



Kevin Boyer (2018)



Cella Wright (2018)



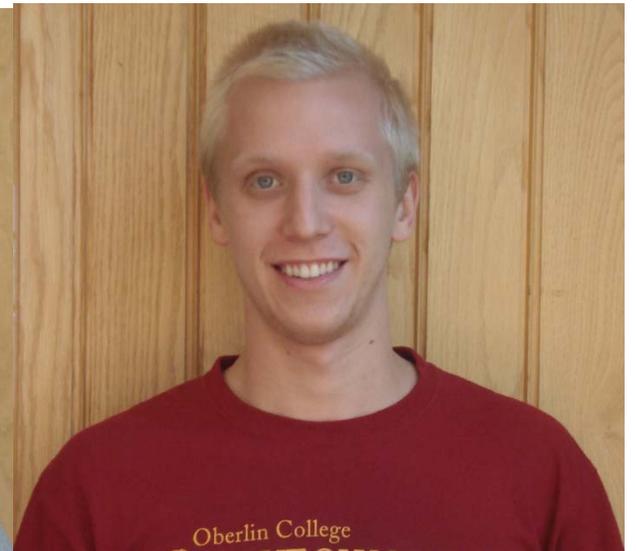
Ben Lovett (2017)



Mercedes Campos-Lopez (2018)



Tempe Shrenker (2019)



Scott Miller (2017)

“The Role of Avian Preen Gland Secretions in Host-Seeking Behavior of *Culex pipiens* Mosquitoes”
Research Advisor: Mary Garvin



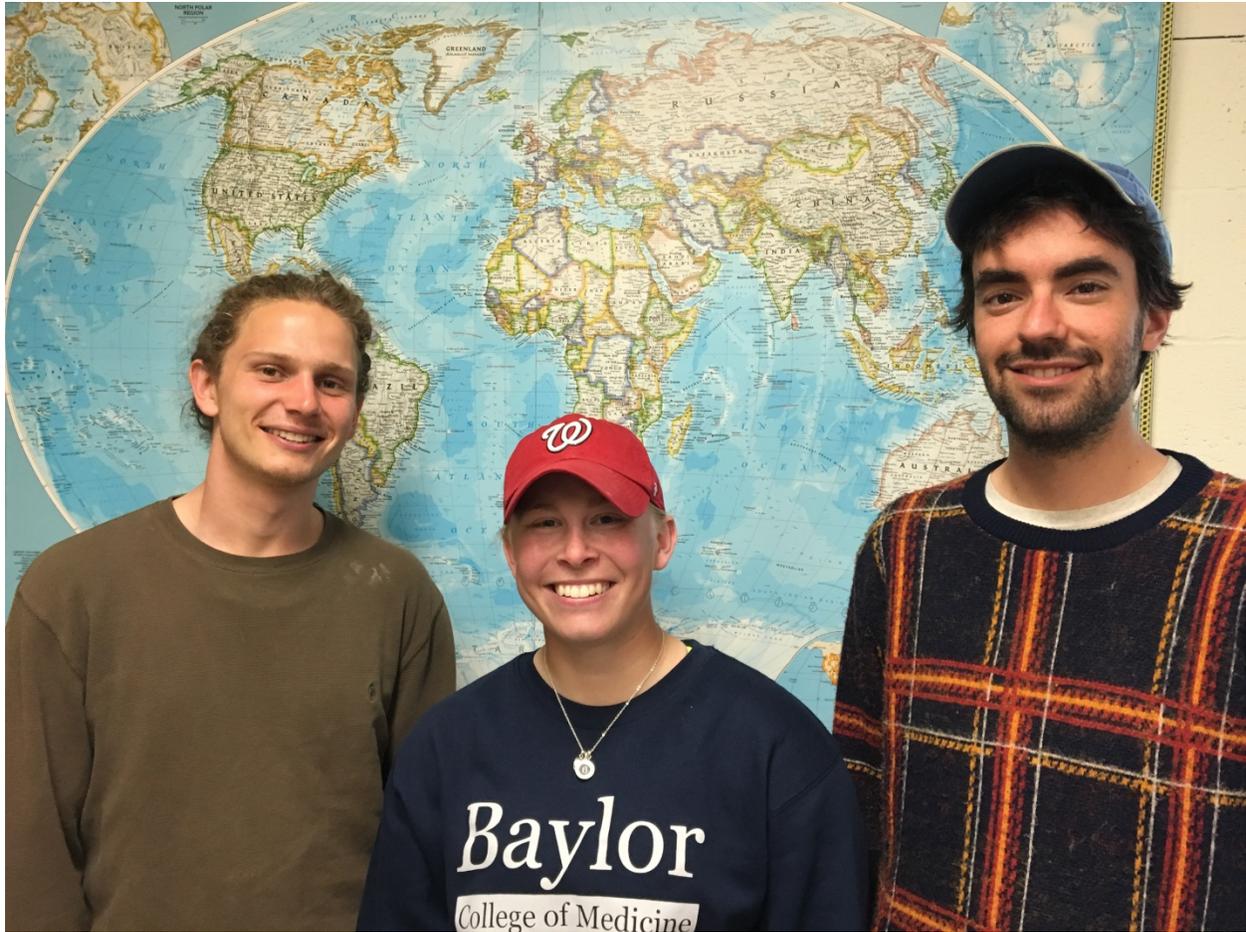
Abbie McCrea (2018)

