PROGRAM IN GENETICS

8th ANNUAL FALL RETREAT

Friday, August 4, 2017

Thomas G. Crowder Woodland Center
The Program in Genetics welcomes you to
The 8th Annual Genetics Fall Retreat!

Say hello to some of our new faces!

2017 – 2018

New Graduate Students for the Program in Genetics

Jacob Deslauriers
Aiden Jones
Morgan Maly
Lossie Rooney
Joseph Tolsma
Monica Zeynalzadeh
Program in Genetics Fall Retreat Schedule

Main Gallery
8:30 AM  Registration check-in
Poster Presentation set-up in Lady Slipper Room
(Presenters - Please note that poster boards are labeled even/odd numbers for convenience during the poster presentation sessions)
Breakfast buffet

Dogwood Room
9:00 AM  Opening remarks by Dr. Trudy Mackay
Director of the Program in Genetics

Faculty Vignettes - Dogwood Room
9:30 AM  Dr. Caroline Laplante
9:40 AM  Dr. Albert Keung
9:50 AM  Dr. Xinxia Peng
10:00 AM Dr. Adriana San Miguel
10:10 AM Dr. Freya Mowat
Main Gallery
10:20 AM  Coffee Break – All day beverage service provided.

Desserts provided by Mel Amor Bakes.

***Fall Retreat Group Photo – Outside, front of Woodland Center***

Postdoctoral Blitz - Dogwood Room
11:00 AM  Dr. Pei-Li Yao
11:10 AM  Dr. Javier Brumos
11:20 AM  Dr. Maggie Wagner
11:30 AM  Dr. Shanshan Zhou
11:40 AM  Dr. Ashley Elias

Lunch - Dogwood Room
12:00 PM  Lunch – Catered by Triangle Catering: Fajita bar, pasta bar, and BBQ buffet

Teaching Genetics Education - Great Reception Ballroom (Room 122)
1:00 pm  Opening remarks about the Undergraduate Program by Dr. Betty Gardner
1:10 pm  Dr. Claire Gordy
1:20 pm  Dr. Joy Little
Social Activity on the Back Deck!

1:30 PM  
Social Activity – Nature Craft - Craft a Genetics Model Organism
Social Leader: Grace Parker

How to Participate:

- Divide into teams of 3 people (maximum).
- Search for nature items on the Woodland trail (ex: leaves, rocks, pinecones, sticks, etc.) Please keep in mind this a protected nature facility.
- Use nature items along with felt, construction paper, markers, scissors, and glue to create/design a model organism found in Genetics!
- The team with the best model organism wins! (Three Starbucks gift cards will be awarded!)

Other social activities include a game of corn hole outside on the deck! Dr. John Meitzen has allowed us to use his boards and to try on “beer goggles” (used at Brain Awareness Night) while playing!

Rain Plan: Assorted board games will be provided for teams to play from 1:30 pm - 2:30 pm.

New Genetics Graduate Student Orientation - Gallery or outside on the deck

2:30 PM  
New students meet with Dr. Trudy Mackay and Melissa Robbins
Poster Presentations - Lady Slipper Room

Enjoy Coffee! – All day beverage service provided by Triangle Catering and desserts provided by Mel Amor Bakes!

2:30 PM  Poster Presentations (Even Numbers)
3:15 PM  Poster Presentations (Odd Numbers)

Student Achievements - Great Reception Ballroom (Room 122)

4:00 PM  Kate Coyle
4:10 PM  Richard Gell
4:20 PM  Brandon Baker
4:30 PM  Jen Baltzegar
4:40 PM  David Bullock
4:50 PM  Anna Rogers
5:00 PM  ADJOURN. Thank you for joining us! We hope to see you next year!
5:15 – 5:30 PM  Take down posters and clean up!
Faculty Vignettes

Dogwood Room

9:30 AM – 10:20 AM
Structural insights into cytokinesis: quantitative high-speed super-resolution imaging in live fission yeast cells

Caroline Laplante

Cytokinesis in animals, fungi, and amoebas depends on the constriction of a contractile ring built from a common set of conserved proteins. Many fundamental questions remain about how these proteins organize to generate the necessary tension for cytokinesis. Using quantitative high-speed fluorescence photoactivation localization microscopy (FPALM), we probed this question in live fission yeast cells at unprecedented resolution. We show that nodes, protein assembly precursors to the contractile ring, are discrete structural units with stoichiometric ratios and distinct distributions of constituent proteins. Anillin Mid1p, Fes/CIP4 homology-Bin/amphiphysin/Rvs (F-BAR) Cdc15p, IQ motif containing GTPase-activating protein (IQGAP) Rng2p, and formin Cdc12p form the base of the node that anchors the ends of myosin II tails to the plasma membrane, with myosin II heads extending into the cytoplasm. This general node organization persists in the contractile ring where nodes move bidirectionally during constriction. We observed the dynamics of the actin network during cytokinesis, starting with the extension of short actin strands from nodes, which sometimes connected neighboring nodes. Later in cytokinesis, a broad network of thick bundles coalesced into a tight ring around the equator of the cell. The actin ring was ~125 nm wide and ~125 nm thick. These observations establish the organization of the proteins in the functional units of a cytokinetic contractile ring.
Synthetic epigenetics

Albert J. Keung

There is a wealth of 'epigenetic' information layered on top of the genomic sequence. Yet our abilities to manipulate, access, and understand it trails behind modern genetic tools. This talk will give a succinct overview of the questions, tools, model systems, diseases, and other applications the Keung Lab is currently working on towards the central goal of revealing epigenetic functions.
Our interest is to use systems approaches to better understand pathogen-host-microbiome interactions and microbial pathogenesis. The goal is to uncover underlying molecular mechanisms of microbial pathogenesis and to identify targets of intervention as well as biomarkers for clinical applications. We focus on computational analysis of high-throughput omics data in combination with targeted experimental validation. The Lab is housed in the College of Veterinary Medicine Research Building located at the NC State Biomedical Centennial Campus, and is part of NC State Bioinformatics Research Center.
Microfluidics for aging and deep phenotyping studies

Adriana San Miguel

We develop tools to extract quantitative phenotypes at multiple levels. We use the multicellular organism C. elegans to characterize in vivo intermediate and downstream phenotypic states such as gene expression, cellular and subcellular morphology, and behavior. By incorporating experimental platforms that enable high-throughput imaging, controlled environmental conditions, and on-line image analysis, we are able to extract quantitative phenotypic data sets that enable identifying underlying biological functions and genetic relationships via statistical and mathematical analysis tools. This is made possible by the integration of customized microfluidic platforms and computer vision which allow fast animal handling, controlled environmental conditions, and quantitative image analysis. In particular, we focus on studying dynamic changes in phenotypes throughout aging.

