Functional characterization of a cysteine peptidase from *Babesia bovis*: its relation to host-parasite biology.

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*Rhipicephalus microplus* tick is the major ectoparasite for bovine in tropical and sub-tropical regions of the globe, responsible for the transmission of pathogens such as *Anaplasma* and *Babesia*. Despite the impact that *R. microplus*-*Babesia* complex has in livestock production, little is known about the mechanism of invasion and survival of *Babesia* genus. In the near past, the identification and characterization of key proteins of protozoan life cycle have been addressed - specially in *Plasmodium* and *Toxoplasma* – and several surface proteins (MSA) and proteases, such as falcipains and subtilisins, were related to parasite survival.

In order to understand the role of *Babesia bovis* proteases in host-parasite biology, the aim of this work is the functional characterization of a cysteine peptidase from *B. bovis*. We perform a genome search for proteases and select a putative transcript for further study: a cysteine peptidase similar to cathepsin L (XP_001612131) named BbCp. The BbCp nucleotide sequence was amplified from cDNA of bovine red blood cell (RBC) infected with *B. bovis* and cloned in the expression yeast vector pPICZαB. Protein expression was carried in the yeast system with *Pichia pastoris*. Preliminary data using the synthetic substrate Z-Phe-Arg-AMC and E64 suggest the presence of an active recombinant BbCP in yeast supernatant, but with low enzymatic activity. It was also found a mutation in BbCp amino acid sequence in the N-terminal region. Our perspective will be to correct the BbCp construction, in attempt to obtain a full active enzyme to perform its biochemical characterization.

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