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Vital Surveillances

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

Shiwen Wang[1,2,&]; Peihua Niu[1,&]; Qiudong Su[1]; Xiaozhou He[1]; Jing Tang[1]; Ji Wang[1]; Yenan Feng[1,2]; Cao Chen[1]; Xiang Zhao[1]; Zhixiao Chen[1]; Wenling Wang[1]; Zeyuan Yin[1]; Yuchao Wu[1]; Changcheng Wu[1]; Lili Li[1]; Aili Cui[1]; Yan Zhang[1]; Caiyun Long[1]; Xiaoyu Yang[1]; Zhongxian Zhang[1]; Hong Bo[1]; Wenbo Xu[1,2,#]; SARS-CoV-2 Genome Working Group

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%,

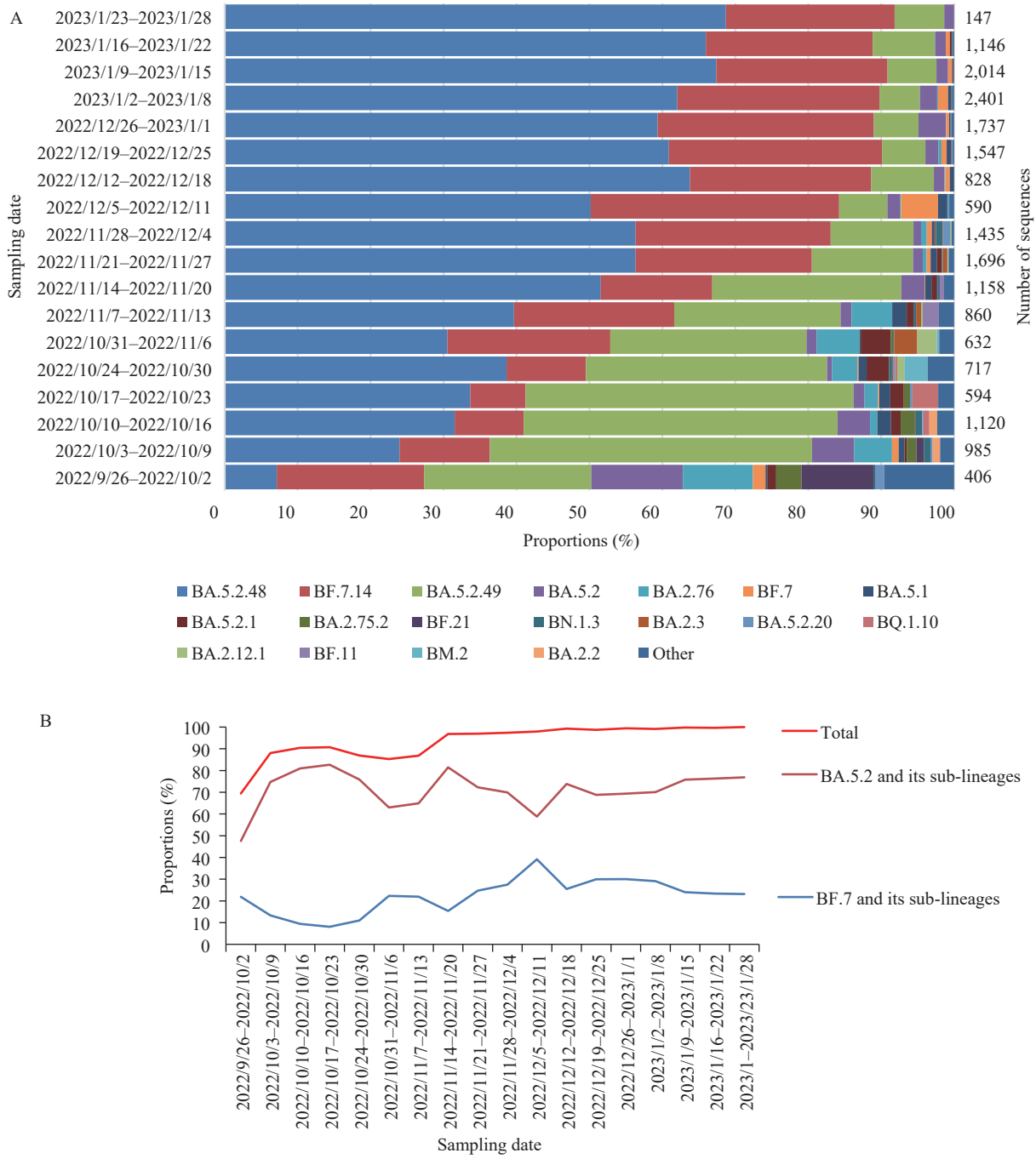

FIGURE 1. Dynamic trends of SARS-CoV-2 lineages of domestic cases in China. (A) All lineages; (B) BA.5.2 and descendent lineages, and BF.7 and descendent lineages.
Note: Collection date interval was from September 26, 2022 to January 28, 2023. The data were derived from valid SARS-CoV-2 genome sequences 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.

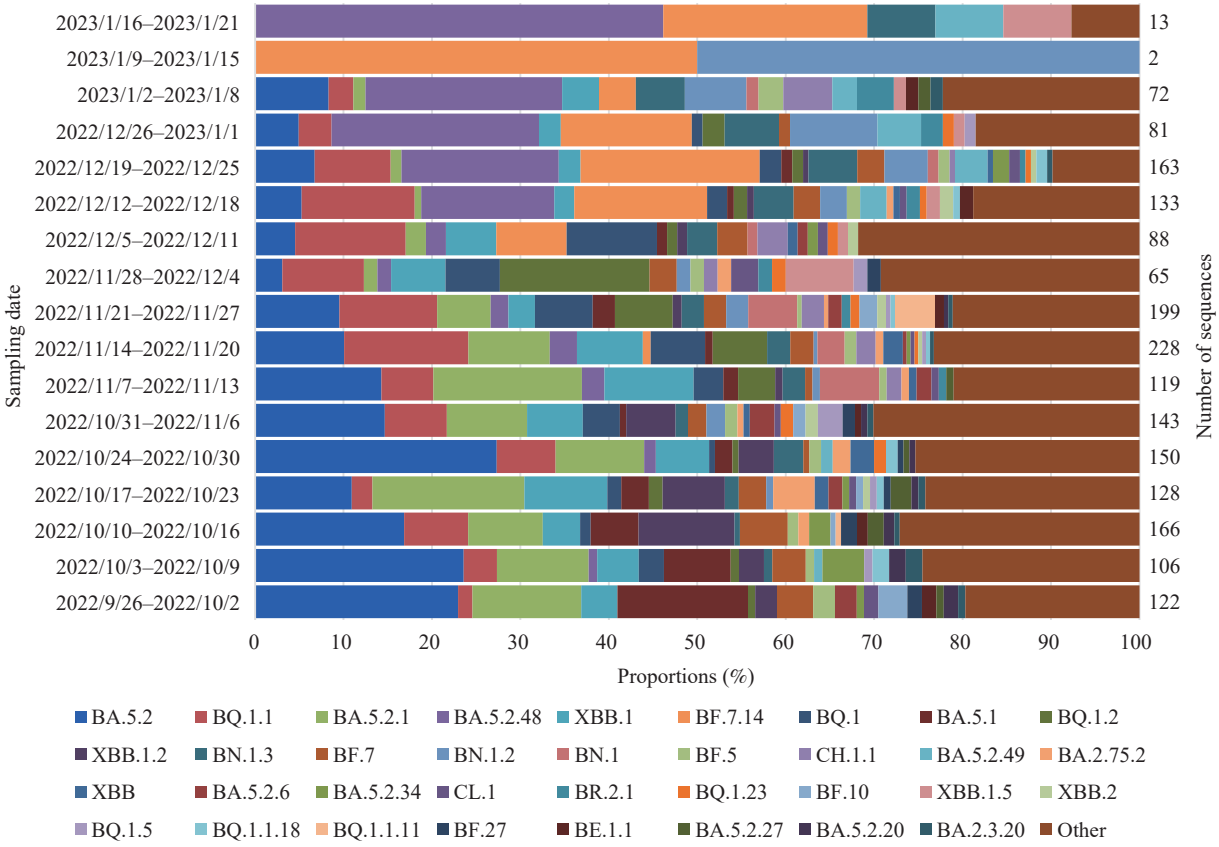

FIGURE 2. Dynamic trends of SARS-CoV-2 lineages of imported cases from September 26, 2022 to January 21, 2023.
Note: Data were derived from valid SARS-CoV-2 genome sequences of domestic cases submitted by PLADs with a deadline of January 29, 2023. Numbers marked on the right of the figure represent the 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).

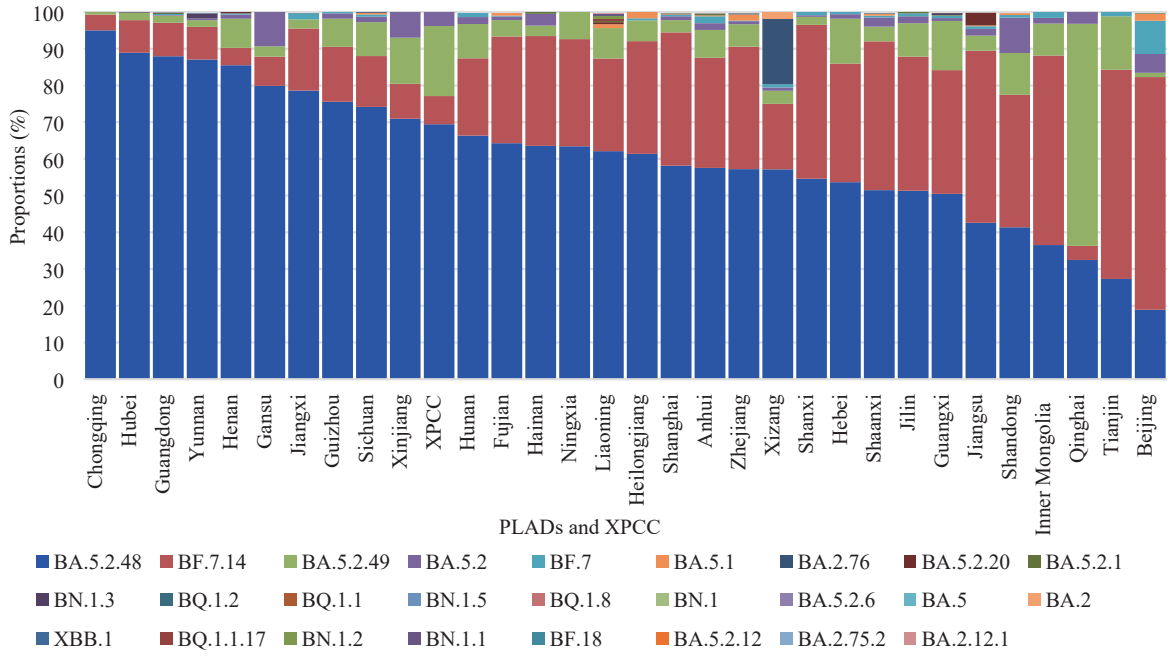

FIGURE 3. Surveillance of the epidemic variant of SARS-CoV-2 in all PLADs and XPCC in China.
Note: Collection date interval was from September 26, 2022 to January 28, 2023. The data were derived from the valid genome sequences of SARS-CoV-2 of indigenous cases submitted by PLADs with a deadline of January 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

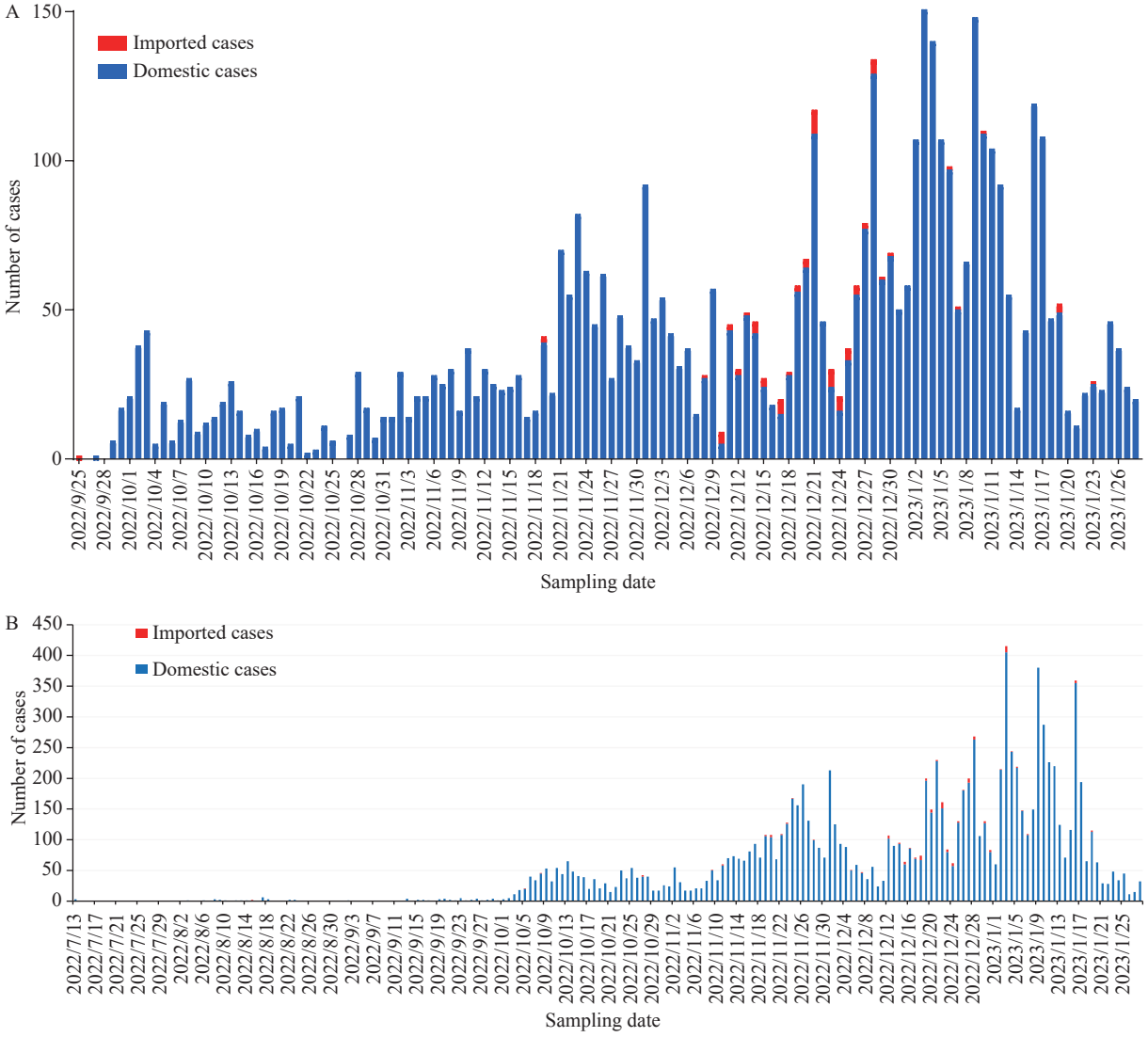

FIGURE 4. Distribution of domestic and imported cases in (A) BF.7.14 lineage and (B) BA.5.2.48 lineage based on sampling time.

