Anna Robinson ² ¹ Program in Ecology and Department of Ecosystem Science and Management, University of Wyoming ² University of Wyoming
		<p>Abstract</p> <p>As glaciers retreat in many parts of the world they leave behind newly exposed land where soil begins to develop. The recently exposed material is composed of mostly minerals from the crushed and broken rocks, but, very quickly, organic material from microbes and plant matter interact with the minerals and soil starts to form. From similar research work in other parts of the world, the older soils had a higher organic matter content, which was likely linked to active plant communities and microbial activity. In addition, pH tended to go down with age, and the microbes which are able to break down N and more complex C sources increased with older soils. At the Dinwoody Glacier, in the Rocky Mountains, we collected soil samples along a chronosequence from the current toe of the glacier to the Little Ice Age moraine, which is about 160 years old, a distance of just over one kilometer. Across five transects, that parallel the toe of</p>

the glacier, we collected replicate soil samples covering the width of the glacier. Organic matter (OM) increased with age of soil, while pH did not follow a trend. However, there was a slight decrease in electrical conductivity (EC) with soil age. Using enzyme activity to evaluate the soil for microbial functional groups as well as more specific microbial families or species will allow us to determine how microbial communities and associated activities change through time since exposure to light and heat. Other research suggests that microbial communities proceed through succession like plant communities but soil pH and in-situ nutrients play important roles for driving that succession.

TIME 4:00 **Species-specific nutrient limitation influences response to altered nutrient availability**

Rebecca Upjohn¹, Tim Collier¹, and Brian Mealor²
¹Ecosystem Science and Management
²Department of Plant Sciences

Abstract

Nitrogen-fixing exotic species, such as Russian olive (*Elaeagnus angustifolia*), may shift nutrient availability within invasions from nitrogen (N)-limited to phosphorus (P)-limited systems over time, which may constrain native plant growth. Altered nutrient availability can persist for several years after removal of the exotic species, complicating recovery or restoration of the system. Determining how native species respond to altered nutrient availability is essential for understanding changes in species composition as a result of exotic plant invasion and selecting appropriate species for restoration of previously invaded areas. Recent theory suggests that plant functional traits may be a useful tool for understanding plant responses to nutrient limitation. Using a greenhouse experiment, I examined the response of three native shrub species (*Ribes aureum*, *Rhus trilobata* and *Shepherdia argentea*) to varying levels of P at low and high N availability both in terms of growth (biomass) and a commonly assessed plant functional trait, Specific Leaf Area (SLA). My results indicate that nutrient limitation is ultimately species-specific, with *R. trilobata* responding primarily to P addition while *R. aureum* and *S. argentea* responded to N addition. Though SLA is often used to indirectly measure nutrient limitation, my data challenges this assumption by demonstrating an inconsistent relationship between SLA and total biomass, a direct and reliable measure of nutrient limitation.

TIME 4:15 **Temporal variation in movement patterns impact the seed dispersal potential of exotic species; evaluating exotic dispersers in a novel ecosystem**

Rebecca Wilcox¹ and Corey Tarwater¹
¹Program in Ecology and Department of Zoology and Physiology, University of Wyoming

Abstract

Seed dispersal is a critical ecosystem function for maintaining the structure and diversity of ecosystems. In vertebrate-dispersed systems, seed dispersal is a unique mutualism that relies on temporal and spatial overlap between long-distance dispersal events and plant fruiting phenology to function properly. Reduced dispersal can result in decreased seedling survival and limit plant distributions. However, we often ignore temporal variation in movement and its impact on seed dispersal potential when evaluating these interactions. This is particularly

important in novel ecosystems where exotic dispersers and native plants have not co-evolved, and decoupling between plant fruiting phenology and long-distance events is likely to occur. Here we examined three key avian dispersers on the island of O‘ahu, Hawai‘i where all of the native dispersers have gone extinct. The Japanese white-eye (*Zosterops japonicus*), red-billed leiothrix (*Leiothrix lutea*), and the red-whiskered bulbul (*Pycnonotus jocosus*) range in their body size, gape size, diet preference, and density. We sought to determine if there was temporal variation in movement for these three species and what extrinsic (precipitation) and intrinsic (age, sex, breeding season and body size) factors might explain that variation. We examined disperser movement by radio-tracking 90 individuals (523 observation hours) between August 2015-July 2017. We found that Japanese white-eye and red-whiskered bulbuls showed temporal variation in movement patterns. We also found that on average males tended to move shorter distances during the breeding season than the non-breeding season. Our study indicates that understanding interspecific differences and factors that influence temporal variation in disperser movement is critical for understanding the impact invasive dispersers have on native plant communities.

