Katie Rotman ’14, Madison Kincaid ’14, and Michelle Rabowsky ‘12

“Determining How Myosin Works aka Why Worms Wiggle”

We are investigating how a molecular motor works, specifically myosin. Myosin is one of the three major molecular motors used to produce movement in eukaryotic cells. Mutations of myosin are linked to lethal diseases such as Familial Hypertrophic Cardiomyopathy: an inherited heart disease causing enlarging of the heart. This motor has naturally occurring mutations that give rise to diversity. However, disease mutations cause disease that we see in clinics. If we can understand how myosin works in general, we would be better able to understand why certain changes lead to disease. We are examining the molecular mechanism by which certain mutations enhance or diminish the speed of myosin found in the model genetic organism, Caenorhabditis Elegans. Our approach to this involves classical genetics, immunobloting, and applications of engineering principles to determine the mechanical properties of wildtype and mutant worms. The data that will emerge from this study should tell us how myosin works, and more specifically how it can be sped up or slowed down as a motor. This information will help explain why certain mutations lead to diseases and why other changes in amino acids are tolerated and give rise to diversity of muscular function in nature.

Madison Kincaid, from Middlebury, Vermont, enjoys photography and playing outdoors as well as playing with mutant worms. Michelle Rabowsky, from Davis, California, enjoys horseback riding and folk music as well as playing with mutant worms. Katie Rotman, from Montreal, Quebec, enjoys studio art and skiing as well as playing with mutant worms.

Research Advisor: Taylor Allen
Amy Austin ‘11

“Characterization of the Semi-Volatile Compounds of the Preen Gland Secretions of Three Avian Reservoir Hosts of West Nile Virus”

The preen or uropygial gland of birds produces secretions that are important in maintaining the health and structural integrity of feathers. These secretions have also been shown to be important in olfactory communication both within and between species. *Culex pipiens*, the primary mosquito vector of West Nile virus, is known to feed preferentially on American robins, over both house sparrows and European starlings, three species believed to be involved in the West Nile virus cycle. We hypothesize that this preference may be mediated by the uropygial gland secretions. For my honors project, I am identifying the semi-volatile components of the uropygial secretions of the American robin, house sparrow and European starling using gas chromatography-mass spectrometry. Upon identification of the compounds, I will compare them among the three bird species to determine their contribution to the observed preference of *Cx. pipiens*.

Honors Advisor: Mary Garvin

Israel Ukawuba ‘11

“2La Chromosomal Inversion and Insecticide Resistance in *Anopheles gambiae*”

*Anopheles gambiae* is the mosquito vector of *Plasmodium falciparum*, the parasitic protozoan that causes malaria. Resistance of *An gambiae* to insecticide greatly impacts efforts to control the disease. We hypothesize that *An gambiae* insecticide resistance is due to a less permeable cuticle, which lowers the rate of insecticide penetration. I will compare insecticide resistance between two karyotypes of *Anopheles gambiae*, 2La and 2L+, which vary in cuticular permeability. I predict that the karyotype with the less permeable cuticle will be more tolerant of insecticide. To assay for resistance, I will expose mosquitoes of both karyotypes to insecticide for varying amounts of time and record mortality after 24 hours. In a second assay, we will expose both karyotypes of mosquito to an insecticide treated bed net and compare time until knockdown.

Honors Advisor: Mary Garvin
Although phyllotaxy, the patterning of leaves in the shoot of the plant, has been widely studied, rhizotaxy, the patterning of lateral organs in the root, is less well understood. Lateral roots are initiated in two files of cells adjacent to the xylem, at the boundary of the elongation zone and the differentiation zone of the main root. Several competing models exist that seek to explain how lateral roots are initiated. In one model, bending of the root leads to auxin accumulation and these local auxin maxima in turn lead to lateral root initiation. It has been established that lateral root initiation on the outside of curves is widespread throughout seed plants. Various influences could be involved including mechanosensing and activation of stretch receptors, or elongation of cells leading to changes in auxin flow. In another model, endogenous cycling of gene expression at 6 hour intervals leads to formation of pre-branch sites, which may or may not lead to a fully emerged lateral root. Using the model plant *Arabidopsis thaliana* I will investigate the various pathways and genes influencing lateral root initiation and emergence hope to elucidate which model most accurately describes the process of lateral root formation.