Max Butler (2017)

“The Role of Avian Preen Gland Secretions in Host-Seeking Behavior of *Culex pipiens* Mosquitoes”

Culex pipiens, a species of mosquito abundant in the eastern United States, is the primary transmission vector of West Nile Virus (WNV). Among the most common reservoir hosts for the virus are American robins, house sparrows, and European starlings. Feeding preferences of *Cx. pipiens* contribute a great deal to the involvement of particular birds as reservoir hosts, although the basis for this preference is not fully understood. We hypothesize that the apparent preferences are the result of mosquito responses to volatile compounds in bird preen gland secretions. The preen gland, located at the base of the tail, produces complex secretions that include heavier oils and waxes believed to waterproof and condition feathers, as well as lighter, volatile compounds hypothesized by many to serve in intra- and interspecific communication. Work in the analytical chemistry lab of our OC collaborator, Rebecca Whelan, has demonstrated that robins, house sparrows, and starlings have species-specific volatile chemical profiles; moreover, house sparrows demonstrate age-specific profiles. This is especially interesting because *Cx. pipiens* prefer to feed on adult house sparrow over juveniles. To test our prediction that *Cx. pipiens* respond differently to house sparrow age-specific preen gland chemical profiles, we are conducting mosquito behavioral assays. These are conducted in an olfactometer, which allows mosquitoes to choose between secretions of adult and juvenile house sparrows. With the results of these trials, we hope to further elucidate the factors determining the *Cx. pipiens* feeding preferences and better understand the WNV cycle.

Research Advisor: Mary Garvin



Robbery Lewis-Nash (2017), Tori Poplaski (2017), Simon Printz (2018)

**“Determination of feeding preference of West Nile virus mosquito vector
Culex pipiens: via blood meal DNA analysis”**

Culex pipiens mosquitoes are the primary vectors of West Nile virus (WNV) among avian reservoir hosts in the eastern United States. The American Robin appears to be the most important species of reservoir host, but the reason for the robin’s important role in the WNV cycle is not known. One explanation is that *Cx pipiens* prefers robins over other competent reservoir host species. To explore this hypothesis, we are testing the prediction that the majority of blood meals collected by *Cx pipiens* are from American Robins. To test this prediction, we are collecting blood-fed *Cx. pipiens*, extracting avian DNA from the abdomens, and conducting polymerase chain reaction (PCR) to amplify the avian mitochondrial cytochrome *b* gene. We then conduct a BLAST analysis on the PCR product, which allows us to search GenBank, a sequence database, for a match that identifies the blood meal to an avian species.

Research Advisor: Mary Garvin



Anah Soble '18, Sune Wolf Pulsiano '18, Zoe Ciantra '18, Linnea Halsten '19, Laura Ingraham '19, Stephanie Gunter '18, Clarissa Guy '17

“Do squirrels attend to “squirrel-relevant” information encoded in chickadee alarm calls?”

Many animals eavesdrop on avian alarm calls in order to obtain low-cost information about potential predation risk. Previous research shows that Eastern Gray Squirrels (*Sciurus carolinensis*) eavesdrop on the alarm calls of various bird species, including American Robins (*Turdus migratorius*) and Black Capped Chickadees (*Poecile atricapillus*). In this study we are investigating whether squirrels respond to information encoded in alarm calls that is useful explicitly to them. Chickadee alarm calls are referential: Calls with more “d-notes” signal the presence of smaller, more agile predators that are highly threatening to chickadees, but less so to squirrels. Calls with fewer d-notes signal the presence of larger, slower predators that are less threatening to chickadees, but are more threatening to squirrels. We present squirrels with audio playbacks of chickadee alarm calls made either in response to a mounted Red-Tailed Hawk, a common predator of squirrels, or a Saw Whet Owl, which is not a predator of squirrels, and observe changes in squirrel vigilance before and after the playback. If squirrels are able to “decode” the information about predator size contained in chickadee alarm calls, they should respond more strongly to chickadee calls made in response to Red-tailed Hawks than to those made in response to Saw-whet Owls. Such a result would indicate that squirrels have the capacity to extract “squirrel-relevant” information from heterospecific alarm calls, even when the squirrel-relevant information is counter to the urgency encoded in the chickadee call.

