24th Annual
Oregon State University
Biology Graduate Student Symposium

Mark O. Hatfield Marine Science Center
Newport, Oregon

January 29, 2011

Symposium Organizers:

Casey Benkwitt (Dr. Hixon Lab)
Sarah Close (Dr. Menge Lab)
Kelly Farrell (Dr. Maddison/Dr. Borer Lab)
Chris Friesen (Dr. Mason Lab)

Angela Poole (Dr. Weis Lab)
Kojun Kanda (Dr. Maddison Lab)
Tye Kindinger (Dr. Hixon Lab)
Jeremy Rose (Dr. Menge Lab)
Message from the 2011 Organizing Committee:

Welcome to the 24th Annual Biology Graduate Student Symposium! This conference, organized for graduate students by graduate students, brings together all the life science departments at Oregon State University. It is a forum to share research with our peers and to facilitate a better appreciation of the breadth of biological investigation that occurs at our university. This gathering is an opportunity to broaden our outlook on the study of biology; to discuss graduate life and current events; and encourage interactions between future researchers in the various life sciences. We hope you have a productive conference and that you will bring away a positive experience to share with other students.
Keynote Speaker:

Chris Pfefferkorn, Deputy Director of Living Collections at the Oregon Zoo

Keynote address: Coming soon…
The 24th Annual Biology Graduate Student Symposium

We gratefully acknowledge the support of the following:

College of Oceanic and Atmospheric Sciences

Department of Geosciences

Department of Zoology

Department of Fisheries and Wildlife

Venue Sponsor

Hatfield Marine Science Center of Oregon State University
General Information:

Presentations: The symposium will take place in the Library Seminar Room (Guin Library) at the Hatfield Marine Science Center (HMSC) (map – p.6). Each talk should be approximately 12 minutes long, followed by 3 minutes for comments and questions. If presenting, please remember that audience members are from diverse fields of biology - please try to make your talk understandable to all. We have computers available to display PC-generated slides from PowerPoint. Please bring a thumb drive or CD with your presentation.

Breaks: Coffee, tea and treats will be provided at all breaks. *Please bring your eco-friendly coffee cups.*

Meals: Breakfast and lunch will be provided at the HMSC in the Staff Lounge (enter through 904 doorway). Dinner will be provided following the symposium at the rental house. There will be vegetarian options at all meals.

BYO Utensils: This is not due to cost; rather, to be eco-friendly *please bring your own plate, fork, drinking vessel for coffee and other beverages of choice.* There will be non-ecofriendly alternatives available.

Saturday Night Dinner/Social: Please join us following the symposium at the rental house. This is a great time to relax and meet everyone. Festivities will begin shortly after the last talk and carry on into the evening. Please feel free to stay overnight. All food and beverages are provided. If you choose to drink something other than soda, beer, or wine please bring it. The rental house is only a few blocks away from Nye beach. Please come and enjoy the food, music and conversation.

Transportation: You will need to find your own way to and from the HMSC. When arriving at the HMSC, enter through the back gate to park. Better yet, carpool with others attending the symposium.

Housing/Parking: The rental house is near Nye Beach (directions below). *If you are staying at the rental house, you will need to bring a sleeping bag and bed roll.* There are only 2-3 spots in front of the house, but plenty within a couple of blocks.
Map of the Hatfield Marine Science Center:

From Corvallis: Take U.S. Highway 20 through Philomath to Newport. In Newport, turn south on U.S. 101. Take the first exit after crossing the Yaquina Bay Bridge and follow the signs to the OSU Hatfield Marine Science Visitor Center parking lot.

The Library Seminar Room at Guin Library is indicated by a star.
Directions to the 2011 BGSS rental house in Newport

Address: 616 NW 9th St., Newport, OR

Directions from HMSC:
Exit Hatfield Marine Science Center and turn right onto Highway 101.
Drive 1.9 miles across the Yaquina Bay Bridge and into Newport.
Turn left onto 6th street.
Turn right onto Coast St.
Turn right onto 9th St (unpaved). The house is on the left.

