

****ABSTRACT NOT FOR CITATION WITHOUT AUTHOR**

PERMISSION. The title, authors, and abstract for this completion report are provided below. For a copy of the full completion report, please contact the author via e-mail at jdrob@msu.edu. Questions? Contact the GLFC via email at slrp@glfc.org or via telephone at 734-669-3020.**

Environmental, biotic, and sampling effects on genetic estimates of adult sea lamprey abundance in Great Lakes tributaries

Ellen M. Weise^{2,3}, Kim T. Scribner², Jean V. Adams⁴, Aaron Jubar⁵, Gale Bravener⁶,
Nicholas S. Johnson⁷, John D. Robinson²

² Department of Biology, Dalhousie University, Halifax, NS, B3H 4R2

³ Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI 48824

⁴ USGS, Great Lakes Science Center, 223 East Steinfest Road, Antigo, WI 54409

⁵ USFWS, Ludington Biological Station, 375 River Street, Manistee, MI 49660

⁶ Fisheries and Oceans Canada, Sea Lamprey Control Centre, 1219 Queen Street East, Sault Ste. Marie, ON P6A 2E5

⁷ US Geological Survey, Great Lakes Science Center, Hammond Bay Biological Station, 11188 Ray Dr., Millersburg, MI 49759

August 2021

ABSTRACT:

Sea lamprey (*Petromyzon marinus*) are a harmful invasive species in the Great Lakes, and a large annual control and assessment program is dedicated to reducing their population size. Sea lamprey assessment is performed using larval electrofishing surveys as well as adult trapping for mark-recapture estimation of the number of adult sea lamprey entering streams to spawn. These assessment data are used to estimate the abundance of adult and larval sea lamprey populations over time to evaluate the effectiveness of control efforts. The number of successfully spawning adults is not currently assessed. Trapping and mark-recapture abundance estimates are conducted in a small number of index streams compared to the number of streams where larval assessment is conducted. In this study, we evaluated the utility of several genetic estimates of abundance as complementary tools to assess the abundance of spawning adults in Great Lakes tributaries.

Effective breeding size and minimum number of spawners were estimated for larval cohorts from 18 Great Lakes tributaries using SNPs generated from RADcapture sequencing. We used these data to evaluate the effects of environmental, biotic, and sampling factors on estimates of effective breeding size (N_b) and the minimum number of spawning adults (N_s). Associations between mark-recapture estimates and estimates of N_b and N_s from genetic data were also examined. Simulations were conducted to evaluate the precision and accuracy of N_b and N_s estimates as sample size, number of SNPs, and true N_b in the population increased. We found that the number of larvae collected and genotyped, a sampling factor, was a significant predictor of empirical N_b estimates; however, there was no statistically significant correlation between mark-recapture estimates and N_b or N_s . Simulations indicated that sample size and the number of SNP loci become increasingly important as true N_b increases. Additionally, the different methods of estimating N_b have different biases. The Chao method of calculating N_s had less bias than the jackknife method when true N_b is large. Overall, our results highlight the utility of N_b and N_s by providing insight into sea lamprey spawning populations, further demonstrate the complicated relationship between N_b and census size, and highlight the importance of representative sampling in empirical data sets.