

Mitochondrial DNA Sequence Variation of the Firefly,
Pyrocoelia rufa (Coleoptera: Lampyridae)

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We have sequenced a portion of mitochondrial COI gene (403 bp) of the firefly, *Pyrocoelia rufa*, to investigate genetic diversity within population, geographic variation, and phylogenetic relationships among haplotypes. A total of seven mtDNA haplotypes ranging in sequence divergence from 0.2% to 1.2% were obtained from 26 fireflies collected at four localities in Korea: Namhae, Pusan, Muju, and Yongin. The samples collected at the urban area, Pusan, were all fixed with one haplotype, differently those collected at the forest and/or agricultural areas. This appears to suggest that habitat fragmentation and population bottleneck caused by urbanization might have been severe in Pusan. On the other hand, from Muju known as the largest habitat and sanctuary for the firefly, four haplotypes with the maximum sequence divergence of 1.0% were obtained, and this estimate was the highest among the areas studied. The fireflies collected at the isolated islet, Namhae, revealed relatively low haplotype diversity ($H=0.25$), but one haplotype (PR7) was phylogenetically differentiated from others. This phenomenon was explained in terms of biogeographic history of the island and gene flow in the recent past. Grouping of Muju-Yongin and Pusan-Namhae, respectively, in the hierarchical genetic analysis suggest the presence of historically occurred, biogeographic barrier against gene flow between them.