TIME 4:30 Assessing reclamation success by measuring ant and beetle recolonization on oil and gas well pads in the Pinedale Anticline, Wyoming

Megan E. Wilson¹ and Timothy Collier¹

¹Program in Ecology and Ecosystem Science and Management, University of Wyoming

Abstract

Wyoming’s economy is largely supported by energy and mineral extraction. Due to the vast and growing nature of natural resource extraction, Wyoming rangelands are increasingly becoming degraded and fragmented ecosystems. The degraded land is reclaimed with the intent to restore the health, integrity and sustainability of the ecosystem. The majority of current restoration practices address plant communities and the wildlife but does not necessarily address community structure of other keystone species, such as invertebrate populations. We addressed ground dwelling ant and beetle recolonization utilizing a chronosequence on oil and gas well pads in the Pinedale Anticline, Wyoming. Preliminary data has shown that ants return to the landscape 10 years post reclamation while beetles recolonize more quickly 1-3 years post reclamation. Many invertebrates such as ants and beetles are essential for survival of other important wildlife, including important bird species as the Greater Sage Grouse. If ground dwelling invertebrate populations are not returning to the landscape, there are serious repercussions for the ecological integrity of the reclaimed site.

POSTER PRESENTATIONS

Poster #1	<p>Structural and functional dynamics of soil microbes following spruce beetle infestation</p> <p>G.F. Custer^{1,2,3}, W. Stump², and L.T.A. van Diepen^{1,3}</p> <p>¹Program in Ecology, University of Wyoming</p> <p>²Department of Plant Sciences, University of Wyoming</p> <p>³Department of Ecosystem Science and Management, University of Wyoming</p>
<p>Abstract</p> <p>Increased mean annual temperatures coupled with management regimes of our national forests have produced conditions conducive to widespread bark beetle induced mortality. This study focused specifically on the Spruce beetle (<i>Dendroctonus rufipennis</i>) and its host, Engelmann spruce (<i>Picea engelmannii</i>). Upon tree death, the soil environment undergoes changes with respect to nutrient availability. The large one-time input of nitrogen rich needles has been shown to effect nutrient cycling by microbes. However, information regarding the effects of beetle kill on belowground microbial communities is lacking. The goal of this study was to investigate the dynamics of microbial community structure and function following beetle kill using a chronosequence approach, in Southeastern Wyoming. Our study demonstrated changes in soil microbial dynamics, causing increased extracellular enzymatic activity following beetle infestation and turnover of the fungal community, represented by lower proportional abundances of ectomycorrhizal fungi (ECM) as well as a relative increase in saprotrophic taxa in dead stands. The bacterial community also changed as infestation progressed. Our findings show the soil environment to be dramatically affected by bark beetle infestation; as demonstrated by increased microbial decomposition and decreased abundance of ECM both of which could affect forest regeneration following disturbance. Despite the large amount of data generated, meaningful conclusions from high throughput community data are difficult, due to gaps in the microbial databases related to taxonomic identity and associated function; a factor which needs immediate attention if scientists wish to fully utilize microbial community datasets.</p>	
Poster # 2	<p>Examining patterns of local community diversity within an adaptive radiation</p> <p>Golcher-Benavides, J.^{1,2}, McIntyre P.B.^{4,5}, and C.E. Wagner^{1,2,3}</p> <p>¹Program in Ecology and Department of Botany, University of Wyoming, Laramie WY</p> <p>²Department of Botany, University of Wyoming, Laramie WY</p> <p>³Biodiversity Institute, University of Wyoming, Laramie WY</p> <p>⁴Center for Limnology, University of Wisconsin-Madison, Madison WI</p> <p>⁵Department of Natural Resources, Cornell University, Ithaca NY</p>
<p>Abstract</p> <p>Ecological and evolutionary mechanisms underlie patterns in functional and phylogenetic diversity of species. Resource availability are commonly implicated as the causes of increased species richness and total abundance in ecological communities via two contrasting mechanisms: (1): higher resource supply promotes specialization resulting in finer-scale niche partitioning and increased coexistence of functionally dissimilar species, or (2) increased resource supply promotes greater coexistence through a relaxation of competition, resulting in greater coexistence of more</p>	

