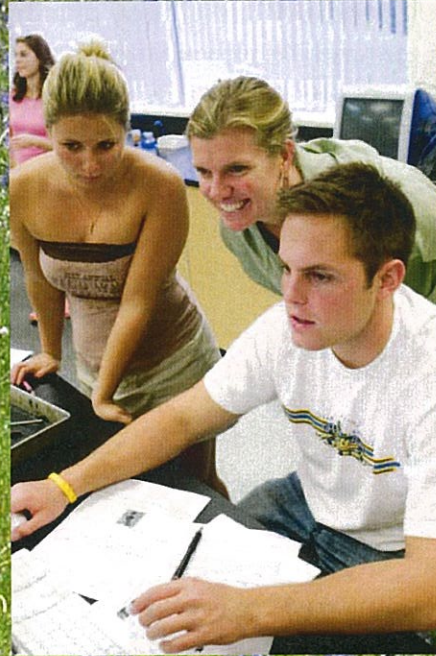


Biology Research Symposium



April 23rd, 2012

2:00-5:15 pm

Refreshments served at 1:45 pm

Cat Cavern Dining Rooms 1 and 2

CONGRATULATIONS TO ALL!

Each of you embarked on a journey of inquiry and discovery that led to this special day of research presentations. You had opportunities to explore on your own and in collaboration with faculty mentors, your peers, and often other professionals and people that have been influential in your lives. We hope you know that the biology faculty are extraordinarily proud of your accomplishments and would love to hear from you in the future as your career paths develop throughout your lives.

In all, as the Biology Faculty we would like to express our sincere congratulations to each of you and wish you the best for the future!

Melissa Marks

Emma Coddington

Jason Duncan

Barbara Stebbins-Boaz

Chris Smith

David Craig

Susan Kephart

Gary Tallman

Jennifer Butler

Sharon Rose

Susie Dunham

Briana Lindh

Jennifer Johns

Biology Research Symposium Schedule

23 April 2012

Session 1 - Cat Cavern Dining Room 1

Moderators: *Susan Kephart and Chris Smith*

Presenter	Time	Title
Gina Pahlke	2:00	Comparing the effect of inflorescence architecture on pollinator visitation patterns and female fecundity for insect-pollinated angiosperms (p8)
Jessica Faust	2:15	Examination of Genitalia Allometry in Parapatric Sister-Species of Female Yucca Moths (p3)
Christin Licata	2:30	Reproductive cost to Yucca brevifolia spp. of obligate mutualism with Tegeticula spp. (p7)
Tom Hallowed	2:45	Assessing the Effects of Phenotype Matching on Reproductive Fitness in an Obligate Pollinator Mutualism (p6)
James Baldwin	3:00	Ecological Niche Modeling of Camassia in Oregon: A tool for understanding species boundaries in rare and common plants (p1)
Hallie Williams	3:15	Morphology and Social Signaling in Canis lupis familiaris (p12)

BREAK

3:30-3:45

Moderator: *David Craig*

Shealyn Friedrich	3:45	Individual Lateralization of Feeding Behavior in a Bill-load Holding Seabird (p4)
Brady Ryan	4:00	Fighting for a fish: Evaluating patterns of sibling rivalry in the Caspian tern (p9)
Emily Bee	4:15	The effects of phytoestrogens on the development and behavior of Danio rerio larvae (pg1)
Brittany Chin	4:30	Using Extrinsic Markers to Identify Individual Eastern Gray Squirrels, Sciurus carolinensis (p2)
Victoria Smith	4:45	Blood Suckers and Babies: Advancements in Biliary Atresia Research (p11)
Kate Gadek	5:00	Ethylene's Regulation of the Floral Transition in Pharbitis nil 'violet' (p4)
Bart Grabman	5:15	Factors That Affect Response Time in Collegiate-Based EMS (p5)

Biology Research Symposium Schedule

23 April 2012

Session 2 - Cat Cavern Dining Room 2

Moderators: *Jason Duncan and Barbara Stebbins-Boaz*

Presenter	Time	Title
Whitney Stannard	2:00	Characterization of Pex 1WU1 Function in the Peripheral Nervous System of <i>Drosophila melanogaster</i> (p12)
Carolyn Gary-Sage	2:15	Bacterial growth inhibiting peptides in the skin secretions of <i>Xenopus laevis</i> (p5)
Justin Etzel	2:30	Factors Influencing Left-Right Determination in <i>Xenopus laevis</i> Embryos (p3)
Alex Johnson	2:45	2,4-Dichlorophenoxyacetic Acid Activates the Raf/MEK Pathway in <i>Xenopus laevis</i> Oocytes while Simultaneously Blocking Maturation (p6)
Emily Simmons	3:00	Promoter Analysis of the Kiss1R Gene to Probe for Estrogenic and Circadian Regulation of Transcription (p10)
Juliane Krause	3:15	An analysis of microbial populations cultured from high traffic areas on Willamette University's campus (p7)

