

28th Annual Biology Graduate Student Symposium

Program and Abstracts

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

February 21st, 2015



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Message from the 2015 Organizing Committee

Welcome to the 28th 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.

2015 Organizing Committee

Trang Dang
Miram Gleiber
Antonio Gomez
Natalie Hambalek
Emily Hartfield Kirk
Dani Long
Haley Ohms
James Pflug
Leah Segui
Jenna Sullivan
Danielle Tom

Acknowledgements

We gratefully acknowledge the support of our sponsors:

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Hatfield Marine Science Center (HMSC)

Department of Integrative Biology

Department of Environmental and Molecular Toxicology

Department of Molecular and Cellular Biology

David Maddison

Trader Joes

And special thanks:

Tara Bevandich for her pivotal role in accounting assistance

Ruben Biel for his time and effort into the BGSS website

General Information

Presentations: The symposium will take place in the Auditorium at the Hatfield Marine Science Center (HMSC) (map – pg. 4). 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: Please BYO utensils, plates, and cups. 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 and 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 at 2148 Hwy 20, Newport (map—pg. 5). Please come and enjoy the food, music, and conversation!

Housing and Parking: A map to the rental house is provided on page. 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, therefore carpooling from Corvallis is encouraged.

Schedule of Talks

Time	Presenter	Department	Title
9:15	Registration; refreshments and coffee		
9:50	Opening Remarks		
10:00	Daniel Ottmann Riera	Integrative Biology	Recruitment patterns, ecology and parental relatedness of juvenile rockfish (<i>Sebastes spp.</i>): a research proposal
10:15	Katherine Dziedzic	Integrative Biology	Coral Reef Thermal Acclimation Association Study
10:30	Alissa Rickborn	Integrative Biology	The Rise of the Planet of the Sponges
10:45	Break		
11:00	Keynote Speaker: Dr. Ivan Arismendi		
12:00	Lunch/Poster set-up		
1:00	Kyle Coblenz	Integrative Biology	Dynamics of trophic specialization with a generalist predator population
1:15	Rachael Kuintzle	Biochemistry	Off the Rocker: Age-dependent Changes in the Rhythmic <i>Drosophila</i> Transcriptome
1:30	Shankar Shakya	Botany and Plant Pathology	Potential effects of diurnal temperature oscillations on potato late blight with special reference to climate change
1:45	Break		
2:00	James Pflug	Integrative Biology	Investigating the systematics and genomics of ground beetles (<i>Carabidae</i>) with next-generation molecular techniques
2:15	Zhian Kamvar	Botany and Plant Pathology	Spatial and temporal analysis of populations of the sudden oak death pathogen in Oregon forests
2:30	Hannah Tavalire	Integrative Biology	Immunological personalities: characterizing variation in immune response in a free-ranging mammal
2:45	Miram Gleiber	Integrative Biology	Copepod Summer Grazing Impact and Carbon Export Along the Western Antarctic Peninsula
3:00	Break		
3:15	Ramya Raman	CBEE	PEO-Tethered Peptides for Capture of Circulating Bacteria and Endotoxin in Sepsis
3:30	Danielle Tom	Integrative Biology	Blobby binning: Separating the Metagenome of an Anemone
3:45	Javier Tabima	Botany and Plant Pathology	Genomic signatures of host jumping onto raspberry and strawberry in two <i>Phytophthora</i> sister taxa
4:00	Cammeron Crowder	Integrative Biology	
4:15	Marisa Litz	Fisheries & Wildlife	The prey quality hypothesis: effects of dietary fatty acids on salmon growth, biochemistry, and aerobic performance
4:30	Kurt Ingeman	Integrative Biology	Novel predators and naïve prey: modeling the effects of predator recognition and adaptive prey behavior in an IGP system
4:45	Head out to rental house		

Keynote Speaker



Dr. Ivan Arismendi

This year, we have the great pleasure of hosting Dr. Ivan Arismendi, an assistant professor, senior research in the Department of Fisheries and Wildlife here at OSU. Dr. Arismendi came here from Chile about six years ago and has been working diverse topics such as the invasion ecology of rainbow trout in Chile and how to predict stream temperature changes in response to climate change. He also has some interesting perspectives on life after graduate school and career options for post-docs, including what to do if you don't land that faculty job immediately afterwards.