We have developed microfluidic platforms that allow longitudinal lifelong monitoring of C. elegans populations, while performing high-resolution imaging. Through these platforms, lifelong spatiotemporal gene expression patterns can be extracted, and correlated with subcellular, cellular and physiological outcomes. These deep-phenotyping tools allow quantitative characterization of intermediate and downstream outcomes (such as spatiotemporal gene expression, cellular and subcellular phenotypes), and thus enable building predictive models that link phenotype and genotype.
Deciphering the genetic cause of inherited blindness in red wolves

FM Mowat, H Mochizuki, FP Giorgino, E Marx, R Ring, W Waddell, M Breen, S Kennedy-Stoskopf

Background
The red wolf (canis rufus) is a critically endangered species and a captive breeding program, established from 14 founders has resulted in significant inbreeding. Retinal degeneration has been identified in related red wolves, warranting further genetic study.

Methods
A cohort of related wolves was phenotyped using clinical examination, tests of retinal function and histology, and a pedigree was constructed to relate these wolves to a historical cohort reported in Tennessee in 1997. Whole genome sequencing was performed in one putative carrier, and whole exome sequencing was performed on 2 affected, 2 unaffected and one putative carrier. Candidate genes relevant to the phenotype were explored using sanger sequencing in a wider cohort.

Results
The ratio of affected males to females was 6:1 and further suspected affected males were described, supporting an x-linked recessive pattern of inheritance, with a predicted high mutant allele frequency. Mutations in Retinoschisin 1 and Collagen 4A5 were excluded by sanger sequencing. Few X chromosome candidate genes known to be causative of inherited retinal disease in humans remained after evaluation of variants from whole exome sequencing and elimination of variants not matching phenotype.

Conclusions
X-linked inheritance is suspected, although the lack of identification of a strong candidate gene may indicate more complex genetics such as the presence of a second modifier, or autosomal inheritance. A GWAS-type approach is underway using the whole exome dataset to identify loci that match phenotype, and further phenotyping of related individuals is planned to expand the cohort.
Postdoctoral Blitz
Dogwood Room
11:00 AM – 11:40 PM
Genetic susceptibility to diethylstilbestrol (DES) in male reproductive system

Pei-Li Yao, Nicole E. Allard, Harlie A. Cope, David L. Aylor

An increasing body of evidence supports that environmental factors during early development influence the individual’s sensitivity to diseases later in life. Thus, it is of interest whether and how individual genotype interacts with the environmental impact, and leads to variable susceptibility during development. Fetal exposure to diethylstilbestrol (DES), a potent synthetic estrogen, is associated with an increased risk of both male and female reproductive tract defects including vaginal cancer, testicular cancer, cryptorchidism, and infertility in human populations. In the present study, a panel of inbred mouse strains was treated with relatively low dose of DES (2 µg) on postnatal days (PND) 1-5. These strains include several from the Collaborative Cross, a mouse genetic reference population that contains most existing natural genetic variation in mice. The changes in male reproductive phenotypes and functions in response to DES exposure were examined at the age of 12 weeks. Neonatal exposure to DES is associated with the reduced testis weight, epididymis weight, seminal vesicle weight, and decreased sperm counts in mice. Some mice exposed to DES also exhibited a mild to severe degeneration of spermatogenic cells in the seminiferous tubules compared to controls, including vacuolization, impaired spermatogenesis, germ cell depletion, Sertoli-cell-only tubules, and testicular atrophy. Importantly, the severity of DES-induced abnormality in male reproductive tracts varies among genetically diverse strains. These observations demonstrate that genetic diversity substantially contributes to DES susceptibility. Our results establish the CC as an ideal platform to identify specific gene by environment interactions in mice.
"Translational genetics" ethylene, the ripening hormone

Brumos J, Alonso JM, Stepanova AN

The current population growth is rising food demand and convergent studies agree that food availability has to increase by 70% in the next 30 years to meet the needs of the growing global population. Hence, increasing worldwide food availability is becoming a major goal of the primary sector of the economy. One of the major challenges of modern agricultural production is to minimize crop losses caused by over-ripening and senescence. A better understanding of how the ripening process is regulated has the potential to reduce spoilage and avoid food waste. Gene expression changes during fruit ripening have been extensively studied at the transcriptional level, however little is known about ripening-associated shifts in the efficiency of transcript translation. We hypothesize that a subset of transcripts display ripening-associated changes in their translational efficiencies. The Ribo-seq technology will be employed to monitor changes in transcript translation at a whole-genome scale and single-codon resolution on different-stage tomato fruits. In parallel, previously characterized cis-regulatory elements that are required and sufficient for the translational inhibition of gene expression in the presence of the ripening hormone ethylene are being tested for their ability to control the timing of fruit softening.

