



# SARS-CoV-2 omicron variant: the black swan of microbiology

Zhangkai J. Cheng<sup>1</sup> · Mingshan Xue<sup>1</sup> · Youpeng Chen<sup>1,2</sup> · Yong Zhang<sup>1</sup> · Baoqing Sun<sup>1</sup>

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## Abstract

The sudden emergence of the SARS-CoV-2 Omicron variant is causing major global concern due to its high number of mutations compared to previous variants, which is a relatively rare but significant event that can change the course of viral evolution, the occurrence of which might have huge consequences for the natural evolution of species in general, prompting us to rethink our knowledge on evolution.

**Keywords** COVID-19 · Omicron · Variant · The black swan

## Background

On 24 November 2021, a new variant of SARS-CoV-2 b.1.1.529 was reported to the World Health Organization (WHO) from South Africa, later named Omicron by WHO (Update on Omicron 2021). Omicron is the most mutated SARS-CoV-2 strain discovered so far, with over 60 known mutation sites, so it immediately attracted the attention of scientists and institutions worldwide and many countries have rapidly increased the level of control. Researchers consider Omicron to be a likely continuous iteration of the earliest strains of the virus, thus covering a wider range of mutational types.

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Zhangkai J. Cheng, Mingshan Xue and Youpeng Chen have contributed equally.

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✉ Yong Zhang  
yongzhangcn@qq.com

✉ Baoqing Sun  
sunbaoqing@vip.163.com

<sup>1</sup> Department of Allergy and Clinical Immunology, Guangzhou Institute of Respiratory Health, State Key Laboratory of Respiratory Disease, National Clinical Research Center of Respiratory Disease, First Affiliated Hospital of Guangzhou Medical University, Guangzhou, China

<sup>2</sup> KingMed Diagnostics and KingMed School of Laboratory Medicine, Guangzhou Medical University, Guangzhou, China

