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## The complete mitochondrial genome of the oriental mole cricket, *Gryllotalpa orientalis* (Orthoptera: Gryllotalpidae)

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The complete nucleotide sequences of the mitochondrial (mt) genome from the oriental mole cricket, *Gryllotalpa orientalis* (Orthoptera: Gryllotalpidae) was determined. The complete genome is 15,521-bp long and contains a typical gene complement, base composition, gene size, and codon usage found in metazoan mt genome. *G. orientalis* contains most common gene order and arrangement, found in several insect species including *Drosophila yakuba*, but differ from *Locusta migratoria*, another orthopteran species sequenced in their entire mt genome. Genes overlap 68 bp in 19 locations ranging in size 1~16 bp and leave intergenic spaces in 78 bp in 9 locations ranging in size 1~34 bp. The A+T-richness also is obvious in the *G. orientalis* mt genome as other insects, but slightly less than those of other insects in all genes. The initiation codon for *G. orientalis* COI gene appears to be ATG and its initiation context does not have the tetranucleotides, which has been postulated to act as an initiation codon for *L. migratoria* COI. The initiation codon for ND2 appears to be GTG. This codon is rare, but has been designated for an initiator of *Tricholepidion gertschi* ND2. All anticodons were identical to *D. yakuba*. The tRNA<sup>Ser</sup>(AGN) could not form stable stem-loop structure in the DHU arm as shown in many other insect tRNA<sup>Ser</sup>(AGN), although other tRNAs formed stable structures. Pairwise comparison of each concatenated tRNAs, rRNAs, protein-coding genes, and all DNAs of the *G. orientalis* mt genome to the corresponding, concatenated genes of other insects resulted in non-inclusive

relatedness among insect orders in many cases. Phylogenetic analysis using the concatenated amino acid sequences of the 13 protein-coding genes confirmed a monophyletic Insecta, but a monophyletic Pterygota was failed due to fluctuating position of singly included apterygotan *T. gertschi*. Furthermore, *L. migratoria* and *G. orientalis* belonging both to Orthoptera never clustered together as a monophyletic group. Except for these a monophyletic Endopterygota (Diptera + Lepidoptera + Coleoptera), a monophyletic Mecoptera (Diptera + Lepidoptera), a monophyletic Diptera, and a monophyletic Lepidoptera were well supported, suggesting that the complete insect mt genome sequence has a resolving power in the diversification events within Endopterygota, but not well reflects the earlier insect diversification event.