

MAPPING OF HEMOGLOBIN PROTEOLYSIS IN THE HARD TICK IXODES RICINUS

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Introduction and objectives: Hemoglobin is the primary energy source for ticks, however, its digestion is poorly understood at the molecular level. We analyzed the hemoglobin proteolysis in the hard tick *Ixodes ricinus*, a vector of Lyme disease and tick-borne encephalitis. **Results and conclusions:** Distribution of peptidases in the tick gut homogenate was determined with the help of two approaches: activity profiling with specific substrates and inhibitors, and imaging of proteases using labeling with selective active site probes. The identified endo- and exopeptidases include (i) aspartic peptidase cathepsin D, and (ii) cysteine peptidases: asparaginyl endopeptidase (legumain), papain-type peptidases cathepsin B and L, and dipeptidyl peptidase I (cathepsin C). The classification of these peptidases was corroborated by determination of their cDNA sequences from the gut cDNA library. The degradation pathway of the hemoglobin substrate was examined in vitro with authentic cocktail of tick gut proteases with an acidic pH optimum. Analysis of the contribution of particular proteases demonstrated that hemoglobinolysis in the ticks is predominated by cathepsin B and D acting in synergy. **Acknowledgements:** GACR 206/06/0865; projects Z60220518 and Z40550506. **Key Words:** hemoglobin, peptidase, tick.