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.

Conflicts of interest: No conflicts of interest.

Author group & contributions: SARS-CoV-2

Genome Working Group includes Yang Pan, Hui Xu, Zhaomin Feng, Fu Li, Shujuan Cui, Bing Lyu, Zhichao Liang, Daitao Zhang (Beijing Municipality); Xiaoyan Li, Zhichao Zhuang, Yue Lei, Ming Zou, Zhaolin Tan, Xin Gao, Baolu Zheng, Xiaochang Liu, Aiping Yu, Xiaohui Lu, Yuan Wang, Yanzhen Han, Ying Wang (Tianjin Municipality); Hui Jiang, Chaonan Wang, Lingyue Yuan, Xiaoxian Cui, Fanghao Fang, Run Li, Jing Zhou, Yuyang Wang, Jiajing Liu, Yong Chen, Xiaoqing Cui, Hongwei Di, Hongyou Chen, Min Chen (Shanghai Municipality); Sheng Ye, Shuang Chen, Yun Tang, Zhen Yu, Zhangping Tan, Mingyue Wang (Chongqing Municipality); Xu Han, Guangyue Han, Shiyou Liu, Zhaoyi Jia, Hongbin Zhang, Minghao Geng, Tong Su, Yanan Cai, Baohua He, Shaoxuan Song, Junli Zhang (Hebei Province); Junyu Zhao, Ruijuan Zhang, Binzhi Ren (Shanxi Province); Lingling Mao, Haibo Sun, Lulu Wang, Shuang Liu, Xuesheng Liu, Xiaoting Xu, Bo Wang, Lu Lei, Ge Song, Sinong Sun, Hanyi Guo, Na Liu, Zhijian Bo (Liaoning Province); Donglin Wu, Xianda Yang, Yao Yang, Jing Li, Hongmin Liu, Leilei Wei, Wei Zhao, Weiyu Zhang, Ben Shi, Hui Wang, Xihui Zang (Jilin Province); Jun Xu, Qi Liang, Chang Shu, Ming Yang, Fengju Ouyang, Lu Tang, Xin Shi, Hua Hua, Yan Leng, Fengying Xia (Heilongjiang Province); Changjun Bao, Liguo Zhu, Shenjiao Wang, Jianguang Fu, Huan Fan, Fei Deng, Huiyan Yu, Zhifeng Li, Lunbiao Cui, Kangcheng Zhao, Xiaojuan Zhu, Yiyue Ge (Jiangsu Province); Yi Sun, Hao Yan, Lingxuan Su, Honghu Chen, Baofeng Zhou, Wenwu Yao (Zhejiang Province); Yong Sun, Weiwei Li, Jun He, Peng Wang, Wenchang Li, Wanrong Luo, Wanxing Lu, Ruan Wu, Xinxin Wang, Tai Ma, Xiaomin Wu, Lingkang Yang, Weixi Fang, Xue Zhou, Juanjuan Liu (Anhui Province); Qi Lin, Zhimiao Huang, Wei Chen, Zhiwei Zeng, Yingxiang Zheng, Quwen Li (Fujian Province); Jianxiong Li, Yong Shi, Bowen Wuyang, Gang Xu, Jun Zhou, Yanni Zhang, Xiaoqing Liu, Qian Wang, Shiwen Liu, Dajin Xiao, Xin Ran, Shuting Wei, Jiabo Du (Jiangxi Province); Zengqiang Kou, Ti Liu, Yan Li, Ming Fang, Mingxiao Yao, Yuwei Zhang, Xiaolin Liu, Hui Lyu, Gaoxiang Sun, Zhongyan Fu, Bo Pang, Shuang Wang, Lu Liu, Julong Wu, Yujie He, Jianxing Wang, Shu Zhang, Ziqing Liu, Zhen Dong (Shandong Province); Hongxia Ma, Baifan Zhang, Yi Li, Sheng Zhao, Haiyan Wei, Dongxiao Li, Shidong Lu, Yun Song, Xiao Hu, Lin Zhu (Henan Province); Bin Fang, Linlin Liu, Xiao Yu, Qiangling Yin, Xiaolu Zhang, Mingwei Peng, Yating Zhang, Cong Liu, Shi Han (Hubei Province); Xingyu Xiang, Zhifei Zhan, Yiwei Huang, Juan Wang, Shuai Chen, Zixiang He, Ran Liu (Hunan Province); Chang Zhang, Zhencui Li, Lijun Liang, Yao Hu, Fangzhu Ouyang, Shen Huang, Jiajun Liu, Zhonghua Zheng, Hanri Zeng, Jing Xu, Qianfang Guo, Jianxiang Yu, Qiqi Tan, Juan Su, Pengfai Jia (Guangdong Province); Lei Cui, Chuyang Sun, Yinggui Cai, Shizhuang Kuang, Xiaoting Gan, Yunting Zeng, Dandan Li, Su Wang, Xin Wei (Hainan Province); Jianan Xu, Li Liu, Zhongping Huang, Mingfeng Jiang, Chenxia Liu, Wenxia Zhao, Qiuhua Yu, Qinghua Huang, Xiaozhen Ma, Ranran Cao, Chaohua Xu, Ying Ding, Hongyu Liao, Rongmei Yuan, Na Li, Ximei Fu, Huiping Yang, Wei Li, Yuliang Feng, Hongrong Zhong, Cheng Wang, Wenbo Li, Lili Liu, Gaopeng Lei, Lin Zhang, Li Liu, Hong Lyu, Na Chen, Yi Zhang, Linzi Zeng (Sichuan Province); Lin Fu, Yonghu Wan, Ping Wu, Li Zhuang, Qian Ke, Ju Zheng, Weifang Shi, Dan Wang, Danya She, Qing Ma, Ying Liu, Chunting Liu, Xinggui Yang, Jingshu Xiang, Qian Zhou, Yuhui Wu, Xiaoyu Wei, Weijia Jiang (Guizhou Province); Meiling Zhang, Ruize Ni, Jienan Zhou, Xiaonan Zhao, Yanhong Sun, Zhaosheng Liu (Yunnan Province); Yao Meng, Shen Li, Bin Chen (Shaanxi Province); Baodi Li, Jianhua Chen, Congshan Xu, Miao Wang, Biao Wang, Zhe Zhao, Xueying Wang, Haizhuo Wu, Hui Zhang, Yingjie Zhao, Guina Zhu, Yu Zhen (Gansu Province); Youju Lei, Meiying Zhong, Qianlan Li, Mengqi Yin, Lifang He, Chonghai Li, Xiaotong Wang (Qinghai Province); Xiaoling Tian, Hai Yan, Wu Yihan, Tana, Lu Yang, Dongyan Zhang, Xinxin Yu, Xueyao Zhang, Ying Chen (Inner Mongolia Autonomous Region); Yu Ju, Fuyin Bi, Huafeng Chen, Ning Kang, Jing Wang, Zhenli Liang, Hang Huang, Bao Lu, Meirong Tang, Chizhen Liao (Guangxi Zhuang Autonomous Region); Hongmei, Qin Wang, Guolong Dai, Suolangdeji, Luoyangcuo, Wentao Zhao, Cidanzhuoga, Suoyang [Xizang (Tibet) Autonomous Region]; Zhonglan Wu, Jianxin Pei, Xiang Liu (Ningxia Hui Autonomous Region); Xin Ma, Jun Zhao, Jia Huang, Zhenguo Gao, Xuan Zhang, Yuan Chen, NIGEDELI·Alitengsaier, Hundezi·Awuxi, Quanxi Li, Rong Wang, Muhtar·Amir (Xinjiang Uygur Autonomous Region); Yuxia Liu, Yao He, Jingxia Guo, Chi Du (Xinjiang Production and Construction Corps). All teams were involved in high-throughput sequencing of the SARS-CoV-2 genome.

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[#] Corresponding author: Wenbo Xu, xuwb@ivdc.chinacdc.cn.

[1] National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China; [2] National Health Commission Key Laboratory for Medical Virology and Viral Diseases, Beijing, China.
[&] Joint first authors.

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Vital Surveillances

SARS-CoV-2 Surveillance Through China Influenza Surveillance Information System — China, December 1, 2022 to February 12, 2023

Xiaoxu Zeng[1,&]; Yiran Xie[1,3,&]; Xiaokun Yang[2,&]; Zhibin Peng[2]; Jing Tang[1,3]; Lei Yang[1]; Shuxia Lin[1]; Jun Han[1]; Yanping Zhang[2]; Dayan Wang[1,#]

ABSTRACT

Introduction: The World Health Organization (WHO) proposed using influenza surveillance systems to carry out coronavirus disease 2019 (COVID-19) surveillance due to the similarity between the two diseases in some respiratory symptoms. To assess the prevalence of COVID-19, we analyzed the influenza-like illness (ILI) and positive rate of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) detections in ILI patients reported to the influenza Surveillance Information System (CNISIS) since late 2022.

Methods: Data related to ILI were reported by national surveillance sentinel hospitals. Positive testing for SARS-CoV-2 and influenza viruses was conducted using real-time reverse transcription polymerase chain reaction (rRT-PCR) detection by the national influenza surveillance network laboratories. Surveillance data were reported to CNISIS.

Results: Beginning on December 12, 2022 (Week 50), the ILI percentage increased dramatically, peaking in Week 51 at 12.1%. Subsequently, the ILI percentage began to decline rapidly from Week 52, 2022, and by Week 6, 2023 (February 6–12), the ILI and ILI percentage had returned to the levels observed at the beginning of December 2022. From December 1, 2022 to February 12, 2023, 115,844 specimens were tested for both SARS-CoV-2 and influenza virus. Of these, 30,381 (26.2%) were positive for SARS-CoV-2 and 1,763 (1.5%) were positive for influenza virus. The positive rate of SARS-CoV-2 tests peaked at 74.1% around December 23 and 25.

Conclusions: Sentinel-based surveillance, previously established for influenza, is an effective way to track the circulation trend of SARS-CoV-2 during community-level epidemics. There was no co-prevalence of SARS-CoV-2 and influenza virus during the outbreak of SARS-CoV-2, even during the winter influenza season. However, it is important to remain vigilant for the potential rise of influenza activities following the COVID-19 epidemic.

Sentinel surveillance of influenza-like illness (ILI) has been recommended by the World Health Organization (WHO) for influenza surveillance for many years due to its sensitivity and rapidity, although it is less specific (*1*). Other respiratory viruses, including rhinovirus, respiratory syncytial virus, parainfluenza, adenovirus, and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), can also present as ILI (*2*–*7*). The China National Influenza Surveillance Network (CNISN) reached its current scale in 2009, consisting of 554 national-level sentinel hospitals and 410 national influenza surveillance network laboratories, as well as hundreds of provincial-level sentinels. During the coronavirus disease 2019 (COVID-19) pandemic, SARS-CoV-2 and influenza virus can be tested simultaneously (*8*). Integrated sentinel surveillance of influenza virus and SARS-CoV-2 can guide public health responses to both public health problems concurrently. SARS-CoV-2 has undergone constant variation, resulting in changes in its pathogenicity and transmissibility (*9*). On December 7, 2022, the Comprehensive Group of Joint Prevention and Control Mechanism for the State Council's Response to COVID-19 Epidemic optimized prevention and control policies. To gain insight into the epidemic trends and provide risk assessment of SARS-CoV-2 in China, this study analyzed the positive rate of SARS-CoV-2 and influenza virus reported by the network laboratories, as well as the ILI cases reported by sentinel hospitals in outpatient and emergency departments.

METHODS

Indicator Description

ILI is characterized by fever (temperature ≥38 ℃) and cough or sore throat. ILI surveillance has been a common symptom surveillance method adopted by WHO member countries around the world over the years.

The percentage of ILI (ILI%) cases among all patients of the sentinel hospitals' surveillance departments was calculated. These departments included: 1) Internal Medicine Outpatient and Internal Medicine Emergency; 2) Pediatric Outpatient and Pediatric Emergency; and 3) Fever Clinic.

Data Resources

Data on ILI were reported by 824 sentinel hospitals, including 546 national influenza surveillance sentinel hospitals and 278 non-national level sentinel hospitals, and were downloaded from the China National Influenza Sentinel Surveillance System (CNISIS). From December 1, 2022 to February 12, 2023 (sample collection date), 402 national influenza surveillance network laboratories submitted their real-time reverse transcription polymerase chain reaction (rRT-PCR) testing results for SARS-CoV-2 and seasonal influenza viruses. Laboratories were required to test both SARS-CoV-2 and influenza virus for each sample; this study only includes samples that were tested for both simultaneously. Sentinel hospitals collected samples of ILI cases and sent them to the network laboratories in viral transportation medium for testing. rRT-PCR testing was conducted according to the influenza and COVID-19 national surveillance guide.

