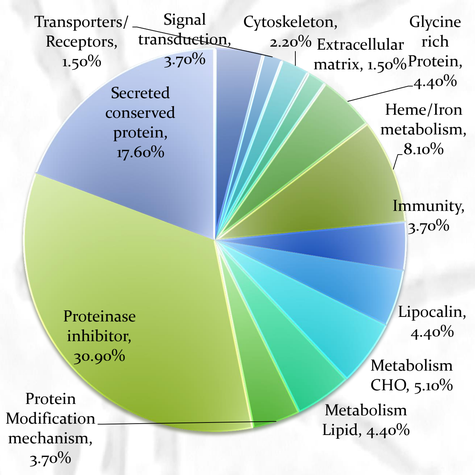
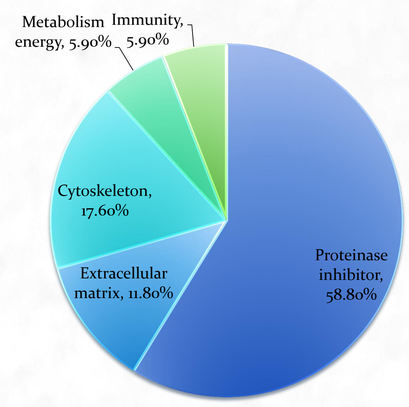
Proteomic characterization of *Haemaphysalis longicornis* saliva and determination of saliva-host interaction during blood-sucking periods

- **Myungjo You*, Mohammad Saiful Islam, Md. Khalesur Rahman, ItabajaraDaSilvaVazJr.**

INTRODUCTION

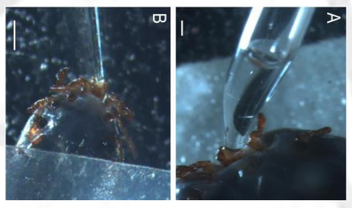
The hard tick *Haemaphysalis longicornis* is a medically and veterinary important vector of many tick-borne disease (TBD). During the feeding process, infected ticks may transmit TBD-causing pathogens.Tick saliva ha s been shown to play a role in pathogen transmission . Therefore, the identification and characterization of nov el *H. longicornis* saliva proteins could point to candidates for the development of anti-tick and transmission-bl ocking vaccines and of new pharmacological active molecules for medical application. *H. longicornis* tick sali va proteome has not been the object of any analysis. The objectives of this study were to identify secreted prot eins in the saliva of fully engorged nymphs (nymphs) and fully engorged adult females (adults) of *H. longicor nis* ticks, comparing the protein profile of these developmental tick stages to evaluate the variation in tick saliv a during feeding of different life stages. This affords to identify tick saliva proteins shared by the two develop mental stages. Such proteins may play an important role in the success of both developmental stages in their fe eding cycle. The novel catalog of tick saliva proteins identified in this study provides a deeper understanding t o the biology of *H. longicornis*.