Research Advisor: Keith Tarvin



Emilia Omerberg '17

“Lake Erie Fisheries”

I do research with the US Geological Survey at the Lake Erie Biological Station in Sandusky Ohio. My Supervisor is Patrick Kocovsky, and Roger Laushman in my faculty advisor for the project. In our research we study the Lake Erie Fishery. We look at diet samples from walleye and yellow perch as well as age analysis to see what different age groups of each fish eat. We have also done work on fish movement in the lake to track breeding movements as well habitat use. Along with this research we also keep tabs on lake dynamics and take water samples to test for the presence and abundance of macro invertebrates, dissolved oxygen and temperature change.

Research Advisor: Roger Laushman



Keyi Feng

“Phylogeography and Potential Speciation among Gypsum Endemic *Mentzelia* Taxa”

The plant genus *Mentzelia* currently has seven gypsum endemic taxa, of which four are closely related and restricted to New Mexico and Texas: *Mentzelia humilis* var. *humilis*, *Mentzelia humilis* var. *guadalupensis*, *Mentzelia perennis*, and *Mentzelia todiltoensis*. However, the species boundaries of these taxa are still uncertain, and preliminary phylogenetic analysis of individuals from several populations of all four taxa suggests there may be additional undescribed taxa. The potential presence of these cryptic taxa suggests that the degree of gene flow among gypsum endemic *Mentzelia* populations is heavily influenced by the distance between their habitats. To investigate these questions, I am isolating DNA from multiple individuals from each population of gypsum endemic *Mentzelia* collected, and sequencing both the nuclear internal and external transcribed spacer regions for all individuals to include in more detailed analyses of phylogenetics and genetic diversity.

Research Advisor: Mike Moore



Abbey Bisesi '17

“Computational Analysis of Models of Gene Rearrangement in Mitochondrial DNA”

The organization of the mitochondrial genome is remarkably conserved in Metazoa. The vast majority of sequenced genomes contain the same 37 genes. However, recent studies have revealed that gene order among these genomes can be highly variable. This variation is presumably neutral, but its existence raises important evolutionary questions. Why is gene order variable in some groups and invariant in others? What are the forces that shape the evolution of gene order? Is it possible to create a computational model of the process of gene rearrangement in order to predict the influence of neutral evolution on gene order? There are several mechanisms currently used to explain changes in gene order over evolutionary time, but the tandem duplication random loss model (TDRL) is considered to be the most relevant in vertebrates. We have available a dataset of crayfish mitogenomes with variant gene order. Computational analysis should lend insight into whether or not the gene rearrangements present in this dataset are predicted by and consistent with the TDRL model. Such investigation of the relative importance of TDRL could provide the basis for comprehensive models of the rearrangement process and serve to improve phylogenetic analyses that rely on comparative gene order.

Honors Advisor: Angie Roles



Ava Field '18

“Localizing Early Pregnancy Factor Secretion in the Lab Opossum”

In mammals, the protein Early Pregnancy Factor (EPF) is the earliest definitive sign of pregnancy, appearing in maternal serum within hours following a fertilization event. EPF has immunosuppressive properties, and has been shown to be associated with certain kinds of cancers. The immunosuppressant role of EPF in pregnancy prevents the embryo from being recognized as an allograft and thus rejected by the maternal immune system. Marsupials were once thought to have no physiological recognition of pregnancy but our lab has shown that several species of marsupials do in fact synthesize EPF during pregnancy. For this project I will be looking for the expression pattern of EPF protein in the ovary and uterus of the lab opossum using immunohistochemical staining, to document its proposed origin in pregnancy ovaries.

Research Advisor: Yolanda P. Cruz



Ave Spencer '17

“Epithelia-Mesenchyme Attributes of Trophoblast and Pluriblast Cells in *Monodelphis domestica*”

I am researching epithelial-mesenchyme transition and location of pluripotent cells in *Monodelphis domestica* (Md). The Md blastocyst first forms from blastomeres that adhere to the zona pellucida and then to the surrounding cells. The blastomeres then flatten against the zona pellucida, and form a monolayer epithelium. The pluriblast is co-planar with the trophoblast and its gene expression pattern is distinct from the trophoblast. Given this, I believe that the pluriblast develops in one of two ways

1. The pluriblast epithelializes similarly to the trophoblast, and then it undergoes an epithelial-mesenchymal transition or,
2. The pluriblast never epithelializes and it remains distinct from the trophoblast during blastocyst formation.

