

**The Mitochondrial Genome of the Firefly, *Pyrocoelia rufa*:
Complete DNA Sequence, Genome Organization, and
Comparisons with Mitochondrial Genome of Other Insects**

Jin Sik Bae¹, Iksoo Kim², Hung Dae Sohn¹ and Byung Rae Jin¹

¹*College of Natural Resources and Life Science, Dong-A University, Busan 604-714, Korea and Department of Sericulture and Entomology, NIAST, RDA, Suwon 441-100, Korea*

The complete nucleotide sequences of the mitochondrial genome from the firefly, *Pyrocoelia rufa* (Coleoptera: Lampyridae) was determined. The circular genome is 17,736 bp-long, and gene complement was identical to that reported from other insects. Gene order was identical to several fly species, but differ from other coleoptera, *Tribolium castaneum*. The longest intergenic spacer located between ND2 and tRNA^{Trp} was observed with 1,724 bp long, consisted of twelve 134 bp tandem repeats plus a partial copy of the repeat composed of 116 bp, and this sequences is extraordinary long compared with other insect intergenic sequences. The overall nucleotide composition was heavily biased towards adenine and thymine as in other mitochondrial genomes. The size and codon usage of thirteen protein-coding genes were similar to other insect mitochondrial genomes. The putative initiation codon for *P. rufa* COI gene was CTA at 3,117 nt, and this codon was not found in Arthropod mitochondrial genome published so far. All tRNAs were able to form a stable clover-leaf structure, except for tRNA^{Ser}(AGN), in which DHU arm is absent. Phylogenetic analysis with amino acid sequence of thirteen protein-coding genes confirmed the current taxonomy of insect orders, but contradicted to the taxonomy of infraclass level. The sequence was deposited in the GenBank under the Accession Number AF452048 on November 23, 2001.