This study will serve as a foundation for future in-depth analyses of novel translation regulation mechanisms involved in fruit ripening and the potential implementation of these regulatory modules as a promising biotechnological tool. The project will pave the path to developing new approaches for controlling fruit and vegetable spoilage.
Patterns and consequences of breeding-induced metagenome variation in maize

Maggie R. Wagner, Peter Balint-Kurti, Posy Busby, Jim Holland

Research demonstrating that beneficial microbes can dramatically alter plant health has spurred calls to incorporate the plant microbiome into crop breeding programs. Previous studies have demonstrated high heritability for some plant-associated microbes, and low to moderate heritability of the microbiome as a whole. However, most studies to date have catalogued differences in microbial diversity between arbitrarily chosen host genotypes. These descriptive approaches typically do not generate clear predictions of how microbiomes might change in realistic breeding scenarios, limiting their applicability. Here I describe ongoing experiments to test predictions about how systematic breeding practices affect microbiome variation by uniting a quantitative genetics framework with methods in community ecology and microbiology. These experiments use high-throughput amplicon sequencing and endophyte re-inoculation experiments in maize (Zea mays L.) to address questions such as: How do hybrid microbiomes compare to those of their parental lines? Does intense artificial selection have side effects on diversity and composition of plant-associated microbial communities? Does introgression of disease-resistance loci have side-effects on beneficial symbionts? If so, do these changes to symbiont communities feedback to affect plant health? Together, answers to these questions will reveal the connections between plant genomic variation, microbiome diversity, and crop health in the contexts of hybridization, artificial selection, and introgression.
A Drosophila model for toxicogenomics: genetic variation in susceptibility to heavy metal exposure


The genetic factors that give rise to variation in susceptibility to environmental toxins remain largely unexplored. Studies on genetic variation in susceptibility to environmental toxins are challenging in human populations, due to the variety of clinical symptoms and difficulty in determining which symptoms causally result from toxic exposure; uncontrolled environments, often with exposure to multiple toxicants; and difficulty in relating phenotypic effect size to toxic dose, especially when symptoms become manifest with a substantial time lag. Drosophila melanogaster is a powerful model that enables genome-wide studies for the identification of allelic variants that contribute to variation in susceptibility to environmental toxins, since the genetic background, environmental rearing conditions and toxic exposure can be precisely controlled. Here, we used extreme QTL mapping in an outbred population derived from the Drosophila melanogaster Genetic Reference Panel to identify alleles associated with resistance to lead and/or cadmium, two ubiquitous environmental toxins that present serious health risks. We identified single nucleotide polymorphisms (SNPs) associated with variation in resistance to both heavy metals as well as SNPs associated with resistance specific to each of them. The effects of these SNPs were largely sex-specific. We used mutational and RNAi analyses to functionally validate 84% of tested genes harboring associated polymorphisms and constructed networks of candidate genes as blueprints for orthologous networks of human genes. The latter not only provided functional contexts for known human targets of heavy metal toxicity, but also implicated novel candidate susceptibility genes. These studies validate Drosophila as a translational toxicogenomics gene discovery system.
Characterization of multiple loci in a complex sex determination system

Ashley Elias, Natalie Roberts, Reade Roberts

Sex determination is one of the most important processes for the functioning and propagation of a sexually reproducing species, yet the “switches” modulating female versus male development are mind-bogglingly diverse. Genetic sex determination has historically been considered as a hard-wired switch, with a single inherited cue driving both primary gonadal sexual development, and producing resounding secondary sexual effects throughout the organism. In vertebrates with genetic sex determination, sex determination alleles act as this switch. The discovery of polygenic sex determination (PSD) has demonstrated that genetic sex determination need not be monogenic in nature. PSD, where multiple genetic factors segregate and interact to direct sexual development, has been discovered in multiple taxa and appears to be a common and stable evolutionary strategy. Since multiple sex genotypes are produced in PSD systems, “sex” is no longer a binary trait. With past research on genetic sex determination largely focused on single gene sex determination systems, certain questions could not be addressed. A PSD system provides the ability to not only make comparisons between sexes, but also within a phenotypic sex and between genetic modes of sex determination. To this end, we used the cichlid fish species Astatotilapia burtoni as a model of PSD. We compared the genomes of four sex genotypes that produce two phenotypic sexes, to complete a comprehensive genomic study of a stable PSD system. Our study not only characterizes the variation between the sex alleles at each loci, but also compares the sex regions within the genome. The development of a model of PSD system will provide the unique ability to address more broad questions about evolutionary transitions and epistatic interactions that take place in gene networks underlying fundamental organismal phenotypes.
Teaching Genetics Education

Dogwood Room

1:00 PM – 1:30 PM
Undergraduate Program in Genetics

Marian (Betty) Gardner

NC State University offers a Bachelor of Science degree in Genetics and a Genetics Minor at the undergraduate level. The Genetics minor was established in 1988 and currently consists of 45 students. The undergraduate Genetics major was established in 2010. Due the major’s relatively small size (currently 86 students), the program facilitates interaction with faculty and other Genetics majors through small classes and enrichment opportunities. Students primarily matriculate into the Genetics program through the Life Sciences First Year Program resulting in classes of sophomores, juniors and seniors, but typically not freshmen. One unique aspect of the undergraduate major is that students are required to complete a laboratory research or teaching research project as part of their degree requirements. There are multiple opportunities for students to present their findings at undergraduate research symposia on campus. Students are also encouraged to participate in the Genetics Club and in outreach opportunities such as Darwin Day and DNA Day at the Museum of Natural Sciences. About a third of our graduates have gone to further education programs including PhD programs in genetics and related fields, Master’s programs including Genetic Counseling programs, and medical and professional school. The remaining graduates have entered the workplace primarily as laboratory research technicians.
Survival in the wild: introduction of a yeast-based CURE in GN 312

