

Genetic Subdivision of the Firefly, *Luciola lateralis* (Coleoptera: Lampyridae), in Korea Detected by Mitochondrial COI Gene Sequences

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This study was carried out to investigate the population genetic structure of the firefly, *Luciola lateralis*, by determining a portion of mitochondrial COI gene sequences (403 bp). Sequence analysis of 80 individuals collected from 12 localities revealed 24 haplotypes, ranging in sequence divergence from 0.2% to 4.0%. Phylogenetic analyses using PAUP, PHYLIP, and networks subdivided the *L. lateralis* into two clades (termed clade A and B) and the nucleotide divergence between them was 2.2%. This haplotype subdivision was also accord with geographic separation: one at Ansung, Suwon, Namhe, Henam, and Muju, and the other at Kwesan, Poun, Yangyang, and Ponghwa. Population genetic analysis subdivided these two population groups with a substantial statistical significance ($p=0.000$), suggesting presence of long-term barrier to maternal gene flow in the firefly populations. We interpreted this phenomenon in terms of geomorphological features of the Korean Peninsula: clade B in the localities neighboring to Bekdudegan, which is the major Korean mountains ranges and clade A in lowlands, deviated from Bekdudegan.