BREAK

3:30-3:45

Moderators: *Melissa Marks and Sharon Rose*

Robin Palmer	3:45	Manipulation of zwf expression and modulation of growth rate in <i>Caulobacter crescentus</i> (p9)
Logan Blair	4:00	Sequencing <i>Nicotiana glauca</i> Polyamine and Ethylene Biosynthetic Genes to Study the Effects of Heat on their Transcription (p2)
Sarah Sonnenfeld	4:15	Corticosterone regulation of vasotocin signaling: An imaging study (p11)
Jacob Munson-McGee	4:30	An investigative study of petroleum hydrocarbon biodegradation by microbial communities in clean and contaminated water (p8)
Stephanie Skelly	4: 45	Identification, Molecular Genetic and Phenotypic Characterization of a fat facets (fafWU2) Allele in <i>Drosophila melanogaster</i> (p10)
Alfredo Zuniga	5:00	The Microtubule Regulatory Protein Stathmin is Essential for Axonal Transport (p12)

Ecological Niche Modeling of *Camassia* in Oregon: A tool for understanding species boundaries in rare and common plants

James Baldwin

Thesis Mentor-Dr. Susan Kephart

Ecological Niche Modeling is a process that enables scientists to evaluate the potential for niche differentiation between species and to test whether niche conservatism occurs across species over time. *Camassia* consists of six species and can be found in wet prairies and woodlands in North America. The peak genetic diversity occurs in Oregon, yet the importance of ecological barriers among these species has been little studied. This experiment examines the realized niches of rare and common species of *Camassia*, which include *C. howellii*, *C. leichtlinii*, *C. quamash* and several of their respective subspecies. The study used environmental layers produced from Worldclim to compare niches for species occurrence in Oregon. The programs Maxent and ENMtools were used to generate and test hypotheses based on occurrence data collected from herbarium loans and direct field observations as well as using 15 environmental layers. We initially hypothesized that statistically differentiated niches exist between species of *Camassia*, due to the broad geographic distribution of the species and prior field data in natural populations. However, the results of this modeling experiment revealed that when the niches of these *Camassia* species were compared based on climate variables, there was no statistical differentiation among species suggesting that these environmental layers are not limiting these species distributions. However, the scale of the climatic analysis may be insufficient to detect local differences in this pilot modeling experiment. Thus, possible explanations for the lack of niche differentiation include the presence of barriers or disjunction in habitable areas, or the existence of untested niche dimensions, including soil type.

The effects of phytoestrogens on the development and behavior of *Danio rerio* larvae

Emily Bee

Thesis Mentor-Dr. David Craig

Phytoestrogens are naturally occurring non-steroidal plant derivatives known as dietary estrogens. Kaempferol, Apigenin, Apigenin-7-glucoside, Epicatechin, Epicatechin-gallate, Enterolactone, Galangin, Biochanin A, Glycitin, Matairesinol, Quercetin, R-Equol, S-Equol and racemic Equol are all phytoestrogenic compounds that mimic endocrine hormone activity when consumed. This study investigated the effects of these compounds on the embryonic development and larval swimming behavior of *Danio rerio*. Non-toxic experimental concentration ranges were determined for each compound, and swimming behavior of larvae exposed to these concentration ranges was observed. At concentrations greater than 10 μ M, nearly all fourteen compounds exhibited toxic properties, resulting in mortalities and debilitating malformations such as pericardial edema, yolk sac edema, curved axes, and truncated body shapes in *Danio rerio* embryos. Behavioral tests were conducted by tracking swimming activity of phytoestrogen exposed larvae under controlled light and dark cycled treatments. Our study found that while exposure to non toxic (less than 10 μ M) concentrations of most compounds did not yield significant results, Quercetin and Galangin exposure resulted in statistically significant differences in swimming behavior under the dark cycle treatment. The results of this study provided preliminary data for continued research into the physiological effects of phytoestrogens on the model organism *Danio rerio*.