RESULTS

Surveillance of Outpatient or Emergency Visits for ILI at Sentinel Hospitals

A total of 92,304,428 outpatient and emergency visit cases were reported by 31 provincial-level administrative divisions and the Xinjiang Production and Construction Corps from September 4, 2022 to February 12, 2023. Of these, 3,512,735 were ILI cases (3.8%). From September to early December 2022, the weekly number of ILI cases in sentinel hospitals ranged from 85,000 to 124,000, with ILI percentages fluctuating between 2.7% and 3.2%. Starting from December 12, 2022 (Week 50), the ILI percentage in Chinese mainland showed a rapid increase, with ILI percentages of 3.6% (Week 49) and 8.5% (Week 50), respectively. In Week 51, the ILI percentage reached its peak of 12.1%. Subsequently, it began to decline dramatically from Week 52 (7.6%). By Week 6, 2023 (February 6–12), it had decreased to 1.4% (Figure 1), with both ILI cases and ILI percentages lower than the levels at the beginning of December 2022.

Further data analysis of different regions revealed that the peak time of ILI% was similar across regions. The ILI% in the Southwest and Central China peaked in Week 50 (11.8% and 9.2%, respectively), while the ILI% in the Northwest, South, East, North, and Northeast China peaked in Week 51 (11.3%, 15.3%, 13.7%, 5.6%, and 11.2%, respectively). Subsequently, the ILI% continued to decline (Figure 1).

Further analysis of different age groups indicated that the groups aged 0–4 years, 5–14 years, 15–24 years, and 25–59 years reached their peaks in Week 51, while the ≥60 years age group reached its peak in the following week, with a slower trend of rise and decline. Currently, the number of ILI cases in all age groups is lower than the pre-epidemic level (Figure 2).

Virologic Surveillance: rRT-PCR Testing of SARS-CoV-2 and Influenza Virus in Network Laboratories

From December 1, 2022 to February 12, 2023 (sample collection date), 402 national influenza surveillance network laboratories reported simultaneous test results of SARS-CoV-2 and influenza virus to CNIISIS. During this period, the network laboratories tested 115,844 specimens, with 30,381 (26.2%) positive detections for SARS-CoV-2 and 1,763 (1.5%) positive detections for influenza virus (Figures 3A and 3B).

According to daily detection, the positive rate of SARS-CoV-2 tests increased from mid-December 2022, reaching a peak of 74.1% around December 23–25, before declining with minor fluctuations. During Week 2 of 2023 (January 9–15), the positive rate of SARS-CoV-2 ranged from 14.3% to 29.1% each day, further fell to as low as 3.4% in February 8 of Week 6 (Figures 3B and 4). During the same period, influenza virus detections remained at a low level, decreasing further since mid-December. The weekly positive rate of influenza virus detections was below 1% from late December until Week 5 of 2023, before increasing

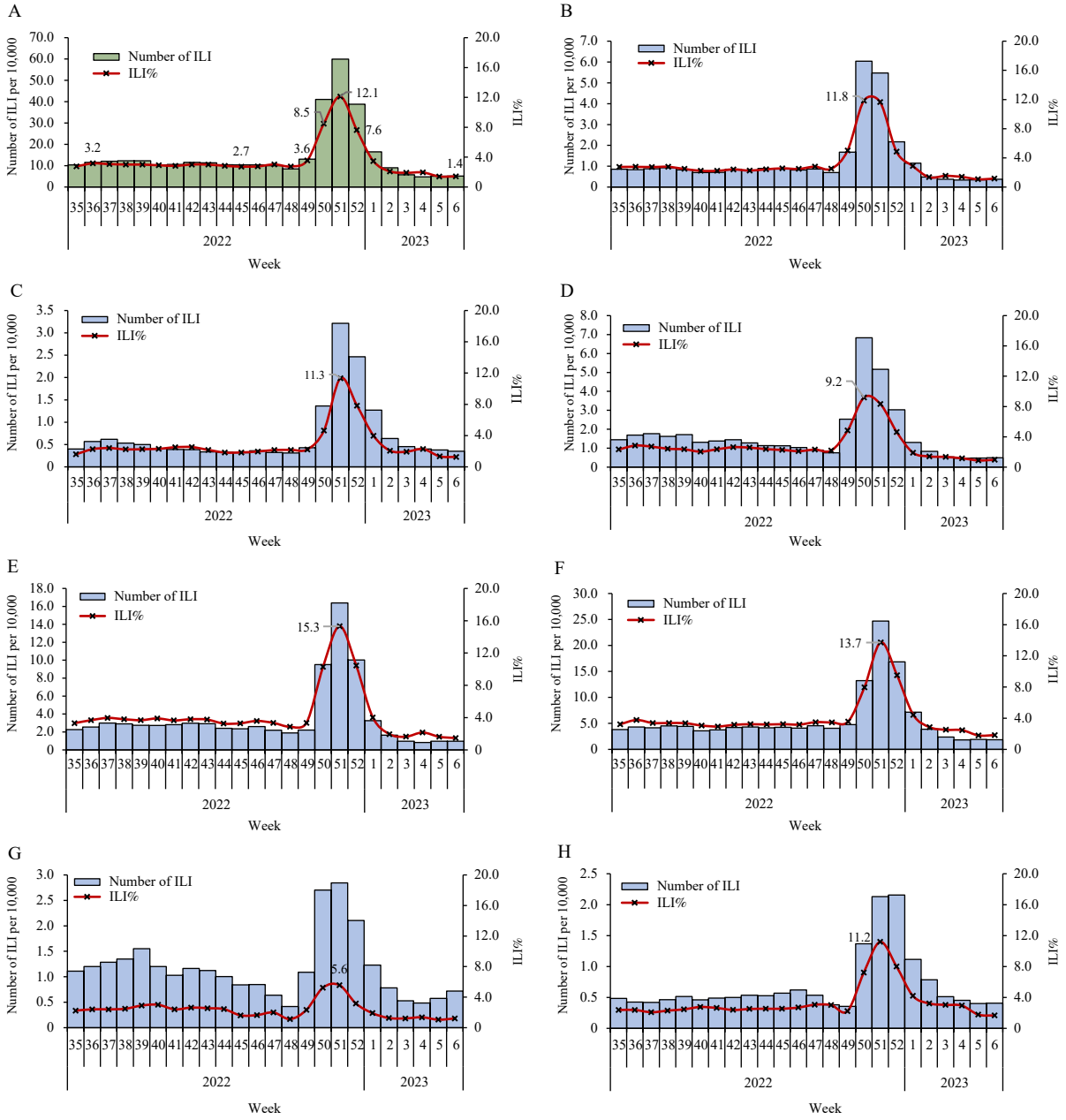

FIGURE 1. Influenza-like illness (ILI) and ILI% as reported by sentinel hospitals from September 4, 2022 to February 12, 2023 in (A) Chinese mainland, (B) Southwest China, (C) Northwest China, (D) Central China, (E) South China, (F) East China, (G) North China, (H) Northeast China.
Note: Southwest China: Guizhou, Sichuan, Xizang (Tibet), Yunnan, Chongqing; Northwest China: Gansu, Xinjiang Production and Construction Corps, Ningxia, Qinghai, Shaanxi, Xinjiang; Central China: Henan, Hubei, Hunan; South China: Guangdong, Guangxi, Hainan; East China: Anhui, Fujian, Jiangsu, Jiangxi, Shandong, Shanghai, Zhejiang; North China: Beijing, Hebei, Inner Mongolia, Shanxi, Tianjin; Northeast China: Heilongjiang, Jilin, Liaoning. The population of each region was 205,148,550, 103,527,786, 223,562,940, 186,220,546, 423,469,844, 169,334,110, 98,514,948 (Data of the 7th National Population Census in 2020), respectively.

in Week 6, which is worthy of attention.

Data analysis of different regions showed that the peak time of the SARS-CoV-2 positive rate was very close. In Southwest, Central, North, and Northeast China, the SARS-CoV-2 positive rate peaked in Week 51 (72.5%, 72.3%, 41.2%, and 37.5%, respectively). In East, South, and Northwest China, the SARS-CoV-2 positive rate peaked in Week 52 (73.0%, 68.0%, and 57.7%, respectively). The positive rate began to decline thereafter (Figure 4).

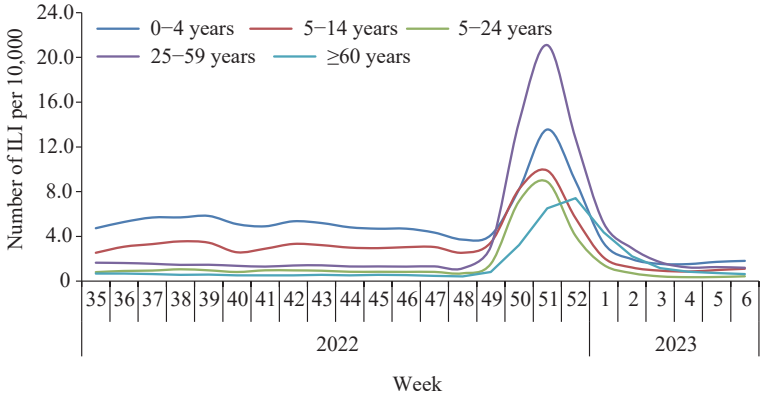

FIGURE 2. Influenza-like illness (ILI) and ILI% reported by sentinel hospitals in different ages from September 4, 2022 to February 12, 2023.

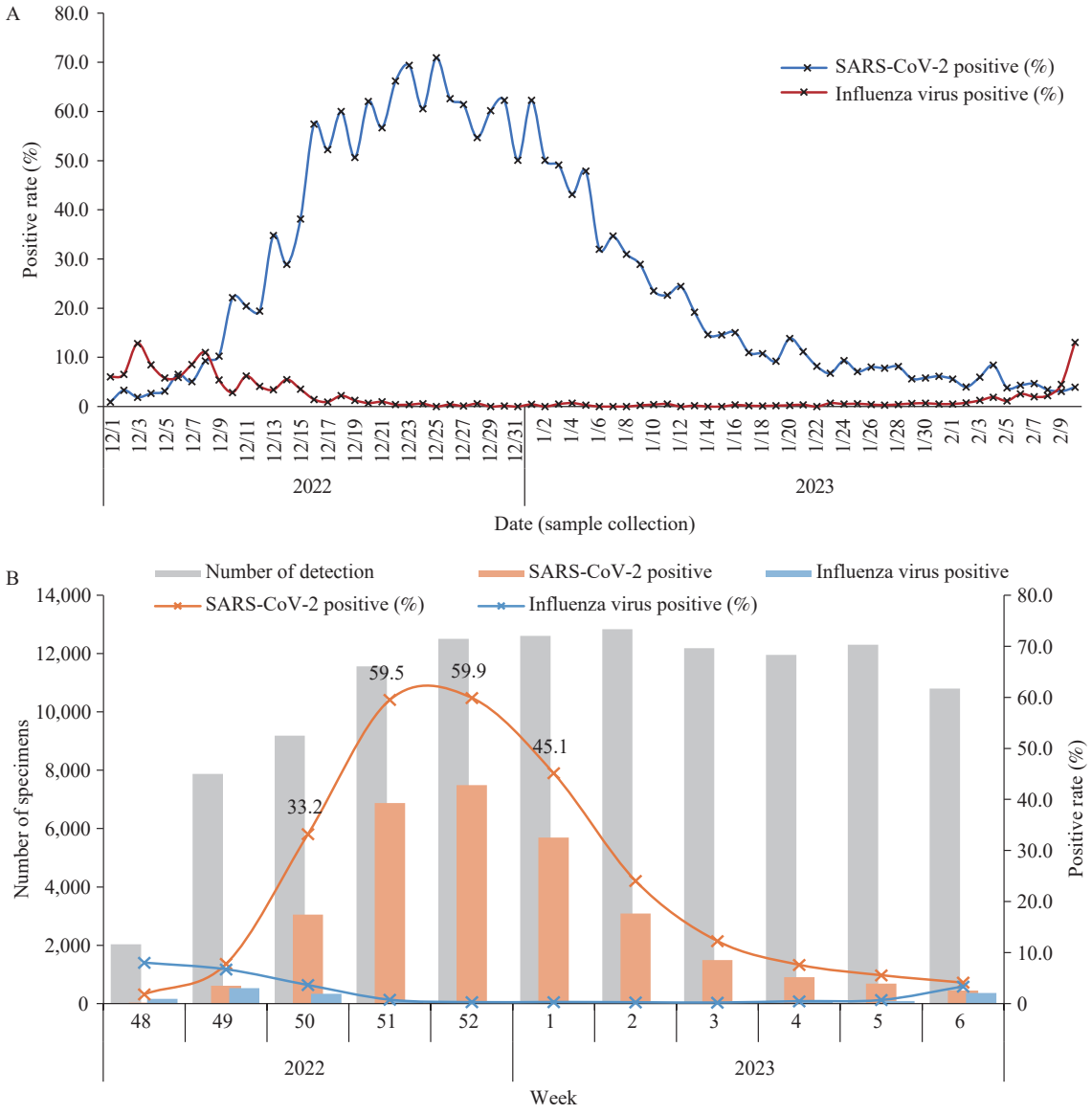

FIGURE 3. SARS-CoV-2 and influenza virus positive tests reported by influenza network laboratories from December 1, 2022 to February 12, 2023. (A) Daily analysis; (B) Weekly analysis.

