Taking Covid-19 virus image at atomic resolution, scientists discovered its chemical infectious nature

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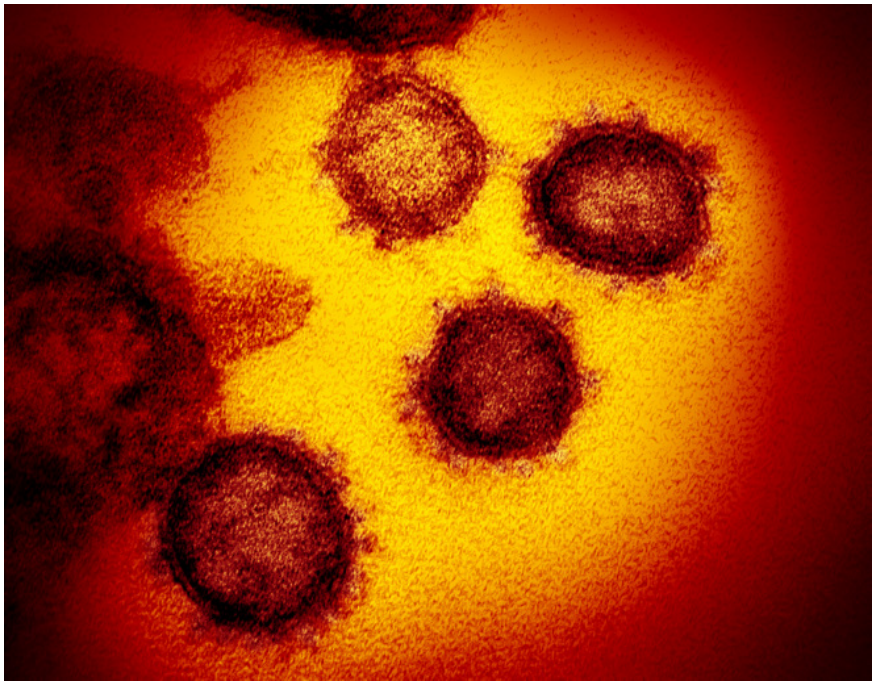
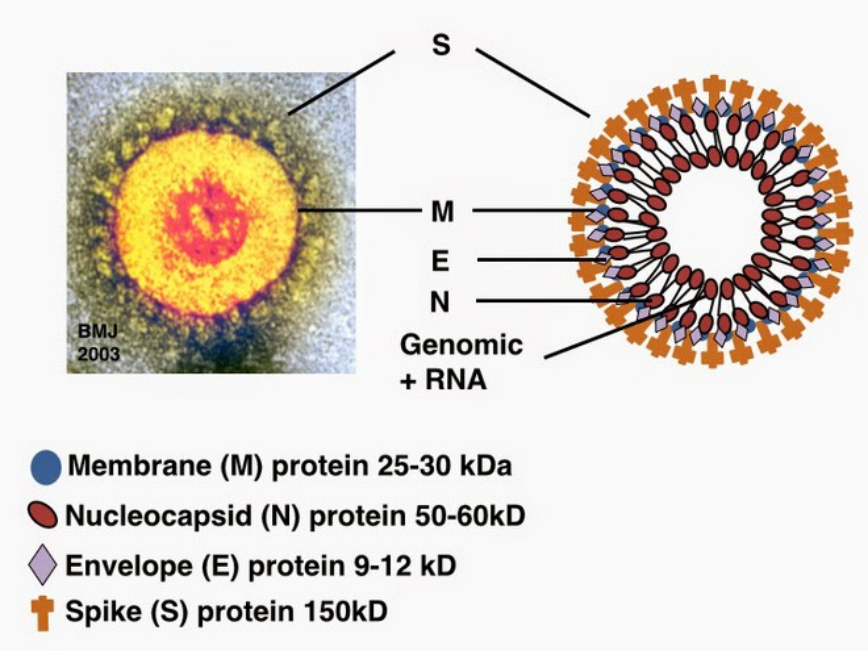
The SARS-CoV-2 virus causing the Covid-19 epidemic is only a spherical particle of size 100 nm. For ease of visualization, it is only 1/900 the diameter of a human hair. Using electron microscopes, a team of scientists at the Rocky Mountains Laboratory last month magnified the virus image 300,000 times, revealing the first detailed images of the structure of SARS-CoV. -2.

These images confirm that SARS-CoV-2 is a corona virus strain with a structure of 4 parts: the nucleus (N), the sheath (E), the membrane (M) and the spines (S). The artificial sheath forms a genetic core. It is again encased in proteins that make up the virus's shell and membrane.



