

## AFSC/ABL: Immature chum salmon allozyme ID of mixed stocks

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Immature chum salmon were collected by the F/V Northwest Explorer between September 5 and October 8, during the 2002 BASIS survey across the eastern Bering Sea shelf and Aleutian Islands (for details, see Murphy et al. 2003). Approximately 1,600 fish were aged, checked for the presence of hatchery thermal marks, and genotyped for allozyme loci. Scale aging and otolith mark identification were done by the Alaska Department of Fish and Game's Mark, Tag, and Age Laboratory in Juneau, Alaska. Otoliths with thermal marks were compared with voucher specimens to verify hatchery of origin. Heart, liver, and muscle tissues were extracted and then analyzed with protein electrophoresis to identify genotypes for the 20 allozyme loci in the chum salmon coastwide genetic baseline (Kondzela et al. 2002). Genetic data were pooled into one of four geographic areas—western Aleutian Islands, eastern Aleutian Islands, southeastern Bering Sea shelf, and northeastern Bering Sea shelf. In the eastern and western Aleutian Islands, the catches were large enough to further stratify the data by ocean age. Regional origin estimates were made for each mixture collection using a conditional maximum likelihood method (Pella and Masuda model in SPAM v. 3.7, ADF&G 2001) and the full 356-population genetic baseline. The 95% nonsymmetric confidence intervals were determined from 1000 bootstrap estimates in which the baseline and mixture were re-sampled.