T lymphocytes epitopes prediction to access immunological response from Chagas diseases patient samples

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Chagas Disease, a pathology caused by the intracellular protozoan Trypanosoma cruzi tackles approximately 16-20 million people in Latin America and is responsible for about 13 thousand deaths per year. There are still few prophylactic measures and pharmacological treatments available. Vaccine development is being broadly assessed by the use of different antigen and delivery vectors. To succeed, it is important that the vaccine induce a strong immune response through the recognition of epitopes presented by the human leukocyte antigen (HLA) to the T lymphocytes, that latter will lead to an immunological memory. Trans-sialidase (TS) and Amastigote Surface Protein – 2 (ASP-2) are two proteins expressed by T. cruzi with high antigenic potential. Both antigens were extensively evaluated in murine models, however a more robust analysis for human immunogenic potential should be performed. To accomplish that, a protein epitope prediction was made considering the great variability existent in the population's HLAs. Three different bioinformatics programs were used: SYFPEITHI, Bimas and The Immune Epitope Database and Analysis Resource (IEDB), once each one worked with a different algorithm. The obtained results were compared, and further analysis was made of every available HLA present in at least two programs. The top five ranked epitopes for each HLA were selected, and the most frequent epitopes were identified in the proteins' amino acid sequence. Considering the great importance of the recognition and affinity of the immune system for the antigen used in vaccination, we intend to screen the selected peptides for the activation of T CD8+ response, measured by the production of IFN-γ upon peptide stimulation. Aiming at screening the peptides, PBMC from Chagas patients will be sensitized with T. cruzi total antigen then re-stimulated with the selected peptides. The data will enlighten the immunological profile of different HLAs under specific binding of the said peptides and open the perspective to pinpoint an immunogenic region of interest of both TS and ASP-2 in order to improve the immunization protocols for humans.

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