Honors Advisor: Yolanda P. Cruz



Aviva Blonder '18

“Do Zebrafish (*Danio Rerio*) Preferentially Associate with Bolder Conspecifics?”

Many species of fish inspect potential predators in groups to decrease the risk to each individual of being eaten. Individuals of several such species have been shown to prefer to associate with conspecifics that get closer to the predator being inspected. The individual closest to the predator is at the highest risk of being eaten and therefore decreases the risk to the other inspecting fish. More closely inspecting predators is considered bolder or more cooperative. I will evaluate the hypothesis that being bolder during predator inspection is an important form of cooperation by testing whether zebrafish, a social species commonly used in the laboratory, prefer to shoal with bolder conspecifics. To do this I will expose trios of zebrafish, each including one focal and two partner fish, to a predator and prevent one of the partner fish from inspecting it. Then, after the predator has been removed, I will measure how much time the focal fish spends with each partner fish. If the focal fish consistently spends more time near the uninhibited partner fish, that indicates that zebrafish prefer to shoal with bolder or more cooperative conspecifics. This opens the door to the possibility that predator inspection is a form of reciprocal altruism in zebrafish as it has been found to be for several other similar species.

Research Advisor: Keith Tarvin



Caroline Edwards

I will be working in Prof. Moore's lab to reconstruct the evolutionary relationships among two sister genera in the Nyctaginaceae (four-o'clock) family, *Abronia* and *Tripterocalyx*. *Abronia* is a genus of approximately 20 species that primarily grow in the western United States and inhabit diverse ecosystems, from Pacific Coast sand dunes to alpine environments in the Sierra Nevada to gypsum soils in New Mexico. *Tripterocalyx* is a small genus of 4 species that grow in sandy environments in the western US. To reconstruct the evolutionary history of habitat preferences in these two genera, I will isolate the DNA from samples of these two groups, amplify and sequence specific regions of chloroplast and nuclear DNA, and use the resulting sequences to build a phylogenetic tree of the two genera.

Research Advisor: Mike Moore



Dorothy DeBiase '19

“Structure and Function of Strident Muscle in Round Worms”

Testing how strident muscles, such as muscles found in the skeleton and heart, turn on and off. More specifically, how does the calcium switch work for strident muscles to propel this mechanism. We know mutation switches due to the calcium switch in the heart lead to fatal diseases. Some diseases that result from the mutation switches are familial hypertrophic cardiomyopathy FHC or HCM as well as dilated cardiomyopathy. There are mutations in the motor function that cause the diseases aforementioned. The mechanism for the calcium switch involves troponin and tropomyosin located in the strident muscle. In this process, calcium binds allowing troponin and tropomyosin to move out of the way which allows for actin and myosin to interact with the strident muscle. In addition, troponin overlaps in a head to tail manner, which proves to be the root of the project. The hypothesis being tested is whether or not the head to tail overlap of troponin tropomyosin along the actin filament is functionally important. The process for approaching this hypothesis is through microscopy and engineering to test for structural and functional alterations and or changes in the mutant organisms. To do this, roundworms are used to test the strident muscles.

Research Advisor: Taylor Allen



Elisa C. Henderson

“Does invasion of *Orconectes rusticus* affect genetic diversity of crayfish along the watershed?”

Introduction of nonindigenous species can have a major impact on ecosystem functioning and can cause loss of biodiversity worldwide. *Orconectes rusticus* is used by humans as live bait, likely causing its range expansion out of its endemic region of Southwest Ohio and Kentucky. It has been introduced into the range of the Sanborn's crayfish (*O. sanbornii*), and has displaced many native crayfish species throughout its expansion. For my Honor's Project, I will research the morphological and genetic impacts of invasion and hybridization in two invaded watersheds in north-central Ohio. I will investigate the genetic composition of populations sampled along the watershed using data from restriction site-associated DNA sequencing (RAD-seq) to test for a trend in genetic resemblance to one species or the other as the populations are found further upstream. I will compare genetic variation in upstream and downstream populations with genetic variation of allopatric populations for both species. Based on personal observation, I hypothesize that downstream populations will have a genetic composition that more closely resembles that of *O. rusticus* native populations, while upstream populations will more closely resemble non-invaded *O. sanbornii* populations. If this pattern holds true in the two sympatric rivers I focus on, the Huron River and the Kokosing River, this supports the hypothesis that landscape characteristics affect the interactions between these two orconectid species. The flow of the river may make it more difficult for Rusty crayfish to travel upstream after their introduction. This could lead to upstream Sanborn's crayfish populations being affected less than those located downstream of or close to the introduction site. If hybridization is prominent in sympatric populations, this could cause an increase in genetic diversity of *O. sanbornii* due to the gene flow from a similar species, as opposed to a replacement of the species. I expect the invaders to have less genetic diversity than allopatric populations because it is likely that only a few individuals were released after use as live bait, causing a bottleneck effect that was followed by population expansion. A closer look at the distribution of genetic diversity along the watershed may provide insight into the consequences of the invasion for both invader and native species, including whether native genetic diversity is maintained in the face of invasion. Comparing genetic diversity along the watershed of two invaded rivers to the genetic diversity of allopatric populations for invasive and native species will provide information regarding the effects that a heterogeneous landscape has on the evolution of these species after the *O. rusticus* invasion.