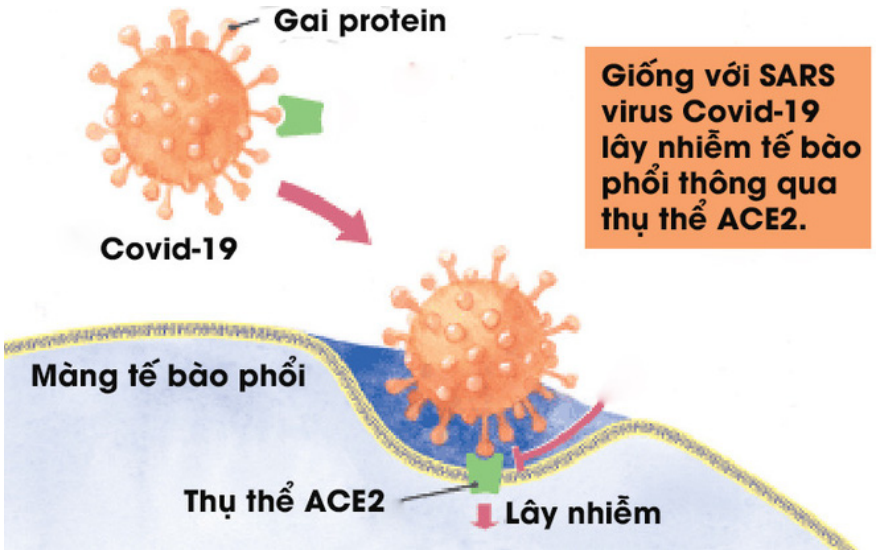


The proteins grow suddenly outside the membrane, forming spines sticking around the SARS-CoV-2 surface, giving it a crown-shaped appearance and emitting halos under an electron microscope.

It was this feature that was used to name them, corona virus with " *corona* " meaning " *crown* " or " *halo* ". And these protein spikes also play a vital role in the transmission of SARS-CoV-2 to the host cell.

Research shows that when the virus's protein spikes find ACE2 receptors (angiotensin 2 conversion enzyme) on the surface of human lung cells, they penetrate inside and begin to take control of the cell to multiply. and cause illness.

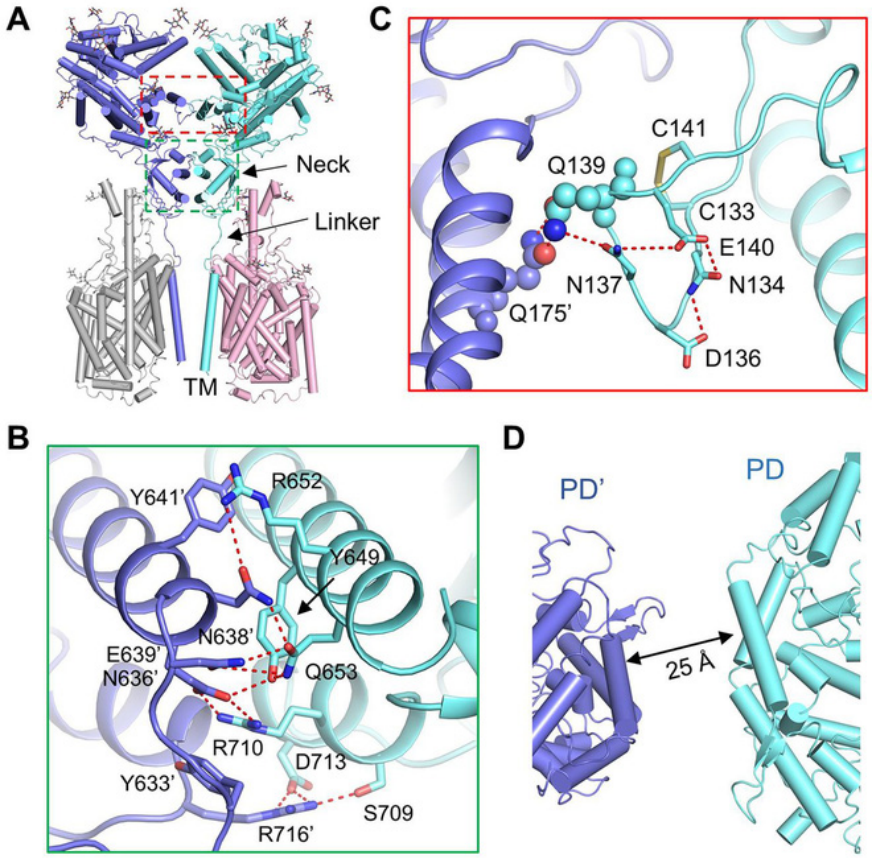
Understanding the mechanism of transmission of SARS-CoV-2 through the ACE2 receptor is an extremely important goal, because from that understanding, scientists can prepare a specific drug for Covid-19 or one type. The vaccine works by blocking this cell's infection mechanism.



