SERINE AND CYSTEINE PEPTIDASES IN INSECTS: STRUCTURE AND FUNCTIONS

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Insects are the most numerous class of animals including more than 1 million species. The major interface of insects with nature is their digestive system. This system is very variable and its proteolytic component is based mainly on serine peptidases from the S1 chymotrypsin family, while several diverse groups of insects rely also on cysteine peptidases from the C1 papain family. We performed a detailed analysis of composition of cysteine peptidases in the genomes of 12 insects from different orders in frame of global i5K project (5,000 Insect and Other Arthropod Genome Initiative). This research revealed new types of cysteine peptidases from C1 family, and allowed us to predict participation of cysteine peptidases in digestion of insects lacking biochemical data on their digestive system. The focus group of our research is the beetle family Tenebrionidae, including the biochemical model *Tenebrio molitor* and the genetic model *Tribolium castaneum*. These stored product pests rely on serine and cysteine digestive peptidases. We studied biochemical characteristics of tenebrionid major serine and cysteine digestive peptidases as well as performed detailed bioinformatics study of structure and functions of peptidases in larval gut transcriptomes obtained by high throughput sequencing. The exact functions of peptidases were also studied using expression patterns of peptidase genes across the beetles’ life cycle, and studying changes in the expression in response to intoxication of *Tenebrio molitor* larvae with Cry3Aa toxin of *Bacillus thuringiensis*.

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