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Immunogenicity of SARS-CoV-2 Epitope Identified by Immune Epitope Database & Analysis (IEDB) Server

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Structured Abstract

Background: In 2020, The World Health Organisation (WHO) has declared a pandemic due to the outbreak of a novel coronavirus 2019 (COVID-19), which is caused by the SARS-CoV-2 virus. It is imperative to stop the virus from spreading and to treat individuals who are affected effectively. Consequently, in order to meet the demands of the global community in fighting the pandemic, vaccine development must go quickly, enable mass production, be cost-effective, safe, and extremely accurate. The current vaccine takes longer to create and is more expensive since it is made using a traditional method that primarily involves live-attenuated whole-pathogen vaccines. A recent development in vaccine manufacture, reverse vaccinology makes more use of bioinformatics tools and computational techniques. Furthermore, it has been demonstrated in previous relevant studies that the use of bioinformatics tools in modern vaccine production yields better results than traditional vaccine production.

Methods: Using the Immune Epitope Database and Analysis (IEDB) website, the T-cell epitopes of the SARS-CoV-2 spike glycoprotein were predicted for this investigation. From the National Centre for Biotechnological Information (NCBI) database, thirty sequences that corresponded to the local population were obtained in this study. The anticipated T-cell epitopes were identified based on their MHC class I and class II binding mechanisms of binding. The two binding sites were differed because they belonged to the categories of helper T cells and cytotoxic T cells, respectively. The Epitope Conservancy Analysis tool in WebLogo 3.0 was utilised to verify the degree of conservation of the projected epitopes. Next, the predicted epitopes were compared to those found in earlier studies.

Results: The two most promising options for vaccination targeting against COVID-19 are EP 2 (IYQTSNFRV) from MHC class II binding and EP 3 (YLQPRTFLL) from MHC class I binding. Both proteins demonstrated 100% conservancy and a satisfactory binding affinity score.

Conclusion: Therefore, it has been demonstrated that using a bioinformatic technique was a reliable substitute for creating a novel epitope-based vaccination targets in order to stop SARS-CoV-2 infection.

Keywords: SARS-CoV-2 virus, IEDB, epitopes, T-cells, vaccine

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