中国科学院北京基因组研究所（国家生物信息中心）
BEIJING INSTITUTE OF GENOMICS CHINESE ACADEMY OF SCIENCES / CHINA NATIONAL CENTER FOR BIOINFORMATION

Molecular epidemiology of the SARS-CoV-2 variant in China revealed a new Omicron BF.7 sub-lineage (proposed to be BF.7.14), October to December 2022

Edition 1, published 8 January 2023

In this edition:
- Overview of epidemic situation in China
- Open released SARS-CoV-2 sequences in China from October to December 2022
- Sequences analysis revealed a new BF.7 sub-lineage

Overview of epidemic situation in China

From November 2022, the COVID-19 epidemic started to spread rapidly in Beijing, China (Figure 1). Most of the reported clinical symptoms were serious, including high fever, severe sore throat, pain, cough, and in some cases lung infection. This seems to be in contrast to the reported situation in previous waves in Shanghai and Guangdong earlier in the year, where there were a large proportion of asymptomatic or mild cases. What are the main epidemic strains? Are there any new variants circulating in China?

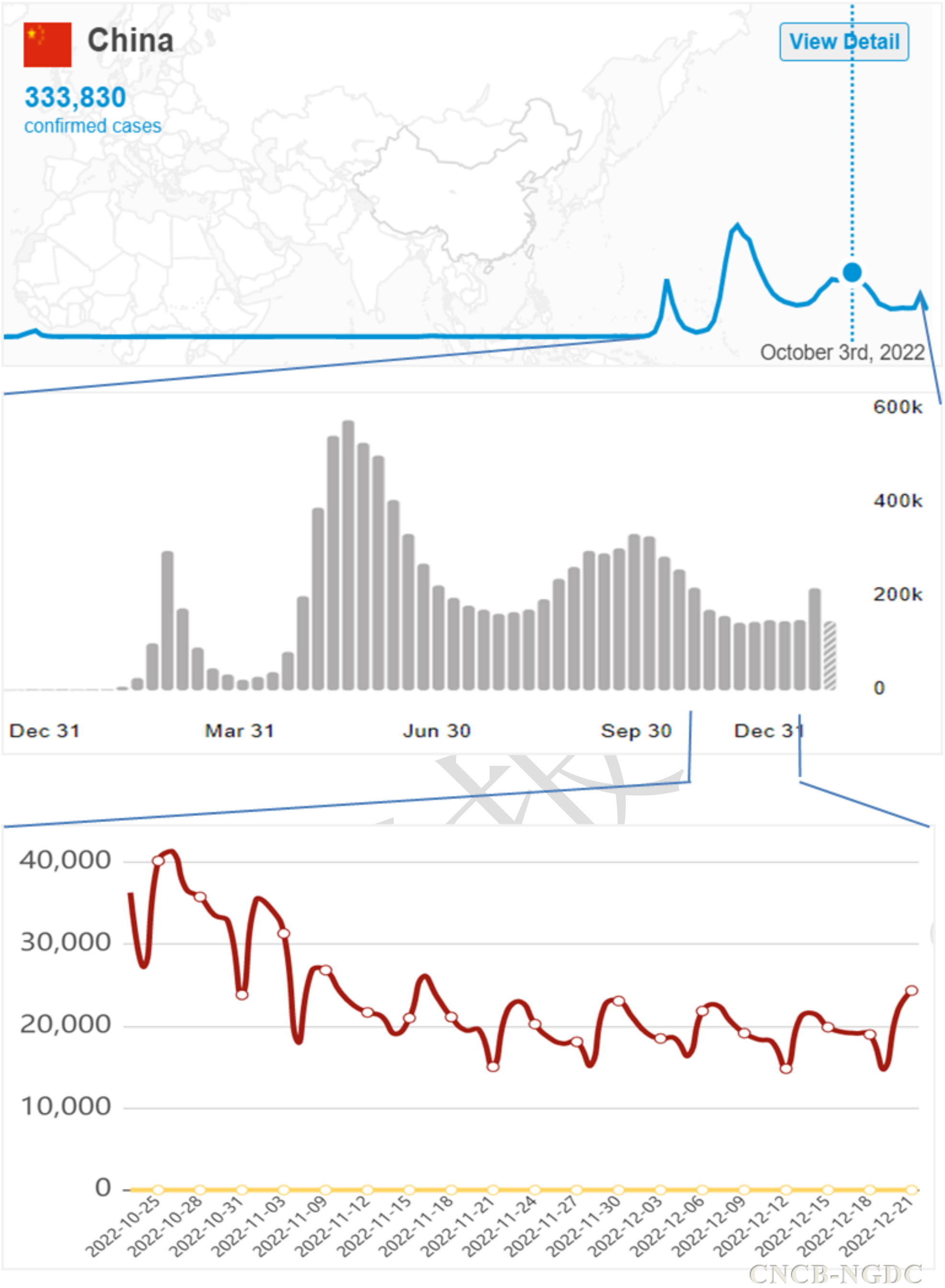

Figure 1 Confirmed COVID-19 cases in China.

Data obtained from WHO (https://covid19.who.int/region/wpro/country/cn) and Wangyi (https://wp.m.163.com/163/page/news/virus_report/index.html).

Released SARS-CoV-2 sequences in China between October and December, 2022

