Antigenic Determinant, a Target for Universal Vaccine in SARS Coronavirus 2

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Abstract

Determination of Antigenic Determinant (Epitope) for an Antigenic Spike Glycoprotein which is an attachment site for an Host to bind antibody to neutralize the Virus is important target for the development of Universal Vaccine against SCoV-2 which is Pandemic throughout the world since December-2019. It is an utmost need for an identification of Antigenic Determinant (Epitope) for SCoV-2 Hence the work proposed.

Keywords: Antigenic Determinant; Vaccine; SARS Coronavirus 2

Introduction

SCOV-2 is pandemic in the world evolved from China (Wuhan) and spread throughout, Different prevention measures are been taken by different countries for the sake of spreading i.e. Lock down and other medical treatment for the infected patients. Gene and Protein Sequences are sequenced for the virus researchers are trying to solve the mystery behind SCOV-2 to Get a permanent remedy through vaccine development. Our work is one of the attempt to predict Conformational Epitope for the virus which will be use a an universal target for the vaccine.

Corona viruses are a large group of RNA Viruses having +ve single stranded RNA and Crown like appearance is caused due to spike protein (S) present in the lipid bilayer. Spike protein(S) is a trimeric protein which is a receptor binding protein and helps in fusion of the envelope of virus to the host cell. This spike protein is responsible for the crown like appearance like a king’s crown. Envelope protein (E) is a pentameric protein that functions as a ion channel protein and allows flow of ions from host to virus and vice-versa. Membrane glycoprotein (M) is the protein that forms a lipid bilayer membrane for the corona virus. Nucleocapsid protein (N) is the RNA binding protein and helps in synthesis of more number of RNA and in the process of translation.
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National Center for Biotechnology Information is a repository for the protein and gene sequence for the SCOV2. Protein sequence were retrieved from the database with an accession number QHD43418.1 for Spike glycoprotein. Conformation or the structure of the protein was predicted by I-TASSER Server with a PDB ID - QHD43418.pdb. There are different isolates of SCOV2 due to mutation rate. They have been classified as Type A, Type B and Type C on the basis of Phylogenetic classification. Bioinformatics tool were used to predict the epitope and its sensitivity and specificity was calculated.

Methodology

1. Sequences were retrieved from the NCBI Protein Database and the Predicted 3 D Structure were taken from the I-Tasser structure prediction server.

2. Ellipro conformational epitope prediction server was used to predict the peptides of the protein.

3. PHI-BLAST was used to screen 20 epitopes/peptides for their Specificity.

4. One specific epitope was identified for the SCOV-2 which can be Used as an universal target.

5. NetNGlyc 1.0 server was used to predict the Glycosylation site.

Results and Conclusion

Ellipro server was used to predict the Peptide for the 3D structure of Spike Glycoprotein 20 Peptides were identified for the structure out of which one peptide was found to be specific with zero false positives and true positives. Serial Number 8 with a start site 64 and end

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site 84 in the sequence was identified as WFHAIHVSGTNGTKRFDNPVL with a length of 21 amino acids and a score of 0.741 as a universal vaccine candidate. Figure 3 shows the ellipro results. And figure 4 shows the N Glycosylation site results for the predicted epitope. WFHAIHVSGTNGTKRFDNPVL TNGKT a Glycylation site.

Figure 3: Ellipro results.

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**Figure**: N glycosylation site prediction.

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