6th Annual Graduate Student Symposium

“Christmas Urchin” by Lingyu Wang

DEPARTMENT OF BIOLOGY
UNIVERSITY OF MIAMI
JANUARY 9, 2015
AT THE FAIRCHILD TROPICAL BOTANIC GARDEN
6th Annual Graduate Student Symposium
Department of Biology
University of Miami
January 9, 2015
At The Fairchild Tropical Botanic Garden

Graduate Symposium Organizing Committee

Faculty
Dr. James Baker
Dr. Kevin Collins
Dr. Carol Horvitz

Graduate Students
Sarah Cowles
Honglin Feng
Jason Presnall
Bo Zhang

Overall Program Schedule

9:15 am - 9:30 am Opening Statements
9:30 am - 10:30 am Talk Session I
10:30 am - 10:45 am Coffee Break
10:45 am - 11:45 am Talk Session II
11:45 am - 1:00 pm Lunch
1:00 pm - 2:00 pm Talk Session III
2:00 pm - 4:00 pm Poster Session
4:30 pm Awards
5:00 pm - 6:30 pm After-Party
DETAILED PROGRAM SCHEDULE

9:15 am - 9:30 am  Opening Statements
Dr. Athula Wikramanayake, Chair of Biology

9:30 am - 10:30 am Talk Session I
Chair: Bo Zhang
9:30 am  Is belowground competition always symmetric?
Joanna Weremijewicz

9:45 am  A Study in Scarlet: the influence of secondary contact on plumage-mediated inter-sexual selection in Myzomela honeyeaters
Jason Sardell

10:00 am  Using RNA-seq to identify differentially localized RNAs along the animal-vegetal axis in the sea urchin embryo
Lingyu Wang

10:15 am  Learning to give the right answer: duet code acquisition in plain wrens
Karla Rivera-Cáceres

10:30 am - 10:45 am Coffee Break

10:45 am - 11:45 am Talk Session II
Chair: Sarah Cowles
10:45 am  Nest site selection by Blue-crowned (Lepidothrix coronata) and Wire-tailed (Pipra filicauda) Manakins in lowland Ecuador
José Hidalgo

11:00 am  Expression of Kruppel-like factors (Klfs) during embryonic development of the ctenophore Mnemiopsis leidyi
Jason Presnell

11:15 am  Light and size influence physiological performance in two co-occurring understory herbs
Andrea Westerband

11:30 am  Degraded ridge-and-slough topographic structure interacting with perturbed water levels decreases shallow water habitat connectivity, fish movement, and biomass accumulation
Simeon Yurek

11:45 am - 1:00 pm Lunch
1:00 pm - 2:00 pm Talk Session III
Chair: Jason Presnell

1:00 pm  Population Genetic Structure and Divergence in a Rufous Fantail (Rhipidura rufifrons) Subspecies Complex
          Douglas Weidemann

1:15 pm  The MIR-23B/-27B Cluster Decreases Metastasis of Aggressive Prostate Cancer
          Meghan Rice

1:30 pm  Quantifying the relationship between plant size and aboveground biomass allocation in the invasive plant, Schinus terebinthifolius
          Kelley Erickson

1:45pm  Amino Acid Transporter Gene Duplications Conserved among Aphids
          Honglin Feng

2:00 pm - 4:00 pm Poster Session
#1  Recessive mutations in SLC25A46 are associated with an optic atrophy “plus” phenotypic spectrum: characterization of an UGO1-like mitochondrial fission protein
    Alexander Abrams

#2  The dynamics of segment formation is regulated by Cdx4 transcription factor during somitogenesis
    Saptaparni Bandyopadhyay

#3  Signal Evolution in an Invasive Species of Tropical Lizard, Anolis distichus
    Winter Beckles

#4  The Phylogeography and Evolutionary History of the Amazilia Hummingbird (Amazilia amazilia) Subspecies Complex
    Sarah Cowles

#5  A comparative look at host/symbiont regulation in sap-feeding insects
    Rebecca Duncan

#6  Comparison of GLUT4 glucose uptake kinetics in frugivorous and insect-eating bats
    Yu-Ching Hsu

#7  Proposed Research: Gut Morphology, Development, and Function in Zebrafish Based Autism Models
    David James
#8 Cdx4 regulates onset of spinal cord neurogenesis
Piyush Joshi

#9 Investigating conserved developmental processes and genetic networks of Autism Spectrum Disorders genes in Yeast and Zebrafish
Robert Kozol

#10 Improvement of the pea aphid genome assembly by optical mapping
Tirtha Lamichhane

#11 Estimating stage-specific demographic rates using a hidden Markov model for juvenile stages in a nymphaid butterfly
Robert McElderry

#12 Age-related Hearing Loss in Zebrafish
Michael Richmond

#13 Phylogenetic placement of Megatritheca (Malvaceae; Byttnerioideae)
Wyatt Sharber