**Honors Advisor: Marta Laskowski**

This year, I will explore lateral root initiation events in the model plant *Arabidopsis thaliana*. Lateral roots grow from the main root, and expand the nutrient uptake ability of the plant. Plants grow these new organs in different numbers and at different points along the roots, such as on the outside of curves, and understanding this behavior has potential benefits for agricultural productivity through increasing nutrient uptake efficiency. There are currently several models for what causes a new lateral root to initiate. The models vary widely and include changing hormone transport, clocks that generate oscillating gene expression, and touch sensing in the roots. I will conduct experiments designed to support or refute these models. My experiments will involve several lines of transgenic plants, including green fluorescing marker lines that I'm examining under a confocal microscope.

**Honors Advisor: Marta Laskowski**
Four native roses (swamp rose – *Rosa palustris*, climbing rose – *R. setigera*, Carolina rose – *R. carolina*, and smooth rose – *R. blanda*) and two invasive species (multiflora rose – *R. multiflora*, and dog rose – *R. canina*) occur in our region. Of the native roses, only smooth rose is in serious decline, listed as state endangered in Ohio and on protected lists in Maryland and Maine. The other three native species bloom in mid- to late summer, whereas smooth rose blooms simultaneously with the two invasive species in late spring to early summer. Sites where smooth rose once occurred are now dominated by multiflora and/or dog rose. Since smooth rose has been shown to hybridize with the invasive rugosa rose (*R. rugosa*) in New England and Quebec, Canada, and rugosa rose and multiflora rose are also known to hybridize, we are investigating the potential hybridization between smooth rose and multiflora rose as a reason for the smooth rose decline. The current effort is focused on comparing morphological traits from existing populations (both sympatric and allopatric) and from herbarium records to better understand character variation patterns over space and time.

**Research advisor: Roger Laushman**
Many plant species in the flowering plant family Nyctaginaceae grow only on outcrops of gypsum (CaSO₄·2H₂O). Several of these gypsum endemic species form diverse clades and are widely dispersed, suggesting a relatively ancient origin for gypsophily. With our project we hope to answer the following questions; 1) How many times did gypsum endemism evolve in Nyctaginaceae? 2) How long ago did gypsophily divergence events occur? In order to date divergence times we need to generate phylogenies and find calibration points, typically dated fossils, for our analysis. Our phylogenetic data will be generated using three protein-coding chloroplast regions; ycf1, ndhF, and matK. Because of the lack of fossil data within Nyctaginaceae, we will include closely related families within the order Caryophyllales to encompass more possible calibration points. Our taxon sampling will include most genera within Nyctaginaceae, all genera in Phytolaccaceae (a closely related family), and some genera from other surrounding families (for example, Sarcobataceae). In addition to the phylogenies generated with chloroplast genes, we will use low copy nuclear genes to resolve phylogenetic discrepancies within Acleisanthes. These phylogenies together will help to resolve relationships within Nyctaginaceae and among closely related families in Caryophyllales, and will allow us to estimate the frequency and timeline of the evolution of gypsophily.

Advisor: Michael Moore
Honors Project: Riva Bruenn
Research Project: Matt Croley and Rebecca Mostow
While the laboratory mouse has been regarded a model animal for mammals, the three-dimensionality of mouse embryonic development does not correlate with the two-dimensional early development of human and other mammalian embryos, which in this respect more closely resemble the embryos of reptiles and birds. Primordial germ cells (PGCs) of reptile and bird embryos arise on the periphery of the extraembryonic ectoderm (ExE), whereas PGCs in mouse arise in the proximal posterior ExE. Using *M. domestica* as a model for other mammals, we would like to see if PGC activity arises on the periphery of the ExE, similar to reptile and bird embryos, by testing for the presence of the mRNA encoded by Blimp-1 gene that is expressed only by PGCs at this embryonic stage. I will be assisting Justin Chen, an honors student in the lab, in this project.

**Research Advisor: Yolanda P. Cruz**

Among the paired sperm of the Laboratory Opossum, *Monodelphis domestica*, only two possibilities exist as to when the acrosome reaction (AR) occurs: either before or after sperm unpairing. Because the AR must occur as close as possible to the moment of fertilization, the unpairing event **must** occur immediately after the AR. I hypothesize that the adhesive proteins holding the paired sperm together are denatured by enzymes released during the AR. Furthermore, I propose that the mechanical force generated by sperm flagella while the AR occurs is sufficient to pull the sperm apart. This model provides a reliable mechanism for unpairing as closely as possible to the zona pellucida, whereas unpairing before the AR will reduce the chances of successful fertilization because single sperm cannot swim as well. I will use various substances known to cause the acrosome reaction in mouse sperm to test this model.

