

Genetic Variation in Asian Populations of Chum Salmon, *Oncorhynchus keta* (Walbaum)

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Asian chum salmon stocks represent a significant portion of all chum stocks feeding in the Pacific ocean. They are of great importance to fisheries of Pacific Rim countries. Effective stock identification in Pacific Ocean mixed-stock fisheries was impossible without a genetic characterization of Asian chum populations. Many aspects of understanding salmon life history, interspecies population structure and ecology in feeding areas in the Pacific Ocean demand knowledge about status and relative abundance of stocks from different continents and spawning regions. The application of mixed-stock fisheries identification techniques is revealing the migration routes of Pacific salmon of different origins in the Pacific Ocean.

The purpose of the present article is to summarize recently collected genetic data with previously published data (Winans et al. 1995) on Asian chum salmon, to characterize genetic diversity among local stocks, to estimate genetic flow and interspecies population structure and create a reliable baseline for identification of Asian chum populations in Pacific Ocean mixed-stock fisheries.

Up to 74 protein loci were screened in 57 sample collections (about 4 thousand fish) from the Northern

Coast of Okhotsk Sea, Chukotka, Northern, West and East Kamchatka, Sakhalin, Amur River, and Prymorie areas.

Genetic diversity was analyzed by several statistical methods - Cavally-Sforza and Edwards chord distances, Nei distances, multidimensional scaling and gene diversity analysis. Several well distinguished clusters were revealed. In general, they are in accordance with a geographical origin of populations. Clusters of the Anadyr River, Amur River and rivers from Sakhalin, Prymorie and Japan significantly differed from each other. In populations from the Northern part of the Okhotsk Sea and Kamchatka Peninsula the clustering of genetic traits is not so clear in spite of highly significant genetic differences among stocks. The G-test analysis revealed a highly significant heterogeneity within all geographical regions. The most different were the artificially reared populations of Sakhalin.

Estimates of genetic flow made by F-statistic analysis showed a significant correlation between gene flow and distances between river mouths ($r^2=0.208$, $P<0.001$).