Considering epitopes conservity in targeting SARS-CoV-2 mutations in variants: a novel immunoinformatics approach to vaccine design

Bagherzadeh MohammadAref, Izadi Mohammad, Baesi Kazem, Mofazzal Jahromi MirzaAli, Pirestan Majid.

Abstract

Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) has gained mutations at an alarming rate in the past years. Developing mutations can increase the virus's pathogenicity and virulence; reduce the efficacy of vaccines, antibodies neutralization, and even challenge adaptive immunity. So, it is essential to identify conserved epitopes (with fewer mutations) in different variants with appropriate antigenicity to target the variants by an appropriate vaccine design. Yet as, 3369 SARS-CoV-2 genomes were collected from global initiative on sharing avian flu data. Then, mutations in the immunodominant regions (IDRs), immune epitope database (IEDB) epitopes, and also predicted epitopes were calculated. In the following, epitopes conservity score against the total number of events (mutations) and the number of mutated sites in each epitope was weighted by Shannon entropy and then calculated by the Technique for Order of Preference by Similarity to Ideal Solution (TOPSIS). Based on the TOPSIS conservity score and antigenicity score, the epitopes were plotted. The result demonstrates that almost all epitopes and IDRs with various lengths have gained different numbers of mutations in dissimilar sites. Herein, our two-step calculation for conservity recommends only 8 IDRs, 14 IEDB epitopes, and 10 predicted epitopes among all epitopes. The selected ones have higher conservity and higher immunogenicity. This method is an open-source multi-criteria decision-making platform, which provides a scientific approach to selecting epitopes with appropriate conservity and immunogenicity; against ever-changing viruses.