Map of the Hatfield Marine Science Center

From Corvallis: Take US HWY 20 through Philomath to Newport. In Newport, turn south on US 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 will be held 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.



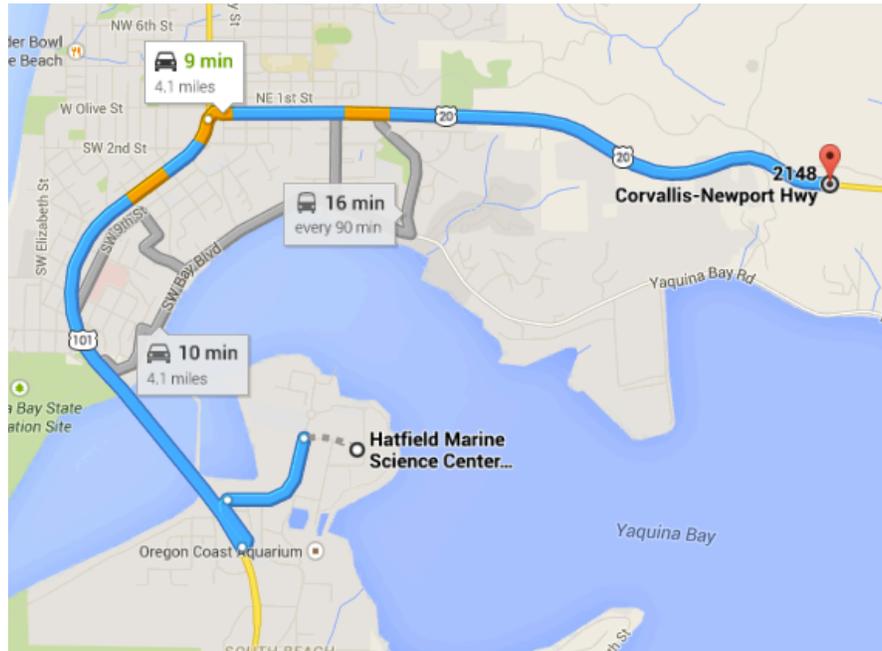
Map to the Rental House from HMSC

The rental house is located at the Bay View Retreat, a 10-minute drive from HMSC.

2148 Hwy 20
Newport, OR 97365

Driving Directions and Parking Information:

Leaving Newport on Hwy 20, 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 drive way. 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 home.



Abstracts

Daniel Ottmann Riera, Integrative Biology

Recruitment patterns, ecology and parental relatedness of juvenile rockfish (*Sebastes spp.*): a research proposal

The Pacific rockfishes (genus *Sebastes*) are a highly diversified group of fishes in the California Current, but some stocks collapsed in the past century as a consequence of overfishing. Hence, management institutions aim to maximize the knowledge of rockfish ecology and life cycle to improve the effectiveness of their programs. By studying spatial and temporal patterns of recruitment to Oregon coasts I will assess potential habitats that are essential to complete the life cycle of rockfishes and evaluate the adequacy of recently established marine reserves. I will complement these observations with data of age at settlement and early growth rates of these juveniles to relate ecological traits with larval dispersal and juvenile settlement. Additionally, I will perform a kinship analysis to find out whether parental related individuals settle together after having spent their first months of life in a pelagic environment. The results of this research can improve the effectiveness of management programs based on ecological knowledge and provide new insights to the currently debated question of whether siblings disperse and recruit together.

Alissa Rickborn, Integrative Biology

The Rise of the Planet of the Sponges

Sponges- what are they? What do they do? Why should you care? Poriferans have profound impacts on ecological communities and environments, and yet, have been traditionally ignored in the scientific literature. This talk will highlight some cool facts about poriferan biology, ecology, and an argument for why you should care about these amazing metazoans.

