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Preplanned Studies

Asymptomatic Norovirus Infection Among Children in Kindergartens and Primary Schools — Beijing Municipality, China, 2021

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Summary

What is already known about this topic?

Children in kindergartens and primary schools are the high-incidence groups of norovirus acute gastroenteritis. However, asymptomatic norovirus infection among them is seldom reported.

What is added by this report?

The norovirus positive rate was 3.48% among asymptomatic children in kindergartens and primary schools in Beijing Municipality in June 2021, the most common genotype was GII.4 Sydney, and no acute gastroenteritis outbreak was reported over the study period.

What are the implications for public health practice?

The asymptomatic norovirus infection was relatively low among kindergarten children and primary school students in summer. Norovirus genotypes in asymptomatic children were similar to those circulating in the symptomatic cases. Asymptomatic norovirus infection may play a limited role in causing acute gastroenteritis outbreaks.

Norovirus is the dominant causative agent of acute gastroenteritis (AGE) throughout the world, and both symptomatic and asymptomatic persons may be the source of infection (*1*–*3*). Asymptomatic persons have no obvious clinical symptoms and are easily neglected. Children in kindergartens and primary schools are the high-incidence groups of AGE due to norovirus (*1*–*2*), but asymptomatic infection among them is seldom reported. In this study, norovirus was detected among 460 healthy children, with a positive rate of 3.48%, and GII.4 Sydney was the dominant genotype, the same as in children with AGE. The results suggested that noroviruses circulating in asymptomatic children had a common source with those in AGE cases. However, there were no acute gastroenteritis outbreaks in schools or kindergartens 4 weeks before and after the sampling, suggesting that asymptomatic children may have a limited role in causing AGE outbreaks.

This is a cross-sectional study in Fengtai District in Beijing in June 2021, and children aged 3–9 years without symptoms of AGE within 4 weeks were recruited in kindergartens and primary schools. According to the economic development levels and geographical characteristics, three communities were selected, including developed FZ (Fangzhuang) community in the east, moderately developed FT (Fengtai) community in the middle, and less developed WZ (Wangzuo) community in the west. A total of 3 kindergartens and 2 primary schools were selected from each community; 10 children were selected from each of the senior, middle, and junior classes in each kindergarten; and 10 students were selected from each of the 1st, 2nd, and 3rd grades in each primary school. Noroviruses were detected using the real-time RT-PCR detection kit (XABT, Beijing, China). Following the kit instructions, if the Ct value ≤35, or the Ct value of two PCR tests is between 35–40, the result is judged positive. Semi-nested RT-PCR assays for partial VP1 gene of the norovirus genome were performed, using COG1F/G1SKR and G1SKF/G1SKR for norovirus GI, COG2F/G2SKR and G2SKF/G2SKR for norovirus GII, yielding 330 bp and 344 bp PCR products, respectively (*2*,*4*–*5*). The PCR products were sequenced directly or by cloning sequencing, and the sequences were genotyped using Norovirus Typing Tool Version 2.0 (https://www.rivm.nl/mpf/typingtool/norovirus). The phylogenetic trees were constructed using the maximum likelihood method through MEGA software (version 6.0, Mega Limited, Auckland, New Zealand). The initial data was collated and imported into WPS Spreadsheets 2016 (Kingsoft Inc., Beijing, CHN), and statistical analyses were done using SPSS 19.0 software (SPSS, Chicago, IL, USA). Chi-square test was used to compare the positive rates,

and $P<0.05$ was considered statistically significant.

In this study, a total of 460 stool specimens were collected, and the positive rate of norovirus was 3.48% (16/460). There was no significant difference in the positive rates among children of different genders, institutions, and communities (Table 1).

In this study, the norovirus positive rate was 8.33% (6/72) in children aged 6 to 7 years, followed by 6.25% (4/64) aged 7 to 8 years, 3.33% (4/120) aged 3 to 4 years, and 2.41% (2/83) aged 4 to 5 years. No norovirus was detected in children aged 5 to 6 years (0/82) and aged 8 to 9 years (0/39).

Of 16 positive stool specimens, 5 were positive for GI, with a median Ct value of 32.6 (range 26.32–37.05); 10 were positive for GII, with a median Ct value of 35.12 (range 24.01–38.23); and 1 was mixed infection of GI (Ct value 33.9) and GII (Ct value 36.5). Of the GI positive stool specimens, 4 GI strains were sequenced successfully, 3 strains were identified as GI.3d and 1 strain was GI.5a (GenBank accession numbers: ON197358–ON197361). GI.3d strains had the highest identities (99.3%–99.6%) with reference strains MW255382/Hu/2020/Chengdu/CHN, MN922742/Hu/2019/Taiwan/CHN and MZ022026/Hu/2020/KRChengdu/CHN/2020, MN922742/Taiwan/CHN/. GI.5a strains had the same identities as reference strains MK121731/Hu/2018/Sichuan/CHN,OK562729/Hu/2021/Guangzhou/CHN,LC544080/Hu/2018/MY (Figure 1). Of 11 GII positive stool specimens, 9 were sequenced successfully, 4 were infected with single genotypes (1 GII.2, 1 GII.6a and 2 GII.4 Sydney), 5 were infected with mixed genotypes (2 GII.2 and GII.4 Sydney, 1 GII.2 and GII.17, 2 GII.6a and GII.4 Sydney). The GenBank accession numbers of 14 GII strains were ON197537-ON197550. GII.4 Sydney were most common (6/14), which had the highest identities (99.2%–100%) with reference strainsOL336382/Hu/2019/Beijing/CHN, OL336366/Hu/2021/Beijing/CHN,MW205658/Hu/2019/Beijing/CHN, OM368736/Hu/2019/Beijing/CHN, MW205667/Hu/2020/Beijing/CHN, MW205571/Hu/2019/Beijing/CHN (Figure 2).

