

**A107** Genetic Relationships of *Rana amurensis* by Mitochondrial Cytochrome *b* Gene Sequences

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Inter- and intraspecific genetic relationships between *Rana amurensis* from Korea and Russia and other brown frogs were investigated by nucleotide sequence of a 504 base pair (bp) fragment of mitochondrial cytochrome *b* gene. Nucleotide sequence similarities among Korean populations of *R. amurensis* ranged from 99.6% to 97.6% and 98.8% within Russian populations. The nucleotide sequence similarity between Korean and Russian *R. amurensis* ranged from 86.9% to 85.5%. Based on Kimura-2-parameter distance, the sequence divergence between *R. amurensis* from Korea and Russia was 16.18% and 18.04% among other related brown frogs. Interspecific sequence divergences among *R. amurensis* and other related brown frogs were diverged by 20.3%. Using an estimate of 2%-4% mitochondrial DNA sequence divergence per million years, Korean and Russian *R. amurensis* was diverged about 8 to 4 million years ago (Mya) and other brown frogs were diverged about 9 to 5 Mya from ancestral frogs and distributed from North Asia to Sakhalin in a short time. In the neighbor-joining and UPGMA tree, *R. amurensis* was clustered into two groups with Korean and Russian populations, and the other brown frogs were grouped separately with diverged trichotomous clusters (*R. dybowskii* and *R. pirica*, *R. okinavana* and *R. tsushimensis*, and *R. japonica* and *R. longicrus*).

**A108** The First Record of a Brown Frog *Rana huanrenensis* (Family Ranidae) from Korea

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We report a brown frog species unrecorded from South Korea. This species is closely related to *Rana dybowskii*, *R. chensinensis*, *R. ornativentris*, *R. pirica*, and *R. huanrenensis* characterized by 2n=24 chromosomes, but is differ from the first four species by the ecological, morphological, and genetical characteristics (habitat of mountain stream-breeding, absence of a vocal sac, and a significant genetic differentiation). This frog is identified as *R. huanrenensis*, recently reported from China, based on the morphology, ecology and genetic analysis. We also report the taxonomic status and relationships of this species in comparison with 24 chromosome members of brown frogs from east Asia.