

Bioinformatics analyzes to evaluate the vacinal potential of the D3 peptide mimetic to *Strongyloides stercoralis* antigen

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Strongyloidiasis is an intestinal helminthiasis, caused by *Strongyloides stercoralis*, which can lead to severe clinical cases (hyperinfection and disseminated infection) or remain asymptomatic for long periods, becoming chronic. It has a global distribution, prevailing in poor countries. There are anti-helminthic drug treatments for the infection, but there are still no immunoprophylactic measures, such as vaccines. Reverse vaccinology technology uses *in silico* assays for the detection of peptides and antigenic proteins for various microorganisms, including intestinal helminths. The D3 peptide, *Strongyloides* antigen mimetic was analyzed in the present study for the verification of its vaccine potential. Alignment of the peptide sequence with three proteins, nuclear hormone receptor of the steroid / thyroid hormone receptors superfamily (NHR), SMAD-1 and cytochrome C oxidase subunit I was detected. The presence of signal peptides in the analyzed proteins was not detected. As for the prediction of B cell epitopes capable of activating the humoral immune response, the study sequence presented characteristics favorable to B cell interaction, such as accessibility, antigenicity, linearity, flexibility and hydrophilicity. Regarding the T cell-mediated immune response, there were low interactions with MHC I and ability to align with the MHC II binders. The theoretical modeling of the study proteins was carried out for later editing of the images to visualize the accessibility of the peptide of interest in the proteins. The peptide of interest was marked and visualized on the protein surface of the three proteins analyzed. The validation of the generated three-dimensional models showed unsatisfactory scores with respect to the amino acid loads in relation to the compatibility between 1D / 3D structure. As conclusion, it was obtained that the peptide D3 possesses favorable aspects to the design of a peptide vaccine, being able to stimulate humoral and cellular immune responses. Bioinformatics tools play an essential role in the development of new generations of vaccines, aiding in the search for the eradication of parasitic diseases, as well as reducing costs, minimizing risks and shortening the time of research using experimental models. In the future the D3 peptide vaccine potential will be tested in experimental animals for *in vivo* substantiation of its ability to generate humoral immune response.

Key-words: *Strongyloides stercoralis*, reverse vaccinology, epitope prediction, *in silico*, bioinformatics.

Financial support: FAPEMIG, CNPq, CAPES