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Immunogenicity Of SARS-CoV-2 Epitopes Identified By Combination Prediction (COMPRED) Server

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Structured Abstract

Background: The World Health Organisation (WHO) declared the COVID-19 outbreak to be caused by the SARS-CoV-2 virus in 2020. Therefore, it is critical to develop a vaccine that is safe, affordable, and effective in order to halt the virus's spread and stop additional disease and fatalities. Nevertheless, the need for a quick and efficient vaccine production process was not provided by the conventional vaccine production approach. The most recent approach to producing vaccines utilising bioinformatics tools is appropriate and satisfies all needs for quick, efficient vaccine manufacture. Therefore, the purpose of this work was to use prediction methods to analyse the pattern of the SARS-CoV-2 virus and forecast the cytotoxic T lymphocyte cell epitope of the virus in order to quickly and effectively manufacture a vaccine.

Methods: In this work, the SARS-CoV-2 epitopes were predicted using a computer method. Thirty SARS-CoV-2 amino acid sequences from the spike (S) gene were obtained from the NCBI database and assigned to a Malaysian sample. Then, using the combination prediction (COMPRED) database, the cytotoxic T lymphocyte cell (CTL) epitopes of the SARS-CoV-2 spike protein were predicted. Using the conservation analysis tool, the most conserved epitopes were identified, and the Weblogo 3.0 database was used to visualise them.

Results: A total of eight CTL epitopes were chosen using a 0.5 cutoff score and four had been selected for further study. The conservation analysis for EP1 (VVVLSFELL), EP2 (WTFGAGAAL), EP3 (RLNEVAKNL), and EP4 (GLTVLPPLL) was 100%. Out of the four anticipated epitopes, EP1 (VVVLSFELL) achieved the highest peptide score of 2.079, making it the most promising candidate peptide for vaccine design.

Conclusion: In summary, out of the eight CTL epitopes that were predicted using the COMPRED prediction method, only four were found to be the most promising candidates for vaccine development. Therefore, in comparison to the conventional and traditional way, this bioinformatic approach demonstrated a potential effective and quick strategy for vaccine design.

Keywords: SARS-CoV-2 virus, epitope, COMPRED, cytotoxic T lymphocyte cell (CTL), vaccine.

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