Honors Advisor: Angie Roles



Emma K. Rast '17

**“Impact of EAB-induced Ash Mortality on Herbaceous Understory Vegetation in
Chance Creek Preserve”**

The Emerald Ash Borer (EAB) is an invasive phloem-feeding pest native to northeastern China that has caused widespread ash death throughout eastern North America (Herms 2014). While several studies have documented the effect of EAB-induced ash mortality on forest structure and composition, little research has been done concerning its impact on herbaceous understory vegetation. This is an important area of study, as the herbaceous layer accounts for the majority of plant biodiversity in forest ecosystems. Furthermore, the herbaceous layer can influence the future composition of a disturbed forest due to the impact of interspecific competition between herbaceous species and regenerating overstory seedlings (Gilliam 2007). Our research focuses on examining the impact of EAB-induced ash mortality on fall herbaceous understory vegetation within Chance Creek Preserve. We will collect data on canopy closure, groundcover, and herbaceous species diversity using thirty-three 0.04 ha permanent plots established in 1974 and compare high, medium, and low ash-loss permanent plots.

Honors Advisor: Roger Laushman



Jessica Jimenez '17

“Investigating the molecular pathways causing lifespan extension in a *C. elegans* intestinal mutant”

Organisms allocate their energy stores appropriately in response to environmental conditions. In stressful situations organisms prioritize self-preservation over reproduction. In *Caenorhabditis elegans* (*C. elegans*), reduction of caloric intake and decreased intestinal cell-cell communication correlate with increased lifespan. To examine the role of the intestine in longevity we utilize an intestinal gap junction mutant, innexin (*inx-16*), which displays deficiencies in intestinal calcium wave propagation. We have shown that *inx-16* mutants experience increased lifespan; now we are working to understand the molecular pathway connecting intestinal signaling to longevity. Several stress response pathways are known to induce longevity in *C. elegans*. Previous work suggests that *inx-16* mutants activate a stress response related transcription factor, SKN-1, which can increase expression of antioxidants and other stress response factors. I will assess whether SKN-1 responsive genes are upregulated in the *inx-16* mutant, utilizing transcriptional reporter gene constructs in which GFP is driven by the normal stress response gene's regulatory sequences. GFP fluorescence levels will be compared between *inx-16* and normal animals as a readout of SKN-1 transcriptional activation. This study may determine if the SKN-1 pathway is involved in the observed *inx-16* longevity and provide a deeper understanding of intestinal calcium waves in organismal physiology.

Research Advisor: Maureen Peters



Josh Goodman

"Regulation of Embryonic-Lineage Specification Factors in *Monodelphis domestica* via Promoter DNA Methylation."

I will be investigating the role of promoter CpG methylation in the temporal regulation of embryonic-lineage specification factors in *Monodelphis domestica*, the South American gray short-tailed opossum. Direct CpG methylation is known to inhibit gene expression, but its role in metatherians (a clade including marsupials) is not well understood, especially in comparison to its function in eutherians (the clade containing most other mammals). I will use bisulfite sequencing and qPCR to determine the extent of DNA methylation in the promoter regions of a number of pluripotency factors (e.g. Nanog and Oct2) and other cell fate-specification factors (e.g. Wnt3a and FGF8) over the course of *Monodelphis* embryonic development, as well as in adult tissue, in order to see if promoter methylation seems to direct changes in gene expression necessary for proper development. FISH will also be utilized to quantify mRNA expression over time, in order to demonstrate if transcription amount is indeed correlated with promoter methylation in this setting. On the whole, I hope to shed light on the role of promoter methylation in the tightly controlled *Monodelphis* developmental program.

