

Mitochondrial DNA Phylogeography of Chum Salmon in the Pacific Rim

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Chum salmon (*Oncorhynchus keta*) are the most widely distributed species of salmon and trout (Salo, 1991). However, factors implicated in the geographical distribution of chum salmon populations are mostly unknown to date.

The present study aimed to clarify the influence of historical events on the genetic population structure of chum salmon around the Pacific Rim. We estimated the genetic relationship among populations of chum salmon, using the nucleotide sequence data of the mitochondrial (mt) DNA control region and genealogy and geographical distribution of mtDNA haplotypes from Sato et al. (2004) and newly analyzed data of 1,444 individuals from 28 populations (20 Russian and 8 North American populations).

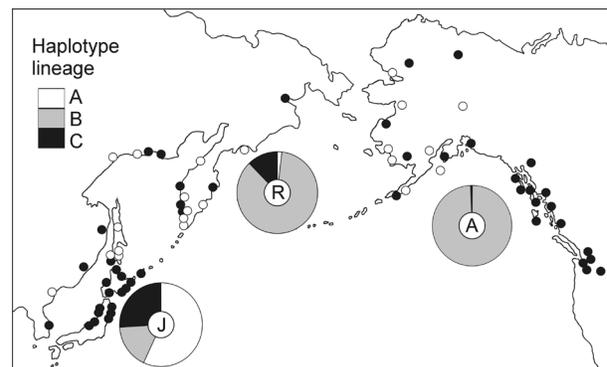
The mtDNA haplotypes of three clades (A, B, and C) observed in 28 additional populations were the same as those identified in previous results (Sato et al. 2004), and further advocated an association with geographic region, in that clade A and C haplotypes characterized Asian and Russian populations and clade B haplotype distinguishes North American population. Clade B is also the most frequent haplotype in Russia and a significant portion in Japan (Fig. 1).

Nucleotide diversity was highest in the clade B lineage (0.0047 ± 0.00039), followed by those of clade C (0.0033 ± 0.00064) and clade A (0.0031 ± 0.00053). Nucleotide divergence was also highest in clade B (0.0044), followed by those of clade C (0.0033) and clade A (0.0027). The number of net nucleotide substitution per sites between clade A and C (0.0019) was lower than those between clade A and B (0.0034) and between clade B and C (0.0052). This finding suggests that the genetic kinship is close between A and C but distant between B and C lineages.

The significant pairwise F_{ST} estimates were greater between Japan and North America (0.450–0.996) than between Japan and Russia (0.085–0.995) or Russia and North America (0.000–0.846). The relationship between genetic (F_{ST}) and geographical distance among populations within three regions (Japan, Russia and North America) showed a clear regional equilibrium, suggesting influence of gene flow with isolation by distance rather than genetic drift on the population structure (Fig. 2).

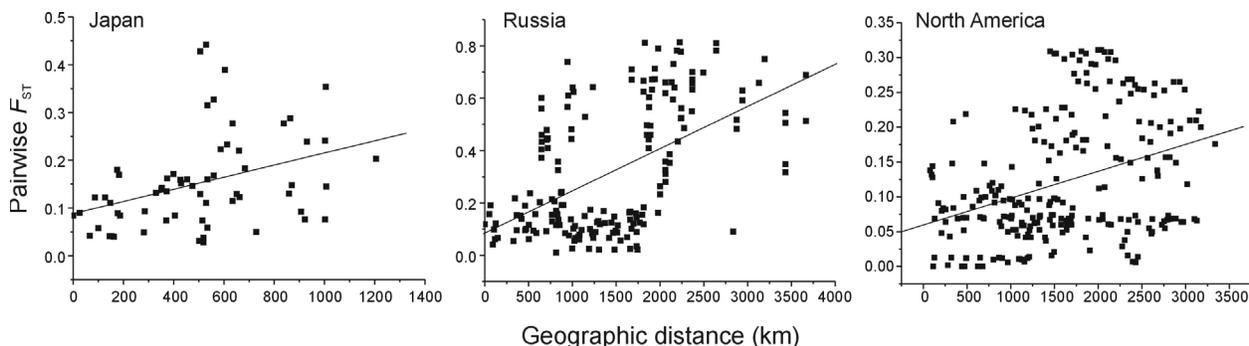
The geographical association of haplotypes was examined by nested clade phylogeographical analysis (NCPA; Templeton et al. 1987; Templeton 2004) and probable causes of associations of chum salmon populations in the Pacific Rim were inferred from mtDNA. The NCPA is a test for significant correlation of an independent variable (geographical distance for phylogeographic studies) with an intraspecific haplotype genealogy. The results of NCPA showed that observed geographical distribution of chum salmon haplotypes was influenced by the major process of contiguous range expansion. This process indicated that chum salmon dispersed from adjacent regions counterclockwise around the Pacific Rim from Japan to North America (Alaska Peninsula/Southcentral Alaska) via Russia (Sakhalin). This result may indicate historical demography of chum salmon driven by glaciation cycles and sea level changes during the Pleistocene, or even earlier, although historical factor(s) implicated in the formation of genetic structure within regional populations was not observed at present. The suggested dispersal route of chum