Parking:
The house only has about three parking spaces in front of it but there is plenty of curbside parking around the block.

Map to rental house:
<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Department</th>
<th>Title of Talk</th>
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<tbody>
<tr>
<td>8:30</td>
<td>Registration and Breakfast</td>
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<tr>
<td>9:10</td>
<td>Opening Remarks</td>
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<td>9:30</td>
<td>Emily Uhrig</td>
<td>Zoology</td>
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<td>9:45</td>
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<td>Danielle Lightle</td>
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<td>You're gluing what to that bug? Using EPG to understand insect resistance in raspberry</td>
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<tr>
<td>10:15</td>
<td>Julia Buck</td>
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<td>The impacts of <em>Batrachochytrium dendrobatidis</em> on aquatic food web dynamics and implications for amphibians</td>
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<td>1:00</td>
<td>Mark A. Albins</td>
<td>Zoology</td>
<td>Effects of the invasive Pacific red lionfish on Atlantic coral-reef fish communities</td>
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<td>1:15</td>
<td>Rosie Gradoville</td>
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<td>Comparison of N\textsubscript{2} fixation response by Trichodesmium to pCO\textsubscript{2} perturbations using gas bubbling and acid/base approaches</td>
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<td>Not just a chastity belt: the role of copulatory plugs in Red-sided garter snakes revisited</td>
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<td>Angela Brandt</td>
<td>Zoology</td>
<td>Effects of disturbance and resource supply on traditional and phylogenetic community diversity</td>
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<td>2:00</td>
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<tr>
<td>2:15</td>
<td>Timothy Pusack</td>
<td>Zoology</td>
<td>Gene flow and larval dispersal in a metapopulation of a coral-reef fish</td>
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<td>Investigating pheromone variability in a terrestrial woodland salamander</td>
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<td>Molecular and Cellular Biology</td>
<td>The role of Mcl-1 in Respiratory Syncytial Virus infection</td>
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<td>3:00</td>
<td>Kaitlin Bonner</td>
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<td>There's no such thing as a &quot;free lunch&quot;: Problems with using vector control to eradicate Schistosomiasis</td>
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<td>Botany-Plant Pathology</td>
<td>Is plant population growth driven by climate?</td>
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<td>Top predators versus the abiotic environment: what determines community structure in arid-land streams?</td>
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<td>4:00</td>
<td>Allison Barner</td>
<td>Zoology</td>
<td>Few costs to selfing in the sea palm kelp</td>
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<td>4:15</td>
<td>Concluding Remarks</td>
<td>Proceed to poster presentations in hallway!</td>
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MARK A. ALBINS (Zoology)
Effects of the invasive Pacific red lionfish on Atlantic coral-reef fish communities
Pacific red lionfish (*Pterois volitans*) initially introduced to Atlantic waters in the mid to late 1980s, have undergone an extremely rapid range expansion and population explosion over the last decade. This invasive predator is now found across most of the Caribbean Sea, the Gulf of Mexico, and the southeastern coast of the United States. Lionfish are voracious fast-growing predators of small crustaceans and especially fishes, they are well defended from predators by numerous large venomous fin spines, and they are reaching far greater densities in the invaded range than any reported from their native range. Invasive lionfish have the potential to cause deleterious changes to Atlantic coral-reef communities via both direct and indirect interactions with native species. Field experiments in the Bahamas have demonstrated that lionfish cause significant reductions in the abundance, richness, and diversity of native coral-reef fishes, and that the effects of lionfish on native fish communities are greater than the effects of an ecologically similar native predator, the coney grouper.

