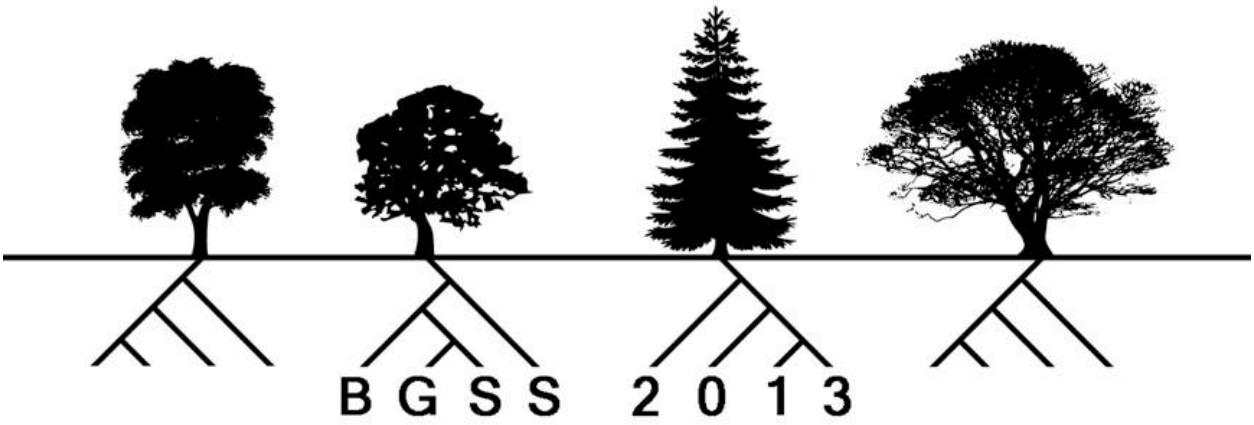
26th Annual Biology Graduate Student Symposium

Program and Abstracts

Oregon State University
Mark O. Hatfield Marine Science Center
Newport, Oregon

March 2nd, 2013



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Message from the 2013 Organizing Committee

Welcome to the 26th Annual Biology Graduate Student Symposium! This conference, organized by and for graduate students, brings together students from 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.

2013 Organizing Committee

Casey Benkwitt
Elizabeth Cerny-Chipman
Cammie Crowder
Emily Hartfield
Tye Kindinger
Sheila Kitchen
Dani Long
Trang Nguyen
Jessie Reimer
Chenchen Shen
Hannah Tavalire

Acknowledgements

We gratefully acknowledge the support of the following sponsors:

OSU Departments:
Department of Fisheries and Wildlife
Department of Zoology
College of Earth, Ocean, and Atmospheric Sciences
College of Education
College of Science
Graduate School

Venue:
Hatfield Marine Science Center of Oregon State University

Refreshments and Food:
First Alternative Co-Op
Fred Meyer
Rogue Brewery
Safeway

General Information

Presentations: The symposium will take place in the Auditorium at the Hatfield Marine Science Center (HMSC) (map – p. 13). 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. Please bring a thumb drive with your presentation.

Meals: *BYO utensils, plates, and cups* but we will have plastic disposables available for those who forgot or don't care. Coffee, tea and treats will be provided at all breaks. Lunch will be at HMSC and dinner will be at the rental house. There will be vegetarian options at all meals.

Saturday Night Dinner/Social: Please join us following the symposium at the rental house. This is a great time to relax and meet everyone. Please feel free to stay overnight. All food and beverages are provided. If you choose to drink something other than soda or beer please bring it. The rental house is located on Hwy 20 just 2 miles east of Newport (map – p. 14). Please come and enjoy the food, music and conversation!

Housing/Parking: A map to the rental house is provided on page 14. If you are staying at the rental house, you will need to bring a sleeping bag and pillow. There is somewhat limited parking at the house and therefore, please try to carpool from HMSC or from Corvallis.