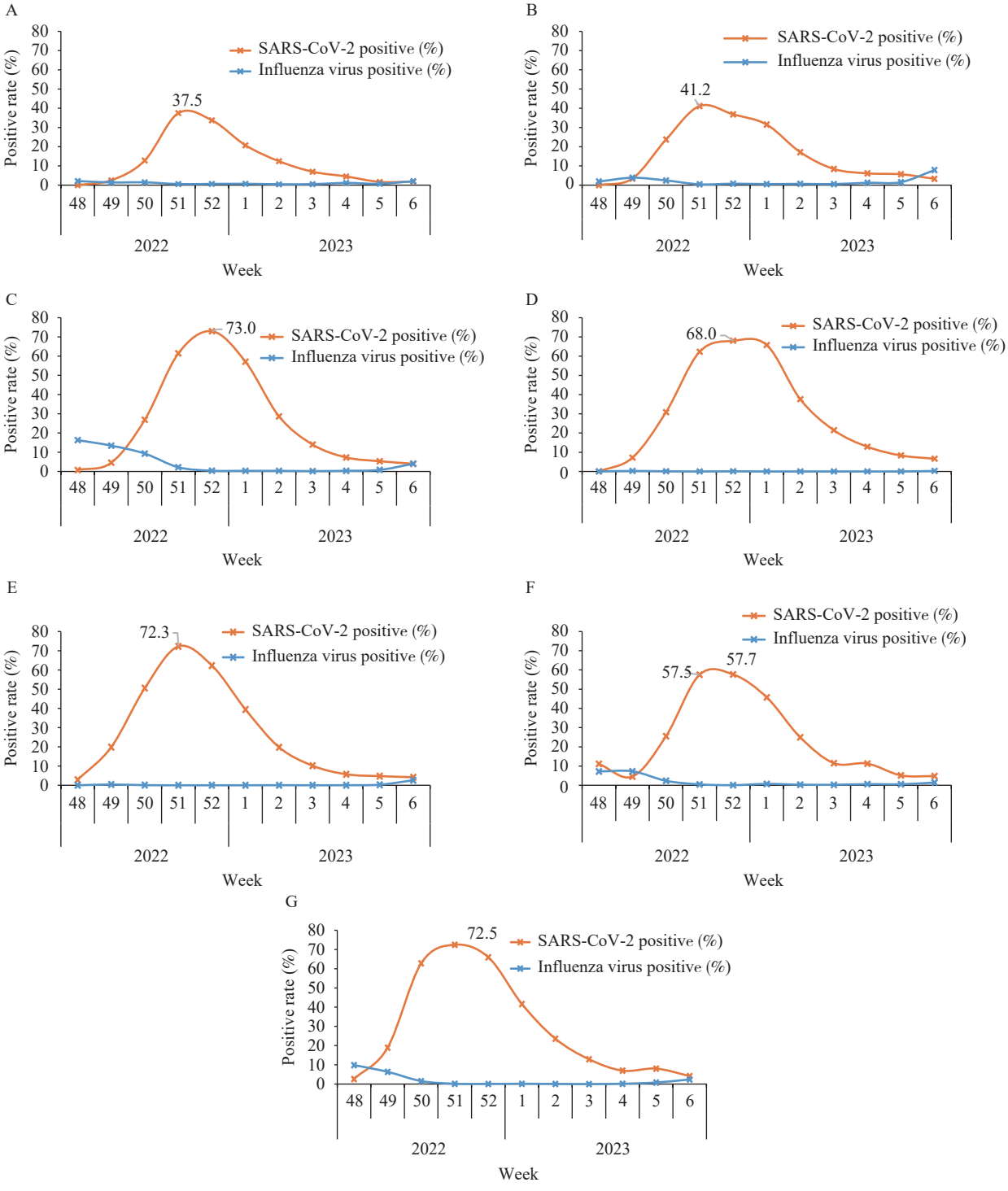

FIGURE 4. The positive rate of SARS-CoV-2 and influenza virus in ILI samples from sentinel hospitals in seven regions of Chinese mainland from December 1, 2022 to February 12, 2023. (A) Northeast China; (B) North China; (C) East China; (D) South China; (E) Central China; (F) Northwest China; (G) Southwest China.

Note: Northeast China: Heilongjiang, Jilin, Liaoning; North China: Beijing, Hebei, Inner Mongolia, Shanxi, Tianjin; East China: Anhui, Fujian, Jiangsu, Jiangxi, Shandong, Shanghai, Zhejiang; South China: Guangdong, Guangxi, Hainan; Central China: Henan, Hubei, Hunan; Northwest China: Gansu, Xinjiang Production and Construction Corps, Ningxia, Qinghai, Shaanxi, Xinjiang; Southwest China: Guizhou, Sichuan, Xizang (Tibet), Yunnan, Chongqing. The population of each region was 98,514,948, 169,334,110, 423,469,844, 186,220,546, 223,562,940, 103,527,786, 205,148,550 (Data of the 7th National Population Census in 2020), respectively.

DISCUSSION

The influenza surveillance network, which was designed to address influenza, also serves as a critical resource for countries responding to non-influenza emergencies. Some of the clinical symptoms in SARS-CoV-2 infection patients meet the definition of an ILI case. Therefore, monitoring the proportion of ILI cases in sentinel hospitals can provide insight into the circulation of SARS-CoV-2 during the COVID-19 outbreaks. The CNISN and CNISIS have been established for many years as well-coordinated and quality-controlled systems. When there is a community-level epidemic, sentinel-based surveillance is a sensitive, convenient, and effective way to conduct SARS-CoV-2 surveillance. Additionally, simultaneous testing of SARS-CoV-2 and influenza virus in ILI patients can assess the risk of SARS-CoV-2 and influenza epidemics.

From December 1, 2022 to February 10, 2023 (sample collection date), 402 of 410 national influenza surveillance network laboratories submitted their rRT-PCR testing results for SARS-CoV-2 and influenza virus. The proportion of SARS-CoV-2 was significantly higher than that of influenza virus, and influenza activity in the Chinese mainland was at a very low level (*10*–*11*). Combined with the number of ILI, ILI%, and virologic surveillance results, it suggested that the increase of ILI in December was mainly caused by SARS-CoV-2 infection. Although it was the influenza season during the study period, our data indicated that influenza virus and SARS-CoV-2 did not peak and circulate together, which was consistent with other studies (*12*). However, the rise of influenza activity may occur after the COVID-19 epidemic, so it is essential to continuously strengthen surveillance and improve the capacity of early warning of infectious diseases.

Compared to other age groups, the increase and decrease of ILI cases in the elderly group was relatively slow. This may be attributed to the fact that elderly people tend to have fewer social activities and fewer opportunities to come into contact with infected individuals, resulting in a slower spread of SARS-Cov-2 in this age group and a later onset and flatter peak of infection. It is important to note, however, that our study was based on outpatients; the age group characteristics of inpatients may differ.

In this study, it is evident that even when SARS-CoV-2 was highly prevalent, there was still a proportion of both SARS-CoV-2 and influenza virus negative ILI samples, suggesting that other pathogens may also be present. Surveillance of respiratory samples for multiple pathogens can provide information on the epidemic trend and disease burden of different pathogens.

This study had some limitations. We did not compare sentinel-based ILI surveillance with the prevalence of SARS-CoV-2 from other surveillance systems. The sentinel surveillance was based on ILI cases in departments of outpatient, emergency, and fever clinics, so the data cannot directly predict the number of SARS-CoV-2 infections in the entire population.

Conflicts of interest: No conflicts of interest.

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[#] Corresponding author: Dayan Wang, wangdayan@ivdc.chinacdc.cn.

[1] National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention; WHO Collaborating Centre for Reference and Research on Influenza, Beijing Municipality, China; [2] Chinese Center for Disease Control and Prevention, Beijing Municipality, China; [3] Key Laboratory for Medical Virology, National Health Commission, Beijing Municipality, China.
[&] Joint first authors.

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Vital Surveillances

Trends of SARS-CoV-2 Infection in Sentinel Community-Based Surveillance After the Optimization of Prevention and Control Measures — China, December 2022–January 2023

Jue Liu[1,&]; Fan Ding[2,&]; Yu Wu[1]; Wenzhan Jing[3]; Wenxin Yan[1]; Chenyuan Qin[1]; Fangyuan Li[2]; Yanping Zhang[2]; Min Liu[1,#]; Wannian Liang[3,#]; Qun Li[2,#]

ABSTRACT

Introduction: On December 7, 2022, China implemented the "Ten New Measures" to optimize its prevention and control measures for coronavirus disease 2019 (COVID-19). To provide the latest data after the optimization, we evaluated trends of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection among the community population in China.

Methods: We utilized data from the National Sentinel Community-Based Surveillance (NSCS) system in China to assess trends of SARS-CoV-2 infection. NSCS is a national community-based surveillance cohort with 0.42 million participants from all 31 provincial-level administrative divisions (PLADs) and Xinjiang Production and Construction Corps (XPCC). Participants were tested for infection twice a week (a total of eight rounds) from December 16, 2022 to January 12, 2023. SARS-CoV-2 infection was defined as testing positive for SARS-CoV-2 nucleic acid or antigen. We calculated the daily average of newly positive rates of SARS-CoV-2 infection.

Results: In this national cohort, the daily average newly positive rate of SARS-CoV-2 infection decreased from 4.13% in Round 1 (December 16–19, 2022) to 0.69% in Round 8 (January 10–12, 2023). The epidemic peak occurred in Round 2 (December 20–22, 2022). Similar trends were observed in urban areas (decreasing from 4.65% to 0.73%), rural areas (decreasing from 2.83% to 0.57%), the eastern region (decreasing from 4.18% to 0.67%), the central region (decreasing from 5.43% to 0.61%), and the western region (decreasing from 3.01% to 0.77%).

Conclusions: NSCS data showed that the peak of SARS-CoV-2 infection in China had passed. SARS-CoV-2 infection in community populations in China is currently at a low epidemic level.

Since its emergence in late 2019, coronavirus disease 2019 (COVID-19) has been a global threat for over three years (*1*). After experiencing a large-scale epidemic in February 2020, China entered a normalization stage of prevention and control that began in May 2020 (*1*–*2*). During this normalization stage, comprehensive measures were taken to reduce the impact of COVID-19 on health, the economy, and society (*2*). With the high coverage of COVID-19 vaccines in China, accumulated experience in prevention and treatment, and the presence of the highly infectious but less virulent Omicron variants BA.5.2 and BF.7, "Ten New Measures" were implemented on December 7, 2022 to further optimize prevention and control measures of COVID-19. A recent modeling study estimated the transmission dynamics of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Omicron BF.7 in Beijing (*3*). However, no study has evaluated national and regional trends of SARS-CoV-2 infection among the general community-based population in late 2022 and early 2023 during the widespread transmission of Omicron variants BA.5.2 and BF.7 throughout China. To fill this knowledge gap, we evaluated national and regional trends of SARS-CoV-2 infection among the general population using a community sentinel surveillance system during December 2022 and January 2023 to provide SARS-CoV-2 infection data during this critical period.

METHODS

Using aggregated data from the National Sentinel Community-Based Surveillance (NSCS) system in China, we assessed trends of SARS-CoV-2 infection. NSCS is a national community-based sentinel surveillance cohort with 0.42 million participants from

all 31 provincial-level administrative divisions (PLADs) and Xinjiang Production and Construction Corps (XPCC). Multistage stratified cluster sampling was used to recruit participants. Each PLAD was required to select one provincial capital city, one other large city, and one county. At least 2,000 households (≥ 5,000 individuals) were sampled in each provincial capital city; at least 1,500 households (≥3,000 individuals) were sampled in each selected large city; and at least 1,000 households (≥2,500 individuals) were sampled in each selected county. The minimum sampling unit was the household, and all selected households were included in the cohort. Each site conducted nucleic acid or antigen testing twice a week in every household. Neighborhood committees (village committees) in each surveillance sentinel site were responsible for the implementation of the investigation and data reporting. The district CDC of each sentinel site was responsible for collecting information and reporting to other levels. All participants in the monitored communities were tested voluntarily for infection twice a week (a total of eight surveillance rounds) from December 16, 2022 to January 12, 2023.

SARS-CoV-2 infection was defined as testing positive for either SARS-CoV-2 nucleic acid or antigen (*4*). The daily average newly positive rate of SARS-CoV-2 infection and its 95% confidence interval (*CI*) (*5*) were used to reflect the average daily new infection levels in the community sentinel surveillance populations during a specific surveillance round. This rate was calculated as the percent of investigated people with positive SARS-CoV-2 nucleic acid or antigen tests in a specific surveillance round divided by the number of days in the surveillance round. From the daily average newly positive rates we calculated estimated daily percentage change (EDPC) between rounds, which is a widely used measure of trends in rates over specified time intervals (*6*). We fit regression lines to the natural logarithm of the positive rate as $y= \alpha + \beta x$, where y is ln(incidence rate) and x is the surveillance round. EDPC reflected incidence trends between different rounds and was calculated as $100 \times (e^{\beta} - 1)$; its 95% *CI* was calculated as $[100 \times (e^{\beta\ lower\ bound} - 1), 100 \times (e^{\beta\ upper\ bound} - 1)]$. *P*-values were calculated for hypothesis testing as $t= \beta / SE_{\beta}$, with degrees of freedom as the number of rounds minus 2. Trends of incidence were considered downward (or upward) when EDPC values were below (or above) zero. SAS (version 9.4, SAS Institute Inc., Cary, USA) and Office Excel (version 2010, Microsoft Corp., Redmond, WA., USA) were used to analyze and draw statistical figures.

RESULTS

A total of 419,984 people were recruited into the community sentinel surveillance cohort of NSCS. The average daily rate of newly positive SARS-CoV-2 infections decreased from 4.13% in Round 1 (December 16–19, 2022) to 0.69% in Round 8 (January 10–12, 2023), with an estimated daily percentage change of –26.1%.

The daily average newly positive rate of SARS-CoV-2 infection in the eight surveillance rounds was found to be statistically significant ($P<0.05$, Table 1). The rates were 4.13%, 6.36%, 5.18%, 3.96%, 2.43%, 1.87%, 0.97%, and 0.69%, respectively. The epidemic peak occurred during Round 2 (December 20–22, 2022).

