

## **Mitochondrial DNA single nucleotide polymorphisms detected in the Pacific Rim populations of chum salmon**

Syuiti Abe<sup>1</sup>, Moongeun Yoon<sup>1</sup>, Shunpei Sato<sup>2</sup>, Shigehiko Urawa<sup>2</sup>, Lisa W. Seeb<sup>3</sup>, Vladimir Brykov<sup>4</sup>, Nataly Varnavskaya<sup>5</sup>, Richard L. Wilmot<sup>6</sup>, James E. Seeb<sup>3</sup>, and Akihisa Urano<sup>7</sup>

<sup>1</sup>Division of Marine Biosciences, Graduate School of Fisheries Sciences, Hokkaido University, Hakodate, Japan

<sup>2</sup>Genetics Section, National Salmon Resources Center, Sapporo, Japan

<sup>3</sup>Alaska Department of Fish and Game, Anchorage, AK

<sup>4</sup>Institute of Marine Biology, Vladivostok, Russia

<sup>5</sup>Kamchatka Research Institute of Fisheries and Oceanography, Petropavlovski-Kamchatsky, Russia

<sup>6</sup>Auke Bay Laboratory, National Marine Fisheries Service, Juneau, AK

<sup>7</sup>Division of Biological Sciences, Graduate School of Science, Hokkaido University, Sapporo, Japan

The non-coding control region of animal mitochondrial (mt) DNA is often hypervariable compared with the coding regions, and recommended for assessing genetic variation within the species of interest. In an attempt to develop molecular markers and baseline information for chum salmon (*Oncorhynchus keta*) to address stock identification problems and related issues, we performed nucleotide sequence analysis of about 500 bp portion from the 5' end of the mtDNA control region in more than 3,800 individuals representing 88 Pacific Rim populations including 41 North American, 29 Russian, 17 Japanese, and one Korean populations. So far, a total of 22 variable nucleotide sites have been detected in the analyzed portion, where 21 biallelic and one triallelic nucleotide polymorphisms included 14 transitions, 7 transversions, and one each of deletion and insertion. Alignment of the observed single nucleotide polymorphisms (SNPs) resolved 32 haplotypes of three genealogical clades (A, B and C) on a parsimony network. Nucleotide diversity and divergence were highest in the clade B lineage, followed by those of clade C and clade A. The number of net nucleotide substitution per sites between clade A and C was lower than those between clade A and B and between clade B and C, suggesting a closer genetic kinship between A and C than between B and C lineages. The occurrence of haplotypes was mostly associated with regions, in that clade A and C haplotypes characterized Asian populations and clade B haplotypes distinguished North American populations. Clade B was also the most frequent haplotype in Russia and a significant portion in Japan. 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. The analysis of molecular variance, contingency  $\chi^2$  tests and pairwise population  $F_{ST}$  estimation demonstrated strong structuring among Japanese/Korean, Russian and North American populations, and a definite geographic structuring among local populations within regions.

The observed mtDNA control region SNPs would thus become a useful genotyping tool of chum salmon, thereby providing a potential means for estimation of the stock origin in high seas mixed populations and for the migratory studies.