This study found 4 cluster asymptomatic infections in the 4 classes in primary schools, of which 3 were caused by GII noroviruses and 1 was caused by GI noroviruses, and 2 or 3 children were involved in each incident. No norovirus related outbreaks were reported in the asymptomatic infection children's classes 4 weeks after sampling.

DISCUSSION

In this study, the prevalence of asymptomatic norovirus infection in summer was 3.48% in Beijing Municipality, and reports of norovirus outbreaks in Beijing were fewer during the summer (*2*). The positive rate of norovirus among outpatient children with diarrhea in summer was far lower than that in the whole year (9.5% *vs.* 16.5%) in Beijing (*4*). Cheon et al. also found that the prevalence of norovirus in asymptomatic children aged 4 to 6 in summer was lower than that in winter (2.9% *vs.* 5.5%) in the Republic of Korea (*6*). Asymptomatic norovirus infections were observed in 11.7% (19/163) and 13.1% (12/90) in Nicaragua and Brazil (*7*–*8*), significantly higher than that in this study. The reason may be that their enrolled children were under 5 years old, and most asymptomatic children were under 2 years old (*7*–*8*), the age group with a higher incidence

TABLE 1. Epidemiological characteristics of asymptomatic norovirus infection in children.

Group	Total number	Number of positives	Positive rates (%)	χ^2	*P* value
Gender					
Male	219	7	3.20	0.099	0.753
Femal	241	9	3.73		
Institution					
Primary schools	190	10	5.26	3.072	0.08
Kindergartens	270	6	2.22		
Community					
FZ	160	8	5.00		
FT	150	4	2.67	1.692	0.429
WZ	150	4	2.67		

Abbreviation: FZ=Fangzhuang, FT=Fengtai, WZ=Wangzuo.

