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**Complete Sequence and Genome Organization of the Mitochondrial Genome of the Firefly, *Pyrocoelia rufa***

**Jin Sik Bae, Hung Dae Sohn and Byung Rae Jin**

*College of Natural Resources and Life Science, Dong-A University, Busan 604-714, Korea*

The complete sequence of the mitochondrial genome of the firefly, *Pyrocoelia rufa*, was determined. The circular genome is 17,736 bp long and contains a standard gene complement, i.e. thirteen genes encoding mitochondrial proteins, twenty-two transfer RNA (tRNA) genes, the large and small ribosomal RNA subunits, and the (A+T)-rich region. The gene order and arrangement was identical to that reported for other insects. The longest intergenic spacer which located between ND2 and tRNA<sup>Trp</sup> was observed with 1,724 bp long. It is composed of twelve 134 bp tandem repeats plus a partial copy of the repeat composed of 116 bp of the beginning and longest intergenic spacer in insect. The overall nucleotide composition was heavily biased towards adenine and thymine, which accounted for 77.4% of all nucleotides as in other mitochondrial genomes. Size and codon usage of thirteen protein-coding genes were similar in other insect mitochondrial genomes. The putative initiation codon for *P. rufa* COI gene was CTA at 3,117 nt, but this codon was not found in Arthropoda mitochondrial genome published so far. All tRNAs were showed stable canonical clover-leaf structure of other mitochondrial tRNAs, except for tRNA<sup>Ser</sup>(AGN). However DHU arm of tRNA<sup>Ser</sup>(AGN) could not form stable stem-loop structure. In PHYLIP and PAUP analyses with amino acid sequence of thirteen protein-coding genes are correctly distributing the order level, e.g., *P. rufa* and *Tribolium castaneum*, and flies and mosquitos species each formed a strong monophyletic group with high bootstrapping values. But, these results are not correctly distributing the infraclass level.