Schedule of Talks

Time	Presenter	Dept.	Title
9:15	Registration; refreshments and coffee		
9:50	Opening remarks		
10:00	Erin Gorsich	Zoology	Consequences of brucellosis infection and co-infection for survival: immunity and disease
10:15	Krissi Hewitt	Sci. Ed.	Socioscientific Issues-based Laboratory Curriculum: Creating Motivating Environments for University Biology Students
10:30	Kate Boersma	Zoology	Community trajectories in fragmented arid-land streams: Combined effects of extreme environmental conditions and aerial dispersal
10:45	Break		
11:00	Keynote speaker: Dr. Kathleen Dean Moore		
12:00	Lunch/poster set up		
1:00	Erin Bredeweg	MCB	Control and Function of Two Fatty Acid Regulators in Neurospora crassa
1:15	Stephen Meck	F&W	Range-use estimation and sighting probability for juvenile Steller's sea lions in the Gulf of Alaska
1:30	Tara Chestnut	Env. Sci.	The Red Queen in the Arctic Arms Race: Amphibian chytrid fungus in the boreal environment
1:45	Break		
2:00	Zhian Kamvar	Botany	Poppr: An R package for genetic analysis of populations with mixed (clonal/sexual) reproduction
2:15	Emily Uhrig	Zoology	Garter snakes and their endoparasites
2:30	Deb Bailey	Sci. Ed.	The Practice of School Gardening
2:45	Break		
3:00	Jessica Reimer	Zoology	Drift Algae as an Ecological Subsidy on Sand Shores: Variation Along the Upwelling Gradient of the Oregon Coast
3:15	Kojun Kanda	Zoology	A candle in the night: molecular phylogenetics illuminate the wonders of the darkling beetles (Coleoptera: Tenebrionidae)
3:30	Brianna Beechler	Env. Sci.	The role of an emerging disease, Bovine Tuberculosis, in a Rift Valley Fever outbreak in African Buffalo
3:45	Trang Nguyen	Zoology	Stranger(s) in a strange land: strain variation in an emerging infectious disease
4:00	Closing remarks and poster session		
5:15	Head out to rental house		

Keynote Speaker

This year we have the great pleasure of hosting Dr. Kathleen Dean Moore, Distinguished Professor of Philosophy here at OSU and co-founder and Senior Fellow of the Spring Creek Project for Ideas, Nature, and the Written Word. As an environmental philosopher, Dr. Moore explores environmental ethics and our moral, spiritual, and cultural relationships to the natural world. Dr. Moore has written widely about environmental philosophy in professional journals, popular journals, and in several books and essays. Her latest book is Moral Ground: Ethical Action for a Planet in Peril.

Oral Presentation Abstracts *(in alphabetical order)*

DEB BAILEY (Science and Math Education)

The Practice of School Gardening

This project proposes to explore the world of a summer gardening program from the perspective of adolescent youth. This research study seeks to discover the underlying experiences that adolescents have which shape their science perspective and identity. Specifically this study focuses on those experiences developed during a coordinated youth gardening experience. The gardening program is targeted to 14-20 year old youth and specifically provides support for rural disadvantaged youth. This summer garden experience is a partnership between Oregon State University and 5 rural communities in Oregon.

Research has shown that out-of-school learning experience may provide positive outcomes in the development of science identity to rural (Exstrom & Mosher, 2000) and under-resourced (Fine 2005) youth. This study will build upon this research by using a phenomenological approach and a communities of practice theoretical lens to describe the essential experience of gardeners from the perspectives of disadvantaged rural youth. In detailing these perspectives, this study will provider a deeper understanding into the processes within a gardening experience that contribute (or not) to positive science perspectives. To further aid educational researchers, garden curriculum developers, and effective gardening pedagogy, this study will map the perceived STEM experiences of rural under-resourced youth to their gardening activities. In doing so, this project will come away with a greater understanding about how gardening with youth may contribute to science identity and what student experiences should be built into a garden curriculum.

