

Use of genotyping-by-sequencing data to develop a high-throughput and multi-functional set of genetic markers for conservation applications in Pacific lamprey

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Next generation sequencing data can be mined for highly informative single nucleotide polymorphisms (SNPs) to develop high throughput genomic assays for non-model organisms. However, choosing a set of SNPs to address a variety of objectives can be difficult because SNPs are often not equally informative. We developed an optimal combination of 96 high throughput SNP assays from a total of 4,439 SNPs identified in a previous study of Pacific lamprey (*Entosphenus tridentatus*), and used them to address four disparate objectives: parentage analysis, species identification, and characterization of neutral and adaptive variation. Nine of these SNPs are *FST* outliers, and five of these outliers are localized within genes and significantly associated with geography, run-timing, and dwarf life history. Two of these SNPs were diagnostic for two other lamprey species which are morphologically indistinguishable at early larval stages and are sympatric in the Pacific Northwest. The majority (85) of SNPs in the panel were highly informative for parentage analysis- i.e. putatively neutral with high minor allele frequency across the species range. Results from three case studies are presented to demonstrate the broad utility of this panel of SNP markers in this species. Specifically, we applied them to the following conservation directives: 1) validate reproductive success of a set of translocated adults, 2) identify species of early life stages of lamprey, and 3) link genotypes with phenotypes (i.e. adult migratory traits). As Pacific lamprey populations are undergoing rapid decline, these SNPs provide an important resource to address critical uncertainties associated with conservation and recovery of this imperiled species.