Population Structuring of Chum Salmon, *Oncorhynchus keta,* Populations in Far East Asia

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Keywords: chum salmon, microsatellite DNA, population structure

Chum salmon, *Oncorhynchus keta*, is the most widely distributed species among all the Pacific salmon, ranging from Korea and Japan, northward to the Arctic coast of Russia and North America, and southward to the Oregon coast.

The significant genetic differentiation among and within regions for Pacific Rim chum salmon reflects contemporary restrictions on gene flow (Yoon et al. 2008). In the northeastern Pacific, genetic data have been used to define the evolutionarily significant units (ESUs) and the conservation unit under the Endangered Species Act for chum salmon. However, the historical events and processing of chum salmon genetic structure in the northwestern Pacific still remain unclear.

In the present study, microsatellite DNA (msDNA) was analyzed to estimate the genetic structure of chum salmon populations in Far East Asia. Analyses using four polymorphic loci (OKM4, OKM5, OKM7 and OKM8) were performed using 1,000 fish from 31 populations from Korea, Japan, and Russia (Fig. 1). The assignment tests of individuals was based on an admixture model (K = 2) set of baseline samples, and the neighbor-joining phonogram of chum salmon populations was based on the allelic frequencies between populations.
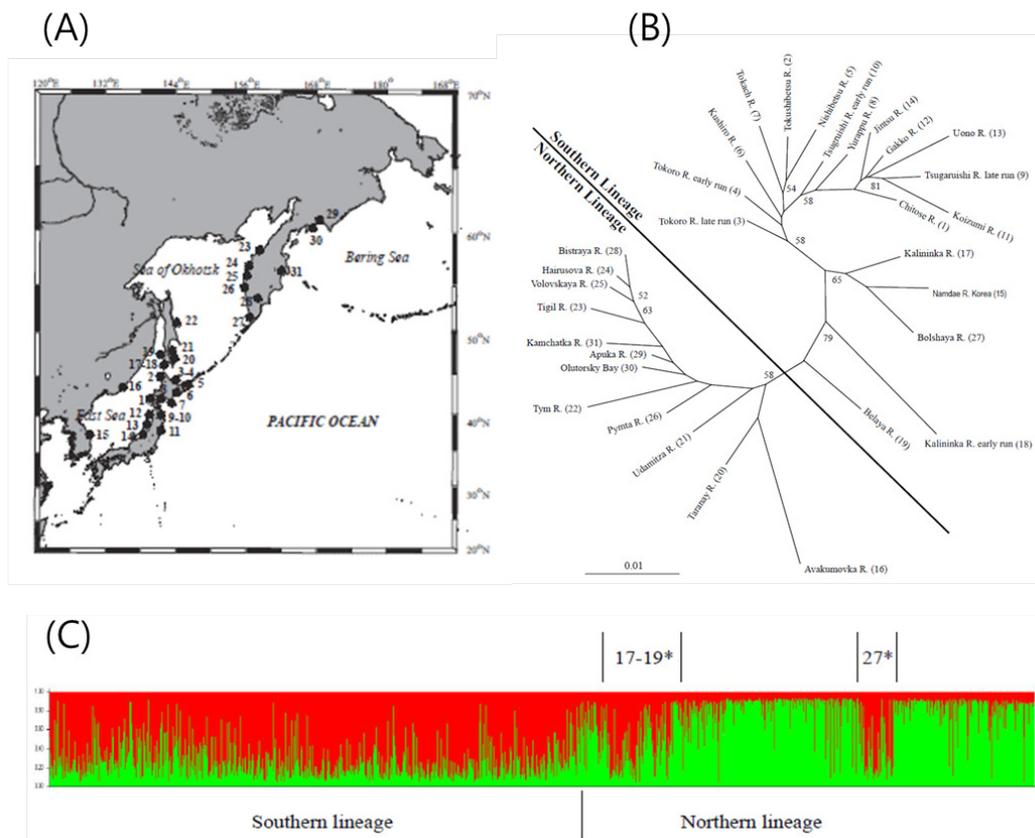
Fig. 1. Map of Far East Asia showing river locations where chum salmon were sampled (A), neighbor-joining phonogram based on allelic frequencies of microsatellite DNA (B), Bayesian analysis of the admixture structure; the optimal cluster number (K) was determined to be two.

The msDNA data reveal clear geographic structuring in the Far East Asian chum salmon among regions (Fig. 1). The analyses showed differentiation between groups of Korean and Japanese populations and Russian populations. In an earlier study, five Russian populations were grouped together with other local populations within the rim of the Okhotsk Sea and West Bering Sea (ROWB) region for management purposes (Yoon et al. 2008). In terms of genetic differentiation, our results suggest that some Russian populations may be intermediate between Korean, Japanese, and other Russian populations. Russian populations shown to be genetically grouped with the Korean and Japanese populations by msDNA data suggests that separate management consideration may be needed for this region. Our results suggest that the observed geographic pattern of the two regions is congruent with patterns obtained in earlier allozyme and mtDNA studies of the same populations (Yoon et al. 2008). Hence, msDNA analysis will be useful for population genetic studies of chum salmon.

Our analyses (msDNA) and an earlier study (mtDNA Yoon et al. 2008) provide differentiation between two regions for effective population size. These findings together might suggest that long-term historical events, such as postglacial re-colonization from different glacial refuges, may influence genetic population structure. Perhaps the Pleistocene ice ages influenced not only historical demographic evidence, glacial population extinctions, and interglacial colonization, but also influenced the contemporary populations of phylogroups of chum salmon along the coasts of Far East Asia.

In conclusion, based on the high degree of chum salmon genetic divergence among geographical groups of populations revealed by msDNA, the genetic markers used in this study will be applicable to identifying the origin of mixture samples collected from salmon aggregations on the high seas, and can be used to further evaluate the discriminative genetic stock identification potential in chum salmon.

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