The relationship between receptor expression and function in patterned generators in crustacean nervous systems

Emily Oleisky, Class of 2020

Central pattern generators (CPGs) are small neural networks that produce rhythmic motor output to generate behaviors such as breathing, chewing, and walking. In order to respond aptly to the environment, CPGs are capable of modulating their outputs, resulting in a variety of patterned behaviors. CPG flexibility can be achieved through neuromodulation. Previous work that I have conducted in the Dickinson Lab has shown the effects of myosuppressin, a well-characterized crustacean neuromodulator, on the CPG of the cardiac neuromuscular system of the American lobster, the cardiac ganglion (CG). During my time at the USDA Arid Lands Research Center in Maricopa, AZ, I was hoping to analyze RNA from tissue samples collected and frozen last spring to understand the myosuppressin receptor distribution across the two cell types of the CG. However, due to the ongoing government shutdown, the focus of my weeks shifted and broadened to include bioinformatics work to create primers for future molecular analysis and physiological data analysis of the stomatogastric nervous system (STNS) of *Cancer* crabs.

Peptides, short strings of amino acids linked by amide bonds, compose the largest class of neuromodulators. These neuromodulators interact with receptors in corresponding neurons to elicit a physiological response, which can be quantified as a change in the burst characteristics of the neurons. Utilizing a list of peptide precursor sequences known to exist in the lobster brain, I utilized BLAST software and a well-vetted bioinformatics workflow to search a previously generated *Homarus* CG transcriptome (Christie et al., 2017) for similar sequences, to identify peptide precursors that exist in the CG. I then used Geneious, a bioinformatics software platform, to design over twenty sequences needed for future experiments to assess peptide abundance, including the sequence for myosuppressin, my peptide of interest.

In addition to the CG, the STNS is a model system for studying the modulatory ability of crustacean neuropeptides, and another system in which the myosuppressin receptor was found. I analyzed recordings of the physiological response of the *Cancer borealis* STNS to myosuppressin and RYamide. These data revealed the ability of these neuropeptides to modulate the rhythmic output of the *Cancer* crab STNS, and have been synthesized with analysis into a scientific paper under review for publishing.

References:
Christie, A. E., Roncalli, V., Cieslak, M. C., Pascual, M. G., Yu, A., Lameyer, T. J., . . . Dickinson, P. S. (2017). Prediction of a neuropeptidome for the eyestalk ganglia of the lobster Homarus americanus using a tissue-specific de novo assembled transcriptome. General and Comparative Endocrinology, 243, 96-119.