

**F103**

Geographic variations of cytochrome *b* sequence in Korean  
*Rana rugosa*.

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The nucleotide sequence of 501 base pair (bp) fragment of mitochondrial cytochrome *b* (cyt *b*) gene was analysed for 9 populations of *Rana rugosa* using the polymerase chain reaction (PCR) and direct silver sequencing. Two genetically distinct groups (A and B types) were found in populations. The level of mitochondrial DNA (mtDNA) sequence differences were ranged from 0.0 to 0.6% within populations and 0.0 to 0.8% among 6 populations of type A, and from 0.0 to 1.0% among 3 populations of type B. However sequence differences between A and B types were ranged from 5.4 to 6.6%. Type B inhabit in restricted regions (Yongdok, Chungsong and Pohang). Using Kimura two-parameter and Tamura-Nei distance, the level of genetic sequence divergence between A and B types was 6.50% and neighbor-joining tree was completely supported in 99% of the bootstrap iteration.

**F104**

The genetic variation of partial sequence of cytochrome *b* gene in 6  
species of Korean *Rana*

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The analysis of the partial sequence of mitochondrial cytochrome *b* gene was performed to investigate the interspecific variation and relationship among 6 species of the genus *Rana* (*Rana amurensis*, *Rana dybowskii*, *Rana rugosa*, *Rana plancyi*, *Rana nigromaculata*, *Rana catesbeiana*). The sequence of the 504 nucleotides were analysed encoding 168 amino acid residue. The published sequence of *Xenopus laevis* was utilized for outgroup comparison. Sequence differences of cytochrome *b* gene were ranged 6.35%–19.64% between *Rana* species, and 22.22%–26.59% between *Rana* species and *X. laevis*. Transition occurred more frequent than transversion at synonymous sites. Based on Tamura-Nei distance, percent sequence divergence was estimated 21.64% among *Rana* species and 30.53% between *Rana* species and *X. laevis*. The sequence divergence was found in *R. rugosa* from two localities, which estimated 6.75%, as subspecies or interspecies level. Phenogram showed that *R. catesbeiana* and *R. rugosa* clustered as one group and all the remaining species claded into another group.