Vital Surveillances

Genomic Surveillance for SARS-CoV-2 — China, September 26, 2022 to January 29, 2023

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ABSTRACT

Introduction: The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has generated 2,431 variants over the course of its global transmission over the past 3 years. To better evaluate the genomic variation of SARS-CoV-2 before and after the optimization of coronavirus disease 2019 (COVID-19) prevention and control strategies, we analyzed the genetic evolution branch composition and genomic variation of SARS-CoV-2 in both domestic and imported cases in China (the data from Hong Kong and Macau Special Administrative Regions and Taiwan, China were not included) from September 26, 2022 to January 29, 2023.

Methods: Analysis of the number of genome sequences, sampling time, dynamic changes of evolutionary branches, origin, and clinical typing of SARS-CoV-2 variants submitted by 31 provincial-level administrative divisions (PLADs) and Xinjiang Production and Construction Corps (XPCC) was conducted to assess the accuracy and timeliness of SARS-CoV-2 variant surveillance.

Results: From September 26, 2022 to January 29, 2023, 20,013 valid genome sequences of domestic cases were reported in China, with 72 evolutionary branches. Additionally, 1,978 valid genome sequences of imported cases were reported, with 169 evolutionary branches. The prevalence of the Omicron variants of SARS-CoV-2 in both domestic and imported cases was consistent with that of international epidemic variants.

Conclusions: This study provides an overview of the prevalence of Omicron variants of SARS-CoV-2 in China. After optimizing COVID-19 prevention and control strategies, no novel Omicron variants of SARS-CoV-2 with altered biological characteristics or public health significance have been identified since December 1, 2022.

China has adhered to its dynamic COVID-zero policy and strategies to tackle both imported and domestic infections since the outbreak of coronavirus disease 2019 (COVID-19) (*1*). Based on the Protocol on Prevention and Control of Coronavirus Disease 2019, China has systematically conducted severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) genome surveillance on the virus strains causing domestic outbreaks and imported virus strains (*2*). Surveillance data confirmed that all domestic cases of sporadic and outbreaks in China after May 2020 were caused by imported cases or imported contaminated SARS-CoV-2 cargoes (*3*).

Since the Omicron variants were reported in November 2021, different Omicron lineages have circulated around the world, reflecting their strong transmission ability (*4*). As the global number of infections continues to increase and vaccination rates improve, numerous studies and clinical data have indicated that the pathogenicity of Omicron is significantly reduced compared to the original strain and other variants of concern (VOCs) such as the Delta variant (*5*). In December 2022, China optimized and adjusted its epidemic prevention and control policies according to the characteristics of Omicron and the global epidemic trend. Following this, the number of infections in China increased significantly.

In this study, we analyzed the prevalence of Omicron lineages in domestic and imported cases before and after the adjustment of China's dynamic COVID-zero policy in China. This provided information about the source and evolution of SARS-CoV-2 variants Omicron during this period.

METHODS

Data Sources

In this study, SARS-CoV-2 variant genome data was included for all cases of COVID-19 that had been sequenced in the SARS-CoV-2 laboratory network from September 26, 2022 to January 29, 2023 in China (the data from Hong Kong and Macau Special Administrative Regions and Taiwan, China were not included. Data was reported in real time by 31 provincial-level administrative divisions (PLADs) and Xinjiang Production and Construction Corps (XPCC) to the COVID-19 Notifiable Surveillance System of the National Institute for Virus Disease Control and Prevention, covering all regions in China.

The China COVID-19 Case Database is a laboratory-based surveillance system that receives real-time electronic data on laboratory-confirmed cases of SARS-CoV-2 from PLADs in China.

Data collection criteria included selecting three sentinel hospitals in three different regions of 31 PLADs and XPCC, with no fewer than 25 valid sequence tests completed weekly for each sentinel hospital in each PLAD. Additionally, surveillance of SARS-CoV-2 variants among inbound people was conducted at land, water, and airport ports.

Sequencing Strategy and Data Analysis

The complete genome sequence of SARS-CoV-2 was obtained using Oxford Nanopore, Illumina, and BGI sequencing systems. Genomic analysis of all files was performed using CLC Genomics Workbench (version 21.0.4; Qiagen, Germany) and Nextclade webservers. The whole genome spliced sequence, sequence quality test, mutation sites, and the number of mutation sites were obtained.

