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**Genetic Structure of Returning Chum Salmon (*Oncorhynchus keta*)
Populations Inferred from 10 Microsatellite DNA Marker**

by

Sang Gyu Kim and Eun Ah Kim

Aquatic Living Resources Division, Korea Fisheries Resources Agency (FIRA)
4, Idong-gil, Icheon-ri, Ilgwang-myeon, Gijang-gun, Busan 46041
Republic of Korea

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Genetic Structure of Returning Chum salmon (*Oncorhynchus keta*) Populations Inferred from 10 Microsatellite DNA Marker

Abstract

Genetic structure of chum salmon (*Oncorhynchus keta*) was examined in a total of 1,208 samples collected from thirteen geographical groups by using 10 microsatellite DNA markers.

In Asia populations included five localities (Myeongpa River, Buk River, Namdae River, Yeongok River and Taehwa River) on the east side of the Korean Peninsula and two localities (Kushiro and Tokushibetsu River) on the Hokkaido Island of Japan. In North America populations included six localities on the Alaska (Holokuk and Wells River) with United States (Green River and Hoodspport), and two localities of Canada (Conurna and Nimpkish River).

The results of genetic diversity analysis are shown in Table 1. The mean N_a (number of alleles) ranged from 16.70 (Wells River) to 23.60 (Tokushibetsu River). The H_o (observed heterozygosity) and H_E (expected heterozygosity) per populations ranged from 0.686 (Wells River) to 0.780 (Conurna River) and from 0.765 (Wells River) to 0.836 (Kushiro River), respectively. In addition, the mean PIC (polymorphism information content) index ranged from 0.747 (Wells River) to 0.822 (Kushiro River). In conclusion, Wells River population showed lower than genetic diversity from between thirteen populations.

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

Populations	Average of genetic diversity between thirteen geographical populations of chum salmon						
	N	N_a	AR	H_o	H_E	PIC	FIS
Myeongpa River, Korea	93.50	20.80	16.77	0.711	0.820	0.806	0.118
Buk River, Korea	88.50	19.90	16.18	0.693	0.811	0.797	0.142
Namdae River, Korea	92.20	21.10	16.68	0.729	0.803	0.788	0.099
Yeongok River, Korea	90.90	21.30	16.73	0.742	0.808	0.793	0.088
Taehwa River, Korea	58.20	19.20	16.67	0.722	0.797	0.780	0.080
Green River, United State	94.30	18.10	14.93	0.764	0.795	0.770	0.037
Hoodspport, United State	92.90	18.30	14.60	0.753	0.807	0.780	0.074
Holokuk River, Alaska	93.40	20.10	16.34	0.731	0.807	0.791	0.116
Wells River, Alaska	86.30	16.70	14.43	0.686	0.765	0.747	0.119
Conurna River, Canada	95.10	19.00	15.38	0.780	0.800	0.779	0.027
Nimpkish River, Canada	81.50	19.70	16.43	0.756	0.800	0.779	0.059
Kushiro River, Japan	92.00	23.50	18.78	0.756	0.836	0.822	0.090
Tokushibetsu River, Japan	93.20	23.60	18.81	0.750	0.826	0.814	0.087
Total average	88.62	20.10	16.36	0.7364	0.8057	0.7881	0.087

* 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 (FIS)

The results of population structure, each population bifurcated into two groups corresponding to the migratory pathways of salmon by PCoA and phylogenetic (NJ and UPGMA) analysis based on Nei's genetic distance. The F_{ST} values showed lower than genetic distance from between thirteen populations.

