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**Genetic Structure of Cherry Salmon (*Oncorhynchus masou*) Populations
Inferred from Mitochondrial DNA Variation**

by

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Genetic Structure of Cherry Salmon (*Onchorhynchus masou*) Populations Inferred from Mitochondrial DNA Variation

Abstract

Genetic structure of cherry salmon (*Onchorhynchus masou*) populations was examined by analyzing NADH dehydrogenase subunit 5 gene (553bp) of 364 individuals collected from 6 geographical groups: 1 localities (Kangwondo Gosung) on the demilitarized zone of the South Korea, 4 localities (Shiribetsu River, Shari River, Ichani River and Tokushibetsu River) on the Hokkaido Island, Japan and 1 locality on Russia. 11 haplotypes were defined. Haplotype and nucleotide diversities were greater in the populations in Japan and South Korea than in those in Russia. The most populations showed genetic differentiation ranged from 0.0677 to 0.0415 ($P < 0.05$) between geographical populations, respectively. However, Tokushibetsu river and Shari river populations showed no genetic differentiation ($P < 0.05$).

Keywords: Genetic structure, population structure, mtDNA, NADH dehydrogenase subunit 5

Table 1. Measures of mtDNA diversity calculated for each population of cherry salmon

Country	Migration behavior	Sampling location	Abbreviations	Individuals	No. of Haplotypes	Haplotype Diversity(h)	Nucleotide diversity(π)
South Korea	Non-anadromous	Gosung	'15OmGSKR	42	2	0.4181±0.0613	0.000756±0.000782
Japan	Non-anadromous	Shiribetsu River	'15OmShiriJP	40	6	0.6949±0.0515	0.001790±0.001373
		Shari River	'15OmShariJP	40	3	0.6090±0.0417	0.002666±0.001831
		Ichani River	'17OmIchaniJP	96	6	0.4772±0.0578	0.001424±0.001156
		Tokushibetsu River	'17OmTokuJP	96	6	0.7024±0.0381	0.002831±0.001887
Russia	Anadromous	Russia	'15OmRu	50	1	0.0000±0.0000	0.000000±0.000000

Table 2. Genetic differentiation between the eight populations of cherry salmon, Pairwise F_{ST} (below the diagonal) and Nei's genetic distance (above the diagonal)

	'15OmGSKR	'15OmShiriJP	'15OmShariJP	'17OmIchaniJP	'17OmTokuJP	'15OmRu
'15OmGSKR	0	0.0016	0.0027	0.0014	0.0025	0.0005
'15OmShiriJP	0.2072	0	0.0032	0.0019	0.0029	0.0011
'15OmShariJP	0.3874	0.3155	0	0.0023	0.0028	0.0021
'17OmIchaniJP	0.1701	0.1400	0.1842	0	0.0023	0.0008
'17OmTokuJP	0.2222	0.1712	0.0232	0.0677	0	0.0019
'15OmRu	0.2891	0.1970	0.4415	0.1046	0.2085	0

* Bold text, $P < 0.05$

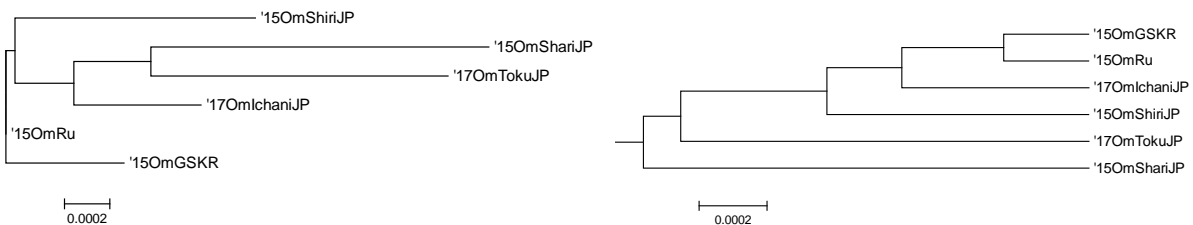


Figure 1. Neighbor-Joining tree (left) and UPGMA tree (right) of the eight populations

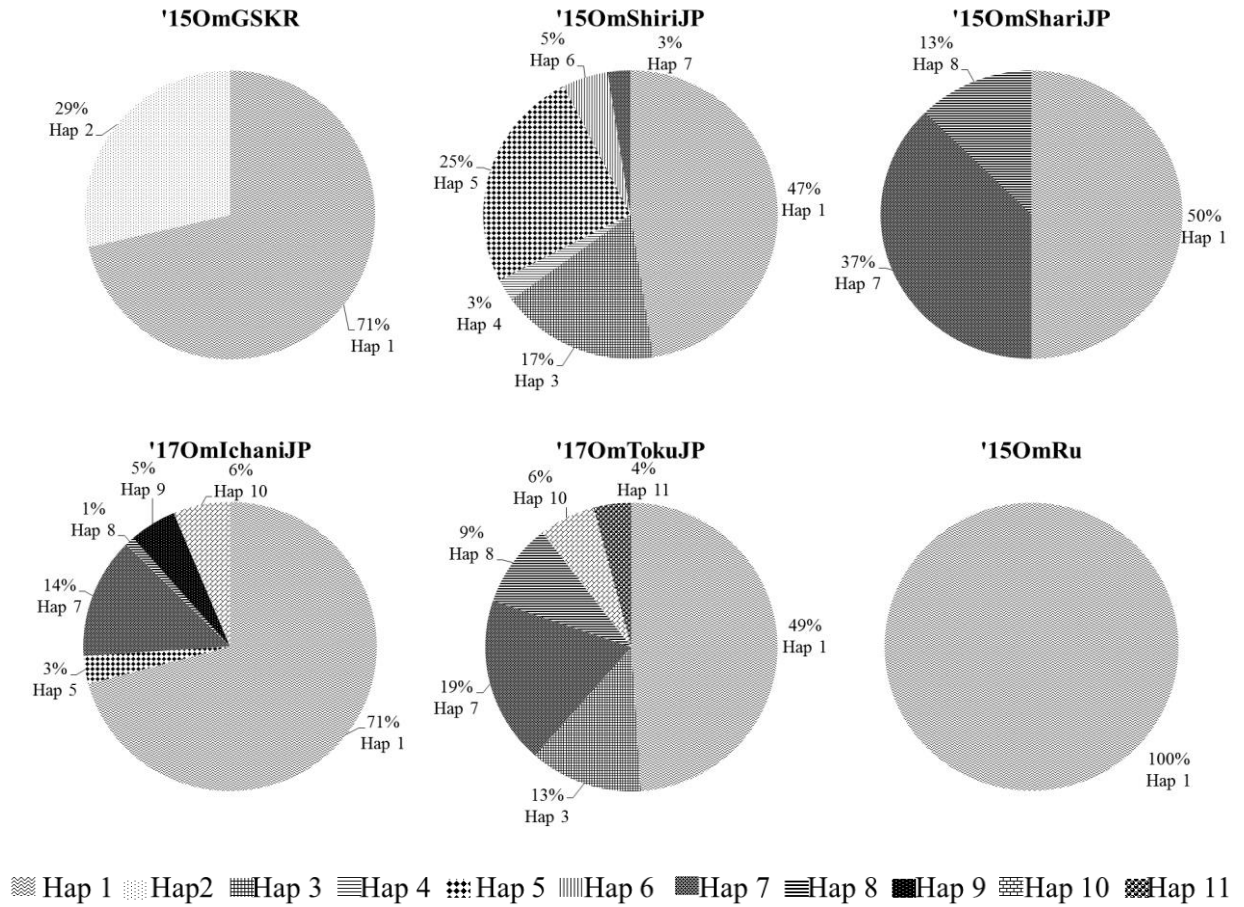


Figure 2. Haplotype frequency for each 6 population are shown with pie chart