RESULTS

The Dynamic Trend of SARS-CoV-2 Variants from Domestic Cases in China

From September 26, 2022 to January 29, 2023, 20,013 valid genome sequences of COVID-19 from domestic cases were reported by all 31 PLADs and XPCC, with 72 lineages. The predominant lineages were BA.5.2.48 (52.42%), BF.7.14 (22.70%), and BA.5.2.49 (16.30%), followed by 15 other lineages with proportions ranging from 0.11% to 2.46%, including BA.5.2, BA.2.76, BF.7, BA.5.1, BA.5.2.1, BA.2.75.2, BF.21, BN.1.3, BA.2.3, BA.5.2.20, BQ.1.10, BA.2.12.1, BF.11, BM.2, and BA.2.2. Additionally, 54 minority lineages with proportions below 0.10% accounted for 1.07% (Figure 1A). The proportion of BA.5.2.48 gradually increased from 7.14% (September 26–October 2, 2022) to 68.71% (January 23–28, 2023), while the proportion of BA.5.2.49 declined from 44.16% (October 3–9, 2022) to approximately 6%. Additionally, the proportion of BF.7.14 rose from 7.58% (October 17–23, 2022) to 34.07% (December 5–11, 2022), before decreasing to 22.70% (January 23–28, 2023) (Figure 1A).

BA.5.2 and its descendant lineages, including BA.5.2, BA.5.2.1, BA.5.2.12, BA.5.2.16, BA.5.2.20, BA.5.2.21, BA.5.2.26, BA.5.2.27, BA.5.2.28, BA.5.2.34, BA.5.2.48, BA.5.2.49, BA.5.2.6, and BA.5.2.7 (Figure 1B), increased from 47.54% (September 26–October 2, 2022) to 82.66% (October 17–23, 2022), then decreased to 62.97% (October 31–November 6, 2022), increased again to 81.43% (November 14–20, 2022), and then decreased to 58.81% (December 5–11, 2022), finally reaching about 76%. BF.7 and its descendant lineages, including BF.7, BF.7.5, and BF.7.14 (Figure 1B), decreased from 21.92% (September 26–October 2, 2022) to 8.08% (October 17–23, 2022), then increased to 22.31% (October 31–November 6, 2022), decreased again to 15.37% (November 14–20, 2022), and then rose to 39.15% (December 5–11, 2022), finally reaching about 24%. When considering BA.5.2 and its descendant lineages and BF.7 and its descendant lineages together, their proportions increased from 69.46% (September 26–October 2, 2022) to about 100.00% (January 23–28, 2023).

Local BQ.1 and its descendent lineages (BQ.1.1, BQ.1.2, BQ.1.5, BQ.1.8, BQ.1.10, BQ.1.13, BQ.1.23, and BQ.1.1.17) were identified from October 10, 2022, with a total of 63 relative cases. Of these, BQ.1.10 and BQ.1.1 accounted for 50.79% (32/63) and 14.29% (9/63), respectively. Local XBB.1 and XBB.1.2 were identified from October 14, 2022, with a total of 16 relative cases.

The Dynamic Trend of SARS-CoV-2 Variants from Imported Cases

From September 26, 2022 to January 29, 2023, a total of 1,978 valid genome sequences of COVID-19 imported cases were reported, with 169 evolutionary lineages. BA.5 and its descendant lineages were dominant in the imported mutant strains. Among them, BA.5.2, BF.7, BQ.1.1 (and BQ.1.2), and XBB.1 variants accounted for 18.17%, 8.63%, 11.26%,