Sequencing *Nicotiana glauca* Polyamine and Ethylene Biosynthetic Genes to Study the Effects of Heat on their Transcription

Logan Blair

Thesis Mentor-Dr. Gary Tallman

Though the negative effects of heat stress on plant growth have been well documented, we still do not fully understand the cellular and molecular mechanisms underlying these effects. *Nicotiana glauca* (Graham), tree tobacco, has evolved a high basal thermotolerance. Cultured *N. glauca* guard cell protoplasts (GCP) do not regenerate cell walls, dedifferentiate, re-enter the cell cycle, or divide under heat stress (38°C), and heat suppresses activation by auxin of the *BA* auxin-responsive transgene promoter in *N. glauca* GCP. L-N⁶-monomethyl arginine (L-NMMA), an inhibitor of nitric oxide (NO) production in animals and plants, mimics the effects of heat stress by suppressing activation of the *BA* promoter, linking reduced NO levels to suppressed auxin signaling and function. Both polyamine-dependent NO biosynthesis and ethylene biosynthesis require S-adenosyl methionine (SAM) as a precursor. We hypothesize that heat stress increases the rate of the ethylene biosynthetic pathway at the expense of the polyamine-dependent NO biosynthetic pathway, thereby reducing NO dependent auxin signaling and inhibiting plant growth. qPCR probes are being designed to determine whether enzymes in the polyamine and ethylene biosynthetic pathways are transcriptionally regulated by heat. I isolated and sequenced two of four partial cDNA targets, one for S-adenosylmethione decarboxylase involved in the polyamine and ethylene biosynthetic pathways and the other for 1-aminocyclopropanecarboxylic acid oxidase involved only in the ethylene biosynthetic pathway. These sequences will be used to design *N. glauca* gene-specific qPCR primers to study the effects of heat on transcription of polyamine and ethylene biosynthetic genes.

Using Extrinsic Markers to Identify Individual Eastern Gray Squirrels, *Sciurus carolinensis*

Brittany Chin

Thesis Mentor-Dr. David Craig

There are currently multiple methods used for identifying individual squirrels. However, all are intrusive to the animal involving trapping and subsequent tagging with skin piercing ear tags, spray paint, and wrapping bands. Trapping, catching, and tagging squirrels takes up a lot of valuable time and resources that may be put to better use, especially in urban environments where squirrels are easy to observe. This paper looks at the efficacy of using naturally occurring extrinsic markers to identify individual eastern gray squirrels, *Sciurus carolinensis*. Footage of squirrels was collected over 4 different days at the Capitol in Salem, Oregon initially. Three weeks after initial footage days more data was gathered to test if extrinsic markers are viable over time. Photos were taken from this footage for comparison. On any given day the maximum number of squirrels was 15, indicating the number of squirrels that use the area of study. Of those 15 at least 4 are easily identifiable, but data suggests that at least half the squirrels could be identified with time. The extrinsic markers used to differentiate squirrels include: variation in ear tufts, variation in coat patterns, and scars/tail deformations. Research that could use this new method is to determine if squirrels can differentiate between individual people. Understanding if squirrels are capable of recognizing individual people could explain why squirrels have successfully adapted to urban environments and contribute to the field of urban ecology and conservation.

Factors Influencing Left-Right Determination in *Xenopus laevis* Embryos

Justin Etzel

Thesis Mentor-Dr. Michael Danilchik, Oregon Health & Sciences University

Left-right body patterning in most vertebrates is influenced by a common pathway. It involves unidirectional cilia-generated flow in the archenteron of neurulating embryos to establish an asymmetry. The frog, *Xenopus laevis*, was used as a model system to further investigate the details of this pathway. In a previous investigation, 2-3 butanedione monoxime (BDM), a putative myosin ATPase inhibitor, was shown to disrupt left-right pattern formation in *Xenopus* embryos. Specifically, organ placement was randomized or reversed, known as *situs invertus*. To begin identifying the target of this inhibitor, the present study was carried out to determine the developmental stage most sensitive to BDM-induced organ randomization. Embryos were exposed to 20 mM BDM for 2 h periods at selected developmental stages between cleavage and neurulation. Confocal microscopy and fluorescent polystyrene microspheres (FluospheresTM) were used to monitor archenteron development and track ciliary flow, respectively. These experiments identified gastrulation as the developmental time point during which embryos were most susceptible to the randomizing effects of BDM. Developmental delays and changes in archenteron morphology were also observed. Further analysis is needed to determine BDM's effects on cilia-generated flow. These results support an alternative pathway for left-right body patterning that occurs prior to neurulation.

Examination of Genitalia Allometry in Parapatric Sister-Species of Female Yucca Moths

Jessica Faust

Thesis Mentor-Dr. Chris Smith

Obligate pollinator systems, systems in which both the sole pollinator and the pollinated angiosperm depend on one another for reproduction, have been predicted to facilitate diversification of both the angiosperm and pollinator species. Moreover, obligate pollinator systems are prone to coevolution as the plant species and its pollinator diversify in parallel. One such system is that of the Joshua Tree (*Yucca brevifolia*; Agavaceae) and its obligate pollinator, the yucca moth (*Tegeticula spp.*) in which observed phenotype matching between the moth's ovipositor length and the width of the yucca's stylar canal has caused speculation of a history of coevolution. Body size and its effect on ovipositor length were examined between two species of yucca moth (*Tegeticula synthetica* & *Tegeticula antithetica*) to gain a better understanding of whether ovipositor length is increasing allometrically with body size, indicating that selection is acting specifically on ovipositor length. Results show that body size is not significantly correlated with ovipositor length for either species of moth, and that the interaction between the morphological features is not significantly different between the two species. We conclude that we are unable to reject the null hypothesis of isometry.

