

**Z101 The longest small subunit ribosomal RNA in Crustacea (Nucleotide sequence and predicted secondary structure of the SSU rRNA of the Crustacea, *Armadillidium vulgare* )**

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The complete nucleotide sequence of SSU rRNA gene from *Armadillidium vulgare* (Crustacea, Isopoda) was determined. It is 3214bp long with a GC content of 56.3%. This is not only the longest SSU rRNA gene in Crustacea but longer than any others except that of strepsipteran insect, *Xenos vesparum* (3316bp), which is the longest ever known. Among the variable regions, V2, V4, and V7 were strongly expanded. The portion of the gene represented by V4 and V7 occupies more than half of total length. Comparison of these portions among unusually long SSU rRNAs implies that the increase of length of SSU rRNA mainly due to the expansion occurred in these two regions. RT-PCR analysis of these regions proved that they exist in mature rRNA. Sequence simplicity analysis of V4 and V7 shows that slippage motifs exist. On the other hand, the V9 region was shorter than those of other crustaceans.

We constructed putative secondary structure of complete SSU rRNA gene of *A. vulgare*. It represents typical for eukaryotes except V2, V4 and V7 regions. In V2, bulges located between helices 8 and 9, and 9 and 10 become larger. In V4 and V7, stem E23-3 is dramatically expanded with small branched stem and stem 43 is branched and expanded by insertions.

**Z102 The Analysis of Partial Sequence of Mitochondrial Cytochrome *b* Gene of *Rana dybowskii* in Korea**

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The genetic differentiation based on partial nucleotide sequences of the mitochondrial DNA of Korean brown frog *Rana dybowskii* was investigated. Korean *Rana dybowskii* is distributed in south Korea widely, among them phylogenetic relationships of 4 populations analysed with 560 base pairs of mitochondrial cytochrome *b* gene and compared with Japanese brown frogs.