A total of 817 SARS-CoV-2 sequences collected since October 2022 in mainland China have been released, covering 79 Pangolin lineages (https://ngdc.cncb.ac.cn/ncov/monitoring/country/China). The main epidemic lineages are different between the north and south part of China. The 304 sequences in the north are distributed in 12 lineages, and the two main lineages are BF. 7 (72%) and BA. 5.2 (19%). The 494 sequences in the south, however, are more diversified and fall into 73 lineages, with the following top three lineages:

BA. 5.2 (35%), BF. 7 (12%) and BQ. 1.1 (11%) (Figure 2). It should be pointed out though, the high number of lineages in the south are mostly contributed by imported cases in Shanghai.

One of the largest lineages is BF.7 (278, 34%), whose sequences were mainly collected from Beijing (208, 74.8%), Shanghai (30, 10.8%) and Fujian (18, 6.5%), between October and December 2022. Actually, it was circulating in Inner Mongolia as early as late September 2022 before the abandonment of the zero-COVID-19 policy. Its high prevalence in China is presumably due to a founder effect, not the selection pressure from immune escape.

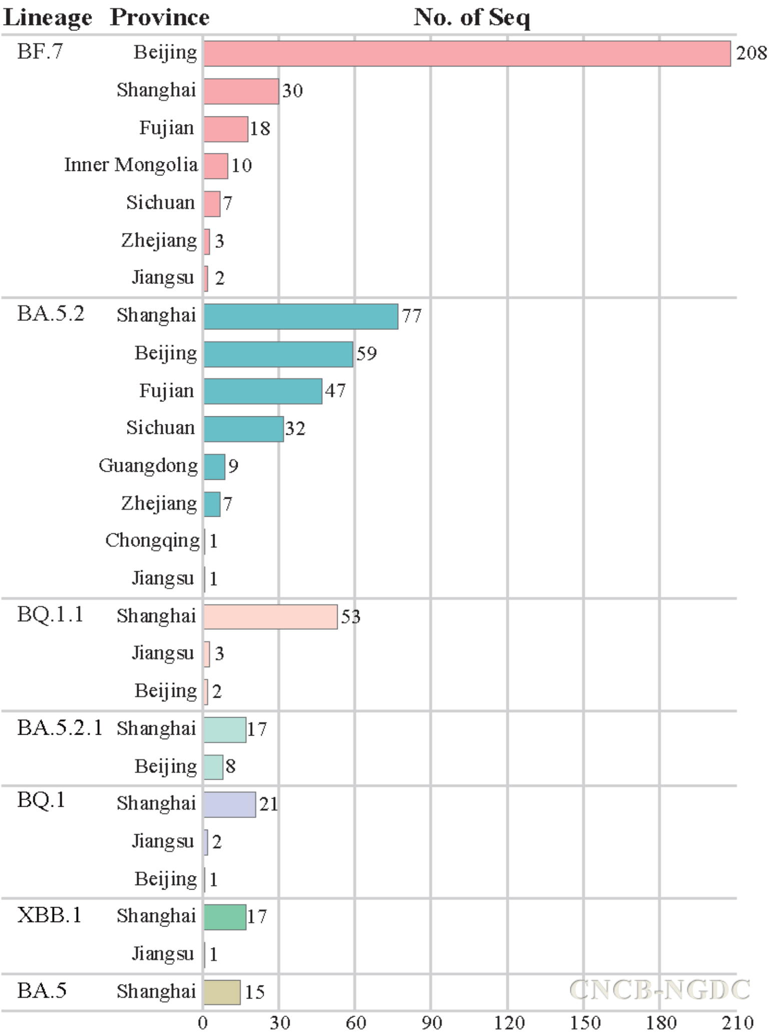

Figure 2 Distribution of the pangolin lineages for all public available sequences collected from October to December 2022 in China.