#14 Characterization of the Green Sea Turtle Juvenile Aggregation in Habitats of la Guajira, Colombia, Southern Caribbean
Catalina Vasquez-Carrillo

#15 Identification and functional characterization of Dishevelled-interacting proteins in the micromeres of sea urchin embryos
Wei Wu

#16 Effects of arginine on the reproduction in Acyrthosiphon pisum
Shuang Xu

#17 Altered Synapse Distribution during Recovery of Swimming Behavior in a Zebrafish Glycine Transporter 1 Mutant
Qing Yan

#18 When and where ecosystems shift? -A model study of hammock/mangrove shifts in South Florida, US
Lu Zhai

#19 Modeling the dynamics of the invasive tree, Melaleuca quinquenervia, in the Everglades, with and without Biological Control
Bo Zhang

4:30 pm Awards
5:00 pm – 6:30 pm After Party
THANK YOU

Thank you for attending the 6th Annual Graduate Student Symposium! The Graduate Symposium Organizing Committee would like to thank The Fairchild Tropical Botanic Garden and staff for all the help in planning and allowing us to use their facilities for our event.

The Graduate Student Organizers would like to thank Dr. James Baker, Dr. Kevin Collins, and Dr. Carol Horvitz for their help on the Organizing Committee.

On behalf of all the graduate students, we would also like to thank all of the faculty members for their attendance and support during the Annual Symposium, which plays an important role in our professional development.
9:30 - Is belowground competition always symmetric?
Joanna Weremijewicz and David Janos
From the Janos Lab

A long-established principle of plant competition is that belowground interactions are symmetric, that is, proportional to root system size. In native ecosystems, however, besides having overlapping roots, neighboring plants may be interconnected by common mycorrhizal networks (CMNs) of branched, arbuscular mycorrhizal fungus hyphae. Like roots, CMNs influence the distribution of limiting mineral nutrients, and thereby can affect belowground competition and plant size hierarchies. I investigated the roles of CMNs versus roots by manipulating belowground interactions. I found that in the absence of root overlap, CMNs amplified size inequalities, resulting in a fifty-fold dry-weight difference between the largest and smallest plants. When roots alone interacted, size distributions were relatively equitable with the largest plants only fifteen times heavier than the smallest plants. By separating the effects of CMNs and roots, these results challenge the long-established principle that all belowground interactions are symmetric.

9:45 - A Study in Scarlet: the influence of secondary contact on plumage-mediated intersexual selection in Myzomela honeyeaters
Jason M. Sardell
From the Uy Lab

Two species of Myzomela honeyeaters coexist on Makira in the Solomon Islands: a native melanic species (M. tristrami) and a recent invader with carotenoid-based red plumage (M. cardinalis). Previous research suggests that plumage likely plays an important role in driving asymmetric mate choice and hybridization in this system, and that alleles for melanic plumage are introgressing from M. tristrami to M. cardinalis. In this study, we assess the role of intra-sexual selection in maintaining plumage diversity in Myzomela. Sympatric males of each species were presented with taxidermy mounts of a conspecific, heterospecific, or ecological competitor and resulting aggressive behavior was recorded. Surprisingly, both species are statistically more likely to show increased aggression toward mounts with red plumage relative to melanic mounts or controls. Further investigation is needed to determine whether this result is driven by ancestral sensory bias or whether it is a consequence of secondary contact and/or genetic introgression.
10:00 - Using RNA-seq to identify differentially localized RNAs along the animal-vegetal axis in the sea urchin embryo
Lingyu Wang
From the Wikramanayake Lab

The sea urchin is an excellent system to study primary body axis formation and germ layer specification because of the unique unequal cell division patterns in 16-cell stage embryos. At this stage, three embryonic cell tiers with distinct sizes and cell fates form along the primary embryonic axis. The eight middle-sized mesomeres at the animal pole are primarily fated to ectoderm, while the four large-sized macromeres and four small-sized micromeres are primarily fated to endomesoderm. This fixed pattern of germ layer specification is determined by the maternal molecular polarities already established in an unfertilized egg. However, the molecular mechanisms are poorly understood. To characterize the molecular polarities and assemble a complete picture of such polarities in sea urchin embryos, I designed a RNA-seq project to identify differentially localized RNAs along the primary embryonic axis. I will discuss ongoing studies characterizing the respective roles of these molecules in sea urchin embryogenesis.