And recently, a team of Chinese scientists at the Zhejiang Province Biological Structure Key Laboratory took the first images of the ACE2 receptor and the SARS-CoV-2 protein spike to such an extent that 2.9 angstrom (0.29 nm) resolution, asymptotic to atomic size (0.1-0.5 nm).

These 2D images were then folded and modeled using 3D software for the first time explaining the nature of the chemical contagion of SARS-CoV-2: Which molecular cluster of protein spikes has been somewhat linked to of ACE2 receptors, by what chemical bonds?

** Stay up to date with the latest research results and information on the worldwide outbreak of Covid-19* ***here.***



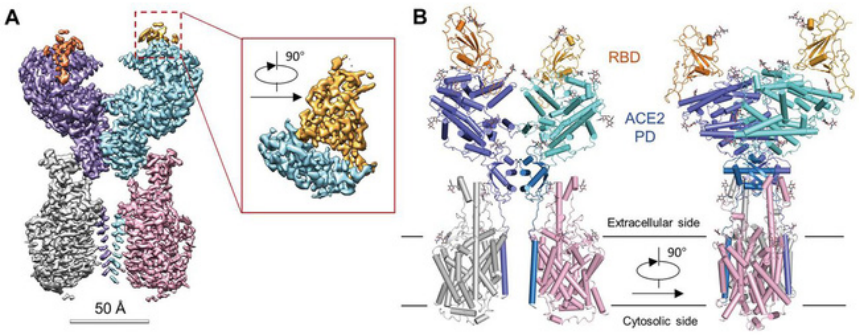
ACE2 receptor image is 3D rendered with atomic resolution.

Based on this 3D-realistic image, the scientists found that the SARS-CoV-2 protein spikes consisted essentially of S1 and S2 subunits.

S1 contains the receptor binding domain (RBD), which is the weapon that viruses use to bind to the peptisase (DP) domain on the ACE2 receptor of lung cells. Meanwhile S2 on the spikes works to serve the virus itself, which is responsible for fusion on its protective film.

The image was taken under a frozen electron microscope (cryo-EM), a photographic technique that can provide resolution to individual atoms. In it, Chinese scientists ordered recombinant and refined protein spikes, then mixed it with the ACE2 they synthesized themselves.

This means that the entire study did not use the full SAR-CoV-2 virus. They are just taking pictures of the " *curated* " virus spines, like studying the fangs of a poisonous snake.

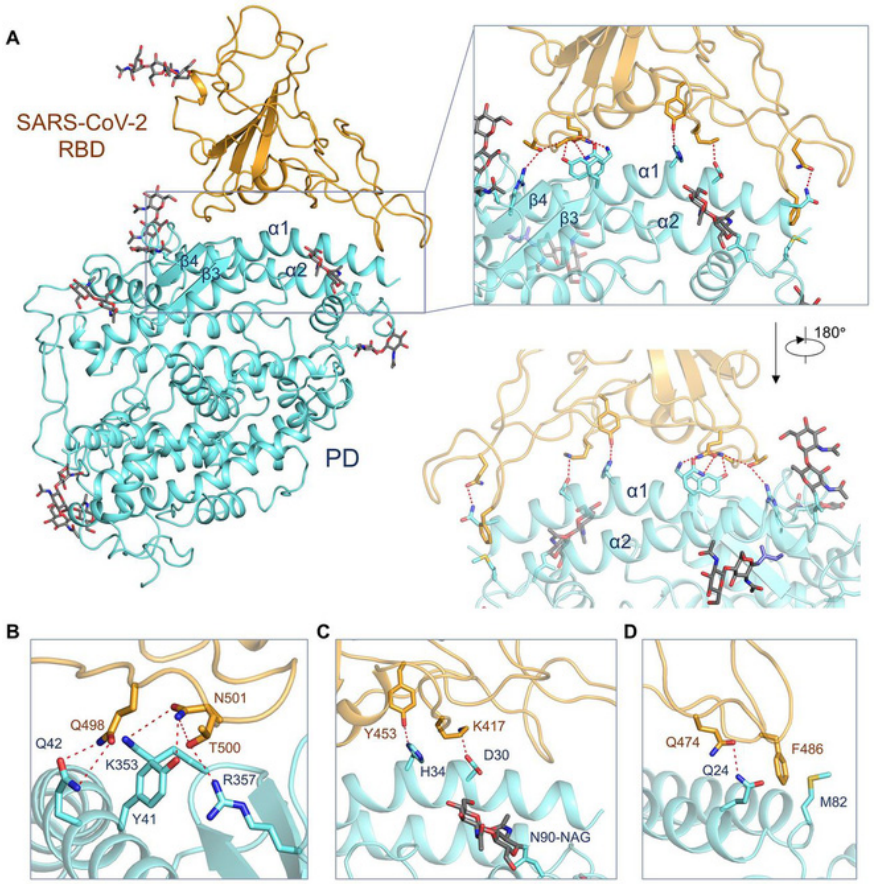


Receptor binding domain (RBD), which is the weapon that the virus binds to the peptisase (DP) domain on the lung cell's ACE2 receptor.