Sequences analysis revealed a new BF.7 sub-lineage

Sequence comparison revealed that the recent BF.7 sequences in China are completely distinct from BF.7 and its 18 sub-lineages (as of January 7, 2023, Figure 3). There are additional five new mutations concurrently to BF.7, namely V274L in ORF1a, L238F in ORF1b, C1243F in S, H47Y in ORF7a, and C29632T in ORF10 (Figure 4). This suggests that there is an independent BF.7 sub-lineage spreading in China, which had also been proposed (https://github.com/cov-lineages/pangodesignation/issues/1470) and has been designated as BF.7.14 recently in Pangolin. Although these mutations are not located in domains with obvious functions such as the RBD of the S protein, their effects on virus transmissibility and pathogenicity deserve further investigations.

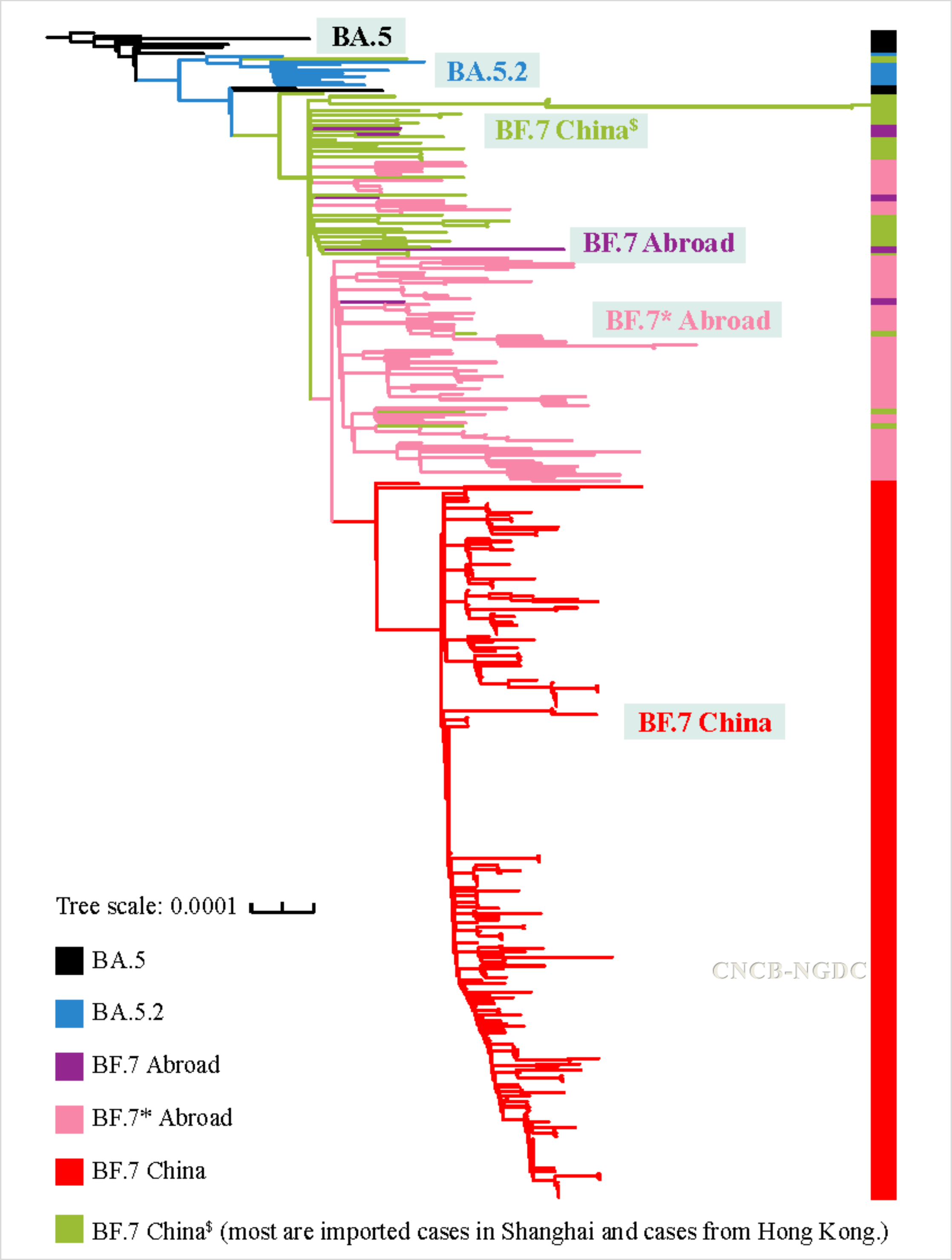

Figure 3 The phylogenetic tree of all BF.7 sequences from China and sequences sampling from BA.5, BA.5.2 and BF.7* aboard.

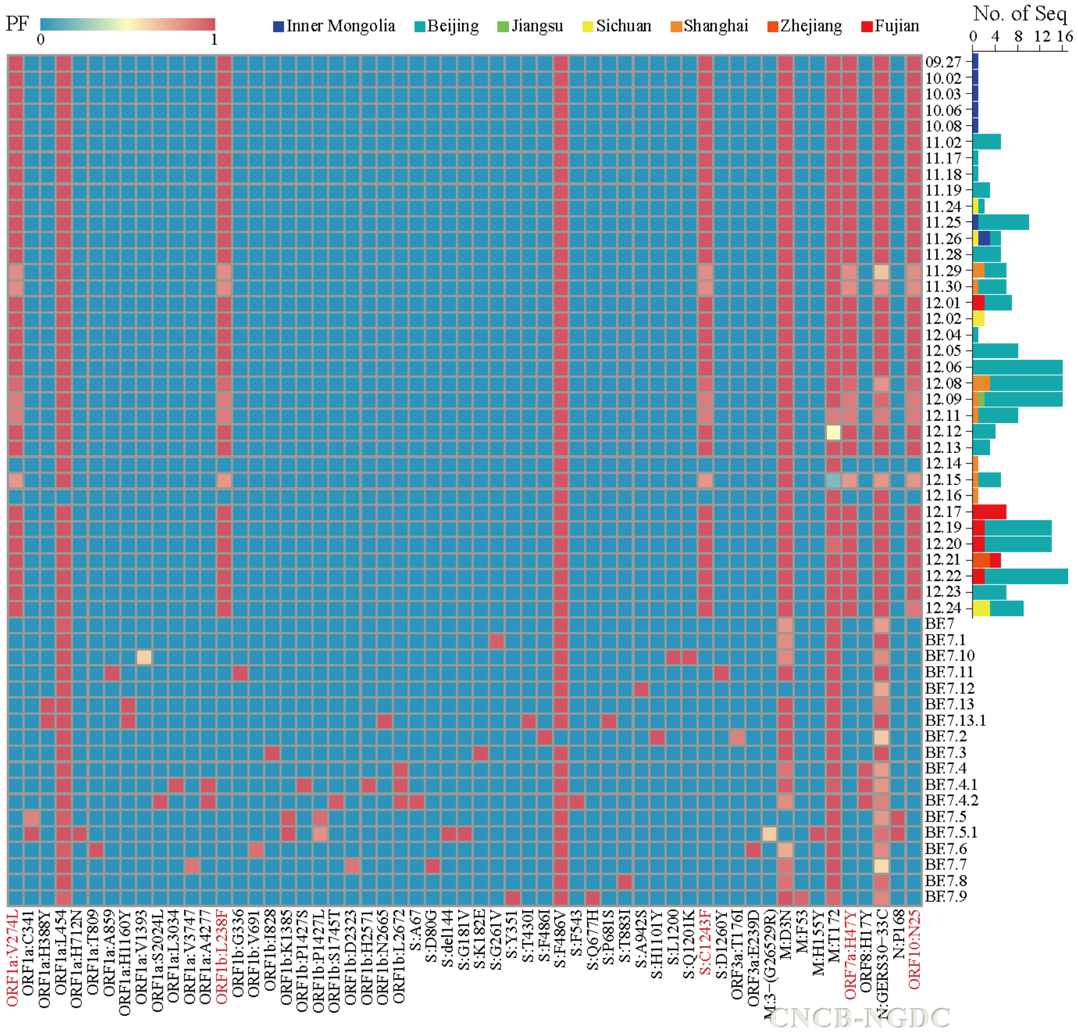

Figure 4 Distribution of population frequency of mutated allele from sequences on different collection time (between Oct. and Dec., 2022) in China, and sequences representing different BF.7* lineages. The five new mutations concurrently to BF.7 are labelled in red in X-axis. In the right panel, we also show the number of high quality sequences and their location.