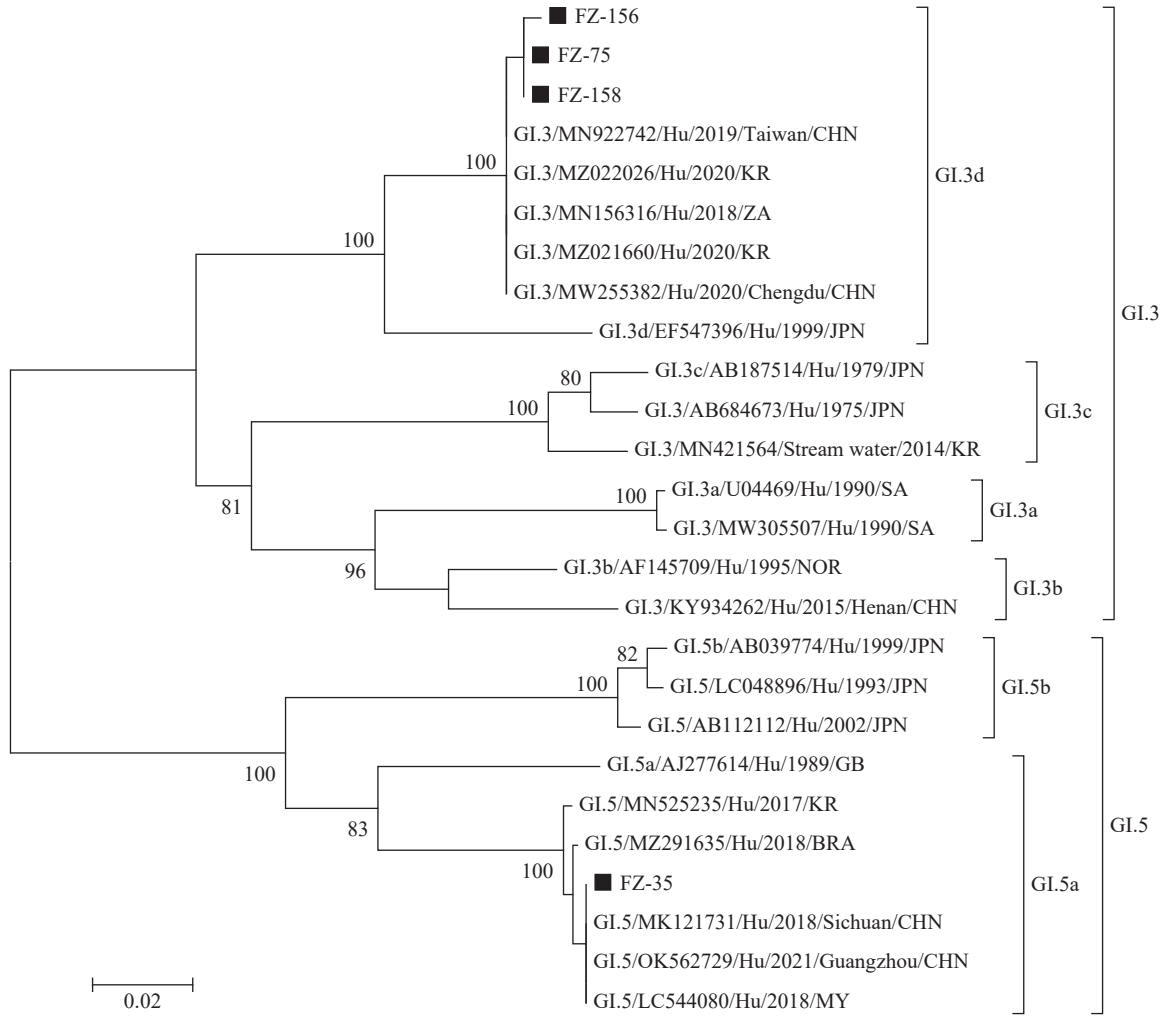

FIGURE 1. Phylogenetic analysis of GI noroviruses based on partial VP1 gene (291 bp).
Note: Norovirus strains detected in this study were marked with black squares. The reference sequences were retrieved from GenBank. The trees were generated using the maximum likelihood method with the nucleotide substitution model Kimura 2-parameter + Gamma + Invariant sites. Bootstrap values, estimated from 1,000 replicates, are indicated at each node. The scale bar indicates the number of nucleotide substitutions.

of norovirus infection (*4*,*9*).

A higher positive rate of norovirus cases was found in the developed FZ community in this study, and norovirus outbreaks also occurred mainly in economically developed areas in China (*1*–*2*). This trend may be caused by the high population density and rapid population mobility in economically developed regions, which facilitate the spread of infectious diseases. The positive rate in primary school was higher than that in kindergarten (5.26% *vs.* 2.22%), similar to those in Changzhou City, Jiangsu Province (4.70% *vs.* 2.68%) (*10*). It could be because the children in primary school have more social activities than those in kindergarten, and more children, both in class and school, have a higher chance of contracting an infection.

This study's reported genotypes were consistent with those in symptomatic children in Beijing, and GII.4 Sydney was the most common genotype (*4*). This result suggests that asymptomatic and symptomatic infections have a common source.

We found that the Ct values of norovirus in children with asymptomatic infection were higher, and the optimal Ct value cutoff for attributing infectious intestinal disease to norovirus was reported as 31 (*11*). A recent study also showed that the Ct values of GII norovirus in children with diarrhea were significantly lower than those without diarrhea. GII norovirus was associated with diarrhea when the Ct value was ≤25 (*11*). Shioda et al. found that the Ct value of norovirus infection in symptomatic cases (25.3±1.2) was lower than in asymptomatic persons (28.5±1.4) (*12*). In this