Ramya Raman, Chemical, Biological, and Environmental Engineering

PEO-Tethered Peptides for Capture of Circulating Bacteria and Endotoxin in Sepsis

Severe sepsis is a blood infection that affects over 750,000 people each year in the US alone, killing 28-50% (more than prostate cancer, breast cancer and AIDS combined). Symptoms result from a highly dysregulated immune response, which, if untreated, can lead to multiple organ failure and death. Currently, treatment uses wide-spectrum antibiotics, but this is hindered by the rise of antibiotic-resistant 'superbugs'. One potential novel treatment is a high-throughput microfluidic hemoperfusion device, which specifically removes circulating bacteria and cell wall fragments ("endotoxin") from blood. Microfluidics offer enhanced mass transfer and control of particle trajectory, as well as very high surface-to-volume ratios. A microfluidic device with a biocompatible and bioactive surface coating could selectively bind circulating bacteria and endotoxins from blood, enabling rapid, safe treatment of bacterial sepsis. WLBU2 is an α -helical, cationic amphiphilic peptide (CAP) with 13 positively-charged arginine and 11 hydrophobic tryptophan/valine residues oriented on opposite faces of the helix. WLBU2 has high anti-microbial activity against a variety of pathogens, and integrates into bacterial cell membranes (Deslouches, et al. J. Antimicrob. Chemother. 2007; 60: 669-672). WLBU2 retains its helical structure when bound to a surface, and immobilized WLBU2 binds

bacteria and endotoxin. Biocompatible, non-fouling surfaces can be made by covalently tethering a dense brush of polyethylene oxide (PEO) polymer chains at the surface. Longer PEO tethers terminated with WLBU2 should enable increased mobility and solvent accessibility to tethered WLBU2, allowing it to bind bacterial cells/endotoxin, without compromising the biocompatibility of the coated surface.

Miram Gleiber, Integrative Biology

Copepod Summer Grazing Impact and Carbon Export Along the Western Antarctic Peninsula

Copepods are important grazers on phytoplankton and contributors to carbon export through production of sinking fecal pellets, but their impact on both is poorly known along the Western Antarctic Peninsula (WAP), a region of rapid climate warming. We conducted copepod grazing and fecal pellet production experiments in the WAP each January from 2012-2014. Gut evacuation and ingestion rates linearly increased with increasing chlorophyll a for most species, with ingestion rates 4-70 times greater in the productive coastal region than in offshore waters. Copepods had a lower grazing impact on phytoplankton biomass (<1%) and productivity (1%, up to 11%) compared to the dominant macrozooplankton in the WAP. Calculated body rations indicated copepods were likely feeding on other sources of carbon (i.e., protozoans and metazoans) to meet metabolic demands, although copepod reliance on phytoplankton varied with chl a and productivity. We found high egestion rates, even in low chl a conditions, but relatively high retention of fecal pellets in the upper water column. Thus, compared to krill, copepods may not be efficient exporters of carbon to depth in this region.

Kyle Coblenz, Integrative Biology

Dynamics of trophic specialization with a generalist predator population

Extensive theory has been developed for the interactions between predators and their prey. However, the majority of existing theory focuses on predators which specialize on a single prey species, though most predators in nature are generalists, feeding upon multiple prey species. Furthermore, a large body of evidence suggests that generalist predator populations are heterogeneous, comprised of individuals that vary from being specialists on a single prey species to generalists that feed across multiple prey species. Therefore, theory is required that accounts for both the generality of a predator at the population level and the heterogeneity among predators at the individual level. Here I present a mathematical model of a one predator-two prey system in which the predator population is compartmentalized into three sub-populations: one that is a generalist on both prey species and two sub-populations that are specialists each on one of the alternative prey species. I present a preliminary numerical analysis of the dynamics of the system assuming a variety of possible functions for distributing predators among the three compartments. I then discuss the possible ramifications of this theory for our understanding of predator-prey dynamics and the stability of predator-prey interactions.