Claire Gordy and Joy Little

The Elementary Genetics Laboratory (GN 312) is a one-credit hour course required of all Genetics majors and minors to supplement the concepts of the Elementary Genetics Lecture course GN 311. Students cross Drosophila melanogaster to evaluate concepts in meiosis, linkage, sex-linkage, and population genetics in the first part of the course. The second half of the course is meant to introduce molecular topics and has historically relied on a series of “cook-book” lab modules. Starting in Fall 2017, this second half of the course will be a multi-week student-directed Saccharomyces cerevisiae course-based undergraduate research experience (CURE). Students will develop hypotheses and experiments designed to evaluate genetic differences that contribute to fitness of a wild yeast strain as compared to the lab S. cerevisiae yeast. This project will introduce various molecular approaches and has multiple avenues for expansion in future terms and/or for independent projects. This talk will introduce the experimental framework for the new yeast genetics module with a focus on the techniques and skills the students will gain.
Encouraging TH!NKing in GN312

Joy Little and Claire Gordy

The Elementary Genetics Laboratory (GN 312) is a one-credit hour course required of all Genetics majors and minors to supplement the concepts of the Elementary Genetics Lecture course GN 311. Starting in Fall 2017, this second half of the course will be a multi-week student-directed Saccharomyces cerevisiae project. Students will develop hypotheses and experiments designed to evaluate genetic differences that contribute to fitness of a wild yeast strain as compared to the lab S. cerevisiae yeast. This talk will focus on the higher-order skills and behaviors students will be asked to practice as a consequence of this lab module.

Students will be given multiple opportunities to assess data and develop new questions and hypotheses based on their results. Students will be asked to communicate their experimental design clearly, both before proceeding and after completion. As such, there will be multiple opportunities for reflection on alternative approaches and to explain the reasoning behind each decision. Students will also have the opportunity to put together their data in a graphical format to effectively communicate their findings. In sum, students will be working through the NCSU TH!NK criteria throughout this yeast genetics module by 1) raising questions and formulating problems; 2) gathering and assessing relevant information; 3) synthesizing and generating ideas; 4) considering alternatives; 5) reaching reasoned conclusions; and 6) effectively communicating their findings, their process, and their ideas.
Poster Presentations
Lady Slipper Room

2:30 PM - 3:15 PM
Poster Presentations (Even Numbers)

3:15 PM - 4:00 PM
Poster Presentations (Odd Numbers)
Comparative analysis of the larval gut transcriptome of cichlid fishes across trophic levels

Aldo Carmona Baez, Kate Coyle, Amanda Cass, David Reif, Reade Roberts

Several characteristics of gut morphology and physiology correlate with trophic levels. For instance, vertebrates with a plant-based diet generally have longer digestive tracts compared to animals at higher trophic levels. This trend is also seen among recently diverged Malawi cichlid species, even when raised in the lab on the same diet, supporting a genetic basis for gut length differences. Here, we produce and analyze expression data from the intestine of several cichlid species across different trophic levels at ~21 days post fertilization, a time point at which cichlids have consumed their yolk sac, but prior to external feeding. This dataset is the first gut transcriptome study in cichlids, and we use it to explore genes involved in gut development prior to interactions with diet and species-specific microbiota. The comparison of gut expression data of species adapted to different diets will help us detect potential genes and mechanisms involved in rapid dietary adaptation and transitions across trophic levels.
(Poster 2)

The genetic and genomic basis of species divergence

Allison Schloop, Richard Lyman, Trudy Mackay

Understanding the genetic basis of species divergence remains an unsolved problem in biology. The genetic basis of speciation – the process by which one interbreeding population evolves into two reproductively incompatible populations – is thought to be due to the accumulation of mutations in each lineage that have deleterious epistatic interactions in the background of the other lineage, leading to hybrid infertility and/or inviability. The species pairs Drosophila melanogaster and D. simulans have been extensively investigated. These species are thought to have diverged 5.4 million years ago. Matings of D. melanogaster females to D. simulans males yield viable, but sterile females. The reciprocal cross is rarely successful, but when it is, hybrid males are viable but sterile. Two mutations, Lethal hybrid rescue and Hybrid male rescue, can give viable males in the former cross. Genetic analyses at the level of whole chromosomes indicate that the genetic basis of divergence between these species is more complicated, however. Trudy Mackay’s lab has generated the D. melanogaster Genetic Reference Panel (DGRP) of 205 inbred, sequenced lines. Recently, Dr. Richard Lyman generated a comparable D. simulans Genetic Reference Panel (DSRP) of ~290 inbred lines. Preliminary data has shown a wide range of hybrid female viability and wing phenotypes when the D. simulans lines are crossed to a common D. melanogaster strain, indicating that there is natural variation in hybrid performance in this population. I will use these panels to identify genes that are highly divergent between these two species, perform genome wide association analyses to map genetic variant affecting hybrid viability and wing phenotypes, and assess genome-wide allelic-specific gene expression in hybrids.
A novel platform for identifying aging phenotypes in *C. elegans*

*Daniel Midkiff* and *Adriana San Miguel*

In flowering plants the gynoecium (seedpod) is critical for reproductive success. The mature seedpod serves as protection during seed maturation until dehiscence (pod shatter) occurs allowing for seed dispersal. The valve margin (VM), longitudinal furrows in the walls of the seedpod made of a lignified and cell separation layer, is required for pod shatter.

The transcription factor, SHATTERPROOF2 (SHP2) is important for VM development; plants with mutations in the paralogs SHATTERPROOF 1 (SHP1) and SHP2 lack a VM and are indehiscent. Regions of high sequence similarity have been identified phylogenetically in the promoter/enhancer regions of SHP2. Subsequent functional analyses have highlighted a 1kb region that is capable of giving late SHP2 expression primarily in the VM.

