HIGH-THROUGHPUT SEQUENCING, ASSEMBLY AND ANALYSIS OF WHOLE-BODY TRANSCRIPTOMES FOR ADULT AND IMMATURE TOBACCO THRIPS

Sally Taylor
Jaap van Kretschmar
Manal Farouk
George G. Kennedy
Clyde E. Sorenson
Jack S. Bacheler
R. Michael Roe
North Carolina State University, Department of Entomology
Raleigh, North Carolina

Abstract

Separate whole-body RNA extractions of adult and larval tobacco thrips, *Frankliniella fusca* (Hinds), were used to construct cDNA libraries for high-throughput sequencing on the Illumina® Genome Analyzer IIx sequencing platform. Together, adults and larval thrips of the 1st and 2nd instar comprise the actively-feeding life stages of this species. The sequence data generated were comprised of a total of 131 million reads for the immature library and a total of 105 million reads for the adult library. The sequence reads for each life stage were then assembled *de novo* using Trinity® software into128,027 contiguous sequences (contigs) for the immature sample and 114,980 contigs for the adult sample. The assembled contigs were each batch BLASTed, mapped and annotated against the NCBI non-redundant database using Blast2GO® software and an E-value cut-off set at E-3 (10^{-3}). The resulting contigs with BLAST hits numbered at 40,330 for immature thrips and 36,052 for adult thrips. Gene ontology assignments of the top BLAST hits were compared between the life stages and used to identify potential targets for gene-silencing techniques that are present throughout the crop-damaging life stages of this insect. The possible targets that were expressed in both immature and adult tobacco thrips included putative transcripts that may regulate key hormonal pathways and those that are currently targeted by commercial insecticides. Furthermore, transcripts responsible for proteins that potentially provide insecticide resistance were found, including xenobiotic and steroid metabolizing enzymes. The prospects for the exploration of thrips control using RNAi approaches is discussed, in addition to a comparison of gene expression levels across the life cycle of this species.