HIGH-THROUGHPUT SEQUENCING GIVES INSIGHT INTO THE BIOLOGY AND POTENTIAL FOR GENETIC CONTROL OF TOBACCO THRIPS

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Abstract

The tobacco thrips, *Frankliniella fusca*, is a major economic pest of cotton in the Southeastern United States. There are increasingly limited choices for the management of this pest. The identification of genes essential to the growth, development and homeostasis of this insect provide potential targets for RNAi transgene therapies. We sequenced whole-body transcriptomes of larval and adult tobacco thrips using Illumina® high-throughput technology. The resulting 236 million 100 base pair reads were assembled, batch BLASTed, mapped, and annotated into over 25 thousand contiguous sequences per life stage, to be further analyzed to identify function. To illustrate the depth of contig information in our global, putative functional analysis, messages are characterized which are involved in hormonal regulation of development, steps in juvenile hormone (JH) biosynthesis and degradation, ecdysteroid metabolism, known commercial insecticide targets, and enzymes involved in insecticide detoxification. We have identified putative proteins associated with reproductive pathways in larval thrips, illustrating the need for species-specific and life stage-specific sequencing across insect taxa. Our data provide a critical first step in understanding the unique physiology, and exploring the future molecular control, of this species.