## How common are mutations in SARS-CoV-2, and do the mutations lead to changes in the severity of the disease?

A small study convincingly shows that coronavirus may have more mutations than previously expected, but more data is needed on whether these mutations actually change how deadly the virus is.

## Key takeaways

- Though this study only used samples from 11 patients, it was well
  designed and used super deep sequencing technique to show that the
  coronavirus has more mutations than previously thought.
- The data on how quickly the virus reproduces and how deadly it is needs much more testing and verification to see if this is true outside of a petri dish. We wouldn't put too much stock in this finding just yet.

 Finding live virus in patient's stool is a new finding that merits further investigation

## Why is this important?

This research is important for a couple reasons. Figuring out what mutations there are and how quickly the coronavirus mutates is important for researchers working on treatments and vaccines so that they can target the right areas of the virus. Second, if different strains of the virus are more infectious or more lethal than others, this could help different countries and regions better manage their outbreaks.

This study has recently been taken up by media outlets, mainly focusing on the possibility that mutations might make some strains of the coronavirus more deadly than others. Let's take a look at those claims.

## What did the study do?

SAMPLING



Extracted live virus samples from 11 patients

The 11 patients came into the researchers' hospital in China in January 2020, and were confirmed to have coronavirus. The researchers found that they

were able to isolate functioning viral particles from poop <u>a</u>

## **OUR TAKE**

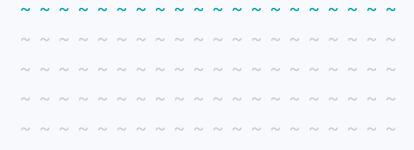


Finding active coronavirus in poop is a new finding that should be further investigated, as it may affect how people protect themselves from contracting the virus.

## Lack of standardization in virus sampling

A challenge in virus research is making sure you have the same amount of live virus in each sample because this can make a huge difference in the results.

**Example:** Let's say a sample has 100 virus particules, but only 20 of them are living, meaning they can actually reproduce.



Sample A

Meanwhile, another sample has only 50 virus particles, but all 50 of them are living.

Sample B

Standardizing between both samples before you start measuring how quickly they kill cells is super important because you could mistakenly conclude that sample B is more deadly when really it just started with more living virus particles.

There are techniques for balancing these differences out, but the researchers don't provide any detail on whether or how they did this.

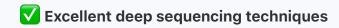
## ! Only one sample per patient

Growing the virus can vary a lot from sample to sample so generally researchers try to take multiple samples from the same patient or samples from multiple patients who have similar strains of the



This was a two part study. In the first part, they isolated coronavirus from these patients and determined if they had any mutations in their genome using deep sequencing.

### **OUR TAKE**



The researchers have excellent evidence to show how much the virus mutates. The genetic sequencing technique they used was more sensitive and of higher quality than prior studies, which allowed them to pick up more mutations.

MEASURING



Measured how fast the virus could reproduce in cells grown in a dish, and how fast they killed those cells

In the second stage, they grew the different strains of virus in the lab and measured how rapidly the strains could reproduce in (and subsequently kill) cells growing in a dish.

### **OUR TAKE**



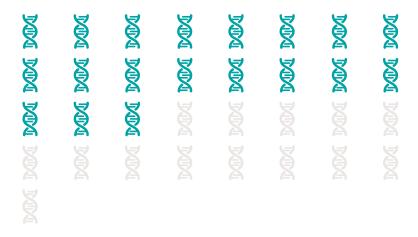
Samples grown in monkey cells, not humans

The cells that the authors used in the study were monkey kidney cells, which are commonly used in studies of viruses, and specifically for coronaviruses like SARS and the current coronavirus. It's always challenging to know if these findings would apply in living humans.

RESULTS



33 total mutations found with 19 brand new mutations



The fastest growing samples of the virus grew **270 times faster** than the slowest.

CONCLUSION



SARS-CoV-2 mutates more than we had previously thought, and different strains of the virus *might* reproduce and kill cells at different rates

### **OUR TAKE**

The authors have not demonstrated that the mutations that they detected actually changes how

sick humans get. The data on how quickly the virus reproduces and how deadly it is needs much more testing and verification to see if this is true outside of a petri dish. We wouldn't put too much stock in this finding just yet.

## ! Small sample size

Since they only took samples from 11 patients who were all very different (their ages alone ranged from 4 months to 62 years), it is impossible to say if the mutations are why some were sicker than others. This would require a lot of data and further study.

## How was it reported?

BAD

Coronavirus has mutated into more than 30 strains, study finds

## THE HILL

The article incorrectly claims that the virus was tested in human cells when it was tested in monkey kidney cells. At least it brings in one outside source to comment.

BAD

# Coronavirus has mutated into at least 30 different strains, study finds

## **FOX NEWS**

The article has minimal details on the study itself, but at least acknowledges that the results are preliminary and not peer reviewed.

VERY BAD

Coronavirus's ability to mutate has been vastly
 underestimated, and mutations affect deadliness of
 strains, Chinese study finds

### SOUTH CHINA MORNING POST

The article has a misleading subheading claiming that this study showed New York to have a deadlier strain from Europe even though the study makes no such claim. There's also no acknowledgment of the weaknesses in the study or comments from other scientists.

The original paper is a preprint study. It has *not* been certified by peer review from other researchers, and information presented may be erroneous. Do not use it to guide clinical practice! Learn more  $\rightarrow$ 

Original Paper DOI: 10.1101/2020.04.14.20060160

Patient-derived mutations impact pathogenicity of SARS-CoV-2 [PDF]

## **Additional Reading**

For more details and technical discussion of the study, we recommend reading the following resources:

• Podcast - This Week in Evolution (start at 9:49)

## **Share This Explanation**

