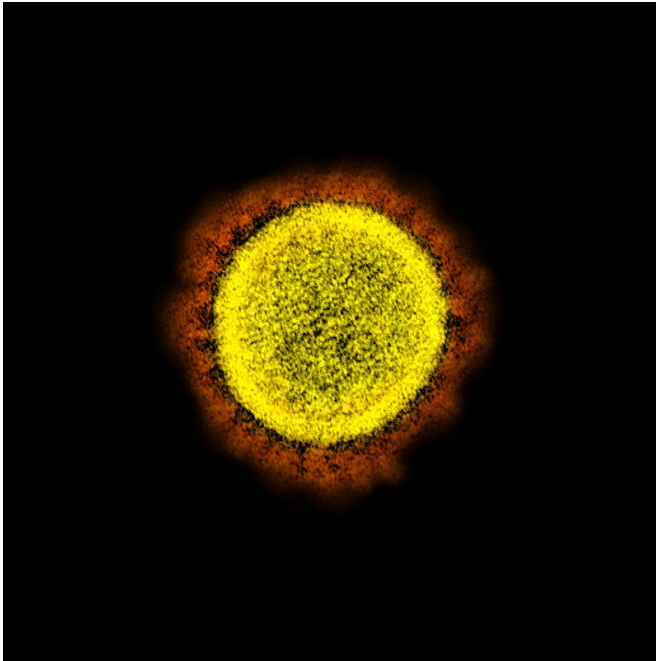


RNA analysis shows most SARS-CoV-2 variants rarely persist through secondary transmissions

12 March 2021, by Bob Yirka



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

A large team of researchers affiliated with a host of institutions across the U.K. has found that most SARS-CoV-2 variants rarely persist through secondary transmissions. In their paper published in the journal *Science*, the group the RNA sequencing of nearly 1,400 nasal swabs from patients between March and June of last year, and what they found by doing so.

As the global pandemic has progressed, attention has turned to variants of the virus that infect people with COVID-19. A growing fear is that some

of the new variants will prove to be immune to the vaccines that are being given to combat the original form of the virus, setting off a whole new pandemic. This new effort was conducted late last year, before most of the new variants had made their way into news headlines. The researchers sought to better understand the danger posed by these SARS-CoV-2 variants. More specifically, they wanted to know more about how frequently they arise and how easily they can spread.

The work by the team involved obtaining 1,313 nasal swabs collected from infected people in the U.K. between March and June of last year—most of whom exhibited symptoms of COVID-19. Each of the samples was then subjected to RNA sequencing to identify variants.

The researchers found that most of the infected people had only one or two variants, most of which were not able to survive [transmission](#) to other people. They did find that a few of those infected had variants that could survive transmission, though they found very few instances of them transmitted between households.

The researchers suggest their findings indicate that, at least during early infection, [mutations](#) that are able to survive attacks by antibodies are quite rare. That being said, they did find evidence of variants whose mutations gave them a better chance of surviving an immune response. Such mutations, they note, would be more likely to spread as [vaccine](#) use becomes more widespread. They suggest that monitoring will have to be stepped up to quickly identify variants that may not be weakened by current vaccines.

More information: Katrina A. Lythgoe et al. SARS-CoV-2 within-host diversity and transmission, *Science* (2021). [DOI](#):

[10.1126/science.abg0821](https://doi.org/10.1126/science.abg0821)

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