Editorial

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Editorial Note on Immunoinformatics

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Editorial Note

Clostridium perfringens is a bacterium found in the Gastro-Intestinal Tract (GIT) of both sick and healthy people and animals. In addition, this bacterium is responsible for 5–15% of all antibiotic-associated diarrhoea cases, which occur in 5%-40% of all antibiotic-treated patients. It also causes enteritis necroticans, a human condition that is typically fatal. Although *C. perfringens* is well-known, the underlying mechanisms that cause various characteristics of disease are unknown. Using immunoinformatics methods, this study predicts an efficient epitope-based vaccine against *Clostridium perfringens* fructose 1,6-biphosphatealdolase (FBA) enzyme.

The sequences were obtained from NCBI, and numerous prediction tests were run to look for potential epitopes for B-cell, T-cell, and MHC class I and II MHC molecules. The most promising epitopes' tertiary structure was discovered. B-cells showed high binding affinity for 48 epitopes, while MHC I and MHC II showed high binding affinity for five epitopes. The findings suggested that a vaccination with population coverage of more than 98% may be developed. We hope that these potential epitopes will be used as a disease prevention measure in the future, and we propose further *in-vivo* and *in-vitro* research.

Plasmodium falciparum is one of four parasite species found in humans, all of which belong to the genus Plasmodium. It is responsible for 50% of all malaria cases worldwide. It is the deadliest, accounting for 98% of all fatalities. Because no prior reports of an effective epitope-based vaccine against *Plasmodium falciparum* TCTP enzymes had been reported, this study used immunoinformatics to predict an effective epitope-based vaccine against *P. falciparum* TCTP enzymes. The TCTP sequences of *Plasmodium Falciparum* were obtained from the National Center for Biotechnology Information (NCBI) database. To predict B-cell, T-cell MHC class I and II, the conserved areas were added to the IEDB analysis database. The most promising epitope's 3D structure was discovered. SYVQQDPFE, a proposed and promising peptide, exhibited a strong binding affinity to B-cell, MEAGIIYSY, which showed a strong binding affinity to MHC I alleles, and IYSYYKGEEITPRFV, which showed a strong binding affinity to MHC II alleles. The findings indicated that a vaccination with more than 93.73% global coverage and 82.13% in Sudan may be developed, omitting particular MHC II alleles. The most promising peptides as universal vaccines should be evaluated *in-vivo* and *in-vitro*, according to this study. The sequences were obtained from NCBI, and numerous prediction tests were run to look for probable epitopes for B-cell, T-cell, and MHC class I and II MHC class I and II.

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