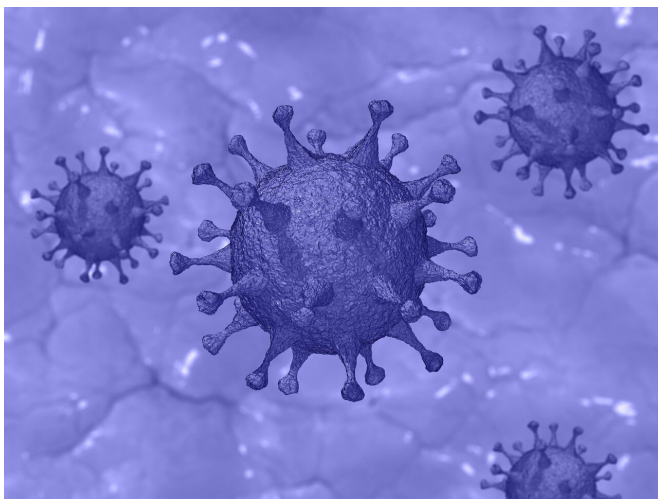


Genetic differentiation and diversity of SARS-CoV-2 Omicron variant in its early outbreak

5 August 2022



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More mutations have been carried by the SARS-CoV-2 omicron variant than previously reported variants. However, the genetic differentiation and diversity within omicron variant that occurs during its early spread remains unclear.

At the end of 2021, a new SARS-CoV-2 variant omicron appeared in South Africa. It had 50 consensus mutations, of which 31 mutations were in the S protein. Omicron had remarkable immune evasion ability and extremely fast transmission speed. As the infection cases increase, there is currently a large number of genome sequences from the early stage of the omicron outbreak.

In this article the authors comprehensively analyze the genetic differentiation and diversity of the [omicron variant](#) during its early outbreak. More deletions on omicron genome were accumulated than other four SARS-CoV-2 variants in the same timescale. Seven new notable non-synonymous

mutations emerged in addition to 50 known consensus mutations. The rapid spread of the omicron variant might lead to its high genetic differentiation and diversity in the population.

This study shows that omicron had remarkably rapid genetic differentiation and mutational diversity with its rapid spread. In [conclusion](#) more attention should be paid to the emerging omicron sub-lineages in [disease prevention](#) and control.

The research was published in *Biosafety and Health*.

More information: Shenghui Weng et al, Genetic differentiation and diversity of SARS-CoV-2 Omicron variant in its early outbreak, *Biosafety and Health* (2022). [DOI: 10.1016/j.bsheal.2022.04.004](https://doi.org/10.1016/j.bsheal.2022.04.004)

Provided by Compuscript Ltd

APA citation: Genetic differentiation and diversity of SARS-CoV-2 Omicron variant in its early outbreak (2022, August 5) retrieved 16 November 2022 from <https://medicalxpress.com/news/2022-08-genetic-differentiation-diversity-sars-cov-omicron.html>

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