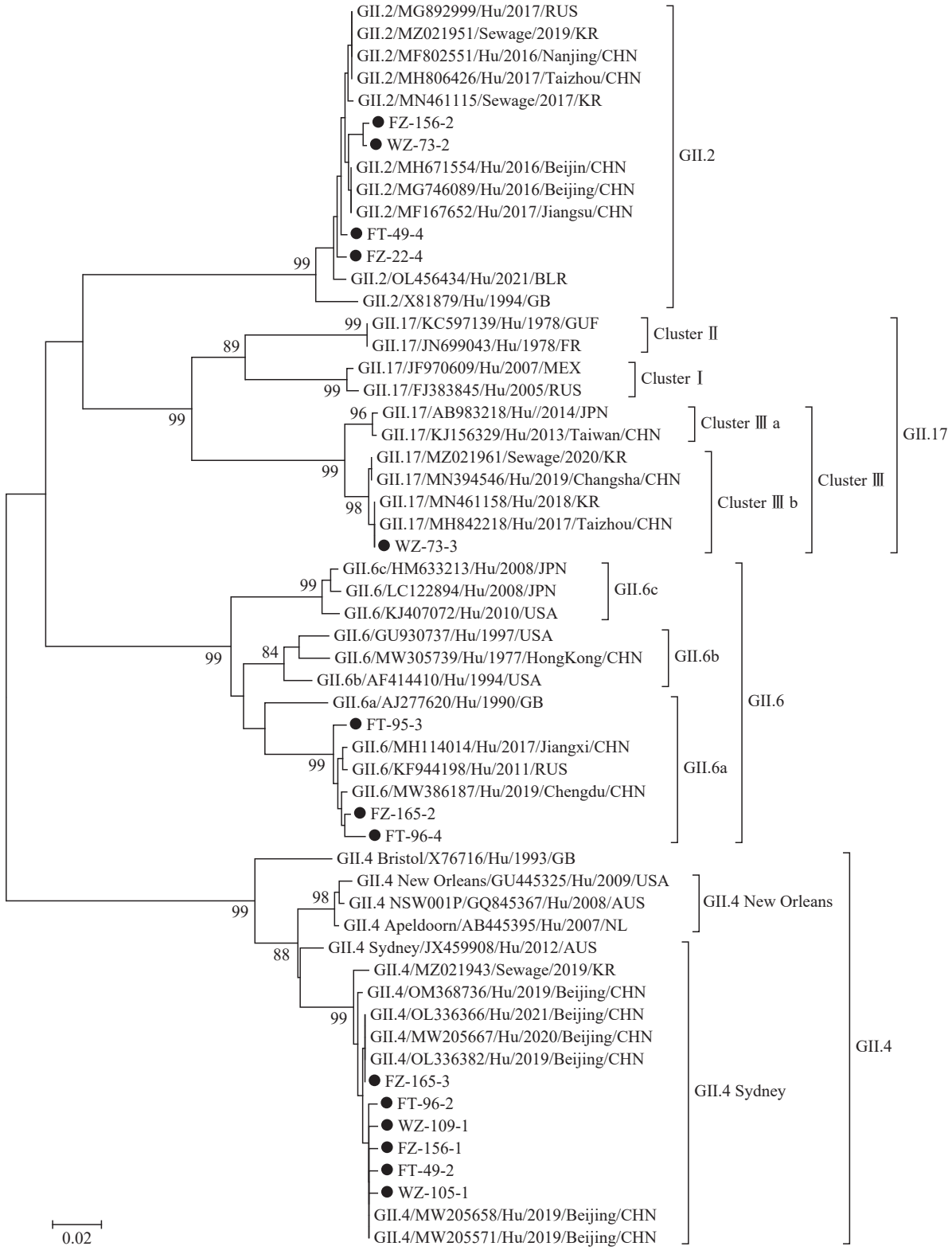

FIGURE 2. Phylogenetic analysis of GII noroviruses based on partial VP1 gene (283 bp).
Note: Norovirus strains detected in this research were marked with black dots. The reference sequences were retrieved from GenBank. The trees were generated using the maximum likelihood method with the nucleotide substitution model Kimura 2-parameter + Gamma. Bootstrap values, estimated from 1,000 replicates, are indicated at each node. The scale bar indicates the number of nucleotide substitutions.

study, the median Ct value of GI was 32.6, and GII was 35.1. This is consistent with the results of Kobayashi et al. for Ct values in asymptomatic adults, GI (34.4) and GII (35.4) (*13*). These results prove that asymptomatic norovirus infections have higher Ct values.

In this study, 4 clustered asymptomatic infections were found, but no norovirus outbreak was reported 4 weeks before and after sampling. This finding suggested that asymptomatic infection was not easy to cause the outbreak. The possible reasons are the low viral load and the high temperature in summer, which lead to the decline in virus survival and transmission. Benjarat et al. also found that asymptomatic people were more likely to cause family clustered infections in winter than in summer and that most were asymptomatic clustered infections (*3*).

This study was subject to some limitations. First, this is a cross-sectional study in one month, not throughout the year. Second, the source of asymptomatic infections was not investigated, for example, whether it came from infected family members.

The norovirus-positive rate was 3.48% among asymptomatic children in kindergartens and primary schools in summer, and norovirus genotypes in asymptomatic children were similar to those circulating in the symptomatic cases. Asymptomatic infected children present a lower viral load and may have a limited role in causing AGE outbreaks.

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Preplanned Studies

A Questionnaire Survey on Extrapulmonary Tuberculosis Control and Prevention — China, 2021

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Summary

What is already known about this topic?

Tuberculosis (TB) is a multisystem disease that might affect any organ. Currently, the National TB Program (NTP) issued by the State Council of China, only covers pulmonary tuberculosis (PTB), and the status of extrapulmonary tuberculosis (EPTB) remains unclear nationwide.

What is added by this report?

The survey conducted by China CDC reported that there were no specific health facilities responsible for diagnosis, treatment and management of EPTB in China, while more than half of counties thought it should be included into NTP.

What are the implications for public health practice?

China should include EPTB into NTP to achieve the target of End-TB strategy, a world free of TB. Zero deaths, disease and suffering due to TB.

Tuberculosis (TB) is a multisystem disease that could affect any organ (*1–2*). Extrapulmonary tuberculosis (EPTB) cases account for 13.37% to 53.00% of TB cases globally, which were 11.93% to 33.40% of cases found in China (*3*). The National TB Program (NTP) sponsored by the State Council of China only covers control and prevention of pulmonary tuberculosis (PTB). The control and prevention status of EPTB remains unclear. It has been found that EPTB has played an important role in achieving the promoted target of End-TB strategy (*4*). Therefore, it is essential to understand the status of EPTB in China to develop an action plan to address this important issue. A nationwide questionnaire survey to investigate current diagnosis, treatment, and management of EPTB at county level was conducted by China CDC in 2021. It was found that at county level in China, there were no unified diagnostic criteria and methods for EPTB, and patient management was also disparate. Currently, not enough attention has been paid to the control and prevention of EPTB. It is suggested that EPTB be included in NTP.