10:15 - Learning to give the right answer: duet code acquisition in plain wrens
Karla D. Rivera-Cáceres, Esmeralda Quirós-Guerrero
From the Searcy Lab

One of the most striking properties of avian duets is the occurrence of answering rules (“duet codes”) that individuals use to link their own song types to those of their partners. Yet, it is not clear how duet codes develop. We recorded the duets of juvenile plain wrens (Cantorchilus modestus zeledoni) and performed a removal experiment in adult plain wrens to determine at which stage duet codes are acquired. We found that juvenile plain wrens a) use the same phrase types as the adults they duet with, b) use their codes with less precision than adults and c) improve with time. This indicates that individuals learn their codes during early development. We also found that adult plain wrens rarely answer to unfamiliar phrase types and that, when they do, their coordination is poorer than for familiar phrases. This suggests that individuals can potentially modify their duet codes during adulthood.
10:45 - Nest site selection by Blue-crowned (*Lepidothrix coronata*) and Wire-tailed (*Pipra filicauda*) Manakins in lowland Ecuador
José R. Hidalgo, John G. Blake, Bette A. Loiselle, Thomas B. Ryder, Renata Durães, and Wendy P. Tori
*From the Uy Lab*

This study examines nest-site selection by two manakin species, Blue-crowned *Lepidothrix coronata* and Wire-tailed *Pipra filicauda* (Aves, Pipridae), that co-occur in lowland wet forest of eastern Ecuador. Both species build simple open-cup nests and both experience high rates of nest predation. Surrounding vegetation was measured for 25 and 27 nests of *L. coronata* and *P. filicauda*, respectively. Corresponding measurements were made of vegetation at random locations near nest sites. The two species used several host-plant species in common for nest building but with different frequencies. Despite some overlap in characteristics of vegetation that surrounds nests, the two species differed in nest-site locations. Similarity in nest sites was greater among nests of a given species than between species. Vegetation surrounding nest sites differed from that at random locations, suggesting that manakins select specific aspects of the environment when building nests.

11:00 - Expression of Kruppel-like factors (Klfs) during embryonic development of the ctenophore *Mnemiopsis leidyi*
Jason S Presnell and William E Browne
*From the Browne Lab*

Klf transcription factors are defined by a highly conserved DNA binding domain composed of three C-terminal C2H2 zinc fingers. Collectively the *Klf/Sp* genes play key roles in a variety of critical biological processes including metabolism, cell proliferation, stem cell maintenance, and embryonic development. Very little is known about the *Klf* gene family and its expression during development in non-bilaterians. Here we provide the first description of *Klf* gene expression in a non-bilaterian metazoan, the ctenophore *Mnemiopsis leidyi*. *Mnemiopsis* has two *Klf* genes, *MleKlfα* and *MleKlfβ*. Both of these genes are ubiquitously expressed during early stages of development, with expression patterns becoming spatially restricted after gastrulation. Regions of high *MleKlf* gene expression correspond to areas of high cell proliferation. By investigating the expression of *Klf* genes in an early branching metazoan, we may gain insight into the ancestral function of this ancient transcription factor gene family.
11:15 - Light and size influence physiological performance in two co-occurring understory herbs
Andrea Westerband
From the Horvitz Lab

On the forest floor, light strongly influences growth, survival, and reproduction in understory plants. Plants that grow more are in turn, able to acquire more light. In the summer of 2013 and 2014, I used a portable photosynthesis system to measure physiological performance in 42 individuals of Heliconia tortuosa and Calathea crotalifera in a Costa Rican tropical rainforest. Size was estimated using total leaf area and height, and canopy openness was measured as a proxy for light availability from 2012 to 2014. I tested for correlations among size, change in size, light availability, photosynthetic capacity and efficiency, and respiration. We found correlations among size and light, but these were not uniform across species and years. We found few correlations among physiological performance and leaf area, but height was correlated with photosynthetic efficiency and respiration, suggesting that height may be the best predictor of a plant’s ability to use light.

11:30 - Degraded ridge-and-slough topographic structure interacting with perturbed water levels decreases shallow water habitat connectivity, fish movement, and biomass accumulation
Yurek, S., DeAngelis, D., Trexler, J., Larsen, L.
From the DeAngelis Lab

GEFISH, a simulation model of forage fish population growth and dispersal within a food web, was developed to compare biomass accumulation and concentration in natural and degraded Everglades ridge-and-slough habitats. Fish were assumed to disperse between shallow water habitats, seeking foraging opportunities and predator refuges. Spatiotemporal connectivity of these habitats depends upon persistent movement corridors in the topographic structure. A twelve-year time series of empirical water level data was applied to realistic topographies derived from georeferenced vegetation community maps using empirical vegetation patch elevations. Three fish groups competed for the same resources with different parameters for depth affinity, stranding and feeding. The organized ridge-and-slough landscape had interconnected, braided networks and seldom dried out completely, resulting in a high persistence of directional connectivity and net fish movement, while the degraded landscape had isolated pools and longer drought periods, resulting in low persistence of connectivity and fish movement.
1:00 - Population Genetic Structure and Divergence in a Rufous Fantail (Rhipidura rufifrons) Subspecies Complex
Douglas E. Weidemann and J. Albert C. Uy
From the Uy Lab

Studying the evolutionary history, population structure, and patterns of gene flow of diverging populations can provide important information on how populations diverge. The Rufous Fantail (Rhipidura rufifrons) is a highly variable species of Australasian flycatcher found across the Pacific. Many adjacent island populations have diverged substantially in morphology, providing good opportunities to study divergence. This study focuses on three subspecies endemic to southeastern Solomon Islands, which show divergence in color patterns (especially the head and tail) across islands separated by narrow bodies of water (< 20 km). Nuclear and mitochondrial markers were sequenced for 56 individuals from throughout the study region, which were then used to examine population structure and evolutionary relationships within the group. Despite narrow water barriers separating the adjacent populations, R. r. ugiensis is distinct both morphologically and genetically, suggesting that either low dispersal or strong selection is maintaining the differences between it and the other populations.

