VAC_02 - Identification of immunodominant proteins from the *Viannia* and *Leishmania* subgenera for the composition of a pan specific vaccine for leishmaniasis

Prisciliana Jesus de Oliveira[1]; Luzinei S. Couto[1]; Nathalia Pinho[1]; Patricia Cuervo[1]; Alda M. da Cruz[1]; Adriano Gomes da Silva[1]; Eduardo Fonseca Pinto[1].
[1]Fundação Oswaldo Cruz (Fiocruz).

Introduction: About 20 species of *Leishmania* cause at least two main clinical forms of leishmaniasis (tegumentary and visceral). Although immunization of the population would be an efficient control alternative, so far there are no effective control measures. Our group demonstrated that *L. (Viannia)* naiffi antigens induce well-modulated responses and that sera from volunteers cured of cutaneous cutaneous leishmaniasis recognized fractions considered to be immunodominant of the soluble antigen of this species. Other experiments by the group demonstrated that total antigens of this species and of *L. (Leishmania) amazonensis* induce protective immunity against *L. (V.) braziliensis*, when administered by the intranasal immunization route in hamsters.

Objective: Thus, this work aimed to identify the immunodominant proteins present in the soluble fractions of the total antigen of *L. (L.) amazonensis* and *L. (V.) naiffi*, more conserved within of the genus *Leishmania*, as candidates to compose a panspecific vaccine for the control of leishmaniasis.

Methodology: The soluble antigens were subfractionated on a polyacrylamide gel and the bands with molecular weight between 35 and 100KDa were extracted and analyzed by mass spectrometry for proteomic identification. The most abundant proteins were analyzed for similarity to host proteins. Epitopes recognized by B lymphocytes and high-affinity ligands to HLA class I and II molecules of antigens proteins with low similarity (<30%) to human proteins were predicted. These proteins were also selected for their high promiscuity to the considered HLA alleles. Thus, in addition to the potential for activating T lymphocytes, the predicted epitopes also have a broad capacity for antigenic presentation in the human population, due to the high predicted promiscuity regarding the binding capacity of these epitopes to HLA alleles.

Results: A subproteome with 328 validated proteins was obtained, of these, 128 presented low similarity value to human, dog and hamster proteins. 16 more immunodominant proteins were identified in terms of the number of epitopes with high binding affinity to BCR and promiscuous to HLA I and II. The homology analysis allowed the identification of 11 proteins with the most orthologs among *Leishmania* species.

Conclusion: This work demonstrated the potential of these proteins as promising vaccine targets for the formulation of a vaccine prototype capable of inducing a humoral, cellular and pan-specific immune response in humans, in the prevention of visceral and cutaneous leishmaniasis.

Keywords: Leishmaniasis; Vaccine prototype; Immunodominant epitopes