BRIANNA BEECHLER (Environmental Sciences)

The role of an emerging disease, Bovine Tuberculosis, in a Rift Valley Fever outbreak in African Buffalo

Most ecological studies focus on single infections and fail to consider that most free-living populations are exposed to and are infected with multiple pathogens at one time. These pathogens interact within the host, via competition and facilitation, and can alter the survival of each other. We investigated interactions between the emerging bacterial disease bovine tuberculosis (BTB) and the native viral disease Rift Valley fever (RVF) in a competent reservoir

host, African buffalo using data from a natural outbreak of RVF in an buffalo breeding facility in 2008 with data collected from a neighboring free-living herd of African buffalo in Kruger National Park. African Buffalo previously infected with BTB were 1.7 times as likely to subsequently acquire RVF in the captive population and 2.3 times more likely to be seropositive for RVF in the natural population. In addition coinfected buffalo were twice as likely to exhibit the clinical signs of RVF (abortion) than buffalo singly infected with only BTB. Future work will focus on whether these alterations in individual host susceptibility to RVF, due to BTB, can increase the frequency or intensity of RVF outbreaks. However this data indicates that the consequences of emerging infections are not limited to direct effects of the emerging infection, but can potentially alter the dynamics of native infectious diseases in free-ranging wildlife populations.

KATE BOERSMA (Zoology)

Community trajectories in fragmented arid-land streams: Combined effects of extreme environmental conditions and aerial dispersal

As precipitation in arid regions becomes more variable, arid-land streams will be subject to increasing fragmentation. Ecological theory predicts that species composition in fragmented communities may become more similar (converge) or more distinct (diverge) through time, but there has been little consensus on the mechanisms behind either trajectory. In arid-land streams during the dry season, extreme abiotic conditions and aerial dispersal are two important drivers of community structure, but these factors have been associated with either convergence or divergence, depending on the study and the system. Given the vulnerability of arid-land aquatic fauna to environmental changes, understanding these dry-season community trajectories is of imminent conservation concern. To distinguish between community convergence and divergence in arid-land streams, we compared invertebrate communities collected at the beginning and end of the dry season under various abiotic conditions and levels of aerial dispersal. We found that environmental extremes were associated with community convergence, but that aerial dispersal caused surprising divergence, both taxonomically and functionally. An understanding of dry-season community dynamics will allow us to project how communities will respond to the increasingly extreme environmental conditions predicted for arid-land aquatic habitats.

ERIN BREDEWEG (Molecular and Cellular Biology)

Control and Function of Two Fatty Acid Regulators in Neurospora crassa

The filamentous saprotroph Neurospora crassa, containing single copies of many genes, is an excellent model for describing the behavior of transcriptional regulators. We aim to describe globally the behavior of two Fatty Acid Regulators or FAR proteins, transcription factors that modulate the response of Neurospora to the presence of fatty acids. We used ChIP-Seq to find the localization of FAR-1 and FAR-2 under nutrient conditions targeting short and long chain fatty acid carbon sources, with sucrose as a control. Bioinformatic analyses describe variant binding sites for FAR-1 and FAR-2, with overlap in ChIP-seq targets of about 1/3. Functions under control of ChIP-Seq targets was further examined with phenotypic assays: siderophore production, oxidative stress, and linear growth rate. These experiments found reduced siderophore production, and oxidative stress vulnerability in far-1 mutants, but not far-

2. Linear growth showed a carbon specific slow growth rate for far-2, and Tween-20 sensitivity and conidiation deficiency for far-1. RNA-Sequencing identified transcripts changing within the ChIP-Seq targets, and others affected by the absence of one or both FARs. These analyses identified groups of co-regulated proteins not previously known to be affected by the FAR transcription factors, in addition to control of the core cellular machinery for energy production by beta-oxidation.

TARA CHESTNUT (Environmental Sciences)

The Red Queen in the Arctic Arms Race: Amphibian chytrid fungus in the boreal environment

