Mechanisms underlying differential responses to neuropeptide allatostatin-C (AST-C) in the cardiac ganglion (CG) of the lobster, *Homarus americanus*

Tess Lameyer, Class of 2016; Devlin Shea, Class of 2018; Meredith Stanhope, Class of 2018

Central pattern generators (CPGs), neural networks found in most animals, produce rhythmic patterned outputs that control basic functions, such as breathing, walking and chewing. Several CPGs exist in the American lobster, *Homarus americanus*, making it an ideal model organism for understanding CPGs. The cardiac ganglion (CG), the CPG of the lobster heart, is composed of nine neurons that produce quantifiable outputs1. In order for lobsters to respond to environmental and physiological stressors, the CG requires flexibility in these outputs. Neuropeptides, signal molecules essential to the neuronal communication that regulates behavior, act as one method of altering the electrical output of CPGs. This peptide-driven neuromodulation is advantageous when stressors demand different cardiac outputs, as is the case when lobsters molt.

Previous research in the Dickinson lab found that one such peptidergic modulator of the CG is allatostatin-C (AST-C). AST-C perfusion through the heart causes a consistent decrease in contraction frequency; however, the peptide causes either increases or decreases in contraction amplitude among different individuals2. Further research showed that AST-C acts directly on the CG, indicating there is a change in the neuronal activity in the CG itself that causes the differential response to the peptide. These differential responses to the peptide tended to cluster around certain times of the year, suggesting a possible correlation between AST-C response and lobster molt stage2. Molting exerts additional stress on the lobster and many physiological factors are altered during this time (e.g. blood flow through the heart) creating a need to adjust the CG output. Thus, it is not hard to imagine that AST-C is acting differently in the CG depending upon the expression of relevant molecular players. In related arthropods, two AST-C receptors exist. Therefore, it was hypothesized that the mechanism responsible for this variability in response was induced by molt-related factors, more specifically a change in number and/or type of receptor expressed in individual lobsters.

To record receptor expression, transcriptomes can be assembled from isolated RNA. Since factors related to molting may exist in other nervous system tissue, RNA isolated from the CG, heart muscle, eyestalk, brain, and hypodermis tissue will be used to make reference transcriptomes representative of different stages of the molt cycle. Additional transcriptomes representative of the differential response to AST-C will be constructed and mapped against the reference transcriptomes to identify factors that may change during the molt cycle. Specifically, we will look at whether different preparations show a shift in the number of one type of receptor or a shift in the proportion of each type of receptor in regards to different responses to AST-C and various molt stages.

Another lobster transcriptome previously assembled from inter-molt nervous tissue was assessed for peptides relevant to neuromodulation3. Bioinformatic analysis identified the AST-C peptide and at least two AST-C receptors. These findings support our hypothesis regarding the CG’s differential response and reinforce the notion that at least two AST-C receptors exist. Future bioinformatic assessment of transcriptomes related to molting and AST-C response will confirm these findings and provide the foundation for understanding the molecular mechanisms underlying neuromodulation in this species.

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References:
3. Transcriptome from David Schulz, University of Missouri; Eve Marder, Brandeis University