Rachael Kuintzle, Biochemistry

Off the Rocker: Age-dependent Changes in the Rhythmic *Drosophila* Transcriptome

A robust circadian clock is well known to be an integral part of healthy aging. Senescent flies and mammals exhibit irregular behavioral and sleep rhythms, which are associated with neurodegeneration and increased susceptibility to oxidative stress. In flies, these phenotypes are exacerbated in clock gene mutants, suggesting that the ability to maintain strong clock function may slow down aging and extend healthspan. However, the molecular basis for age-related circadian dysregulation is unknown. To investigate this, we performed RNA sequencing (RNA-Seq) and compared the temporal expression profiles of circadian transcripts in young and old *Drosophila melanogaster*. Our hypothesis that aging of the circadian clock may lead to dampened oscillations in the expression of clock-controlled genes was supported by a large group of genes which lose amplitude or become arrhythmic in old flies. Unexpectedly, we also identified a subset of genes which are arrhythmic in young flies but adopt a rhythmic expression pattern during aging. Our data also revealed a potential novel, multi-exonic, age-activated noncoding gene with rhythmic expression. This study demonstrates extensive and diverse effects of aging on rhythmic RNA levels and provides a genome-wide map of isoform-resolution expression in senescent *Drosophila*.

Shankar Shakya, Botany and Plant Pathology

Potential effects of diurnal temperature oscillations on potato late blight with special reference to climate change

Global climate change will have effects on diurnal temperature oscillations as well as on average temperatures. Studies on potato late blight (*Phytophthora infestans*) development have not considered daily temperature oscillations. We hypothesize that growth and development rates of *P. infestans* would be less influenced by change in average temperature as the magnitude of fluctuations in daily temperatures increases. We investigated the effects of seven constant (10, 12, 15, 17, 20, 23, and 27°C) and diurnally oscillating (± 5 and $\pm 10^\circ\text{C}$) temperatures around the same means on number of lesions, incubation period, latent period, radial lesion growth rate, and sporulation intensity on detached potato leaves inoculated with two *P. infestans* isolates from clonal lineages US-8 and US-23. A four-parameter thermodynamic model was used to describe relationships between temperature and disease development measurements. Incubation and latency progression accelerated with increasing oscillations at low mean temperatures but slowed down with increasing oscillations at high mean temperatures ($P < 0.005$), as hypothesized. Infection efficiency, lesion growth rate, and sporulation increased under small temperature oscillations compared with constant temperatures but decreased when temperature oscillations were large. Thus, diurnal amplitude in temperature should be considered in models of potato late blight, particularly when predicting effects of global climate change on disease development.

James Pflug, Integrative Biology

Investigating the systematics and genomics of ground beetles (Carabidae) with next-generation molecular techniques

Next generation sequencing techniques are rapidly changing the nature of evolutionary biology and systematics. Even modest projects are capable of generating large amounts of useful sequence data with minimal effort. Here we present preliminary analyses of shallow-

scale genome sequences obtained from several of beetles in suborder Adephaga, with an emphasis on potential phylogenetic utility and applications.

Zhian Kamvar, Botany and Plant Pathology

Spatial and temporal analysis of populations of the sudden oak death pathogen in Oregon forests

A disease known as Sudden Oak Death was discovered in California in the mid 1990's. It was formally described as the clonal Oomycete, *Phytophthora ramorum* in 2000. Known to infect a wide range of hosts including *Rhododendron*, *Quercus*, and *Notholithocarpus* species, *P. ramorum* has a large impact on forest health. It was first detected in Oregon forests in 2001 by aerial surveys, and was followed by an ongoing and aggressive eradication effort by the Oregon Department of Forestry in Curry County. Populations from symptomatic tanoaks were sampled from 2001 to 2014, genotyped using microsatellite markers, and studied to infer population genetic history. While there are three clonal lineages found in nurseries on the North American west coast, only the NA1 lineage has been discovered in OR forests. Since the initial introduction event into the Joe Hall area, the pathogen has spread North, West, and Southwest within Curry county. A discovery in the Hunter Creek area in 2011 appears to be a second introduction as it does not cluster with the early introduction or subsequent infections. Utilizing population genetic analyses appropriate for clonal organisms with data from OR forests and west coast nurseries, we give support for a most parsimonious scenario of at least two distinct introduction events from Oregon or California nurseries. Continued vigilance and eradication of nursery populations of *P. ramorum* are important to avoid further emergence and potential introduction of other clonal lineages.

