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The analysis of partial sequence of mitochondrial cytochrome *b* gene of the Family Hynobiidae (*Hynobius*, *Onychodactylus*) in Korean

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The genetic differentiation and phylogenetic variations based on partial nucleotide sequence of the mitochondrial cytochrome *b* gene of Korean salamander *Hynobius leechii* and *Onychodactylus fischeri* were investigated. According to previous study of Korean *H. leechii* using isozymic and morphological analysis by Yang *et al.* (1997), this species was genetically divided into three groups (A, B, C). Based on Yang's analysis, we are trying to compare phylogenetic relationships of the isozymic result and cytochrome *b* gene sequence analysis (4 populations of the *H. leechii* and 2 populations of the *O. fischeri*).

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Genetic differentiation among 2 species of the Genus *Rana* in Korea.

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An analysis of the partial sequence of the mitochondrial cytochrome *b* gene was performed to investigate the intra- and interspecific differentiation among 2 species of the genus *Rana* (*R. nigromaculata*, *R. plancyi*). The sequence of the 315-base pairs, which cover approximately 28% of the cytochrome *b* gene, was determined by PCR-directed silver sequencing method. The sequence of *Xenopus laevis* (Roe *et al.*, 1985) was utilized for outgroup comparison. Levels of mtDNA sequence differences were ranged from 0.3 - 3.2% within species, 3.8 - 6.4 % between 2 *Rana* species and 24 - 28% between 2 species and *Xenopus laevis*. Transition is more frequent than transversion at synonymous site. Transitions were dominated at the third position of the codon. In amino acid analysis, number of amino acid differences were 14 amino acids between *Rana* species and *X. laevis*. Genetic distance was calculated by Tamura-Nei (1993).