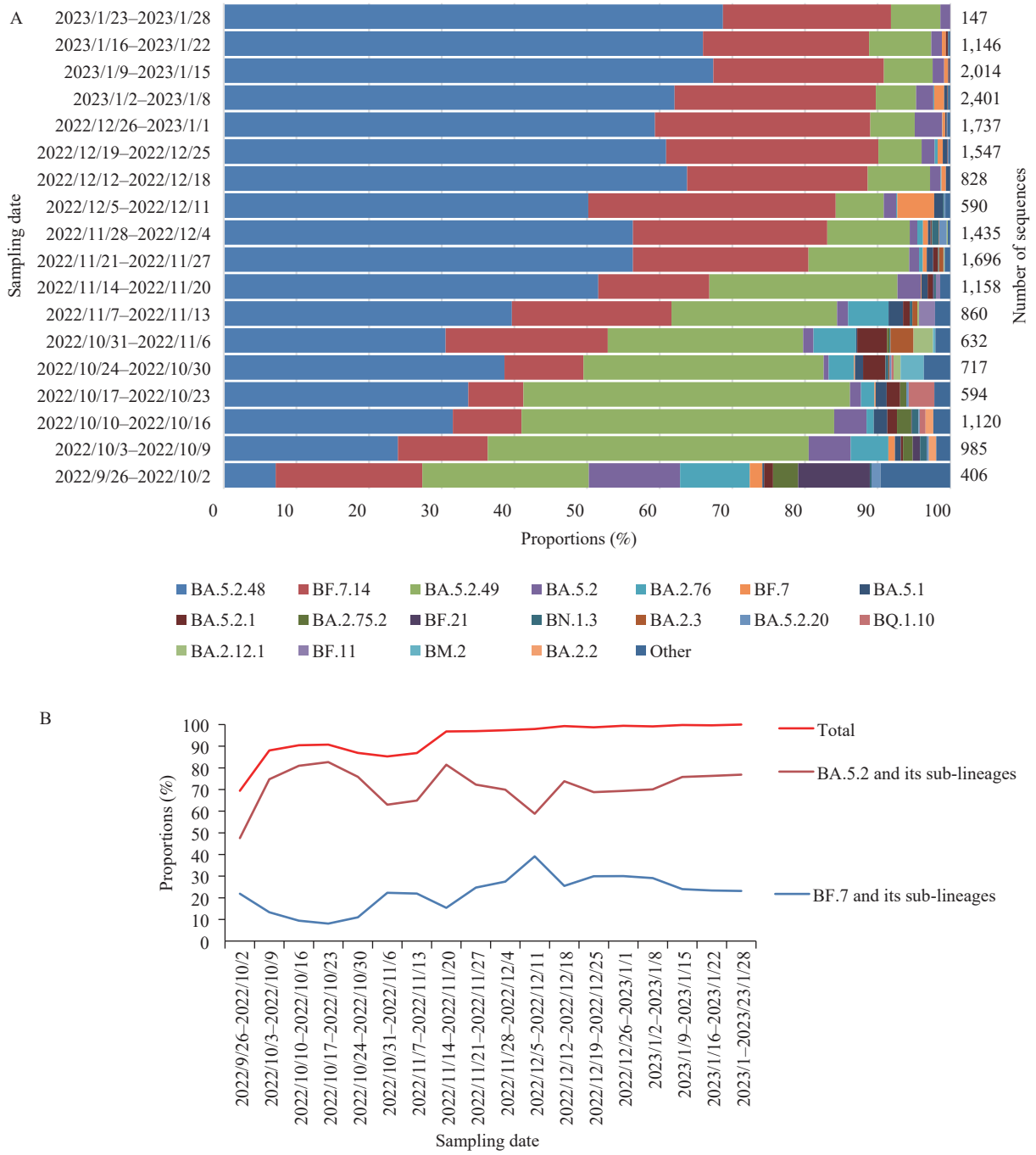

FIGURE 1. Dynamic trends of SARS-CoV-2 lineages of domestic cases in China. (A) All lineages; (B) BA.5.2 and descendent lineages, and BF.7 and descendent lineages.

Note: Collection date interval was from September 26, 2022 to January 28, 2023. The data were derived from valid SARS-CoV-2 genome sequences of domestic and imported cases submitted by PLADs with a deadline date of January 29, 2023. The numbers marked on the right of the figure represent the number of valid genome sequences per week for all lineages. "Other" refers to lineages with proportions of Omicron variants less than 0.1% of domestic cases. The other 54 lineages include BA.2.75.1, XBB.1, BN.1.5, BY.1, BS.1.1, BA.5.2.27, BQ.1.1, BA.2, BA.5.1.7, BQ.1.2, BA.5.9, BE.1, BA.5.1.23, BF.5, BN.1.2, BA.5.2.26, BE.1.1, BQ.1.8, BQ.1.23, BA.5, BF.23, BQ.1, BF.4, BA.5.6, BE.4, BN.2, BQ.1.5, BF.7.5, BM.1.1, BF.18, BN.1, BA.5.2.34, BF.26, BA.5.2.6, BN.1.9, BA.5.2.28, BA.2.75.8, BA.5.2.16, BA.2.38, BS.1, XBB.1.2, BA.5.1.3, BA.5.2.21, BA.5.2.7, BA.2.3.20, BA.5.1.30, BA.2.5, BA.2.75.9, BA.2.2.1, CA.3, BQ.1.13, BA.5.2.12, BN.1.1, and BQ.1.1.17.