Individual Lateralization of Feeding Behavior in a Bill-load Holding Seabird

Shealyn Friedrich

Thesis Mentor-Dr. David Craig

Behavioral lateralization, or the preferential use of one side of the body over the other within the context of a given activity, has been documented in a wide range of vertebrate species. Such directional asymmetries are believed to be reflective of specialized brain function and can occur either at the population or the individual level. Several studies have found evidence for avian visual lateralization which may provide insight into the functional specialization of the brain's separate hemispheres. In this study, we recorded the feeding events of Caspian tern chicks (a piscivorous bill-load holding bird), ages one to four weeks, to determine whether this species exhibits individually lateralized feeding behavior with respect to fish orientation and eye use. For three of the four lateralization measures generated, there was a significant tendency for individuals to demonstrate a right side bias. This was particularly true with respect to eye use. Although positive correlations were found for the relationship between the directionality of lateralization and feeding efficiency, none of these correlations were significant. This research adds to a growing body of evidence for the presence of behavioral and cerebral lateralization among birds and other vertebrates at the individual level.

Ethylene's Regulation of the Floral Transition in *Pharbitis nil* 'violet'

Kate Gadek

Thesis Mentor-Dr. Alison Fisher, Chemistry

The phytohormone ethylene is involved in many plant developmental processes, from seed germination to fruit ripening. However, ethylene's role in plant flowering is not well understood. In this study, the effects of altered ethylene biosynthesis or perception on expression of specific genes involved in the floral transition of *Pharbitis nil* 'violet' (Japanese morning glory) were examined. Previous data have shown that ethylene regulates the expression of the *FLOWERING LOCUS T (FT)* homologs, *PnFT1* and *PnFT2*, in *Pharbitis*. The objective of this study was to examine ethylene's regulation of *GIGANTEA (PnGI)* and *APETALA-like2 (PnAP2-like)*, two potential upstream regulators of *PnFT1/2*. Plants were treated with 1-aminocyclopropane-1-carboxylic acid (ACC; the biosynthetic ethylene precursor that increases ethylene production), aminoethoxy-vinylglycine (AVG; an inhibitor of ethylene biosynthesis), or silver thiosulfate complex (STS; an inhibitor of ethylene receptor binding). Plants were then induced to flower with a single 16-hour dark period or exposed to continuous light (control). *PnGI* and *PnAP2-like* transcripts were quantified using reverse transcription coupled with quantitative PCR (RT-qPCR). Our results indicated that ethylene does not regulate *PnGI* expression. Our results also demonstrated an increased amount of *PnAP2-like* transcripts in non-flowering control plants, suggesting that *PnAP2-like* may act as a floral repressor.

Bacterial growth inhibiting peptides in the skin secretions of *Xenopus laevis*

Carolyn Garey-Sage

Thesis Mentor-Dr. Sharon Rose

The peptide-containing slime coat of *Xenopus laevis* is produced by granular glands that develop from epidermal cells during the metamorphic period. These peptides have antimicrobial properties and serve as the first line of defense against certain pathogens. The purpose of this study was to determine if there was a difference in the effectiveness of bacterial growth inhibition between the slime coat of *X. laevis* that were raised in their natural environment and the slime coat of frogs that were raised in a lab environment. If wild-type frogs were better adapted to inhibit bacterial growth, this could indicate that the wild environment had possibly selected for individuals that had more peptides or peptides that were effective at inhibiting bacterial growth. This particular study did not indicate any significant difference between lab-bred and wild type organisms, however there was a significant inhibition of *Staphylococcus aureus* growth in the presence of lower concentrations of both wild raised and lab bred frog slime as compared to inhibition from tap water.

Factors That Affect Response Time in Collegiate-Based EMS

Bartholomew Grabman

Thesis Mentor-Dr. David Craig

Minimizing response time in collegiate-based emergency medical services (CBEMS) may improve provider-patient relations, increase the quality of care patients receive, and, most importantly, maximize survivability for critical patients. However, while several studies have focused on response time in traditional EMS systems, the applicability to CBEMS is limited. CBEMS face unique and additional challenges, including a lack of available resources, limited patient transport capabilities, and a younger patient population. Using Pre-Hospital Care Reports from the last 15 years (1997-2011; n=840) collected through Willamette University EMS, factors affecting response time, including time of day, the type of emergency, whether a patient was transported to another medical care facility, and whether a patient ingested alcohol, will be discussed in detail.