ALLISON BARNER (Zoology)
Few costs to selfing in the sea palm kelp
Naturally isolated populations have conflicting selection pressures for successful reproduction and inbreeding avoidance. These species with limited seasonal reproductive opportunities may use selfing as a means of reproductive assurance. We quantified the frequency of selfing and the fitness consequences for inbred versus outcrossed progeny of an annual kelp, the sea palm (*Postelsia palmaeformis*). Using experimentally established populations and microsatellite markers to assess the extent of selfing in progeny from six founding parents, we found the frequency of selfing was higher than expected in every population, and few fitness costs were detected in selfed offspring. Despite a decline in heterozygosity of 30% in the first generation of selfing, self-fertilization did not affect individual size or reproduction, and correlated only with a marginally significant decline in survival. Our results suggest both that purging of deleterious recessive alleles may have already occurred and that selfing may be key to reproductive assurance in this species with limited dispersal. Postelsia has an alteration of a free-living diploid and haploid stage, where the haploid stage may provide increased efficiency for purging the genetic load. This life history is shared by many seaweeds and may thus be an important component of mating system evolution in the sea.

KATE BOERSMA (Zoology)
Top predators versus the abiotic environment: what determines community structure in arid-land streams?
Extreme abiotic conditions fundamentally structure arid-land aquatic communities. However, top-down processes may be equally important determinates of community assembly in seasonally-intermittent arid-land streams. These habitats shrink to fragmented pools during the summer, restricting faunal movement and increasing insect densities. To explore relationships between abiotic factors, top predators and community structure, we conducted complementary observational and experimental studies. First, we documented invertebrate communities and abiotic factors in pools within a single fragmented arid-land stream in southeastern Arizona. Second, we established experimental mesocosm communities and applied treatments with and
without top predators. Ordination of observational data revealed that pools with little canopy cover and pools with extensive canopy cover contain distinct invertebrate communities, and presence of top predators is associated with unshaded pools. Experimental results suggested that top predators affect algal growth and invertebrate community composition, even under extreme abiotic conditions. A warming and drying climate is predicted to trigger local extinctions of aquatic predators and intensify environmental extremes in arid-land aquatic ecosystems. Therefore, studying these factors’ relative influences on aquatic communities will be important to understand the future of arid-land streams.

KAITLIN BONNER (Zoology)
**There's no such thing as a "free lunch": Problems with using vector control to eradicate Schistosomiasis**
Neglected tropical diseases have a greater combined global disease burden compared to both malaria and tuberculosis, despite being comparatively heavily under-funded. Efforts to eradicate neglected tropical diseases, including Schistosomiasis, are thwarted by poor living conditions, such that a lack of sanitation, infrastructure for drug treatment and adequate removal of vector populations all greatly hinder eradication efforts. Schistosomiasis causes 200,000 deaths per year and nearly 200 million are infected and 400-600 million are exposed to the parasite in 54 countries yearly. Successful eradication efforts include a combination of both vector control and drug treatment. To date, the most commonly used vector control methods involve broad application of molluscicides containing chemical pollutants leading to environmental degradation and harmful human exposure to chemicals. This study examines the potential for vector control by introgression of resistance genes into natural populations through breeding programs using local populations. Adequate examination of fitness consequences of carrying resistance genes is required for successful introduction of resistance organisms into natural populations. In this study we demonstrate a clear cost associated with resistance to parasite infection. However, a cost was not found associated with the only previously described resistance gene in this system, copper-zinc superoxide dismutase (SOD1).

ANGELA BRANDT (Zoology)
**Effects of disturbance and resource supply on traditional and phylogenetic community diversity**
Disturbance and resource supply are two important processes that can impact community diversity and assembly, and may interact in their effects. However, traditional metrics of species diversity may not fully represent the diversity of a community because species are not independent entities. We are examining the effects of disturbance and nitrogen manipulation on plant community diversity, comparing effects on species richness and evenness with effects on phylogenetic diversity (PD) and phylogenetic abundance evenness (PAE). Furthermore, we are exploring how community composition, both for independent species and by incorporating species’ phylogenetic relationships, differs among treatments and over time. Our preliminary results suggest that disturbance increases diversity regardless of the metric used, but resource supply differentially affects richness and evenness metrics. Disturbance and resource supply also tend to interact in their effects on richness, evenness, and community composition. The temporal stability of treatment effects also differs for richness and evenness. Phylogenetic results do not appear grossly different from those using traditional species diversity metrics,
however further investigation, particularly into which species and clades differ among treatments, is needed.

