

NPAFC

Doc. 911

Rev. _____

Genetic stock identification and gene flow estimation among the chum salmon populations in the North Pacific using the nucleotide variations in mtDNA, COIII-ND3-ND4L region

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submitted to the

North Pacific Anadromous Fish Commission

by

Republic of Korea

October 2005

THIS PAPER MAY BE CITED IN THE FOLLOWING MANNER:

Lee, Y., G. Kang, W. Jung, G. Kim, C. Kim, K.B. Seong, S. Kang, J.E. Seeb, P. Beerli, Y.-J. Won, S. Kim. 2005. Genetic stock identification and gene flow estimation among the chum salmon populations in the North Pacific using the nucleotide variations in mtDNA, COIII-ND3-ND4L region. (NPAFC Doc. 911) 2 p. Korea Ocean Research and Development Institute, Ansan P.O. Box 29, 425-600, Korea.

Genetic stock identification and gene flow estimation among the chum salmon populations in the North Pacific using the nucleotide variations in mtDNA, COIII-ND3-ND4L region

Korea Genetic stock identification has employed a number of different methods. In terms of accuracy, reproducibility and comparability, single nucleotide polymorphisms (SNPs), which use difference in DNA sequences are getting more acceptances. For the chum salmon, we identified 53 variable sites within the 744 nucleotide-long region of mtDNA, COIII-ND3-ND4L, from the comparison of 186 individuals, 48 from Korea, 44 from Japan, 45 from Alaska, 29 from Canada and 20 from the United States. SNPs in these variable sites comprise 49 haplotypes, some of which are specific to a certain population. Based on these SNPs, population-specific PCR primers were designed in a way that the most 3'end nucleotide becomes specific to each haplotype and that the second to the last nucleotide at the 3'end mismatches the conserved nucleotide at the site. PCR with these primers amplified DNA distinctively depending on the origin of samples. On the other hand, some haplotypes are common in different populations, indicating presence of individual migration among them. Parsimony network of individual genealogies corroborates such gene flow and shows close genetic relationship between Korea and Japan populations and among Canada, Alaska, and the United States populations. Major gene flow occurs asymmetrically from Alaska to Canada populations (16 ± 6) individuals per generation), from the United States to Canada populations (5.7 ± 1.9), from the North America to the Asia populations (1.4 ± 0.2), and from Japan to Korea populations (10 ± 3). In the last example of the gene flows (from Japan to Korea), however, human-mediated transplantation of stocks for hatchery operation should be considered in its interpretation.