

A105

The genetic variations of the mitochondrial ND2 and tRNA^{Trp} gene for six species of Korean genus *Rana*

Hyuk Lee, Suh Yung Yang, and Hei Yung Lee*

Department of Biology, College of Natural Sciences, Inha University

The genetic variations among six species of Korean genus *Rana* were investigated using 508 bases of mitochondrial DNA sequences for the genes encoding ND2 (subunits one of NADH dehydrogenase) and tRNA^{Trp}. These genes were the same in the organization as those found in the mammalian, *Xenopus laevis* and *Rana catesbeiana* mitochondrial genomes.

The nucleotide sequences of 508-bp segment of ND2 and tRNA^{Trp} genes were identified using 6 species of genus *Rana* (*R. nigromaculata*, *R. plancyi*, *R. dybowskii*, *R. sp.*, *R. rugosa*, *R. amurensis*) in Korea. A sequence alignment provided 103 variable sites. The sequence divergences were 0.1 - 0.9% within species and 6.4 - 19.5% among 6 species of genus *Rana*. The secondary structure of tRNA^{Trp} was not found compensatory changes potentially could confound phylogenetic inference.

A106

Genetic Relationship of the Mitochondrial Cytochrome *b* Gene among Six Species of Korean Genus *Rana* (Amphibia; Ranidae)

Jung Eun Lee, Suh Yung Yang, and Hei Yung Lee*

Department of Biology, College of Natural Sciences, Inha University

The genetic relationships among six species of the genus *Rana* were investigated by complete nucleotide sequences of mitochondrial cytochrome *b* gene (1143 bp) and structure-functional model. Interspecific genetic distance based on Kimura-2-parameter distance were ranged from 0.0783 to 0.2500. The genetic distance between *R. nigromaculata* and *R. plancyi* was 0.0783, 0.0847 among two types of *R. rugosa* (A, B), 0.1642 between the brown frogs (*R. amurensis* and *R. dybowskii*), 0.1611 among two types of *R. dybowskii* (A, B), and between pond frogs (*R. nigromaculata* and *R. plancyi*) and *R. catesbeiana* was 0.1236. Based on UPGMA tree, the genus *Rana* was grouped by trichotomous cluster. In the first cluster, *R. catesbeiana* was grouped with *R. nigromaculata* and *R. plancyi* by iteration of 62%. Secondly, *R. amurensis* and *R. dybowskii* (A) were grouped with 40% iteration. In the third cluster, *R. dybowskii* (B) and *R. rugosa* (A, B) were grouped with 81% of bootstrap iteration. Based on structure-functional model of cytochrome *b* gene, nucleotide sequences were divided into three parts; 513 bp of the transmembrane, 336 bp of the outer surface and 294 bp of the innersurface. The most variable sites were within transmembrane (8.1%) and inner surface (4.2%), but outer surface (2.6%) where Q₀ redox center was less variable.