MOLECULAR APPROACH TO CONTROL SLUGS: TRANSCRIPTOME OF THE GRAY GARDEN SLUG

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The gray garden slug, \textit{Deroceras reticulatum} (Müller) (Gastropoda: Pulmonata), is one of the most common terrestrial molluscs native in Europe with global distribution including North America, causing serious damages in many vegetables and crops. Studies on \textit{D. reticulatum} have focused on its ecology, biology, pest status, and control methods using chemical molluscicides, cultural practices and natural enemies. However, less attention has been paid to its molecular biology due to lack of genetic information, which is crucial for the development of alternative pest management strategies such as RNAi-based control and for the molecular approaches.

Here we report the whole body transcriptome of \textit{D. reticulatum} which provide a rich molecular information on the terrestrial slug pest. Illumina high-throughput sequencing of the whole body transcriptome of \textit{D. reticulatum} generated about 5.9 billion raw paired-end reads. Reads were \textit{de novo} assembled by Trinity, resulting in 143,575 transcripts and further filtrated into 120,553 unigenes. Gene Ontology (GO) terms were assigned to 30,588 unigenes composed of biological process (36.9%), cellular component (30.2%) and molecular function (32.9%). Functional annotation of transcriptome by blastx found out 39,987 unigenes with blast hit and many genes were categorized into important functional groups, such as cytoskeleton (2,403), immune-related (1,438), detoxification (678), G-protein coupled receptors (358), ribosomal proteins (284), ion channels (279), neuropeptide (138), and RNAi machinery (36). Expression abundance measured by FPKM indicated that several genes related to slime production and muscle contraction are highly expressed.

The slug’s peculiar biology includes mucous slime production, strong and flexible muscle contraction, hermaphroditic reproduction, omnivorous herbivory, and so on. The rich transcriptome information will pave a molecular avenue on understanding biological functions of the slug and applying novel molecular approaches to control the slug pest (e.g. RNAi-based control).
Figure 1. Analysis of the *Deroceras reticulatum* transcriptome. (A) Size distribution of transcripts and unigenes after Trinity assembly. (B) Species distribution of the best BLASTx-hit of transcripts against the nr database in NCBI. (C) Portions of BLASTx hits (dark gray) and no-hits (light gray) and three major classes of Gene Ontology (GO). (D) Functional GO classification of the unigenes.