

The Genetic Basis for the Propensity to Migrate in a Sequestered Population of Rainbow and Steelhead Trout

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ABSTRACT:

Little is known of the underlying genetic basis of migration in any species despite the tremendous ecological benefits these species provide to their communities, and their rapid global decline. Using next generation sequencing of restriction-site associated DNA (RAD) tags we genotype thousands of SNPs in two wild populations of migratory steelhead and resident rainbow trout (*Oncorhynchus mykiss*) from the Pacific Northwest of the United States. One population maintains a connection to the sea, whereas the other population has been sequestered from its access to the ocean for more than fifty years. Here we perform a genome-wide association study to identify several genetic regions and hundreds of RAD SNP markers associated with the propensity to migrate in both the free marine access, and sequestered wild trout populations. Our results corroborate results found in quantitative trait loci (QTL) analysis and provide new evidence for additional loci associated with this complex life history. Additionally we determine that despite sequestration the landlocked population continues to harbor genetic variation associated with a migratory life history. Furthermore we demonstrate the tremendous utility of genotyping by next generation sequencing and how these RAD-tag SNP data can be readily compared between studies within this species.