A region of high sequence similarity with several binding sites specific to MADS domain proteins, transcription factors that help to specify organ identity during plant development, has been found within the 1kb fragment. Functional analysis shows that proximal consensus sequences for BASIC PENTATCYSTEINE (BPC) proteins that have been shown to interact with MADS proteins to repress transcription may regulate SHP2 through this region. Mutagenesis of specific MADS protein binding sites, potentially including AGAMOUS-LIKE 15 and AGAMOUS-LIKE 18, also suggests a role in SHP2 regulation during late seedpod patterning.
Tail morphology in fishes can have a profound impact on swimming mechanics, and consequently, adaptive fitness. Wide, rounded tail fins provide increased stroke power, while a ‘forked’ shape reduces drag for longer bouts of swimming. Additionally, tail fin tissue has the ability to regenerate after trauma with species-specific morphological patterns. Following broader evolutionary trends within the fishes, open-water Lake Malawi cichlids have more forked tails, and shore-dwelling species have more rounded tails. These cichlids are ideal model to study how genetic changes can lead to evolutionary change, as we can perform QTL mapping between interspecies hybrids in the lab, and compare the resultant peaks to regions of differentiation (high Fst) between species across the lake. Photographs were used to quantify metrics of tail shape (roundedness, forkedness, and tail base width) in Metriaclima mbenjii (rounded tail) and Aulonocara koningsii (forked tail), as well as their F1 and F2 offspring. We genotyped our F2 using restriction site associated DNA sequencing (RADseq), and resultant markers were used for single locus interval mapping. Mean Weir Cockerham Fst between 19 rounded tail and 6 forked tail species was calculated for the genomic intervals under QTL peaks with LOD=3, using a 10 Kbp sliding window analysis. Here, we identify QTL peaks related to forkedness on chromosome 17, roundedness on chromosome 8, and tail base width on chromosome 4. This information allows further insight into the genetic changes impacting fin shape, as well as the potential to link this trait to other adaptive changes in the cichlid morphology.
Across different animal groups, there are multiple mechanisms for sex determination, including genetic or environmental factors. African cichlid fishes are an extremely diverse group that has undergone an explosive radiation of speciation through the evolution of many different traits, including genetic sex determinants. One species, Astatotilapia burtoni, has been historically studied for behavioral adaptation, including reproductive and social behaviors. While there has been much work on understanding the neurological and physiological aspects of these social and reproductive interactions, the sex determining system has not been characterized. We performed a genetic mapping study and found two distinct sex determining systems on separate chromosomes, demonstrating a polygenic sex determining (PSD) system. We aim to understand the epistatic or potentially additive interaction of the sex determining alleles and identify the sex determining genes, using known breeding experiments. Understanding this allows for categorization of sex based not only on phenotype but also genotype, giving framework for understanding how different sex alleles can still work to produce the same sex. Here using a poolseq strategy, we sequenced the sex determining loci to identify SNPs unique to each locus to narrow and identify any potential candidate variants for the sex determining alleles.
Genomic regulation of limited lifespan and reproductive senescence in Drosophila melanogaster

Grace Parker and Trudy F. C. Mackay

Limited lifespan and senescence are near-universal phenomena. These quantitative traits exhibit variation in natural populations due to the segregation of many interacting loci and from environmental effects. Due to the complexity of the genetic control of lifespan and senescence, our understanding of the genetic basis of variation in these traits is incomplete. Our goal is to identify causal genes associated with increased lifespan and postponed reproductive senescence in Drosophila melanogaster by functional analyses of genetically divergent genes between five long-lived (O) lines selected for postponed reproductive senescence and five unselected (B) lines. Preliminary data assessing productivity of the reciprocal crosses of the O and B lines suggest that genes influencing reproductive senescence are maternally-controlled. Therefore, all of the candidate genes tested are expressed in the ovaries of females. To determine which of these candidate genes exhibit a quantitative change in lifespan or reproductive productivity, we assessed lifetime reproduction of candidate genes from the Vienna collection of RNAi lines in which gene expression is knocked down weakly throughout the body. We identified genes that limit and genes that extend longevity and are required for proper reproductive function. Identifying evolutionarily conserved genes affecting increased lifespan and delayed reproductive senescence is the first step towards understanding the evolutionary forces that maintain segregating variation at these loci in nature and may provide potential targets for therapeutic intervention to delay senescence in populations with increasing lifespans.
As a science teacher, it is vital to continually draw on current research and lab techniques in order to communicate with students the importance of technology and knowledge in their everyday lives. Making lessons relevant, yet still rigorous, is a balance and a challenge to inspire curiosity and questioning. In this case, examples from research in the Dr. Reade Roberts lab served as a template for lessons crafted for middle and high school lessons.
Maternal overnutrition and metabolic syndrome susceptibility: a model of epigenetic programming

Marine Baptissart, David Reif, Michael Cowley

Maternal high-fat diet (mHFD) exposure during perinatal life predisposes offspring to metabolic disorders including obesity and non-alcoholic fatty liver disease (NAFLD). However, the relative contributions of prenatal and postnatal mHFD exposure on disease programming remains poorly appreciated. Moreover, the nature of the primary molecular events responsible is still unknown. Epigenetic modifications, which can be modulated by the environment during perinatal life and are heritable through cell division, represent a strong candidate mechanism for mediating developmental programming. In this context, our study aims to: 1. discriminate the metabolic changes induced by either prenatal or postnatal mHFD exposure, and; 2. draw a comprehensive epigenetic and transcriptional signature underlying the relative contributions of these distinct time-windows on disease susceptibility.

Using a crossfostering strategy, C57Bl/6J mice were exposed to mHFD (45% fat), or corresponding control diet, during prenatal and/or postnatal development. Mice were weaned onto control diet or challenged with HFD during adulthood. At birth, weaning and adulthood, we performed metabolic tests and characterized histological and molecular changes in the liver.

At weaning, mice exposed to postnatal but not prenatal mHFD exhibit increased fat accumulation and excess hepatic lipid storage, a hallmark of NAFLD. Exposure to mHFD also programs susceptibility to metabolic deficiencies in adulthood, with distinct phenotypes observed depending on the perinatal exposure window.

