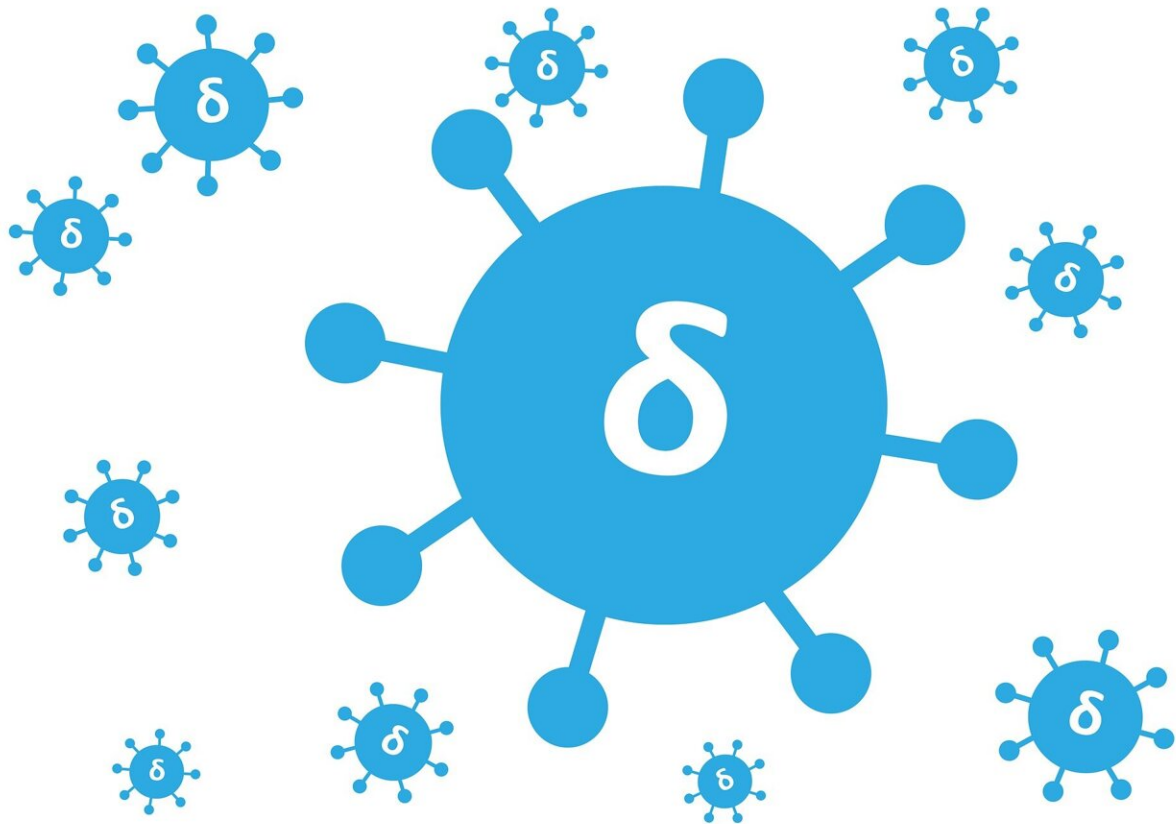


Study shows a single 'lucky' substrain of coronavirus delta variant to account for 90% of infections in Russia

December 7 2021



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Skoltech scientists and their colleagues have looked at the genetic

makeup of the dominant strain of the coronavirus, the delta variant, in Russia. According to them, just one viral subvariant quickly came to be responsible for an overwhelming majority of the cases, unlike in many other countries. The team concluded this probably happened by sheer chance and not because the substrain is more infectious or resistant to immunity. Reported in a preprint on medRxiv, the findings suggest that early on in a new pandemic wave, every case counts and tight travel regulations are an effective countermeasure.

Researchers are monitoring the rise and spread of distinct coronavirus subvariants, technically known as lineages, to keep an eye on the evolving virus and find out early enough about some of the nastier mutations it may acquire—those that make it better at infecting people, resisting natural or vaccine-based immunity, and evading test kits.

"But a sublineage may also turn out to be successful just because it got lucky. And understanding such scenarios is also important for making sense of the epidemic and predicting how it will evolve," the study's principal investigator, Georgii Bazykin of Skoltech and the Kharkevich Institute for Information Transmission Problems of RAS, commented. "This has apparently happened with the [delta variant](#), which dominated the Russian epidemic between April and October 2021."

The researchers found that one specific lineage called AY.122 "was responsible for 85% of all Russian infections in April 2021 but only for 0.5% of the cases worldwide," the paper says. Over 90% of the viral samples analyzed in the study exhibited a telltale set of mutations, which strongly suggests that they had all descended from a single infection case "imported" from abroad. Although the [genetic evidence](#) also points to several other import events, those proved relatively unsuccessful.

Neither the spread of delta in most other countries nor the pre-delta coronavirus waves in Russia have been characterized by one substrain

dominating the domestic epidemic to the extent revealed in the study. This puts Russia in one group with Singapore, Australia, the U.K., Turkey, and Japan, where no particular genetic diversity is seen in the delta variant. At the opposite pole are nations including Poland, Greece, Romania, and the Czech Republic, which saw the rise of multiple competing substrains.

"While the success of the sublineage prevalent in Russia apparently has nothing to do with its adaptedness, the biggest takeaway is perhaps this: We can clearly see how the number of infection imports from other countries can have a huge effect early on in a new wave of the epidemic, because even a single import of a not particularly nasty subvariant can rapidly get out of hand," Bazykin said.

This suggests that tight travel restrictions imposed at an early stage can play a decisive role in delaying the time when the next wave hits and stretching it out. This is helpful for reducing the load on the health care system and making maximum use of the facts that emerge as we become more aware of which path the evolution of the virus is taking.

"I see these findings in a hopeful light. Namely, since the number of cases imported to a country, say, in a week turns out to be so important early on, this means smart policy-making can actually be effective," the researcher concluded.

More information: Galya V. Klink et al, The rise and spread of the SARS-CoV-2 AY.122 lineage in Russia (2021). [DOI: 10.1101/2021.12.02.21267168](https://doi.org/10.1101/2021.12.02.21267168)

Provided by Skolkovo Institute of Science and Technology

Citation: Study shows a single 'lucky' substrain of coronavirus delta variant to account for 90% of infections in Russia (2021, December 7) retrieved 3 May 2024 from <https://medicalxpress.com/news/2021-12-lucky-substrain-coronavirus-delta-variant.html>

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