

Congruence of Population Genetic Profiles Obtained from Mitochondrial and Microsatellite DNA Analyses in the Pacific Rim Chum Salmon Populations

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Chum salmon have received considerable attention due to their high commercial importance and wide geographic distribution in the Pacific Rim (Quinn 2005). Stock identification of chum salmon in mixed aggregations in high seas is therefore a fundamental international issue. Genetic stock identification using polymorphic mitochondrial and nuclear DNA markers could become a competent method with high resolution power and technical ease compared with the conventional allozyme analysis.

In this study, we performed nucleotide sequence analysis of the mitochondrial (mt) DNA using 96 populations recruiting 20 additional populations from North America to previously analyzed 76 populations (Yoon et al. 2004), to improve estimation of the genetic diversity and population structure in the Pacific Rim chum salmon. In addition,

Fig. 1. Distribution of the three mtDNA lineages (A, B, and C) of chum salmon in Japan/Korea (JK), Russia (RU), and North America (NA) along the Pacific Rim. Dots indicate geographical position of sampling site.

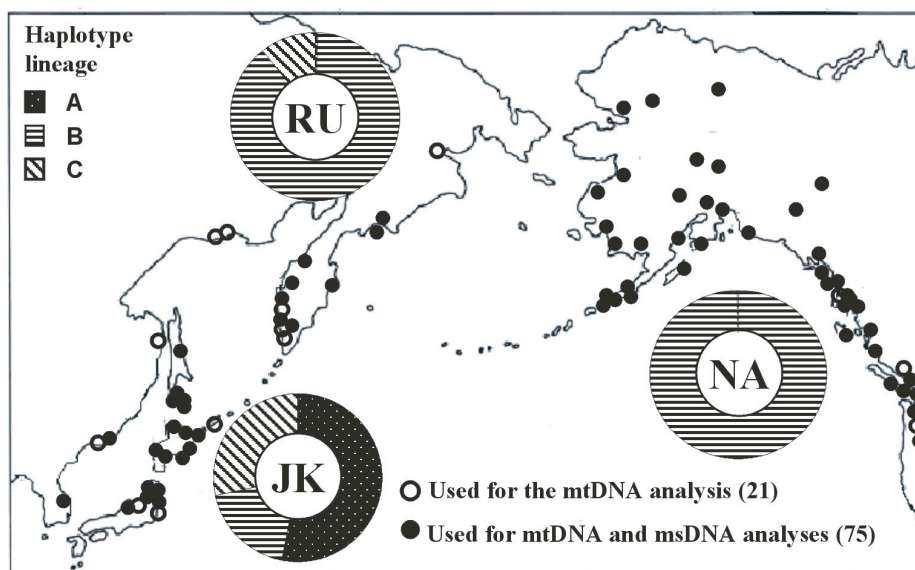


Table 1. Results of the hierarchical analysis of molecular variance based on mtDNA and msDNA for chum salmon. The percentage of variance (%), probability estimated from permutation (P), and the F-statistic (Φ) are given at hierarchical level (Excoffier et al. 1992). Indicated data are depicted from four different analyses.

Variance component	mtDNA			msDNA		
	%	P	Φ	%	P	Φ
Analysis I						
Among regional groups (Japan, Russia and North America)	68.7	$P < 0.001$	0.68	5.1	$P < 0.001$	0.05
Analysis II						
Among regional groups in Japan	7.8	$P < 0.001$	0.09	0.6	$P < 0.01$	0.01
Analysis III						
Among regional groups in Russia	29.0	$P < 0.001$	0.31	4.3	$P < 0.001$	0.04
Analysis IV						
Among regional groups in North America	2.1	$P < 0.001$	0.02	5.3	$P < 0.001$	0.05

nuclear microsatellite (ms) DNA analysis was performed with four polymorphic loci (OKM4, OKM5, OKM7 and OKM8) (Abe et al. 2002) using more than 3,000 individuals from 75 of the above 96 populations, including those of Japan and Korea (15), Russia (15) and North America (45), to compare the genetic features obtained from the mtDNA analysis (Fig. 1).

Estimation of the 481 bp sequence in the 5' variable portion of chum salmon mtDNA control region disclosed 22 variable sites in 4,243 individuals from 96 populations examined, which defined a total of 32 haplotypes of three clades (A, B, C) including the previously defined 30 haplotypes (Sato et al. 2004) and newly identified two haplotypes of clade B from the 20 additional North American populations. Pairwise net nucleotide divergence among the three lineages ranged from 0.0019 (between clade A and B) to 0.0053 (between clade C and B), indicating a shallow haplotype genealogy. The occurrence of haplotypes was in keeping with our previous observations (Sato et al. 2004) and further advocated a geographic association of haplotypes, in that clade A and C haplotypes characterized Asian and Russian populations and clade B haplotypes distinguished North American populations (Fig. 1).