Fig. 1. Distribution of the three mtDNA lineages (A, B, and C) of chum salmon in the three regions (Japan/Korea = J, Russia = R, and North America = A) of the Pacific Rim. Dots indicate the sampling locations in the Pacific Rim: Open circles observed new sampling locations and closed circles indicated previous analysis locations reported by Sato et al. (2004).



salmon in the Pacific Rim seems overlap the hypothetical migration route of Japanese chum salmon from the Sea of Okhotsk to the Bering Sea and east to the Gulf of Alaska (Urawa 2000; Urawa *et al.* 2001). Furthermore, a previous study demonstrated that the surface circulation in the North Pacific Rim has been conserved since the Pleistocene (Romine 1985). All together, the present mtDNA phylogeographical study suggests Asian origin of chum salmon.

Fig. 2. Scatter-plots of pairwise population F_{ST} estimates against geographic distances (kilometers) separating each pairwise combination populations within each region. The scatter-plot of F_{ST} values and geographical distances for Japan, Russia and North America showed a clear association of genetic and geographical distance across all population range in each region, suggesting a regional equilibrium. The correlation coefficient was significantly positive for the populations of Japan ($r = 0.37094$, $p < 0.01$), Russia ($r = 0.53542$, $p < 0.0001$), and North America ($r = 0.35903$, $p < 0.0001$).



REFERENCES

- Romine, K. 1985. Radiolarian biogeography and paleoceanography of the North Pacific at 8 Ma. *In* The Miocene Ocean: Paleoceanography and Biogeography. Edited by J.P. Kennett. The Geological Society of America, Bolder, Colo. pp. 237–272.
- Salo, E.O. 1991. Life history of chum salmon (*Oncorhynchus keta*). *In* The Pacific Salmon Life Histories. Edited by C. Groot and L. Morgolis. UBC Press, Vancouver, pp. 231–309.
- Sato, S., H. Kojima, J. Ando, H. Ando, R.L. Wilmot, L.W. Seeb, V. Efremov, L. LeClair, W. Buchholz, D.-H. Jin, S. Urawa, M. Kaeriyama, A. Urano, and S. Abe. 2004. Genetic population structure of chum salmon in the Pacific Rim inferred from mitochondrial DNA sequence variation. *Environ. Biol. Fish.* 69: 37–50.
- Templeton, A.R. 2004. Statistical phylogeography: methods of evaluating and minimizing inference errors. *Mol. Ecol.* 13: 789–809.
- Templeton, A.R., E. Boerwinkle, and C.F. Sing. 1987. A cladistic analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping. I. Basic theory and an analysis of alcohol dehydrogenase activity in *Drosophila*. *Genetics* 117: 343–351.
- Urawa, S. 2000. Ocean migration route of Japanese chum salmon with a reference to future salmon research. National Salmon Resources Center Newsletter 5: 3–9 (In Japanese).
- Urawa, S., Y. Ueno, Y. Ishida, L.W. Seeb, P.A. Crane, S. Abe, and N.D. Davis. 2001. A migration model of Japanese chum salmon during early ocean life. *N. Pac. Anadr. Fish Comm. Tech. Rep.* 2: 1–2.