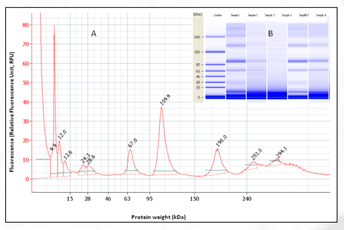


MATERIALS AND METHODS

Tick saliva collection



On chip electrophoresis

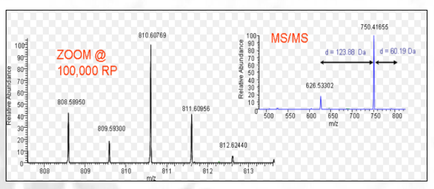


Protein digestion & sample preparation

Precolumns & analytical columns

LC MS/MS





Data analysis

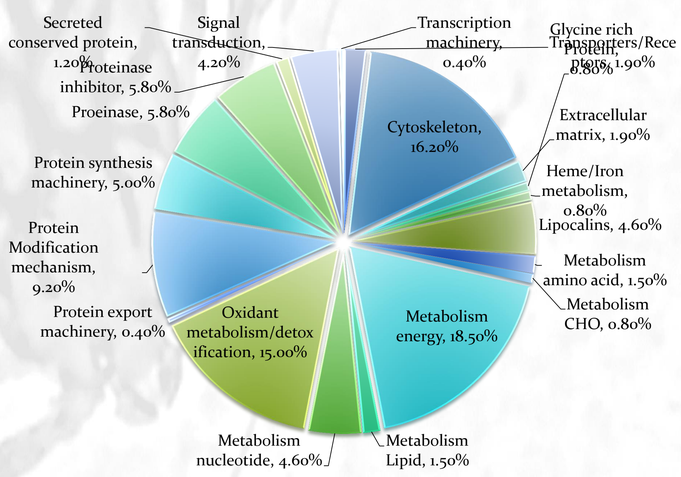
Functional annotation & classification of proteins

RESULTS

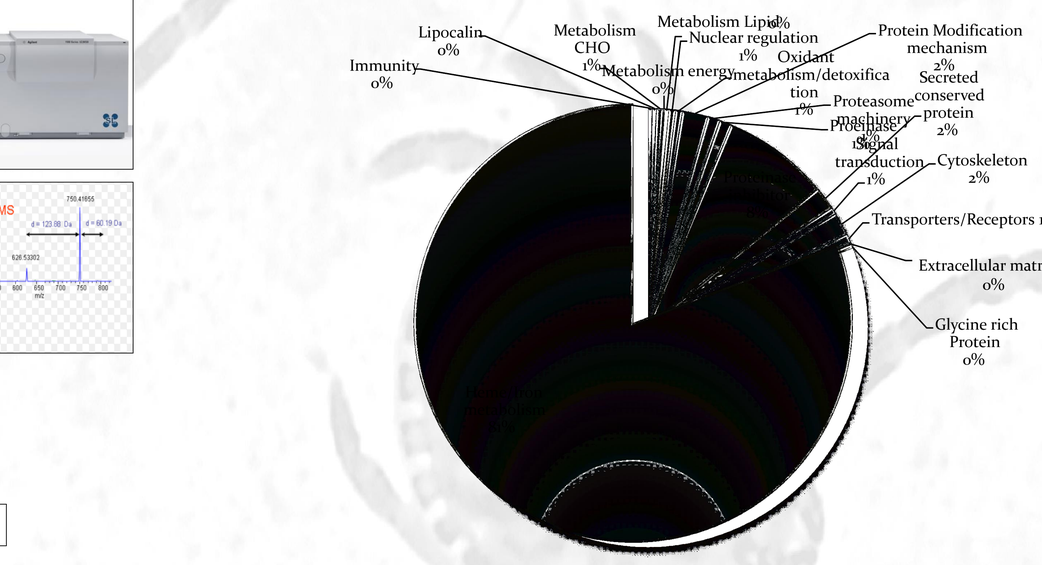
Identified protein groups

Group	Example
1. Heme/iron metabolism-related	Hemelipoproteins ,ferritin, serotransferrin, hemopexin
2.Oxidation/detoxificati on functions	Glutathione S-transferase, aldehyde dehydrogenase, glutathione peroxidase, and catalase
3. Enzymes	Serine proteinases, cysteine proteinases, metalloexopeptidases, carboxypeptidases, and aspartic proteases
4. Proteinase inhibitors	Serpin, cystatin, alpha-2-macroglobulin, trypsin inhibitor-like (TIL), and Kunitz families
5. Tick-specific protein	Lipocalin (histamine-binding proteins), glycine-rich proteins, and the group of secreted conserved proteins
6. Cytoskeletal functions	actin-depolymerizing factor, myosin tail
7. Protein modification	lysosomal & prostatic acid phosphatase
8. Signal transduction	TGF-beta-induced protein ig-h3, cyclophilin 1
9. Transporters and receptors	Apolipophorin, glutamate receptor 1-like
10. Metabolism	Phosphoserine aminotransferase (amino acid) ATP synthase subunit beta (energy) Transketolase (carbohydrate) Farnesoic acid o-methyltransferase (lipid) GDP dissociation inhibitor (Nucleotide)