Under the cryo-EM microscope, the scientists observed that during S1 binding to the ACE2 receptor, another cleavage site on S2 was exposed and cut off by the host proteases, an The process is very important for virus infection.

Each PD cluster on the ACE2 receptor gives only one RBD cluster of the virus to bind to. An extended loop region of RBD extends the spiral ?1 circular sequence of ACE2-PD like a bridge.

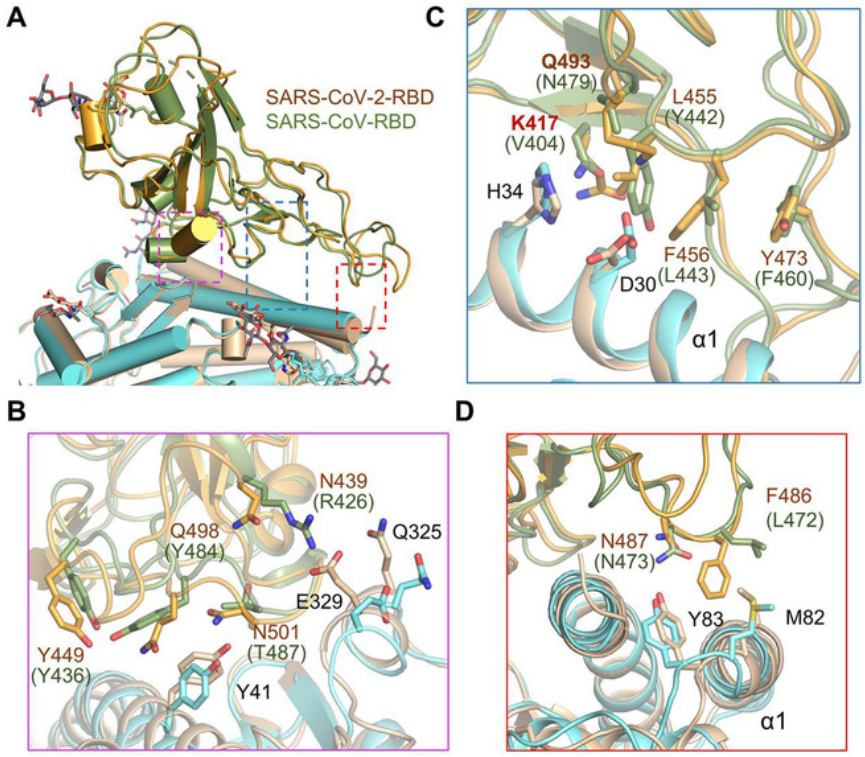
The helix ?2 and a loop connecting the non-parallel chains ?3 and ?4, of the PD, also contribute a limited contribution to the coordination of RBD. In the figure, these interactions are represented by a red dashed line:



Spines of SARS-CoV-2 virus (yellow), ACE2 receptors on lung cells (green) and chemical bonds between them.

The " *cement* " that binds the RBD cluster north from the virus to the ?1 of the PD interacts with the amino termini (N) and carboxyl (C). The endpoint of N binds to RBD by hydrogen bonding. While some other segments of RBD bind to ACE2 through van der Waals forces.

Basically, the chemical bonds that SAR-CoV-2 used to invade human cells are similar to what SARS did in the 2003 pandemic. However, there are some differences. The study showed a higher level of affinity for the virus with cells, as well as the stronger spread of the current Covid-19 epidemic compared to SARS 17 years ago:



Compare linkage image of SARS-CoV-2 with ACE2 (orange and green) by superimposing it on the link of SARS virus with the same receptor (green and yellow)

Scientists say that both SARS and Codid-19 attack ACE2 receptors on the surface of lung cells. In addition, SARS has previously attacked both the patient's intestines and kidneys, where cells also contain this receptor. The heart also contains ACE2, but both SARS and Covid-19 release the hearts of patients, something scientists have not understood why.

Finally, with this new study, the scientists hope to shed light on the infectious nature of the SARS-CoV-2 virus, providing an important document that allows us to develop different types of virus. Covid-19 therapeutic drugs and vaccines prevent entry.

The research has been published in Science.