To identify primary molecular events involved in this programming effect, we are performing global and targeted transcriptomic and epigenetic analyses. Of note, we identify increased expression of the imprinted transcription factor Zac1 in the liver of weanling mice exposed to mHFD during postnatal development. Zac1 controls a coordinately expressed
Imprinted Gene Network (IGN) for which genetic manipulations are interestingly associated with abnormal hepatic lipid storage. Overexpressing Zac1 in vitro, we demonstrate for the first time the ability of Zac1 to control the IGN within liver cells. Future approaches aim to explore the role of the Zac1 dependent network in controlling hepatocyte lipid metabolism in a cell autonomous manner.

Altogether our results support the hypothesis that the IGN contributes to NAFLD programming, and that Zac1 constitutes an epigenetic mediator between mHFD and metabolic disease in later life.

In addition to driving a programming effect within a single generation, a number of studies have shown that epigenetic memory allows transmission of disease susceptibility across generations. Thus, we will determine whether the metabolic deficiencies programmed by developmental mHFD exposure persist through the paternal germline to an F2 generation, and study the underlying epigenetic mechanisms that may be responsible.
Genetic approaches to produce male only-strains of *Lucilia cuprina*

**Megan E. Williamson, Ying Yan, and Max J. Scott**

The Australian sheep blowfly, *Lucilia cuprina*, is a major agricultural pest in Australia and New Zealand. Genetic approaches, such as the sterile insect technique (SIT), have been considered for use for control in *L. cuprina*. For over 60 years, SIT has been used successfully to control the New World screwworm (NWS), a blowfly that is a close relative of *L. cuprina*. However, more efficient genetic systems would facilitate control of NWS in areas where it remains endemic. In SIT programs, females cost money to rear and can hinder the effectiveness of the program by competing with wildtype females to mate with the sterile males. For this reason, transgenic sexing systems have been developed that produce only males when fed a diet lacking tetracycline. Our lab has developed a two component transgenic sexing system in *L. cuprina* that consists of a driver containing an early cellularization gene promoter and a tetracycline transactivator, and an effector, containing *tetO* binding sites and a proapoptotic gene separated by a female specific intron. This work created male-only lines but had an issue with leaky expression- some males were dying along with the females. My work has been focusing on the use of different early cellularization gene promoters and proapoptotic gene combinations in the aim of identifying a better combination. This work shows promising combinations of driver and effector lines. These transgenic sexing systems combined with an SIT program could lead to more efficient systems for genetic control of *L. cuprina* and NWS.
(Poster 10)

Allele-specific gene expression in hybrid Drosophila

Meredith Hemphill

Hybrid offspring of two breeds or species, while mostly resembling their parents, can have unique traits that are unlike either parent. Sometimes this leads to hybrid vigor, wherein the hybrid has higher fitness than either parent. However, the hybrid’s distinct biology can also manifest as decreased fitness, or outbreeding depression. Overdominance and the interaction of novel combinations of dominant alleles may contribute to this phenomenon, but the causal genes remain unknown. In this study, we address the genetic basis of hybrid vigor and outbreeding depression by profiling allele-specific gene expression (AGE) in Drosophila melanogaster/Drosophila simulans hybrids. AGE profiling compares the mRNA levels of each transcript from the respective parents to the hybrid offspring. We crossed females from a homozygous D. melanogaster strain (CSB) to males from 20 lines of D. simulans from the Drosophila similans Reference Panel which had a wide range of hybrid viability with CSB females. The offspring of these crosses were sterile females which often exhibited wing abnormalities. We collected third instar larvae from the hybrids and the pure species parents and performed whole-genome RNA sequencing for AGE analysis. The hybrids are expected to have transcript values similar to one parent or within the range of both for most loci, but extreme values are likely at loci associated with female fertility and wing development. This study will lead to a deeper understanding of the mechanism of unique hybrid phenotypes, which in turn could aid the improvement of animal and plant breeding programs.
A gene encoding maize caffeoyl-CoA O-methyltransferase confers quantitative resistance to multiple pathogens

Qin Yang, Yijian He, Mercy Kabahuma, Amy Kelly, Timothy Chaya, Eli Borrego, Yang Bian, Farid El Kasmi, Li Yang, Judith Kolkman, Mike Kolomiets, Rebecca Nelson, Randall Wisser, Jeffrey Caplan, Xu Li, Jeffery L Dangl, Nick Lauter, Peter Balint-Kurti

Alleles that confer multiple disease resistance are valuable in crop improvement though molecular mechanisms underlying their functions remain largely unknown. A quantitative trait locus, qMdr9.02, associated with resistance to three important foliar maize diseases, southern leaf blight, gray leaf spot and northern leaf blight had been identified on maize chromosome 9. Through fine mapping, association analysis, expression analysis, insertional mutagenesis, and transgenic validation, we demonstrate that ZmCCoAOMT2, which encodes a caffeoyl-CoA O-methyltransferase enzyme associated with the phenylpropanoid pathway and lignin production, is the gene within qMdr9.02 conferring quantitative resistance to both southern leaf blight and gray leaf spot. We suggest that resistance might be caused by allelic variation at the level of both gene expression and amino acid sequence causing differences in levels of lignin and other metabolites of the phenylpropanoid pathway and in regulation of programmed cell death.
(Poster 12)

Effects of allelic variants on Drosophila olfactory behavior

Sneha Mokashi

Drosophila chemoreceptors have been studied extensively but little is known about how genetic variation affects individual variation in olfactory perception. Previously, genome-wide association analyses in the Drosophila melanogaster Genetic Reference Panel identified candidate genes associated with variation in olfactory responses to 14 structurally diverse odorants, including the standard odorant benzaldehyde. We performed principal component analysis on single nucleotide polymorphisms (SNPs) identified from these studies for sexes separately and genome wide association analyses on the principal components to identify key genes likely associated with variation in olfactory behavior. We focused on 49 genes that showed associations with significant P-values in multiple analyses, were present in genetic interaction networks, expressed in the central nervous system and involved in neuronal function. To functionally assess the effects of these 49 candidate genes on olfactory behavior, we used Mi{ET1} mutants and UAS-RNAi lines crossed to a neuronal Gal4 driver. Analyses of variance of dose response curves of mutants compared to co-isogenic controls showed a significant line term or line by concentration interaction term for three Mi{ET1} mutants, corresponding to pk, ppk11 and fas3, and four RNAi-targeted genes, corresponding to pitslre, pax, mam and fz2. Following analyses for linkage disequilibrium and rare alleles to identify haplotypes around the SNPs identified by previous genome-wide association analyses, I will examine the effects of alternative SNPs within these genes on olfactory behavior through allelic replacement by CRISPR-Cas9.
Student Achievements
Dogwood Room
4:00 PM – 5:00 PM
Pancreatic alpha-amylase: a candidate gene for trophic level evolution in Lake Malawi cichlids