Amphibians are among the most vulnerable taxa due to synergistic effects of habitat loss, disease, and climate change. The amphibian chytrid fungus, Batrachochytrium dendrobatidis (Bd), causes an infectious disease, chytridiomycosis, that is associated with mass mortalities of many amphibian species and local extinctions in disturbed and pristine landscapes in both temperate and tropical regions. The 'boreal' is the largest terrestrial ecoregion on the planet, yet largely because of its remoteness, it is one of the least sampled for Bd. Our research investigates the distribution of Bd in the boreal environment, and the relationship between water quality and Bd occupancy in amphibians and their aquatic habitats. In spring/summer 2009–2011, we examined Bd occurrence in water samples from 29 amphibian breeding sites in Alaska (USA) across a latitudinal range from approximately 60 to 67 degrees north. These latitudes were chosen to represent the northern-most latitude of Bd that were reported in the literature (60 degrees) and the known northern-most extent of the wood frog (Lithobates sylvaticus) in Alaska (67 degrees). In 2009 and 2011, in addition to Bd water samples, we also collected skin swabs from wood frogs. We measured the following water quality parameters: temperature, pH, specific conductance, and turbidity. We used qPCR for Bd quantification, and analyzed the results using an occupancy approach with the program PRESENCE 4.1, with AIC as a measure of parsimony for model selection. We found Bd at 38% of sites and as far north as 67 degrees latitude, at very low densities (max. = 8.96 zoospore equivalents per liter of water filtered). All detections except for one occurred in spring. Predicted climate change scenarios are expected to influence both wood frog and Bd distributions in Alaska. Future work will test the Red Queen Hypothesis, e.g. the evolutionary arms race between host and pathogen, to examine if wood frog physiology and their extreme cold-tolerance allows resiliency to Bd, and whether increased temperatures due to climate change will increase susceptibility to chytridiomycosis.

ERIN GORSICH (Zoology)

Consequences of brucellosis infection and co-infection for survival: immunity and disease

In natural populations, hosts are infected with many, simultaneous infections, presenting a strong selection pressure on the host immune system. We studied brucellosis and intestinal parasite co-infections in a free-ranging African buffalo population during an experimental worm-removal study. Survival analysis shows that worm removal decreases mortality in buffalo co-infected with brucellosis. One hypothesis to explain this pattern is that co-infection with intestinal parasites affects the hosts' immunological response to brucellosis infection, thereby altering disease progression or persistence. In this talk, I examine infection, immunity and survival patterns in African buffalo.

ZHIAN KAMVAR (Botany and Plant Pathology)

Poppr: An R package for genetic analysis of populations with mixed (clonal/sexual) reproduction

Analysis of populations with mixed reproductive systems, including a blend of sexual and clonal reproduction, remains a challenge. We developed an R package implementing existing approaches for analysis of mixed populations. R is a multi-platform, open source statistical environment that has gained popularity over the past few years. While there are a plethora of packages in R that perform population genetics analyses, many standard analysis methods for populations with mixed modes of reproduction remain hard to accomplish. Poppr aims at providing functions to facilitate rapid analyses of this data, particularly including methods for analysis of recombination (index of association), clone-censored analysis of full datasets in a hierarchical manner over all levels of sampling, genotypic diversity analyses, and distance analyses. As implemented, poppr requires minimal commands with convenient summary functions while providing compelling graphics. Unlike many platform dependent, standalone programs, poppr can be used for batch processing of data including all kinds of population genetic data (dominant/codominant; microsatellites, AFLP, SNPs). Poppr is available as a beta release for testing upon request and continues to be improved.

KOJUN KANDA (Zoology)

A candle in the night: molecular phylogenetics illuminate the wonders of the darkling beetles (Coleoptera: Tenebrionidae)

Tenebrionidae is a morphologically and ecologically diverse family of beetles containing over 20,000 described species. To date, morphology has not been able to resolve early divergences within this lineage. This study represents the first time molecular data has been used to explore phylogenetic relationships within the Tenebrionidae. Results from the analysis of a dataset containing four genes sequenced for 160 tenebrionids spanning the diversity of the family suggest a need to revise the subfamilial classification in this group. The analyses also revealed interesting evolutionary patterns regarding the evolution of defensive glands and various traits associated with surviving in xeric habitats.

