

DNA Standardization for Pacific Salmon Commission Studies: SNP Variation Contrasting Geographic Scales

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We review recent SNP data collected at Alaska Department of Fish for populations of Chinook and chum salmon from around the Pacific Rim and contrast variation at differing geographic scales. Sixteen Chinook salmon populations ranging from Russia to the Columbia River were examined for nine SNP loci including both mitochondrial and nuclear loci. We also examined multiple populations within four large river systems, the Yukon, Kuskokwim, Copper, and Columbia drainages. On a Pacific Rim scale, the major lineages previously identified by other molecular markers are well resolved by the SNPs. The largest differences across the entire range occur between stream and ocean-type Chinook salmon from the Columbia River. On a drainage-wide scale, individual drainages include multiple smaller lineages often associated with run timing. We also examined nine chum salmon populations from the Pacific Rim ranging from Japan to Washington State as well as populations within the Kuskokwim River drainage for 28 SNPs. Similar to Chinook salmon, previously identified major lineages of chum salmon are well differentiated. On a drainage level, summer and fall chum salmon are clearly differentiated by the SNP loci in the Kuskokwim drainage.

Collaborations to develop additional SNP loci are also reviewed with particular emphasis on the *Genetic Analysis of Pacific Salmonids* (GAPS) group funded by the U.S. Section of the Chinook Technical Committee of the Pacific Salmon Commission.