Peptide Targets to SARS-CoV-2

Sir,

The major difficulty in developing a drug against the novel coronavirus (SARS-CoV-2) causing COVID-19 is due to the fascinating job done by the virus itself through mutational program of evolution. There is a provision to search the drug by high-throughput screening of natural to synthetic chemical libraries. Peptide libraries are good choice for the therapeutic development against human pathogens.[1,2] Beside the conventional approach following isolation, screening, purification, and characterization of antiviral peptides, the engineered peptide library may be synthesized easily and performance evaluation is not a time-killing job.

The surface spike glycoprotein of SARS-CoV-2 helps to enter into the cell through the highly expressed (in the tongue, upper respiratory tract, and lung) angiotensin-converting enzyme-2 (ACE2) receptor.[3] The regions of their binding sites are analyzed to design the possible inhibitor of either ACE2 receptor or receptor-binding domain (RBD) of S-protein. Here, the approach has been undertaken to design and develop peptide-based therapeutics to effectively control COVID-19.[4-6] The S-glycoprotein firmly binds to ACE2 in the region of 607–614 amino acid residues as STDWSPYA.

The region of S-glycoprotein from 1095 to 1104 amino acid residues (GLN 1095, ILE 1096, ILE 1097, THR 1098, THR 1099, ASP 1100, ASN 1101, THR 1102, PHE 1103, and VAL 1104) are responsible for the binding. The RBD has an extended loop of α-helix connected to an antiparallel β-sheet [Figure 1]. The approach is to solid-phase synthesis of peptides guided by both the regions from S-glycoprotein of 1095–1104 amino acid residues (QIITTDNTFV) and the sequence (STDWSPYA) of Chain A of ACE2 which is responsible for binding with S-protein. It is necessary to develop two peptide libraries from the target site of ACE2 and S-protein, separately. The molecular design of the peptide confirmed the presence of the α-helix loop connected to the antiparallel β-sheet. The development of combinatorial synthesis by an automated solid-phase peptide synthesizer is required to analyze the properties of a large number of peptides in a short period of time. It is necessary to develop the peptide libraries by the systematic combination along with their possible modifications of target sites. The active peptide may be useful to block the target site of either ACE2 receptor or RBD of S-protein by competitive inhibition.
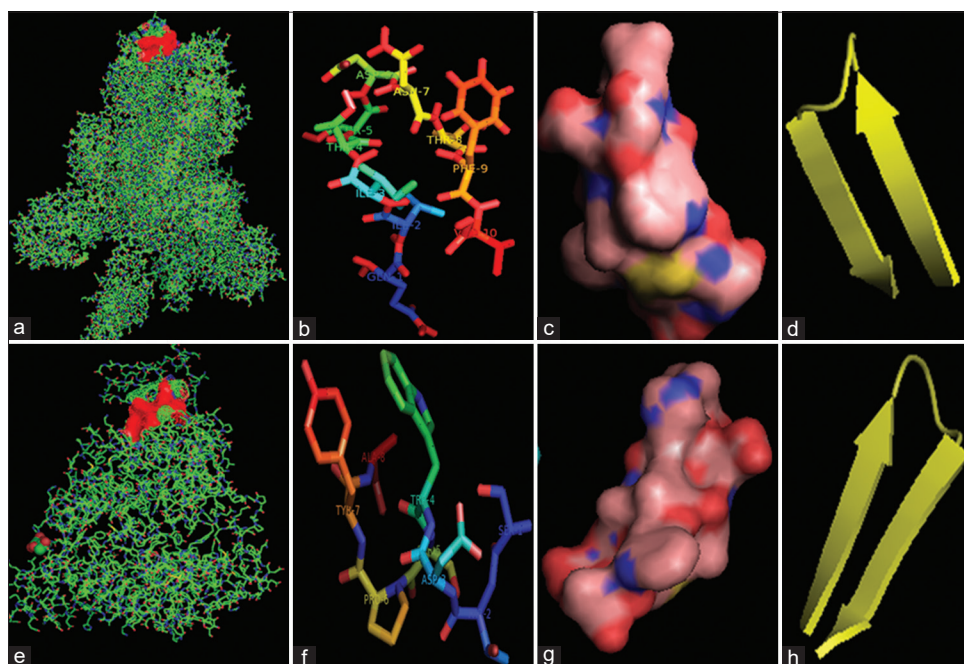
Figure 1: Identification of target region in receptor and receptor-binding domain in S-glycoprotein of SARS-CoV-2. Chain A of S-glycoprotein (PDB: 5 × 5B) and their receptor-binding domain are recognized with red highlight (a). Molecular design of the angiotensin-converting enzyme-2 binding peptide in receptor-binding domain comprised with QIITTDNTFV amino acid sequences (b) and their surface view (c). The peptide has an extended loop of α-helix connected to an antiparallel β-sheet (d). Similarly, Chain A of angiotensin-converting enzyme-2 (PDB: 1R42) and red color highlight the binding region of receptor-binding domain (e), the binding peptide sequence, STDWSPYA and its stick view (f), and their surface view (g). The peptide has an α-helix loop connected to the antiparallel β-sheet (h)

Conflicts of interest

There are no conflicts of interest.

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