JULIA BUCK (Zoology)
The impacts of *Batrachochytrium dendrobatidis* on aquatic food web dynamics and implications for amphibians
Parasites are often excluded from food web analyses because their abundance and impact can be difficult to quantify, and they typically exist at low biomass. However, parasitism represents the most common consumer strategy, and the inclusion of parasites in food webs generally increases connectance. The emerging infectious diseasechytridiomycosis is caused by *Batrachochytrium dendrobatidis* (Bd), a fungal pathogen of amphibians. Although the implications of community structure on disease dynamics of Bd have received only a cursory examination, a series of previous studies showed that the free-living infective stage of a different chyrid fungus is consumed by zooplankton, thus providing protection for its phytoplankton host. Similarly, I hypothesize that consumption of infective Bd zoospores by zooplankton will provide a protective effect for larval amphibian hosts and also have effects that cascade through the food web. I conducted a 2x2x2 factorial experiment in which I crossed the presence or absence of tadpoles, zooplankton, and Bd. I measured growth rate, development, and survival of larval amphibians, and also recorded the community response by quantifying zooplankton abundance, phytoplankton concentration, and periphyton biomass. Preliminary results indicate that zooplankton and Bd caused decreased growth and development of tadpoles and there was a significant interaction of the two treatments. Evidence that the effects of consumption of Bd zoospores by zooplankton could cascade through the food web was not found. qPCR analysis will be conducted on a portion of the metamorphic amphibians to confirm infection and determine treatment effects. Analysis of community variables confirmed a negative effect of tadpoles on periphyton biomass and a negative effect of zooplankton abundance on phytoplankton concentration. Interestingly, an indirect negative effect between zooplankton abundance and tadpoles was revealed, suggesting that this interaction needs to be reexamined. I conclude that consumption of Bd zoospores by zooplankton is unlikely to protect amphibians from infection, but community structure may change disease dynamics in other ways.

ADAM CHOUCINARD (Zoology)
Investigating pheromone variability in a terrestrial woodland salamander
The communication system of Plethodontid salamanders relies heavily upon chemical signaling. Pheromone molecules convey a tremendous amount of information to conspecifics, and facilitate a wide variety of the essential social functions of these animals. Much of the information contained within the pheromone mixture is variable from one individual to the next, such as the ability to recognize specific individuals, the size of the sender, and the relative “quality” of the signal. In order for variable information to be conveyed through chemical signals, the corresponding variability must be contained within the pheromone mixture itself. This variability may exist as a gradient of total volume, changes in the relative ratios of components, and even structural variability of the specific pheromone molecules. These aspects of pheromone variability will be explored in two Plethodontid salamanders (*Plethodon cinereus* and *P. shermani*) using biochemical methods and the phenomenon of female mate-choice as a behavioral measure.
CHRIS FRIESEN (Zoology)

**Not just a chastity belt: the role of copulatory plugs in Red-sided garter snakes revisited**

In promiscuous mating systems, postcopulatory selection and sexual conflict drive male investment in ejaculates. Copulatory plugs (CP) are a gelatinous mass deposited by the male during copulation that can represent a significant proportion of the ejaculate. Passive mate-guarding is the principle function attributed to the CP because it occludes the opening of the female’s reproductive tract and prevents intromission by subsequent males. The CP may also prevent a female from expelling sperm from an “undesirable” male after coerced copulation or when precopulatory choice is otherwise limited. During the spring emergence of Red-sided garter snakes (*Thamnophis sirtalis parietalis*) in Manitoba, Canada, the operational sex ratio is strongly skewed toward males who scramble to locate and court newly emerged females. Litters usually exhibit multiple paternity suggesting that the females are promiscuous; males deposit copulatory plugs suggesting mate-guarding is a wise investment. However, precopulatory female choice is limited in the largest mating aggregations, thus sexual conflict may place a premium on preventing females from ejecting male sperm.