Abbreviations: SARS-CoV-2=severe acute respiratory syndrome coronavirus 2; PLADs=provincial-level administrative divisions.

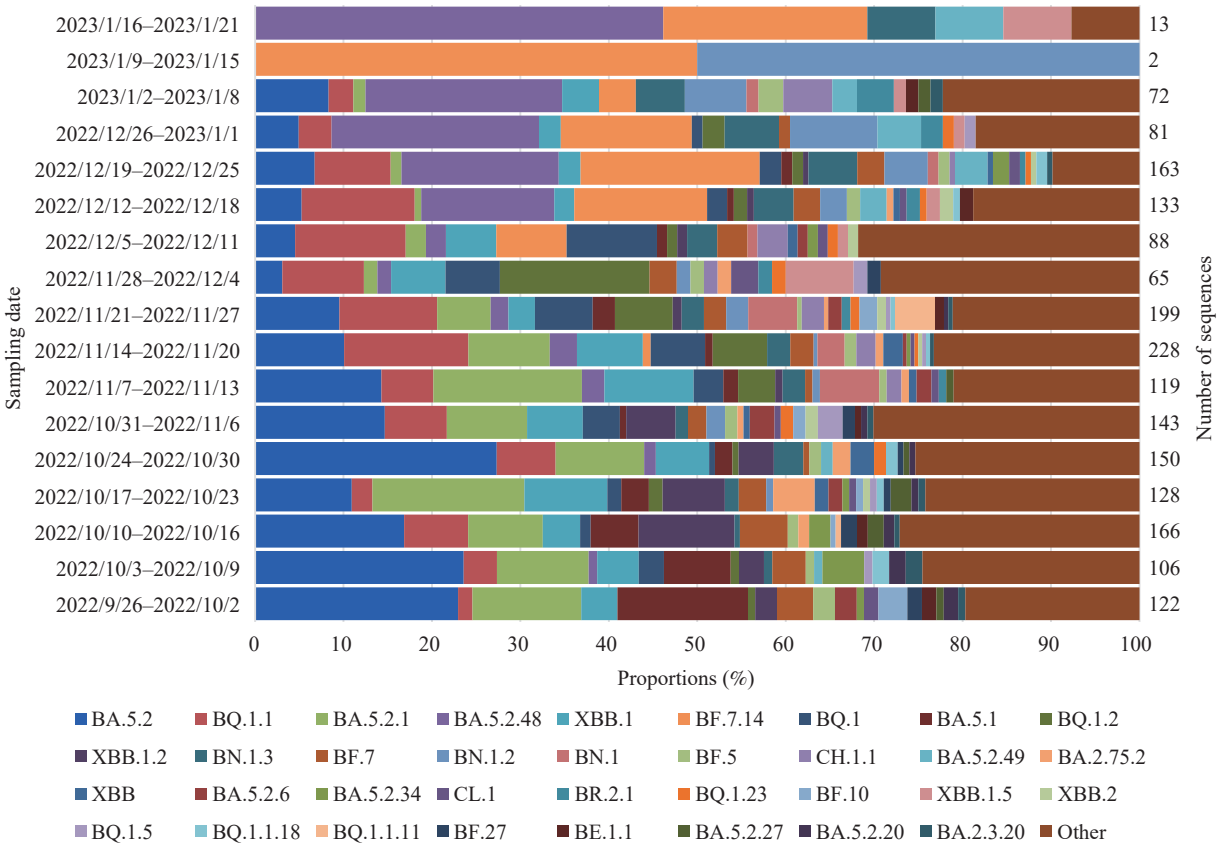

FIGURE 2. Dynamic trends of SARS-CoV-2 lineages of imported cases from September 26, 2022 to January 21, 2023.
Note: Data were derived from valid SARS-CoV-2 genome sequences of domestic cases submitted by PLADs with a deadline of January 29, 2023. Numbers marked on the right of the figure represent the number of valid genome sequences per week for all lineages. "Other" refers to lineages with proportions of Omicron variants less than 0.5% of imported cases. The other 158 lineages included BA.5.2.47, XBB.3, CM.12, BN.1.4, BQ.1.12, XBB.1.1, BA.5.9, BF.7.4.1, BQ.1.8, BN.1.5, BQ.1.25, BF.7.5, BA.2.75.5, CK.1, BQ.1.1.4, BE.1, BA.4.6, BN.1.9, BQ.1.11, BF.11, BN.1.3.1, BF.21, XBB.1.4, BA.5.2.19, BA.5.2.43, BQ.1.1.31, CM.4, BA.5.2.16, BQ.1.13, BA.5.2.28, BA.5.6, BA.2, BQ.1.1.1, BF.7.4, CM.5, BA.5, BF.28, BL.1, BF.7.6, BQ.1.14, BQ.1.1.3, BA.5.2.9, BA.5.2.24, BA.5.2.7, CK.2.1, BA.5.1.30, BQ.1.1.8, BF.4, BA.2.3.7, BA.5.2.36, BF.14, CP.1, BA.4, XBB.1.3, CM.2, BA.2.10.1, BA.5.1.22, BY.1, BA.5.1.10, CH.1.1.1, BQ.1.3, DQ.1, CR.1.1, BN.3.1, XBF, XBB.1.9, BW.1.1, BQ.1.24, BA.5.1.25, BA.5.2.3, BA.5.6.4, BE.1.1.1, BA.5.2.26, BS.1, BA.5.1.24, BA.5.1.6, BA.5.1.5, BA.5.2.13, BL.1.4, BM.1.1.3, DA.1, BA.5.2.25, BN.6, BQ.1.13.1, CN.1, CR.1.3, BA.5.5, BA.5.2.23, BA.5.1.28, BQ.1.1.13, BR.2, CR.1, BE.8, CK.2.1.1, BN.1.1, BF.26, BE.4.2, CM.5.1, BN.1.1.1, BQ.1.1.10, BE.1.4.2, CK.1.2, BF.7.15, BQ.1.27, BA.5.2.18, CZ.1, BA.2.75, BA.4.7, BM.1.1.1, BA.5.1.31, XBB.3.1, BA.5.3.1, BA.5.2.44, BA.4.1.8, BA.5.1.9, BF.31.1, XBB.4, BA.2.75.8, BA.5.2.21, BA.2.2, BA.5.2.14, BS.1.1, BM.4.1.1, XBB.2.1, BQ.1.1.22, CM.8.1, BF.11.2, BM.1.1, XBB.3.2, BE.10, BM.1, BA.5.5.1, BJ.1, BL.2, DG.1, XBB.2.2, BU.1, BQ.1.22, CJ.1, BF.7.13.2, BE.7, BQ.1.7, BQ.1.26, BA.5.1.1, BR.3, BQ.1.1.27, BF.25, BA.5.2.32, DE.2, BQ.1.1.2, BL.6, BQ.1.10.1, BQ.1.1.5, CH.1.1.3, BQ.1.1.32, BA.5.1.3, BN.1.3.2, and BE.9.