To better understand the relationship of BF.7 and other Omicron lineages, a schematic diagram in provided in Figure 5.

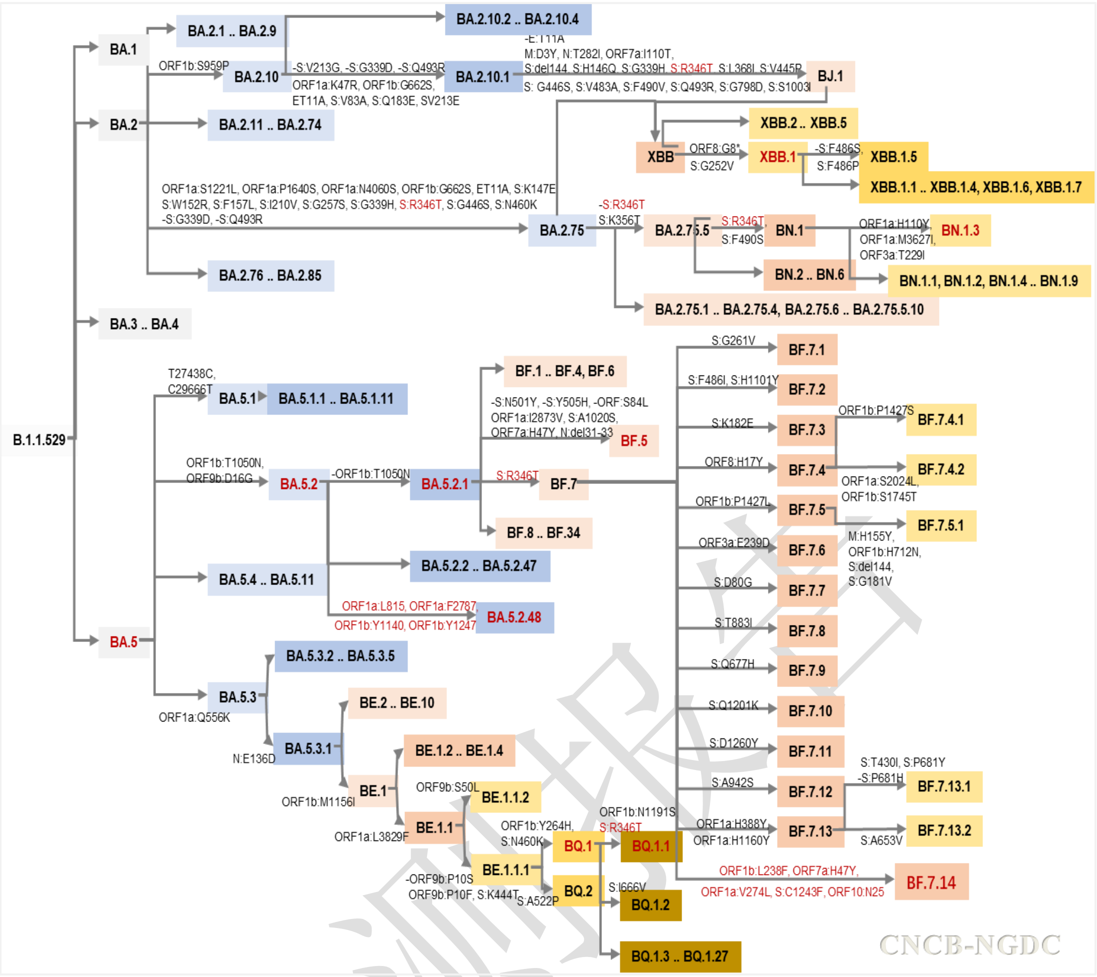

Figure 5 Schematic diagram of the evolution relationship for major Omicron lineage.