**Research Advisor: Yolanda P. Cruz**
Katherine Hampilos ‘11

“Comparative Anatomy and Development of Berries in the Monocotyledons”

The monocot clade, containing over 65,000 species across 12 orders, is one of the most morphologically varied and ecologically successful of the early-divergent clades of angiosperms, and contains such plants as grasses, palms, orchids, and bromeliads. As a result of the group’s diversity, a cohesive understanding of monocot phylogeny and patterns of morphological divergence has not yet been completed. The morphology and evolution of fruit type within the monocots has yet to be thoroughly examined. Most monocot flowering plants are characterized by a dry capsule-type fruit, which splits open to release seeds. However, a number of distantly related monocot families and genera have evolved fleshy berries for fruit instead. Previous research has disproved the hypothesis that berry-like fruit types were present in the ancestor of monocots, indicating that berries evolved separately several times within the monocot clade. The independent evolution of berries implies that separate lineages will have different developmental pathways, a hypothesis I will study through an examination of the anatomy and development of both flowers and fruit in various monocot species with berries. At the conclusion of my project, I will map morphological data from previous studies as well as my own research on the most recent molecular phylogeny for the monocots to reveal homologies and enhance the understanding of fruit evolution in this clade. All anatomical data found in my studies will also be used in the morphological data matrix for the Monocot Tree of Life project through a partnership with the New York Botanical Garden’s Dr. Dennis Stevenson.

Honors Advisor: Michael Moore

Taylor Fey ‘11

“Kava’s Effect on Bodily Function Using C. elegans as a Model”

Kava is an ethnobotanical drug with a history of use as a social relaxant, especially in Eastern cultures. The literature on Kava to date is scarce, but the current research shows that it affects two potential targets: GABA receptors and Calcium L-type channels. GABA receptors are involved in the physiology of mental disorders such as anxiety and depression, while Calcium L-type channels are highly involved in heart function. I seek to use Caenorhabditis elegans as a model genetic organism to uncover the mechanism by which Kava alters body function. Although previous research has focused on purified forms of Kava, I plan to expose specific GABA and Calcium channel mutant C. elegans to a crude preparation. The findings should be applicable to humans because of the large number of genes they share with C. elegans.

Research Advisor: Taylor Allen
Our research focuses on *Nerisyrenia* (Brassicaceae), a small genus of 11 arid-adapted species that are endemic to the Chihuahuan Desert of southwestern North America and Mexico. With the exception of the widespread species *N. camporum*, all taxa within *Nerisyrenia* are restricted to gypsum soils, which are scattered in an island-like fashion throughout the Chihuahuan Desert. This phenomenon is referred to as gypsophily. As part of a larger effort to understand the age, origins, and phylogeography of gypsophily in the Chihuahuan Desert, I will be using chloroplast and nuclear gene sequences to reconstruct the phylogenetic and phylogeographic history of *Nerisyrenia*. Specifically, we will address the following questions: (1) How many times has gypsophily evolved within the genus?; (2) Is the widespread species *N. camporum* derived from gypsophilic ancestors?; and (3) Is there a strong correlation between biogeographic distribution and genetic diversity within gypsophilic *Nerisyrenia*, both within and between species? Preliminary results indicate that the widespread gypsothile *N. linearifolia* has a significant amount of geographically-correlated sequence variation, and that *N. camporum* shares chloroplast haplotypes with several other species, suggesting a complex evolutionary history. In our continuing work we will improve resolution among species within the genus so that we might determine the ancestral state of *N. camporum* and continue to observe patterns of variation correlated with geography. Toward this end we will sequence DNA from several newly obtained populations of Mexican species of *Nerisyrenia*, and we will sequence DNA of these and previous collections using newly developed nuclear primers.

**Research Advisor:** Michael Moore
Primordial germ cells (PGCs) are the first population of the germ cell lineage that gives rise to oocytes and spermatozoa. PGCs are thus responsible for the transmission of genetic information of a given multicellular species from one generation to the next. In mice and presumably the majority of mammalian species, the segregation of somatic cell and germ cell lineages in the developing embryo is controlled by extrinsic signaling from extraembryonic structures. A critical event during PGC specification is the repression of the somatic germ cell program that would otherwise occur. Astoundingly, the transcriptional repressor Blimp1 is responsible for repressing nearly all genes that are down regulated in PGCs relative to their somatic fated neighbors. Critically, Blimp1-positive cells are lineage restricted to PGC precursor cells and Blimp1 is the earliest marker of the PGC lineage.

This study aims to investigate the behavior of PGCs in *M. domestica*. Because Blimp1 is the earliest marker of the PGC lineage in mice, whole mount in situ hybridization using a probe for Blimp1 mRNA will be used to visualize the location and timing of PGC specification in opossum embryos. This study has the potential to elucidate the location of PGCs when they are first specified (a location that is not yet known in metatherians) and track the migration of PGCs through the opossum embryo. Since mouse and opossum embryos have very different morphology, it is possible that PGC migration patterns will vary between the two species.