KRISSI HEWITT (Science and Math Education)

Socioscientific Issues-based Laboratory Curriculum: Creating Motivating Environments for University Biology Students

Many university biology students participate in “canned” labs that are designed only for verification of facts and concepts and do not help students connect what they are learning to the real world. There is a need for the contextualization of biology concepts that serves to connect content with issues students encounter in their everyday lives. The socioscientific issues-based (SSI) approach to science education provides the context for risk evaluations, collective decision-making and the interpretation of scientific content knowledge. The classroom environment models real-world situations and contexts allowing for transfer and application of knowledge to new settings. This approach to undergraduate biology education not only adheres to the core concepts, competencies, and pedagogical approaches outlined in the AAAS biology education standards document Vision and Change, but also focuses on the development of biologically literate citizens capable of informed decision-making. We are

building new majors biology curriculum laboratory activities that include active learning discussions and reflection sessions that focus on global and local social problems that intersect with science (GMOs, genetic testing, local environmental issues, etc.). They are also being built on the idea that students should be engaged in authentic activities that reflect the current state of biological research. Previous studies in primary and secondary science education suggest that this approach increases student interest and motivation with regard to engaging in class activities, but little work has been done with regard to student motivation at a post-secondary level. In order to assess the effectiveness of this laboratory curriculum, a mixed methods research study based on student surveys and questionnaires is being conducted that compares laboratory sections that participate in the socioscientific issues-based curriculum with the sections that participate in the current curriculum in place. Specifically, we are investigating the motivating aspects of the classroom environment with respect to doing the work for the course, and students' motivation to inform themselves about socioscientific issues. This study includes roughly 1000 biology students in the Biology 213 laboratories and will be instrumental in future curriculum reform efforts at Oregon State University.

STEPHEN MECK (Fisheries and Wildlife)

Range-use estimation and sighting probability for juvenile Steller's sea lions in the Gulf of Alaska

Currently, it is not known how far juvenile Steller sea lions (SSLs) from the endangered western population range from rookeries within Prince William Sound, nor what the probability of sighting a sea lion may be within their core area which often includes surveyed haul-out locations. Weaned (12-25 months) juvenile SSLs were captured in Prince William Sound or Resurrection Bay, Alaska, from 2001-2011. Data from 65 individuals fitted with external satellite-linked SDR-T16 or SPLASH tags (Wildlife Computers, USA) were analyzed to quantify the fine-scale movement patterns of sea lions using minimum convex polygon (MCP) and kernel density estimation (KDE) approaches to estimate both individual and group utilization distributions (UDs). From here, a multistate mark-recapture framework was applied to quantify terrestrial sighting probability and to develop a correction factor for count data. Initial MCP results indicate the total area encompassed by all study SSLs was 92,017 km2, after accounting for land mass. While there was variation inherent within the KDE derived UD, in general the values were similar across individuals. 50% of the population fell within a range of 324-1,387 km2 (mean=690.6 km2, LCL=524.6 km2, UCL=909.2 km2 using a back-transformed 95% confidence interval). There were no significant differences in area use associated with gender or whether the juvenile spent time in captivity (seasonally adjusted $U = 124$, $p = 0.205$, $r = -0.16$ and $U = 87$, $p = 0.285$, $r = -0.13$, respectively). However, there were significant differences in seasonal area use: $U = 328$, $p = 0.011$, $r = -0.31$. There was no relationship between the UD area and the amount of time the tag remained deployed ($H(2) = 45.30$, $p = 0.698$). Comparison of haul-out usage within the multistate framework will be presented.

TRANG NGUYEN (ZOOLOGY)

Stranger(s) in a strange land: strain variation in an emerging infectious disease

Global, newly emerging diseases are a central threat to biodiversity. For small, vulnerable populations existing on the edge of extinction, a single infectious disease outbreak

could prove decimating to species survival. This predicament is exemplified by the fungal pathogen, *Batrachochytrium dendrobatidis* (Bd), and its amphibian hosts. Of the 6000+ species of amphibians, nearly one-third are threatened. The infectious disease caused by Bd, chytridiomycosis, is attributed to play a large role in many current amphibian population declines and extinctions, including those in the U.S. To add further complexity, Bd, like many other pathogens (i.e. viruses, bacteria, fungi, etc.), exists in several genetically different strains with varying degrees of virulence; yet comprehensive knowledge of individual Bd strains is minimal. In order to better understand this devastating wildlife pathogen, research investigating strain variation is urgently needed. In this talk I outline questions of interest I plan on undertaking in my dissertation focusing on pathogen variation.