This study was conducted through questionnaire to investigate the current diagnosis, treatment and management of EPTB nationally in China by China CDC in the first half year of 2021. All Center for Disease Control and Prevention or TB dispensaries at county level were investigated. The professionals responsible for tuberculosis prevention and control work were designated to fill in the questionnaire. Upon completion, the questionnaires were collected and checked by responsible staff of CDCs or TB dispensaries at provincial level. A total of 2,825 questionnaires were distributed with a response rate of 100%. The questionnaire consisted of three parts: basic information of EPTB status, diagnostic capacity for EPTB of the local medical institutions, and opinion on incorporating EPTB into NTP. Data were cleaned in Microsoft Office Excel (version 2019, Microsoft Corp, Washington, USA). The results were summarized with descriptive analysis methods.

As of July 2021, counties in which EPTB was mainly diagnosed by TB designated hospitals accounted for 58.09%, whereas counties in which EPTB was mainly diagnosed by both TB designated hospitals and non-TB designated hospitals accounted for 35.08%; 50.30% of counties adopted individualized treatment regimen for EPTB; 61.77% of counties didn't enter EPTB's information in the routine surveillance system at all; the percentage of counties registered all EPTB cases was just 23.36%; 55.54% counties had the same medical insurance policy for EPTB as for other diseases, while 11.58% counties did not include EPTB in basic medical insurance program; 69.95% of counties did not manage EPTB in the same way as they managed PTB, which has been defined by NTP (Table 1).

Approximately 43.68% TB designated hospitals made EPTB diagnosis based on both pathogenesis and histopathology, while 27.86% TB designated hospitals based on pathogenesis or histopathology, and 26.30%

TABLE 1. Basic information of EPTB in China, 2021.

	Question	Eastern area (*n*, %)	Middle area (*n*, %)	Western area (*n*, %)	Total (*n*, %)
Diagnosis	Q1: Which is the main hospital for EPTB in your district?				
	TB designated hospital	457 (49.51)	510 (61.67)	674 (62.70)	1,641 (58.09)
	Non-TB designated hospital	86 (9.32)	44 (5.32)	43 (4.00)	173 (6.12)
	TB and Non-TB designated hospital	371 (40.20)	271 (32.77)	349 (32.47)	991 (35.08)
	No response	9 (0.98)	2 (0.24)	9 (0.84)	20 (0.71)
Treatment	Q2: Which is the main treatment regimen for EPTB in your district?				
	2HRZE/4HR	72 (7.80)	82 (9.92)	109 (10.14)	263 (9.31)
	2HRZE/7-10HRE	337 (36.51)	343 (41.48)	379 (35.26)	1,059 (37.49)
	Individualized regimen	487 (52.76)	381 (46.07)	553 (51.44)	1,421 (50.30)
	No response	27 (2.93)	21 (2.54)	34 (3.16)	82 (2.90)
Management	Q3: Are EPTB cases registered in routine surveillance system in your district?				
	Yes, they are all registered	158 (17.12)	239 (28.90)	263 (24.47)	660 (23.36)
	Yes, just a part is registered	139 (15.06)	139 (16.81)	121 (11.26)	399 (14.12)
	No, they aren't	617 (66.85)	444 (53.69)	684 (63.63)	1,745 (61.77)
	No response	9 (0.98)	5 (0.60)	7 (0.65)	21 (0.74)
	Q4: What is the medical insurance policy for EPTB in your district?				
	The same as PTB	280 (30.34)	297 (35.91)	307 (28.56)	884 (31.29)
	The same as other diseases	517 (56.01)	423 (51.15)	629 (58.51)	1,569 (55.54)
	Wasn't include in basic medical insurance program	109 (11.81)	99 (11.97)	119 (11.07)	327 (11.58)
	No response	17 (1.84)	8 (0.97)	20 (1.86)	45 (1.59)
	Q5: Are EPTB cases managed in local TB control program?				
	Yes, the same as PTB	86 (9.32)	136 (16.44)	241 (22.42)	463 (16.39)
	Yes, but not as strict as PTB	86 (9.32)	149 (18.02)	126 (11.72)	361 (12.78)
	No, they aren't	738 (79.96)	538 (65.05)	700 (65.12)	1,976 (69.95)
	No response	13 (1.41)	4 (0.48)	8 (0.74)	25 (0.88)
Total		923 (100.00)	827 (100.00)	1,075 (100.00)	2,825 (100.00)

Note: The eastern area included the following provincial-level administrative divisions: Beijing, Tianjin, Hebei, Liaoning, Shanghai, Jiangsu, Zhejiang, Fujian, Shandong, Guangdong, and Hainan; the middle area: Shanxi, Jilin, Heilongjiang, Anhui, Jiangxi, Henan, Hubei, and Hunan; and the western area: Inner Mongolia, Guangxi, Chongqing, Sichuan, Guizhou, Yunnan, Xizang (Tibet), Shaanxi, Gansu, Qinghai, Ningxia, and Xinjiang.
Abbreviation: TB=tuberculosis; PTB=pulmonary tuberculosis; EPTB=extrapulmonary tuberculosis.

based on clinical examination only. As for non-TB designated hospitals, 53.52% of them made EPTB based on clinical examination only, and the percentage of them made EPTB diagnosis based on both pathogenesis and histopathology was 24.25% (Table 2).