1:15 - The MIR-23B/-27B Cluster Decreases Metastasis of Aggressive Prostate Cancer
Meghan A. Rice, Reema A. Ishteiwy, Thirupandiyur Udayakumar, Teresita Reiner, Carlos Perez-Stable, Travis Yates, Derek M. Dykxhoorn, Kerry L. Burnstein
From the Burnstein Lab

Deregulation of microRNAs is increasingly implicated in the progression and metastasis of prostate and other cancers. MicroRNA cluster miR-23b/-27b is down-regulated in human metastatic prostate cancer (PC) compared to primary tumors and benign tissue. The major goal of our study is to determine the effects of miR-23b/-27b on metastatic processes of PC.

Ectopic expression of miR-23b/-27b in aggressive PC cell lines decreases migration, invasion, anchorage-independent growth and increases E-cadherin levels. In vivo, miR-23b/-27b limited metastasis and local invasion in a preclinical PC model using orthotopic prostate xenografts. Manipulation of miR-23b/-27b levels did not affect proliferation or primary tumor growth in either model. Further, we identified a novel, functional target of miR-23b/-27b in PC cells, inversely phenocopying the metastatic processes mediated by miR-23b/-27b.

These findings suggest that miR-23b/-27b are linked to metastasis suppression and may be useful biomarkers of poor prognosis, and have therapeutic potential in advanced, metastatic prostate cancer.
These studies were supported by DOD Grant W81XWH-11-1-0314 (MR and RI) and NIH Grant R01CA132200 (KLB).

1:30 - Quantifying the relationship between plant size and aboveground biomass allocation in the invasive plant, *Schinus terebinthifolius*
Kelley Erickson, Paul Pratt and Carol Horvitz
*From the Horvitz Lab*

The demography of the invasive plant *Schinus terebinthifolius* across its invaded range in Florida remains understudied. A non-destructive measurement of plant size and aboveground biomass allocation is desirable for monitoring annual plant performance. *Schinus* individuals from seven different field sites chosen to represent the range of geographical variation and introductory history of *Schinus* in Florida were measured, and the relationship between various size metrics (including basal diameter, height, and canopy area) and biomass allocation (quantified via the number of leaves, number of fruits, the dry weights of woody material, leaves and fruits) was explored. At the branch level, the square of the branch diameter was the best predictor for each of the biomass allocation variables, with variance increasing with size. These equations will be used to predict the aboveground biomass allocation of *Schinus* individuals in which destructive sampling of individuals is undesirable.

1:45 - Amino Acid Transporter Gene Duplications Conserved among Aphids
Honglin Feng, Rebecca P. Duncan, and Alex C. C. Wilson
*From the Wilson Lab*

Amino acid transporters (AATs) duplicate and evolve independently between aphids and other sap feeding insects. However, evolution of AATs duplications among aphids remains unclear. Here, we generate transcriptomes from guts, bacteriocytes (the aphid cells harboring symbionts), and the whole insects from the green peach aphid, *Myzus persicae*. We assemble these transcriptomes using a *de novo* approach in Trinity. From the assembly, we identified 38 AATs that we confirmed by mapping to the *M. persicae* genome. To compare AAT duplications across aphids, we built a Maximum Likelihood phylogenetic tree using RAxML. Our phylogenetic analyses show that *M. persicae* possesses expansions and duplications identical to those of the pea aphid, *Acrystosiphon pisum*. In addition, AATs recruited to the *M. persicae* bacteriocyte will be identified by differential gene expression analysis using RSEM. This comparative study will elucidate the role of gene duplication in host/symbiont evolution among aphids.
#1 - Recessive mutations in SLC25A46 are associated with an optic atrophy “plus” phenotypic spectrum: characterization of an UGO1-like mitochondrial fission protein