JESSICA REIMER (Zoology)

Drift Algae as an Ecological Subsidy on Sand Shores: Variation Along the Upwelling Gradient of the Oregon Coast

Drift macroalgae and seagrass, also known as wrack, which wash into coastal habitats may be important contributors of nutrients, organic matter and physical structure for coastal communities. These ecological subsidies seem to be especially important on sandy beaches, where there is otherwise little *in situ* primary productivity to fuel higher trophic levels. Since stronger upwelling should deliver more nutrients to algal dominated rocky habitats, macrophyte primary production could potentially be higher in areas of more intense upwelling, and thereby provide higher wrack input to nearby sandy shores. We tested this hypothesis by conducting surveys to measure macrophyte percent cover and biomass at three sites that differ in upwelling intensity along the Oregon coast. Preliminary analyses indicate that sandy beaches with strong upwelling (Cape Blanco, OR) receive a greater amount of wrack than beaches with intermittent upwelling (Boiler Bay, OR and Strawberry Hill, OR). This suggests that regional differences in productivity due to ocean upwelling and the proximity to rocky intertidal habitat can influence the amount of wrack delivered to beaches. Given this pattern, future research will explore how far wrack subsidies penetrate inland, the mechanism of transfer, and the ultimate influence that these subsidies have on coastal food web dynamics.

EMILY UHRIG (Zoology)

Garter snakes and their endoparasites

Red-sided garter snakes harbor several different genera of endoparasites including nematodes and trematodes in the lung as well as trematodes in the visceral fat and the tissue of the tail. The current study examines intrapopulational patterns in parasite distributions and compares parasite burden between two populations.

Poster Presentation Abstracts *(in alphabetical order)*

ROSALINDA GONZALEZ (Fisheries and Wildlife)

Juvenile Coho Salmon Density in Response to Instream Habitat and Large Wood Restoration

Large wood has been utilized in many restoration projects to improve in-stream habitat for fish. However, the benefits of this practice remain the subject of ongoing debate. We addressed the impact of large wood on in-stream habitat and quantified linkages among life stages to provide a more comprehensive understanding of how wood affects juvenile coho salmon (Oncorhynchus kisutch). We hypothesized that influences of large wood on coho salmon depend on 1) the influence of wood on local habitat features, 2) the degree to which these factors influence coho, 3) the influences of habitat characteristics within the surrounding areas (neighborhoods), and 4) proximity to spawning areas (habitat complementation). To evaluate these influences we randomly sampled coho and instream habitat in 45 pools along a 3km reach in a 3rd-5th order stream in southern Oregon (Little Wolf Creek, middle Umpqua River basin). All sampling was conducted during low flows in August through September. Population estimates were obtained via mark recapture using a combination of backpack electrofishing and seining. Measurements of geomorphic channel features sampled in pools included: pool forming feature, pool area, pool depths, pool distance to wood, and pool substrate depth and type. Water temperature was also recorded continuously throughout the survey. Regression analysis will be used to compare these habitat characteristics to coho density and body size distributions (an important covariate commonly associated with density). Characteristics of pools formed by instream large wood will be compared to those found to be important, thus providing a linkage to how wood influences instream habitat, and in turn how those influences affect density and size of juvenile coho salmon.

JIMMY KLICK (Horticulture)

Immunomarking field perimeters to determine *Drosophila suzukii* movement into red raspberries

Drosophila suzukii Matsumura (Diptera: Drosophilidae) is a serious pest of berry and stone fruits along the west coast. Populations of *D. suzukii* in early spring are greatest in field perimeters, suggesting that the fly overwinters in these protected habitats. Current data suggests that the fly may invade berry and stone fruit crops from field perimeters, particularly those containing the noxious weed, Himalayan blackberry (*Rubus armeniacus*). This study was conducted to determine how field perimeters containing an alternate host (*R. armeniacus*) and field perimeters containing a non-host (wheat) influence *D. suzukii* invasion of cultivated red raspberries. In 2011 and 2012 liquid chicken egg whites were sprayed weekly on field perimeters containing *R. armeniacus* or wheat. Traps placed in the perimeters, at the field-perimeter interface, 30 m, 60 m and 90 m into the raspberries were used to collect flies. All flies were assayed using enzyme-linked immunosorbent assay (ELISA). Higher populations of positively marked *D. suzukii* were observed in fields near *R. armeniacus* than fields near wheat suggesting more flies visited or originated from field perimeters with *R. armeniacus* than with a non-host such as wheat. The implications of managing field perimeters to reduce risk to neighboring crops from *D. suzukii* populations as an alternative pest management strategy are discussed.