Haplotype diversity was highest in the populations of Japan (0.607 ± 0.001), followed by those of Russia (0.359 ± 0.001) and North America (0.174 ± 0.001), whereas nucleotide diversity was nearly similar in Japanese (0.0021) and Russian populations (0.0017), but lower in North American populations (0.0005). These findings suggest a greater genetic variation in the populations of Japan than those of Russia and North America.

F_{ST} estimates were significantly greater between Japan and North America (0.667 to 0.905) than between Japan and Russia (0.013 to 0.883) or between Russia and North America (0.000–0.867). The analysis of molecular variance (AMOVA; Excoffier et al. 1992) revealed very strong geographic structuring among Japan, Russia and North America (68.7% of the total variance, $p < 0.001$) and a substantial geographic structuring among local populations within regions (Table 1).

Nearly identical population genetic profiles were obtained from msDNA analysis. The number of alleles per locus was highest at the OKM8 locus (29) in the Japanese populations, and lowest at the OKM7 (13) in the North American populations. The expected heterozygosity of Japanese population (0.702) was higher than Russian (0.498) and North American populations (0.438) (Fig. 2). This supports the findings obtained from mtDNA analysis, in that genetic variation is greater in the populations of Japan than those of Russia and North America. Even though msDNA analysis suggested the low level of genetic differentiation among regional groups in Japan and Russia ($p < 0.01$), substantial structuring among Japan, Russia and North America ($p < 0.001$) and among local groups within regions ($p < 0.001$ to $p < 0.01$) was inferred from AMOVA (Table 1).

In addition, msDNA analysis revealed

Fig. 2. Observed and expected heterozygosity at four msDNA loci in 75 chum salmon populations.

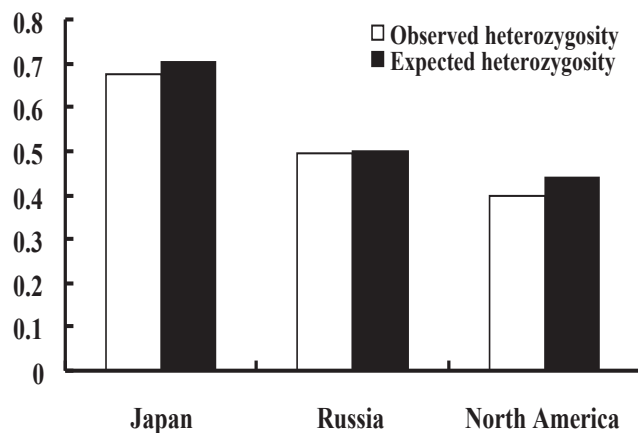
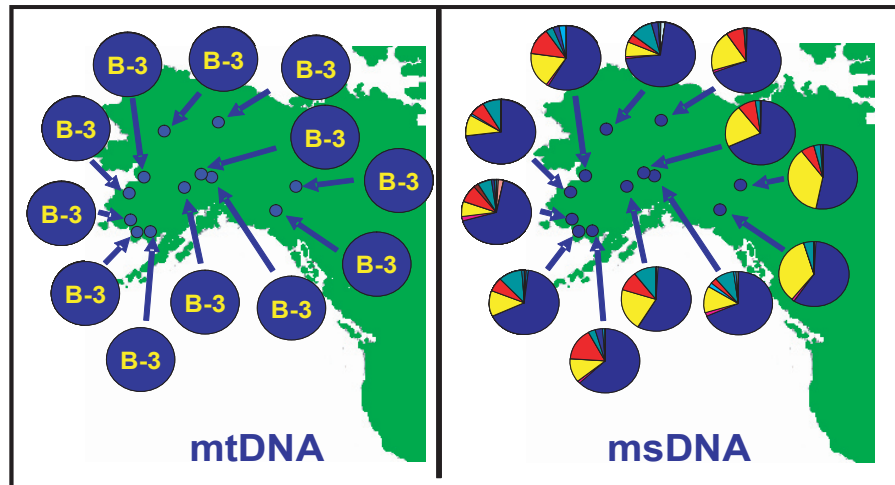


Fig. 3. Direct comparison of allelic frequency at the OKM 5 msDNA locus and mtDNA haplotype frequency among Alaskan populations. Populations with single mtDNA haplotype have a number of msDNA alleles at the examined locus, showing a total of 14 alleles with the observed (0.517) and expected heterozygosity (0.534).



distinct genetic structure in populations with single or a few mtDNA haplotypes of clade B lineage in North America (Fig. 3).

The observed congruence of population genetic profiles obtained from mtDNA and msDNA analyses suggests that a battery of these two DNA markers will become useful for better genetic stock identification of chum salmon in high seas.

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