Alexander J. Abrams¹,², Robert B. Hufnagel³, Adriana Rebelo¹, Claudia Zanna⁴,⁵, Neville Patel², Michael A. Gonzalez¹, Ion J. Campeanu², Laurie B. Griffin⁶,⁷, Saskia Groenewald², Alleene V. Strickland¹, Feifei Tao¹, Fiorella Speziani¹, Leonardo Caporalì⁴, Chiara La Morgia⁴,⁵, Rocco Liguori⁴,⁵, Raffaele Lodi⁸, Zubair M. Ahmed⁹, Kristen L. Sund³, Xinjian Wang³, Laura A. Krueger³, Yanyan Peng³, Carlos E. Prada³, Cynthia A. Prows³, Kevin Bove¹⁰, Elizabeth K. Schorry³, Anthony Antonellis⁶,⁷, Holly H. Zimmerman¹¹, Omar A. Abdulrahman¹², Yaping Yang¹³, Susan M. Downes¹³, Jeffery Prince², Andrea H. Nemeth¹³,¹⁵, Valerio Carelli⁴,⁵#, Taosheng Huang³#$, Stephan Zuchner#$¹, Julia Dallman#²

From the Dallman Lab

Dominant optic atrophy (DOA) and axonal peripheral neuropathy (CMT2) are hereditary neurodegenerative disorders most commonly caused by mutations in the canonical mitochondrial fusion genes OPA1 and MFN2, respectively. In yeast homologs of OPA1(Mgm1p) and MFN2(Fzo1p) work in concert with a third protein, Ugo1p, whose ortholog has not been identified in humans. We present evidence that SLC25A46 is the closest equivalent to Ugo1p in vertebrates and demonstrate that the protein plays an opposing role in mitochondrial fission. Importantly, we also identified recessive mutations in SLC25A46 in four families with a spectrum of phenotypes including optic atrophy, axonal CMT, and cerebellar atrophy. Furthermore, in zebrafish we found that loss-of-function affects the development and maintenance of neuronal processes and is associated with abnormal mitochondrial fission aggregates. Our studies causally link a novel mitochondrial fission gene to a phenotypic spectrum often associated with mitochondrial fusion defects, thus providing additional insight into the pathological mechanisms involved in these mitochondrial disorders.
#2 - The dynamics of segment formation is regulated by Cdx4 transcription factor during somitogenesis
Saptaparni Bandyopadhyay and Isaac Skromne
From the Skromne Lab

The vertebrate body is metameric. As repeating units are generated through segmentation processes, their identity is bestowed through patterning. Segmentation is regulated by dynamic morphogen gradients coupled to a molecular oscillator, the ‘clock and wavefront’ model postulated in 1976 by Cooke and Zeeman. We have investigated the role of a transcription factor Cdx4, likely to be involved in the segmentation process. Despite the fact that Cdx4 deficient embryos have defective somite morphology, its function in somitogenesis has not been established. Our preliminary studies suggest that Cdx4 is important for somite formation through the regulation of the ‘wavefront’ or morphogen gradient, but not the period of the segmentation clock. Loss of wavefront regulation leads to changes in somite size and an overall reduction in embryonic axis length, without affecting the total number of segments. Thus, Cdx4 could potentially be the link regulating somite formation and somite identity.

#3 - Signal Evolution in an Invasive Species of Tropical Lizard, Anolis distichus
Winter Beckles
From the Uy Lab

The effectiveness of visual signals directly depends on an interaction between the signal being sent, the properties of the light illuminating the signal, and the background colors against which the signal is viewed. Anolis distichus is an introduced species of lizard living in a variety of habitats across South Florida. Using a spectrophotometer, I measured the light properties of different A. distichus environments and the reflectance of dewlaps used by the anoles during displays. I found variation in the spectral quality and brightness of light in the different environments, as well as widespread variation in dewlap color. As light properties in a given habitat will dictate the effectiveness of signal colors, variation in dewlap color may be a result of variation in the lighting environment favoring specific dewlap colors. Ongoing work sets out to test this hypothesis by sampling throughout the expanding range of this invasive species in Florida.
#4 - The Phylogeography and Evolutionary History of the Amazilia Hummingbird

*(Amazilia amazilia)* Subspecies Complex

Sarah A. Cowles and J. Albert C. Uy

*From the Uy Lab*

Examining intraspecific variation, evolutionary relationships, and the level of gene flow across differentiated populations of the same species may lend insight into the initial stages of the speciation process. We focus specifically on the Amazilia Hummingbird (*Amazilia amazilia*), a medium-sized hummingbird found in Ecuador and Peru. Six subspecies differ remarkably in phenotypic characters such as size and plumage coloration. Previous research has suggested that the two pairs of northern and southern lowland subspecies form separate clades due to phenotypic similarity. However, the evolutionary relationships of the two highland subspecies in relation to the lowland subspecies remain unresolved. In addition, little is known about the level of interbreeding or intergradation among the subspecies. We will examine the phylogenetic relationships and assess the level of gene flow between the six subspecies using DNA isolated from field-collected blood samples (from Ecuador in 2014) and tissue from museum specimens in a next-generation sequence analysis.