Assessing the Effects of Phenotype Matching on Reproductive Fitness in an Obligate Pollinator Mutualism

Thomas Hollowed
Thesis Mentor-Dr. Chris Smith

In an ongoing study of coevolution between Joshua trees (*Yucca brevifolia* spp.) and their obligate moth pollinators (*Tegeticula* spp.), we are assessing the influence of phenotype matching on the reproductive fitness of female moths. Female moths oviposit by cutting through the ovary wall of the Joshua tree flower, inserting her ovipositor down the stylar canal, and laying her eggs atop the ovules. Previous research found that larval emergence rates were generally higher when the female moth ovipositor was similar in length to the stylar canal of the flower in which she laid her eggs. This evidence suggests that phenotype matching results in greater reproductive fitness for the moth species. Similarly, ovipositors of matching length minimize the harm done to the flower while still allowing the moth to successfully reproduce, so there may be fitness benefits in phenotype matching for the plant as well. What is more, parapatric distribution patterns of moth and tree species correlate with patterns of phenotype matching. It is posited that selection for phenotype matching may be driving an ongoing process of divergent selection that may ultimately lead to speciation. In our study, we utilize an experimental design that involved caging wild Joshua tree inflorescences and treating them with female moths of known ovipositor lengths. A total of 356 larvae were collected and genotyped at nine microsatellite loci. Knowing the genotype of the larvae at these loci, we can assign sibship groups using a computer program called COLONY. Using statistical methods still yet undetermined, we will assess the influence of phenotype matching on the reproductive fitness of the female moths in our study.

2,4-Dichlorophenoxyacetic Acid Activates the Raf/MEK Pathway in *Xenopus laevis* Oocytes while Simultaneously Blocking Maturation

Alexandria Johnson
Thesis Mentor-Dr. Barbara Stebbins-Boaz

Progesterone-induced oocyte maturation in the frog, *Xenopus laevis*, is required for egg formation and subsequent fertilization. During this process full-grown stage VI oocytes advance from prophase I and arrest at metaphase II, marked by germinal vesicle (nuclear envelope) breakdown (GVBD) and the formation of a visible white spot on the pigmented animal pole of the oocyte. Biochemically, these events are regulated by the Mos/MAPK/p34Cdc2/cyclin B1 signaling pathway. Disruption of the pathway by endocrine disrupting chemicals would have negative consequences for species fertility and could contribute to documented global amphibian declines. The widely used hormonal herbicide, 2,4-dichlorophenoxyacetic acid, has been previously shown to block oocyte maturation *in vitro* by inhibiting Mos and p34Cdc2 activation, but unexpectedly, 2,4-D activates MAPK. Here, it was hypothesized that 2,4-D utilizes the Raf/MEK pathway to activate MAPK. Data from Western blot analysis using phospho-specific antibodies suggest that 2,4-D did indeed induce Raf and MEK activation, while progesterone only induced activation of MEK but not Raf. These results suggest that while 2,4-D blocks one upstream activator of MAPK, Mos, it induces an alternative upstream activator, Raf, which is not required for maturation.

An analysis of microbial populations cultured from high traffic areas on Willamette University's campus

Julianne Krause

Thesis Mentor-Dr. Sharon Rose

Methicillin-resistant *Staphylococcus aureus* (MRSA) and *Escherichia coli* (*E. coli*) are pathogenic bacteria known to spread in hospital settings and cause severe secondary illnesses. However, in environments mimicking that of a hospital, with high traffic areas and populations of ill and healthy individuals mixing in a concentrated space, such as a school, MRSA and *E. coli* become viable threats to the health of the general population. To test if the results could be duplicated on Willamette University's campus, keyboard and atmospheric samples were collected from computer labs of varying traffic amounts; samples were incubated under appropriate culture and temperature regimes. There were significantly more gram+ and gram- bacteria collected from keyboards than collected from the atmosphere. However, there was no significant difference in the amount of bacteria cultured and the traffic level of the lab they were sampled from. Most importantly, there was a significant difference in the presence of more gram+ than gram- bacteria because it is suggested that gram+ bacteria cause more severe nosocomial infection outcomes than gram- bacteria. Although not found at an alarming level as compared to the number of pathogens found in a hospital, their presence may have the potential to become a problem in the future.

Reproductive cost to *Yucca brevifolia* spp. of obligate mutualism with *Tegeticula* spp.