Hannah Tavalire, Integrative Biology

Immunological personalities: characterizing variation in immune response in a free-ranging mammal

The fields of ecological immunology and disease ecology have rapidly converged in the past few years to produce studies investigating both the underlying causes for heterogeneity in host response (eco-immunology) and the mechanisms of disease spread in populations and communities (disease ecology). One cause of heterogeneity in host response is variation in underlying immune mechanisms. Recent studies have defined genetically determined patterns in life history response to infection by broad characterizations such as resistance and tolerance (e.g., Raberg & Sim, 2007; Vale & Little, 2012), but most do not directly measure immune response. Furthermore, studies measuring immune response to a particular pathogen take place in controlled laboratory settings, ignoring important environmental factors, including co-infections. No studies have characterized overall "immune phenotype" as an animal trait, though many studies have quantified genetic variation for immune response at certain loci. Immune phenotype consists of an animal's relative investment in basic functional divisions within the immune system. Variation in immune phenotype can manifest in emphasis on constitutive versus inducible and fast versus lasting immunity (innate versus adaptive), as well

as micro- versus macroparasite defenses (TH1 versus TH2). In addition, an immune phenotype allows the animal's tendency toward one pole of these axes to be predictable over time, therefore allowing us to predict infection probability. Here I propose to use a long-term dataset in free ranging African buffalo (*Syncerus caffer*) to define immune phenotype as an animal trait, as opposed to a specific response to a particular infection.

Katherine Dziedzic, Integrative Biology

Coral Reef Thermal Acclimation Association Study

Coral reefs have become vulnerable to climate change, with mass bleaching events, the loss of symbiotic algae (*Symbiodinium spp.*), increasing in both frequency and severity. If bleaching trends continue, models predict > 90% of reef species may face long-term degradation. However, recent evidence has shown that corals may be able to thermally acclimate to increasing sea surface temperatures through adaptive processes of the coral host, their algal symbionts, or both³. Although substantial efforts are being made to understand physiological mechanisms of coral stress tolerance and acclimation, virtually nothing is currently known about the genetic mechanisms that might enable their adaptation to the changing climate. Association studies use genetic variants called single nucleotide polymorphisms (SNPs) to associate phenotypic traits with particular locations along genes. The knowledge gained from these comparative analyses may provide insights into genome organization, evolution and function, providing hope for coral reef studies. In order to examine potential mechanisms of thermal acclimation, I will focus on associating acclimation in the species *Orbicella faveolata* with a study in Bocas del Toro, Panama during Summer 2015.

Danielle Tom, Integrative Biology

Blobby binning: Separating the Metagenome of an Anemone

Javier Tabima, Botany and Plant Pathology

Genomic signatures of host jumping onto raspberry and strawberry in two *Phytophthora* sister taxa

Contrasting the genomes of sister taxa with narrow but different host ranges provides an ideal system for studying host adaptation. Selection pressures imposed by different hosts are expected to lead to adaptation by gradual divergence of populations and eventual speciation due to reproductive isolation. This process of host-mediated speciation is expected to leave signatures (such as mutations, recombination, indels, or duplications) in the corresponding pathogen genomes. Using paired-end approaches on the Illumina HiSeq2000 platform we sequenced and annotated the genomes of two sister species in the plant pathogen genus *Phytophthora*: *P. rubi* and *P. fragariae* to study which genomic signatures are involved in host adaptation (*P. rubi* and *P. fragariae* exclusively infects the genus *Rubus* or *Fragariae* respectively). Genomes were assembled using SOAPdenovo version 1.05. Gene calling was performed using MAKER, AUGUSTUS and SNAP. The genomes of *P. rubi* and *P. fragariae* yielded 9,434 scaffolds and an estimated 18,268 genes for *P. rubi* and 8,511 scaffolds and 17,832 genes for *P. fragariae*. Functional annotation shows a similar number of genes involved in different biochemical pathways, such as sugar processing, metabolism, and amino acid synthesis between the two species. Positive selection (dN/dS) was detected for three pairs of

orthologous effector proteins in the RxLR class. Ongoing work is being conducted to identify other candidate genes under selection and genomic signatures that may have been involved in the process of speciation via host jumping