functionally similar species. In systems where much of the diversity present has evolved in situ, uniting ecological and evolutionary approaches in studying diversity is particularly crucial. We here focus on the littoral fish community of Lake Tanganyika, where over 86% of the species are endemic. Steep bathymetric gradients in this lake result in a rapid decrease in light penetration with water depth, concentrating bio-available habitat and primary production in shallow waters. Using community survey data, we studied the depth distributions of species within these communities via rarefaction techniques and link these data to the genetic relatedness of species, as well as their eco-morphological and dietary diversity. We find evidence for increased coexistence and fine-scale niche partitioning with greater resources. Using taxonomic information and phylogenetic comparative analyses, we unveiled a positive relationship between resource availability and increased coexistence of more functionally similar, closely related species within communities, providing support for more specialization with higher resource availability. These results speak to the value of furthering our understanding of the interaction of ecological and evolutionary processes in understanding the diversity of species-rich communities.

Poster # 3 **The biogeochemical niche of an invasive snail differs from co-occurring native snails**

Michele Larson¹ and Amy Krist¹

¹Department of Zoology and Physiology, University of Wyoming

Abstract

The invasive New Zealand mud snail (*Potamopyrgus antipodarum*) tolerates a wide range of abiotic environmental conditions including temperature and salinity. Yet, less is known about other aspects of the biogeochemical niche (the biotic and abiotic factors occupied by aquatic organisms) of this invasive snail and coexisting native mollusks. We conducted a field survey to assess the biogeochemical niche of native and invasive freshwater mollusks by collecting samples above and below geothermal inputs in five rivers. We also examined the effect of low conductivity on growth and mortality in the invasive and two native snails in a laboratory experiment. For the field survey, we found that density of *P. antipodarum* was positively associated with specific electrical conductivity, ions, elevation, and stream width. Additionally, we found weak statistical support for pH and stream flow positively affecting density of *P. antipodarum* and calcium ions, mollusk richness, and bivalve density negatively affecting density of the invasive snail. In contrast, density of native snails, density of native bivalves, and mollusk richness were not predicted by any of the biotic or abiotic factors that we measured. Our conclusion that the biogeochemical niches of the invasive snail and native mollusks differ was also supported by the laboratory experiment: lower conductivity decreased growth and increased mortality in *P. antipodarum*, but did not affect two native snails. Thus, native mollusks and *P. antipodarum* appear to have different niches with more restrictive biogeochemical conditions required by *P. antipodarum* which may limit the distribution of this invasive species to regions with sufficient electrical conductivity.

Poster # 4 **Relationship between tree seedling recruitment and nutrient availability, enzyme activity, and environmental factors following bark beetle infestation**

Liana Lynch¹, Urszula Norton¹, Linda van Diepen²

¹Program in Ecology and Department of Plant Sciences, University of Wyoming

²Program in Ecology and Department of Ecosystem Science and Management, University of Wyoming