Honors Advisor: Yolanda P. Cruz



Julie Watiker '18

“Further Investigation of the Microanatomy of the *Monodelphis domestica* Prostate”

The mammalian prostate gland secretes fluids that, along with sperm from the testes and fluids from other glands, compose semen. In Marsupials, the anatomy of the prostate gland is not well known. This past summer, my research partner and I designed a project to study the micro-anatomy and the proteins present in the marsupial prostate in comparison to that of the rodent prostate. We used prostate samples from *Monodelphis domestica*, the grey short tailed South American opossum, and *Rattus norvegicus* immunohistochemistry techniques, we aimed to detect the presence of probasin, a prostate specific protein in mammals, in both the rat and opossum prostates. Probasin is known to be found in the lateral lobe of the rat prostate. We discovered that the opossum prostate has probasin producing cells localized to the posterior region and lacks these cells in the anterior region. In the rat, probasin producing cells are found throughout the entire prostate.

This semester, I am continuing this research, hypothesizing that the anterior opossum prostate produces other proteins found in the rat prostate. I will be using immunohistochemistry techniques to determine whether the protein Prostatein, which is present in the ventral lobe of the rat prostate, is present in the opossum and in what regions it is present. The ultimate goal is to further understand the functionality of the opossum prostate as well as the specialization of its different regions.

Research Advisor: Yolanda Cruz



Katherine LaTourrette '18

“*C. elegans* Myosin Muscle Mutations”

My research examines several different *Caenorhabditis elegans* myosin mutations and their effects on a worm's muscle functions. Each strain has a change of one amino acid in a conserved area of myosin. Data is collected using a MATLAB computer program that maps the worm's swimming ability and provides different measures designed to give insight into the proper or improper functioning of the muscle. The other major test I am adding this year is a swimming fatigue test in order to better understand what is happening on a more cellular level during pre-powerstroke, rigor, and post-rigor. I am also analyzing the normal amino acid interactions and the effects of the mutation by looking for changes in amino acid relationships. By combining the data and crystal structure, I am hoping to connect force production, attachment of myosin cross bridges, and ATP use during muscle movement. This will give insight into how muscle movement is formed through the conversion of energy from chemical to mechanical. The information gathered can allow for a better understanding of the role of these amino acids and how small-scale changes in myosin can affect the overall functioning of the entire muscle.

Research Advisor: Taylor Allen



Kobi Griffith

The sperm of New World marsupials pair along their acrosomal face, which could be a possible strategy to improve the motility of sperm and increase the likelihood of fertilization. This year I will be continuing ongoing studies behind the mechanism of sperm pairing in marsupials using the model organism *Monodelphis domestica*. I will study sugar residues of glycoproteins that may be present at the interface of sperm pairing as well as present along the epithelium of the epididymis and oviduct, as these tissues are likely the location of pairing and unpairing of sperm, respectively. I will be using lectin staining, histology and fluorescent staining in my search for these residues. Once the possible sugar residues have been narrowed down I will continue my research by looking into the potential presence of sperm adhesions, a newly researched protein believed to be integral to fertilization, during the pairing process.