In snakes, sperm are produced in the testes and delivered through the ductus deferens, and the copulatory plug is thought to be produced by the renal sexual segment and conveyed through the ureter. We manipulated the delivery of the two fluids separately by ligating the ducts. We found that the CP is not formed in ureter-ligated males and that sperm leaks out immediately after copulation. Further, the CP is analogous to a spermatophore as the protein matrix contains most of the sperm which are liberated over time as the plug dissolves within the female’s vagina.

ROSIE GRADOVILLE (College of Oceanic and Atmospheric Sciences)

**Comparison of N₂ fixation response by Trichodesmium to pCO₂ perturbations using gas bubbling and acid/base approaches**

Recent studies have found that di-nitrogen fixation rates by laboratory cultures of Trichodesmium (strain IMS101) increase when exposed to elevated pCO₂ concentrations. Contrary to these findings, experiments conducted by our research group on a recent cruise in the North Pacific subtropical gyre found the opposite trend: increased pCO₂ concentrations produced lower rates of nitrogen fixation for isolated colonies of Trichodesmium. While the previous studies have manipulated pH by bubbling cultures with CO₂, our shipboard experiment manipulated pH through acid/base additions. Both approaches are accepted by the scientific community as methods to control pCO₂ concentrations in sea water; however, it is essential to explore whether Trichodesmium cultures respond differently to these two acidification methods.

I will present results from laboratory experiments designed to compare nitrogen fixation rates by multiple strains of Trichodesmium spp. over a range of pCO₂ concentrations manipulated through CO₂ bubbling and acid/base additions. These results will be discussed in the context of our recent field observations.

ALISON ILES (Zoology)

**Climate driven trends and ecological implications of event-scale upwelling in the California Current System**

Eastern boundary upwelling systems, such as the California Current System (CCS) in the eastern Pacific Ocean, are among the most productive and lucrative ecosystems on Earth. Although such regions account for less than 1% of the ocean surface, they support 20% of global commercial fishery yields. As upwelling is driven by large-scale atmospheric patterns, global climate change
has the potential to affect a wide range of significant ecological processes through changes in water chemistry, water temperature, and the transport processes that influence species dispersal and recruitment. We examined long-term trends in upwelling event duration and strength for the Oregon and California regions of the CCS. We then associated event-scale upwelling with up to 20 years of barnacle and mussel recruitment, nutrient, phytoplankton, and water temperature data measured at rocky intertidal field sites along the Oregon coast. The results support previous findings for California and suggest that the phenology of event-scale upwelling in Oregon is also changing in ways that are consistent with climate change predictions. Upwelling events are becoming significantly less frequent and longer in duration. Upwelling event duration, calculated from a large-scale regional upwelling index, is associated with lower water temperatures and higher nutrient and chlorophyll-α levels measured at local rocky intertidal field sites in Oregon. Recruitment of barnacles and mussels at these same sites is associated with wind relaxations, which mark the end of each upwelling event. These findings suggest that recent documented cases of hypoxia and anoxia off the Oregon coast are part of a larger climate trend and that future ocean acidification will be exacerbated in coastal upwelling systems.

KOJUN KANDA (Zoology)
The phylogeny of the Tenebrionidae (Coleoptera) inferred from molecular data
The beetle family, Tenebrionidae, contains around 20,000 described species that are divided into 3 main lineages, the tenebrionoids, lagrioids, and pimelioids. To date, morphology and biogeography have not been able to resolve whether it is the pimelioids or the lagrioids that are the sister group to the tenebrionoids. This study represents the first attempt at using molecular data to resolve this deep split in Tenebrionidae. 77 ingroup taxa representing all 9 tenebrionid subfamilies were sequenced at 3 loci: ArgK, CAD, and wingless. Bayesian analyses on individual genes do not resolve the relationship among the lineages. However, analysis of the concatenated dataset shows evidence of lagrioids as the sister group to the tenebrionoids. In addition, the data supports the position of the enigmatic subfamily, Zolodininae, as the sister group to the rest of the clade containing tenebrionoids and lagrioids.