Abstract

Recent outbreaks of bark beetles (*Dendroctonus* spp.) epidemics and associated tree death caused by blue stain fungus (*Grosmannia clavigera*), have caused extensive forest mortality across the western United States. These events have shown to affect belowground biogeochemical processes which include temporary changes to soil organic matter (SOM) accumulation and nutrient cycling. The new knowledge on the ecosystem processes during post- beetle forest recovery over the past ten years have identified the emerging role of the soil microbes in as critical drivers of ecosystem health and function. Plant-microbe relationships are important in successful young tree growth in undisturbed forests as they facilitate release of soil nutrients from SOM and on the other hand, SOM stabilization. Yet, the microbe-plant relationships are not well understood in the post-beetle forest die-off. Moreover, published research and our data collected at the No Name watershed in Medicine Bow-Routt National Forest suggest the tree seedling recruitment and young tree survival in numbers far exceeding the seedling numbers in in beetle- affected forests compared with uninfested forests. The main objective of our study is to evaluate feedbacks between the dynamics of the soil microbial community and seedling recruitment after bark beetle infestation. We collected soil from locations with a 30% beetle kill infestation level on each of the three slopes on the mountain. The cores were taken in between the mature and immature trees to understand how the mature trees, and associated microbes and nutrient cycling, affect the regeneration of the forest. Nutrient availability, enzyme activity of the microbial community, and environmental factors were assessed to help us understand how regeneration changes after the bark beetle outbreak. My future research will contribute to our understanding how microbial communities change after disturbance and how these potential changes are related to natural forest regeneration through seedling recruitment and establishment.

Poster # 5 **Measuring diel stream nitrogen fixation**

Hilary L. Madinger¹ and R. O. Hall Jr.²

¹Program in Ecology and Department of Zoology and Physiology, University of Wyoming

²University of Montana

Abstract

Nitrogen fixation can contribute large fluxes of dissolved nitrogen gas (N₂) into aquatic biofilms, frequently in low nitrate streams. In marine ecosystems nitrogen fixation can occur only at night, only during the day, or continuously. We investigated nitrogen fixation patterns using microcosms over a 30h period to determine when nitrogen fixation occurs. Additionally, we used three methods to measure nitrogen fixation to evaluate the utility of each technique. All techniques showed freshwater stream nitrogen fixation occurs primarily during the day. Measuring the flux of dissolved gases allowed paired measurements of photosynthesis and nitrogen fixation. ¹⁵N₂ isotopes measured the total incorporation of N₂ into biofilms with similar results to the dissolved gas fluxes. Acetylene reduction measured diel nitrogen fixation but variation was largely due to differing temperatures. Gas flux and isotopic measurements of nitrogen fixation represent better estimates of diel nitrogen fixation.

Poster # 6 **Niche expansion and partitioning in stream fish assemblages along longitudinal stream gradients**

Bryan M Maitland¹ and Frank J Rahel¹

¹Program in Ecology & Dept. Zoology and Physiology, University of Wyoming

Abstract

Understanding how emergent properties of food webs (e.g., assemblage niche breadth and overlap) change in response to environmental conditions is necessary for predicting the effects of human alterations on species and ecosystems. Stream food webs are expected to change along longitudinal gradients. The Niche Expansion Hypothesis posits that assemblage-level trophic structure in fish manifests in response to longitudinal stream gradients, predicting that from upstream to downstream, the breadth of trophic resources used by assemblages will increase, as will niche partitioning among species. But recent empirical tests of this hypothesis have shown mixed results. Here, we test the Niche Expansion Hypothesis along longitudinal gradients in mid-order Rocky Mountain—Great Plains streams. We generated a composite predictor variable representing longitudinal gradients in four Wyoming streams using PCA based on in-stream and GIS-derived environmental data. We calculated structural metrics (i.e., assemblage composition, consumer richness, and density) and used stable isotope analysis to estimate assemblage-level dietary niche breadth and overlap. We found that non-native salmonids and centrarchids dominate upstream and downstream reaches, respectively, with native cyprinids and catostomids predominantly observed in mid-gradient reaches. Generalized linear models revealed fish species richness, but not fish density, is positively related to the longitudinal gradient. With respect to food webs, preliminary data suggest assemblage-level trophic niche expansion moving downstream, with concomitant decreases in within- assemblage niche overlap. These findings show the longitudinal gradient has a complex effect on aquatic food webs; it constrains consumer diversity and affects species' niche breadth, with implications for niche partitioning and thus species co-occurrence. Assessing this variation is important for stream restoration and conservation strategies.

