Spike Proteins of SARS –CoV-2: a detailed perspective on structure, receptor binding, antigenicity, vaccine development and neutralization

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Abstract

Spike proteins are heavily glycosylated, small protrusions located on the envelops of coronavirus. These proteins are the characteristic morphological features of coronavirus that give the virus family its name, and are alone responsible for the virulence, pathogenicity, and evolving tropism of these viruses. SARS-CoV-2 shows higher affinity towards its target, ACE-2 receptors in human subjects. This affinity is the result of mutations in its spike protein gene – as revealed through genomic sequencing. Being central to the viral structure, SARS-CoV-2 spike proteins and their receptor binding domains are the preferred platforms for vaccine development. The administration of neutralizing monoclonal antibodies is also being employed along with vaccines to accelerate viral shedding. Various expression and purification strategies are discussed in the paper to provide an updated overview of the SARS-CoV-2 therapeutic landscape. The development of antibody-dependent enhancement (ADE) is still a possible risk linked to the newly developed vaccines and needs to be studied. These challenges demand further research and an innovative approach to expand the therapeutic utility of coronavirus spike proteins.

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