Honors Advisor: Yolanda P. Cruz

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I am continuing the research that I began in ‘08-’09, studying progesterone receptor activity in *Monodelphis domestica* during pregnancy. There is no detectable progesterone-mediated signaling between mother and embryo in marsupials during pregnancy. Several species of marsupials have been examined, and serum progesterone is not statistically different between pregnant and non-pregnant females. An increase in progesterone receptor expression during pregnancy could suggest elevated progesterone receptor-mediated signaling without a change in serum progesterone. Using histology and immunohistochemistry techniques, I will produce slides of uterine and ovarian tissue from *Monodelphis domestica* and stain them to analyze levels of progesterone receptor expression during the course of gestation. I will also measure the concentration of serum progesterone using enzyme-linked immunosorbent assay (ELISA) to show if there are elevated levels of progesterone at some time points during pregnancy. To support this data, I will measure the size of corpora lutea in the ovary, the source of progesterone, whose size should correlate with the amount of progesterone secreted during the various stages of gestation.

Honors Advisor: Yolanda P. Cruz
Lois Immerman ‘11, Matthew Miller ‘11, Latarsha Porcher ‘11 and Monica Raible ‘12

“C. elegans a RNA Interference screen for Defecation Mutants”

A recently discovered process of gene regulation uses small double stranded RNAs to modify the stability of mRNA transcripts and/or their translation. This natural process has been developed into an efficient scientific method for identifying the functions of specific genes, called RNA interference (RNAi). C. elegans is a species of nematode frequently used for genetic analysis that is particularly susceptible to RNAi. When C. elegans ingest a modified form of their normal food source, bacteria expressing RNAi instead of bacteria, an RNAi mutant results. An large library of transgenic bacteria producing RNAi molecules, each strain specific to one of approximately 11,000 genes in the C. elegans genome is being used in the Peters lab. By growing animals on each of these RNAi bacteria sequentially and observing the animal’s traits, the effects of silencing many genes can be tested. All of the worm’s traits are noted but the lab is especially interested in identifying genes involved in the defecation cycle of C. elegans.

Defecation is a highly regulated process that takes place approximately every 50 seconds in a healthy, wild type worm. The cycle involves three distinct muscle contractions: a posterior body contraction, an anterior body contraction, and finally, expulsion. By identifying all of the genes involved in this process, we will be able to better understand the molecular pathways governing it. Lois, Matt, Latarsha and Monica are all analyzing the affects of eliminating about 200-400 genes each per semester.

Research Advisor:  Maureen Peters
“Pregnancy-Related Changes in Progesterone Expression in Monodelphis domestica”

Along with learning various biology research techniques, such as cell culturing and in situ hybridization, I will be helping with the current study of progesterone level reception in the Monodelphis Domestica. Embryo-maternal signaling in marsupials is poorly understood because unlike their eutherian counterparts, serum progesterone remains largely unchanged during pregnancy. (Harder et al. 2008) In eutherians, progesterone increases over the course of pregnancy. However, in marsupials, the progesterone level remains unchanged suggesting that no detectable progesterone-mediated signaling occurs between the mother and the embryo. Progesterone receptor expression may be up regulated, which could show that progesterone signaling might still have a role mediating maternal recognition of pregnancy. This project is designed to determine whether expression of the progesterone receptor (PR) changes with serum progesterone levels in M. domestica over the course of gestation. I will be helping to assess progesterone receptor concentration in ovarian and uterine tissues. Time-mated female M. domestica will be dissected on various days of pregnancy and 3 uteri and one ovary from each of the alternate days 1, 3, 5, 7, 8, 9, 11, and 13 of its 14-day gestation period will be collected. Ovarian and uterine slices will be immunostained for progesterone receptor using primary antibody (1:100 rabbit anti-PR) and secondary antibody (1:200 HRP-conjugated goat anti-rabbit IgG) following a previously published protocol (Lydon 1999). Ovaries are going to be counterstained with hematoxylin. Slides will be viewed in a Nikon Diaphoto under 10X, 20X and 40X and will be photographed with a Nikon Digital Camera DXM 1200. This project could indicate that progesterone receptor activity, rather than progesterone concentration, is involved in maternal response to pregnancy in this marsupial.

Research Advisor: Yolanda Cruz

“Investigating Root Architecture Among Plant Taxa”

Most plants that we encounter in our day-to-day lives, despite their differences in leaves, stems, and flowers, share a common root structure. A main ‘taproot’ grows from the plant beginning as a seedling, and as this root grows downward, new roots emerge from it and grow sideways into the rhizosphere. Other plant lineages instead expand their root networks by bifurcation, or splitting into a Y-shape at the tips of growing roots. I am interested in studying the differences between these types of branching, and the effects on overall plant architecture that they play. To investigate this, I would like to take a phylogenetic survey and use molecular techniques to further elucidate how root growth and branching differs among all plants.