The results of the survey on whether EPTB should be incorporated in NTP management showed that 56.32% of the respondents thought that EPTB should be part of NTP, and only 13.13% of the respondents thought that no attention should be paid to EPTB (Figure 1).

DISCUSSION

To our best knowledge, this is the first national study to address the status of EPTB diagnosis, treatment and management in China, which offers light for policymakers to develop related strategies for EPTB. The study indicated that there were no specific health facilities responsible for diagnosis, treatment and management of ETPB in China, while more than half of counties thought EPTB should be included into NTP.

There is a lack of standardized diagnosis and

TABLE 2. Capability of diagnosis on EPTB in different hospitals in China, 2021.

Region	Only clinical diagnosis		Pathogenesis or Histopathology diagnosis		Pathogenesis and histopathology diagnosis		No response		Total	
	Designated hospital (*n*, %)	Non-designated hospital (*n*, %)	Designated hospital (*n*, %)	Non-designated hospital (*n*, %)	Designated hospital (*n*, %)	Non-designated hospital (*n*, %)	Designated hospital (*n*, %)	Non-designated hospital (*n*, %)	Designated hospital (*n*, %)	Non-designated hospital (*n*, %)
Eastern area	221 (23.94)	407 (44.10)	218 (23.62)	189 (20.48)	458 (49.62)	294 (31.85)	26 (2.82)	33 (3.58)	923 (100.00)	923 (100.00)
Middle area	250 (30.23)	455 (55.02)	223 (26.96)	160 (19.35)	337 (40.75)	183 (22.13)	17 (2.06)	29 (3.51)	827 (100.00)	827 (100.00)
Western area	272 (25.30)	650 (60.46)	346 (32.19)	165 (15.35)	439 (40.84)	208 (19.35)	18 (1.67)	52 (4.84)	1,075 (100.00)	1,075 (100.00)
Total	743 (26.30)	1,512 (53.52)	787 (27.86)	514 (18.19)	1,234 (43.68)	685 (24.25)	61 (2.16)	114 (4.04)	2,825 (100.00)	2,825 (100.00)

Note: The eastern area included the following provincial-level administrative divisions: Beijing, Tianjin, Hebei, Liaoning, Shanghai, Jiangsu, Zhejiang, Fujian, Shandong, Guangdong, and Hainan; the middle area: Shanxi, Jilin, Heilongjiang, Anhui, Jiangxi, Henan, Hubei, and Hunan; and the western area: Inner Mongolia, Guangxi, Chongqing, Sichuan, Guizhou, Yunnan, Xizang (Tibet), Shaanxi, Gansu, Qinghai, Ningxia, and Xinjiang.

Abbreviation: EPTB=extrapulmonary tuberculosis.

management of EPTB throughout the country. Some counties made diagnosis in TB designated hospitals, some in non-TB designated hospitals or TB and non-TB designated hospitals both. The majority of non-TB designated hospitals diagnosed EPTB by only clinical examination, while TB designated hospitals diagnosed EPTB by pathogenesis or histopathology and clinical examination. TB designated hospitals were better than non-TB designated hospitals in diagnostic ability, which was related to the long-term planning of NTP. The NTP required TB designated hospitals to carry out sputum smears, culture and molecular biology examinations for patients, key indicators such as bacteriologically positive rate and treatment success rate had to be a specific level (*5*–*6*). On the contrary, non-TB designated hospitals didn't have the laboratory testing equipment for TB or need to complete the indicators, their diagnostic ability was lower. As a result, EPTB patients cannot be diagnosed accurately, misdiagnoses and missed diagnoses were very likely to occur in non-TB designated hospitals. In addition, not all counties entered EPTB's information in the routine system and the treatment regimens were different across China, which lead to difficulty to accurately determine the epidemic status of EPTB and evaluate the final outcomes of EPTB patients.

Our study also showed that half of the counties had different medical insurance policy for EPTB, the patients had great economic pressure during the process of seeing a doctor. A cross-sectional study calculated the average total medical expenditure for TB treatment was 12,635.5 CNY (*7*). EPTB needs longer hospital stays and higher costs than PTB (*8*), it can be a catastrophic expenditure easily for patients without medical insurance policy.