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

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

	Myeongpa	Buk	Namdae	Yeongok	Taehwa	Green	Hoodsport	Holokuk	Wells	Conurna	Nimpkish	Kushiro	Tokushibetsu
Myeongpa River	0	0.035	0.043	0.037	0.051	0.437	0.406	0.202	0.361	0.352	0.299	0.130	0.119
Buk River	0.001	0	0.052	0.035	0.060	0.407	0.383	0.223	0.356	0.342	0.287	0.142	0.128
Namdae River	0.002	0.002	0	0.043	0.032	0.462	0.408	0.208	0.344	0.336	0.304	0.157	0.123
Yeongok River	0.001	0.002	0.001	0	0.044	0.414	0.380	0.208	0.350	0.326	0.267	0.163	0.111
Taehwa River	0.001	0.002	0.000	0.000	0	0.479	0.450	0.217	0.400	0.378	0.311	0.159	0.118
Green River	0.067	0.067	0.073	0.070	0.075	0	0.109	0.370	0.288	0.153	0.144	0.394	0.328
Hoodsport	0.062	0.062	0.063	0.064	0.072	0.025	0	0.359	0.233	0.101	0.099	0.451	0.314
Holokuk River	0.028	0.032	0.033	0.027	0.032	0.055	0.054	0	0.283	0.306	0.272	0.250	0.210
Wells River	0.077	0.079	0.078	0.077	0.089	0.066	0.052	0.076	0	0.246	0.209	0.437	0.267
Conurna River	0.044	0.043	0.041	0.043	0.050	0.030	0.017	0.027	0.041	0	0.082	0.396	0.286
Nimpkish River	0.044	0.046	0.045	0.045	0.051	0.028	0.017	0.035	0.044	0.008	0	0.321	0.205
Kushiro River	0.020	0.023	0.031	0.026	0.026	0.054	0.064	0.032	0.087	0.048	0.043	0	0.120
Tokushibetsu River	0.018	0.020	0.021	0.020	0.019	0.048	0.048	0.031	0.055	0.032	0.027	0.015	0

*Bold text, $P < 0.05$

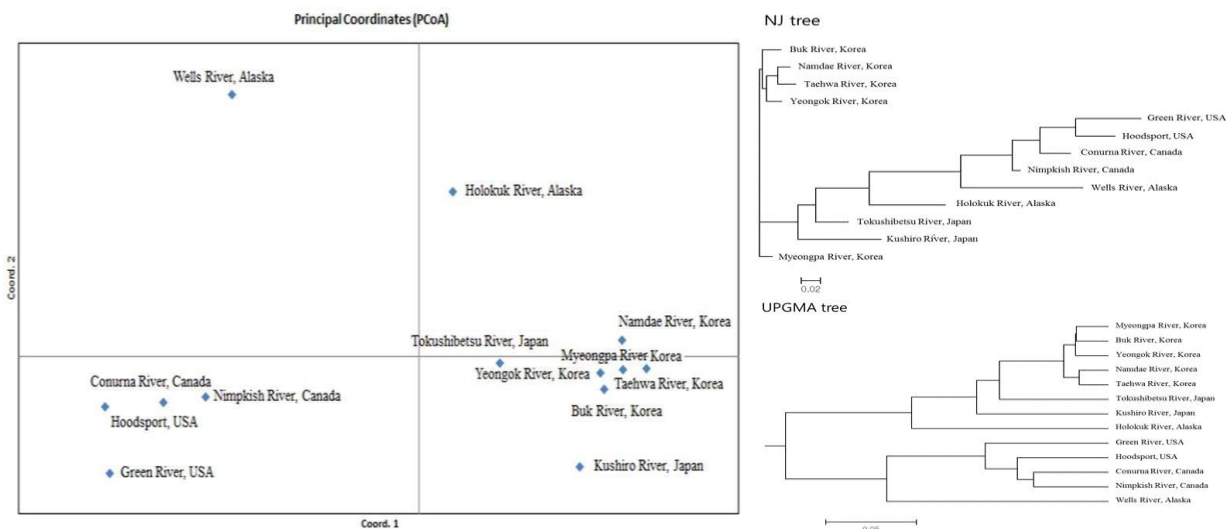


Figure 1. Phylogenetic (NJ and UPGMA) and Principal Coordinates Analysis (PCoA) using Nei's genetic distance