

AFSC/ABL: Chum salmon allozyme baseline

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Allozymes from 46 loci were analyzed from chum salmon (*Oncorhynchus keta*) collected at 61 locations in southeast Alaska and northern British Columbia. Of the 42 variable loci, 21 had a common allele frequency <0.95 . We observed significant heterogeneity within and among six regional groups: central southeast Alaska, Prince of Wales Island area, southern southeast Alaska – northern British Columbia, north-central British Columbia, and two groups in the Queen Charlotte Islands. Genetic variation among regions was significantly greater than within regions. The three island groups were distinct from each other and from the mainland populations. Allele frequencies were stable over time in 14 of 15 locations sampled for more than 1 yr. The geographic basis for heterogeneity among regions is confounded in part by spawning-time differences. The Prince of Wales and Queen Charlotte populations spawn in the fall; the mainland populations spawn mainly in the summer, although some overlap exists. Overall, most genetic diversity (97%) occurred within sampling locations; the remaining diversity was distributed almost equally within and among regions. Our genetic data may provide fishery managers a means to estimate stock composition in the mixed-stock fisheries near this boundary between the United States and Canada.