Christin Licata

Thesis Mentor-Dr. Chris Smith

Coevolution is one mechanism that is thought to promote diversification and speciation, especially in plant-pollinator interactions. The mutualism between Joshua trees (*Yucca brevifolia*) and their pollinators (*Tegeticula* spp) is one system in which plants and pollinators are thought to be coevolving. Joshua trees depend on the moths for pollination, which requires active work by the moth; the moth larvae only eat the seeds of the developing fruit, which imposes a fitness cost to the tree. The current model hypothesizes that the plants are selected for longer floral styles, relative to ovipositor length, which is thought to reduce seed consumption by moth larvae while maintaining the benefits of the interaction (namely, pollination). Here, I report the results of a reciprocal transplant experiment testing this hypothesis. Different subspecies of Joshua tree that differ in style length [*Yucca brevifolia brevifolia* (long-styled) and *Yucca brevifolia jaegeriana* (short-styled)] were experimentally exposed to moths that differ in ovipositor length [*Tegeticula synthetica* (long-ovipositor) and *Tegeticula antithetica* (short-ovipositor)]. The number of seeds eaten per fruit was used as the measure of fitness cost. The results showed strong effects of both tree type and moth species: *Y. b. brevifolia* lost more seeds than *Y. b. jaegeriana* ($p = 0.000$), and *T. antithetica* larvae ate more seeds than *T. synthetica* ($p = 0.001$). However, there was no effect of moth by tree interaction ($p = 0.951$); all differences in fitness cost can be explained by inherent effects of either moth type or tree type. Although confounding effects of statistical non-independence, small sample size, and non-normal distribution mean that these conclusions are strictly preliminary, the results suggest that phenotypic mismatch does not play a role in the fitness costs to the tree.

An investigative study of petroleum hydrocarbon biodegradation by microbial communities in clean and contaminated water

Jacob Munson-McGee

Thesis Mentor-Dr. Sharon Rose

Petroleum hydrocarbons products are some of the most pressing environmental hazards to marine and freshwater environments. While big oil spills are devastating to the local area, small spills are much more common and in total, release more petroleum hydrocarbons into the adjacent environment. In this study I compare the bio degradation ability of microbial populations from small spill environments to those from clean environments. By better understanding the abilities of the existing microbial community to degrade hydrocarbons, we will be better able to utilize bioremediation techniques when a big spill does happen.

Comparing the effect of inflorescence architecture on pollinator visitation patterns and female fecundity for insect-pollinated angiosperms

Gina Pahlke

Thesis Mentor-Dr. Susan Kephart

Maximal seed production in angiosperms is reached when pollinator visitation rates and patterns lead to high rates of pollen deposition but low rates of pollen wastage and intra-plant (geitonogamous) mating. In this study, I explored how variations in inflorescence architecture, including the inflorescence height, length of the raceme, the number of open flowers, and inflorescence floral density influence the rate, duration, and pattern of pollinator visits as well as seed and fruit set. I studied artificial flowers and four natural species (*Camassia quamash*, *Camassia leichtlinii*, *Delphinium nuttallianum*, *Zigadenus venenosus*), all herbaceous perennials that potentially provide important resources for hymenopteran and dipteran pollinator guilds in lowland to montane meadows. Pollinator visitation patterns and subsequent seed set varied among populations due to differences in flowering times and pollinator composition. Pollinators appeared most attracted to, and visited most frequently, inflorescences with more flowers or longer racemes. Pollinators visiting these inflorescences stayed longer and visited a greater number of flowers, but worked a smaller proportion of available flowers and visited individual flowers less frequently than when visiting shorter, few-flowered racemes. In *D. nuttallianum* and *Z. venenosus* maximal seed production is reached by increasing fruit set. In *C. quamash*, it is reached through increases in seeds produced per fruit. Larger inflorescences had both the greatest pollinator visitation rate and female fecundity, leading to the conclusion that geitonogamous mating was not limiting seed set.

Manipulation of *zwf* expression and modulation of growth rate in *Caulobacter crescentus*

Robin Palmer

Thesis Mentor-Dr. Melissa Marks

Changes to the regulation of key genes could potentially alter phenotypic outcomes. When small alterations in gene expression lead to greater fitness, these regulatory mutations influence evolution. Under standard laboratory culture conditions the fresh water bacteria, *Caulobacter crescentus*, has evolved into two distinct strains, NA1000 and CB15. Of interest is a single base pair difference that results in a growth rate polymorphism and is located in the promoter region of *zwf*, a necessary gene in central metabolism. A beta-galactosidase reporter assay has linked decreased *zwf* promoter activity to a 20% faster doubling time in NA1000, as compared to CB15. We designed a series of molecular tools that allow for the manipulation of *zwf* expression *in vivo* to more directly examine the relationship between the amount of transcription and the resulting phenotype. Xylose inducible *zwf* expression plasmids with different origins of replication, and resulting copy number, have been introduced to NA1000. qRT-PCR will provide a way to quantify the amount of *zwf* RNA transcripts in these engineered strains. Measuring the effect of *zwf* expression level in the modified NA1000 strains by monitoring growth rate will bring us closer to understanding the regulation of central metabolism and doubling time in *C. crescentus*.