Kate Coyle and Reade Roberts

Dietary adaptation is a universally important factor in organismal fitness and key driver in the evolution and diversification of species. Response to diet is a complex interaction between both genetic and environmental factors. Because of the massive impact of diet on development and health, there has been significant effort to characterize the contributions of these elements; however, the genetic basis of species divergence in dietary adaptation remains poorly understood. East African cichlids are an excellent model system for studying evolution due to a recent adaptive radiation that has resulted in extreme phenotypic divergence in many traits, including those involved in adaptation to diet. To investigate the genetic factors impacting this process, we sequenced the genomes of 30 cichlid species representing a range of trophic levels, then searched for variants that are alternatively fixed between herbivores and carnivores. One of the most promising candidate genes found is pancreatic alpha-amylase, an enzyme secreted in the foregut to break down dietary starches. Humans and dogs have undergone proliferation in copy number of amylase genes in response to adaptation to an agricultural lifestyle and a starchy diet. In our cichlids, we see both coding and copy number variation between herbivores, carnivores, and the ancestral omnivores. Interestingly, we see increased amylase expression in herbivorous species relative to other trophic levels that is inconsistent with expectations based on amylase copy number in other organisms. Moving forward, we seek to understand the mechanism underlying this pattern and its role in dietary adaptation and, subsequently, trophic level evolution.
Developing the Genetic Map for Aspergillus Flavus

Richard M. Gell and Ignazio Carbone

The carcinogenic mycotoxin aflatoxin is a constant threat and economic burden to corn and oilseed crops grown within the United States and globally. Aflatoxin is produced by species in Aspergillus section Flavi, including A. flavus, A. parasiticus and A. nomius. Within the US and Africa, aflatoxin contamination has been controlled through the application of biocontrols in the form of non-aflatoxin producing A. flavus strains. Current efforts in improving aflatoxin biocontrols involve a population genomics approach and a trait locus mapping approach; both of which rely heavily on alignment to a reference genome of the closely related species A. oryzae.

Development of an A. flavus genetic map began with obtaining genome wide data using double digest Restriction Associated DNA sequencing from 70 progeny strains for three crosses. Initial analysis of recombination frequency supports use of the A. oryzae reference genome to order markers on most chromosomes. Results from all three crosses present a previously unknown arrangement for chromosomes 2 and 6 in A. flavus. This new understanding of genomic organization improves marker selection in future studies and further understand inheritance in A. flavus.
The Genomics of Drug Consumption in Drosophila melanogaster

Brandon Baker and Trudy F. C. Mackay

Abuse and addiction to psychostimulants like cocaine and methamphetamine present a worldwide health issue. Drosophila melanogaster presents a model system to identify genetic and transcriptional networks that underlie variation in effects of drug exposure that can serve as a blueprint for subsequent studies on humans. Drosophila also exhibit many of the effects that are observed in humans when cocaine and methamphetamine are consumed. We have derived an outbred advanced intercross population (AIP) from 37 of the sequenced inbred wild-derived lines of the Drosophila melanogaster Genetic Reference Panel (DGRP). The lines are maximally genetically divergent, have minimal residual heterozygosity, are not segregating for common inversions and are not infected with Wolbachia pipientis. We assessed voluntary consumption of 4% sucrose, 4% sucrose + 1 µg/µL methamphetamine and 4% sucrose + 1.0 µg/µL cocaine of two replicates of 1500 flies for each sex and condition. We found significant phenotypic variation in the AIP, in both sexes, for consumption of both drugs and distinct behavioral effects in some of the tested flies. Using whole genome sequencing and genome-wide association analyses, we can identify and map variants associated with drug consumption and evaluate changes in allele frequencies among high consumers and a random set of flies. To test whether gustatory aversion plays a role in willingness to consume the drug, the proboscis extension response was tested for each sex and drug separately using the same concentrations mentioned above. We found a significant reduction in the proportion of flies that extended for each drug compared to sucrose. With this information, we can identify candidate genes associated with voluntary consumption and their human orthologues that can be used in future human studies.
Evolution of knockdown resistance in Aedes aegypti in Iquitos, Peru

Jennifer Baltzegar

The Yellow Fever mosquito, Aedes aegypti, transmits viruses affecting large numbers of people, including yellow fever, chikungunya, zika, and dengue fever. Historically, yellow fever has been controlled using vaccines, but for the other viruses the most common method of control is the use of insecticides; and pyrethroids are one of the most frequently used insecticide classes because they are effective at killing insects while being less toxic to humans. With frequent applications of pyrethroids to control A. aegypti populations, development of knockdown resistance (kdr) is a major concern. Many genetic loci associated with kdr resistance have been identified. However, two loci shown to be important in Central and South America are F1534C and V1016I. Monitoring the presence and frequency of these alleles in a population provides crucial information needed to develop mosquito control programs for delaying widespread insecticide resistance until more effective and longer-lasting disease prevention measures are available. This study explores the temporal dynamics of two kdr loci as well as fine-scale spatial patterns of insecticide resistance in Iquitos, Peru from 2000 until 2016.
Quantitative Analysis of the Ethylene Response in Arabidopsis thaliana Mutants Using Infrared Imaging