Research Advisor: Marta Laskowski
Most of the sensory systems of more primitive vertebrate clades—the fishes—are retained in land vertebrates. The neural circuits that carry sensory information through the brain are also similarly organized among fishes and land vertebrates. For instance, the neuro-anatomical pathways of the vertebrate auditory system are similar in both fishes and mammals. However, the auditory circuit in bony fish uniquely includes a cell group in the hypothalamus—the anterior tuberal nucleus (AT). The AT is also part of the circuit that carries information from the mechanosensory lateral line system. A previous honors student explored the connections of the anterior tuberal nucleus (AT) in the goldfish with the goal of understanding more completely the functional significance of this hypothalamic area. One of the most exciting results of the study was the discovery of a potential connection between the AT and the gustatory system, thereby implying a potential connection between the auditory and lateral line systems and the gustatory system in goldfish. I will re-explore the connections of the AT in the goldfish using neural tract-tracing methods that are more sensitive than those used in the previous study. One focus of my study will be to determine whether there is, in fact, an interface between the gustatory system and the auditory and lateral line systems. If this interface exists, I will then attempt to fully define the neural circuits that interconnect these systems.

**Honors Advisor:** Catherine McCormick

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Antibiotics rely on differences between prokaryotes and eukaryotes in order to weaken bacteria but not the host organism. In order to develop effective antibiotics, the processes specific to bacteria and their regulation should be well understood. During bacterial cell division, a ring termed the “Z-ring” forms in the middle of the cell. The Z-ring consists of FtsZ, a tubulin-like cytoskeletal protein found only in prokaryotes. The Z-ring contracts and helps split the cell in two. The formation of this Z-ring is very precise; if it does not form properly or in the correct location, the cell may be unable to successfully divide. The process by which the Z-ring forms is known to be regulated by several proteins, such as the transmembrane protein EzrA. However, the mechanism for this is unknown.

My role in this project is observing the properties of a specific mutant of FtsZ, L69W, and how it compares with the wild type. My first goal is to determine the critical concentration (the concentration at which FtsZ readily polymerizes) of both versions of FtsZ. Next, I will aim to compare the bundling activity between the mutant and the wild type. I look forward to a productive year in K215!

**Research Advisor:** Laura Romberg
The uropygial, or preen, gland of birds produces secretions that waterproof and condition feathers. In collaboration with Rebecca Whelan, OC Dept. of Chemistry, volatile components of uropygial secretions of gray catbirds (*Dumetella carolinensis*) have been identified over the past several years via gas chromatography-mass spectrometry. We are conducting a series of bioassays to determine if these volatiles play a role in attracting or repelling mosquito vectors of disease. Assays involve choice trials with approximately 50 female laboratory-raised *Culex pipiens* mosquitoes (5-10 days of age) from a colony maintained by Ohio State University. During each trial mosquitoes are allowed to choose between a control or carboxylic acid-saturated filter paper surrounding cotton dental swabs impregnated with a 10% sucrose solution food source. By testing each uropygial volatile component, we will be able to assess the role of uropygial secretions in attracting or repelling this common species of mosquitoes that severs as a vector for West Nile and other viruses of public health concern.

**Research Advisor:** Mary Garvin
Catherine O’Hare ’11, Miles Pulsford ’12, Jordan Rutter ’12, and Norbeth (Bud) Stracker ‘11

“Characterization of the Volatile Compounds of the Uropygial Secretions of the Gray Catbird (Dumetella carolinensis)”

The uropygial gland (or preen gland) of birds has long been known to produce waxy secretions important in maintaining and waterproofing feathers. Recently, volatile compounds have been identified in these uropygial secretions. Their presence may indicate olfactory communication within or between species. Using gas chromatography-mass spectrometry (GCMS), we have identified linear and branched carboxylic acids as major volatile components of the uropygial secretions of gray catbirds (Dumetella carolinensis). We are now determining if these volatiles play a role in attracting or repelling feather-degrading bacteria and mosquito vectors of viruses such as West Nile Virus. Because males and females have very different roles in breeding, each sex varies in resource allocation and response to environmental pressure. Therefore, we might expect sex-based differences in uropygial secretions. To compare the signal strength of volatiles between male and female catbirds, a sexually monomorphic species, we must determine the gender of each individual sampled. To accomplish this, we identify a sex-specific chromobox-helicase-DNA-binding (CHD) gene using Polymerase Chain Reaction (PCR) and gel electrophoresis.