Poster # 7	Critical thermal limits of bumble bees (<i>Bombus impatiens</i>) are marked by stereotypical behaviors and are unchanged by acclimation, age, or feeding status
	K. Jeannet Oyen ¹ & Michael E. Dillon ¹ Department of Zoology and Physiology & Program in Ecology, University of Wyoming
	<p>Abstract</p> <p>Critical thermal limits often determine species distributions for diverse ectotherms, and have become a useful tool for understanding past and predicting future range shifts in response to changing climates. Despite recently documented population declines and range shifts of bumble bees (genus <i>Bombus</i>), the few measurements of thermal tolerance available for the group have relied on disparate measurement approaches. We describe a novel stereotypical behavior expressed by bumble bee individuals during entry into chill coma. This behavioral indicator of CT_{min} (~3-4°C) was accompanied by a pronounced CO₂ pulse, indicative of loss of spiracle function. CT_{max} averaged ~52-55°C and was indicated by the onset of muscular spasms prior to entering an unresponsive state. Measurements of CT_{min} and CT_{max} were largely unaffected by acclimation, age, or feeding status, but faster ramping rates significantly increased CT_{max} and decreased CT_{min}. This high-throughput approach allows rapid measurement of critical thermal limits for large numbers of bees, facilitating large-scale comparisons among bumble bee populations and species – a key step in determining current and future effects of climate on these critical pollinators.</p>

Poster # 8	Inter- and intraspecific genetic relationships among <i>Lates</i> species in Lake Tanganyika, East Africa
	Jessica A. Rick ¹ , Catherine E. Wagner ¹ ¹ Program in Ecology and Department of Botany, University of Wyoming
	<p>Abstract</p> <p>Africa's Lake Tanganyika (LT) is an exemplary study system for investigating the effects of environmental factors on evolution due to its diverse endemic species radiations and well-studied limnological history. Four LT-endemic Lates fishes (<i>Lates stappersii</i>, <i>L. mariae</i>, <i>L. microlepis</i>, <i>L. angustifrons</i>) are top predators in the lake's pelagic zone that have declined in recent years due to environmental and anthropogenic factors. The Lates species are key components of the LT ecosystem, yet little is known about their evolutionary history and no published genetic work exists for these fishes. I am using these fish as a model for understanding the interplay between population dynamics, environmental change, and diversification over deep timescales. As a first step toward this goal, I have generated reduced-representation genotyping-by-sequencing (GBS) data and whole genome sequences for several individuals from each of these species, to determine how distinct the four species are from one another. In addition, I am analyzing these preliminary data to determine where there is any detectable genetic population structure within each species.</p>

Poster # 9

Methodological development for the study of cognition in the wild

Lauren Stanton¹ and Sarah Benson-Amram¹

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Abstract

Anthropogenic disturbance of the environment is creating novel challenges that wild animals have not experienced in the past. Altering individual behavior in response to novel challenges, such as in resource selection, communication, and vigilance, can facilitate successful adaptation. Animals may therefore rely on cognitive abilities, such as learning, problem solving, and behavioral flexibility, to insure their survival and exploit new opportunities resulting from anthropogenic disturbance. Despite decades of research on animal cognition, however, we are far from understanding the relationship between cognition and contemporary behavioral adaptation. This is because it is difficult both to assess cognition in wild animals and to standardize tests of cognition across multiple species. A lack of adequate tools and methodologies remains one of the largest hindrances for the fields of animal behavior and cognition, impeding not only the advancement of these disciplines, but also any applied knowledge that could be used in the management of wildlife. Here we present progress made towards the development of new methodologies that can be used to study comparative cognition in the wild. We employ advanced technologies to identify and monitor wild mesocarnivores in Laramie, WY. To assess cognition, we blend both traditional and modern cognitive testing approaches to collect data on learning, problem solving, and behavioral flexibility. Each method described presents certain advantages and disadvantages, along with unexpected challenges and opportunities. Our research is not only advancing the study of animal cognition as a discipline, but also addressing important hypotheses regarding the role of cognition in behavioral adaptation to anthropogenic disturbance.