Fighting for a fish: Evaluating patterns of sibling rivalry in the Caspian tern

Brady Ryan

Thesis Mentor-Dr. David Craig

Competition among siblings is widespread among bird and mammal species and in extreme cases can lead to siblicide. Strategies that siblings use in their struggles for dominance vary widely depending on the environment and history, but in most cases the effect of hatching or birth order is a major factor in determining the outcomes of sibling contests. Caspian terns are fish-eating birds that deliver whole prey to their semi-precocious young. Typical nests have two eggs that hatch asynchronously, resulting in an alpha and beta chick. A minority of these family units will raise two chicks at once, but brood reduction to a single offspring is more typical. This project aims to measure how having a sibling affects feeding behavior in Caspian tern chicks. We will look at instances of aggressiveness between siblings in an effort to outcompete their partner and obtain the fish. In collaboration with research of individual lateralization in Caspian terns, we will also be able to compare the lateralization levels and feeding success rates of solo chicks to those of sibling paired chicks to determine how the state of siblinghood affects feeding outcomes.

**Promoter Analysis of the Kiss1R Gene to Probe for
Estrogenic and Circadian Regulation of Transcription**

Emily Simmons

Thesis Mentors- Dr. Barbara Stebbins-Boaz and Patrick Chappell (Oregon State University)

Kisspeptin and its receptor, Kiss1r, are essential in reproductive regulation as deletion or mutation of the gene *kiss1* results in infertility in mice. Data suggest that Kisspeptin and Kiss1R are involved in regulating GnRH neurons, initiators of the GnRH/LH preovulatory surge. The Chappell lab recently found that Kiss1R exhibits circadian rhythms in a line of immortalized GnRH neurons (GT1-7 cells). More specifically these rhythms are seen only under the presence of elevated estradiol. As Kisspeptin appears to be "clock-controlled", this work seeks to investigate the newly characterized promoter regions of the *Kiss1R* gene, examining it for potential regulatory sites where clock factors or estradiol receptors (ERs) could bind. To begin the analysis, sections of the Kiss1R promoter that contain potential regulatory elements were deleted. Luciferase reporter plasmids were used in heterologous cells *in vitro* to examine the regulation of *Kiss1r* transcription by the positive clock components CLOCK and BMAL1. Studies using HEK293, human embryonic kidney cells, indicated that CLOCK/BMAL1 robustly stimulated Kiss1R transcription, but that a deletion of an internal Nde1 restriction site flanked region did not diminish this effect. Currently we are repeating these transient transfections in GT1-7 cells to determine if cell specificity plays a role in clock and estrogen-regulation of *Kiss1R* transcription.

**Identification, Molecular Genetic and Phenotypic Characterization of a *fat facets* (*faf^{wu2}*) Allele in
*Drosophila melanogaster***

Stephanie Skelly

Thesis Mentor-Dr. Jason Duncan

Degradation of cellular proteins is a tightly regulated process carried out by the proteasome. The protein ubiquitin (Ub) functions within this process as a molecular "tag" to identify proteins for degradation. However, within the ubiquitin-proteasome pathway deubiquitinating enzymes (DUBs) serve to effectively rescue proteins from degradation by removing Ub from targeted proteins. Defects in the function of DUB binding have been linked to human disease and cancers. The study of DUBs in *Drosophila melanogaster* has provided clues to their roles in human disease. In particular the *Drosophila fat facets* (*faf*) gene is known to be required for synapse formation and maintenance at the neuromuscular junction. A unique allele of the *Drosophila faf* gene was identified through *cis-trans* analysis. The *faf^{wu2}* allele is the consequence of a transition mutation at nucleotide 1180 in the *faf* open reading frame that converts C¹¹⁸⁹ to T¹¹⁸⁹, altering codon CAG to TAG, converting Gln³⁹⁷ to Stop. Phenotypic analysis of *faf^{wu2}* individuals demonstrates a requirement for *faf* function during eye development. Further investigation for a possible requirement for *faf* function in axonal transport has also begun.

