Can museum specimens help us to understand post-invasion genomic adaption to lampricides in sea lamprey?

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ABSTRACT:

Sea lamprey (Petromyzon marinus) have had profound ecological and economic impacts on the Laurentian Great Lakes and associated waters since their successive invasions during the mid-19th to 20th centuries, prompting decades of intensive control efforts. Despite a dramatic reduction in population sizes following the widespread application of lampricides, persistent survival and potential adaptation among lamprey populations remain concerns for fisheries management and restoration. Understanding the genomic changes and dynamics of sea lamprey populations over time is therefore essential for anticipating future challenges and improving control strategies. However, the lack of DNA-preserved samples from the early invasion period has long hindered such research, as most historical specimens were collected and preserved without consideration for genetic integrity. Recent advances in DNA extraction techniques, especially those applicable to formalin-fixed tissues, present new opportunities to leverage museum specimens for genomic analyses. In this study, we synthesized publicly available records from 82 natural history institutions, generating a comprehensive catalog of 35,193 sea lamprey specimens, with collection dates spanning nearly two centuries. We evaluated the temporal and spatial breadth of these archived samples, focusing on their potential utility for future genetic studies. To test the feasibility of genomic research on historical specimens, we selected gill tissue from 40 individuals representing key geographic locations and time periods, including the Atlantic Ocean, Cayuga Lake, Lake Champlain, and Lake Huron. Using a recently developed method for extracting DNA from formalin-preserved tissues, we successfully performed whole-genome sequencing on the majority of samples, including the oldest-tested specimen from 1854. While sequencing efficiency was lower compared to contemporary samples, sufficient coverage was achieved for mitochondrial DNA analyses, and our results can inform target coverage levels for future nuclear genome studies. Our findings confirm that preserved museum specimens, including those fixed in formalin, can yield genomic data suitable for whole-genome analyses, thus providing a valuable resource for studying the historical and evolutionary trajectories of sea lamprey populations. The newly compiled combined catalog and demonstrated genotyping success lay the groundwork for future research investigating the genetic consequences of control measures, the emergence of resistance, and broader questions of invasion biology.