POPULATION GENOMIC ANALYSIS TO TEST FOR BROAD-SCALE PATTERNS OF GENETIC VARIATION AND SELECTION IN GREAT LAKES SEA LAMPREY

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ABSTRACT:

We found evidence for population genetic structure that can guide population management. There are three distinctive freshwater populations that are themselves genetically distinct from anadromous sea lamprey sampled in the eastern and western Atlantic. The genetic population in the upper Great Lakes appears to be derived from what are likely native freshwater populations. There is evidence for gene flow and, thus, movement of individuals among the freshwater populations and between the freshwater population and the western Atlantic. There was no evidence for trans-Atlantic gene flow. The possibility for continued gene flow between marine and freshwater populations will likely limit the application of some genetic control technologies (e.g., self-perpetuating gene drives). We also found strong evidence for the emergence of genetically based lampricide resistance. The evidence is strong because we tested for evidence for selection on a priori experimentally identified candidate genes associated with gene expression during lampricide treatment. While the evidence for selection is strong, our results cannot speak to the degree to which adaptive responses to lampricide treatment have affected its efficacy. However, given the ongoing success of lampricide treatments in reducing population sizes, the efficacy of current lampricides seems to remain highly effective, with our results pointing to the need for ongoing monitoring of resistance and the continued exploration of new control methods. The evolution of resistance to pesticide treatment is a null expectation when strong selection pressure is applied to pest populations. Additionally, we find evidence for local adaptation across the freshwater and marine range of sea lamprey that should aid the conservation and management of the species throughout its range.