Abbreviation: SARS-CoV-2=severe acute respiratory syndrome coronavirus 2; PLADs=provincial-level administrative divisions.

7.57%, and 6.76% of imported cases, respectively (Figure 2).

Genomic Surveillance of SARS-CoV-2 Variants Among Domestic Cases in Each PLAD from December 1, 2022 to January 29, 2023

From December 1, 2022 to January 29, 2023, the 31 PLADs and XPCC reported 11,311 valid SARS-CoV-2 genome sequences from domestic cases, with 26 evolutionary lineages in total. The most prevalent lineages were BA.5.2.48 (62.08%) and BF.7.14 (26.95%), followed by 6 other lineages, BA.5.2.49, BA.5.2, BF.7, BA.5.1, BA.2.76, and BA.5.2.20, with proportions ranging from 0.16% to 6.88%. The remaining 18 lineages accounted for 0.42%. No novel SARS-CoV-2 Omicron variants with altered biological properties or of public health significance were identified since December 1, 2022.

TABLE 1. Basic information of domestic cases in China from December 1, 2022 to January 29, 2023.

Variable	Number	Proportion (%)
Gender		
Male	6,170	54.55
Female	4,189	37.03
Unknown	952	8.42
Age (years)		
<4	786	6.95
4–18	961	8.50
19–60	4,467	39.49
61–80	2,493	22.04
>80	1,456	12.87
Unknown	1,148	10.15
Periods		
2022/12/1–2022/12/7	1,190	10.52
2022/12/8–2022/12/14	739	6.53
2022/12/15–2022/12/21	1,254	11.09
2022/12/22–2022/12/28	1,748	15.45
2022/12/29–2023/1/4	2,011	17.78
2023/1/5–2023/1/11	2,342	20.71
2023/1/12–2023/1/18	1,546	13.67
2023/1/19–2023/1/25	465	4.11
2023/1/26–2023/1/28	16	0.14
Lineages		
BA.5.2.48	7,022	62.08
BF.7.14	3,048	26.95
BA.5.2.49	778	6.88
BA.5.2	231	2.04
BF.7	106	0.94
Other*	126	1.11
Total	11,311	100