David A Bullock, Jose Alonso and Anna Stepanova

Ethylene is a gaseous phytohormone involved in multiple aspects of plant growth, development, senescence, and stress response. Seedlings that are germinated in the dark in the presence of ethylene undergo specific phenotypic changes known as the triple response. The three elements of this response are the radial expansion and growth inhibition of hypocotyls and roots and an exaggeration of the apical hook curvature. At the molecular level, the developmental effects of ethylene are accompanied by significant changes in gene expression at both transcriptional and post-transcriptional levels. While transcriptional regulation is well established as a critical process in response to ethylene, little is known about the role of ethylene-triggered gene-specific regulation of translation. Through ribosomal footprinting, our group uncovered a key molecular mechanism that links ethylene perception to the activation of a novel gene-specific translational control mechanism. Characterization of one of the targets of this translational regulation, EBF2, indicated that the signaling molecule EIN2 and the nonsense-mediated decay proteins UPFs play a central role in this ethylene-induced translational response, setting a new paradigm of gene-specific translational control. The goal of my project is to test the role of additional candidate genes whose translational efficiency is affected by ethylene. I am characterizing T-DNA knockouts corresponding to ethylene-responsive translational targets and studying their own growth kinetics through a growth response kinetic assay. This test relies on an infrared live imaging system to monitor subtle changes in the rates of elongation in hypocotyls and roots of dark-grown seedlings transiently exposed to the ethylene gas. In parallel, I am also exploring changes in the hypocotyl and root elongation in previously characterized ethylene- and auxin-insensitive mutants. Auxin is another vital plant hormone that controls numerous processes in plant’s life cycle, from
embryo development to fruit ripening. Remarkably, auxin biosynthesis, transport, and signaling are known to be interconnected with the ethylene biosynthesis and signaling pathway. Thus, mutant plants with defects in auxin also show phenotypic deviations in their response to ethylene. My plan is to test a set of previously characterized auxin mutants regarding their dynamic responses to ethylene to determine which stages of the ethylene response and recovery are compromised. Thus, my project is expected to expand our limited knowledge of ethylene-triggered translational regulation and further illuminate the role of auxin in response to ethylene.
Development of genomic prediction models integrating climate data for evaluation of maize hybrid performance

Anna R. Rogers and James Holland

In maize breeding programs with multiple testing environments, breeders are often faced with lines that perform well in one environment but fare poorly in another. In such situations, many breeding programs tend to pick lines that have higher average yield across environments, rather than aiming for specific environmental adaptations. Genotype-by-environment interactions (G×E) underlie these differences in performance, but are problematic to model due to difficulties with including environmental data in statistical models. Problems with including environmental variables in G×E analysis are created by presence of large numbers of predictors that can be highly correlated with one another, each of which only explains a small amount of variance.

Using publicly available for 885 maize hybrids evaluated across 24 locations, we attempt to better model G×E using available data on climate and photoperiod using a mixed modeling approach which combines the climate information with high density DNA marker information. These two sets of information are being employed to develop and evaluate methods to predict the performance of new hybrids in new environments. Such modeling would allow for better prediction of G×E and crop performance in new environments with similarities to those tested in these studies. More accurate estimation of G×E in maize hybrids would give a better depiction of how breeding programs have affected the genetic architecture of adaptive traits that depend greatly on environmental inputs. Breeders could use this information to more effectively breed for high performance for future environmental conditions predicted by climate change models.
Have a question concerning the Program in Genetics?
Contact one of us below!

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Lossie Rooney

Dr. Mary Anna Carbone and Dr. Ignazio Carbone

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Dr. Fred Gould

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Featured Caterers
Triangle Catering Biography

Triangle Catering launched its business as a personal chef service in 1991 and has steadily grown and expanded to include full-service catering and event planning. Our off-premise catering division is capable of serving up to 5,000! Triangle Catering focuses on delivering innovative Southern cuisine and using local North Carolina produce and meats. Owners Michelle and Dodd Aldred have been recognized regionally and nationally for their ongoing support and contributions to the local economy, and they attribute their success to maintaining a family dynamic in their business in spite of their growth and expansion.

Triangle Catering will be treating our event with breakfast, lunch, and an all day beverage service!
Antoinette Love Biography

Antoinette Love is the proud owner of Mel Amor, LLC, which is currently located in Charlotte, NC. She began the company out of her sheer passion for baking. Baking for family and friends started out as just a way to escape the stress from everyday work in Corporate America. With grassroots, word of mouth advertising the demand for her creations continued to grow. Antoinette's baking talents lead her to be selected as a contestant to compete on a nationally aired show, "The Great American Baking Show" and she is a reoccurring guest on local TV stations in Charlotte, NC. Her signature bakes are made special for you for all occasions.

"Our First Ingredient Is Love ".

*Antoinette will be treating our event with French macarons, cream puffs, eclairs, and ooh la la dessert bars!*
Visiting Industry Partner

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About the Company

Since 1979, Denville Scientific has been providing bioresearch laboratories with innovative, cost-effective products and technical solutions designed to improve laboratory efficiency, safety, and results. Our emphasis on quality, value, and customer satisfaction has served our customers and our company well. As a result of our recent growth, we have expanded our facilities, our staff, and our product line to serve you better. In addition to our traditional line of liquid handling products, our new catalog offers detailed descriptions and illustrations on hundreds of new items, many of which demonstrate our commitment to preserving the environment. Our knowledgeable sales staff welcomes your questions and comments. We want to thank our loyal customers for their support and patronage and we welcome those who may be seeing our catalog for the first time. We recognize the vital nature of your research and we realize the significance of our supporting role as a "supplier to science." Denville Scientific is dedicated to providing the scientific community with unique tools and exceptional service. Denville strives to provide American manufactured products of the finest quality. The Denville warehouse is located in Charlotte, NC.

Lisa Sooy will be on site at our event and will be representing Denville Scientific INC. For future inquiries, you may reach Lisa by email at lsooy@denvillescientific.com.
# List of Attendees

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