

**F819**

Intraspecific Variation of Cytochrome b Gene in Korean Frog,  
*Rana amurensis*.

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A fragment(=350 base pair) of mtDNA at the cytochrome b gene site was amplified and sequenced to examine intraspecific variation of *R. amurensis*. The specific oligonucleotide primer set for polymerase chain reaction(PCR) was designed from a comparable published sequence of *Xenopus laevis*. Level of the partial cytochrome b gene sequence divergence was about 3% within species. The values were higher than those of another taxa, because certain regions of the sequence were identified as being particularly differed. The results showed that those regions occur in 31-32 and 75, 78(same numbering for the frog *Xenopus laevis* protein sequence). An interesting finding is that the regions showed higher variation within population. Therefore, these results suggest that the level of cytochrome b gene sequence divergence can be differed on the specific site. We have observed an example for the higher sequence divergence within species in partial cytochrome b gene.

**F820**

**Partial Cloning of Catalase Gene from *Vitreoscilla* sp.**

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Oxidants such as hydrogen peroxide( $H_2O_2$ ) and superoxide anion( $O_2^-$ ) is dangerous in cells and tissues under physiological condition. Catalase is a hemoprotein that is ubiquitously present in aerobic and aerotolerant cells containing a cytochrome system and decomposes the peroxide into water and molecular oxygen. Gram-negative bacterium *Vitreoscilla*, a member of the Beggiatoa family, is an obligate aerobe and produce hemoglobin. The presence of catalase in these cells could prevent the accumulation of peroxide, thus protecting the cells from self destruction when the oxygen concentration is high. To identify *Vitreoscilla* catalase gene, Southern hybridization containing *Vitreoscilla* genomic DNA fragment was performed using a oligonucleotide probe. Also *Vitreoscilla* genomic library constructed 20-25kb fragments of digested *Vitreoscilla* genomic DNA using broad-host-range cosmid vector pVK102 with *Escherichia coli* LE392 as a host. Since pVK102 is sensitive to kanamycin and is resistant to tetracycline, these transformants containing recombinant vectors were selected using antibiotics. These transformants were screened by colony hybridization. We identified catalase gene of *Vitreoscilla* by Southern and colony hybridization.