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Pathways of Insect Protein Digestion: Triatominae (Kissing Bugs)

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Editorial

The majority of insects use serine proteinases like trypsin and chymotrypsin as main enzymes to digest their food [1]. These types of peptidases develop their maximum activity under alkaline to neutral pH conditions [2]. In some insect groups the intestinal lumen is acidic and the digestion switched to cysteine-like proteinases such as cathepsin D or L [3,4]. Some Coleoptera groups (e.g. Bruchidae, Tenebrionidae) developed a digestive system based on such proteinases [2,5]. But the major group using acid proteinases are the Hemiptera. This taxon uses cysteine proteinases because ancestral groups were using plant seeds containing serine proteinases inhibitors as a food source and therefore had to evolve their digestive system [6,7]. The conquest of this food source was a challenge for the digestive system [8] but it certainly contributed to the success of this insect group opening up new niches.

One of the best analyzed hemipteran groups considering their digestion is the Triatominae (Heteroptera, Reduviidae) subfamily. Many species of this group – especially from the genera *Triatoma*, *Rhodnius* and *Panstrongylus* [9] – are medically important because they are able to transmit *Trypanosoma cruzi* (Kinetoplastida, Trypanosomatidae), the causative agent of Chagas disease [10]. In contrast to mosquitoes which develop from egg to adult in few weeks and frequently show low rates of parasitic infection, some long-lived triatomine species needs several months to complete their life cycle [1]. Besides this, kissing bugs takes huge amounts of blood from their vertebrate host at each nymph stage and, consequently usually show higher infection rates (up to about 80%) [1,11-15]. In this insect group several digestive enzymes and their respective genes were identified and characterized. In the beginning of the 1980s activities of cathepsin B and D, aminopeptidase and carboxypeptidase have been shown [16,17]. Later, when the appropriate molecular biology methods were available, different isoforms of genes from different triatomine species have been identified encoding cathepsin B, L and D and serine carboxypeptidase [18-22]. At the same time Borges et al. [23] have demonstrated a significant increase of cathepsin D activity in *Rhodnius prolixus* infected with *T. cruzi.*

However, despite the numerous studies concerning the Triatominae, many questions about their digestive system and its interactions with the parasite are still unanswered. For example, it is quite possible that there are further types of luminal digestive enzymes waiting to be discovered in triatomines. A recent transcriptome analysis of the *R. prolixus* intestine has revealed many genes related to digestive physiology including digestive enzymes lacking some amino acid residues important for enzymatic activity [24]. Furthermore, it would be very important to know whether or not microbiota plays a role in the digestion of triatomines and how strong the influence of *T. cruzi* on the digestive system might be. It would also be interesting to know what modifications in the structure of proteinases were necessary when reduviids changed to hematophagy. Cathepsin B possesses both exo- and endopeptidase activity and its main functions in the triatomine digestion is yet uncertain. The relationship of luminal and lysosomal cathepsins is still an important matter to be clarified. Answering these questions could not only shed new light on the physiology and biochemistry of Triatominae but also opening up new approaches for vector control. An answer to these questions might also answer basic questions of evolution and development of blood-sucking in insects in general.

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