

Project Title: Genomics of maturation age in Yukon Chinook

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Study Location: Yukon River watershed, specifically Chena River and Salcha River spawning populations, and Pilot Station samples of population admixtures.

Abstract: Selective fishing may cause evolutionary changes in harvested fish stocks, but widespread genomic evidence for ‘Fishing Induced Evolution’ remains lacking. Rapid declines in size and age at maturation in AYK Chinook salmon is a potential harbinger of evolutionary change linked to selective fishing. Here we seek to test the overarching hypothesis that variation in age, and therefore size, of adult Chinook salmon in the Yukon River watershed has an underlying genomic basis associated with specific loci. Testing of this hypothesis is the first step towards addressing whether changes in escapement quality are the result of evolutionary change consistent with selective gill net fishing. Our overarching objective is to characterize the genomic architecture of maturation age in Yukon Chinook. To accomplish this goal, we will first search for candidate genes associated with maturation age in two intensely sampled populations (Chena and Salcha rivers). Once candidate genes are identified, we will survey their broad utility using archived samples collected at Pilot Station, which represents an admixture of populations from throughout the Yukon drainage. We anticipate the results to be of broad interest to stakeholders and managers in the AYK region and among salmon researchers more broadly. Identification of specific genomic markers associated with escapement quality is necessary to understand how maturation age and size are likely to respond to management options (e.g. changes in gill net mesh size restrictions) and will inform our understanding of adaptive potential in depressed Yukon Chinook salmon.