Camerron Crowder, Integrative Biology

Corals, the foundational species of coral reefs, suffer reduced fecundity and hindered reproductive development in response to increased ocean temperatures attributed to global warming. However, the molecular and physiological mechanisms governing coral reproduction and the effect increased seawater temperature has on these processes is unknown. Although little is known about the molecular mechanisms of reproduction, multiple environmental variables including temperature and lunar periodicity are correlated with the timing of reproduction in corals. In this study RNA-Seq was used to investigate global gene expression profiles associated with temperature (both high, 28°C and low, 23°C) and lunar phase (new moon, 1st quarter moon, full moon, and last quarter moon) in order to investigate signal transduction and cell signaling pathways involved in cueing reproductive events in the coral *Pocillopora damicornis*. The interaction of lunar phase and temperature together had the largest influence of gene expression profiles and multiple signaling pathways homologous to vertebrate reproductive endocrinological pathways were differentially expressed.

Marisa Litz, Fisheries and Wildlife

The prey quality hypothesis: effects of dietary fatty acids on salmon growth, biochemistry, and aerobic performance

Chinook (king) salmon (*Onchorhynchus tshawytscha*) are a culturally and economically iconic species on the west coast of North America, yet nine ESUs (Evolutionary Significant Units) receive federal protection from the U.S. Endangered Species Act. Chinook salmon experience a period of high mortality (> 90%) upon first entering the ocean as juveniles. It has been hypothesized that ocean conditions influence juvenile salmon mortality by influencing the quality of salmon prey, but research evaluating the effects of prey quality on salmon performance are limited. We conducted a 20-week experiment to quantify the effects of prey quality on juvenile Chinook salmon growth, lipid composition, isotope signatures, and swimming performance. Salmon were reared for 12 weeks on three energetically similar diets enriched with two prey types (anchovy and krill) and two essential fatty acids (docosahexaenoic acid, DHA and eicosapentanoic acid, EPA). Based on previous studies using larvae, we predicted that fish reared on a diet rich in DHA (anchovy diet) would grow faster than fish fed a diet rich in EPA (krill diet) or a diet with equal ratios of DHA to EPA (krill:anchovy diet). From weeks 12-16, we adjusted rations to see if there was a carryover effect of dietary fatty acids on salmon growth and lipid reserves. Finally, from weeks 16-20, ration was withheld from all salmon before measuring critical swimming speed to assess a carryover effect on foraging capabilities and predator avoidance. Growth rates during the feeding study were similar (0.29 to 0.35 mm d⁻¹). However, by the end of the experiment, salmon reared on the anchovy diet were on average 11 mm larger, had 17.9 mg g⁻¹ more lipids, and swam 25 mm s⁻¹ faster than salmon reared on the other formulated diets. These

results provide support for the hypothesis that prey quality is important for juvenile salmon during a critical period in their early life history, and suggests that prey rich in DHA could provide a survival advantage to salmon prior to experiencing their first ocean winter.

Kurt Ingeman, Integrative Biology

Novel predators and naïve prey: modeling the effects of predator recognition and adaptive prey behavior in an IGP system

The introduction of a predator into an existing food web creates a number of novel competitive and trophic interactions, often with non-intuitive effects on species persistence and community stability. For example, introduced and native predators may benefit from an indirect mutualism if anti-predator behavior elicited by one species results in increased predation success in the other. This interaction can also be influenced by prey's ability to accurately evaluate predation risk, potentially yielding competitive advantage to an unrecognized predator (prey naïveté). By incorporating likely features of a predator introduction into an intraguild predation (IGP) model, it is possible to generate hypotheses regarding the effects of invasion on the stability of host communities. My objectives therefore, are (1) to examine the effects of adaptive prey foraging on community structure and stability in an IGP module (2) model generalized prey defense versus antagonistic predation-risk trade-offs, and (3) incorporate prey naïveté in relation to individual predator species in the model community. Each model variation will incorporate adaptive prey foraging behavior in the basal prey resource, whereby prey optimize fitness with regards to the trade-off between predation risk and foraging gain in response to the density of one or both predators. By modifying the anti-predator behavioral response, I will model prey naïveté that is a likely feature of (at least some) predator introductions. Thus, I will generate predictions about whether adaptive prey behavior can stabilize an inherently unstable IGP community, and whether this stability relies on either predator-specific risk trade-offs, perfect knowledge of predation risk, or both.