

AFSC/ABL: Chinook allozyme baseline 2004-2008

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Allozyme variation was used to examine population genetic structure of adult chinook salmon, *Oncorhynchus tshawytscha*, collected between 1988 and 1993 from 22 spawning locations in Southeast Alaska and northern British Columbia. Thirty-five loci and two pairs of isoloci were variable, and of these, 25 loci and one pair of isoloci expressed the most abundant allele with a frequency of less than or equal to 0.95 in at least one collection. A neighbor-joining (NJ) tree of genetic distances defined five regional groups: (1) King Salmon River (the only island collection), which has large allelic frequency differences from other populations in this study; (2) heterogeneous coastal populations from southern southeast Alaska; (3) transmountain collections from the Taku and Stikine Rivers on the eastern side of the coastal mountain range; (4) Chilkat River in northern Southeast Alaska; and (5) northern coastal Southeast Alaska, which consists of the Situk River and the Klukshu River, a tributary of the Alsek River. A second NJ tree that included collections from the Yukon River and British Columbia did not reveal any strong genetic similarity between Southeast Alaska and the Yukon River. The data suggest that Southeast Alaska may have been colonized from both northern and southern refugia following the last glaciation – a period of sufficient time to allow for isolation by distance to occur.