In urban areas, the daily average of newly positive SARS-CoV-2 infections decreased from 4.65% in Round 1 to 0.73% in Round 8, with an EDPC of –27.4% ($P<0.05$, Table 2). In rural areas, the daily average of newly positive cases decreased from 2.83% in Round 1 to 0.57% in Round 8, with an EDPC of –22.4% ($P<0.05$). Both the urban and rural positive rates peaked at Round 2, and the disparity between the two rates decreased as they both declined to less than 1% by Round 8 (Table 2 and Figure 1).

Table 3 shows the epidemic trends of SARS-CoV-2 infection in the three regions. In eastern China, the daily average of newly positive cases of SARS-CoV-2 infection decreased from 4.18% in Round 1 to 0.67% in Round 8, with an EDPC of –28.3% ($P<0.05$). For central and western China, EDPCs were –28.0% (decreasing from 5.43% to 0.61%, $P<0.05$) and –21.6% (decreasing from 3.01% to 0.77%, $P<0.05$), respectively. The daily average of newly positive cases in eastern and western China both peaked during Round 2. As shown in Figure 1, the daily average of newly positive cases converged across regions after Round 6 (January 3–5, 2023), and disparities among regions decreased as all rates declined to 0.6%–0.7% by Round 8.

DISCUSSION

Our findings from a sentinel community-based infection surveillance system showed that new SARS-CoV-2 infections peaked at 6.36% between December

TABLE 1. Trends of SARS-CoV-2 infection among the general population in sentinel community-based surveillance, China, December 2022–January 2023.

Rounds (testing date range)	Number of people investigated (*n*)	Number of newly positive (*n*)	Daily average newly positive rate (%, 95% *CI*)	EDPC (%, 95% *CI*)	*P*-value
Round 1 (December 16, 2022 to December 19, 2022)	139,351	23,019	4.13 (4.03–4.23)	−26.1 (−34.8, −16.5)	0.001
Round 2 (December 20, 2022 to December 22, 2022)	319,488	60,996	6.36 (6.28–6.44)		
Round 3 (December 23, 2022 to December 26, 2022)	405,364	83,912	5.18 (5.11–5.25)		
Round 4 (December 27, 2022 to December 29, 2022)	385,563	45,786	3.96 (3.90–4.02)		
Round 5 (December 30, 2022 to January 2, 2023)	403,471	39,272	2.43 (2.38–2.48)		
Round 6 (January 3, 2023 to January 5, 2023)	387,787	21,722	1.87 (1.83–1.91)		
Round 7 (January 6, 2023 to January 9, 2023)	419,984	16,259	0.97 (0.94–1.00)		
Round 8 (January 10, 2023 to January 12, 2023)	418,836	8,686	0.69 (0.66–0.72)		

Note: EDPC represents estimated daily percentage change from Round 1 to Round 8.
Abbreviation: SARS-CoV-2=severe acute respiratory syndrome coronavirus 2; *CI*=confidence interval; EDPC=estimated daily percentage change.

TABLE 2. Trends of SARS-CoV-2 infection among the general population in sentinel community-based surveillance by location, China, December 2022–January 2023.

Rounds	Number of people investigated (*n*)	Number of newly positive (*n*)	Daily average newly positive rate (%, 95% *CI*)	EDPC (%, 95% *CI*)	*P*-value
Urban areas					
Round 1	99,239	18,471	4.65 (4.52–4.78)	−27.4 (−34.9, −18.9)	<0.001
Round 2	239,464	49,501	6.89 (6.79–6.99)		
Round 3	291,816	62,345	5.34 (5.26–5.42)		
Round 4	295,095	33,749	3.81 (3.74–3.88)		
Round 5	314,079	30,490	2.43 (2.37–2.48)		
Round 6	304,333	15,508	1.70 (1.65–1.74)		
Round 7	326,732	12,290	0.94 (0.91–0.97)		
Round 8	327,044	7,126	0.73 (0.70–0.76)		
Rural areas					
Round 1	40,112	4,548	2.83 (2.67–3.00)	−22.4 (−35.3, −6.9)	0.014
Round 2	80,024	11,495	4.79 (4.64–4.94)		
Round 3	113,548	21,567	4.75 (4.62–4.87)		
Round 4	90,468	12,037	4.44 (4.30–4.57)		
Round 5	89,392	8,782	2.46 (2.35–2.56)		
Round 6	83,454	6,214	2.48 (2.38–2.59)		
Round 7	93,252	3,969	1.06 (1.00–1.13)		
Round 8	91,792	1,560	0.57 (0.52–0.62)		

Note: EDPC represents estimated daily percentage change from Round 1 to Round 8.
Abbreviation: SARS-CoV-2=severe acute respiratory syndrome coronavirus 2; *CI*=confidence interval; EDPC=estimated daily percentage change.

20–22, 2022 and then steadily decreased to 0.69% by January 10–12, 2023. Both urban and rural areas experienced a peak in infection rates during December 20–22, 2022, with the rural area peak being lower than the urban area peak. By January 10–12, 2023, both urban and rural infection rates had declined to nearly identical low levels. Our sentinel community-based surveillance results are consistent with national fever outpatient surveillance at the time of the epidemic peak (December 23, 2022), indicating that the

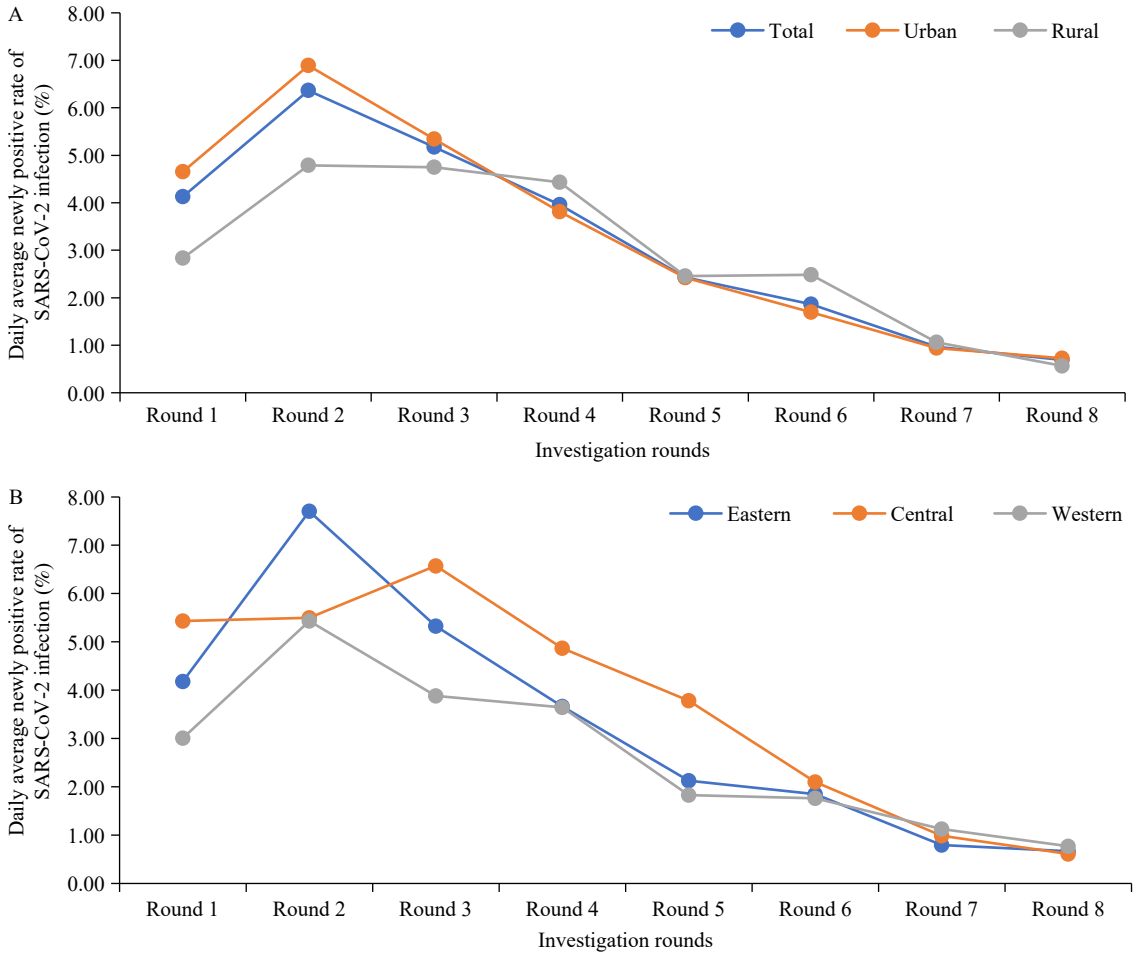

FIGURE 1. Trends of SARS-CoV-2 infection in sentinel community-based surveillance, China, December 2022–January 2023. (A) Stratified by location; (B) Stratified by region.
Note: Investigations in the study were conducted in eight rounds, from December 16, 2022 to January 12, 2023. Round 1 was conducted from December 16–19, 2022; Round 2 from December 20–22, 2022; Round 3 from December 23–26, 2022; Round 4 from December 27–29, 2022; Round 5 from December 30, 2022 to January 2, 2023; Round 6 from January 3–5, 2023; Round 7 from January 6–9, 2023; and Round 8 from January 10–12, 2023.
Eastern region included Beijing, Tianjin, Hebei, Liaoning, Shanghai, Jiangsu, Zhejiang, Fujian, Shandong, Guangdong, and Hainan. Western region included Inner Mongolia, Guangxi, Chongqing, Sichuan, Guizhou, Yunnan, Tibet, Shaanxi, Gansu, Qinghai, Ningxia, Xinjiang, Xinjiang Production and Construction Corps. Central region included Shanxi, Jilin, Heilongjiang, Anhui, Jiangxi, Henan, Hubei, and Hunan.
Abbreviation: SARS-CoV-2=severe acute respiratory syndrome coronavirus 2.

epidemic wave in China had passed following the optimization of prevention and control measures.

The Omicron variant is less pathogenic and more transmissible than the ancestral strain and previous variants of concern, and we now have a deeper understanding of the virus, a broader selection of antiviral drugs, and more experience in the treatment of COVID-19 infection. In late 2022, The State Council Joint Prevention and Control Mechanism issued the "20 Measures (November 11, 2022)" and the "Ten New Measures (December 7, 2022)" to optimize the epidemic prevention and control plan, protect people's safety and health to the greatest extent possible, and minimize the impact of the epidemic on economic and social development. These measures included deployments for strengthening medical resources, promoting vaccination, accelerating drug stockpiling, and strengthening the protection of key institutions and populations (*7*–*8*). These initiatives contributed to our rapid response against the COVID-19 epidemic and enabled us to withstand the peak of the epidemic and its quick decline. In rural areas, comprehensive mapping of key populations, implementing a system of responsibility to ensure prevention and control compliance, and issuing health kits and other measures (*9*) helped to mitigate the

TABLE 3. Trends of SARS-CoV-2 infection among the general population in sentinel community-based surveillance by region, China, December 2022–January 2023.

Rounds	Number of people investigated (*n*)	Number newly positive (*n*)	Daily average newly positive rate (%, 95% *CI*)	EDPC (%, 95% *CI*)	*P*-value
Eastern					
Round 1	39,817	6,654	4.18 (3.98–4.37)		
Round 2	128,620	29,724	7.70 (7.56–7.85)		
Round 3	192,046	40,904	5.32 (5.22–5.43)		
Round 4	145,503	16,003	3.67 (3.57–3.76)	−28.3 (−37.4, −17.8)	0.001
Round 5	150,416	12,806	2.13 (2.06–2.20)		
Round 6	153,315	8,496	1.85 (1.78–1.91)		
Round 7	158,143	5,051	0.80 (0.75–0.84)		
Round 8	157,516	3,154	0.67 (0.63–0.71)		
Central					
Round 1	45,272	9,841	5.43 (5.23–5.64)		
Round 2	81,351	13,425	5.50 (5.34–5.66)		
Round 3	91,777	24,138	6.58 (6.41–6.74)		
Round 4	96,699	14,120	4.87 (4.73–5.00)	−28.0 (−38.2, −16.1)	0.002
Round 5	101,841	15,402	3.78 (3.66–3.90)		
Round 6	81,908	5,162	2.10 (2.00–2.20)		
Round 7	107,850	4,266	0.99 (0.93–1.05)		
Round 8	106,788	1,958	0.61 (0.56–0.66)		
Western					
Round 1	54,262	6,524	3.01 (2.86–3.15)		
Round 2	109,517	17,847	5.43 (5.30–5.57)		
Round 3	121,541	18,870	3.88 (3.77–3.99)		
Round 4	143,361	15,663	3.64 (3.54–3.74)	−21.6 (−30.6, −11.4)	0.003
Round 5	151,214	11,064	1.83 (1.76–1.90)		
Round 6	152,564	8,064	1.76 (1.70–1.83)		
Round 7	153,991	6,942	1.13 (1.07–1.18)		
Round 8	154,532	3,574	0.77 (0.73–0.81)		

Note: EDPC represents estimated daily percentage change from Round 1 to Round 8; Eastern region included Beijing, Tianjin, Hebei, Liaoning, Shanghai, Jiangsu, Zhejiang, Fujian, Shandong, Guangdong, and Hainan. Western region included Inner Mongolia, Guangxi, Chongqing, Sichuan, Guizhou, Yunnan, Tibet, Shaanxi, Gansu, Qinghai, Ningxia, Xinjiang, Xinjiang Production and Construction Corps. Central region included Shanxi, Jilin, Heilongjiang, Anhui, Jiangxi, Henan, Hubei, and Hunan.
Abbreviation: SARS-CoV-2=severe acute respiratory syndrome coronavirus 2; *CI*=confidence interval; EDPC=estimated daily percentage change.

impact of the COVID-19 epidemic.

