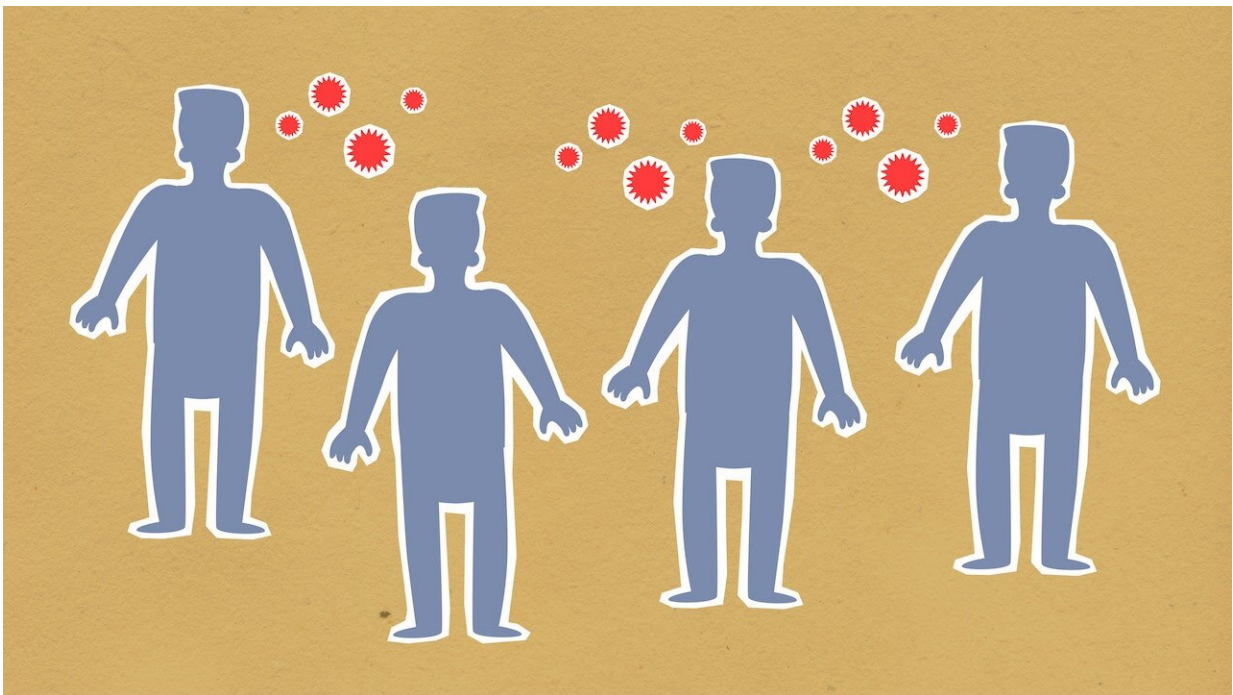


Genetic sequencing could be key to containing future COVID-19 variant outbreaks

October 12 2022



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New COVID-19 variants could potentially be contained where they arise using genetic sequencing, a new study from the University of Georgia has found. But it will require global cooperation.

Published in *PNAS Nexus*, the study found that standard methods that first assess a new [variant](#)'s severity are too slow to stop its spread. Next-generation genetic sequencing, however, offers a feasible alternative to spot new variants with enough time to contain variants where they first appear.

Genetic sequencing is a process by which researchers can determine the genetic makeup of an organism. In the case of COVID-19, some new variants, particularly the more concerning ones, have distinct differences in their [genetic code](#). That means researchers can use genetic codes to detect new troubling variants.

"The bite-sized take-home message of the study is that with the right scale of [genetic sequencing](#), containment of new variants at their source is, in principle, feasible," said Pejman Rohani, co-author of the study and an associate dean in the Odum School of Ecology. "Now the question is whether there's the appetite for doing that."

The British government, for example, recently announced they were no longer going to test asymptomatic individuals for COVID-19, a move that Rohani said is a step in the wrong direction.

"Containment efforts need to be coordinated, and they need to be well designed because variants are not going away," said Tobias Brett, lead author of the study and a postdoctoral researcher in the Odum School of Ecology. "As long as SARS-CoV-2 continues to circulate in [human populations](#), new variants will emerge. Continued surveillance of this virus is absolutely necessary. But it would require global collaboration to work."

Investing in genetic sequencing now could pay off during future disease outbreaks

The concept of using sequencing to identify disease outbreaks isn't new. And it's definitely not unique to the coronavirus.

The researchers developed a [mathematical model](#) that simulates the effects of an emerging variant, tracking its early transmission within a population and its subsequent spread through people traveling from other locations.

The researchers also found that [travel bans](#) that stopped short of quarantining all new arrivals until they are confirmed to not have the virus are unlikely to prevent a variant's geographic spread. At best, a ban that reduces the amount of people coming into a population by 99% would only delay the variant's arrival by about a month, the study showed.

"The tricky thing is policymakers have to make a decision to potentially implement [travel restrictions](#) before they know how big a threat the new variant or disease is," Brett said.

While that does pose the risk of false alarms, the researchers believe making those informed judgment calls could make all the difference.

"Public health authorities have a number of options in terms of what kind of information they would like to invest in," Rohani said. "Some countries have really invested heavily into serology (or the study of examining bodily fluid samples for antibodies), which allows them to have a good idea of how many people have been vaccinated and how many people have been previously infected.

"But in the context of new variants and trying to get ahead of them before they spread globally, our work suggests that sequencing is really going to be your best bet."

More information: Tobias S Brett et al, Containing novel SARS-CoV-2 variants at source is possible with high-intensity sequencing, *PNAS Nexus* (2022). [DOI: 10.1093/pnasnexus/pgac159](https://doi.org/10.1093/pnasnexus/pgac159)

Provided by University of Georgia

Citation: Genetic sequencing could be key to containing future COVID-19 variant outbreaks (2022, October 12) retrieved 3 May 2024 from <https://medicalxpress.com/news/2022-10-genetic-sequencing-key-future-covid-.html>

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