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A proteomic road to acquire an accurate serological diagnosis for human tegumentary leishmaniasis

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Diagnostic tools are important for clinical management and epidemiological evaluation of Tegumentary (TL) and Visceral (VL) Leishmaniasis. Serology is not frequently used for the diagnosis of the TL form because low antibody titers and cross-reaction with VL. Therefore, it is crucial to identify specific and immunogenic antigens from species associated with the TL form. Here, we employed a proteomic (DIGE-MS/MS) and an immunoproteomic (western blot-MS/MS) approach coupled to an *in silico* analysis and identified the most abundant and immunogenic proteins from *L. amazonensis, L. braziliensis* and *L. infantum*. Of 16 species specific proteins, nine were from the species causative of the TL form (*L. amazonensis* and *L. braziliensis*). *In silico* analysis revealed 18 B-cell epitopes with 0% similarity to *T. cruzi* orthologs and therefore, less likely to crossreact with sera of patients with Chagas disease. Two proteins reacted exclusively with serum from TL patients and presented several B-cell epitopes without similarity to *T. cruzi* orthologs: The hypothetical protein GI 134063939 and the metallo-peptidase clan MA(E)-family M3. The immunoassay using peptide array revealed nine peptides with strong reactivity to sera from TL patients. These proteins and peptides may be good candidates to improve the specificity and sensibility of serological tests aiming to diagnose the TL of this neglected human disease.

Biography

Hélida Monteiro de Andrade has completed her PhD from Federal University of Minas Gerais (UFMG), Brazil, and Post-doctoral studies from FIOCRUZ, Brazil. She is the Head of Leishmaniasis Laboratory in Parasitology department from UFMG. She has published almost 50 papers in reputed journals in Parasitology and or Proteomic area, 21 of them using proteomic approaches. She has been advisor of more than 30 students in scientific initiation, Master's, PhD and post-doctoral levels.

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