

Computer-aided protocol to revisit the cDNA library from *Lonomia obliqua* caterpillar: Identification of structural motifs related to inflammatory processes

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Abstract

The skin contact with the bristles of the *Lonomia obliqua* caterpillar leads to poisoning, which is characterized by consumption coagulopathy and secondary fibrinolysis. These events may progress to hemorrhagic syndrome and, consequently, to death. It is well-known that the signaling pathways involved in inflammation and in the coagulation cascade are interrelated. Therefore, we can study such signaling mechanisms in diseases related to inflammatory processes. Osteoarthritis (OA), for instance, is one of these diseases, and is characterized by cartilage degeneration, accompanied by inflammation of the joints, pain and loss of physical functions. The current treatments for OA are limited and involve either pain relief, or total replacement of the joints, in the late stages of the disease. In this regard, the identification of important new molecular targets in the signaling pathways involved in inflammatory processes would be crucial for the development of new and more effective drug candidates to treat OA. The *L. obliqua* cDNA library analysis, using bioinformatics and computer-aided approaches, has provided the identification of structural motifs related to functions involved in inflammatory processes. The re-visitation protocol has allowed the functional annotation and reclassification of 1,503 transcripts from the cDNA library of *L. obliqua*. Twenty-nine predicted protein sequences related to inflammatory functions were identified. The findings allow us to propose five novel peptide constructions (new chemical entities, NCE) to be further synthesized and assayed in human chondrocyte models (experimental validation). Also, the novel peptide constructions will be used as molecular tools for the identification of new molecular targets related to inflammatory processes.

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