Serine Proteases in the Spodoptera Frugiperda Midgut High-Throughput Transcriptome

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The noctuidae moth Spodoptera frugiperda (J.E. Smith, Lepidoptera) is a generalist insect, considered a significant agriculture pest in the western hemisphere. The herbivore insects, using their long evolutionary history, have positively selected different mechanisms to overcome protective obstacles produced by plants. One is the up-regulation of the serine proteases when these moths feed on plants that produce protease inhibitors (PIs). The present work elaborates a database with serine proteases sequences of S. frugiperda. Therefore, a midgut transcriptome from S. frugiperda fed with a dietary enriched with soybean PI was proposed using Illumina/Solexa platform, assembled and evaluated using two different approaches: the proprietary software CLCBIO Workbench and the open source VELVET. Sequences were automatic annotated using Blast2GO. Assembly was enriched using reads data from Spodobase and merged with Illumina data by CAP3 software. The sequences were aligned to bovine chymotrypsinogen using the software Muscle, and analyzed using InterProScan for a possible classification in chymotrypsin and trypsin subfamily. We also propose a phylogenetic clustering of all sequences using Maximum likelihood. In total, 41 sequences with all catalytic residues (His, Asp, Ser) were found. The differentiation among trypsin and chymotrypsin was not possible using only the primary sequence or evolutionary common ancestry, due to difficult to find patterns in the primary sequence and the phylogenetic analyses did not provide monophyletic.

Word Keys: Spodoptera frugiperda, serine protease.
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