

Z 113 Genetic Variation among Korean Treefrogs by Using Mitochondrial Cytochrome *b* Gene

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The partial sequences of mitochondrial cytochrome *b* gene(366bp) was analyzed to investigate inter- and intraspecific genetic variation of *Hyla japonica* and *Hyla suweonensis* from South Korea. Japanese *H. japonica* was used as comparison species. Proportion of variable site between *H. japonica* and *H. suweonensis* was 15% and among *H. japonica* was 9.3%. Because most mutations occurred at third positions of codon, amino acid substitution was observed in only 64th site of wonju and cheju populations. Transition occurred approximately 5 times more than transversion. Based on Tamura-Nei distance, the level of sequence difference shows narrow range (0.55%-3.09%) within Korean *H. japonica*. The sequence difference between Korea and Japanese *H. japonica* was showed 0.55%-8.81% and between *H. japonica* and *H. suweonensis* was 11.43%-12.68%. In the phenogram obtained by the Neighbor-Joining method, Korean *H. japonica* was clustered first with 2.46% sequence divergence, and followed by Japanese *H. japonica* and *H. suweonensis* with 8.17%, 11.81% sequence divergence respectively.

Z 114 The Genetic Variation of Mitochondrial Cytochrome *b* Gene of Microhylid Toad (*Karoula borealis*) in Korea

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The genetic variation within Korean microhylid toad (*Karoula borealis*) was investigated by analyzing partial sequences of mitochondrial cytochrome *b* gene. The nucleotide sequences of 420-bp segment of cytochrome *b* gene was analyzed using fourteen specimens from seven populations of *K. borealis*. Based on the Tamura-Nei distance, the sequence divergence was extremely low in inter- and intra populations of *K. borealis* (0.000-0.0048). The nucleotide substitution rates were also very low (0.00-0.71%) and all the nucleotide substitutions were occurred by only transition. According to the result of sequence divergence, intraspecific genetic variation of *K. borealis* was hardly observed in mitochondrial cytochrome *b* gene.