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Genetic Structure of Chum Salmon, *Oncorhynchus keta* in Korea

by

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Genetic Structure of Chum Salmon, *Oncorhynchus keta* in Korean

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Abstract

Analysis of population genetic structure has been carried out for chum salmon (*Oncorhynchus keta*). In this study, we used ten microsatellite DNA markers to examine genetic diversity and population structure in a total 1,042 samples including seven returning populations in 2018 and four releasing populations in 2019 collected in Korea. The results of genetic diversity analysis are shown in Table 1. The mean N_a (number of alleles) ranged from 16.20 (Taehwa River-releasing) to 22.30 (Taehwa River). The H_o (observed heterozygosity) ranged from 0.7017 (Maup&Osip Stream-releasing) to 0.7795 (Myeongpa Stream). The H_E (expected heterozygosity) ranged from 0.7849 (Taehwa River-releasing) to 0.8263 (Wangpi Stream). Among the four releasing populations, the highest genetic diversity values of N_a (20.60), H_o (0.7250) and H_E (0.8081) were observed from Namdae Stream-releasing population genetically managed by Korea Fisheries Resources Agency (FIRA) than other three releasing populations. The results of genetic differentiations (F_{ST}) and PCoA analysis showed that the seven returning populations were not significantly different (Table 2 and Figure 1). On the other hand, the results of genetic distance of three releasing population: Maup&Osip Stream-releasing, Wangpi Stream-releasing and Taehwa River-releasing managed by local government were significantly different between every populations (Table 2 and Figure 1). In conclusion, among the releasing populations, the highest values of genetic diversity were observed from the Namdae Stream-releasing population which of genetic diversity was managed. In addition, result suggests genetic management of releasing salmon fry should be expanded.

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

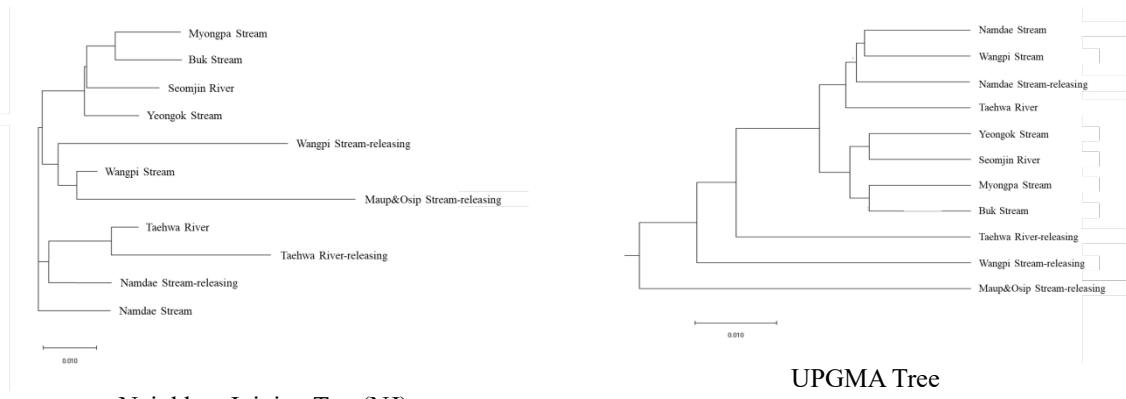
Populations		N	Na	Ar	H_o	H_E	PIC	FIS
Retuning populations in 2018	Myeongpa Stream	93.60	22.00	21.41	0.7795	0.8180	0.8044	0.049
	Buk Stream	95.30	21.21	21.90	0.7389	0.8108	0.7960	0.090
	Namdae Stream	96.00	22.30	21.49	0.7427	0.8213	0.8074	0.098
	Yeongok stream	94.10	22.30	21.66	0.7462	0.8121	0.7990	0.075
	Wangpi Stream	92.90	22.10	21.55	0.7770	0.8263	0.8127	0.059
	Taehwa River	84.90	22.30	22.17	0.7648	0.8088	0.7953	0.048
	Seomjin River	93.10	21.40	20.90	0.7335	0.8196	0.8061	0.103
Releasing populations in 2019	Namdae Stream-releasing	94.10	20.60	20.10	0.7250	0.8081	0.7942	0.094
	Maup&Osip Stream-releasing	95.40	18.80	18.24	0.7017	0.8142	0.7973	0.122
	Wangpi Stream- releasing	93.70	18.30	18.09	0.7324	0.8251	0.8104	0.102
	Taehwa River- releasing	95.00	16.20	15.96	0.7197	0.7849	0.7685	0.074
Total average		93.46	20.68	20.32	0.7419	0.8136	0.7992	0.0830

* Number of samples (N), number of alleles (Na), allelic richness (Ar), observed heterozygosity (H_o), expected heterozygosity (H_E), polymorphism information content (PIC), and inbreeding coefficient (Fis)

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)

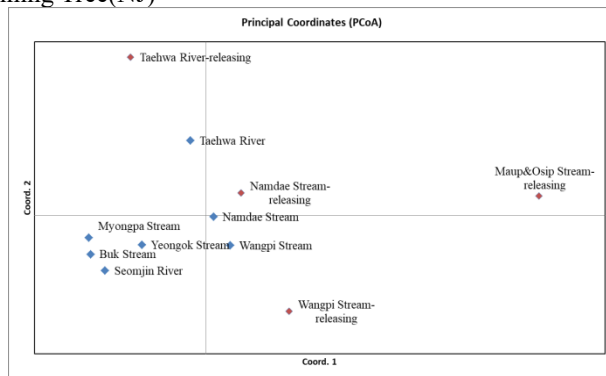
	Myeongpa Stream	Buk Stream	Namdae Stream	Yeongok stream	Wangpi Stream	Taehwa River	Seomjin River	Namdae Stream-releasing	Maup&Osip Stream-releasing	Wangpi Stream-releasing	Taehwa River-releasing
Myeongpa Stream	-	0.025	0.004	0.003	0.028	0.044	0.034	0.043	0.092	0.071	0.058
Buk Stream	0.003	-	0.005	0.003	0.031	0.045	0.029	0.048	0.090	0.073	0.064
Namdae Stream	0.042	0.043	-	0.032	0.026	0.030	0.034	0.027	0.071	0.061	0.060
Yeongok stream	0.030	0.026	0.004	-	0.027	0.035	0.025	0.034	0.077	0.066	0.062
Wangpi Stream	0.003	0.004	0.003	0.003	-	0.005	0.003	0.029	0.056	0.055	0.062
Taehwa River	0.005	0.005	0.004	0.004	0.032	-	0.040	0.030	0.073	0.069	0.035
Seomjin River	0.004	0.003	0.004	0.003	0.029	0.005	-	0.040	0.093	0.062	0.068
Namdae Stream-releasing	0.005	0.005	0.003	0.004	0.004	0.004	0.004	-	0.065	0.058	0.052
Maup&Osip Stream-releasing	0.010	0.010	0.008	0.009	0.006	0.010	0.010	0.008	-	0.010	0.015
Wangpi Stream-releasing	0.007	0.008	0.006	0.007	0.006	0.008	0.006	0.007	0.094	-	0.012
Taehwa River-releasing	0.008	0.008	0.008	0.008	0.009	0.004	0.009	0.007	0.104	0.091	-

*Bold text, $p < 0.05$



Neighbor-Joining Tree(NJ)

UPGMA Tree



* Blue diamond - returning populations, Red diamond - releasing populations

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