

SEQUENCE ANALYSIS AND STRUCTURAL PREDICTION OF THE PROTEIN HEMOLIN FROM *Lonomia obliqua*

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In lepidoptera, an adhesion molecule named hemolin was associated with neurite outgrowth during the metamorphosis process. Recently, it was described some molecules from bristles or haemolymph of *L. obliqua* able to induce proliferative and antiapoptotic effects on different cellular cultures. The aim of this work is to obtain the complete sequence of hemolin's transcripts expressed into a cDNA library constructed previously from bristles and to analyze the three-dimensional model. Complete nucleotide sequence was obtained by primer walking. Based on amino acid coding region, a molecular model was built using Modeller 8v1 using *Hyalophora cecropia* Hemolin (HcHemolin) as template. Hemolins represent 21 clones grouped into seven clusters. The complete nucleotide sequence of hemolins (1239 bp) include a signal peptide and the mature protein with 18 and 395 amino acid residues, respectively. Hemolins revealed variable percentages of identity with cell adhesion molecules involved in development of the nervous system: HcHemolin (76%), Neuroglian (34%) from *Drosophila melanogaster* and human L1-NCAM (26%). Hemolins are composed mainly by beta-strands that form four Ig domains that, in turn, are arranged into an overall globular shape. Several hemolin motifs are conserved. The domain 3 has a motif associated with cell adhesion giving rice intracellular signals. The characteristic of hemolins (present in bristles and haemolymph) could explain the effect observed in different cellular cultures.

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