

Genetic variation among coho salmon populations from the Kuskokwim Region and application to stock-specific harvest estimation

Genetic variation at 15 microsatellite loci was surveyed in coho salmon *Oncorhynchus kisutch* sampled from 12 locations in the Kuskokwim Region. These data were combined with data from a previous study to survey genetic variation of coho salmon in the region. Genetic diversity patterns showed 1) populations from the Goodnews, Kanektok and Arolik rivers were genetically distinct from Kuskokwim River populations and 2) South Fork Kuskokwim River and Highpower Creek in the upper Kuskokwim River were extremely divergent from populations lower in the drainage. Simulation studies indicated that five population aggregates could be identified in mixtures: Kuskokwim Bay (Middle Fork Goodnews, Arolik, and Kanektok rivers); Low-Middle Kuskokwim (Kwethluk, Kisaralik, Tuluksak, Salmon, George, Kogruklu, and Tatlawiksuk rivers); Takotna River; South Fork Kuskokwim River; and Highpower Creek. Data were applied to estimate the stock contribution of a catch sample made from the commercial fishery on August 13, 2001, and the majority of fish originated from the lower and middle Kuskokwim River (87%), with smaller contributions from Kuskokwim Bay and upper Kuskokwim River.

Citation: Crane, P., D. Molyneaux, C. Lewis, and J. Wenburg. 2007. Genetic variation among coho salmon populations from the Kuskokwim Region and application to stock-specific harvest estimation. U.S. Fish and Wildlife Service, Alaska Fisheries Technical Report 96, Anchorage.