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A Phylogenetic Study in Some Long-Horned Beetles (Coleoptera: Cerambycidae) Using Mitochondrial COI Gene and 16S rRNA Sequences

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Two regions of mtDNA genome, cytochrome oxidase subunit I (COI) and 16S ribosomal RNA (16S rRNA) genes, were sequenced for 15 species of the long-horned beetle belonging to four subfamilies and geographic samples of mulberry longicorn beetle, *Apriona germari*, from two localities in Korea. Ten samples of *A. germari* collected from Suwon and Busan revealed three COI haplotypes ranging in nucleotide divergence of 0.3% to 0.5%, and the two populations shared one common COI haplotype (80%). The sequence divergence among 15 species of the long-horned beetle was much higher in COI gene (12.3%~39.4%) than 16S rRNA gene (7.2% to 23.1), and the maximum value in the COI gene is exceptional compared with other relevant studies, including that of Coleoptera. The greatly increased divergence in the COI gene, in fact, was stemmed from a peculiar sequence of *Prionus insularis* belonging to Prioninae, divergence of which ranges from 31.2% to 39.3% from other species. We discussed possible reason of the divergence in this species. Due to the abnormality of COI gene divergence, decrease in phylogenetic signal was severe in COI nucleotide and, subsequently, the converted amino acid sequences, rendering us to put more confidence on the 16S rRNA gene data. Although the molecular phylogeny confidently supports the monophyletic origin of Lepturinae, the presence of discrepancy between molecular data and traditional taxonomic view also is a testable hypothesis. One such discrepancy includes taxonomic position of *Sophronica obrioides* and *Theophilea cylindricollis* belonging to Lamiinae.