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## Proteomic informed by transcriptomic towards candidate vaccine selection

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The animal products consumption is expected to drastically increase in the next decades in parallel with their market price, and, huge losses in productivity may be expected due to animal diseases. Among these, tick-borne diseases remain a rising risk to animal as well to human health and control measures based on acaricides have shown severe limitations. Therefore, vaccines are an alternative option, by-passing acaricide resistance ticks, being environmentally friendly and economically rewarding. Current vaccines have shown restricted achievement due to deficient antigen selection which may be surpassed by "omics" approach.

Having as main target the selection and evaluation of new antigens aimed at vaccine trial, we performed RNA sequencing and compared the transcriptome and proteome of different *Rhipicephalus* spp. tacking in account parasite infection. After mass spectrometry, proteins were identified using the proteomic informed by transcriptomic method which combines deep sequencing transcriptomics and MS/MS allowing protein identification in the absence of a reference proteome. Proteomic results validated transcriptomic analysis and, the combination of these two approaches, provided strong support for the identification of relevant pathways in ticks. Based on these achievements we selected several genes for functional analysis and further cattle vaccination trials with recombinant antigens. The results showed both reduced tick infestation and parasite infection, strongly suggesting the involvement of selected proteins in vector-pathogen interactions, recommending its inclusion in a vaccine targeting both arthropods from *diverse locations* and multiple pathogens.

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## Potential use of non pathogenic living trypanosomes in combination with specific recombinant antigens of pathogenic protozoan for immunisation or immunotherapy in Chagas' disease

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*Trypanosoma* cruzi is the etiological agent of Chagas' disease, discovered in 1909 by Carlos Chagas in Brazil. It is unclear the mechanism involved in the pathogenic process in humans, which is an accidental host in the life cycle of the parasite. *T. cruzi* shows a characteristic distribution of genotypes in the American Continent which seems to be associated with different clinical form of the disease in the chronic stage. No cure is available in the chronic stage and the only two drugs for the treatment of the disease in the acute stage, nifurtimox and benznidazol, have very low effectiveness with high toxicity and in many cases severe side effects. No vaccine exist to prevent the infection, meanwhile Chagas' disease has become a worldwide threat due to blood transfusion or organ transplant from infected donors, as well as congenital transmission to the newborn from infected mother. In an endemic area of Venezuela we have found children infected with *T. cruzi* or with the no pathogenic *T. rangeli* but no children with co-infection. In the same area we have found a species of triatomine bug vector, *Rhodnius prolixus*, either infected with *T. cruzi* or *T. rangeli*, as well as co-infected with both species. On the other side, several recombinant proteins have shown partial protection against *T. cruzi* infection and also immune response in the chronic stage in murine models. Chagas' disease remains killing people in Latin America and demands to join effort in the search for novel strategies against this worldwide threat.

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