This project is in collaboration with Prof. Rebecca Whelan, Dept. of Chemistry.

Research Advisor: Mary Garvin
Our research is part of a larger project focusing on Chihuahuan Desert plants of the southwestern United States and northern Mexico, specifically those which grow on gypseous (CaSO4·2H2O) soils. The three genera we will be studying make up the subtribe Flaveriinae and include Flaveria, Haploësthes, and Sartwellia. Many taxa within Flaveriinae are gypsophilic (endemic to gypsum), including most taxa within Sartwellia and Haploësthes. Like many other gypsophilic plant groups, genera in Flaveriinae are geographically widespread, despite the island-like distribution of gypsum outcrops in the Chihuahuan desert. Morphological and phylogeographic evidence suggests that these widespread gypsophiles may be relatively old. As a first step toward understanding the phylogeography and evolutionary history of gypsophily within Haploësthes and Sartwellia, we are reconstructing a comprehensive phylogeny of these genera. Through DNA sequence data and analysis we aim to reconstruct evolutionary relationships within Flaveriinae in order to understand how many times gypsum endemism evolved. We are also examining geographic variation within species of Sartwellia and Haploësthes to test whether gene flow is ongoing among populations or whether populations on different deposits have been isolated for long periods of time. Preliminary results based on chloroplast and nuclear sequence data indicate geographic structure within Flaveriinae and one origin of gypsophily in Sartwellia and Haploësthes. By completing our data set and acquiring more nuclear regions, we aim to create a more comprehensive phylogeny of Flaveriinae and increase our understanding of gene flow and phylogeography within gypsophilic clades of the Chihuahuan Desert.

**Research Advisor:** Michael Moore
“Epigenetic Variation in *Arabidopsis thaliana*”

Genes and variation in genotype are typically thought of as the underlying code to determine phenotype. However, there is a growing body of evidence that suggests other features of DNA can have an effect on phenotype as well. For instance, methyl groups can be attached to DNA strands to silence expression of those regions of DNA. Evolution is usually thought to occur through natural selection acting on genetic variation. However, the evidence that epigenetic variation can affect phenotypic variation and perhaps be inherited indicates an important role in evolution. I will expose different genotypes of *Arabidopsis thaliana* to an environmental stressor and compare methylation patterns using methylation-sensitive restriction enzymes. I will also compare these to a mutation line with differential expression of chromomethyltransferase3, an enzyme responsible for maintaining methylation of DNA in plants. I hope to answer the following questions: 1. Does the variation in expression of CMT3 affect the methylation patterns in *A. thaliana*? 2. Can the environment induce a change in methylation pattern? Does exposure to a stressor affect the methylation pattern, and how does the change compare to the mutant? 3. Are environmentally induced changes in the methylation pattern heritable?

Honors Advisor: Angela Roles

“Investigating Hybridization in a Crayfish Invasion”

The rusty crayfish, *Orconectes rusticus*, is an invasive species throughout much of North America. These crayfish were introduced to the nearby Huron River several decades ago, and have been spreading upstream from Lake Erie since, competing with and pushing out the native Sanborn’s crayfish, *Orconectes sanbornii*. The Roles lab monitors five sites along the Huron each summer, taking measurements and DNA samples from crayfish of both species. During these trips, crayfish of intermediate morphology are observed, indicating possible hybridization between the two species. Last year, Katherine Muller showed using allozyme and mitochondrial DNA data that hybridization is occurring. I will expand on Katherine’s results, using nuclear DNA markers (as well as allozymes and mitochondrial DNA) and a larger sample of crayfish to investigate the rate of hybridization and introgression (gene flow from one species to another) in the Huron. I also hope to develop a quantitative method for identifying hybrids in the field using simple calculations based on easy-to-take measurements on the crayfish.

Honors Advisor: Angela Roles
“Examining Failure of Day-5 Embryos in the Laboratory Opossum”

I will be organizing and examining various photographs of embryos of *Monodelphis domestica*, the laboratory opossum, specifically images and data on Day-5 embryos. Over the years, it seems that day-5 is a difficult stage for the embryos to successfully complete. When embryos are collected for use in other projects, many are usually failed at this particular stage. It also seems that if one embryo has failed, all the other embryos in the litter are also failed at the same time. The embryos could be unfertilized, or there could be something wrong with the mother, but many other factors could be at play. I will be examining photos taken of these embryos as an attempt to rationalize the constant failure at Day-5.