DANIELLE LIGHTLE (Horticulture – Entomology)
You're gluing what to that bug? Using EPG to understand insect resistance in raspberry
Electrical penetration graph (EPG) technique is a unique method that measures hemipteran insect feeding behavior by wiring the insect and plant into an electrical circuit. Changes in the electrical current over time create waveforms that are characteristic of different feeding behaviors such as salivation or phloem feeding. In this study, EPG will be used to help elucidate the mechanism of aphid resistance in red and black raspberry by comparing how the aphid feeding behavior changes on susceptible and resistant varieties, as well as to understand how the mechanism of resistance will affect virus transmission by the aphid vector.

MACIEJ MASELKO (Molecular and Cellular Biology)
The role of Mcl-1 in Respiratory Syncytial Virus infection
Respiratory Syncytial Virus (RSV) is the leading cause of infant respiratory failure in the U.S. The apoptosis of infected cells early during infection is considered to be an antiviral strategy to protect uninfected cells. Mcl-1, an anti-apoptosis protein, was previously found to be upregulated early in RSV infection presumably as a viral strategy to block apoptosis. However, we have found that knockout mouse embryonic fibroblast cells lacking Mcl-1 produce
considerably more virus than wild type cells and are no more apoptotic early during infection.

IAN PFINGSTEN (Botany and Plant Pathology)
Is plant population growth driven by climate?
Plant population demographers typically use random fluctuations in vital rates to represent environmental variation. We intend to explain some of that variation with site-specific climate in the hopes to create sophisticated models that project population trends with greater precision. We chose five, rare, Oregon native populations from sites in and out of the Willamette Valley. Most populations tended to increase with temperature or precipitation in growing seasons, while decreasing with precipitation during dormant seasons. Effects sizes ranged from 80% to 40% explained variation for the best models of each population, however not all climate variables were included in the models. Forecast projections using demographic models parameterized with estimates from general circulation models showed positive and negative trends for populations, with only three deviating from null models. Our expectations of population viability may change when including explicit environmental variation.

TIMOTHY PUSACK (Zoology)
Gene flow and larval dispersal in a metapopulation of a coral-reef fish
Marine metapopulations consist of separate local populations connected by larval dispersal. Understanding marine metapopulation dynamics is critical to inform fisheries management, guide marine reserve design, and establish effective conservation efforts. Because larval dispersal patterns characterize metapopulations, we examined the genetic structure of multiple cohorts of a common coral-reef fish over 4 years. We used neutral genetic markers (10 microsatellite loci) to identify dispersal patterns in bicolor damselfish (Pomacentridae: Stegastes partitus). We genotyped samples from 3647 fish (1601 adults and 2046 recruits) collected from 4 islands surrounding the Exuma Sound, Bahamas, from 2005 through 2008. Bayesian parentage analysis indentified several parent-offspring pairs and directly documented self-recruitment at each island. Principal coordinates analysis revealed that recruits from each site clustered in the same multivariate space as the adults from the same site, and did not cluster with individuals from other sites. This indirect evidence indicated that self-recruitment likely occurred at all sites. While measures of genetic differentiation (e.g., Fst,) suggested high levels of gene flow among populations over longer time periods, there are differences in population structure among years in both adults and recruits. Our findings suggest that connectivity among subpopulations explained metapopulation structure on evolutionary time scales. However, since we found evidence of self-recruitment and locally independent sweepstakes events over multiple years, local larval production is probably important to structuring metapopulations on ecological time scales.

