

Abstract

High Throughput Sequencing and Annotation of *Hellula undalis* (Fabr.) (Lepidoptera: Pyralidae)[†]

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Abstract: The cabbage webworm, *Hellula undalis* (Fabricius) (Lepidoptera: Pyralidae), is a significant pest of brassicas and other cruciferous plants in warm regions worldwide. Transcriptome analysis is valuable for investigation of molecular mechanisms underlying the insect development and reproduction. *De novo* assembly is particularly useful for acquiring complete transcriptome information of insect species when there is no reference genome available. In case of *Hellula undalis*, only 17 nucleotide records are currently available throughout NCBI nucleotide database. Genes associated with metabolic processes, general development, reproduction, defense and functional genomics were not previously predicted in the *Hellula undalis* at the genomic level. To address this issue, we constructed *Hellula undalis* transcriptome using Illumina NovaSeq6000 technology. Approximately 48 million 125 bp paired-end reads were obtained from sequencing. A total of 30,451 contigs were generated by *de novo* assembly of sample and were compared with the sequences in the NCBI non-redundant protein database (Nr). In total, 71% of contigs were matched to known proteins in public databases including Nr, Gene Ontology (GO), and Cluster Orthologous Gene Database (COG), and then, contigs were mapped to 123 via functional annotation against the Kyoto Encyclopedia of Genes and Genomes pathway database (KEGG). In addition, we compared the ortholog gene family of the *Hellula undalis* transcriptome to *Spodoptera frugiperda*, *spodoptera litura* and *spodoptera littoralis* and found that 2,749 orthologous gene families are specific to *Hellula undalis*. This study is the first transcriptome data for *Hellula undalis*. Additionally, it serves as a valuable resource for identifying target genes and developing effective and environmentally friendly strategies for pest control.

Keywords: *Hellula undalis*; Transcriptome; Annotation; Orthologous gene

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