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**Molecular Cloning of the Sec61p  $\gamma$ -Subunit Homologue Gene from the Mole Cricket, *Gryllotalpa orientalis***

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The Sec61 trimeric complex ( $\alpha$ ,  $\beta$ , and  $\gamma$  subunits) is one of the Sec-complex responsible for posttranslational protein translocation across the membrane of the endoplasmic reticulum in diverse organisms. In this study, a cDNA encoding the Sec61p  $\gamma$ -subunit homologue was isolated from the cDNA library of the mole cricket, *Gryllotalpa orientalis*. Sequence analysis of a 442-bp cDNA clone showed it to contain an open reading frame of 68 amino acid residues consisted of 204-bp. The homologues of the gene were found in the GenBank database in a diver organism including insect, mammals, and fungi. The deduced amino acid sequence of Sec61  $\gamma$ -subunit homologue of the mole cricket showed the highest homology to the gene of the singly known insect, *Drosophila melanogaster* (93% identity), and the least homology to that of the baker's yeast, *Saccharomyces cerevisiae* (37.2%). Phylogenetic analysis also confirmed a close relationship between the insect Sec61  $\gamma$ -subunit homologues from *G. orientalis* and *D. melanogaster*. Hydrophathy analysis of the cricket mole including a few other organisms and published data suggest that the hydrophobic segment close to C-terminus is predicted to be putative membrane anchor. Alignment of the Sec61  $\gamma$ -subunit homologue with that of other organisms showed the presence of several conserved domains including the conserved proline at position 28.