The last universal common ancestor (LUCA) represents the last ancestor shared by the Archaean, Prokaryotic, and Eukaryotic domains of life. First proposed by Charles Darwin in 1885, the construct of the universal ancestor has since been corroborated by the comparison of genomes across the tree of life. Several studies have proposed possible genomes represented by LUCA, and though these studies tend to agree on the functional categories of genes represented in the ancestor, they differ in their predictions of its genome size and precise gene content. I am conducting a meta-analysis of the results of these studies, looking for consensus between their predictions. Because these studies were performed by different methods, identifying areas of agreement between them should yield a much more accurate view of the content of LUCA's genome.
Culex pipiens, a species of mosquito abundant in the eastern United States, is the primary means of transmission of West Nile virus (WNV) among birds, which serve as important reservoirs for the virus. American robins, house sparrows, and European starlings are believed to be among the most common reservoir hosts, however, models of WNV transmission reveal that robins contribute most to the viral cycle. Culex pipiens has been shown to disproportionately feed on American robins; the reason for this preference is not known. We seek to better understand this relationship. Preen glands, located at the base of the tail, produce complex secretions that include oils and waxes believed to waterproof and condition the feathers, as well as lighter, more volatile compounds. Foundational work, conducted in the lab of Rebecca Whelan, demonstrates that robins, house sparrows, and starlings have species-specific volatile chemical profiles. We hypothesize that the secretions of the robin preen gland, have species-specific chemical profiles that contribute to its relative attractiveness. We specifically predict that Cx pipiens will be attracted to the volatile components of robin secretions. To test this prediction, we use an olfactometer to conduct behavioral trials in which mosquitoes are allowed to choose between two stimuli, thus allowing us to determine the innate preferences of Cx pipiens for the three bird species.

Research Advisor: Mary Garvin
VASA is a highly conserved gene that codes for the VASA protein—an RNA-binding helicase involved in germ cell development and differentiation. This gene is expressed relatively late in the embryonic development of most mammals, such as mice, compared to reptiles and birds. However, previous work by Nico Lara in Professor Cruz’s lab found evidence that the gene may be expressed earlier in marsupials than in placental mammals, as *vasa* mRNA was detected in cleavage-stage *Monodelphis domestica* embryos. If this is indeed the case, then germ cell specification in marsupials may resemble that in reptiles and birds more than it does in placental mammals. I will be testing for the presence of the VASA protein at various stages of embryonic development in *Monodelphis domestica* by immunostaining embryos and confocal microscopy.

**Research Advisor: Yolanda P. Cruz**
Live organisms must balance energy output with their available energy stores. In stressful situations, such as low food availability, organisms will prioritize survival of self, over their ability to reproduce. In Caenorhabditis elegans (C.elegans) reduction in caloric intake correlates with decreases in progeny number, and increases in lifespan. A key transcription factor, DAF-16, orchestrates the cellular response to limited caloric intake. C. elegans with lower caloric intake typically have higher DAF-16 activation levels resulting in lower brood sizes and longer lifespans. Recent studies suggest that effective digestion, caloric absorption, and defecation may be linked. Worms with intestinal problems resulting in constipation have lower fat stores and deficiencies in nutrient uptake. Our lab has extensively studied the INX-16 gap junction protein found in the intestine of C.elegans, without which, mutants are constipated. We hypothesize that the INX-16 mutation disrupts nutrient uptake, lifespan and brood size of the organism through the activation of DAF-16 and deficiencies in production and/or secretion of yolk protein from the intestine.

Honors Advisor: Maureen Peters
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**
Emma Lucore

“How does the presence of information derived from birds in the environment influence the foraging efficiency and vigilance responses of Eastern Grey Squirrels?”

