

Comparative midgut transcriptome analysis of *Helicoverpa armigera* feeding on natural conditions

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Abstract

The cultivation of different annual crops may provide ideal conditions for feeding and survival of lepidopteran pests presenting generalist feeding habits. With occurrence in Brazil since 2013, one of the most important species from Noctuidae family is *Helicoverpa armigera*. It has a high capacity to tolerate many insecticides. Both private companies and public policy makers seeks to develop an integrated pest management approach to reduce the usage of pesticides and the emergence of populations. In addition, the main enzymes responsible for the digestive process in insects are peptidases involved in the initial digestion of plant proteins. Thus, to develop efficient ways to control pests, it is mandatory first to know which genes are involved in the digestive and detoxifying processes. *Helicoverpa armigera* individuals feeding on natural conditions were collected in order to characterize differentially expressed transcripts associated with soybean, cotton and bean diets. Total RNA from midgut was extracted and cDNA libraries sequenced (paired-end) using an Illumina HiSeq 2500. A de novo assembly of the short reads using both Mira and Trinity resulted in 145,284 transcripts (1000 bp N50) and a length of 98.63 Mb. We identified 31 transcripts differentially expressed between dietary conditions. The largest number of differentially expressed transcripts was obtained in the cotton versus soybean contrast, where 26 transcripts were found up-regulated in cotton diet. From these, 11 transcripts were also found to be up-regulated in cotton diet relative to bean. Functional analysis showed that these transcripts are involved in biological processes like proteolysis, electron transport chain and lipid catabolic process. This is the first study of *H. armigera* transcriptome feeding under natural conditions and assembled transcripts are a powerful resource for future research promoting an improved understanding of the gene regulation of digestive peptidases.

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Link to Video: