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Immunome Research

Editorial

Immunoinformatics

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Editorial Note

Clostridium perfringens is a member of the gastrointestinal tract (GIT) microbial community of both diseased and healthy humans and animals. Also, this bacterium is responsible for around 5–15% of all circumstances of antibiotic-associated diarrhea, which develops in 5–40% of all patients receiving antibiotic therapy. In addition, it causes enteritis necroticans; an often-fatal human disease. C. *perfringens* is clear and defined the underlying factors responsible for specific aspects of pathology remains uncertain. This study predicts an effective epitope-based vaccine against fructose 1,6-biphosphate aldolase (FBA) enzyme of *Clostridium perfringens* using immunoinformatics tools. The sequences were retrieved from NCBI and several prediction tests were conducted to analyze possible epitopes for B-cell, T-cell MHC class I and II. Tertiary structure of the most promising epitopes was obtained. 48 epitopes showed high binding affinity for B-cells, while five epitopes showed high binding affinity for MHCI and MHCII. The results were promising to formulate a vaccine with more than 98% population coverage. We hope that these promising epitopes serves as a preventive measure for the disease in the future and recommend *in vivo* and *in vitro* studies.

Plasmodium falciparum is one of four human's parasitic species that belongs to the genus Plasmodium. It is responsible for causing 50% of malaria incidence throughout the world. It is the most lethal and accounts for 98% of all lethal cases. No previous reports were found in *Plasmodium falciparum* epitope based vaccine, so this study aimed to predict an effective epitope-based vaccine against TCTP enzymes of *P falciparum* using immunoinformatics approaches. *Plasmodium Falciparum* TCTP sequences were retrieved from (NCBI) database. The conserved regions were introduced into IEDB analysis resource to predict B-cell, T-cell MHC class I and II. 3D structure of the most promising epitope was obtained. The proposed and promising peptide SYVQQDPFE showed a potent binding affinity to B-cell, MEAGIIYSY with a very strong binding affinity to MHC I alleles, and IYSYYKGEEITPRFV that showed a very strong binding affinity to MHC II alleles. The results were promising to formulate a vaccine with more than 93.73 % population coverage worldwide and 82.13 % in Sudan, excluding certain MHC II alleles. This study recommends an in vivo and in vitro assessment for the most promising peptides as universal vaccine. The sequences were retrieved from NCBI and several prediction tests were conducted to analyze possible epitopes for B-cell, T-cell MHC class I and II. Tertiary structure of the most promising epitopes was obtained. 48 epitopes showed high binding affinity for B-cells, while five epitopes showed high binding affinity for MHCI and MHCII. The results were promising to formulate a vaccine with more than 98% population coverage. *Plasmodium Falciparum* TCTP sequences were retrieved from (NCBI) database. The conserved regions were introduced into IEDB analysis resource to predict B-cell, T-cell MHC class I and II. 3D structure of the most promising epitope was obtained. This study recommends an *in vivo* and *in vitro* assessment for the most promising peptides as universal vaccine. The sequences were retrieved from NCBI and several prediction tests were conducted to analyze possible epitopes for B-cell, T-cell MHC class I and II. Tertiary structure.

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