Previous research shows that Eastern Gray Squirrels (Sciurus carolinensis) eavesdrop on various avian species and increase their vigilance in response to alarm calls that signify a higher predation risk. Vigilance behaviors detract from time that squirrels could be spending foraging or eating, so maintaining constant vigilance against predators is costly. With this project, I seek to study whether squirrels exhibit fewer vigilance responses and forage more efficiently when in the presence of avian species that produce “squirrel-relevant” alarm calls by noting the frequency of vigilance responses and the foraging efficiency of squirrels when presented with recordings of chatter from avian mixed species foraging flocks versus under control conditions. If squirrels can rely on other species to relay information about predation risk, then they should be able to forage while keeping the potential cost of becoming prey relatively low.

Research Advisor: Keith Tarvin
Erin Johnson

“Exploring the Phylogenetic Position of a Bizarre, Poorly Known Gypsum Endemic Plant: *Hedyotis teretifolia* (Rubiaceae)”

*Hedyotis* (Rubiaceae) is a taxonomically difficult genus that includes a number of arid-adapted species in North America. Most North American *Hedyotis* species are small, herbaceous plants with narrow leaves and do not display a preference for one soil type. However, the northern Mexican species *Hedyotis teretifolia* is restricted to gypsum soils in southwestern Coahuila and is characterized by several morphological features that are bizarre for the family, including strong succulence, petals that persist on the flowers during fruit development, and an unusual ovary position. It appears that *Hedyotis teretifolia* diverged from the other major lineages in the *Houstonia* Clade early on in the history of the clade, and the unusual morphology and soil preferences of *H. teretifolia* may mean that this taxon became adapted to gypsum soon after it split from the rest of the *Houstonia* Clade, perhaps several million years ago. This divergence suggests this species may be a relatively ancient lineage and perhaps distinct enough from the other species in the *Houstonia* Clade to warrant treatment as a new genus. To test these hypotheses, we will continue to generate DNA sequence data for *H. teretifolia* and several other North American taxa in the genus, including three chloroplast loci (*trnL/F* spacer *atpB/rbcL* spacer, and the *rps16* intron) and one nuclear locus (ITS). Phylogenetic analyses based on these sequences and all other Spermacoceae sequences on GenBank will help to explain the evolutionary history of North American *Hedyotis*.

Research Advisor: Mike Moore
In North Carolina, loggerhead turtles (*Caretta caretta*) nest from May through August, totaling ~750 nests/year on average. This summer, as part of an REU internship at the Duke University Marine Lab, I examined the trend in the curved carapace length (CCL) of nesting loggerhead sea turtles at Bear Island, North Carolina, from 1979 through 2015. On this island—a part of Hammocks Beach State Park—nighttime monitoring of nesting females has been conducted in summer months since the late 1970’s. The range of sizes of the nesting females on Bear Island since the late 1970’s is similar to those reported in other nesting locations in the NW Atlantic, north of Florida. There was an increasing trend in CCL from the beginning to the middle of the study period, and a decreasing trend in CCL from the middle to the end of the study period. I am currently working on publishing my findings in the Marine Turtle Newsletter and preparing a poster for presentation at the 2016 International Sea Turtle Symposium in Lima, Peru. I intend to use the extensive data from the Bear Island nesting assemblage to model the status of the assemblage into the future.

Research Advisor: Roger Laushman
Trees culture the microbial community in the soil surrounding their roots in ways that affect the fitness of future generations. These effects, called plant-soil feedbacks, influence the likelihood that trees will be able to recruit under their own canopy and ultimately patterns of forest composition. My research will involve determining whether bur oaks foster facilitative or detrimental soil microbial communities by comparing the growth of seedlings in soils taken from under bur oaks with soil taken from under other co-occurring trees. I will also be describing the microbial communities in the soils using molecular and genetic techniques. The combination of a growth experiment with microbial characterization will allow me to correlate differences in growth with the presence and abundance of specific microbial species in the soil.

Honors Advisor: Roger Laushman
My research is on a species of flowering plants called *Tiquilia palmeri* which grow in certain regions of Southern California. Last semester I isolated and sequenced genes in both the nuclear and chloroplast regions of the DNA from various specimens of this species from regions of Southern California and we created a phylogenetic tree. The resulting tree showed strong evidence that *T. palmeri* is a cryptic species, which are groups that are isolated geographically and have become morphologically different from each other. I plan to build on these results by isolating more specimens and to see how they fit into the tree.

