

SNPs resolve populations of Chinook salmon in the Yukon River

William Templin, Christian Smith and Lisa Seeb

Alaska Dept. Fish and Game, 333 Raspberry Road, Anchorage, AK 99518 USA

Anadromous Chinook salmon bound for United States and Canadian spawning grounds migrate through the U.S. portion of the Yukon River where they are targeted by a gauntlet of fisheries. To fulfill treaty obligations between these two countries, fishery managers need to know what portion of fish caught in the U.S. are of Canadian origin. Allozyme markers have been used to assign mixed fishery samples to U.S. and Canadian portions of the Yukon River; however, these markers are limited by sampling difficulties and by the number of available loci. Microsatellite markers have been considered as an alternative; however, no standardized database exists for these markers. We present the use of 26 single nucleotide polymorphism (SNP) markers that combine the ease of sampling and large number of potential loci of DNA markers with universally transportable data. Simulations and analyses of known fish suggest that the SNP baseline can be used to assign mixture components to country-of-origin with >96% accuracy. Additional resolution to seven fine-scale reporting groups (U.S. – Lower Yukon, Middle Yukon; Canada – five groups) is possible with better than 90% accuracy. The SNP baseline described here may be used to provide rapid and accurate estimates of the proportions of U.S. and Canadian Chinook salmon caught in Yukon River fisheries.