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IN A BOOST TO VACCINE DEVELOPMENT, STRUCTURE OF SARS-COV-2 KEY PROTEIN MAPPED

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Mapping the 3D structure of the protein — spike (S) glycoprotein — will allow better understanding of how the virus binds to the human cells. Knowing the structure of the spike protein will, in turn, allow scientists to develop vaccines and antivirals against the virus and even better diagnostics.

Like other coronaviruses, SARS-CoV-2 virus particles are spherical and have mushroom-shaped proteins called spikes protruding from their surface, giving the particles a crown-like appearance. The spike binds and fuses to human cells, allowing the virus to gain entry.

The spike protein of the novel coronovirus shares 98% sequence identity with the spike protein of the bat coronavirus, the researchers say. The results were published in the journal *Science.*

The researchers also found that like in the case of the SARS coronavirus, the spike protein of the novel coronavirus (SARS-CoV-2) that causes COVID-19 disease binds to the cellular receptor called angiotensin-converting enzyme 2 (ACE2), which serves as the entry point into human cells. But unlike in the case of SARS, the spike protein of the novel coronavirus binds to the cell receptor with much higher affinity — 10- to 20-fold higher.

The much greater binding affinity to the cell receptor explains the apparent high human-to-human transmissibility of the virus compared with the SARS coronavirus.

“The high affinity of the 2019-nCoV S for human ACE2 may contribute to the apparent ease with which the 2019-nCoV can spread from human-to-human,” the researchers write. “Additional studies are needed to investigate this possibility.”

Since both the SARS coronavirus and the 2019 novel coronavirus share structural similarity and bind to the same receptor, the researchers tested three monoclonal antibodies specific to SARS virus for their ability to bind to the novel coronavirus. But none of the three antibodies tested were found to be effective in inhibiting the novel coronavirus from binding to the human receptor ACE2 and prevent or treat the disease.

However, the 3D map of the S protein will help researchers design new antivirals to stop the virus from binding and infecting human cells.

“Knowing the atomic-level structure of the 2019-nCoV spike will allow for additional protein engineering efforts that could improve antigenicity and protein expression for vaccine development,” the researchers write.

The researchers were able to determine the structure of the spike protein as the Chinese researchers shared the whole genome sequence data in the global database.

The WHO had to come up the name in line with the 2015 guidelines between the global agency, the World Organisation for Animal Health and the Food and Agriculture Organization.