

Genetic stock identification of Kuskokwim Area Chinook salmon

The subsistence fishery for Chinook salmon in the Kuskokwim Management Area is one of the largest and most significant in Alaska. Low returns in recent years have yielded shortfalls in escapements basin-wide and resulted in fishing restrictions, which directly affect local communities. Sustained productivity of salmon relies on maintenance of genetic diversity through informed management of the resource. We investigated the genetic diversity of Chinook salmon from the Kuskokwim River using two types of genetic markers, microsatellites and single nucleotide polymorphisms, to understand the population structure. Analysis of genetic data found evidence of significant structure among these Chinook salmon populations. However, much of the diversity was associated with two populations in the upper drainage. Populations were assigned to three groups based on genetic characteristics and geographic proximity, two within the Kuskokwim River (Upper and Lower/ Middle) and the third in Kuskokwim Bay. Simulations using these groups indicate that the Lower Kuskokwim and Kuskokwim Bay groups are not sufficiently identifiable for mixed stock analysis using currently available genetic data. These genetic data provide comprehensive representation of Kuskokwim Chinook salmon in rangewide baselines that can be used in studies of Chinook salmon on the high seas.

Citation: Templin, W.D., N.A. Decovich, J.D. Guyon, S.E. Gilk-Baumer, D.B. Molyneaux, and L.W. Seeb. 2011. Genetic stock identification of Kuskokwim Area Chinook salmon. USFWS Office of Subsistence Management, Fisheries Resource Monitoring Program, Final Report for Study No. 05-305, Anchorage, Alaska.