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Design and in Slico Study of the Truncated Spike-M-N SARS-CoV-2 as a Novel Effective Vaccine Candidate

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Abstract : Background:The emerging COVID-19 pandemic is a serious concernfor the public health worldwide. Despite the many mutations in the virus genome, it is important to find an effective vaccine against viral mutations. Therefore, in current study, we aimed at immunoinformatic evaluation of the virus proteins immunogenicity to design a preventive vaccine candidate, which could elicit humoral and cellular immune responses as well. Methods:Three antigenic regions are included;Spike, Membrane, and Nucleocapsid amino acid sequences were obtained, and possible fusion proteins were assessed andcompared by immunogenicity, structural features, and population coverage. The best fusion protein was also evaluated for MHC-I and MHC-II T-cell epitopes and the linear and conformational B-cell epitopes. Results: Among the four predicted models, the truncated Spike protein in fusion with M and N proteins is composed of 24 highly immunogenic human MHC class I and 29 MHC class II, along with 14 B-cell linear and 61 discontinues epitopes. Also, the selected protein has high antigenicity and acceptable population coverage of 82.95% in Iran and 92.51% in Europe. Conclusion: The data indicate that the truncated Spike-M-N SARS-CoV-2form which could be potential targets of neutralizing antibodies. The protein also has the ability to stimulate humoral and cellular immunity. The in silico study provided the fusion protein as a potential preventive vaccine candidate for further in vivo evaluation.

Keywords : SARS-CoV-2, immunoinformatic, protein, vaccine
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