Structural and Immunological Characterization of the Fusion Core of the SARS-coronavirus Spike Protein

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Severe Acute Respiratory Syndrome (SARS) has been one of the most epidemic diseases threatening the lives of human beings in the 21st century. The SARS-CoV spike (S) protein, a glycoprotein essential for viral entry, is a primary target for vaccine and drug development.

The polyclonal antibodies produced by recombinant S2 protein were tested for the antigenicity of the two heptad repeats. Two peptides denoted HR-N(SN50) and HR-C(SC40), corresponding to the Leu/Ile/Val-rich heptad-repeat regions from the N-terminal and C-terminal segments of the SARS-CoV spike S2 sequence, respectively, were synthesized and predicted to form trimeric assembly of hairpin-like structures. The crystallographic study of the SARS spike HR-N/HR-C complex presents the crystal belongs to the triclinic space group P1 and the data-set collected to 2.98 Å resolution showed noncrystallographic pseudo-222 and 3-fold symmetries. Based on these data, comparative modeling of the SARS-CoV fusion core was performed. Structural and biophysical studies of SARS-CoV spike fusion core with inhibitor are in progress. The immunological and structural information presented herein may provide a more detailed understanding of the viral fusion mechanism as well as the development of effective therapy against SARS-CoV infection.

Keywords: SARS, spike, x-ray crystallography