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Inside the gut: Revelations of metatranscriptomic and transcriptomic analyses of *Spodoptera frugiperda* larvae from an organic maize plantation at 2283 meters above sea level (Tafí del Valle, Tucumán)

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Spodoptera frugiperda is a noctuid moth that devastates various crops, including corn, and is found in most of the American continent. Transgenic crops that produce insecticidal proteins from *Bacillus thuringiensis* are currently the most successful biotechnological pest management application, but *S. frugiperda* has developed field-evolved resistance. In this regard, insect gut microbiota conform a complex community that establishes symbiotic relationships with its host, contributing to its viability. For this reason, metatranscriptomic and transcriptomic analyses of insect guts in their natural environment are invaluable to better comprehend their biology and to identify genes as targets for pest control. We previously captured *S. frugiperda* specimens from different environments, altitudes and food sources in the province of Tucumán (Argentina). For all samples, total RNA extracted from fifth instar larval guts was submitted to a one-step reverse transcription and PCR sequence independent amplification procedure, and then pyrosequenced. In this study we analysed one of these samples, namely, larvae that were captured in an organic maize field in Tafí del Valle (26°55'40.75''S, 65°45'19.90''W; Tucumán province) at 2283 meters above sea level. Sequence reads were trimmed and assembled. Homology searches were performed against various NCBI databases. Taxonomic and functional contents were analysed with MEGAN. The metatranscriptome, in which we identified sequences from archaea, bacteria, fungi, nematodes and plants, revealed potential biocontrol candidates for this pest, and others related with host metabolism and digestion. Furthermore, the host transcriptome showed that most transcripts were associated with the digestive tract structure and development, among others. Some of these genes could be possible targets for pest control *via* RNA interference (RNAi). In summary, this study has shown the potential effects of this particular food source (*i.e.*, organic maize) and of the environmental conditions (altitude, among others), on the expression profile of *S. frugiperda* larval guts, their associated metatranscriptome, and putative interactions between them. Future studies will test the potential biocontrol candidates that we identified.



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