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**Population Genetic Structure of Chum salmon (*Oncorhynchus keta*)  
from Republic of Korea**

by

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# Population genetic structure of Chum salmon (*Oncorhynchus keta*) from Republic of Korea

## Abstract

Genetic structure of chum salmon (*Oncorhynchus keta*) was examined in a total of 465 samples collected from seven geographical groups by using ten microsatellite DNA markers. In Korea, populations included seven localities (Myeongpa Stream, Buk Stream, Namdae Stream, Yeongok Stream, Maup&Osip Stream, Wangpi Stream and Taehwa River) on the east side of the Korean Peninsula. The results of genetic diversity analysis are shown in Table 1. The mean  $N_a$  (number of alleles) ranged from 12.70 (Maup&Osip Stream) to 21.70 (Namdae Stream). The  $H_o$  (observed heterozygosity) per populations ranged from 0.6466 (Yeongok Stream) to 0.7814 (Wangpi Stream). The  $H_E$  (expected heterozygosity) per populations ranged from 0.8060 (Myeongpa Stream) to 0.8204 (Maup&Osip Stream). In addition, the mean PIC (polymorphism information content) index ranged from 0.7834 (Wangpi Stream) to 0.8026 (Buk Stream). In conclusion, the analyses showed similar level of genetic diversity from between seven populations. The microsatellite markers revealed that genetic differentiation ( $F_{ST}$ ) between populations is generally low (Table 2), suggesting a moderate level of gene flow taking place among those populations. In addition, the result of PcoA shows that Maup&Osip Stream and Wangpi Stream population are clearly distinguished from the others respectively (Figure 1).

**Keywords:** genetic structure, population structure, microsatellite, genetic distance

**Table 1.** Genetic diversity observed at 10 microsatellite markers in seven populations of chum salmon (*Oncorhynchus keta*).

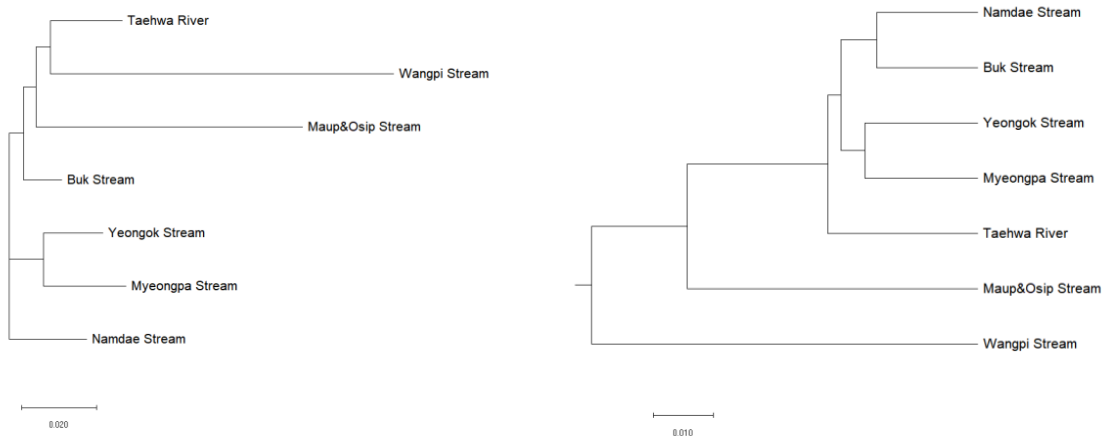
Populations	Average of genetic diversity between seven geographical populations of chum salmon						
	N	$N_a$	Ar	$H_o$	$H_E$	PIC	$F_{IS}$
Myeongpa Stream	83.70	19.40	12.02	0.6490	0.8060	0.7899	0.177
Buk Stream	86.50	20.90	12.83	0.7282	0.8173	0.8026	0.100
Namdae Stream	95.70	21.70	12.85	0.7788	0.8159	0.8014	0.040
Yeongok Stream	84.10	19.20	12.10	0.6466	0.8109	0.7961	0.179
Maup & Osip Stream	19.70	12.70	12.25	0.7354	0.8204	0.7853	0.104
Wangpi Stream	31.20	13.30	11.38	0.7814	0.8095	0.7834	0.031
Taehwa River	44.70	18.40	13.15	0.7340	0.8143	0.7955	0.124
Total average	63.66	17.94	12.37	0.7219	0.8135	0.7935	0.108

\* Number of samples (N), number of alleles ( $N_a$ ), allelic richness (Ar), observed heterozygosity ( $H_o$ ), expected heterozygosity ( $H_E$ ), polymorphism information content (PIC), and inbreeding coefficient ( $F_{IS}$ )

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

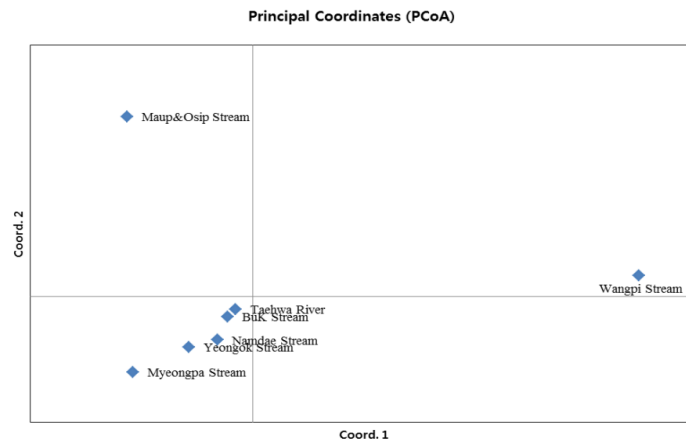
	Myeongpa Stream	Buk Stream	Namdae Stream	Yeongok Stream	Maup&Osip Stream	Wangpi Stream	Taehwa River
Myeongpa Stream	-	0.039	0.050	0.038	0.111	0.149	0.053
Buk Stream	0.003	-	0.034	0.047	0.084	0.104	0.043
Namdae Stream	<b>0.004</b>	0.002	-	0.048	0.101	0.118	0.054
Yeongok Stream	0.002	<b>0.004</b>	<b>0.006</b>	-	0.100	0.125	0.051
Maup&Osip Stream	0.007	0.004	<b>0.010</b>	0.006	-	0.170	0.091
Wangpi Stream	<b>0.021</b>	<b>0.012</b>	<b>0.014</b>	<b>0.016</b>	<b>0.017</b>	-	0.111
Taehwa River	<b>0.004</b>	0.000	0.002	0.003	-0.001	<b>0.008</b>	-

\* Bold text,  $P < 0.05$



Neighbor-Joining Tree (NJ)

UPGMA Tree



**Fig. 1.** Phylogenetic (NJ and UPGMA, above) and Principal Coordinates Analysis (PCoA) using Nei's genetic distance (below).