BREANNA POWERS (Fisheries and Wildlife)

Butterfly and nectar source abundance and diversity among upland prairie, oak savanna, and oak woodlands in the Willamette Valley

In the Willamette Valley, prairie-oak butterfly species are rapidly declining; this is mainly attributed to loss and degradation of prairie-oak ecosystems upon which these obligate prairie-oak species rely. Butterflies are crucial ecosystem integrity because they provide services such as pollination, prey species (energy transfer), and decomposition. The aim of this study is to evaluate butterfly and nectar resource community structures (abundance and species diversity) among upland prairie, oak savanna, and oak woodlands in the Willamette Valley, Oregon. The objectives of this research are to: (1) assess butterfly species richness and abundance responses across a canopy cover gradient (2) characterize community composition of nectar resources and environmental variables known to be important for individual butterfly species, and (3) correlate butterfly community characteristics with nectar source community characteristics across the environmental gradient. A minimum of 20 circular variable plots (8 m2) were established along a line-transect (≥ 500m) at each study site (12 total) were used for collecting butterfly abundance and species diversity. To obtain data on nectar sources (abundance and species diversity) along with abiotic and host variables, surveys were conducted within each variable plot with a 2m2 vegetation plot. Preliminary results will include an examination of the relationship of butterfly community structure along several environmental gradients (including nectar) with a joint-plot ordination. These finding should guide long term management efforts for the restoration or conservation of remnant prairies, oak savannas, and oak woodlands in the Willamette Valley.

STEPHANIE ROSALES (Microbiology)

Metagenomics to discover unknown neurotropic viruses in a harbour porpoise (Phocoena phocoena) stranded along the Oregon coast

Marine mammals are top predators that are essential for stabilizing coastal marine community, structure, and function.1 Since the 1990s NOAA has continuously documented yearly unusual mortality events (UME) of marine mammals with cetaceans making up 55% percent of deaths.2 Surprisingly, the cause of ~50% of UME have yet to be determined.2 Importantly, research efforts continuously find that marine mammals are susceptible to neurological viral infections, such as Phocine Distemper Virus and Morbillivirus; 3,4 therefore we hypothesized that undetected and/or emerging neurotropic viruses contribute to cetacean stranding events. The discovery of novel viruses with standard techniques (e.g., marker genes degenerate PCR, microarrays, or microscopy) requires some prior knowledge of viral genome sequence or capsid morphology. To circumvent these limitations we approached our question using viral metagenomics. In order to evaluate possible unknown or undetected viruses, we acquired tissues from a male harbor porpoise (Phocoena phocoena) found stranded along the Oregon Coast in June of 2011. The animal was collected by the Marine Mammal Institute in Oregon and was diagnosed by Oregon State University (OSU) veterinarians with possible viral encephalitis. A subsample of brain tissue was used for RNA extraction and depleted of rRNA. Next, extracted RNA was sent to OSU's Center for Genome Research and Bicomputing for cDNA library construction and then pair-end metagenomic sequencing on the Illumina HiSeq 2000 platform. Resulting read lengths were 100 base pairs long, and after quality filtering contigs

were assembled with Velvet. Contigs were then compared to CAMERA's (Community Cyberinfrastructure for Advanced Microbial Ecology Research and Analysis) viral nucleotide database using tblastx. From our metagenomic sequence analysis, it was found that novel retroviruses and Herpesviridae viruses are present in Phocoena phocoena brain tissues. The presence of these sequences indicates that marine mammal stranding events may be associated with novel viral infection and that these viruses may lead to future epidemics in marine mammals.

