## TITLE: Prediction of epitopes for the diagnosis of sexually transmitted infections

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## ABSTRACT:

Sexually transmitted infections (STIs) are considered a public health problem, mainly because of the ease of transmission. Several microorganisms are associated with STIs, including Mycoplasma hominis, M. genitalium and Chlamydia trachomatis. These bacteria are the most prevalent in causing little or no symptoms, making diagnosis and treatment impaired. The diagnostic methods currently available for such infections have a high aggregate cost in addition to the need for qualified individuals. Bioinformatics has been a practical method for predicting epitopes that can be used for the development of diagnostic methods. In this way, the aim of the present study was to perform bioinformatics analysis to identify probable epitopes for the development of a rapid test for M. hominis, M. genitalium and C. trachomatis. Reference proteomes were analyzed using cell localization programs (PSTORb, TOPOCONS). Proteins expressed as extracellular or membrane proteins were predicted through the BEPIPRED, LBTOPE and IEDB programs to identify reagent epitopes for B cells. After identification of the epitopes a conservation analysis was performed with the non-redundant proteomes of each species. In total, 1862 proteins were analyzed considering the sum of the three proteomes. One hundred seven proteins (5.75%) were predicted as extracellular. Subsequently, 949 proteins probable B cell-reactive epitopes were identified and 10% were conserved between the species. The tools of bioinformatics enabled the development of a consensus since several prediction programs were used, thus guaranteeing accuracy in the prediction and also facilitating the selection of good epitopes for the later phases. Thus, it is believed that the resulting epitopes can be used in future stages in the development of the screening test, since they presented good characteristics during the prediction phase.

Key words: Recombinant protein, diagnosis and infection.

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