Research Advisor: Yolanda P. Cruz

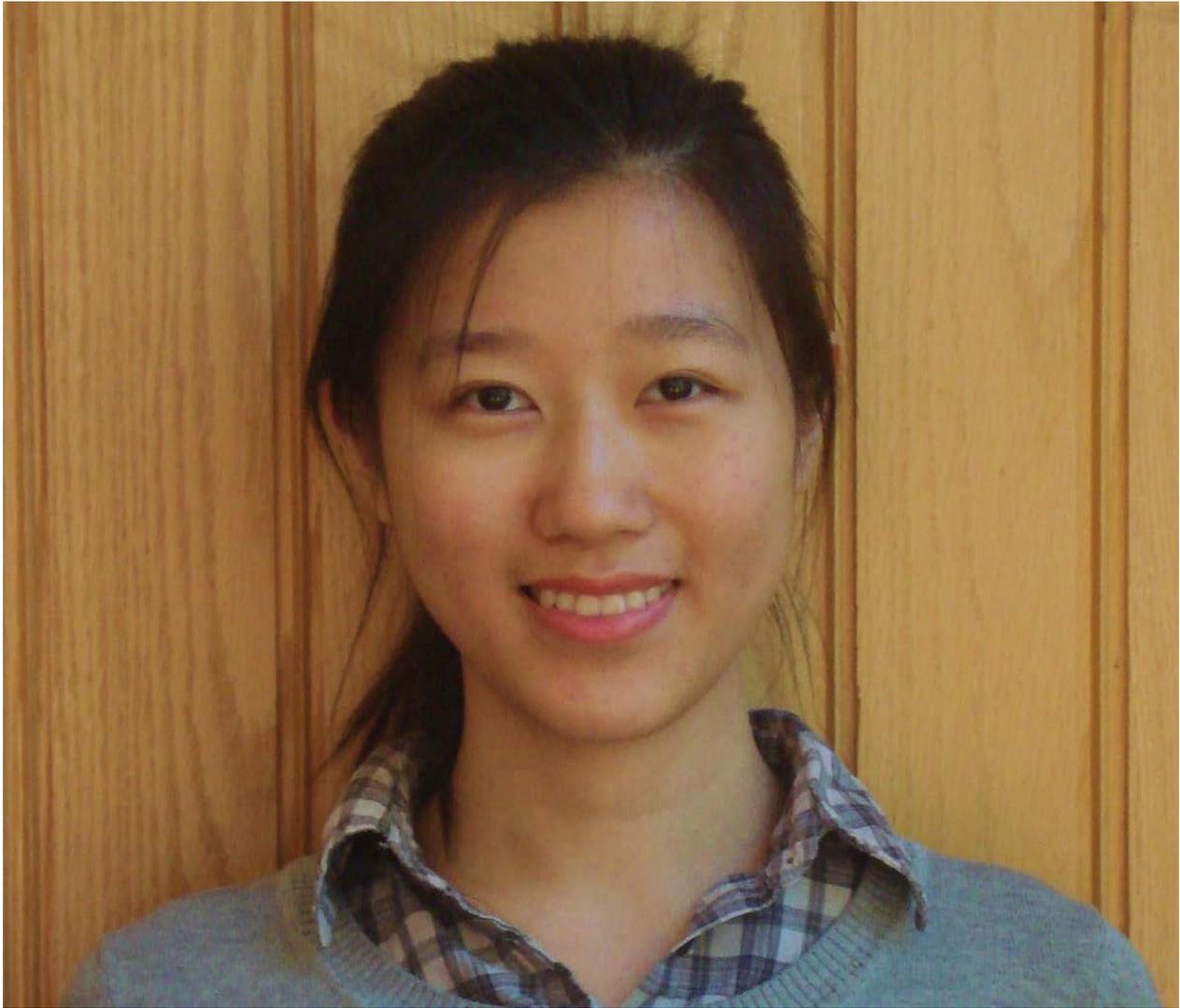


Marie Lilly '17

“Bird chatter as an indicator of safety: To what extent do Eastern Grey squirrels rely on public information?”

Many studies have shown that Eastern Gray squirrels and other small mammals exploit heterospecific alarm calls as indicators of danger. There have not, however, been any investigations of what environmental cues small mammals recognize as signs of safety. The objective of my study is to test the hypothesis that eavesdroppers such as Eastern Grey squirrels use bird chatter as a measure of safety. If bird chatter indicates safety, I predict that squirrels will be less vigilant following a playback of a predator (Red Tailed Hawk) call when bird chatter is played than when no bird chatter is present. Behavior of the squirrels will be monitored and recorded before and following playback trials. The recorded behavior will later be analyzed to provide information about relative change in levels of vigilance in response to danger in the presence or absence of bird chatter. This study will add to the body of knowledge about the role of eavesdropping in behavioral ecology.

Honors Advisor: Keith Tarvin



Nina Li '17

“Investigation on the caloric restriction in a long-lived *C.elegans* mutant, *innexin-16*”

We have isolated a long-lived mutant, innexin (*inx-16*), caused by a loss of function mutation in an intestinal gap junction subunit. Phenotypically, *inx-16* animals have traits associated with caloric restriction such as small size, long life, and low brood size. Therefore, we hypothesized that *inx-16* strain experiences poor nutrient absorption and the resulting changes in autophagy, which is known to be associated with increased longevity. To evaluate the validity of this hypothesis we have developed aims that identify alterations in nutrient intake and measure markers of starvation. First, we tested whether *inx-16* strain has a food intake defect by analyzing the activity of the worm’s stomach-like organ, the pharynx. Then we tested whether *inx-16* has nutrient absorption defects by measuring fat storage, which should reflect energy acquisition and allocation. We found that *inx-16* has a similar pharyngeal movement rate but decreased body fat compared to wildtype, supporting our hypothesis of poor nutrient absorption. Currently, we are investigating cellular changes associated with caloric restriction, such as the induction of autophagy. Autophagic activity is being analyzed using a GFP tagged autophagy related protein, LGG-1, which is incorporated into pre-autophagosomal and autophagosomal membranes. We expect to observe increased numbers of LGG-1 protein aggregates in *inx-16* compared to wildtype, which will indicate elevated autophagic activity.