* "Other" refers to lineages with proportions of Omicron variants less than 1% of imported cases. The other 158 lineages include BA.5.1, BA.2.76, BA.5.2.20, BA.5.2.1, BN.1.3, Q.1.2, BQ.1.1, BN.1.5, BQ.1.8, BN.1, BA.5.2.6, BA.5, BA.2, XBB.1, BQ.1.1.17, BN.1.2, BN.1.1, BF.18, BA.5.2.12, BA.2.75.2, and BA.2.12.1.

Table 1 shows that 54.55% of the cases were male, 37.03% were female, and 8.42% were unknown. The 19–60-year age group had the highest proportion (39.49%), followed by the 61–80-year age group (22.04%). The numbers of subjects in the <4 and 4–18-year age groups were similar, and 10.15% of the subjects had no information regarding their age. From December 1, 2022, the number of subjects gradually increased to 2,342 cases (January 5–11, 2023). The main lineages after December 2022 were BA.5.2.48 and BF.7.14, which together accounted for 89.03% of the total.

Overall, BF.7 and its descendant lineages were predominant in Beijing and Tianjin Municipalities. The prevalence rates of BF.7 and its descendant lineages and BA.5.2 and its descendant lineages in Jiangsu Province and Inner Mongolia Autonomous Region were approximately equal. BA.5.2 and its descendant lineages were predominant in other PLADs (Figure 3).

Prevalence of BF.7.14 and BA.5.2.48 in China

According to the latest data from the Pango nomenclature, the strain BF.7 was identified as containing four characteristic amino acid mutation sites (ORF7a:H47Y, ORF1b:L238F, S:C1243F, and ORF1a:V274L) and one characteristic nucleotide mutation site (C29632T), and was designated BF.7.14.

Among the domestic cases, the lineages of BF.7.14 accounted for 99.52%, suggesting that the main prevalence of BF.7 was BF.7.14. In the imported cases, BF.7.14 lineages accounted for 61.90%, indicating that BF.7.14 had been found in the imported cases from international sources to our country. The earliest reported BF.7.14 domestic cases were from the Inner Mongolia Autonomous Region on September 27, 2022. Subsequent cases were mainly distributed between November 21 and December 6, 2022, and from December 19, 2022 to January 19, 2023. The earliest reported BF.7.14 imported case was from Belarus on September 25, 2022. Subsequent BF.7.14 imported cases were mainly concentrated in December 2022 (Figure 4A).

According to the latest data from Pango nomenclature, BA.5.2 containing four additional characteristic nucleotide acid mutation sites (C2710T, C8626T, C16887T, and T17208C) was named BA.5.2.48. The BA.5.2.48 subvariants accounted for 69.18% of BA.5.2 in domestic cases and 9.08% in imported cases in China. The earliest domestic case of BA.5.2.48 was reported in Guangdong Province on July 13, 2022. The earliest reported BA.5.2.48 imported case was a case who entered the country from Russia on August 15, 2022 (Figure 4B).

