B3

Molecular Cloning and Characterization of Cuticle Protein Genes from the Mulberry Longicorn Beetle, *Apriona germari*

Seong Ryul Kim¹, Hyung Joo Yoon², Nam Sook Park¹, Sang Mong Lee³, Jae Yu Moon⁴, Sook Jae Seo⁵, Byung Rae Jin¹ and Hung Dae Sohn¹

¹College of Natural Resources and Life Science, Dong-A University, Busan 604-714, Korea. ²Department of Sericulture and Entomology, National Institute of Agricultural Science and technology, Suwon 441-100, Korea. ³Department of Sericultural and Entomological Biology, Miryang National University, Miryang 627-130, Korea. ⁴College of Agriculture and life Science, Seoul National University, Suwon 441-744, Korea. ⁵Division of Life Science, Gyeongsang National University, Chinju 660-701, Korea

We have cloned three major larval cuticle protein genes (LCPs) designated as AgLCP9.2, AgLCP12.3 and AgLCP12.6 in the larval stage of the mulberry longicorn beetle, *Apriona germari*. The cDNA clones for these AgLCPs were sequenced and characterized. Sequence analysis of AgLCP9.2, AgLCP12.3 and AgLCP12.6 revealed an open reading frame of 103, 132 and 136 amino acid residues, respectively. The deduced protein sequences of AgLCP9.2, AgLCP12.3 and AgLCP12.6 are identical to *Bombyx mori* LCP18 (60%), *B. mori* LCP17 (32%) and *B. mori* LCP17 (46%), respectively. The deduce protein sequence alignment analysis of AgLCPs identified the conserved residues within the consensus sequence among the cuticle proteins. Phylogenetic analysis was performed with known insect larval cuticle protein genes. Northern blot analysis indicated that AgLCPs showed larval epidermis-specific expression pattern at the transcriptional level.