

# The emerging Omicron sublineages

What led to the recent outbreak of COVID-19 cases in China? What are the SARS-CoV-2 lineages circulating in the country? Which Omicron sublineages has the WHO put under the 'Omicron subvariants under monitoring' category?

## EXPLAINER

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### The story so far:

Since the initial outbreak in 2019 in Wuhan, China, the world has seen multiple repeated waves of COVID-19 infections over the past few years, largely driven by the emerging variants of concern (VOCs) of the causative virus, SARS-CoV-2. However, until recently, China remained successful in containing the spread of the disease owing to its zealous "zero-COVID" policy, which included mass quarantines, lockdowns, and early vaccination programmes. As a result of the abrupt lifting of the policy, the country is now facing a surge of COVID-19 cases.

### What are the SARS-CoV-2 lineages circulating in China?

Over the course of the pandemic, genome sequencing of the virus and rapid sharing of data has been key to tracking the evolution of SARS-CoV-2 and early identification of emerging variants. SARS-CoV-2 sequencing data previously submitted from China to GISAID, a globally accessible repository of SARS-CoV-2 genome sequences, shows that over the months, the country has seen isolated cases linked to multiple variants of the virus seen previously. These include Delta and its sublineages in 2021, and Omicron and its sublineages in 2022. Only 30 sequences of SARS-CoV-2 collected between October-December 2022 are available on GISAID from China. These belong to 14 different lineages of SARS-CoV-2, all of which are Omicron sublineages, including BA.5.2, BQ.1.1, BF.7, BF.5, BA.2.75 and the recombinant lineage XBB.

Of the 14 genomes from China available on GISAID for the month of December, two genomes each belong to the Omicron sublineages BF.7, BF.5 and BA.2.75, while one genome belongs to the recombinant lineage XBB. Lineages BF.5 and BF.7 of SARS-CoV-2, while first detected in January



On a rise: Medical staff assist patients at a clinic treating COVID-19 patients, in China. GETTY IMAGES

2022 in France, have also been previously detected in India in May and July 2022, respectively, while lineage BA.2.75 was first detected in India as early as December 2021. The recombinant lineage XBB has also been previously detected in early 2021 in multiple countries in Asia, including India and Singapore. With the limited number of genomes available corresponding to the ongoing outbreak, we are still in the dark about the variants driving the wave in China.

### Which Omicron sublineages are under monitoring?

Owing to the large-scale spread of Omicron and its sublineages across the world, the World Health Organisation (WHO) has added another category of variants referred to as 'Omicron subvariants under monitoring'.

Currently, the Omicron subvariants being monitored under this category include BA.2.75, BA.4.6, XBB, BA.2.3.20 and sublineages of BA.5 including BF.7 and BQ.1. While the first sample belonging to lineage BA.4.6 dates back to December 2021, lineage BA.2.3.20 was detected in multiple

countries recently in August 2022.

### What is the XBB lineage?

The SARS-CoV-2 virus has the potential to evolve by exchanging large fragments of the genome, called recombination. First detected in January 2022, the XBB lineage of SARS-CoV-2 resulted from recombinant between Omicron sublineages BA.2.10.1 and BA.2.75. The lineage was largely detected in genomes from Singapore and India, with the largest number of genomes on GISAID belonging to the U.S. and India. Although detected in over 30 countries, there has been no observed association of the lineage with a sustained increase in new cases in India but has become now the dominant variant in many countries seeing an uptick in infections. Monitoring the prevalence of XBB and its sublineages will therefore be essential in the days to come.

Although BA.5 was first detected in November 2021, certain BA.5 sublineages having mutations at key antigenic sites in the virus have emerged over the months, including BF.7, BF.14 and BQ.1. Lineage BQ.1 is a BA.5 sublineage having the muta-

tions K444T and N460K in the spike protein of the virus. Accounting for over 5% of global cases, the variant has been seen to have a growth advantage over other lineages in highly vaccinated regions including Europe and the U.S., thus making it important to monitor the spread and evolution of this sublineage.

With waning immunity to vaccination and prior Omicron waves leading to reinfections, genomic surveillance will be the key to understanding the continuing evolution of Omicron. Being immune-naïve to Omicron, an overwhelming surge of cases in a populous country such as China will not only cause massive loss to life but will also allow the virus to mutate with the potential to create new variants. Wide-ranging efforts are thus urgently required to monitor the COVID-19 situation in China and other countries, including genomic surveillance and the use of time-tested methods with significant scientific evidence.

(The authors are researchers at the CSIR Institute of Genomics and Integrative Biology in Delhi. All opinions expressed are personal)

## THE GIST

Until recently, China remained successful in containing the spread of the disease owing to its zealous "zero-COVID" policy. However, the abrupt lifting of the policy has led to a surge of COVID-19 cases.

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