Research Advisor: Mike Moore
I am investigating temperature sensitive myosin mutations in C. Elegan mutants e1301 and e1157. These mutations are unique in the fact individuals affected with the mutation only display it at 25°C and will appear almost identical to wild types at 15°C. When a worm displays the mutation, the worm is almost entirely paralyzed because the myosin heads are not interacting correctly with other proteins to create muscle movement. These differences are able to be seen morphologically through a polarized light microscopy. The muscle striations in mutant type C. Elegans are more muddled and have far less distinction than wild type C. Elegans. Along with the microscopy, I will also be using a computer program developed by Pennsylvania State University to record other evidence of these mutations by placing the worms in a buffer and recording their swimming cycles. The program maps these cycles in order to create a model of flexibility and movement that allows the rigidity of the worms to be recorded and compared through measurements such as tissue viscosity, young’s modulus, frequency, and speed. These tests will hopefully allow for further exploration of ideas such as the mutation effects on homozygotes vs. heterozygotes, haploid insufficiency vs. poison peptides, and dominance vs. semi-dominance.

Research Advisor: Taylor Allen
My project involves histological analysis of the marsupial (the lab opossum) prostate, a poorly studied reproductive organ. This will require collecting tissue samples as well as dehydrating, embedding, mounting, slicing, staining, preserving, and photographing them. I will employ immunohistochemistry in order to establish which portions of the opossum prostate correspond functionally to that of the rat (a eutherian mammal) for this I will use the prostate-specific protein Probasin. The use of a primary antibody (goat polyclonal antibody raised against a peptide mapping near the C-terminus of probasin of mouse origin) and a secondary antibody (Biotinylated Rabbit anti-Goat IgG antibody) allow for the immunolocalization of the same kinds of cells in both the opossum and the rat prostate.

Research Advisor: Yolanda P. Cruz
In lab strains of Gram-negative bacteria, excess levels of the TolQ protein interact with the cell division protein FtsN, hindering the completion of cell division. This phenotype is rescued by the over-expression of FtsN. My project involves isolating natural strains of Gram-negative bacteria and transforming them with TolQ expression plasmids. Transformants will be assessed for division phenotypes upon over-expression of TolQ. Techniques include aseptic isolation of natural Gram negative bacteria, Gram staining, microscopy, differential and selective testing to identify Gram-negatives, antibiotic sensitivity assays, bacterial transformation, plasmid-encoded protein over-expression, and the phenotyping of transformants upon over-expression of TolQ alone and of TolQ and FtsN concurrently. The goal of this project is to determine the degree of conservation of TolQ’s role in cell division beyond the Gram negative laboratory strains.

Research Advisor: Mary Teleha
"Investigation of the Role of Caloric Restriction in a Long-lived *C. elegans* Mutant"

We are what we eat. Evidence indicates that caloric intake influences the rate of aging in many animals such as *C. elegans*, and, possibly, humans[1]. In the Peters lab we are investigating the cause of a *C. elegans* mutant with a longer than normal lifespan. The animal’s mutation alters an intestinal gap junction subunit, *innexin-16* (*inx-16*). Intestinal gap junctions function in a periodic intestinal calcium wave and are essential for proper execution of rhythmic defecation motor program[2]. Since low caloric intake correlates with longer life in *C. elegans*, we hypothesize that the *inx-16* animals’ lengthened life is due to caloric restriction. Reduction in calories could be due to reduced eating or poor nutrient absorption. My project is to compare the food intake and nutrient absorption in *inx-16* and control animals. To evaluate food intake the activity, or pumping, of the pharynx, an organ that functions like a mouth and stomach, will be determined. If the pumping rate is slow, it means the worm does not get enough food intakes due to pharyngeal defects. Nutrient absorption will also be assessed by measuring worm body fat. Lower body fat content indicates fewer nutrients are absorbed in intestine (REF). The results of these assays will provide insight into which, if any of the digestion steps is altered in the *inx-16* mutant.