Given the presence of highly infectious Omicron variants BA.5.2 and BF.7, it was of utmost urgency to quickly and accurately assess infection rates and trends in community populations. Compared to other surveillance methods, the positive rate we observed in the NSCS was lower than seen in hospital-based sentinel surveillance during the same period. This difference may be attributed to the different surveillance methods and population characteristics. Hospital-based survey populations are clinic populations, in which people are seeking medical attention, possibly for SARS-CoV-2 infection, resulting in a higher positive rate than the general population in a community. As a national community-based sentinel surveillance cohort with nearly 420,000 participants from 31 PLADs and XPCC, NSCS has effectively filled the current research and knowledge gap, providing near-real-time data and technical support for assessing the epidemic situation and estimating medical treatment resource needs at the national, regional, and provincial levels. China has

passed the peak of COVID-19 infection and is now at a low epidemic level. In the future, it will still be necessary to adjust prevention and control measures flexibly and actively respond to the dynamic situation to consolidate the current COVID-19 achievements.

This study has several strengths. First, a large sample size of households was selected from cities and counties of all 31 PLADs and XPCC. Second, NSCS conducted regular, frequent, and periodic testing of participants during a time that captured the peak of the epidemic in both rural and urban populations.

The study also has some limitations. First, due to this being an emergency surveillance project supported by the National Bureau of Disease Control and Prevention, the sampling methods varied by PLAD and included both population-proportional-to-size random sampling and convenience sampling. This, combined with the large sample size, allowed us to reflect the dynamic infection level of SARS-CoV-2 in the community population, but the conclusions may not be generalizable to other populations. Second, we analyzed aggregated NSCS data without individual-level data and therefore could not analyze the differences in the average daily incidence rate of SARS-CoV-2 infection among people with different characteristics (such as age, gender, and presence of underlying chronic diseases).

In conclusion, after optimizing prevention and control measures, sentinel surveillance data from community populations suggest that the peak of SARS-CoV-2 infection in China occurred in December 2022. Currently, SARS-CoV-2 infection in community populations across China is at a low level.

Conflicts of interest: No conflicts of interest.

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[#] Corresponding authors: Min Liu, liumin@bjmu.edu.cn; Wannian Liang, liangwn@tsinghua.edu.cn; Qun Li, liqun@chinacdc.cn.

[1] School of Public Health, Peking University, Beijing Municipality, China; [2] Chinese Center for Disease Control and Prevention, Beijing Municipality, China; [3] Vanke School of Public Health, Tsinghua University, Beijing Municipality, China.
[&] Joint first authors.

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Preplanned Studies

Epidemic Features of COVID-19 and Potential Impact of Hospital Strain During the Omicron Wave — Australia, 2022

Jingli Yang[1,2]; Hannah McClymont[1]; Liping Wang[3]; Sotiris Vardoulakis[4,5]; Wenbiao Hu[1,5,#]

Summary

What is already known about this topic?

Hospitals have experienced a surge in admissions due to the increasing number of Omicron cases. Understanding the epidemiological features of coronavirus disease 2019 (COVID-19) and the strain it places on hospitals will provide scientific evidence to help policymakers better prepare for and respond to future outbreaks.

What is added by this report?

The case fatality rate of COVID-19 was 1.4 per 1,000 persons during the Omicron wave. Over 90% of COVID-19-related deaths occurred in individuals aged 60 years or older, with pre-existing chronic conditions such as cardiac conditions and dementia, particularly among males aged 80 years or older.

What are the implications for public health practice?

Public health policy is essential for preparing and preserving medical resource capacity, as well as recruiting additional clinicians and front-line staff in hospitals to address the increased demand. High-risk individuals should be prioritized for healthcare, vaccines, and targeted interventions.

In the past three years, coronavirus disease 2019 (COVID-19) has become one of the major public health crises worldwide. As severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) sequences mutated and vaccination coverage increased, the severity of COVID-19 appears to have gradually decreased. Many countries, including Australia, have gradually allowed SARS-CoV-2 to circulate in communities. This study aimed to summarize the epidemic features of COVID-19 and explore the impact of hospital strain during the Omicron wave in Australia. A Quasi-Poisson regression model was used to explore the associations between the number of deaths, intensive care unit (ICU) admissions, and hospital admissions caused by COVID-19. Results showed that the single-day maximum numbers of deaths, hospital admissions, and ICU admissions caused by COVID-19 in Australia were 1,875,571, and 224 during the Omicron wave, respectively. Additionally, 73.5% of confirmed cases and 72.5% of deaths were recorded at the Omicron wave. About 92.9% of the deaths caused by COVID-19 occurred in people over 60 years old, with the highest risk in males and pre-existing chronic conditions, including chronic cardiac conditions and dementia, especially for those over 80 years old. The research findings could help policymakers to better prepare for and respond to future outbreaks.

We aimed to summarize the epidemic features and explore the impact of hospital strain on the COVID-19 Omicron wave in Australia. Data were obtained from Our World in Data (*1*) and the Australian Bureau of Statistics. The formulas for case fatality rate (CFR), case hospitalization rate (CHR), case ICU rate (CICUR), and mortality fatality index (MFI) caused by COVID-19 can be found in the Supplementary Material (available in https://weekly.chinacdc.cn/). To more comprehensively understand the severity of COVID-19, we developed MFI considering COVID-19 confirmed cases and deaths, and the population. CFR, CHR, MFI, and CICUR were described chronologically using scatter plots with regression lines. The stringency index, a composite measure of the government's prevention and control of COVID-19 developed by OxCGRT (*2*), was based on nine response indicators including school closures, workplace closures, and travel bans, rescaled to a value from 0 to 100 (100=strictest). Spearman's rank correlation was used to detect the correlation coefficients (r). Since the number of patients in hospitals caused by COVID-19 was a count and its mean and variance were unequal, a Quasi-Poisson regression model was used to overcome the overdispersion and assess the associations between the number of deaths, ICU, and patients in hospitals caused by COVID-19. Chi-square tests were used for mortality comparisons by sex and age groups. All statistical analyses were completed using R version

4.1.3 software (R Foundation for Statistical Computing, Vienna, Austria).

On December 15, 2021, the Omicron strain of COVID-19 was detected in Australia and quickly displaced previous variants, with the Omicron strain accounting for 100% of SARS-COV-2 sequences by February 14, 2022. As of December 19, 2022, the total number of confirmed cases of COVID-19 in Australia was 10,979,204, with an infection rate of 43.2%. The total number of deaths caused by COVID-19 was 16,712, and the mortality rate was 60 per 100,000 persons. Of these, 73.5% of the confirmed cases and 72.5% of the deaths caused by COVID-19 occurred during the Omicron wave. About 92.9% of the deaths caused by COVID-19 occurred in people over 60 years old (Figure 1A), and the mortality of men in all age groups was significantly higher than that of women (Figure 1B and Supplementary Table S1, available in https://weekly.chinacdc.cn/). During the Omicron wave (from February 14 to December 19, 2022), the CFR caused by COVID-19 was 1.4 per 1,000 persons overall, and the CFR was 1.5, 6.6, 27.5, and 69.5 per 1,000 persons in the 60–69, 70–79, 80–89, and 90+ years age groups, respectively (Figure 1A). After the stringency index reduced to its lowest level on July 6, 2022, the CFR, CHR, MFI, and CICUR gradually reached their peak (lasting for about 4 months) (Figure 2). The CFR was 1.02 per 1,000 persons between February 14 and July 6, 2022, and 2.49 per 1,000 persons between July 6 and December 19, 2022 (Supplementary Table S2, available in https://weekly.chinacdc.cn/). Additionally, the daily death rate per million had a peak after the stringency index reduced to its lowest level (Supplementary Figure S1, available in https://weekly.chinacdc.cn/). During the Omicron wave, the single-day maximum number of deaths,

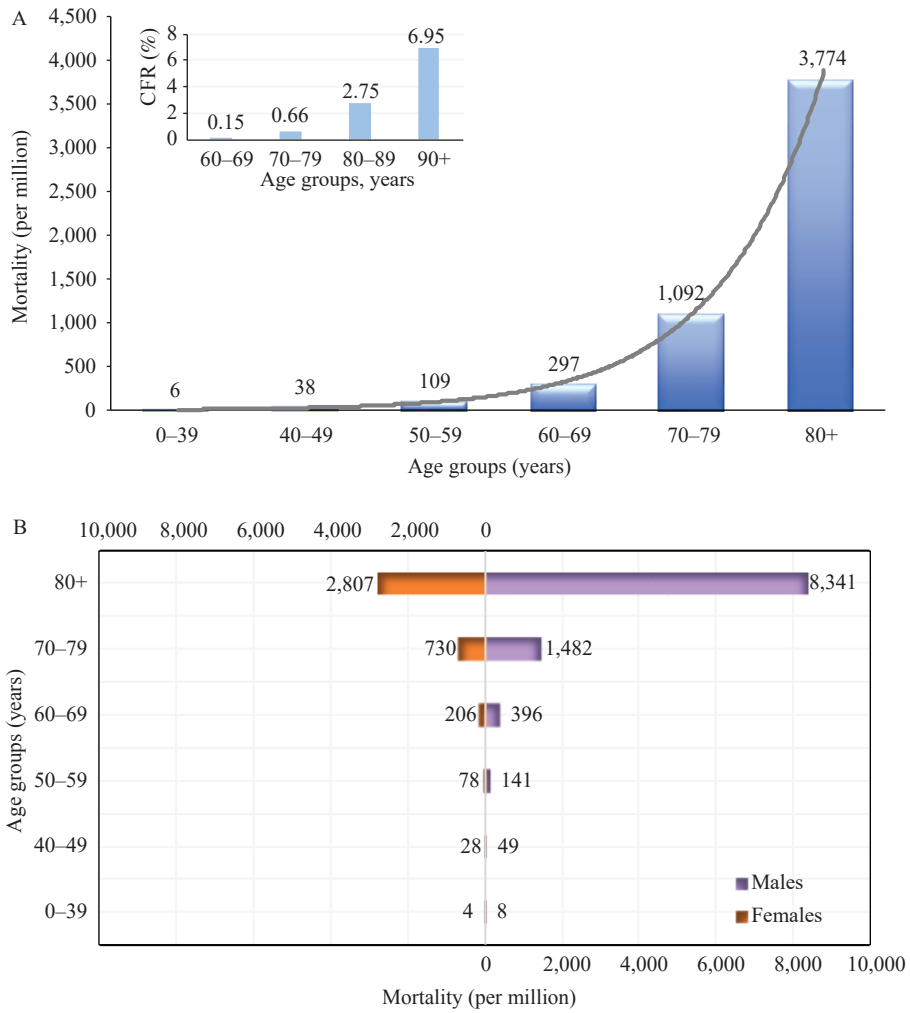

FIGURE 1. Deaths caused by COVID-19 by (A) age during Omicron period and (B) sex up to November 2022 in Australia.
Abbreviation: COVID-19=coronavirus disease 2019.

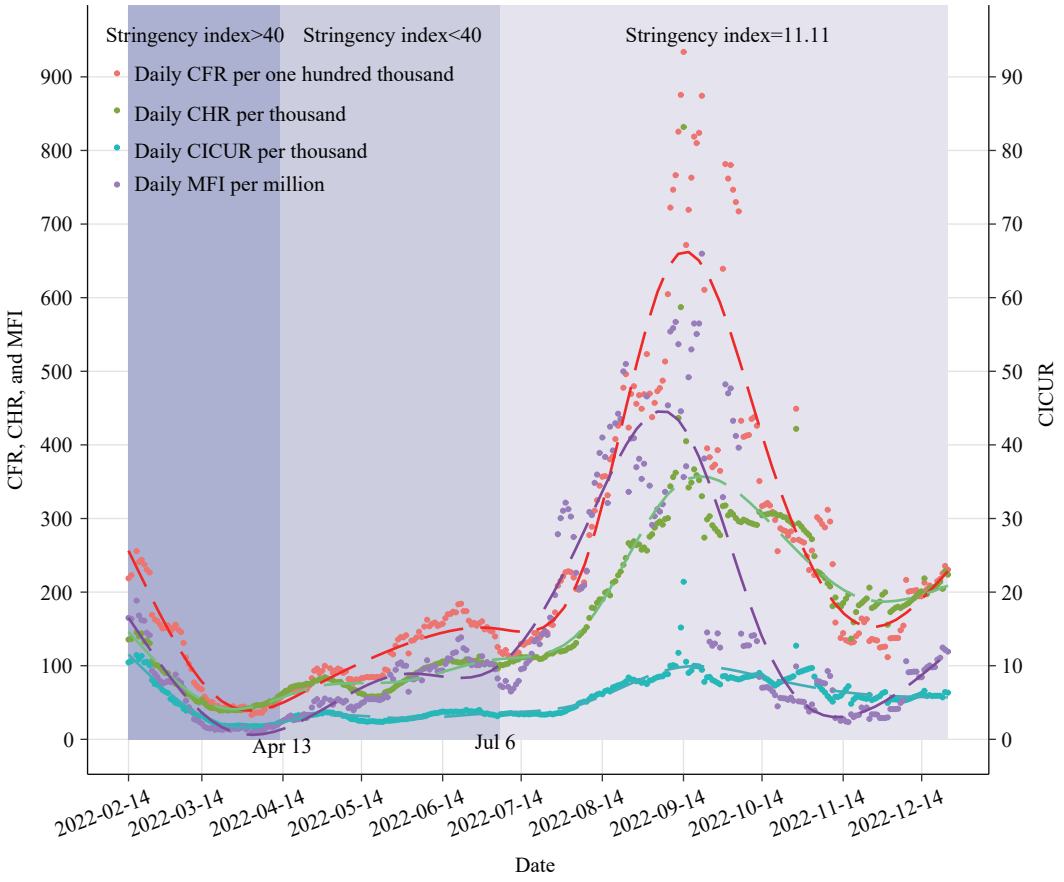

FIGURE 2. The trends of case fatality rate, case hospitalization rate, and case ICU rate in Australia during the Omicron period.
Note: CFR, CHR, MFI, and CICUR are described chronologically using regression lines ('dash line') and scatter plots ('dotted'). The stringency index is a composite measure based on nine response indicators including school closures, workplace closures, and travel bans, rescaled to a value from 0 to 100 (100=strictest).
Abbreviation: ICU=intensive care unit; CFR=case fatality rate; CHR=case hospitalization rate; MFI=mortality fatality index; CICUR=case ICU rate.

hospital admissions, and ICU admissions caused by COVID-19 were 187, 5571, and 224, respectively. Furthermore, the number of deaths (r=0.82, P<0.01) and ICU admissions (r=0.70, P<0.01) increased with the increase in the number of COVID-19 hospital admissions (Figure 3). The CFR (r=0.86, P<0.01), MFI (r=0.59, P<0.01), and CICUR (r=0.90, P<0.01) increased with the increase in CHR (Supplementary Figure S2, available in https://weekly.chinacdc.cn/). Of the deaths caused by COVID-19, 39.3% had a history of chronic cardiac conditions, 30.3% had a history of dementia, and 17.8% had a history of chronic respiratory disease (Supplementary Figure S3, available in https://weekly.chinacdc.cn/). Pneumonia (61.0%) and respiratory failure (14.9%) were the main causes of death caused by COVID-19 (Supplementary Figure S4, available in https://weekly.chinacdc.cn/). In December 2022, only 20.0% of detected cases were reinfections in the Australian Capital Territory, and the proportion of reinfection increased over time (Supplementary Figure S5, available in https://weekly.chinacdc.cn/).

