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Determining sampling effort necessary to assess effects of lampricide treatments delays
due to the COVID-19 pandemic

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ABSTRACT:

Invasive sea lamprey have a complex life history that makes their control challenging and requires ongoing management efforts. In particular, they have a protracted larval stage and lack homing behavior to their natal streams. The lack of homing behavior presents challenges because the elimination of larval lamprey in an infested stream does not prevent future reproduction of individuals that emerged from that stream and does not prevent the future colonization of that stream after lampricide treatment. A current outstanding question in sea lamprey research and control is identifying the source of spawning adults, as they represent individuals that have escaped interventions targeting earlier life stages. In this pilot study, we assessed the feasibility of using genetic pedigree reconstruction to generate demographic estimates and link individuals to natal stream. Using a sample of 1,900 fin clips collected in 2023 from spawning adults in the Manistique River, we used a newly developed GT-seq panel targeting microhaplotypes. Additionally, to test our ability to detect siblings across life stages, we incorporated the data from this pilot with RAD capture data collected in previous years for the SupCon program. This is possible because the GT-seq panel was developed based on RAD capture data. Then, we used the Colony program, which uses a full-likelihood approach to infer full and half sibling family groups within spawning adults and across life stages. We estimated the frequency of sibling relationships and used simulations to assess the statistical power of our genotyping panel. We conducted two independent simulations: (1) we assessed the accuracy and precision of using adult pedigree data to infer N_b , or the effective population size within a cohort, and (2) we estimated Type I and Type II error rates for full and half sibling estimates. We found that within a sample of spawning adults and across several replicates, 9% of individuals had at least one other full sibling in our sample. Using sibling relationships across life stages, we found two individuals that could be linked back to natal stream. However, we also found several dozen impossible sibling relationships, i.e. full siblings detected between larvae from different streams. The process of subsetting the RAD capture data to the loci present in the GT-seq panel results in missing data at a large number of loci, and the individuals participating in impossible dyads appear to have high locus missingness. Thus, more work is needed to effectively screen for missing data. Our simulations found that estimates of N_b were dependent on the number of offspring sampled, with small sample sizes leading to underestimation. Finally, we found overall low Type I and Type II error rates for both full and half siblings, however error rates were higher for half siblings. Interestingly, we found that error rates

decreased with increasing parent population size. We hypothesize that this may be due to small parent populations resulting in many related individuals. Half siblings are mathematically similar to aunt-niece relationships, thus a large number of potential second-order relationships may result in incorrect pedigree inference. More work is needed to understand the role of parent population demographics to more confidently infer half siblings in the sea lamprey system. Overall, these results demonstrate that pedigree reconstruction using a GT-seq microhaplotype panel is a promising tool for inferring demographic parameters and linking spawning adults to natal streams. As a pilot study, this work identifies key challenges related to missing data and half sibling inference that will be addressed as part of an expanded GLFC-funded project.