

Single nucleotide polymorphism discovery in Pacific salmon

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Single nucleotide polymorphisms (SNPs) are a class of genetic marker that are well suited to a broad range of research and management applications. Although advances in genotyping chemistries and analysis methods continue to increase the potential advantages of using SNPs to address molecular ecological questions, the scarcity of available DNA sequence data for most species has limited marker development and thus applications. As the number and diversity of species being targeted for large-scale sequencing has increased, so has the potential for using sequence from sister taxa for marker development in species of interest. We evaluated the use of *Oncorhynchus mykiss* and *Salmo salar* sequence data to identify SNPs in three other species (*O. tshawytscha*, *O. nerka* and *O. keta*). Primers designed based on *O. mykiss* and *S. salar* alignments were more successful than primers designed based on *Oncorhynchus*-only alignments for sequencing target species, presumably due to the greater number of sequences available for the former alignments. In sequencing ~89Kb we observed a frequency of 4.30×10^{-3} SNPs per bp. Approximately half (52/101) of the subsequently designed validation assays resulted in high-throughput SNP genotyping markers. We speculate that this conversion rate may reflect the duplicated nature of the salmon genome. Our results suggest that a large number of SNPs could be developed for Pacific salmon using sequence data from other species. While the costs of DNA sequencing are still significant, these must be compared to the costs of using other marker classes for a given application.