#5 - A comparative look at host/symbiont regulation in sap-feeding insects

Rebecca P. Duncan & Alex C. C. Wilson

*From the Wilson Lab*

Aphids are sap-feeding insects that host intracellular bacteria (*Buchnera*), and both host and symbiont rely on each other for the production and provisioning of amino acids for protein synthesis. How partners coordinate to regulate amino acid provisioning has been a mystery until recently – aphid amino acid transporter ApGLNT1 transports the precursor, aphid-produced glutamine into bacteriocyte cells where *Buchnera* reside, and glutamine uptake is inhibited by downstream, *Buchnera*-produced arginine. We are testing the generality of this elegant model of regulation across evolutionary space by examining ApGLNT1 orthologs in two additional sap-feeding and two non sap-feeding insects. If other sap-feeders evolved the same mechanism of regulation with the same gene, we predict that (1) they depend on symbionts for arginine provisioning, (2) ApGLNT1 orthologs will be expressed in bacteriocytes, and (3) glutamine transport by ApGLNT1 orthologs is inhibited in the presence of arginine. Here, we present our preliminary results for this project.
Glucose transport 4 protein (GLUT4), encoded by the gene Slc2a4, is a transmembrane protein that plays a major role in regulating skeletal muscle glucose uptake for maintenance of whole-body glucose homeostasis. In mammals, high glucose uptake will lead to insulin resistance and type II diabetes. Remarkably, frugivorous and nectarivorous bats have the ability to ingest large quantities of sugar in short time periods while maintaining normal blood glucose. In an earlier molecular evolution study, it has been shown that Slc2a4 has experienced adaptive evolution in old world fruit bats compared with the insect-eating taxa. Here we test the hypothesis that the kinetics of glucose transport by GLUT4 in old world fruit bats differs from that of their insect-eating sister taxa.

Despite the fact that Autism Spectrum Disorders (ASD) are diagnosed by behaviors associated with altered brain function, more than 50% of individuals with ASD also suffer gastrointestinal symptoms (GS). We are interested in testing the hypothesis that neuro-developmental delays typically linked with ASD could affect gastrointestinal function. Recent clinical studies have noted physiological abnormalities in the gut of individuals with ASD. To determine root causes of abnormal gastrointestinal phenotypes, we propose to create several zebrafish ASD models. Utilizing the CRISPR/cas9 system, we will create mutations in select ASD-linked genes including Shank3, MET, CDX2, and GTF2IRD2. With these mutants, gut development and functionality in the context of ASD can be determined through assays of lipid metabolism, enteric and vagal innervation, and the generation of genetically chimeric embryos to test which phenotypes are direct versus indirect consequences of mutations in genes linked to ASD.
#8 - Cdx4 regulates onset of spinal cord neurogenesis
Piyush Joshi, Isaac Skromne
From the Skromne Lab

Spinal cord neurogenesis is initiated at posterior most region of the neural plate, termed the stem cell zone. As stem cells in these precursor zones undergo differentiation, they leave the region behind and become part of the progressively growing spinal cord. While the molecular components driving spinal cord stem cell proliferation and differentiation are being elucidated, the molecular components driving the proliferation to differentiation switch are poorly understood.

Here we show that Cdx4, a transcription factor essential for neural tube antero-posterior patterning, regulates the proliferation to differentiation switch in spinal cord neural stem cells. In gain and loss of function experiments in chicks, we show that Cdx4 functions as a differentiation switch by activating neurogenic factor Pax6 while repressing the pluripotency factor Cash4. Bioinformatics analysis supports a direct regulation of Pax6 by Cdx4, as Pax6 has two clusters of Cdx4 binding sites that are evolutionarily conserved among vertebrates.

#9 - Investigating conserved developmental processes and genetic networks of Autism Spectrum Disorders genes in Yeast and Zebrafish
Robert A Kozol1*, Wiley DJ2, D’Urso G2 and JE Dallman1
1) Department of Biology, University of Miami, Coral Gables, FL; 2) Department of Molecular and Cellular Pharmacology, University of Miami Miller School of Medicine, Miami FL.
From the Dallman Lab

Autism Spectrum Disorder (ASD) is a heterologous disease that may be the result of hundreds of monogenic causes converging on similar developmental processes. Utilizing two complimentary models we can address both common developmental processes and gene networks affected by ASD gene mutations. First, we are developing zebrafish mutant models of two synergistic ASD genes, SHANK3 and SYNGAP1, to identify common neurodevelopmental processes affected by gene disruption. Second, we have recently established a method called Yeast Augmented Network Analysis (YANA) that couples yeast interaction assays with previously published protein-protein interaction data to identify disease susceptibility networks. Together these two models will help to identify common cellular processes affected by ASD gene mutations and the underlying developmental gene networks that are susceptible to perturbations. Our goal is to exploit the evolutionary conservation of eukaryotic genetic interactions and cellular mechanisms to identify genetic or molecular modifiers that can ameliorate developmental disruptions in ASD.
Improvement of the pea aphid genome assembly by optical mapping
Tirtha Lamichhane
From the Wilson Lab

Pea aphids are of great interest to biologists because of their intriguing biological traits such as bacterial endosymbiosis, plant virus transmission, extreme developmental plasticity, clonal and sexual reproduction and rapid development of resistant to insecticides. Improved understanding of these diverse phenomena will be facilitated by improvement of the assembled genome. A new approach to genome mapping, high throughput optical mapping makes improvement of the pea aphid genome assembly feasible. In this method, high quality molecular DNA will be extracted from whole nuclei isolated from aphid embryos. The resulting ordered high-resolution restriction maps will be valuable for sequence verification, identification of errors in contig joining and final assembly. In contrast to earlier methods, optical mapping is highly efficient for reduction of gap number, improved scaffolding and orientation and, is fast and inexpensive.