DISCUSSION

In February 2022, Australia reopened its international borders (share of residents with a complete initial vaccine protocol: 78.1%). By April 2022 (share of residents with a complete initial vaccine protocol: 82.0%), Australian jurisdictions had begun to lift mask mandates, and airport mask mandates were removed in June 2022. When the stringency index decreased to its lowest level in July (share of residents with a complete initial vaccine protocol: 82.7%), community levels of COVID-19 peaked and remained at this level for four months. Our findings indicated

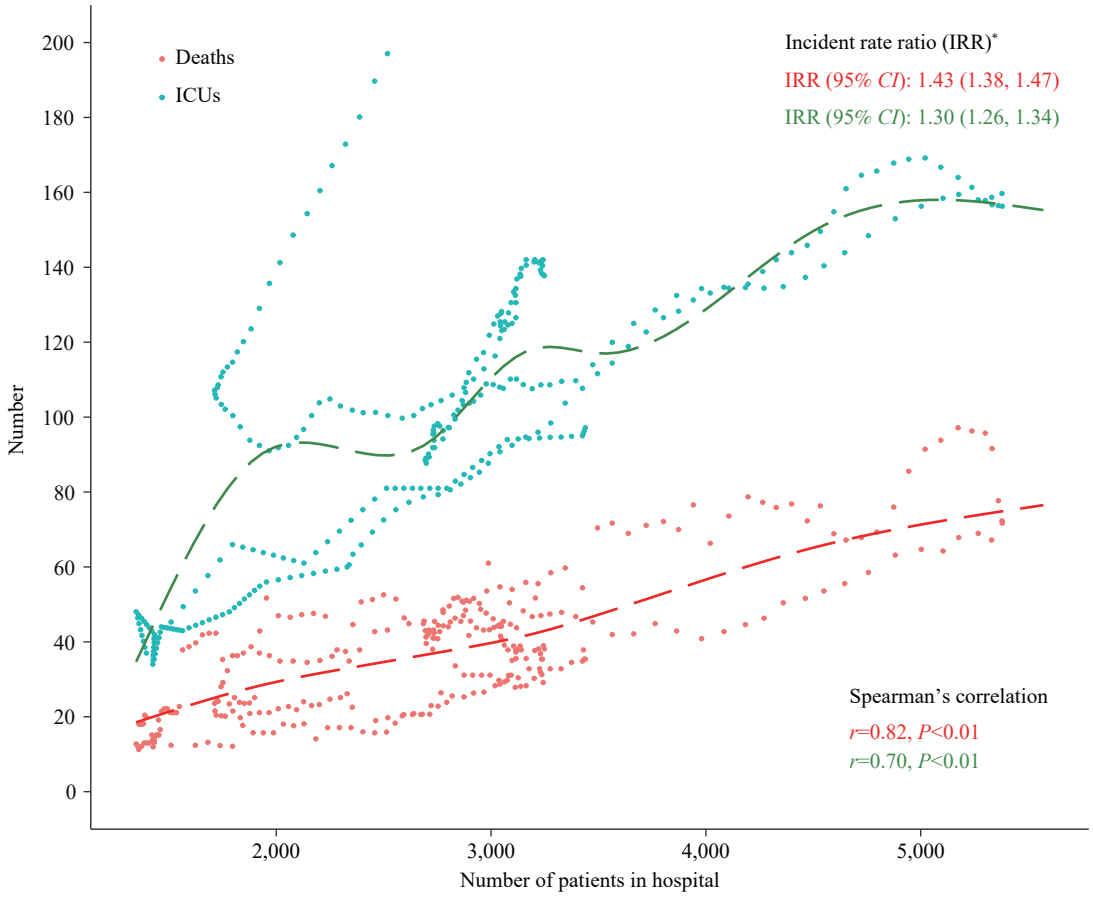

FIGURE 3. Scatter plot and Spearman's correlation between number of deaths, ICU, and patients in hospitals caused by COVID-19 in Australia during the Omicron period.
Note: The dash lines were the fitted curve using regression lines. Incident rate ratio in daily number of deaths and ICUs for 1,000-increase in daily number of patients in hospitals caused by COVID-19 in Quasi-Poisson regression model.

that the CFR, MFI, and CICUR increased significantly with the increase in CHR during the Omicron wave, which is consistent with several previous studies (*3*–*4*). This increase in hospital burden contributed to the rise in COVID-19 deaths. Vaccination and non-pharmaceutical interventions (NPIs) will remain important measures to suppress the peak of the epidemic and reduce hospital strain (*5*). Additionally, a new Omicron subvariant XBB was detected in Australia at the end of September 2022, and its proportion of SARS-COV-2 sequences had risen to 3.0% as of January 16, 2023 (*1*).

This study found that 92.9% of deaths in Australia occurred in people over 60 years old, with the highest risk in men and those with pre-existing chronic conditions, including chronic cardiac conditions and dementia. Research has shown that individuals diagnosed with dementia have three times the risk of developing severe COVID-19 compared with those without dementia (*6*), which may be due to social isolation, delayed clinical care, and worsening mental health (*7*). Additionally, risk factors for dementia (such as age, obesity, and cardiovascular and metabolic diseases) are also risk factors for SARS-CoV-2 infection and severe COVID-19 (*8*). People with dementia may have difficulty understanding and following public health recommendations, so it is essential to provide additional support during the COVID-19 outbreak (*9*).

This study has several limitations. First, we do not have individual clinical information about deaths due to COVID-19 in Australia during the Omicron wave. However, 72.5% of the deaths attributed to COVID-19 occurred during the Omicron wave, suggesting that the distribution of deaths included in this study is a good representation of the Omicron wave. Second, case numbers may be underestimated due to inadequate detection, which could lead to overestimation of the CFR, CHR, and CICUR. Nevertheless, the quality of the reported data is

unlikely to vary significantly within the temporal scales of our analysis.

The epidemiological features of COVID-19 in Australia provide an important reference for other countries currently experiencing high levels of COVID-19 transmission during the Omicron wave. To reduce mortality and relieve strain on healthcare systems, health authorities should prioritize the following: 1) Minimizing the chance of infection through strengthening NPIs and vaccinating vulnerable populations; 2) Providing effective COVID-19 health education strategies to reduce fear and confusion; 3) Mitigating the risk of co-infections by improving access to non-hospital care, outdoor fever/testing clinics, and telehealth services; 4) Developing effective early warning systems to improve the efficiency and accuracy of surveillance and management of COVID-19 (*10*).

Conflicts of interest: No conflicts of interest.

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[#] Corresponding author: Wenbiao Hu, w2.hu@qut.edu.au.

[1] School of Public Health and Social Work, Queensland University of Technology, Brisbane, Australia; [2] College of Earth and Environmental Sciences, Lanzhou University, Lanzhou City, Gansu Province, China; [3] Division of Infectious Diseases, Chinese Center for Diseases Control and Prevention, Beijing Municipality, China; [4] National Centre for Epidemiology and Population Health, College of Health and Medicine, The Australian National University, Canberra, Australia; [5] Healthy Environments And Lives (HEAL) National Research Network, Australia.

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SUPPLEMENTARY MATERIAL

Definition

Stringency Index

The indicators of government response include nine policies recorded on an ordinal scale, namely, school closures, workplace closures, cancellation of public events, restrictions on public gatherings, closures of public transport, stay-at-home requirements, public information campaigns, restrictions on internal movements, and international travel controls. The stringency index is composed of a series of individual policy response indicators. For each indicator, we create a score by taking the ordinal value and subtracting half a point if the policy is targeted rather than general, if applicable. We then rescale each of these by their maximum value to create a score between 0 and 100, with a missing value contributing 0. These scores are then averaged to obtain the composite indices. This calculation is described in the equation below, where k is the number of component indicators in an index and I_j is the subindex score for an individual indicator. Sources: A global panel database of pandemic policies (Oxford COVID-19 Government Response Tracker) | Nature Human Behaviour (Source: https://www.nature.com/articles/s41562-021-01079-8).

$$\textbf{Stringency Index} = \frac{1}{k}\sum_{j=1}^{k} I_j$$

Daily CFR, CHR, CICUR, MFI

The outcomes included daily case fatality rate (CFR), case hospitalization rate (CHR), case ICU rate (CICUR), and mortality fatality index (MFI) caused by COVID-19, calculated as follows:

$$\textbf{Daily CICUR} = \frac{\text{7 days moving average of daily number of patients in ICU}}{\text{7 days moving average of daily number of new confirmed cases 10 days earlier}} \times 1,000,000$$

$$\textbf{Daily CHR} = \frac{\text{7 days moving average of daily number of patients in the hospitals}}{\text{7 days moving average of daily number of new confirmed cases 10 days earlier}} \times 1,000,000$$

$$\textbf{Daily CFR} = \frac{\text{7 days moving average of daily number of new confirmed deaths}}{\text{7 days moving average of daily number of new confirmed cases 10 days earlier}} \times 1,000,000$$

$$\textbf{Daily MFI} = \frac{\text{7 days moving average of daily number of new confirmed deaths}^2}{\text{7 days moving average of daily number of new confirmed cases 10 days earlier} \times \text{Total population}} \times 1,000,000$$

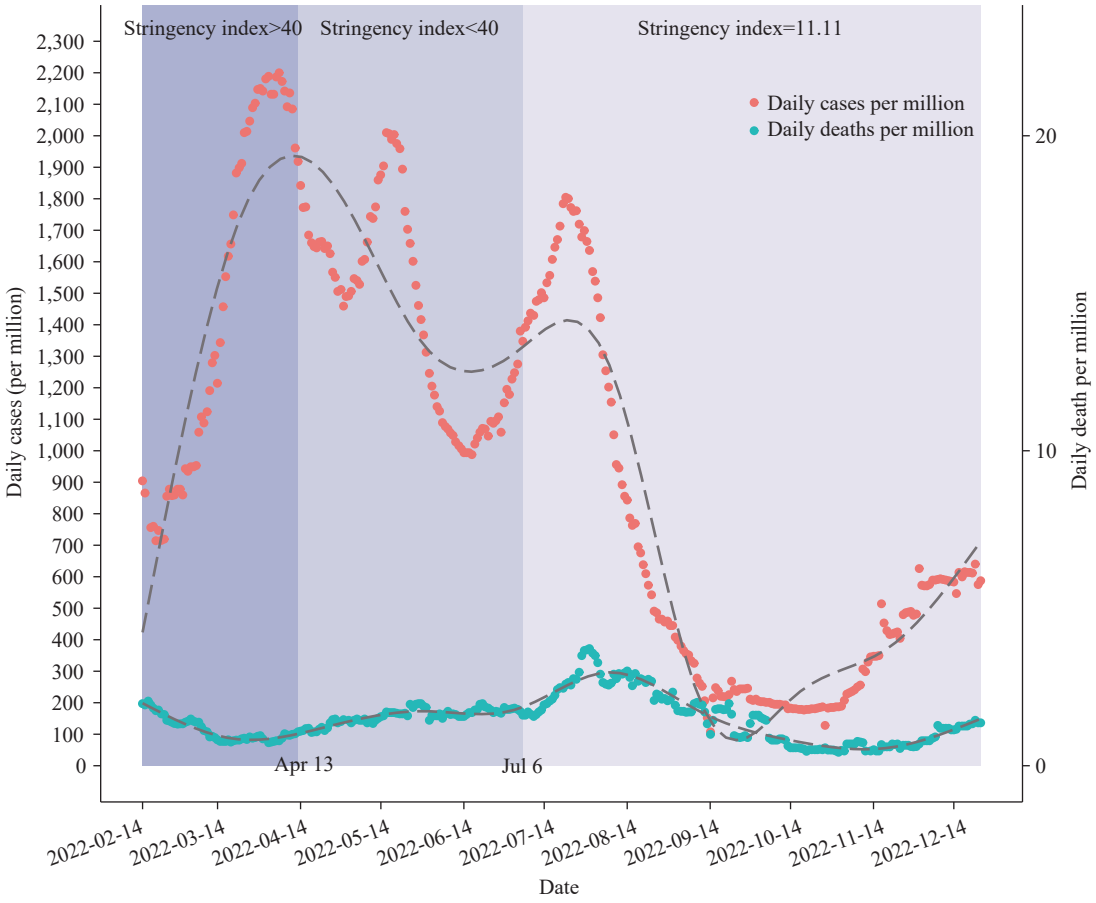
When calculating the daily CFR, we keep consistent with Our World in Data using the number of new confirmed cases 10 days earlier since confirmed cases often do not die on the same day. Furthermore, the deaths caused by COVID-19 in this report have been coded to ICD-10 code U07.1 COVID-19, virus identified or U07.2 COVID-19, virus not identified as the underlying cause of death.

