

Comparative analysis of genetic networks of *Anticarsia gemmatalis* Hübner, 1818 (Lepidoptera: Erebidae) obtained from transcriptomes of strains resistant and susceptible to the protein Cry of *Bacillus thuringiensis*

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Abstract

The larvae of the pest *Anticarsia gemmatalis* Hübner, 1818 (Lepidoptera: Erebidae) are capable of generating serious economic losses in the soybean industry and, although efficient methods are known to combat them, such as chemicals, less aggressive techniques are chosen to human health. Biological technology that uses organisms or by-products of biocontrollers, such as Cry toxins from *Bacillus thuringiensis*, is capable of acting efficiently and specifically on the insect pest without generating serious environmental impacts. However, cases of resistance of *A. gemmatalis* to Cry toxin have been reported. Therefore, the objective of this project is to perform a comparative analysis of genetic networks of transcripts of *A. gemmatalis* obtained from a resistant colony and another sensitive to the Cry protein of *B. thuringiensis* subsp. *Kurstaki* Lineage HD-73. The project is based on the data set of the work of Forim et al., 2017, which reports information on transcriptomes of *A. gemmatalis* resistant and susceptible to this toxin. Each treatment and control will be carried out in triplicate for resistant and susceptible, resulting in 12 experimental units. Our consensus software are adopted to analyze differentially expressed genes. The produced data set (active and inhibited genes) are performed adopting the DimReduction software to infer the genetic networks. Subsequently, the metabolic pathways corresponding to the target genes are investigated using the computational tools of the KEGG database. As a result, some relevant genes in the process of resistance and susceptibility to Cry protein are identified, as well as the metabolic pathways in which they participate.

Funding:

Link to Video: