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Dynamics of digestive proteolytic system during blood feeding of the hard tick *Ixodes ricinus*

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Abstract

Background: Ticks are vectors of a wide variety of pathogens causing severe diseases in humans and domestic animals. Intestinal digestion of the host blood is an essential process of tick physiology and also a limiting factor for pathogen transmission since the tick gut represents the primary site for pathogen infection and proliferation. Using the model tick *Ixodes ricinus*, the European Lyme disease vector, we have previously demonstrated by genetic and biochemical analyses that host blood is degraded in the tick gut by a network of acidic peptidases of the aspartic and cysteine classes.

Results: This study reveals the digestive machinery of the *I. ricinus* during the course of blood-feeding on the host. The dynamic profiling of concentrations, activities and mRNA expressions of the major digestive enzymes demonstrates that the *de novo* synthesis of peptidases triggers the dramatic increase of the hemoglobinolytic activity along the feeding period. Overall hemoglobinolysis, as well as the activity of digestive peptidases are negligible at the early stage of feeding, but increase dramatically towards the end of the slow feeding period, reaching maxima in fully fed ticks. This finding contradicts the established opinion that blood digestion is reduced at the end of engorgement. Furthermore, we show that the digestive proteolysis is localized intracellularly throughout the whole duration of feeding.

Conclusions: Results suggest that the egressing proteolytic system in the early stage of feeding and digestion is a potential target for efficient impairment, most likely by blocking its components via antibodies present in the host blood. Therefore, digestive enzymes are promising candidates for development of novel 'anti-tick' vaccines capable of tick control and even transmission of tick-borne pathogens.