Estimating stage-specific demographic rates using a hidden Markov model for juvenile stages in a nymphalid butterfly
Robert M. McElderry
From the Horvitz-Nutt Lab

In butterflies, little is known about the dynamics of demographic rates (survival and stage transitions) among juveniles in nature. I repeatedly censused 510 caterpillars in their natural environment for one month, and ask how the probability of surviving and transitioning between stages varies in time, testing for effects of temperature and density. The demographic process was “hidden” by imperfect detection of caterpillars, and was modeled as a hidden Markov process. Detection, survival, and stage transition probabilities were estimated given each individual encounter history. During this survey, caterpillar densities attracted multiple insect and arachnid predators. Survival declined as per capita predation rate increased. Transition rates increased with warming spring temperatures, likely due to increased feeding and metabolism. These demographic rates will parameterize the juvenile stages of a periodic stage-structured matrix model that characterizes the life cycle of this bivoltine butterfly in 3-day time steps over one year.
#12 - Age-related Hearing Loss in Zebrafish
Michael T. Richmond and Steven Denyur, Coauthors: Luis Cai, Willy J. Chertman
From the Lu Lab

Presbycusis, age-related hearing loss is one of the most common sensory disorders affecting elderly people. The NIH reports that nearly one-half of individuals over the age of 75 are afflicted with presbycusis. While the zebrafish (Danio rerio) has been extensively used to model mechanisms of sensorineural hearing loss, no previous studies have reported age-related hearing loss in any fish species. Using auditory brainstem recordings (ABR) on young and old adult zebrafish, we have demonstrated for the first time that zebrafish also undergo age-related hearing loss. The mechanism by which this hearing loss occurs is still unknown especially considering the ability of zebrafish to regenerate hair cells. Presbycusis may be caused by the inability of zebrafish to regenerate hair cells and/or that the inability of hair cells to transduce vibrational information declines with age. In summary, our preliminary results indicate that the zebrafish is a potentially useful vertebrate model for presbycusis.

#13 - Phylogenetic placement of Megatritheca (Malvaceae; Byttnerioideae)
Wyatt V. Sharber
From the Whitlock Lab

The genus Megatritheca has long been recognized as closely related to Byttneria, Rayleya, and Ayenia because of the shared traits of antipetalous stamens and constricted petals fused at the apex to the staminal column. However, more precise phylogenetic placement has been uncertain due to a combination of traits found in the other three genera. Megatritheca shares with Ayenia unusual trithecate anthers (anthers are dithecate in Byttneria, Rayleya, and most other Angiosperms), but has fleshy petal bases of Byttneria and Rayleya (petal bases are filamentous in Ayenia). The two species of Megatritheca are restricted to Central and West Africa, overlapping with the pantropical distribution of Byttneria while Rayleya and Ayenia are restricted to the New World. I present plastid DNA sequence data from Megatritheca grossedenticulata from Gabon. Phylogenetic analyses reconstruct M. grossedenticulata as sister to the combined Byttneria/Rayleya/Ayenia clade. I discuss implications for morphological evolution and historical biogeography of this clade.
The Long-lasting juvenile stage of the green sea turtle Chelonia mydas limits the intrinsic growth rate of populations. Habitats that allow juvenile long-term survival and connectivity, contribute more individuals to reproductive stages and therefore to populations growth. However, the characteristics and locations of these habitats are still unknown. The Guajira region of Colombia harbors extensive seagrass beds and mangrove forest and is a candidate juvenile habitat in need to be characterized. Here, a preliminary characterization of the green sea turtle aggregation and their habitats in La Guajira is presented. All turtles sampled here were juveniles (<76cm Straight Carapace Length). High genetic diversity and a mixture of genotypes from two genetic connectivity regions were found. Evidence of residency at least for three years and a spatial pattern on the location of juveniles were found; smaller turtles were located on embayed, forested areas whilst larger turtles were found in open ocean areas.

