

ANALYSIS OF THE SELECTED GLYCOSYLTRANSFERASES IN THE TRANSCRIPTOME OF THE TICK IXODES RICINUS

Věchtová Pavla^{a,b}, Štěrbá Ján^{a,b}, Erhart Jan^b, Čegan Radim^c, Beneš Vladimír^d, Grubhoffer Libor^{a,b}

^aFaculty of Science, University of South Bohemia, České Budějovice, Czech Republic; ^bInstitute of Parasitology, Biology Centre of the Academy of Sciences of the Czech Republic, České Budějovice, Czech Republic; ^cFaculty of Science, Masaryk University, Brno, Czech Republic, ^dGenomics Core Facility, EMBL Heidelberg, Germany

E-mail: liborex@paru.cas.cz

Glycosylation is a process of glycan attachment to proteins which further extends or modulates the function of the glycoproteins in the cell. Glycans render the cell many specific functions, amongst which the most pronounced is the participation in cell interactions, which not only covers signalling among the cells of the same organisms but also involves the interactions of unicellular invaders with the host organism.

Studying glycans and the process of glycosylation as a potential mediator of bacterial or viral pathogenesis thus offers promising object for infection treatment and vaccine development.

Our study focuses on the analysis of transcriptome of castor bean tick *Ixodes ricinus*. The differential expression of selected glycosyltransferases has been investigated in fed and unfed life stages of *I. ricinus* in order to determine their possible role in tick feeding and development. A special attention was given to fucosyltransferases which previously proved important to the process of pathogen transmission through the tick body. Additionally, the expression of sialyltransferases was also examined as the presence of sialylation in adult ticks was previously disproven and the origin of sialic acid in tick glycans was thus assigned exclusively to host blood. Finally, the expression of the two highly conserved oligosaccharyltransferase isoforms (STT3) was studied due to their role in the process of *N*-glycan attachment to glycoproteins during protein translation.

The analysis of transcriptomic data suggests that the expression of both STT3 isoforms is rather similar in all life stages, which is explained by the importance of the enzyme for the entire process of *N*-glycosylation. Similarly, the studied fucosyltransferases showed also a steady expression level throughout the tick life-stages.

Conversely, the expression of sialyltransferase proved rather different among the tick life-stages. In particular, its expression was restricted to early stages of tick development and rather in low amounts. Similar observations were reported in the model invertebrate *D. melanogaster*, where the pathway for sialylation was only activated to a limited extent during short period of embryogenesis, and the brain formation. This project was funded by the project Postdok_BIOGLOBE

(CZ.1.07/2.3.00/30.0032) co-financed by the European Social Fund and the state budget of the Czech Republic and by the Grant Agency of the University of South Bohemia [GAJU 04-155/2013/P].