

Summary of SARS-CoV-2 variants of concern for increased infectivity/transmissibility and antigenic changes (no. 26)

Updated March 24, 2023, at 9:00 am
National Institute of Infectious Diseases, Japan

*This is a provisional translation of the summary of the report entitled "*kansen-denpasei no zoukaya kougenseino henkaga kenensareru SARS-CoV-2 no henikabunituite (dai26hou)*" (<https://www.niid.go.jp/niid/ja/2019-ncov/2551-cepr/11879-sars-cov-2-26.html>). In the case of any dispute over translation, Japanese text prevails.

Overview of SARS-CoV-2 variants

The Omicron, the B.1.1.529, and its descendent lineages are still dominant globally among SARS-CoV-2 variants, with no significant changes in epidemiological trends compared to the No. 25 report. The World Health Organization (WHO) refers to all B.1.1.529 sub-lineages and recombinants as Omicron, whereas NIID has classified omicron variants as variants of concern (VOCs).

The omicron variants are genetically divergent, and WHO and European Centre for Disease Prevention and Control (ECDC) have classified them as variants under monitoring (VUM), variants of interest (VOIs), and VOCs. The WHO has classified XBB.1.5 as currently circulating variants of interest (VOIs), and BQ.1, BA.2.75, CH.1.1, XBB and XBF as currently circulating variants under monitoring (VUMs), respectively, since March 15. However, the information lacks significant changes in viral characteristics such as severity or infectivity/transmissibility, apart from the predominance of the increased number of infected cases and the possibility of immune escape between subvariants. Thus, NIID continues the current classification of the subvariants. It is important to continue monitoring and collecting information on sub-variant outbreaks through genomic analysis in the country and quarantine.

They accounted for 98.4% of the sequences submitted to GISAID from February 13 to March 13, with few reports of other lineages (WHO, 2023). The XBB variant accounted for 44.8% of the detected subvariants and became dominant in five of the six WHO regions, except the Western Pacific region, in the 8th week of 2023 (February 20-26).

The top three variants globally were XBB.1.5 (35.1%), BQ.1 (15.1%), and XBB, excluding XBB.1.5 (9.7) (WHO, 2023). In Japan, BA.5 replaced BA.2 around July 2022, and the relative sequence prevalence among circulating variants has been dominated by BA.5, followed by an increasing proportion of BQ.1 (a sub-lineage of the BA.5.3 lineage) and BA.2.75 (a sub-lineage of the BA.2 lineage) since October 2022.

Some subvariants, such as BQ.1 and XBB, exhibit characteristic mutations in the spike protein that allow the virus to evade neutralizing antibodies through vaccination, infection, and/or show a growth advantage. Some subvariants, such as XBB.1.5, are increasing in North America and may have a growth advantage over existing sub-lineages in certain regions. However, there were no findings that they spread more rapidly than the other variants.

Omicron subvariants have emerged with specific characteristics that primarily contribute to immune escape. There were no significant differences from the other variants except for them. Global immune status and some public health interventions in each country have resulted in less influence of variant-specific nature on epidemic dynamics. It is crucial to determine appropriate interventions based on regular monitoring of variant prevalence and changes in variant-specific features, including virulence, transmissibility, vaccine and antiviral resistance, clinical presentation, and rapid risk assessment for each variant.

COVID-19 surge has been reported in China since November 2022. China decided to cease the zero-COVID-19 policy on December 7, 2022. The number of daily cases started increasing in late December 2022, and there was a late increase in severe or hospitalized patients in early January 2023. Recent reports have demonstrated a decreasing trend in the number of daily cases. According to sequences submitted to GISAID from China, BA.5.2.48 and BF.7.14 were considered dominant. These subvariants are thought to have no significant effect on immune escape, transmissibility, and severity compared with BA.5.2 and BF.7, which have already been detected in Japan.

Japan conducted screening tests for all passengers with a travel history of China (excluding Hong Kong and Macau) (within seven days) and all passengers directly from China (excluding Hong Kong and Macau) as they arrived from December 30, 2022. These test results revealed that BA.5.2 and BF.7 are dominant in these passengers from China. The quarantine testing policy has changed since March 1 to test a maximum of 20% of the samples from passengers from China (excluding Hong Kong and Macau).