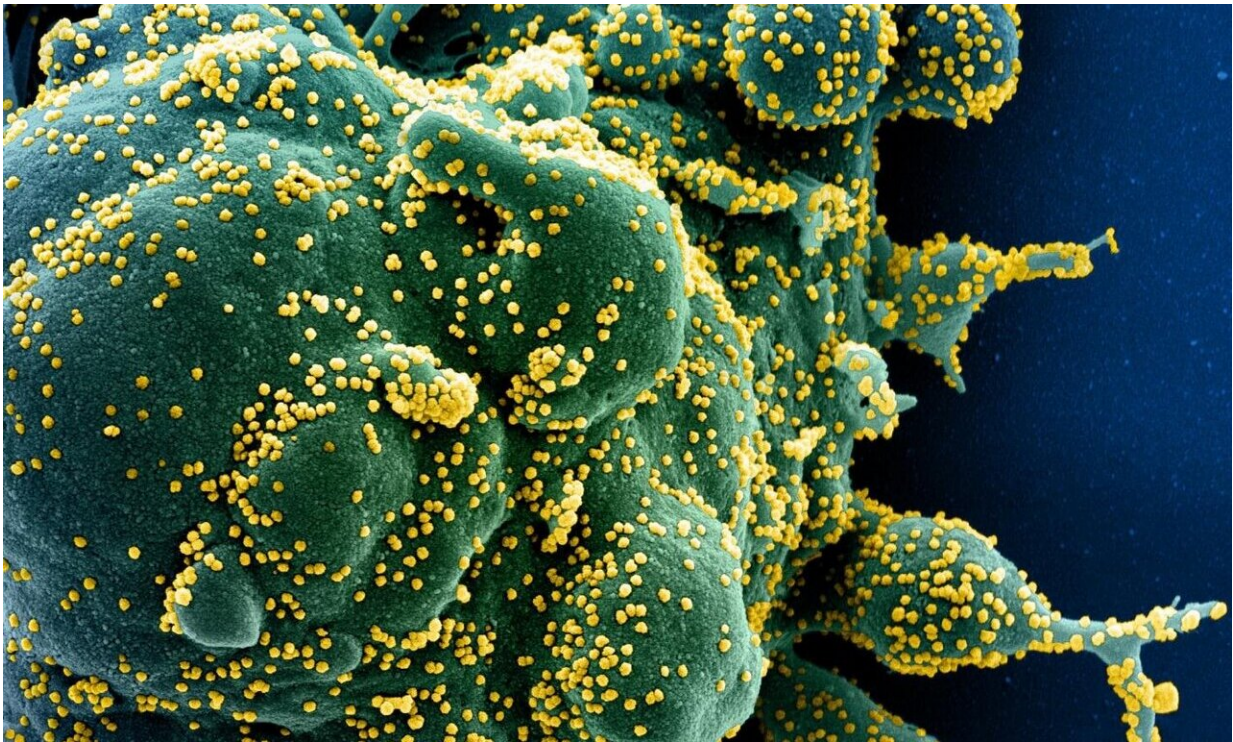


Research may help identify more dangerous strains of the virus that causes COVID-19

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Colorized scanning electron micrograph of an apoptotic cell (green) heavily infected with SARS-COV-2 virus particles (yellow), isolated from a patient sample. Image captured at the NIAID Integrated Research Facility (IRF) in Fort Detrick, Maryland. Credit: NIH/NIAID

Viral mutations during the COVID-19 pandemic could cause the SARS-CoV-2 virus to become more dangerous. A new study published in

Genetic Epidemiology has examined the genetic code of SARS-CoV-2 viruses that have infected patients, looking for links between different mutations and patient deaths.

For the study, investigators analyzed 7,548 SARS-CoV-2 genomes of COVID-19 patients worldwide and looked for an association between genomic variants and mortality. In total, 29,891 locations in the [viral genome](#) were assessed.

One location was significantly linked with patient mortality. Mutations at this location cause changes in part of the SARS-CoV-2 spike protein, which plays a key role in viral entry into host cells.

"When, in the fall of 2020, we applied methodology from [genome-wide association studies](#) to COVID-19 genomes, we noticed one locus in the COVID-19 genomes from Brazil that was associated with mortality and that later became part of the definition of the P.1 strain from Brazil," said co-lead author Georg Hahn, Ph.D., of Harvard University. The P.1 strain was behind a deadly COVID-19 surge in the Latin American country. It's more contagious and more resistant to antibodies than the original strain.

More information: Georg Hahn et al, Genome-wide association analysis of COVID-19 mortality risk in SARS-CoV-2 genomes identifies mutation in the SARS-CoV-2 spike protein that colocalizes with P.1 of the Brazilian strain, *Genetic Epidemiology* (2021). [DOI: 10.1002/gepi.22421](#)

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