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Identification of adaptive genes associated with Lake Trout Survival and recruitment in different and changing Great Lake Environments

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ABSTRACT:

We developed novel genomic resources that will be fundamental for advancing a new generation of research on lake trout including a high-density linkage map, an annotated and chromosome-anchored genome assembly, and three high-throughput genotyping panels for the species. We used these resources to identify genomic regions with signals of adaptive divergence between hatchery strains, which likely underlie differences in fitness (survival and reproduction) between strains in the contemporary Lake Huron environment. Loci associated with differences in fitness between Seneca and Great Lakes origin strains were localized using local ancestry inference (i.e. admixture tract mapping) and local ancestry outlier tests. By evaluating locus specific allelic contributions of the ancestral Seneca Lake and Great Lakes-derived hatchery strains to naturally-produced wild Lake Huron populations across the genomes of F2 wild born individuals, we were able to determine that a subset of 7 genomic regions contributed to differences in fitness between Seneca Lake and Great Lakes origin individuals during the re-emergence of wild lake trout in Lake Huron. We also identified 2 genomic regions where Great Lakes origin alleles were favored by selection, 4 regions associated with hybrid vigor, and 2 regions potentially associated with hybrid inferiority in recovering wild lake trout populations. We also found that certain Seneca origin alleles are only favored by selection on certain genetic backgrounds. For instance, F2 hybrids between the Seneca strain and Lake Michigan origin strains have an excess of Seneca origin haplotypes on chromosome Sn11, while this is not the case in hybrids between Lake Superior and Seneca origin individuals. Collectively, these results indicate that elevated performance of the Seneca strain can at least be partially attributed to a number of adaptive alleles at a small subset of genes. Additionally,

the fact that Great Lakes origin alleles were favored by selection at two loci indicates that native strains contain some variation that provides a fitness advantage in Lake Huron. These admixture outlier regions contained a significant excess of genes related to swimming behavior and negative regulation of vascular wound healing, which strongly suggests that differences in fitness between strains are due to behavioral and physiological factors associated with the ability to avoid and survive predation by Sea Lamprey. Additionally, we carried out two studies seeking to identify genetic variation associated with habitat occupancy and phenotypic variation in lake trout. First, we carried out a quantitative trait locus (QTL) mapping study in which we identified loci associated with length and condition related traits, skin pigmentation, and body shape.

We produced a linkage map for lake trout as a prerequisite for this work. The information on locus order obtained from the linkage map was also critical to the assembly of the lake trout genome. Recombination rate estimates obtained from the linkage map were critical to the goal of assigning haplotype segments to their hatchery strain of origin for wild-born Lake Huron individuals. This study also allowed us to determine the location of the lake trout sex determination locus, determine centromere locations, and characterize structural differences (i.e., chromosomal inversions and translocations) between lake trout and other salmonid species. Second, we performed a genome-wide scan for loci associated with eco-morphological divergence in Lake Superior lake trout (specifically between lean, siscowet, and hump forms), and identified numerous regions with abnormally high levels of divergence between forms. These loci likely underlie variation in traits that differentiate forms, as well as traits that contributed to reproductive isolation historically. For example, the genomic region most strongly associated with length and condition (from our QTL mapping study) was also associated with eco-morphological divergence in Lake Superior. Interestingly, we find that hybridization primarily occurred between humpers and siscowets and humpers and leans immediately preceding a genetic homogenization event that occurred in the late 1990s or early 2000s. Using a collection of samples over a multi-decade time series collected from the Apostle Islands, we show that levels of hybridization with humpers increased substantially starting in the 1980s.