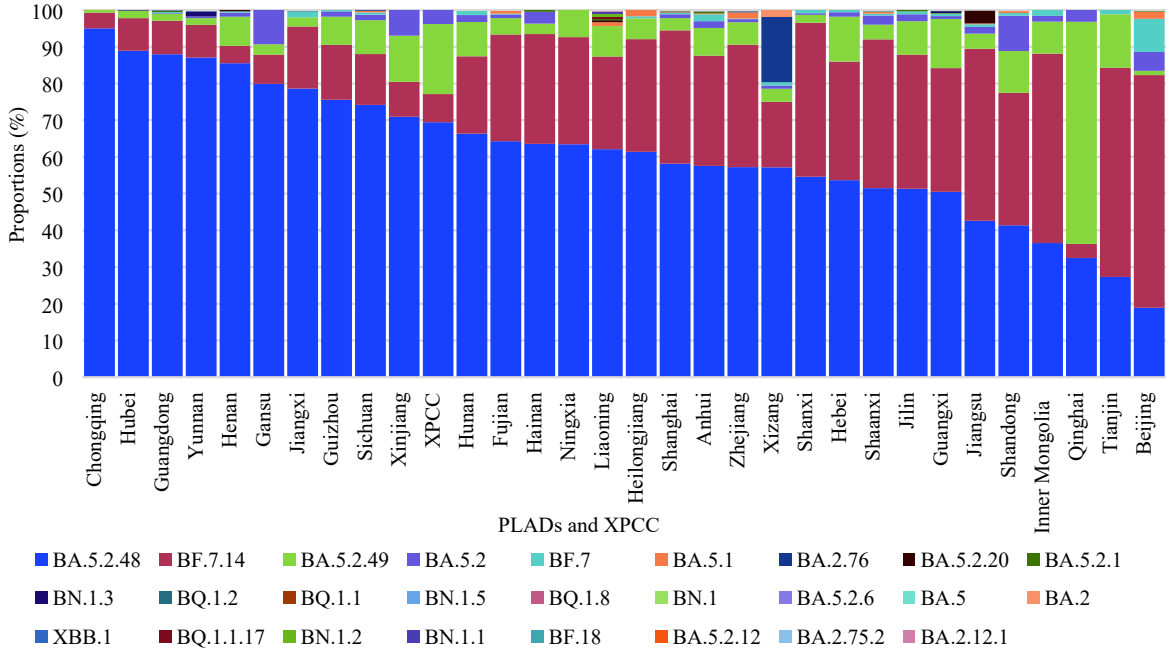

FIGURE 3. Surveillance of the epidemic variant of SARS-CoV-2 in all PLADs and XPCC in China.
Note: Collection date interval was from September 26, 2022 to January 28, 2023. The data were derived from the valid genome sequences of SARS-CoV-2 of indigenous cases submitted by PLADs with a deadline of January 29, 2023.
Abbreviation: SARS-CoV-2=severe acute respiratory syndrome coronavirus 2; PLADs=provincial-level administrative divisions; XPCC=Xinjiang Production and Construction Corps.

Relationship between Clinical Types and Genotypes in Domestic Cases

The chi-square test revealed statistically significant differences in the proportions of three clinical types of cases (asymptomatic, mild, and severe) between BA.5.2 and BF.7 ($P<0.05$) (Table 2). The proportions of asymptomatic and severe cases of BA.5.2 were higher than those of BF.7, while the proportion of mild cases was lower than that of BF.7. Additionally, there was no statistically significant difference in the proportions of the clinical type cases of ordinary and death between BA.5.2 and BF.7.

CONCLUSIONS

Data from September 26, 2022 showed that the predominant lineages circulating in China were domestic cases of BA.5.2 and BF.7, accounting for 93.95% of the total. The proportion of BA.5.2 fluctuated from rising to falling before entering a plateau period, while the proportion of BF.7 experienced two declines and rises before also entering a plateau period. This suggests a counter-balancing relationship between the two main epidemic strains, with the other lineages gradually decreasing.

According to the World Health Organization (WHO), from December 30, 2022 to January 30, 2023, the Omicron variant of concern (VOC) accounted for 99.9% of sequences reported in the GISAID database in the past 30 days globally (6). BA.5 and its descendent lineages remain dominant globally (6). Major subvariants BF.7, BQ.1 (and BQ.1.1), and XBB, which are currently being tracked by WHO, also accounted for an important proportion of imported cases in China, suggesting that the imported SARS-CoV-2 variants in China were consistent with the international epidemic variants.

Surveillance of domestic and imported cases revealed that, following the adjustment of China's dynamic COVID-zero policy in December 2022, BA.5.2 and BF.7 quickly became the predominant circulating lineages and caused widespread epidemics in the country. No novel SARS-CoV-2 Omicron variants were identified that resulted in altered biological properties or were of public health significance. The COVID-19 epidemic Omicron variants in China were associated with imported cases, in line with the overall global situation.