SUPPLEMENTARY TABLE S1. Deaths caused by COVID-19 by sex and age groups during Omicron wave in Australia.

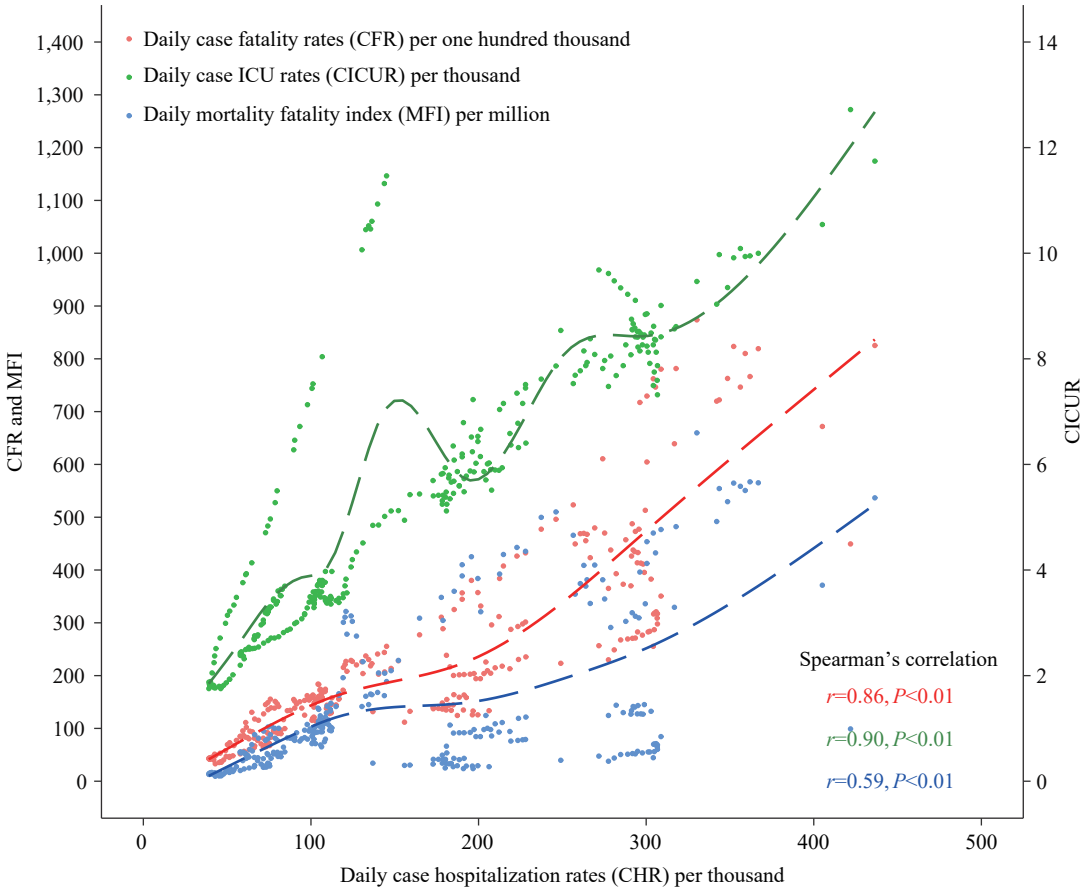
Age group, years	Sex	Death	Frequency	χ^2	*P*-value
0–39				5.633	0.018
	Males	No	6,632,889		
	Males	Yes	51		
	Females	No	6,505,979		
	Females	Yes	29		
40–49				9.153	0.002
	Males	No	1,616,847		
	Males	Yes	79		
	Females	No	1,667,830		
	Females	Yes	47		
50–59				28.373	<0.001
	Males	No	1,541,189		
	Males	Yes	217		
	Females	No	1,611,329		
	Females	Yes	126		
60–69				83.845	<0.001
	Males	No	1,336,528		
	Males	Yes	529		
	Females	No	1,429,210		
	Females	Yes	294		
70–79				256.834	<0.001
	Males	No	952,498		
	Males	Yes	1,414		
	Females	No	1,028,023		
	Females	Yes	751		
80+				1601.200	<0.001
	Males	No	459,055		
	Males	Yes	3,861		
	Females	No	632,252		
	Females	Yes	1,780		

SUPPLEMENTARY TABLE S2. The cases, deaths and case fatality rates caused by COVID-19 during the Omicron wave (from February 14, 2022 to December 19, 2022).

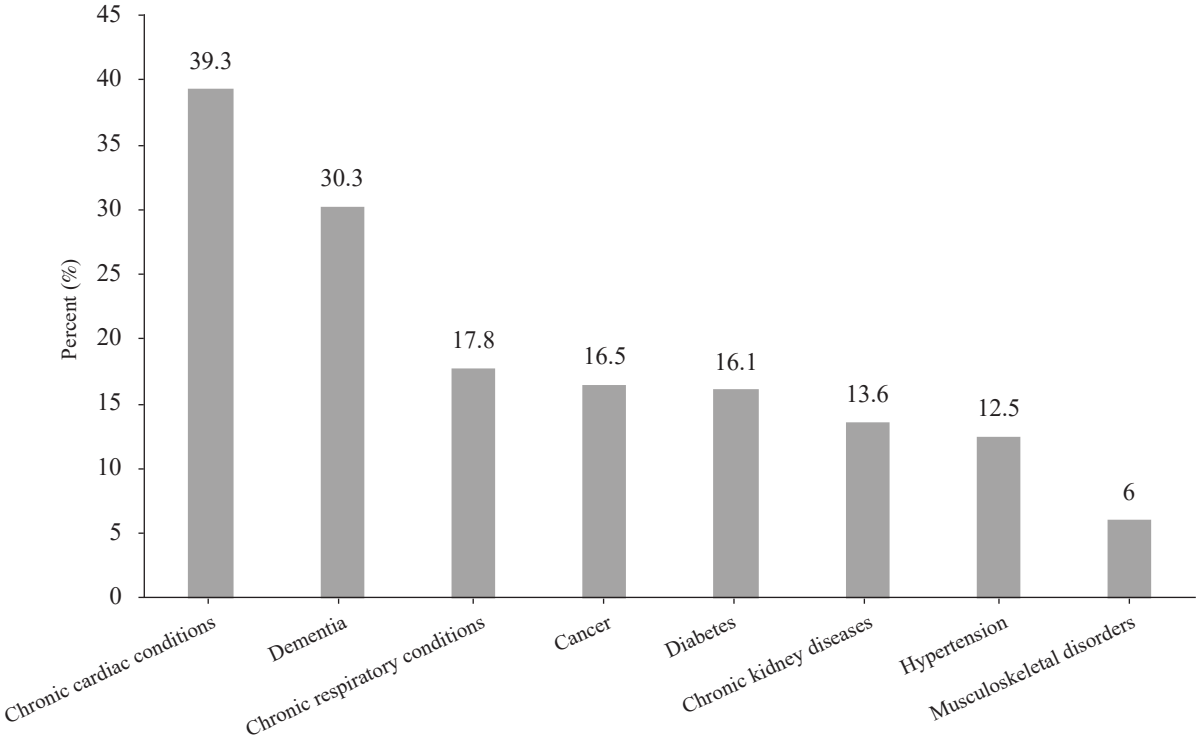
Outcome	February 14 to July 5	July 6 to December 19	February 14 to December 19
COVID-19 confirmed cases	5,420,219	2,644,402	8,064,621
COVID-19 confirmed deaths	5,526	6,582	12,108
Case fatality rates	0.102%	0.249%	0.150%



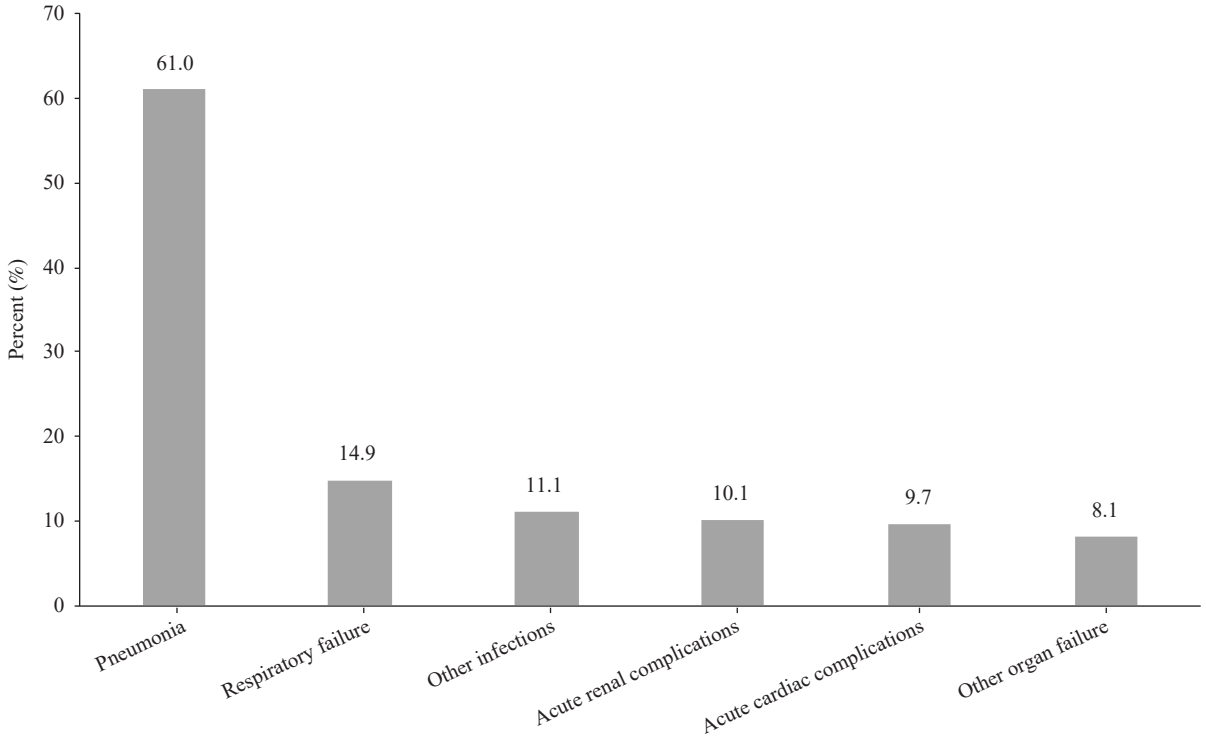
SUPPLEMENTARY FIGURE S1. The trends of confirmed cases and deaths in Australia during the Omicron wave.
Note: The dash lines were fitted curve using regression lines.



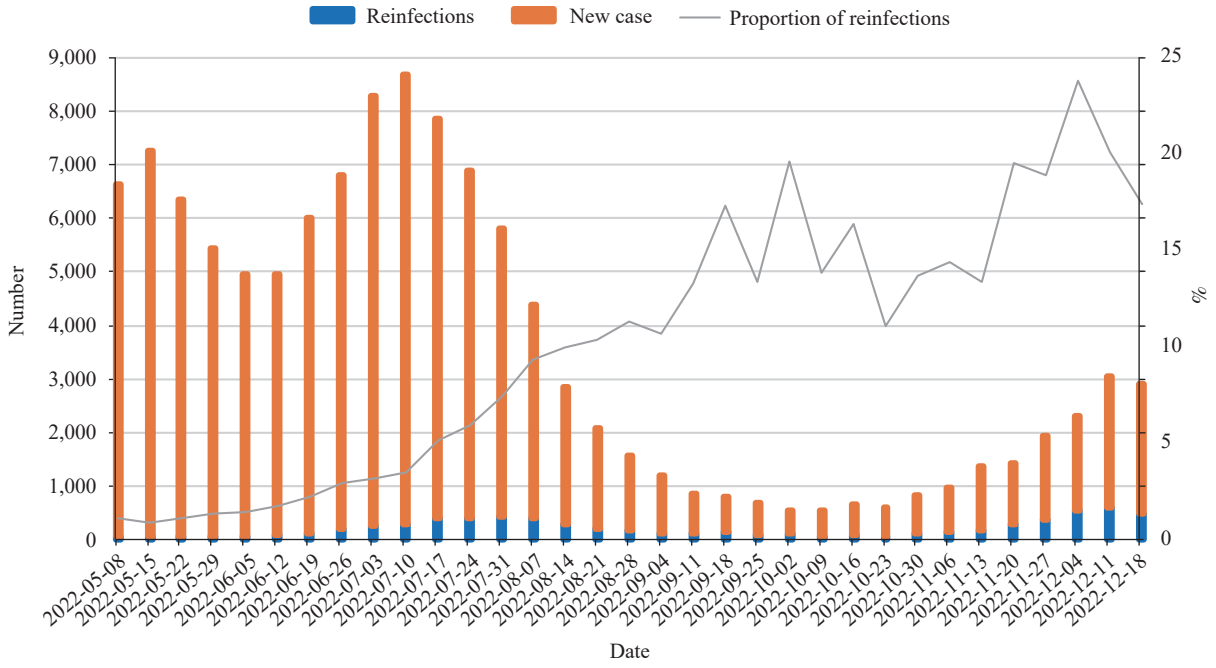
SUPPLEMENTARY FIGURE S2. Scatter plot and Spearman's correlation between case fatality rate, case ICU rate and patients in hospitals in Australia during the Omicron wave.
Note: The dash lines were the fitted curve using regression lines.



SUPPLEMENTARY FIGURE S3. Deaths caused by COVID-19: pre-existing chronic conditions in Australia between 2020 and 2022.
Source: https://www.abs.gov.au/



SUPPLEMENTARY FIGURE S4. Deaths caused by COVID-19: conditions in the causal sequence in Australia between 2020 and 2022.
Source: https://www.abs.gov.au/



SUPPLEMENTARY FIGURE S5. Weekly reported cases by previous infection status in the Australian Capital Territory in 2022.
Source: https://www.abc.net.au/news/2023-01-04/latest-surge-infecting-people-who-have-not-had-covid19/101794332

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