Epitopic mining on Spike protein of SARS-CoV-2 as a candidate target for vaccine design: An in-silico analysis

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Abstract

The outbreak of novel SARS-CoV-2 virion has wreaked havoc with a high prevalence of respiratory illness and high transmission due to a vague understanding of the viral antigenicity augmenting dire challenge to public health globally. This viral member requisite the expansion of diagnostic and therapeutic tools to track its transmission and confront through vaccine development. Therefore, prophylactic strategies are mandatory. Virulence-related spike proteins can be the desirable candidate befitting computational design of vaccines targeting SARS-CoV-2 followed by meteoric development of immune epitopes. This study aims to characterize Spike protein using the existing knowledge related to the immunological profile of SARS-CoV-2 to predict immunogenic epitopes based on antigenicity, allergenicity, toxicity, immunogenicity, and population coverage. Applying in-silico approaches, a set of twenty-four B lymphocyte-based epitopes and forty-six T lymphocyte-based epitopes (MHC-I and MHC-II) were selected. The predicted epitopes were evaluated for their intrinsic properties. Physico-chemical characterization of epitopes qualify them for further *in vitro* and *in vivo* analysis pre-requisite vaccine development. This study presents a set of screened epitopes that binds to the HLA- specific allelic proteins that can be employed for designing a multi-epitopic peptide vaccine construct (MEPVC) against SARS-CoV-2 that will confer vaccine-induced protective immunity due to its structural stability.

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