Research Advisor: Yolanda P. Cruz

“Population Genetics of a Crayfish Invasion”

I am studying the structure of genetic variation in the native Sanborn’s crayfish (*Orconectes sanbornii*) and the invasive rusty crayfish (*O. rusticus*). In order to do this, my first goal will be to test and optimize polymerase chain reaction (PCR) conditions for a set of microsatellite markers. Tissue samples were collected from watersheds across northern Ohio between 2006 and 2009 and DNA isolations have already been performed. With working genetic markers, I will genotype the resulting PCR products from these samples to analyze trends in genetic variation in both species. Rusty crayfish have invaded many, but not all, nearby rivers so local watersheds give me an excellent opportunity to compare the patterns in genetic variation found in a native and nonnative species. One challenge faced by invasive species is a lack of genetic diversity due to founder effects, so I expect to find less diversity in the invasive species than in the native species (though this is not necessarily true if multiple introductions have bolstered genetic variation). Also, behavioral experiments show that rusty crayfish often outcompete sanborn’s crayfish for shelter and therefore rusty presence may increase gene flow and reduce among population variation in the native species. Additionally, molecular evidence suggests that the two species can hybridize in the wild and I may be able to detect some evidence of allele transfer between species. A thorough assay of the genetic diversity in both species followed by calculating classic population genetics measures should allow me to address these important ecological questions.

Research Advisor: Angie Roles
"Phylogeny and Phylogeography of Gypsophily in Gaillardia (Asteraceae)"

In the Moore lab, we study the evolution of gypsophily in plants that grow in the Chihuahuan Desert of the southwestern US and northern Mexico. Gypsophilic plants grow only on surface gypsum deposits, which are scattered throughout the Chihuahuan Desert region in an island-like fashion. Gaillardia is a genus in the sunflower family (Asteraceae) whose center of diversity is in the Chihuahuan Desert. Of the 20 species of Gaillardia, six are gypsophilic. Our earlier work places these gypsophilic species in three distinct lineages. However, data from plastid DNA support different relationships within Gaillardia than the relationships supported by nuclear DNA data. Part of our project will be to resolve these incongruencies using data from a second nuclear locus. Eventually we hope to generate a multi-locus phylogeny including multiple representatives of each species of Gaillardia and individuals of the other genera in subtribe Helenieae. Once the evolutionary relationships within this genus are known, this information can be used to study the age and phylogeographic history of gypsophily within Gaillardia. Some questions we hope to answer include: Where, when and how many times did gypsophily evolve within Gaillardia? And does Gaillardia share any phylogeographic patterns with any other gypsophilic plant groups?

Advisor: Michael Moore
Honors Project: Carolyn Stange
Research Project: Flora Samis
In the Chihuahuan Desert region, there are 200 taxa in more than 30 plant families that grow only on the substrate gypsum. Although gypsum appears in discontinuous islands throughout the Chihuahuan Desert, many of these taxa are geographically widespread. *Nama*, a genus in the Boraginales clade, has eight species that are endemic to gypsum. Collectively, these eight species are distributed across the Chihuahuan Desert. A recent phylogenetic study of the genus indicated that seven of the eight gypsophiles form a well-supported clade. This implies that speciation on gypsum has occurred, and that the gypsophilic character state is relatively old. However, this study included only one or two individuals for each of these gypsum endemic species. We will expand sampling to include many additional populations of each species. We hope that this phylogeographic approach will give us insight into the origin and diversification of gypsophily in the Chihuahuan desert. Specifically, we will be testing several hypotheses regarding the distribution of *Nama* during the Pleistocene period:

1. **Recent speciation hypothesis:** Gypsophilic *Nama* did not appear until after the Pleistocene. Based on this hypothesis, we would expect to see minimal variation between species in the gypsum endemic clade.
2. **Refugium hypothesis:** Gypsum endemism evolved in *Nama* before the Pleistocene, and was forced into a few isolated refugia or pockets during the Pleistocene.
3. **Wide distribution hypothesis.** Gypsum endemism evolved in *Nama* before the Peistocene, and was able to remain in basically its current distribution during periods of cooling.

**Research Advisor:** Michael Moore
“The Effect of Garlic on the Growth of Pathogenic and Normal Vaginal Microbiota”

Bacterial vaginosis (BV) is one of the most prevalent vaginal conditions in adult women worldwide. Associated complications include preterm delivery, increased risk of pelvic inflammatory disease, and increased susceptibility to HIV acquisition and transmission. BV is characterized by an imbalance of the vaginal flora, in which the usually predominant Lactobacilli species are replaced by an overgrowth of anaerobic pathogenic bacteria that form a polymicrobial biofilm. The common drug treatment is metronidazole; however, with a recurrence rate of over 50%, more effective treatments are needed. Garlic, or Allium sativum, is known to be antimicrobial, as it hinders the growth of many bacterial species. Additionally, it inhibits cell wall synthesis of Candida albicans, the causative agent in vaginal yeast infections. I work with Gardnerella vaginalis, a bacterium highly associated with BV, and Lactobacillus crispatus, a common strain in the healthy vagina. I am testing the effects of fresh garlic extract, metronidazole, and a chemical isolate from garlic, diallyl disulfide, on the growth of both species of bacteria. The aims of my project are 1) to determine the minimal inhibitory concentration of each chemical for both bacteria, and 2) to test the minimal bactericidal concentration of each chemical for G. vaginalis grown as a biofilm.

