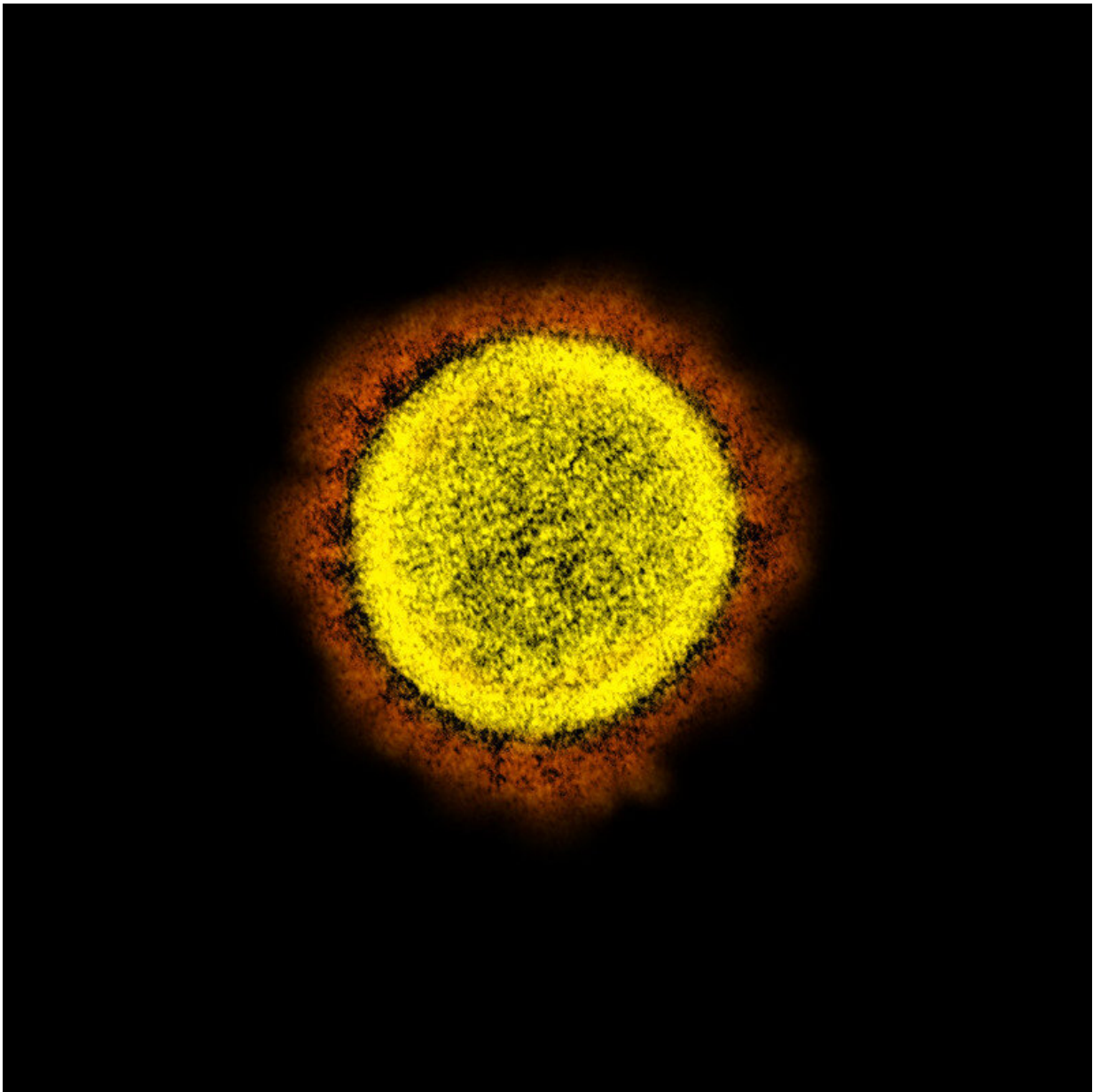


Understanding the evolution of SARS and COVID-19 type viruses

February 25 2021, by Andy Fell



Novel Coronavirus SARS-CoV-2 Transmission electron micrograph of SARS-CoV-2 virus particles, isolated from a patient. Image captured and color-enhanced at the NIAID Integrated Research Facility (IRF) in Fort Detrick, Maryland. Credit: National Institute of Allergy and Infectious Diseases, NIH

As COVID-19 sweeps the world, related viruses quietly circulate among wild animals. A new study shows how SARS-CoV-2, the virus that causes COVID-19, and SARS-CoV-1, which caused the 2003 SARS outbreak, are related to each other. The work, published recently in the journal *Virus Evolution*, helps scientists better understand the evolution of these viruses, how they acquired the ability to infect humans and which other viruses may be poised for human spillover.

"How did these viruses come to be what they are today? Why do some of them have the ability to infect humans while others do not?" said Simon Anthony, associate professor of pathology, microbiology and immunology in the School of Veterinary Medicine at the University of California, Davis, and senior author on the paper.

Both SARS-CoV-1 and SARS-CoV-2 belong to a group called the sarbecoviruses, Anthony said, but they are actually quite different from each other. Scientists have divided the sarbecoviruses into five lineages, with SARS-CoV-1 belonging to lineage 1 and SARS-CoV-2 to lineage 5.

Even though these two viruses belong to different lineages they both get into human cells using the ACE2 receptor.

"That is striking," Anthony said, "because there are other viruses more closely related to SARS-CoV-1 that do not use ACE2. So how did SARS-CoV-1 end up having similarities to a [virus](#) that is more distantly related?"

A family tree of viruses

Anthony and Heather Wells, a [graduate student](#) at Columbia University, constructed a family tree of all the SARS-like viruses. They found that lineage 5—which contains SARS-CoV-2—is the ancestral lineage. They concluded that most of the [lineage](#) 1 viruses related to SARS-CoV-1 lost the ability to use human ACE2 receptors long ago because of deletions in their genome. But SARS-CoV-1 and a few other viruses regained the ability to use [human](#) ACE2 at some point.

That probably occurred through a process called recombination, Wells said. For that to happen, two different viruses must have infected the same animal at the same time, producing a hybrid virus with the ability to infect humans through ACE2.

The family tree also gives insight into the geographic origins of these viruses, Wells said. So far, all ACE2-using viruses have been detected in Yunnan province, implying that SARS-CoV-2 did not originate in Wuhan, where the first cases of COVID-19 were reported, but elsewhere in China.

One unanswered question is, why did SARS-CoV-2 emerge now? If this virus has always targeted ACE2, it may long have had the ability to infect humans. So what prompted it to emerge at this time?

"There have to be other factors involved," Anthony said. "Having the genetic capacity to infect humans is only part of the story."

This study provides evolutionary context for why these viruses behave as they do, Anthony said. It allows researchers to place newly discovered viruses within the [family tree](#) and estimate whether they have the potential to infect humans.

"We now know that having the genetic potential for spillover doesn't mean it will happen—but it is important to identify the viruses that are high risk. We can then use epidemiological or ecological studies to investigate how and if people come into contact with bats or other animals that carry these viruses," Anthony said.

"It's also a nice reminder that there are a whole lot of viruses out there that we need to understand better—SARS-CoV-1 and 2 won't be the only ones," he said.

More information: H L Wells et al, The evolutionary history of ACE2 usage within the coronavirus subgenus Sarbecovirus, *Virus Evolution* (2021). [DOI: 10.1093/ve/veab007](https://doi.org/10.1093/ve/veab007)

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