

Z6 17 **Phylogenetic Relationships of Korean Salmonids Based on Mitochondrial DNA Control Region Sequences**

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We determined complete sequences from mtDNA control region of six salmonid species in Korean Waters: lenok (*Brachymystax lenok*), cherry salmon (*Oncorhynchus masou masou*), Ishikawa's cherry salmon (*O. masou ishikawai*), chum salmon (*O. keta*), rainbow trout (*O. mykiss*), and its albino mutant. The aims of this study are to provide the genetic basis information on levels of mtDNA polymorphism among these species for genetic stock identification; to discuss phylogenetic relationships among three *Oncorhynchus* species; to demonstrate the utility of control region sequence data as a genetic marker for distinguishing between Korean salmonids. The estimated interspecific sequence divergences from PCR/direct sequencing data, range from 5.146% to 16.487%. The organization of this region is similar to that of other vertebrates. A 81 bp tandemly repeated sequence, associated with length variation was observed in the 3' end of the salmonids control region in this study. In addition, we estimated the phylogenetic relationship based on the control region sequences, the tree supported that cherry salmon was closer to chum salmon than to rainbow trout, and that lenok was most distantly related species in six salmonid species. In the end, this region has proven useful for evaluation of relative levels of genetic variability in populations and for examination of the phylogenetic relationships of the six salmonid species.

Z6 18 **Mitochondrial rRNA Gene Sequence Variation of Korean Salmonid Species**

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We surveyed DNA sequence variation of the mitochondrial rRNA genes among six salmonid species in Korean Waters: lenok (*Brachymystax lenok*), cherry salmon (*Oncorhynchus masou masou*), Ishikawa's cherry salmon (*O. masou ishikawai*), chum salmon (*O. keta*), rainbow trout (*O. mykiss*), and its albino mutant. Our purposes of this study have been to provide the genetic basis information on levels of mtDNA polymorphism among these species for genetic stock identification; discuss phylogenetic relationships among three *Oncorhynchus* species; demonstrate the utility of ribosomal RNA gene sequence data as a genetic marker for distinguishing between Korean salmonids. We determined sequences from these gene regions of *Oncorhynchus* species (2530 bases) and *B. lenok* (2531 bases included one insertion) for the first time in Korea. PCR/direct sequencing data indicated the following consistent results: 1) Common substitutions detected in all six species were transitional mutations. 2) The significant differences were not shown in the intraspecific variation values of salmonid ribosomal RNAs. The percentage sequence divergence values were ranged from 0.066 to 0.212%. 3) The interspecific divergences were greater than the intraspecific variation. Nevertheless, ribosomal RNA genes were more conserved among species than the other mitochondrial genes, and they showed potentiality as a marker for intergenus systematics. In addition, phylogenetic trees were constructed from this data by using the maximum likelihood and the neighbor-joining methods. The resultants supported that cherry salmon was closer to chum salmon than to rainbow trout, and that lenok was most distantly related species in six salmonid species.