***Identifying and Analyzing Neuropeptides and Receptors that are Present in the Cardiac Neuromuscular System of Homarus Americanus***

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Central pattern generators (CPGs) are networks of neurons that generate rhythmic patterns of output to drive behaviors such as eating, walking, and breathing. These CPGs are relatively fixed networks of neurons that produce consistent, stereotypical patterns in the absence of other inputs. However, neuromodulators like peptides acting on the network enable flexibility in the motor outputs. Rhythmic behaviors need to be flexible to allow organisms to adjust to changes in the environment and sensory input.

 Neuromodulators have been shown not only to exert effects on the CPGs themselves, but also to alter the muscle movements by acting on the peripheral sites, such as the neuromuscular junction or the muscle itself.

 This study was performed on the cardiac neuromuscular system of the American lobster (*Homarus americanus*). The simplicity of crustacean CPGs made the American lobster an optimal experimental model. The lobster’s heart is neurogenic, so it requires neural impulses to contract. These neural impulses come from a cluster of neurons on the heart wall known as the cardiac ganglion (Cooke, 2002). Neuromodulators exerting their effects on the cardiac neuromuscular system are known to modulate the contraction of the system at multiple sites. The Dickinson lab is interested in the pathways involved in the signaling of these neuromodulators. To better understand the signaling pathways, the Dickinson lab has collaborated with researchers at the University of Hawaii at Manoa who have used a new method of *in silico* transcriptomics that has predicted a variety of neuropeptides and receptors present within the small and large cells of the cardiac ganglion, cardiac muscle, brain, and other tissue in the American lobster (Christie et al, 2015). Transcriptomics is a method in which the messenger RNA (mRNA) is extracted from the tissue. The mRNA holds the genetic information that leads to the formation of proteins like neuropeptides and receptors. Using query sequences from either *Homarus americanus* or *Drosophila melanogaster,* we were able to determine the homologous sequences of the predicted neuropeptide and receptor in the selected tissue. Well-vetted programs were used to help predict the identity of the novel neuropeptides and receptors present in different tissues in the lobsters. Identifying the location of these neuropeptides and receptors will go on to help the Dickinson lab understand their role in the tissue and the mechanics of their signaling.

 In my research this summer, I looked at five neuropeptide families and nine receptor families, which included the neuropeptides myosuppressin, tachykinin, CCAP, proctolin, RPCH, and the receptors for myosuppressin, tachykinin, CCAP, proctolin, RPCH, and multiple amines. Stretch sensitive receptors, like TREK-1, PIEZO, and TRPGamma, were also analyzed. Studying stretch sensitive receptors is an important part of understanding the cardiac muscle’s contraction that is initiated by the positive feedback loop from the stretch response which is modulated by a variety of neuropeptides.

 The neuropeptides and receptors identified can be further analyzed to understand their structural composition and their localization using mass spectrometry and immunohistochemistry which can inform our understanding of CPGs.

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**References**

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