

Unusual mitochondrial DNA polymorphism of the oriental mole cricket, *Gryllotalpa orientalis* (Orthoptera: Gryllotalpidae) in Korea

Iksoo Kim, So young Cha, Mi Ae Kim and Jae Sam Hwang

Department of Agricultural Biology, The National Institute of Agricultural Science and Technology, Suwon 441-100, Korea

The mole cricket, *Gryllotalpa orientalis*, is an insect pest widely distributed in the world. Biological information on this species is very limited, and genetic aspect of the species/populations is nearly unavailable. Thus, we sequenced a portion of mitochondrial (mt) COI gene (405 bp) and A+T-rich region (~920 bp) to understand the magnitude and pattern of genetic diversity within species. Maximum parsimony (MP) analysis of the COI gene revealed the presence of two reciprocally monophyletic groups in this species (group A and group B) and consistent pattern was observed with A+T-rich region. Further, we sequenced a portion of mt 16S rRNA gene from each one individual from each group and incorporated these into three GenBank-registered homologous *Gryllotalpa* sequences. MP analysis showed a strong sister group relationship of group A to the GenBank-registered *G. orientalis*, excluding group B sequence. Taken these together, *G. orientalis* occurring in Korea, which is known to be a single species seems to contain unidentified another species immigrated from outside study area or be composed of two reciprocally monophyletic groups.