EMILY UHRIG (Zoology)
Interspecific variation in the female sexual attractiveness pheromone of garter snakes
During the breeding season, female garter snakes produce a sexual attractiveness pheromone composed of a homologous series of saturated and monounsaturated methyl ketones. This pheromone, expressed in the skin lipids of females, elicits courtship behavior from males, who rely extensively on the pheromone for recognition of suitable mates. Utilizing four garter snake species, including two pairs of sympatric species, the current study is designed to investigate whether the chemical profile of the female sexual attractiveness pheromone exhibits interspecific
variation. Pheromone samples were collected from females of each species: the red-sided garter snake (*Thamnophis sirtalis parietalis*) and the plains garter snake (*Thamnophis radix*), which are sympatric in Manitoba, Canada, as well as the red-spotted garter snake (*Thamnophis sirtalis concinnus*) and the northwestern garter snake (*Thamnophis ordinoides*), which are sympatric in Oregon. Chemical analyses revealed significant qualitative variation in the chemical profile of the pheromone between all four species. This dissimilarity was particularly evident within the sympatric groups. These results suggest that the female sexual attractiveness pheromone of garter snakes may function as a mechanism of prezygotic reproductive isolation allowing males to distinguish between conspecific and heterospecific females.

**Symposium Poster Abstracts – Alphabetical Order**

ANKITA JUNEJA (Biological and Ecological Engineering)
**Effect of flashing light on photosynthetic efficiency of algae**
Microalgae are potential feedstocks for advanced biofuels production due to their high lipid, carbohydrate contents and biomass productivity. Algae production in open ponds is constrained by contamination and low production. Photobioreactors can address some of these issues they are limited by high cost of production, which can be offset by maintaining higher biomass productivities. Algae are typically autotrophic organisms, utilizing light, CO$_2$ and other inorganic nutrients for their growth. Higher growth rates can be obtained by increasing the light and CO$_2$ utilization efficiency. As maximum CO$_2$ uptake is mass transfer limited, light uptake efficiency can be increased to enhance algae growth rate. Many studies have shown that continuous illumination at high light intensity can cause photoinhibition. While light utilization efficiency is higher at lower light intensities, algae growth rates are correspondingly much lower. Some of the studies have suggested utilizing the flashing effect at high light intensities to simultaneously increase light utilization efficiency and biomass productivity while avoiding photoinhibition effects. This study focuses on simulating the dark and light times of the flash for increasing the photosynthetic efficiency in turn augmenting the algae growth.

TIMOTHY LEE (Environmental Sciences)
**Describing benthic invertebrate assemblages on the continental shelf of the Pacific Northwest**
The coastal waters of western North America hold some of best locations for renewable wave energy development installations. Little however is known about benthic biological communities in these continental waters. To assess the potential effects of these developments on biological communities, a program was proposed to survey structure-forming and non-structure-forming invertebrate diversity and species-habitat associations in continental shelf waters of Pacific Northwest. Prior to initiating fieldwork, historical dives from areas near the proposed sites were reviewed in order to make comparisons of species assemblages over time. Invertebrate assemblages and habitat patches were surveyed using six ROV Delta submersible videos filmed during September 1995 at 60-150 m depths in Gray’s Harbor, Washington. Six different habitat patches were recorded using laser beams and transects. A total of six taxa and 9,831 individuals were found for structure-forming types, and fourteen taxa and 355 individuals for non-structure forming types. Majority of habitat patches surveyed were composed of mud with occasional cobble mixture and isolated boulders. Over 90% of structure-forming
invertebrates observed were composed of Subselliﬂorae sea pens, which were predominantly found in plain mud and mud-cobble patches. The infaunal Luidia foliolata comprised majority of non-structure forming invertebrates in mud habitats. An occasional isolated boulder in predominantly mud patch was densely covered with Metridium farcimen. Both structure and non-structure forming taxa increased numerically and taxonomically with increasing depth as seabed features revealed more patches comprised of gravel, cobble and boulder. Higher densities of Gorgonian corals and shelf sponges were found with increasing boulder abundance; greater concentrations of Asterina miniata, Florometra serratissima, and Pandalus platyceros were found in cobble-dominated patches. Given that relatively little is known about benthic diversity in Pacific Northwest’s continental waters, this study can provide baseline data on potential habitats and species to be affected in sites targeted for offshore renewable energy development.