This study was subjected to some limitations. First, we didn't survey the epidemic situation of EPTB in China, for example the incidence and mortality of different EPTB, and the policy-makers may not fully understand the importance of EPTB control and prevention. Secondly, our study did not investigate the hospitals and patients linked to EPTB, more targeted policies and practices need to be based on epidemiological and clinical characteristics of patients, costs of medical care, difficulties in seeking medical treatment etc. Therefore, studies based on hospitals and patients should be carried out in the future.

Achieving a TB-free world is a desirable goal with respect to human, animal, and environmental health — according to the tenets of One Health (*9*). Both PTB or EPTB belong to tuberculosis, ending

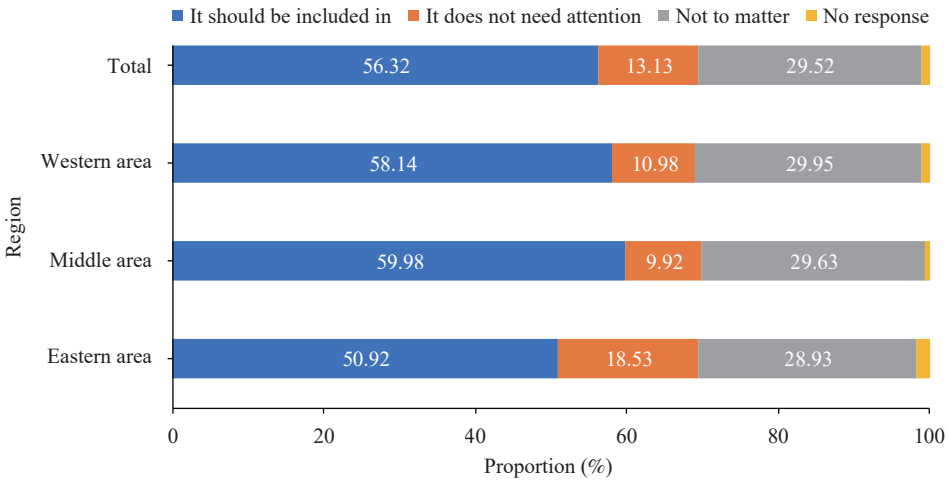

FIGURE 1. Results of the survey on whether EPTB should be incorporated in NTP management in China, 2021.
Note: The eastern area included the following provincial-level administrative divisions: Beijing, Tianjin, Hebei, Liaoning, Shanghai, Jiangsu, Zhejiang, Fujian, Shandong, Guangdong, and Hainan; the middle area: Shanxi, Jilin, Heilongjiang, Anhui, Jiangxi, Henan, Hubei, and Hunan; and the western area: Inner Mongolia, Guangxi, Chongqing, Sichuan, Guizhou, Yunnan, Xizang (Tibet), Shaanxi, Gansu, Qinghai, Ningxia, and Xinjiang.
Abbreviation: EPTB=extrapulmonary tuberculosis; NTP=National TB Program.

tuberculosis epidemic needs paying attention to control and prevention of EPTB, this study implied that EPTB should be included in NTP. The governments at all levels need to provide adequate personnel, funding, and policy support for EPTB. TB prevention and treatment organization should establish standards of the diagnosis, treatment and management to EPTB. Whether TB designated hospitals or non-TB designated hospitals need to improve their capacity of recognition and diagnosis to EPTB and enter EPTB information in the routine surveillance system. CDCs and TB dispensaries should actively carry out EPTB screening and strengthen monitoring EPTB in order to grasp the epidemiological trends. Further studies about drugs and treatment regimens for TB are also necessary to do, which will give the patients more effective treatment and reduce their medical burden.

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Vital Surveillances

Dynamic Changes of ORF1ab and N Gene Ct Values in COVID-19 Omicron Inpatients of Different Age Groups — Beijing Municipality, China, November–December 2022

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ABSTRACT

Introduction: In November 2021, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Omicron variant was identified as the variant of concern and has since spread globally, replacing other cocirculating variants. To better understand the dynamic changes in viral load over time and the natural history of the virus infection, we analyzed the expression of the open reading frames 1ab (ORF1ab) and nucleocapsid (N) genes in patients infected with Omicron.

Methods: We included patients initially admitted to the hospital for SARS-CoV-2 infection between November 5 and December 25, 2022. We collected daily oropharyngeal swabs for quantitative reverse transcriptase-polymerase chain reaction tests using commercial kits. We depicted the cycle threshold (Ct) values for amplification of ORF1ab and N genes from individual patients in age-specific groups in a time series.

Results: A total of 480 inpatients were included in the study, with a median age of 59 years (interquartile range, 42 to 78; range, 16 to 106). In the <45-year-old age group, the Ct values for ORF1ab and N gene amplification remained below 35 for 9.0 and 11.5 days, respectively. In the ≥80-year-old age group, the Ct values for ORF1ab and N genes stayed below 35 for 11.5 and 15.0 days, respectively, which was the longest among all age groups. The Ct values for N gene amplification took longer to rise above 35 than those for ORF1ab gene amplification.

