Proteomics-based Identification of Hemolymph Proteins from *Spodoptera frugiperda* Larvae (Lep., Noctuidae)

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INTRODUCTION: Insect pests cause economic losses in worldwide crops. Knowledge of insect physiology is of great importance to the development of new pest control technologies. It contribute to our understanding concerning of insect resistance and environmental adaptation mechanisms developed in the field. **OBJECTIVE:** To carry out phenotypic analyses of the constitutive expression of hemolymph proteins from *S. frugiperda* larvae by mass spectrometry. **MATERIAL AND METHODS:** Three biological replicates of the hemolymph samples collected in different periods from 5th-instar *S. frugiperda* larvae. Following, trypsin-digested sample were prepared for LC–MS/MS onto Sep Pak C-18 desalting column. Tryptic peptides were separated by liquid chromatography (EASY-nLC II) coupled to a mass spectrometer (LTQ-Orbitrap Velos). Raw MS/MS data were analyzed using MASCOT software, against NCBInr database containing 8,196 protein sequences. Variable modifications contained oxidation of M and phosphorylation of S, T, and Y. (CAM)-modified cysteine was set as fixed modification. The precursor and fragment ions mass tolerance were 10 ppm and 0.5 Da, respectively. **RESULTS AND DISCUSSION**: From 140 proteins already identified, they were involved in a variety of cellular functions, including metabolism, development, defense, nutrient transport and reserve. However, it is known that proteins present in the hemolymph vary in amount according the larval development. Gene ontology analysis showed that 25.8% of these proteins have metabolic process activities and 11.6% were involved with catalytic activity. Pathway analysis revealed that 24 proteins with common targets were involved in many biological processes such as extracellular region, response to stimulus, metabolic and cellular process. These results suggested that a complex biological network is coordinating the multiple functions of hemolymph. **CONCLUSION:** This approach would help in futures applied studies aiming to improve better understanding between genotypic information and the phenotypic expression of the fall armyworm.

Keywords: Lepidoptera, Hemolymph, Phenotype, Proteomics.
Supported by: FUNDECT and CNPq