Welcome to The14th Annual P.U.R.E. Symposium *"Fall Session"!*

Thursday Nov 29th, 2017, LSF 102
Snacks 3:45, Talks begin at 4:00pm

This Semester's Presentations and Speakers:

4:00 – 4:12pm:

"Genotyping of *Procambarus braswelli* to Facilitate Conservation Efforts Against *Procambarus clarkii* via E-DNA Capture."

Student: Andrew Westfall; Faculty Mentors: Dr. David Malakauskas and Dr. Jeff Steinmetz

Procambarus braswelli is a native crayfish species that is only known to inhabit Horry, and possibly Marion, counties in South Carolina. It is currently classified as a vulnerable species due to factors such as the expansion of *Procambarus clarkii*, an aggressively territorial invasive species that has been shown to reduce the range of native species. Conservation efforts for *Procambarus braswelli* are hindered by imprecise knowledge of the distribution of the crayfish and limitations to current sampling methodologies, which are slow and require much manual labor. Furthermore, these methods fail to sample certain crayfish habitats, especially cavities in the benthic regions of waterbodies. Before conservation efforts can be developed, it is necessary to accurately determine the current distribution of *P. braswelli* in South Carolina. Our goal is to develop an eDNA assay to supplement traditional sampling methodologies. Our assay will allow natural resource agencies to detect the presence of *P. braswelli* by simply testing water samples. This information will be used by management agencies to formulate and implement a conservation strategy that will preserve the rare *P. braswelli* from extinction.

4:12 – 4:24pm:

"Survey of crayfish diversity in northeastern South Carolina and the evaluation of crayfish sampling methods."

Student: Geraldine Cuypers; Faculty Mentors: Dr. David Malakauskas and Dr. Jeff Steinmetz

Crayfish are aquatic arthropods that serve important roles in nutrient cycling and ecosystem food chains, and a number of crayfish species are used as bioindicators in water quality monitoring. Although the southeastern United States is a hotspot in crayfish biodiversity, not much is known about species distributions throughout the state. One crayfish of particular conservation interest is the Waccamaw Crayfish (*Procambarus braswelli*). This crayfish is known from a single watershed in South Carolina, and it is believed that *P. braswelli* populations are being threatened by an aggressive, invasive crayfish, *P. clarkii*. Before a conservation plan is developed, the precise distribution of *P. braswelli* must be determined. Our aim was to collect and document distributions of *Procambarus* species in northeastern South Carolina. We collected crayfish using dip nets and baited traps in the summer of 2018. We collected 69 individuals, with the dominant taxa being *P. acutus*, *P. blandingii*, and *P. clarkii*. To date, we have not collected *P. braswelli*, and our results suggest this species is rare. Together with future collections, our specimens will be used to construct a genetic database that can be used to design an eDNA assay for more sensitive detection of *P. braswelli* populations.

4:24 – 4:36pm:

"Delineating Southeastern Crayfish Species Using the CO1 Barcoding Gene."

Student: Alacia Witherspoon; Faculty Mentors: Dr. David Malakauskas and Dr. Jeff Steinmetz

Traditionally, crayfish identification has relied on morphological traits to determine species. However, use of morphological traits is challenging, and genetic evidence suggests morphological traits have more limited utility than previously believed. As a result, researchers are turning to a molecular alternative called DNA barcoding to help identify and delineate crayfish species. DNA barcoding uses the cytochrome *c* oxidase subunit I gene (or COI gene) from the mitochondrial genome to determine an organism's species. CO1 gene is a subunit of the enzyme cytochrome c oxidase, which is a large transmembrane protein complex found in the mitochondria of bacteria, archaea, and eukaryotes. This experiment was performed to test the effectiveness of the COI barcoding gene in crayfish species collected from the Southeastern region of the U.S.. DNA from freshly collected gill tissue was amplified using PCR and sequenced for genetic analysis. The data from this experiment show that CO1 gene is indeed effective in crayfish identification, and also suggest that some crayfish species have been misidentified using the traditional morphological method. Because there were some confounding results, it is recommended that more genetic testing be performed on crayfish to achieve a more efficient system in identifying these species.

4:36 – 4:48pm:

"Investigating Transduction Efficiencies Of Gene Therapy Vectors."

Student: Luke Fennell; Faculty Mentor: Dr. Jennifer Lyles

Gene therapy is a cutting-edge technique used to treat genetic disorders by introducing a functional copy of a mutated or absent gene. This type of treatment requires a vector for delivery of the functional gene, and among the most successful gene therapy vectors is Adeno- associated virus (AAV). Gene therapy using AAV vectors has demonstrated tremendous success over the last decade, including the approval of the first commercially available gene therapy treatment for clinical use. AAV vectors are known for their long-term persistence following a single administration of the vector, a property that is critical to the success of the therapy. A potential barrier to long-term persistence is the initial entry of the vector into the host cell. It is known that different "serotypes" of AAV have different affinities for various cell types. Traditionally, AAV-2 has been the most widely used and widely studied serotype. However, it has been demonstrated that alternative serotypes may have greater affinities for certain cell types than AAV-2, resulting in greater transduction efficiency and ultimately a greater therapeutic effect. As a result, the field has shifted towards the use of alternative AAV serotypes depending on the target tissue – for example, AAV-9 is now used to target hepatocytes (liver cells). Additionally, AAV vectors may contain either single-stranded (ss) or self-complementary (sc) genomes. The configuration of the vector genome upon nuclear entry has also been shown to have an effect on transduction efficiency. While preliminary data demonstrates that both the vector serotype and genome configuration affect transduction efficiency, there is still much characterization that needs to be done. Characterizing the transduction efficiencies of each AAV serotype in common laboratory cell lines and cataloging this information will aid in establishing a vector "toolkit". Researchers and clinicians will be able to use this information to ensure that the most suitable vector is being used for the appropriate target tissue or cell line in order to maximize transduction efficiency and therapeutic effect. Specifically, the transduction efficiency of AAV-DJ—a newly engineered serotype of AAV with a hybrid capsid derived from eight serotypes—is being investigated in several mammalian cell lines, including HEK293 cells (human), HeLa cells (human), and C2C12 cells (mouse). AAV-DJ is currently a leading candidate for liver gene therapy.

4:48 – 5:0pm:

"A comparison of lung function values among divers and in comparison to a non-diver population."

Student: Gabriel Hudson; Faculty Mentor: Dr. Erin Eaton

The purpose of this study was to investigate possible correlations between lung function values (PEF, IRV, ERV, and FVC) among a diver population, as well as in comparison to a non-diver population. Independent variables for both populations were biological sex, age, and weekly physical activity. Independent variables for the diver population were dive tenure, number of logged dives, certification level, and gas mixture used. A spirometry test was conducted to collect lung function values of both populations. Data from this study suggest a statistically significant relationship between diver and non-diver sex and FVC, dive age and ERV, diver sex and ERV, and non-diver FVC and weekly physical activity.

The Department of Biology at FMU strongly encourages student participation in research activities. We offer many opportunities for undergraduates to assist in faculty research or develop their own independent research projects. Students can earn academic credit through Special Studies (BIOL 497) and Honors Independent Study.

If you are interested in learning more about P.U.R.E. or available research opportunities, please visit our website at: *http://people.fmarion.edu/tbarbeau/PURE_symposium.htm*. You can also contact Dr. Barbeau (tbarbeau@fmarion.edu), the coordinator of P.U.R.E., to answer any questions you might have and get you started on a research project!