ABSTRACT

The mulberry silkworm, *Bombyx mori*, is a domesticated insect bred by humans for about five thousand years due to its ability to produce natural silk fibers. Nowadays, this insect is also often used for the production of recombinant eukaryotic proteins or as a model organism for pest control studies. The life cycle of the mulberry silkworm is well described, its genome was sequenced in 2004, but the number of its proteins which were structurally characterized is very low. For instance, there are approximately 500 structures of fruit fly proteins deposited in the PDB, whereas in the case of mulberry silkworm this number is 10 times lower, showing that structural proteomics of *B. mori* is a vastly uncharted territory.

The silkworm life cycle can be divided into three main stages: larval, pupal and adult. Protein expression is at a very high level during the fifth larval instar - many important proteins are then secreted to hemolymph which is an analog of blood. Among the hemolymph proteins two major groups can be distinguished: high molecular weight storage proteins (hexamerins of a molecular weight of about 500 kDa) and 30-kDa lipoproteins (LPs).

The main goal of this project was the determination of crystal structures of major hemolymph proteins, followed by detailed structural analysis.

This dissertation describes the complete methodological path of the studies on major hemolymph proteins: starting from the isolation and purification procedure of the most abundant proteins; through protein crystallization; X-ray diffraction data collection; structure solution, refinement and validation; protein identification, mainly based on the electron density maps supported by other methods (Edman degradation, mass spectrometry); to the final structural analysis of the obtained structures. Six crystal structures have been determined, analyzed and described, three of Bmlp7, two of Bmlp3 (both, Bmlp7 and Bmlp3, belong to 30-kDa LPs) and the structure of a hexameric complex of two storage proteins, SP2 and SP3.