

## Stock Identification of Chum Salmon by Mitochondrial DNA Sequence Analysis

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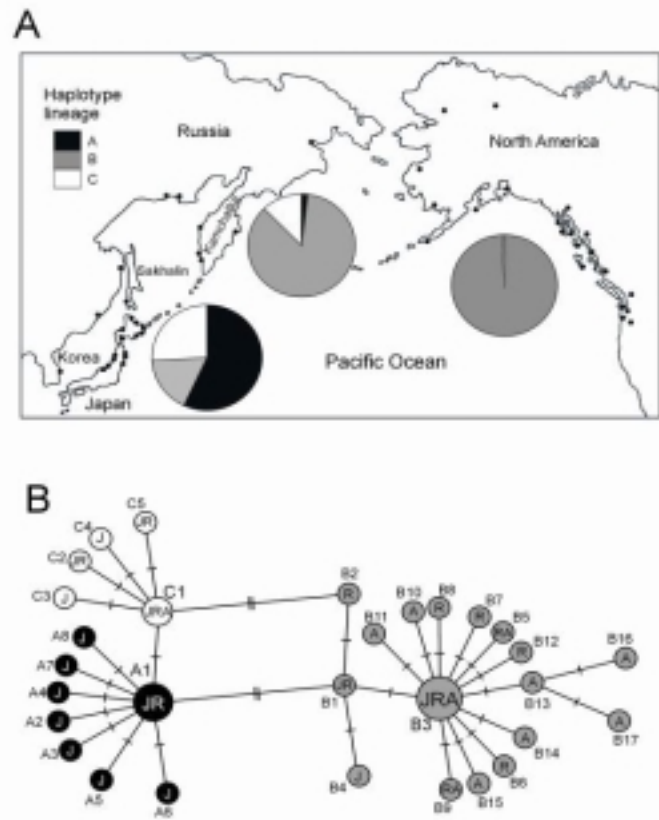
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Polymorphic nucleotide sites were found in about 500 bp sequence from the 5' end of the control region of the mitochondrial (mt) DNA of chum salmon (*Oncorhynchus keta*) (Sato et al. 2001). The observed nucleotide sequence variation has so far defined 30 mtDNA haplotypes of three genealogical groups (clade A, B and C) in more than 2,100 individuals representing 48 populations from Japan, Korea, Russia, and North America including Alaska, British Columbia and Washington (Sato et al. in press). 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 (Fig. 1).

The haplotype diversity was highest in the Japanese populations (0.64), followed by Russian (0.43) and North American populations (0.34), suggesting a greater genetic variation in the populations of Japan than those of the other two regions. The AMOVA, contingency chi-square test and pairwise population  $F_{ST}$  estimation showed a distinct genetic differentiation among Japanese, Russian and North American populations (Sato et al. in press). In addition, a moderate but significant differentiation was suggested in the populations within Japan and among northwestern, central and southeastern Alaska, British Columbia and Washington in North America (Fig. 2). The populations from Northwest Alaska were found to be genetically distant from other North American populations but closer to Russian populations (Sato et al. in press).

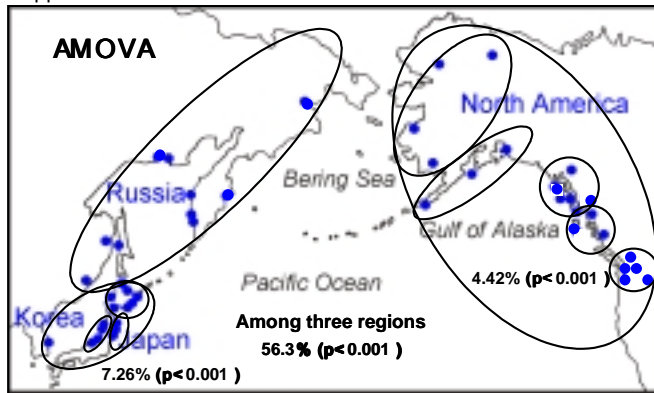
Using the above mtDNA data as a baseline, SPAM estimation was performed for regional stock contribution in the mixed ocean chum samples. In summer, Japanese and Russian stocks were nearly 100% in the central Bering Sea (Fig. 3A), whereas North American stocks were predominant in the Gulf of Alaska, particularly in the north (about 94%) (Fig. 3B). In the central North Pacific Ocean, Russian stocks were more abundant than Japanese and North American stocks (Fig. 3C).

**Fig. 1.** A. Geographical distribution of the three mtDNA haplotype lineages for three regions of chum salmon in the Pacific Rim. Dots indicate the sampling locations in the Pacific Rim. B. Parsimony network for genealogy of the 30 mtDNA control region haplotypes (481 bp) of chum salmon with geographical association. J: Japan, R: Russia, and A: North America.



The present results suggest that mtDNA sequence analysis will become a useful means for genetic stock identification of chum salmon (Abe et al. 2002) with improvement of the baseline data by incorporation of more populations from Russia and North America.

**Fig. 2.** Genetic differentiation of 48 chum salmon populations among or within regions inferred from AMOVA (analysis of molecular variance, Sato et al., in press). Dots indicate the sampling locations in the Pacific Rim. Degree of differentiation is shown by the percent of variation with indicated statistical support.



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**Fig. 3.** Stock composition of chum salmon estimated by the SPAM program on mtDNA haplotype data. A. Chum salmon collected in the Bering Sea (178°W 56°N) July 2000 (50 fish) and 2001 (64 fish). B. Chum salmon collected in the North (145°W 56°N, 45 fish) and South station (145°W 50°N, 79 fish) of the Gulf of Alaska July 2000. C. Chum salmon collected in the central North Pacific Ocean (180° 41°N–46°N, 60 fish) July 2000.