Tick Nymph protein (Unique30/135)

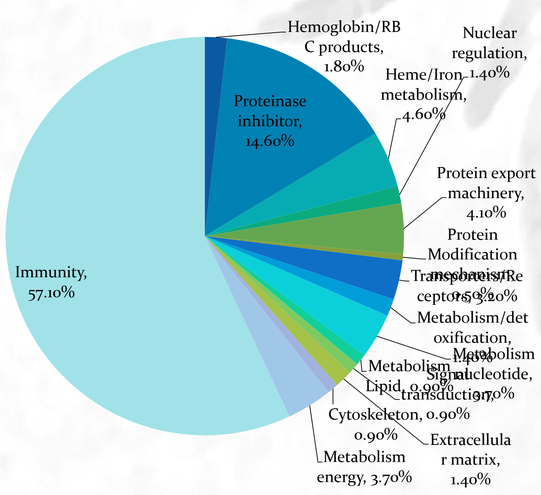


Tick Adult (Unique74/135)

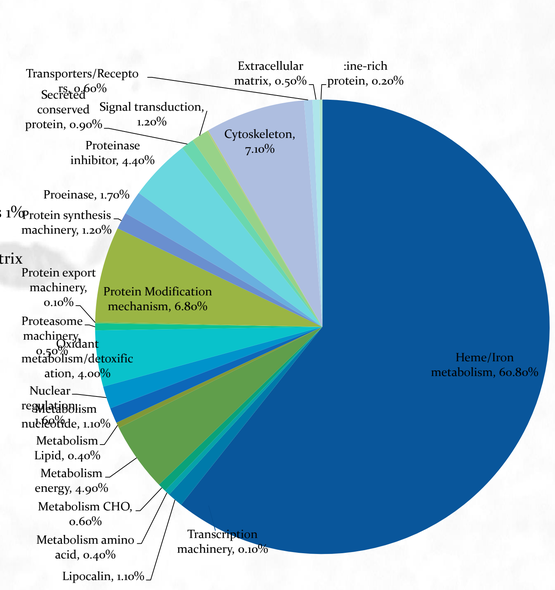


Tick nymph(total 61/135)

Host Nymph (unique13/100)



Host Adult (unique48/100)



Tick Adult (total 105/135)

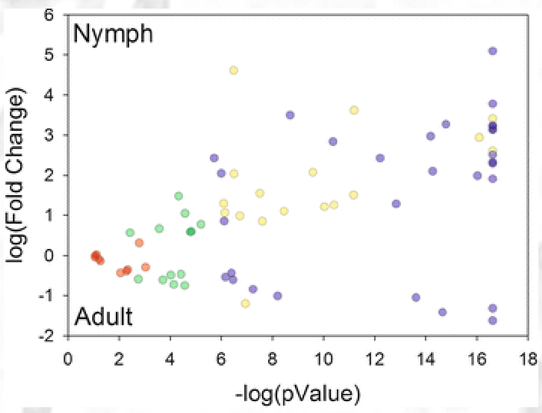


Figure shows volcano plot changes in expression levels were observed for 11 of the 31 identified tick proteins detected in both stages.

CONCLUSIONS

This study describes the first proteome analysis of saliva of nymph and adult *H. longicornis.* Identify several tick proteins that can provide useful information for basic and applied aspects of the host-parasite interaction. Salivary components may improve the understanding of tick physiology, aiding the identification of a new target for tick control.

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2. Tirloni L, Reck J, Terra RM, Martins JR, Mulenga A, Sherman NE, et al. Proteomic analysis of cattle tick Rhipicephal (Boophilus) microplus saliva: a comparison between partially and fully engorged females. PLoS One. 2014;9:e94831.

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