Research Advisor: Maureen Peters
Progesterone is the hormone of pregnancy in placental mammals. Elevated levels of serum progesterone are required for maintaining pregnancy. Interestingly, this noticeable increase in progesterone is absent in marsupials. How is it that marsupials sustain pregnancy if serum progesterone remains at pre-pregnancy levels? We hypothesize that as the levels of progesterone do not increase, then the number of nuclear progesterone receptors expressed must, for progesterone to have a role in marsupial pregnancy. We will use uterine samples obtained from the marsupial Monodelphis domestica (gray short tailed opossum) at different points of gestation. Histology, and immunohistochemistry techniques will be used to assess expression levels of progesterone receptor in the endometrium and uterine glands. Mouse uterine samples will make up the positive control, as their progesterone receptor expression during pregnancy is well documented.

Research Advisor: Yolanda P. Cruz
Anthropogenic noise from roads and industrial equipment has been shown to have a significant negative impact on wildlife. For example, 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 pitches in close proximity to feeders, and comparing the number and species diversity of birds that come to feed during different playbacks. This may enable us reducing impact on birds by restricting noise pollution frequencies, or by altering machinery or designing selective noise-canceling devices.

Research Advisor: Keith Tarvin
Permanent plots are a useful ecological tool for examining change over time, succession, and the effects of disturbance on vegetation. A grid of permanent plots was established in 1974 in the Chance Creek Natural History Reservation as part of a tree species survey. The plots were sampled again in 1986, 1998, and 2015 (this study). We re-sampled the plots to explore the effects of the widespread death of ash trees due to the invasive emerald ash borer. As in previous studies, we measured for all stems > 2.54 cm in thirty-three 0.04 ha plots. We also recorded count data for seedlings and saplings in smaller plots. Present composition and structure will be compared to the data from past surveys using standard diversity measures (Percent Similarity; Shannon’s $H'$ and Pielou’s $J$), and we will use canonical correspondence analysis to correlate species composition with various ecological variables, such as slope, aspect, light (PPFD), and edaphic characteristics (organic matter; N, P).

Honors Advisor: Roger Laushman
Lisa Learman

“Intestinal gap junction INX-16 mediates a social foraging behavior in C. elegans”

Groups of organisms exhibit social behavior that is thought to improve survival and reproduction. Different forms of social interaction are present in all sorts of organisms, from bacteria forming microfilms to flocks of birds navigating a migration. However, the molecular mechanisms responsible for these behaviors remain poorly understood. We are investigating the role of an intestinal gap junction in a C. elegans behavior known as social feeding, in which worms cluster together while foraging. In wild isolates this behavior is due to a single nucleotide polymorphism in neuropeptide receptor NPR-1. NPR-1 is a G protein-coupled receptor that suppresses social feeding when active. NPR-1 can be activated by FLP-21, a peptide expressed in many neurons and the posterior intestine. The intestine can act as a neurosecretory organ in C. elegans and many peptides are found there. We identified a social feeding defect in strains with mutated intestinal gap junction INX-16 and have conducted research showing that INX-16 and NPR-1 act in a common pathway to mediate social feeding. We hypothesize that in inx-16 mutants defective FLP-21 secretion from the intestine leads to insufficient activation of the NPR-1 receptor to promote social feeding. Current and future research will attempt 1) to show that FLP-21 and INX-16 act in the same pathway to mediate social foraging 2) to determine where FLP-21 functions to suppress aggregation and 3) whether FLP-21 is properly synthesized, packaged, released, and received in inx-16 mutants.

Honors Advisor: Maureen Peters
The epiblast is an embryonic tissue that forms during early development in amniote embryos. In the laboratory mouse and other placental mammals, the epiblast contains pluripotent cells, known as Epiblast stem cells (EpiSCs). Marsupial mammals also have epiblasts, but marsupial EpiSCs have yet to be isolated and grown in vitro. This study began last year and aims to formulate a culture protocol that will enable us to grow marsupial EpiSCs in vitro for use in future experiments on cell differentiation. We will use embryos of the laboratory opossum, *Monodelphis domestica*, for our work.