WEI WEI (Microbiology)

Novel Proteins Involved in Agrobacterium Plant Transformation

Agrobacterium species can transfer a portion of their DNA (T-DNA) and virulence proteins to plant cells. This technology is this the preferred means to create transgenic plants because transgenes delivered by Agrobacterium have lower copy numbers and undergo fewer rearrangements than genes transferred to plants by other methods. To target T-DNA to the nucleus, A. tumefaciens secrete single-stranded DNA-binding protein (VirE2) to plant cells, whereas A. rhizogenes secrete a novel helicase-strand transferase (GALLS), which our lab discovered. The GALLS protein provides an alternative route for nuclear uptake of transferred DNA. The GALLS gene from A. rhizogenes pRi1724 complements a virE2 mutation in A. tumefaciens, and GALLS is essential for virulence in A. rhizogenes strains that lack VirE2. By examining the functional domains of GALLS, we noticed a lack of obvious similarities to virE2, and thus we predict the mechanism in which GALLS helps integrate T-DNA into the host nucleus is very different than that of VirE2. We also discovered that GALLS interacts inside the nucleus with a plant protein (GALLS Interacting Protein; GIP) that is also important for gene transfer. Overexpression of GIP in transgenic A. thaliana stimulates Agrobacterium-mediated transformation up to 15-fold. We hypothesized that GALLS acts as a "molecular tractor", interacting with other secreted bacterial proteins and host proteins such GIP to pull T-DNA into the host nucleus. Currently we are investigating the importance and roles of these proteins in GALLS mediated transformations. We are looking at the importance of proteins involved in VirE2-mediated gene transfer for GALLS-mediated gene transfer by creating mutations in desired genes and observing how the mutations affect virulence. We are also investigating the role of GIP in transformation and how it increases susceptibility of A. thaliana to GALLS mediated transformation by using RNAseq to document changes in the A. thaliana transcriptome when GIP is overexpressed in roots. The findings from these experiments will hopefully improve upon the major limitations of current methods of Agrobacterium plants transformations, which include low or zero transformation frequency in recalcitrant hosts and the hundreds of events required to make one commercially useful transgenic line.

KATIE WOOLLVEN (Marine Resource Management)

Beyond content knowledge: The role of explicit instruction in volunteer learning outcomes for a large-scale citizen science program

Citizen science has gained tremendous popularity in recent years. Because volunteers collect data used in authentic scientific research and resource management, citizen science programs may be ideal settings to promote understanding of the resource management decision-making process. Comparisons have been drawn between volunteer understanding of

data use in policy and education literature on nature of science learning. Three decades of research indicate that nature of science learning requires explicit and reflective instruction, but large citizen science programs often provide instruction for science content only. Citizen science program COASST (Coastal Observation And Seabird Survey Team) has several intended outcomes related to volunteer understanding of how data are used in science and resource management, but formal instruction provided to volunteers about this topic is minimal. However, COASST volunteers are motivated by a deep concern about the environment and may be intrinsically motivated to learn about the end use of their data. This study uses semi-structured volunteer interviews and existing survey data to investigate the following questions: (1) Do COASST volunteers think about the use of their data in science and resource management, and if so, what program features encourage this reflection? (2) How do COASST volunteers describe science, the process of management decision-making, and the role of their work and their data in each? (3) What patterns exist among volunteers who received high/low scores on COASST's assessment of volunteer understanding of the role of their data in professional science and decision-making? Most citizen science research focuses on designing programs to maximize outcomes for science, participants, and society. Information from this study can be used to plan and evaluate similar programs, and to increase the potential for a triple bottom line in the future.

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.

This year BGSS is in the Auditorium in the HMSC Visitor Center, indicated by a star. Registration and breakfast is in the break room/kitchen across the hall from the visitor's center. In the morning, you may need to enter the building through the "After hour access to Ed Wing" entrance and walk down the hallway to the break room/auditorium. This entrance is indicated by a dot on the map.

Directions to the Rental House from HMSC

From Hatfield, get back on Hwy 20 leaving Newport.

Travel east about 2 miles.

You will pass a bright blue building on your right (an auto body shop) and just as you exit the next sweeping curve to the left, you will turn RIGHT into the driveway. The Drive is marked by a statue of a Blue Heron on top of a log post.

There are double gates at the entrance to the house. Outer buildings are not for guest use or access. You may park in the open 3-bay garage and in the very spacious driveway.

The house is located at **2148 Hwy 20, Newport, OR**.