

Genetic variation and population structure of chum salmon inferred from the mitochondrial and microsatellite DNA analyses

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We investigated nucleotide sequence variation in the mitochondrial (mt) DNA control region and allelic polymorphism at four nuclear microsatellite (ms) DNA loci in chum salmon (*Oncorhynchus keta*) to estimate the genetic variation and population structure of this species in the Pacific Rim.

Nucleotide sequence variation in the mtDNA control region of chum salmon defined 32 haplotypes of three genealogical groups (clade A, B and C) in more than 4000 individuals representing a total of 96 populations from Japan, Korea, Russia and North America. The observed haplotypes were mostly associated with geographic regions, in that clade A and C haplotypes characterized Asian populations and clade B haplotypes distinguished North American populations. The haplotype diversity was highest in the Japanese populations, suggesting a greater genetic variation in the populations of Japan than those of Russia and North America. Population genetic analyses with AMOVA and pairwise F_{ST} estimates suggested distinct genetic differentiation of populations among and within regions and clear geographical structure in the Pacific Rim. Similar population genetic analysis with msDNA using more than 1,800 fish representing 36 populations from Japan (14) and North America (22) also disclosed a genetic diversity in the populations of Japan than North America and a distinct genetic differentiation between and within geographical groups of populations. The observed geographic pattern seems to be influenced with isolation by distance and low or restricted gene flow between local groups within regions.

The present results suggest that mtDNA and msDNA analyses may become a powerful battery to estimate the genetic variation and population structure of chum salmon in the Pacific Rim, which will provide a useful baseline for the genetic stock identification of mixed chum salmon populations in high seas.