Research Advisor: Maureen Peters



Olivia Tsang '18

“Forest Community Structure and Invertebrate Diversity”

Eastern deciduous forests consist of subtypes such as floodplain, upland, slope, and successional forests. Invasive species such as the emerald ash borer (EAB) cause rapid changes in forest structure in the understory and ground layers. Consequently, we are examining understory vegetation and invertebrate diversity among four habitats (floodplain, high ash-loss, successional forest, and undisturbed). During summer 2016, we surveyed invertebrate taxa (including beetles, spiders, and ants) using pitfall-traps in eight of the 33 permanent plots at Chance Creek Experimental Research Reservation. The invertebrate diversity will be analyzed in correspondence with vegetation and abiotic factors such as light (canopy cover, PPFD) and soil (moisture, pH, organic content). We have a particular interest in ant distribution, given that approximately 70% of understory flora are myrmecochorous (ant-mediated seed dispersal).

Research Advisor: Roger Laushman



Rachael McMinimy

“Characterizing the Developmental Profile and Growth Pattern of a *C. elegans* Mutant with intestinal defects”

Dietary restriction has been demonstrated to delay developmental progression from larvae to adult in *Caenorhabditis elegans* (*C. elegans*), leading to extended lifespan and increased reproductive longevity. Previous work by the Peters lab has shown that *C. elegans* with a mutation in an intestinal gap junction subunit, innexin-16 (*inx-16*) have longer lifespans than wild-type worms. Additionally, preliminary visual analysis has suggested that *inx-16* worms may experience delayed growth and reduced size in comparison to wild-type. INX-16 forms gap junctions between intestinal cells; these gap junctions are essential for cell communication of a cyclic calcium wave. This wave is required for normal digestive motor programs leading to waste release. We believe that dysfunction of INX-16 may compromise intestinal function in other ways, leading to poor nutrition and subsequently causing lifespan extension. In order to investigate this hypothesis, I am comparing the growth profile of *inx-16* worms to two other mutants known to have nutritional deficits. Comparison of the *inx-16* mutant against these worms at larval stage 4 (L4) and adult ages will help to reveal the significance and severity of *inx-16* growth delay relative to other mutants with established nutritional deficits.

Research Advisor: Maureen Peters



Tadhg Young

“Investigations into phase related lateral root formation in response to wounding”

The life cycle of a plant presents many distinct phases, germination of a plant, through leaf production, to the end of its reproductive phase. How a plant reacts to stimuli can vary depending the particular phase in which that stimuli are perceived. One such example is how wounding of a primary root causes lateral roots to form above the damaged site. When specific genes that contribute to the synthesis of an important hormone in lateral root formation, auxin, are knocked out we see a loss of this lateral root formation in response to wounding, but only at specific ages. My research investigates how genetic manipulation of phase affects the wounding response.

Honors Advisor: Marta Laskowski



Vera Hutchison

“Spatio-Temporal Expression of Vasa in Primordial Germ Cell Determination in *M. domestica*”

Work in the Cruz lab focuses on marsupial development by using the laboratory opossum, *Monodelphis domestica*. My work concerns two germline proteins and their spatio-temporal expression throughout embryonic development. I use immunohistochemistry, confocal imaging, and mRNA analysis to locate these two proteins and quantify their levels. We hope to understand the developmental evolutionary history of *M. domestica*, as these animals show developmental patterns similar to both mammals and reptiles.

Honors Advisor: Yolanda P. Cruz



Victor Lau '17

“Effect of Ash Tree Loss on Tree Species”

The emerald ash borer (EAB) is an invasive beetle species that has decimated ash tree populations since their accidental introduction in the United States in the 1990s. We have woody species data from 33 permanent plots at the Chance Creek Natural History Reservation recorded in 1974, 1986, 1998, and 2015, which documents species diversity both before and after the EAB introduction. The ash tree population has decreased by 98% since 1998, so the focus of my research concerns the effects of ash tree loss on other tree species. I am examining these tree species using data from plots that experienced high ash-loss with plots that had little or no ash-loss with the goal of identifying positive or negative response patterns.

Research Advisor: Roger Laushman



Wren Leader

“What’s that Noise?: A Study of Auditory Masking in Birds”

Anthropogenic noise from roads and industrial equipment has been shown to have a significant negative impact on avian wildlife, with lower population density and diversity of species in areas with lots of noise pollution. Some bird species have been known to increase the pitch of their songs and calls in high-noise areas, and species with higher-pitched vocalizations are more likely to persist in areas with large amounts of anthropogenic noise, which tends to be low frequency. This is presumably to prevent “masking”: when a sound is drowned out by noise of similar frequencies. Masking can be particularly devastating for birds due to their heavy reliance on information from hetero and conspecific alarm calls. I will be investigating whether masking of avian communication by anthropogenic noise is a significant factor in avian behavior by playing masking and non-masking white noise in close proximity to feeders, and comparing the number and species diversity of birds that feed during different playbacks. This may enable us to reduce impact on birds by restricting noise pollution frequencies, or by altering machinery or designing selective noise-canceling devices.

Research Advisor: Keith Tarvin