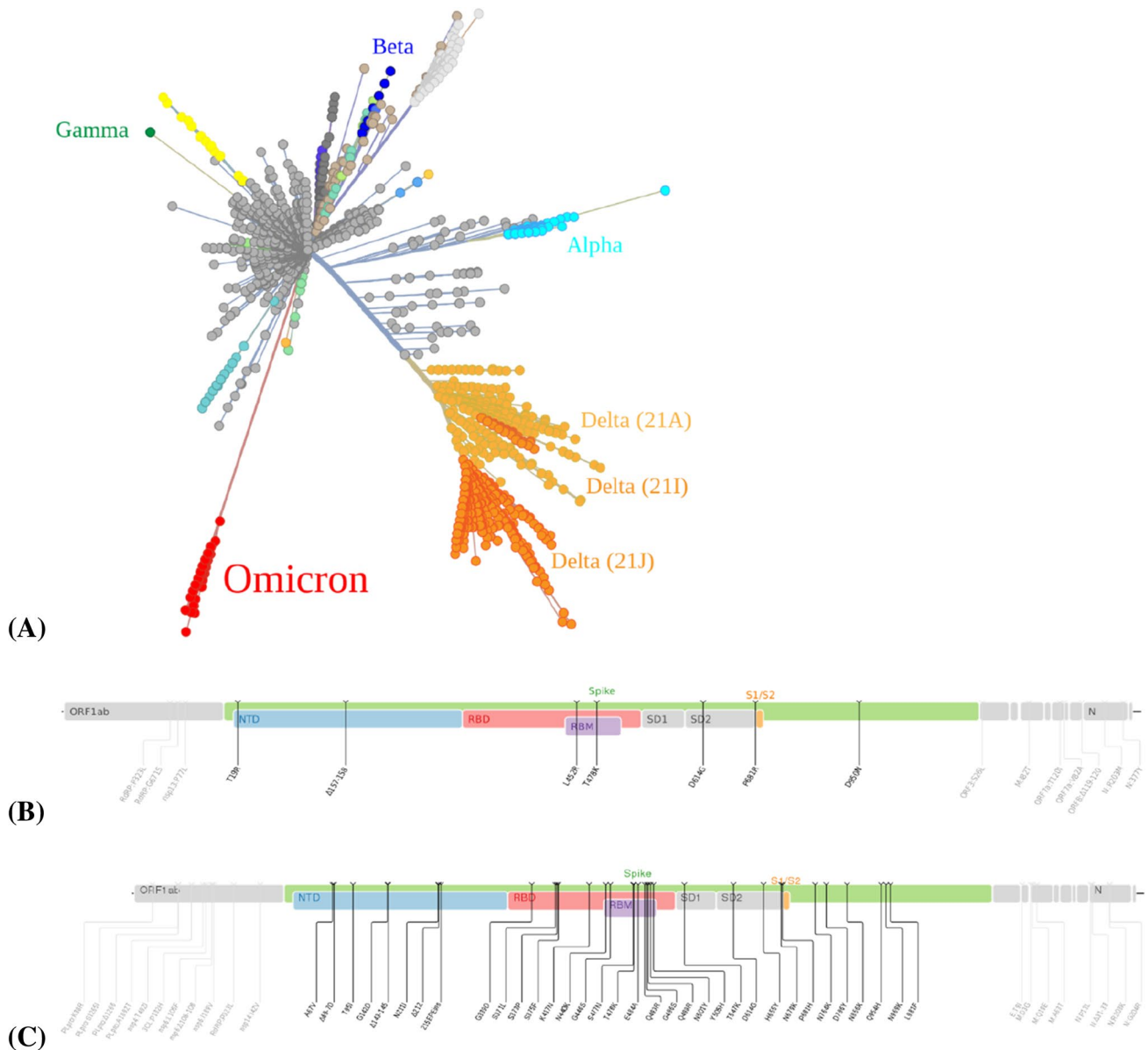
## Main text

Much remains unclear about Omicron, but studies have shown that with many mutations, the mutation has high potency for immune evasion (Kupferschmidt 2021a, b; Wang et al. 2022; Accorsi et al. 2022). With more than quadrupling the number of mutation sites compared to the Delta variant, the sudden emergence of Omicron broke the conventional understanding of viral evolution. Due to the constant mutation and iteration as the virus spreads, new strains and mutations should semi-periodically appear on an ongoing basis. The probability that any individual base will be erroneously replaced when the genome replicates were shown to be around 3/1,000,000 in a recent study (Borges et al. 2021), and this amounts to 0.1 mutations each time the genome replicates. Five replication cycles during a typical infection would result in a new mutation for every two people. However, almost all mutations never make it out into the wider world due to them being harmful/useless mutations (Morales et al. 2021). With a huge host population created by the pandemic, the overall rate of evolution is still quite high.

After two years of continuous transmission and mutation, the Delta variant had accumulated only 13 (15 or 17, depending on whether more common mutations are included) mutation sites, in line with the natural rate of evolution (Novelli et al. 2021). The independently evolved new variant of Omicron shows a markedly greater number of mutations compared to the previous SARS-CoV-2 variants (Kandeel et al. 2022). Being the most highly mutated SARS-CoV-2 strain discovered to date, the Omicron variant carries a total of 60 known mutation sites compared to

the original wildtype strain: 50 nonsynonymous mutations, 8 synonymous mutations, and 2 non-coding mutations (Nie et al. 2022). Figure 1 compares the genetic variations for different SARS-CoV-2 strains. With such a high number of mutations, the emergence of Omicron broke this observed rate of evolution. This new mutation set has a significant competitive advantage, as Omicron has become the globally dominant strain. The reason for its emergence may be that Omicron stemmed from a particular environment,

such as in individuals with particular chronic diseases, or reinfection from non-human species, or that vaccine suppression accelerates the mutation of the virus. A leading theory is that Omicron results from accumulating evolutionary mutations in a patient with AIDS (Kupferschmidt 2021b).



**Fig. 1** SARS-CoV-2 mutations. **A** Omicron variant and other major or previous variants of concern of SARS-CoV-2 depicted in a tree scaled radially by genetic distance. Image by Soupvector—CC BY-SA 4.0, [https://commons.wikimedia.org/w/index.php?curid=](https://commons.wikimedia.org/w/index.php?curid=112983798)

[112983798](https://commons.wikimedia.org/w/index.php?curid=112983798). **B** Mutations of SARS-CoV-2 Delta variant with a focus on the spike. **C** Nonsynonymous mutations of SARS-CoV-2 Omicron variant with a focus on the spike. Image by Stanford HIVDB Team—<https://covdb.stanford.edu/page/mutation-viewer/>

## A black swan

The black swan theory, according to its developer Taleb, refers to unexpected and catastrophic events characterized by three conditions (Taleb 2010):

1. The event should be statistically anomalous and have exceptional value.
2. The event should have an extreme impact.
3. Human nature would rationalize the event and provide it with after-the-fact predictability.

According to Taleb himself, the COVID-19 global pandemic is a white swan instead of a black swan, due to being something that would eventually take place with great certainty (Taleb 2020). The outbreak of the SARS-CoV-2 Omicron variant, on the other hand, is typical of a black swan event, due to it being improbable but significant, as it changes the course of the viral evolution. The occurrence of such an event suggests that similar mutation events might occasionally occur in nature. In a short time, favorable evolutionary conditions may lead to a sudden leap in the evolution of a species, breaking the stable rate of natural evolution, and may even result in the creation of a new species or gain new functions. If similar black swan events appeared in the history of evolution, they would greatly influence the evolution speed and the impact on the population ecology of different species (such as viruses, plants, animals).

## Conclusions

Further study of this event may point to new problems and challenges of conventional evolutionary theory, prompting us to reconsider the mechanism of evolutionary events, species differentiation, and chronology determination of species origin and differentiation.

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**Consent for publication** All authors gave consent for publication.

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