Honors Advisor: Yolanda P. Cruz
Mackensey Saxton

“Sperm Pairing in Monodelphis domestica”

New World marsupials exhibit the unique reproductive strategy of sperm pairing. Developing sperm pair along the acrosomal face in the epididymis of the male’s reproductive system and remain paired after being introduced into the female reproductive system. Paired sperm then swim together to the female’s oviduct where they unpair in the oviductal crypts. Paired sperm have a significantly higher success rate of arriving in the ampulla of the oviduct, where fertilization occurs. The biochemical mechanisms behind sperm pairing and unpairing are not well studied and remain a mystery. I will be looking into these mechanisms to try to deepen our understanding of the specific processes of sperm pairing. Past research suggests that sperm pairing is mediated by cell-surface glycoproteins. My first objective is to narrow down the list of probable sugar moieties present on these acrosome-surface glycoproteins. I hope therefore to create a “map” of the sugars that mediate pairing. Once I have completed this aspect of my project, I will shift my focus to the mechanism behind sperm pairing in the epididymis and sperm unpairing in the oviduct. Past work showed that sperm in the corpus epididymis, where sperm pairing is known to take place, adhere to the epididymal epithelium. Likewise, paired sperm in the oviductal crypts adhere to the oviductal epithelium prior to unpairing. I hypothesize that sugars are also responsible for these adhesion or binding interactions. I intend to identify the specific sugar residues present at these surfaces and their effect on sperm pairing.
Maya Muenzer

“The Significance of the Giant Exon in Troponin-t3 for Muscle Development, Structure, and Function in Caenorhabditis Elegans”

Maya Muenzer is a senior Biology and Dance double major. She is currently working the Allen Lab. The lab focuses on the interaction between the proteins that control striated muscle contraction using the model organism c. elegans. Mutations in these proteins may affect the function and structure of muscles; ultimately, mutations in these proteins may culminate in hyper cardiomyopathies and dilated cardiomyopathies in humans. Maya’s research focuses on the protein troponin, specifically its tethering component, troponin-T. She is investigating the function of a giant exon present in some transcripts of this protein.

Honors Advisor: Taylor Allen
As global warming causes worldwide water levels to rise, the habitat available to wading birds will be dramatically altered. Increased water levels create less accessibility to primary prey species found in shallow waters. In this study, we seek to better understand foraging habitat selection patterns among wading birds to create a more accurate model of their behavior. Our study is being conducted at Old Woman Creek National Estuarine Research Reserve, a joint branch of both the National Oceanic and Atmospheric Administration and the Ohio Department of Natural Resources’ Division of Wildlife, in Huron, Ohio. Data is collected via cameras and active transects conducted in the estuary. We hypothesize wading birds will not use areas of tall, dense emergent vegetation as much as less dense emergent vegetation and open water. We also reexamine Bancroft et al.’s (2002) hypothesis that wading birds will not use water depths greater than 40cm. Our results will inform management strategies for both natural and newly created wetlands thereby promoting the overall health of these ecosystems.

Honors Advisor: Mary Garvin
Nicolas Lara

“In what tissues are filovirus genes present in the genome of *Monodelphis domestica* expressed?”

“At what points during embryonic development are sequences coding for vasa protein expressed in *Monodelphis domestica*?”

I am working on two projects this semester, both on gene expression in *Monodelphis domestica*, a species of Brazilian gray opossum. The first is to try to determine in which organs filovirus genes—genes left over from the class of viruses of which ebola is a member—are expressed, and thus to come closer to understanding what purpose they serve. The second is to determine at what stages in embryonic development the vasa protein is coded for. Vasa is a protein that is essential for germ cell development: preliminary research done this summer suggests that in *Monodelphis domestica*, vasa protein behaves more like it does in chickens than like it does in rats, suggesting that *Monodelphis domestica* and related marsupials could develop more similarly birds than to other mammals during embryonic development.

