

Beta-Fructosidases Present in the Midgut and Hemolymph From *Lonomia obliqua* (Lepidoptera)

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Introduction: Although the most studied aspect of *Lonomia obliqua* larvae is their involvement in human coagulation accidents, other aspects of their physiology could be explored. Previous data indicated the activity of two sucrose hydrolases in the hemolymph and midgut from *L. obliqua*, which were identified as β -fructosidases with distinct kinetic properties. **Objectives:** Identify the transcripts of β fru in Illumina sequencing of cDNA from *Lonomia obliqua* and correlate these with proteomic data from β fru enriched activity fractions. **Material and Methods:** *L. obliqua* larvae (6th instar) whole body cDNA was isolated and used to HiSeq analysis while the cDNA from hemolymph (HE), Malpighi tubule (MT), midgut epithelium (ME) and carcass (CA) were used to RT-PCR analysis. Proteomic nano LC-MS/MS analysis was done using the β fru enriched active chromatographic fractions. Transcriptome and proteomic data were used to identify β fru. **Results and Discussion:** The analysis of the transcriptome data indicated the presence of two complete transcripts of β fru (β fru1 and β fru2). Chromatographic fractions from HE and ME enriched on β fru activity submitted to proteomic analysis allowed the identification of 9 peptides from β fru1 and 1 from β fru2, in both samples, corroborating the transcriptome data. Preliminary RT-PCR data showed that β fru are distinctly expressed in *Lonomia* tissues, and are mainly expressed in ME and MT. **Conclusions:** This study expands the knowledge of β fru in caterpillars' tissues.

Keywords: Beta-fructosidases, *Lonomia obliqua*, hemolymph and midgut

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