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Analysis of Expressed Transcripts generated from *Apriona germari* Hope (Coleoptera)

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Objectives

The *Coleoptera* is one of the most species-rich order of animals, adapted to most terrestrial and freshwater aquatic habitats. Among them, the mulberry longicorn beetle, *Apriona germari* Hope, is widely distributed in eastern Asia and became one of the major pests of mulberry tree in Korea. To obtain genetic information on the mulberry longicorn beetle, we have constructed cDNA library from the larvae whole-body. Here, we report *Apriona germari* ESTs profiles determined the 5' most end of 3072 clones.

Materials and Methods

• Animal: Apriona germari larvae

• Library construction: Uni-ZAP XR vector (Stratagene, USA)

• Plasmid isolation: MWG RoboPrep 2500 (Germany)

• Sequence: ABI PRISM 377 autosequencer (Perkin Elmer, USA)

• Database analysis : DNAstar

Result and Discussion

cDNA library of Apriona germari have been partially sequenced and functionally annotated searching the nucleotide and protein databases in the GenBank and other public sources using BLASTX. The average length of sequences was 457nt. We sequenced and analyzed 3072 ESTs from whole body of Apriona germari larvae and assembled the 2349 ESTs sequences into 1358 contigs, 321 of which contained two or more ESTs sequences and 1037 remained singletons. Overall, 866 contigs are found similar to existing sequences in GenBank and 492 are novel. Most of the best matches originated from insects. They are Drosophila melanogaster(39.6%) and Anopheles gambiae(15.1%). Also, these genes are categorized into 13 groups.

Average - length	457nt
Sequenced	3072
Identified (ESTs%)	2349
Different (Unigene%)	1358
Unknown	492

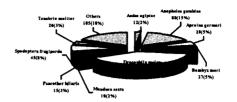


Table 1. Summary of *Apriona germari* EST clones lower taxo.

Fig 1. Percent of sequence with top hits in

Reference

Hyungjoo Yoon and Yongil Mah., 1999, Life cycle of the mulberry longicorn beetle *Apriona germari*Hope on an artificial diet, J. Asia-Pacific Entomol 2(2) 169-173.