Research Advisor: Yolanda P. Cruz
In Professor Salter’s lab this semester we are working on a cell culture project to cure a human leukemic cell line of mycoplasma – a genus of bacteria that lack a cell wall, and thus are resistant to most antibiotics. Mycoplasma have a number of detrimental effects on eukaryotic cells: mycoplasma interference can lead to nutrient competition; alter host metabolism and cellular morphology via their fermentative pathway (changes pH); alter eukaryotic membrane composition by a dependence of cholesterol and lipids; and chromosomal mutations can be induced by mycoplasma activating lymphocytes and cytokines. We are using the sterile technique to grow multiple cell lines in complete media with serial BMC antibiotic treatments: BMC1 is a pleuromutilin (inhibits protein synthesis by binding to the 5OS ribosomal subunit) and BMCII is a tetracycline (inhibits protein synthesis with multiple mechanisms). To determine the concentration of surviving cells after each day (cell viability), we use a hemocytometer to do microscopic cell counts. Infection with mycoplasma will be determined by PCR using primers specific for 16A rRNA coding regions in the mycoplasma genome. After each week’s treatment, we re-isolate a sub-population of the cell colony and grow it in fresh medium to repeat the next round of antibiotics. We hope at the end of the semester we will have generated a cell line completely free of mycoplasma contamination.

Research Advisor: Robin Salter
Anika Burg, Victor Lau, Wren Leader, Emma Lucore, and Sune Wolf Pulsiano

“Is Response to Heterospecific Alarm Calls in Eastern Gray Squirrels: Learned or Innate?”

Eastern gray squirrels (*Sciurus carolinensis*) respond to heterospecific alarm calls of American robin (*Turdus migratorius*) (Getschow et al. 2013; Ethology 119: 983-992). American robins share many of the same predators as gray squirrels. Therefore, robin alarm calls reflecting the presence of predators may be useful to both robins and squirrels. We are attempting to determine whether heterospecific alarm call recognition is learned or innate. Gray squirrels are born in late May or June and leave the nest in late June or July. In the early fall, we expect the population to have a greater percentage of naive juveniles, which could lead to a lower population-level response rate to robin alarm calls. Using playback experiments, we will compare squirrel response rate in the fall to their response rate in the winter, when a greater proportion of the population has had opportunities to associate heterospecific alarm calls with predators. If squirrel recognition of heterospecific alarm calls is innate, then we expect no difference in the proportion of positive responses to alarm playbacks; however, if squirrels learn to associate alarm calls with predators based on experience, we expect to see an increase in the proportion of positive responses over time.

Research Advisor: Keith Tarvin
Lateral roots grow horizontally from the primary root of a plant and improve plant’s ability to reach soil, water, and nutrients. The pattern of lateral root formation is highly controlled by complicated genetic pathways within the plant. In our model plant *Arabidopsis thaliana*, we discovered that a hormone transporter could greatly affect lateral positioning. Because this transporter can be found in multiple cell types of the root, we do not know which of these expression site(s) is/are the most important in regulating lateral root growth/positioning. To study the mechanism by which this transporter induces lateral root growth, we are trying to express this transporter in only one root cell type of plants that lack this transporter. By analyzing the change of lateral root positioning, we can advance our understanding about the overall mechanism of lateral root formation.

**Honors Advisor:** Marta Laskowski
While horizontal gene transfer (HGT) is not the dominant mode of gene transmission in organisms today, it has been hypothesized that early life – predating the last universal common ancestor (LUCA) – may have undergone significant HGT at a much higher rate. In our research, we hope to use computational modeling of organismal ecology and evolution to elucidate whether this transition was driven by any overarching ecological principals. We hope to develop model systems in which the degree of organismal partition can adjust freely in response to changes in input and parameters, thus allowing us to determine which parameters are important in prescribing the degree of vertical versus horizontal gene flow. We hope to do this across several distinct models to show that the results represent ecological principles and not just idiosyncrasies of the models.

Honors Advisor:  Aaron Goldman