

2-6. Analysis of expressed sequence tags from *Protaetia brevizarsis*(*Coleoptera*).

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The *coleoptera* is the most species-rich order of animals. Relatively little is known about *Coleoptera* genes and genome.

We describe here the construction and DNA sequencing of cDNA libraries from *Protaetia brevizarsis*, a fruit tree pest in Korea. We sequenced and analyzed 3072 ESTs from wholebody of *Protaetia brevizarsis* larvae. The average length of sequences was 513nt. Then we assembled the 2826 ESTs sequences into 1051 contigs, 236 of which contained two or more ESTs sequences and 816 remained singletons. Overall, 511(48.6%) contigs are found similar to existing sequences in GenBank and 540(51.4%) are novel. Most of the best matches originated from insects. They are *Drosophila melanogaster*(39.9%) and *Anopheles gambiae*(35.3%). These genes are categorized into 13 groups. Groups that expressed at high level are (1) cellular organization(41.1%) (2) unclassified protein(33.4%) (3) metabolism(17.1%) (4) transcription(11.4%) (5) protein synthesis(10.4%) (6) protein fate (9.3%) (7) cellular transport and transport mechanisms(8.6%) (8) cell rescue defense cell death and aging(5.9%) (9) cellular communication signal transduction(3.6%) (10) energy(3.2%) (11) regulation of interaction with cellular enviroment(1.9%) (12) classification not yet clear-cut(1.2%) (13) subcellular localisation(0.4%).