Dishevelled (Dsh) protein is highly enriched and differentially modified in a specialized vegetal cortical domain (VCD) of the sea urchin egg and vegetal blastomeres of early embryos. Functional analysis has shown that Dsh activity is essential for the initial activation of canonical Wnt signaling in the 16-cell stage micromeres. To understand how Dsh is activated by its regulatory partners in the micromeres, it is critical to identify and functionally study Dsh interacting proteins (DIPs) in isolated micromeres. Dsh Co-immunoprecipitation coupled with mass spectrometry was applied to pull down and sequence DIPs. DIPs were then functionally annotated by Blast2GO. Potential DIPs were further characterized by RNA in situ hybridization. Functional studies will be performed to determine roles of potential DIPs in regulating Dsh activity. This work will provide critical insight into the molecular basis underlying the asymmetric activation of Wnt signaling that leads to the specification of endomesoderm in sea urchins.
#16 - Effects of arginine on the reproduction in *Acyrthosiphon pisum*

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Pea aphids, *Acyrthosiphon pisum*, feed on plant phloem sap, which is deficient in essential amino acids. *Buchnera aphidicola*, housed in aphid bacteriocyte cells, utilizes glutamine as a precursor to synthesize ten essential amino acids and supplies them to *A. pisum*, forming an obligate nutritional symbiotic partnership. Glutamine is transported by ApGLNT1 on the bacteriocyte plasma membrane from hemolymph to bacteriocytes, but its transport is competitively inhibited by arginine. Recently, ApGLNT1 was also localized to the maternal follicular sheath of aphids, leading to an hypothesized model that bacteriocytes not only provide essential amino acids to pea aphids but also to embryos. Since arginine is a negative regulator of ApGLNT1, we hypothesize high concentration of arginine inhibits reproduction of aphids. We will manipulate the concentration of arginine in *A. pisum* hemolymph by microinjection and determine the impacts of arginine on aphid fecundity.

#17 - Altered Synapse Distribution during Recovery of Swimming Behavior in a Zebrafish Glycine Transporter 1 Mutant

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The nervous system is endowed with the remarkable ability to maintain essential behaviors even in the presence of external or internal perturbation. For example, zebrafish *glycine transporter 1* (*glyt1*) mutants suffer from embryonic paralysis, but recover their motor behaviors naturally as they mature, indicating that the mutant spinal circuit function is maintained by intrinsic mechanisms. One possible mechanism that contributes to *glyt1* mutant recovery is the regulation of synapse number and distribution in the territory of the spinal cord neuropil. To test this hypothesis, we immuno-labeled and quantified the number and relative location of excitatory and inhibitory synapses to monitor the number and distribution of synapses. We found that early-on in recovery, compared to wild-type, mutants exhibit higher densities of both excitatory and inhibitory synapse distribution as well as motor neuron dendrites more extensively branched. These results indicate that the mutant spinal circuit can actively regulate synapse distribution in response to perturbation.
When and where ecosystems shift? - A model study of hammock/mangrove shifts in South Florida, US
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With sea level rise and the subsequent intrusion of saline seawater, an increase in soil salinity will cause South Florida saline-intolerant vegetation (e.g. hardwood hammocks and pinelands) to be replaced by saline-tolerant vegetation (e.g. mangroves or salt marshes). Although vegetation shifts can easily be monitored by satellite imagery, it is hard to predict the particular area or even the particular tree that is vulnerable to such shift. In order to find an appropriate indicator for potential vegetation shifts, we incorporated $^{18}$O abundance as a tracer in various hydrologic components in a previously published model describing an ecosystem shift between hammock and mangrove communities in South Florida. Our simulations found that: (1) there was a linear relationship between salinity and $\delta^{18}$O value in the water table, whereas this relationship was curvilinear in the vadose zone; (2) hammock trees with higher replacement probability had higher $\delta^{18}$O values of plant stem water, and this difference could be detected three years before the replacement occurred; (3) individuals that were replaced by mangroves from the hammock tree population with a 50% replacement probability had higher stem water $\delta^{18}$O values three years before their replacement compared to those from the same population which were not replaced. Overall, these simulation results suggest that it is promising to track the yearly $\delta^{18}$O value of plant stem water in hammock forests to predict the replacement probability and the timing. This model requires further improvements for use in conservation practices, e.g. combining with more complex demography and geography structure, and more vegetation growth factors.

Modeling the dynamics of the invasive tree, Melaleuca quinquenervia, in the Everglades, with and without Biological Control
Bo Zhang, Don DeAngelis, Min Rayamajhi
From the DeAngelis Lab

Melaleuca quinquenervia is an invasive tree that has spread over the freshwater ecosystems of southern Florida, displacing native vegetation. Suppression of Melaleuca appears to be progressing through the introduction of insect species. It’s important to project the long-term effects of the biocontrol on the suppression of the Melaleuca. The individual based model, JABOWA, was used as a basis for developing a model to simulate successional processes occurring in areas of Everglades occupied by Melaleuca, both in the absence and presence of the biological control agents. Our model assumes that the bio-control negatively influences the growth and reproduction of Melaleuca. Our simulation results show that the density and total basal area of Melaleuca decreases after the bio-control, and that native species, such as pond cypress, saw grass, tend to increase in density and total basal area. Therefore, it appears that the bio-control will help in the reestablishment of the native community.