

2019 Belmont Undergraduate Research Symposium

Honors – Biology and Neuroscience

Moderator: John Niedzwiecki, Ph.D.

April 11, 2019, 6:15-7:15 p.m.
Ayers 5001

6:15 p.m. - 6:35 p.m.

Evaluating Composition and Overall Comprehension of the *Desmognathus fuscus* Cutaneous Microbiome

Samantha Chu

Faculty Advisor: John Niedzwiecki, Ph.D.

The microbiome consists of all bacteria, fungi, and other microscopic organisms that reside within a given area. In humans, for instance, the microbiome of the GI tract aids in digestion and helps maintain overall bodily health. In other organisms, an example that has been of much interest in the past few decades is the cutaneous microbiome of amphibians. This is because of chytridiomycosis, an emerging infectious fungal disease that has caused declines or extinctions of amphibian populations on six of the seven continents. However, it has been found that some amphibian populations are resistant to this disease because of certain beneficial bacteria in their cutaneous microbiome. In this research project, we studied the cutaneous microbiome of five *Desmognathus fuscus* salamanders with the aim of examining the diversity and richness of each salamander's microbiome makeup. Furthermore, we analyzed how microbiome diversity changed with experimental sample size. After swabbing each salamander, plating what we found on three different nutrient media, and characterizing all bacterial isolates, we found that each salamander had a rich community of cutaneous microbes. However, comparing these makeups revealed that the microbiomes were not as similar to each other as expected; one bacterial type was shared by at most three salamanders. Sensitivity analyses also showed us that five salamanders was not a sufficient sample size for representing the *D. fuscus* cutaneous microbiome.

6:35 p.m. - 6:55 p.m.

Breaking Down the Communication Barriers in Healthcare: An Analysis of Communication Gaps Between Patients and Healthcare Providers

Crystal Lemus

Faculty Advisor: Lori McGrew, Ph.D.

Effective communication is a hallmark of safe patient care. Based on previous case studies it is safe to assume that miscommunication, regardless of the source, can account for issues with very serious consequences. These consequences vary from the upbringing of law cases, physically and mentally traumatizing experiences for those involved, and can even go as far as to causing undue death. While the severity of these issues is not up for debate, the source(s) of these issues is.

Taking a more preventative measure and focusing on education, this thesis turns to the education and training of nurses, nurse practitioners, and physicians. Through curriculum analysis of varying programs, one on one interviews, surveys, and a turn to the digital humanities, this thesis looks at an overarching amount of information in order to help explain why miscommunication incidences take place with the aim of potentially opening the door to new preventative measures that can be taken in the future in order to stop similar occurrences from happening at such an alarming rate. Findings from this thesis could later be implemented in curriculums in order to introduce well-rounded medical professionals in the future.

6:55 p.m. - 7:15 p.m.

Phylogeny of the Streamside Salamander in Tennessee: A Window into Hidden Biodiversity

Joanna Bellan

Faculty Advisor: John Niedzwiecki, Ph.D.

Biodiversity, the measure of natural variation from the genetic level to the biosphere, is the reflection of evolutionary patterns that have shaped the tree of life. The emergence of mitochondrial DNA (mtDNA) analysis has revealed cryptic species, populations that are morphologically similar but genetically distinct, throughout the taxonomic system including the Ambystomatid (mole salamander) family. First distinguished from its sister group *Ambystoma texanum* (smallmouth) thirty years ago, a recent mtDNA study has suggested the *Ambystoma barbouri* (streamside) contains a further split within the species. This follow up study aimed to build a phylogenetic tree using mtDNA to determine whether the Tennessee and Kentucky *A. barbouri* populations hold distinct genetic lineages. The method included sample collection from three Tennessee counties (Rutherford, Sumner, Wilson), mtDNA extraction, amplification of the mitochondrial D-loop region, sequencing, alignment, and bootstrapped tree generation using *Ambystoma mabeei* and *A. texanum* as outgroups.

The resulting likelihood and parsimony models both recovered the same mixed nesting patterns for the Tennessee and Kentucky clades, suggesting a more complex pattern of gene flow than the Kentucky River barrier proposed in previous studies would provide. Interestingly, the model also suggests the smaller Tennessee populations contain a higher level of genetic diversity. This makes the species particularly relevant to conservation efforts since genes translate to potential adaptive ability in the future. When considering conservation concerns, it is also helpful to examine the value of biodiversity from biological, economic, philosophical, and literary perspectives because these all shape our relationship with the natural world.