China will continue to conduct comprehensive monitoring of the variation in the SARS-CoV-2 genomic sequences. If emerging lineages with

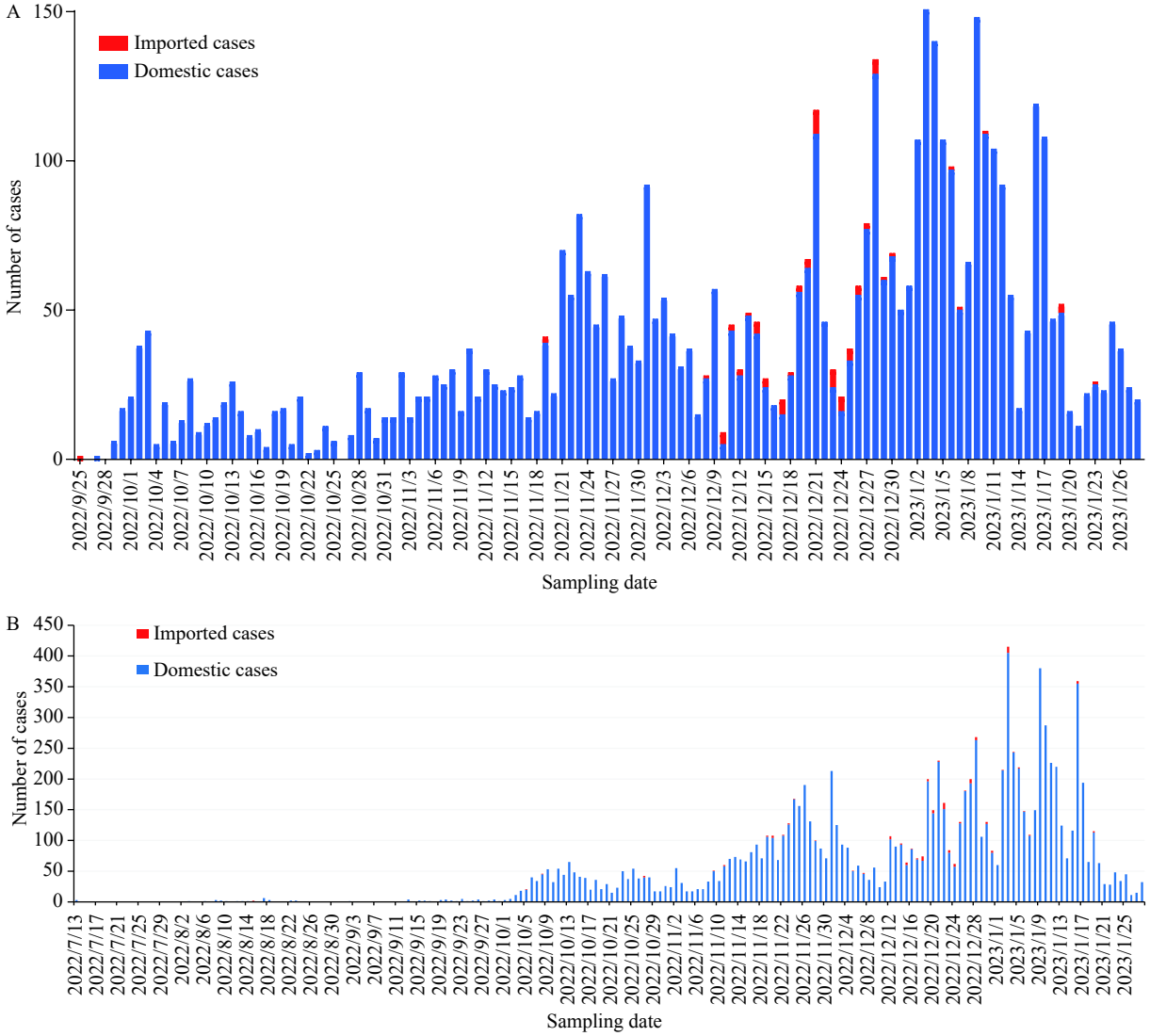

FIGURE 4. Distribution of domestic and imported cases in (A) BF.7.14 lineage and (B) BA.5.2.48 lineage based on sampling time.

TABLE 2. The relationship between clinical types and genotypes in domestic cases of China from December 1, 2022 to January 29, 2023.

Clinical type	BA.5.2		BF.7		χ^2	*P*
	Number	Proportion (%)	Number	Proportion (%)		
Asymptomatic	290	5.69	68	3.84	9.141	0.002
Mild	2,516	49.40	970	54.77	15.162	<0.001
Ordinary	1,052	20.66	362	20.44	0.037	0.847
Severe	1,220	23.95	368	20.78	7.450	0.006
Death	15	0.29	3	0.17	0.381	0.537
Total	5,093	100	1,771	100		

Note: Percentages may not total 100 because of rounding.

mutations of interest are detected, closer attention will be paid, and the genome sequence will be shared globally via GISAID or other international genome databases.

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Author group & contributions: SARS-CoV-2

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