LIA MURTY (Environmental and Molecular Toxicology)
Detection of lolitrem B in bovine urine and feces by LC-MS/MS
(1)Lia Murty, (2)Jennifer Duringer, (3)Sara Livesay, (3)Ashley Galen, (3)A. Morrie Craig
(1)Department of Natural Products & Medicinal Chemistry, OSU
(2)Department of Environmental & Molecular Toxicology, OSU
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Perennial ryegrass (PRG) is a hardy cool-season grass that is used on lawns, parks and athletic fields, for erosion control and animal forage. It is infected with the endophytic fungus Neotyphodium lolii, which enables the plant to be insect repellant and drought resistant, lowering the use of insecticides and fertilizers. However, this fungus also produces the compound lolitrem B (LB, m/z 686.4) which causes the tremorgenic neurotoxicity syndrome ‘ryegrass staggers’ in livestock. Further, human health concerns have arisen from a study which found LB in bovine fat after they were fed PRG containing LB. However, limited data exists on the fate and metabolism of LB in cattle. We developed a LC-MS/MS method for quantification of LB in bovine urine and feces samples from a feeding trial of 23 beef steers fed PRG containing LB. Urine was diluted in 0.1M phosphoric acid, followed by solid phase extraction on a Waters Oasis HLB cartridge. Feces were dissolved in ethyl acetate and the organic layer applied to a Strata X Silica cartridge. Extracts were analyzed by (+)APCI via multiple reaction monitoring using 686.4→237.9, 686.4→196.3, 686.4→628.4 and 686.4→238.3 as transitions. The limit of detection and quantitation for LB were 13 ng/mL and 42 ng/mL, respectively. Extraction recoveries for urine and feces were 58.3% and 79.3%, respectively (10 ng/mL LB matrix spike). Through standard addition, it was determined that the control group contained 2 µM fecal LB. Development of this assay will allow for detection of LB in matrices which will assist in research and clinical cases of perennial ryegrass staggers.

ERIK ROWLEY (Zoology)
Genome sequencing and resource development of agriculturally important accessions of European hazelnut
European hazelnut (Corylus avellana) possesses several characteristics that make it an attractive Betulaceae model. Using data obtained from whole genome shotgun sequencing and transcriptome sequencing (RNA-seq), resources assisting in genetic mapping of important agronomic traits and marker assisted breeding efforts were developed and a draft genome was
assembled for the reference hazelnut accession ‘Jefferson’. Currently a final genome assembly and annotation is underway for ‘Jefferson’, with 7 additional diverse accessions of agricultural importance being sequenced for reference-guided assembly and establishment of genetic resources.

KEVIN WEITEMIER

Intra-genomic rDNA sequence diversity across 84 milkweeds (Asclepias, Apocynaceae)

Nuclear ribosomal DNA (rDNA) has been one of the most widely used molecular markers in plant phylogenetic studies of both deep (18S-5.8S-28S) and shallow (ITS) relationships. Even after the recognition of factors limiting the phylogenetic utility of these regions, such as intra-genomic sequence variation and confusion between orthology and paralogy, they remain in wide use today. Additionally, while these regions are thought to exhibit concerted evolution, the high copy number of rDNA regions has hampered efforts to characterize intra-genomic variation between copies. The use of next-generation sequencing can alleviate this problem through detection of variation present at low copy number. We have used Illumina sequencing to investigate the rDNA regions of 92 members of the milkweeds (66 taxa within Asclepias, 8 other genera in Apocynaceae). We characterize rDNA sequence variation within individuals and between functional and spacer regions. The large dataset allows intra-genomic variation to be compared across the genus. In agreement with previous studies in yeast, preliminary results indicate that variation present at high frequency (>20% of reads) may be rare across the region. However, polymorphisms present at lower frequencies may be much more common, and heterogeneity may exist between the functional and spacer regions. Analysis of intra-genomic variation in a phylogenetic context can indicate whether polymorphisms present within the rDNA array of an individual are a product of recent mutations or represent ancestral variation in lineages of Asclepias.