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Immunogenicity of SARS-CoV-2 Epitope Identified by BepiPred 2.0 Server

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Structured Abstract

Background: The escalating incidence of infections necessitated the development of antiviral medications and vaccinations as COVID-19 cases persisted and constituted a threat to worldwide health. The promotion of healing and immunological defense against the virus depended heavily on B cell activation. Nevertheless, it was shown that the conventional approaches to developing vaccines, including using live or dead attenuated microbes, were costly, time-consuming, difficult, and inefficient. Immunoinformatics technologies were utilized to overcome the above-mentioned problem related to vaccine development of COVID-19. Therefore, this study set out 3 objectives: - 1) to use the BepiPred 2.0 Server to predict the SARS-CoV-2 epitope, 2) to investigate the use of the BepiPred 2.0 server as an appropriate prediction tool in immunogenetics research and 3) to identify the most conserved epitope using the Epitope Conservancy Analysis Tool.

Methods: Thirty SARS-CoV-2 spike protein sequences, originating from Malaysia, were obtained from the NCBI Virus database. Additionally, the BepiPred 2.0 server successfully predicted six linear B-cell epitopes of the SARS-CoV-2 spike protein. The most conserved epitopes were identified using Epitope Conservancy Analysis Tools, and WebLogo 3.0 was used to visualize the data. The anticipated epitopes were then contrasted with those found in earlier studies.

Results: Along with EP4 (^{330}PNITNLCPFGEVFNATRFASVYAWNRK^{356}) and EP6 (^{36}1ADYSVLYNSASFSTFKCYGVSPTKLNDLCF^{390}) at 96.67%, EP1 (^{1131}VNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGI^{1170}) emerged as the most conserved epitope at 100%, suggesting these epitopes as strong candidates for vaccine formulation against SARS-CoV-2. Using bioinformatic methods, the immunogenicity of anticipated B-cell epitopes of the SARS-CoV-2 spike protein was determined.

Conclusion: The creation of the COVID-19 vaccine benefited greatly from these epitopes, which outweight the conventional wet lab techniques. Thus, considering its ease of use, efficacy, and lack of labour and time requirements, bioinformatics-based epitope prediction is a promising method for creating a COVID-19 vaccine.

Keywords: SARS-CoV-2, BepiPred 2.0, Epitopes, B-cells, Vaccine

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