Blood Suckers and Babies: Advancements in Biliary Atresia Research

Victoria Smith¹

Dr. James L. Boyer^{1,2}

Thesis Mentor-Dr. David Craig

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The sea lamprey (*Petromyzon marinus*) undergoes a stage of metamorphosis during which it loses its bile ducts and gall bladder. It is unknown whether the lamprey undergoes cholestasis, but its inability to secrete bile shares a direct link to patients with biliary atresia. Although, in contrast to human infants facing biliary atresia, who develop progressive cholestasis and eventual liver failure, the lamprey will continue to grow and develop regardless of their lack of bile ducts. In our initial investigations we examined bile salt concentration and excretion methods in adult migrating lampreys as well as the regulation of vital bile salt transporters between pre and post-metamorphosis lampreys. Our results indicate that the sea lamprey is a unique cholestatic animal model that employs novel methods of excretion in order to adapt to the loss of the biliary tree.

Corticosterone regulation of vasotocin signaling: *An imaging study*

Sarah Sonnenfeld

Thesis Mentor-Dr. Emma Coddington

Acute stress has many effects on animal behavior and physiology, including behavioral changes due to hormonal fluctuations. These rapid changes are critical to survival and reproduction, yet their mechanisms are relatively unknown. The roughskin newt was used to investigate the relationship between CORT (stress hormone) and VT (peptide hormone). We conducted a confocal imaging study using VT tagged to a fluorescent probe. Newts received an injection of CORT, followed by administration of VT-OG directly to the hindbrain. Results showed CORT had no effect on VT-OG internalization, suggesting either another possible mechanism, or a limitation in experimental set-up.

**Characterization of *Pex 1^{WU1}* Function in the
Peripheral Nervous System of *Drosophila melanogaster***
Whitney Stannard
Thesis Mentor-Dr. Jason Duncan

Peroxisomes are a ubiquitous organelle found in all eukaryotic cells. They have many different functions including degradation of reactive oxygen species (ROS) and breakdown of very long chain fatty acids (VLCFA) through β -oxidation. The genes responsible for the transport of peroxisomal matrix enzymes are known as Pex genes. Mutations in Pex genes in humans cause peroxisome biogenesis disorders (PBD) such as Zellweger's syndrome. We identified and isolated a mutation in the *Pex 1* gene of *Drosophila melanogaster*. *Pex 1* is a AAA (ATPase Associated with diverse Activities)-ATPase that helps facilitate cargo translocation into the peroxisome. *Pex 1^{WU1}* encodes a severely truncated *Pex 1* protein, resulting in adult lethality, as well as shortened life span and crawling defects in the homozygous *Pex 1^{WU1}* and *Pex 1^{WU1}/Df(3L)ED4536* adult survivors. We analyzed the *Pex 1^{WU1}* larvae for crawling defects and immunostained their peripheral nervous system to assess the axonal transport system. The nervous system of the *Pex 1^{WU1}* larvae looked comparable to wild type and we conclude that the observed phenotypes are not due to defects in axonal transport.

Morphology and Social Signaling in *Canis lupis familiaris*
Hallie Williams
Thesis Mentor-Dr. David Craig

Paedomorphosis, the retention of juvenile morphology at maturity, is believed to be an important process in generating evolutionary change. The domestic dog, *Canis familiaris*, was domesticated from the wolf, *Canis Lupus*, and is a distinct species. The domestic dog displays great morphological diversity that is believed to be derived from both global and local paedomorphosis. This study investigates how differing morphologies and levels of paedomorphosis affect the exchange of agonistic visual signals in the domestic dog. Data gathered through observation of dogs at play, assigning each dog a morphology score and observing the number of agonistic signals displayed. Methods and results will be discussed.

The Microtubule Regulatory Protein Stathmin is Essential for Axonal Transport
Alfredo Zuniga
Thesis Mentor-Dr. Jason Duncan

Neurons utilize a microtubule-based transport system to bidirectionally transport proteins, vesicles, and organelles between the cell body and the synaptic terminal. We have identified the protein stathmin (*stai*), which regulates the dynamics of the microtubule cytoskeleton, as a component required for axonal transport in *Drosophila*. We have isolated mutations in the *stai* gene that cause neuronal dysfunction resulting in phenotypes consistent with severe defects in axonal transport. Mutant third instar larvae exhibit a posterior paralysis, or 'tail flip' phenotype indicative of a disruption in axonal transport. Immunostaining of the axons of the segmental nerves displays "clogs" caused by a build up transported components. In addition, mutant animals have a significantly reduced lifespan and exhibit an age-sensitive seizure phenotype. A Genetic reversion as well as a genetic rescue helps demonstrate that all observed phenotypes are caused entirely by the loss of *stai* function. Collectively our data identifies a novel, conserved role for *stai* in the regulation of microtubule-based axonal transport.