

Genomic Structure and Polymorphism of the A+T-rich Region of Mitochondrial DNA in the Oriental Mole Cricket (*Gryllotalpa orientalis*)

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The complete A+T-rich region of mitochondrial DNA (mtDNA) has been cloned and sequenced from 48 individuals of *G. orientalis* (Orthoptera: Ensifera) collected in five Korean localities. Thirty-six haplotypes ranged in size from 917 to 925 bp, sequence divergence from 0.2% to 14.1%, and A+T content from 74.5 to 76.3%. Structural analysis of the region in search of the conserved structural elements previously described in the caeliferan Orthoptera and the Diptera showed most elements were not conserved in the *G. orientalis* A+T-rich region. The most well conserved structural element in the *G. orientalis* A+T-rich region was a stretch of [TA(A)]_n sequence, which has been postulated to be involved in transcription or replication control. More than a dozen of sequence stretches in the A+T-rich region have the potential to form stem-and-loop structure, but the 3' flanking sequence "G(A)_nT", which is well conserved in a diverse organism including the caeliferan Orthoptera and the Diptera was not conserved in the *G. orientalis* A+T-rich region. Phylogeographic analysis of the *G. orientalis* haplotypes revealed the presence of two clearly differentiated mitochondrial clades in Korea, separated by 13.4% of a minimum uncorrected pairwise sequence divergence. This mtDNA polymorphism was explained in terms of the recent admixture of two long-term isolated populations of *G. orientalis* or, alternatively, by recent immigration of unknown, similar *Gryllotalpa* species to Korean Peninsula.