Binding Affinity and Interaction of SARS-CoV-2 Epitopes with Major Histocompatibility Complex

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SARS CoV-2 has been affecting the world since 2019. It caused 245 million cases of infection and around 5 million deaths worldwide. The most important strategies for the development of vaccines against SARS-CoV-2 are inactivated or weakened virus, replicating or non-replicating viral vector-based approaches, DNA, RNA, virus particle like approaches and epitope-based approaches. The epitope-based approach is rapid, accurate, cost-effective, and reliable against pathogens. By presenting epitopes (antigen peptides) on antigen-presenting cells (APCs), the major histocompatibility complex (MHC), also recognized as the human leukocyte antigen (HLA) system in humans, plays an essential role in triggering T-cell immune responses. The focus of this study is to identify the binding motif of the epitopes generated from the structural proteins such as spike, membrane, and nucleocapsid of SARS CoV-2 with the MHC. Two HLAs including HLA-DQ and HLA-A*30 were considered for this study. The three-dimensional structure of the epitopes was modelled by the PEP-Fold server. All the three-dimensional models of the epitopes have extended alpha-helix structures with short-coiled C-termini. The interactions of these epitopes with the MHC complexes were noticed. Using a molecular docking approach, the binding affinity and non-bonding interactions between the MHC and epitope were measured and identified by PATCH-DOCK and FIRE-DOCK. In HLA-DQ, the epitopes showed binding affinities ranging from -36.58 to -82.31 kcal/mol, whereas in HLA-A*30 all epitopes showed comparatively lower binding affinities, ranging from -34.90 to -59.78 kcal/mol. Some of the epitopes were accurately bound to the residues in the peptide-binding grooves of HLA complex while some were in the vicinity of the binding site. Our results can provide more understanding of HLA supertypes and pave the way for SARS-CoV-2 epitope screening and vaccine development based on the binding motifs of different supertypes.