Honors Advisor: Taylor Allen

Cynthia Minter ‘12

“The Influence of Diet on Belly Color of Fossorial Snakes”

Several North American fossorial snake species have brightly colored bellies, and there is often variation in the intensity of color among individuals of the same species. Being fossorial, these species spend most of their time underground, and usually only come to the surface after dark. This combination of bright coloration and a dark existence is paradoxical – why would natural selection favor potentially expensive coloration if nobody is likely to see it? We hypothesize that belly color reliably signals the unprofitability of the snake to the predator because the intensity of the color reliably reflects the toxicity of the snake as a food item. The link between color and toxicity might arise if color production itself is costly, such that being both colorful and toxic imposes costs that only high quality individuals can afford to bear. Alternatively, snakes that are successful at tolerating toxic prey items (such as salamanders, which produce skin toxins from the food they eat) may become more toxic themselves. We will maintain ring-necked snakes (Diadophis punctata), northern red-bellied snakes (Storeria occipitomaculata), and brown snakes (Storeria dekayi) in captivity, allocate them to different diet treatments hypothesized to influence toxicity and measure belly color to test whether diet affects belly color within individuals. We will periodically collect cloacal secretions for chemical analysis and for use in future behavioral experiments with predators to determine whether toxicity levels of the snakes themselves are affected by diet treatment. We hope this study will shed light on the evolutionary mechanism by which fossorial snakes maintain their colored underbellies.

Research Advisor: Keith Tarvin
“The Effects of Sublethal Exposure to Metolachlor on the Agonistic Behavior of Two Congeneric Crayfish Species in the Lake Erie Basin”

Water quality in the Lake Erie Basin is affected by many factors, including anthropogenic changes in land use. Pesticide and fertilizer load from agriculture and livestock production in Northeast Ohio has contributed to many problems in the Lake Erie Basin, causing eutrophication and accumulation of toxins in many of Ohio's rivers and streams. Though many of these chemicals are present in sublethal levels in the Lake Erie Basin, they may still have deleterious effects on the aquatic communities that inhabit streams and rivers. For benthic invertebrates such as crayfish, these toxins may interfere with sensory organs vital for defense and interspecies interactions. Because crayfish compete for resources like food, mates, and shelter, changes in aggressive behavior can have important consequences. I am studying the effects of a particularly common herbicide, metolachlor, on the agonistic behavior of two congeneric crayfish species, *Orconectes sanbornii* (Sanborn's crayfish) and *O. rusticus* (rusty crayfish). *Orconectes rusticus* is an invasive species of crayfish currently hybridizing with and possibly displacing the native *O. sanbornii* in the Huron River watershed. I am studying the effects of metolachlor on the agonistic responses of these two species of crayfish to determine whether metolachlor pollution is a factor that favors the invasion of *O. rusticus* in the Lake Erie Basin.

Honors Advisor: Angela Roles

“Tradeoff in American Goldfinches’ Bill Color and Level of Immunoglobulin Y (IgY) due to Stress”

Signal theory predicts that the reliability of conspicuous signals is maintained by costly tradeoffs with other physiological functions. Over the summer of 2010, I and members of the Tarvin lab conducted a field study to determine the effects of stress on bill color and immunocompetence among American Goldfinches. We captured and clipped the primary feathers of the goldfinches, which would force the birds to exert more energy while flying, thus increasing the levels of daily stress. Experimental birds were captured twice, before and one to three weeks after their feathers are clipped. We also had control birds which undergone the same overall procedure, with the exception that their feathers were not clipped. Each time we captured a bird, we measured the bill color with a spectrometer, and collected blood samples. My work this fall is to investigate the correlation between bill color and the level of immunoglobulin Y in the goldfinches’ plasma, and the increased daily stress in the goldfinches due to increased exertion of energy in their day-to-day activities. I will do this using Enzyme-Linked Immunosorbent Assay (ELISA), which will enable me to gauge the amount of IgY in the goldfinch plasma samples collected in the summer.

Research Advisor: Keith Tarvin