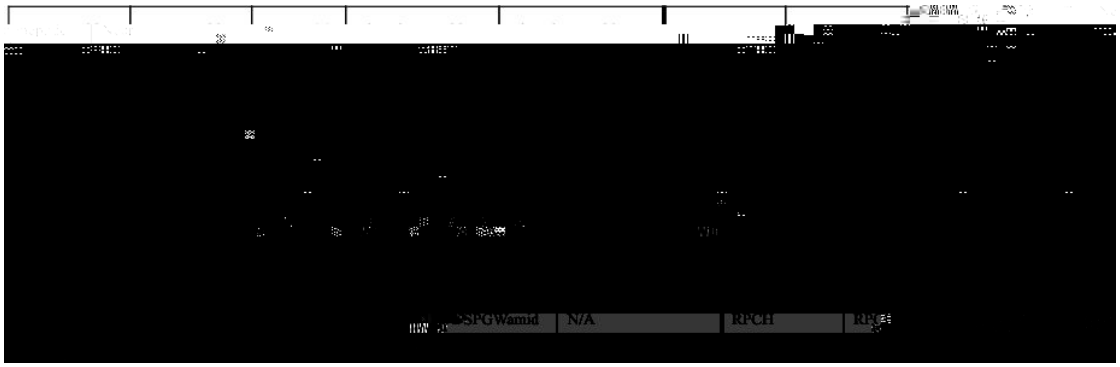
crab ***Pugettia producta.*** Behavioral flexibility is the ability an organism has to interact appropriately with changes in its environment and is mediated by modulation.

While I specifically looked at the crab ***Pugettia,*** other students in the Dickinson Lab focused on ***Libinia emarginata.*** Both crabs are part of the same superfamily Majoidea, but ***Pugettia*** is a specialist feeder while ***Libinia*** is an opportunistic feeder. Due to the limited diet of ***Pugettia,*** the Dickinson lab predicted that ***Pugettia*** has less neuromodulation in the STNS (stomatogastric nervous system) which controls the foregut movement necessary for feeding, compared to opportunistic feeders such as ***Libinia***. Physiological recordings confirm that ***Pugettia*** is less responsive to exogenously applied neuromodulators than opportunistic feeders. My research this summer took the first step in determining whether the differential expression that was observed during physiological recordings in ***Pugettia*** is due to the differences in ability to respond to modulators. Bioinformatics and transcriptome data mining enabled us to explore and determine sequences of neuropeptides and receptors in the brain and STG that can be used in the future to test this hypothesis, consider how these sequences differ between ***Pugettia*** and ***Libinia,*** and tentatively predict the processing of neuropeptides.

Regarding our techniques, we followed a simple bioinformatics workflow focusing on five neuropeptides and receptors for those peptides. Each neuropeptide or receptor search began by using protein query sequences collected from previously annotated brain and eyestalk transcriptomes to search a public access CLC BLAST search tool (University of Hawaii). The BLAST returned sequences (notated by TRINITY numbers) that we used to search the ***Pugettia*** transcriptome. The ***Pugettia*** transcriptomes (brain and STG) allowed us to have a snapshot of the RNA present in ***Pugettia*** and determine which proteins ***Pugettia*** cells are expressing. I then translated the nucleotide sequences gathered from the transcriptome to a protein sequence (Expasy translate tool). Homology- based BLAST searches

results.



I am extremely grateful to Professor Dickinson, Professor Stemmler, the Student faculty research fellowship, and Bowdoin's resources for the opportunity to be part of this exciting project.

Patsy S. Dickinson

Student faculty research fellowship supported by the National Science Foundation