

Genetic Variations and Differences of Chum Salmon (*Oncorhynchus keta*) along the North-Pacific Realm

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Introduction

It has been suggested that molecular technique of genetic variation is a promising tool for stock identification of fish populations. Especially, the recent advance of mitochondrial analysis reveals genetic differences among species and populations. We estimated the genetic variations and differences among the chum salmon from Korea, USA, and Russia including the Bering Sea by analyzing the haplotype (H) and nucleotide diversity (π) in the mitochondrial DNA control regions.

Materials and Methods

We collected 1040 salmon specimens from seven areas (Korea:2, USA: 3, Russia: 1, and Bering Sea: 1) and about 739 (71%) of specimens were analysed. A total of 554bp sequences were aligned, compared and translated using the DNASIS ver. 2.5 program (Hitachi Software Engineering Co., Ltd.). Nucleotide sequences of all salmon samples were used in phylogenetic analysis. The bootstrap analysis (1000 replicates) was performed with the taxon input order randomized once for each replicate.

Results and Discussion

Numbers and frequencies of haplotype in 7 populations from 4 regions indicate 101 distinct haplotypes distribution. Bering Sea population had the most haplotypes, 94 of 101. While the haplotype 2 was the main type for 2 populations from Korea, the haplotype 3 was the main for 4 populations from USA (F and K), Russia and Bering Sea and haplotype 5 for another population from USA (N). Haplotype diversity (H) was highest in the Bering Sea salmon (0.692), followed by those of Russia (0.495),

USA (K: 0, F: 0.423) and Korea (2003: 0.295, 2004: 0.433). Nucleotide diversity (π) had a tendency which was similar in Haplotype diversity (H). With regard to genetic distances in intra-populations, Korean populations had lower value (0.00112) than those of Russia (0.00151) and Bering Sea (0.00489). In inter-populations genetic distances, USA (N) population was genetically close to USA (K) population but Korean and Bering Sea population were very far.

Summary

Genetic variations and differences of chum salmon were analysed by using haplotype and nucleotide diversities in the mitochondrial DNA control region in Korea and the North Pacific realm. In this research, based on haplotype distribution and diversities, we can infer Korean populations entered Bering Sea and mixed with their populations.

References

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