Conclusion: The time to test negative varied among different age groups, with viral nucleic acid shedding taking longer in older age groups compared to younger age groups. As a result, the time to resolution of Omicron infection increased with increasing age.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in late 2019 and has been prevalent for over three years (*1*–*3*). As of January 8, 2023, more than 659 million confirmed cases and over 6.6 million deaths have been reported globally (*4*). The continuous evolution of SARS-CoV-2 has produced multiple variants of concern, including Alpha, Beta, Gamma, Delta, and Omicron, which have caused several waves of coronavirus disease 2019 (COVID-19) during the pandemic (*5*).

The Omicron variant was first detected in November 2021 in South Africa and contained extensive mutations that enhanced its transmissibility, allowing it to spread globally within a month (*6*). As a result, Omicron quickly replaced the other cocirculating variants worldwide.

As indicated in the Diagnosis and Treatment Protocol for Novel Coronavirus Pneumonia (Trial Version 9), a sample with cycle threshold (Ct) values greater than 35 for both open reading frames 1ab (ORF1ab) and nucleocapsid (N) genes by two consecutive tests (with at least 24 hours in between) is the laboratory criterion for hospital discharge of the patient. Quantitative reverse transcriptase-polymerase chain reaction (qRT-PCR) of nasopharyngeal swabs or oropharyngeal swabs is recommended for clinical diagnosis of SARS-CoV-2 infection (*7*). The Omicron variant has a shorter incubation period compared to that of previous variants. Currently, patients infected with the Omicron variant generally recover within 7 days. However, the dynamic changes of SARS-CoV-2 infection have not been systematically analyzed. In this study, we collected samples from 480 patients with SARS-CoV-2 and assessed the amplification of target SARS-CoV-2 genes to describe the natural history of SARS-CoV-2 Omicron variant infection through the

viral load over time in infected patients.

METHODS

Between November 5 and December 25, 2022, patients hospitalized in Beijing Ditan Hospital, the designated hospital for clinical treatment of COVID19 in Beijing,with confirmed COVID-19 in the early stages of acute infection, whose Ct values of SARS-CoV-2 gradually decreased after admission, were enrolled in this study. All infections belonged to the Omicron BF.7 sub-variant, as established via next-generation sequencing. Oropharyngeal swabs were collected daily from the enrolled cases during hospitalization, and viral RNA was extracted from the swabs using a Nucleic Acid Extraction System (Xi'an Tianlong Science and Technology CO., Ltd., Xi'an, China). qRT-PCR was used to detect SARS-CoV-2 RNA from patient samples, with RNA expressed from the N and ORF1ab genes of SARS-CoV-2 being detected. Ct values based on amplification from detected RNA were used as indicators of the copy number of SARS-CoV-2 RNA in specimens; lower Ct values represented a higher viral load in the specimens. Additionally, general and clinical information of the patients was collected, including sex, age, and underlying medical comorbidities. Patients were divided into four groups according to their age, and a boxplot of Ct values over time was plotted.

RESULTS

A total of 480 cases were enrolled from November 5 to December 25, 2022, with a median age of 59 years (interquartile range, 42 to 78; range, 16 to 106). The male-to-female sex ratio of all cases was 0.81. Patients were divided into four age groups: <45, 45–59, 60–79, and ≥80 years old (Table 1), containing 130, 112, 128, and 110 patients, respectively. The proportion of male and female patients in each age group was similar. In the <45-year-old age group, 93.8% of patients had no underlying medical comorbidities, whereas 88.2% of patients in the ≥80-year-old age group had one or more underlying medical comorbidities (Table 1). The risk of developing underlying medical comorbidities increased with increasing age.

The Ct values for amplification of ORF1ab and N RNA changed over time during hospitalization, initially decreasing and then increasing (Figure 1 and Supplementary Table S1, available in https://weekly.chinacdc.cn/). This indicated that all cases were in the early stages of infection. Except for those in the <80-year-old age group, the Ct values for the ORF1ab and N genes were lowest at day 3, indicating the highest viral load at the inflection point. However, in the ≥80-year-old age group, the Ct values were lowest at day 2 (Figure 1 and Supplementary Table S1), which differed from the other age groups. As the viral load peak was reached, the Ct values gradually increased, indicating a gradual decrease in viral load.

The median time for the Ct value for ORF1ab RNA amplification to reach >35 in the <45-year-old group was 9 days (range: 4 to 26) (Figure 1), whereas this was 11.5 days for the Ct value for N RNA to reach >35 (range: 7 to 26). In the 45–59-year-old group, the Ct values for ORF1ab and N genes reached >35 after a median of 9 (range: 7 to 23) and 11 days (range: 8 to 23), respectively (Figure 1). In the 60–80-year-old group, these medians were 11 (range: 6 to 24) and 14 days (range: 7 to 28), respectively. In the ≥80-year-old group, the times for the Ct values for ORF1ab and N

TABLE 1. Baseline characteristics of the enrolled coronavirus disease 2019 patients by age group in Beijing (*n*=480).

Variable	Age group			
	<45 years (*n*=130)	45–59 years (*n*=112)	60–79 years (*n*=128)	≥80 years (*n*=110)
Sex, *n* (%)				
Male	53 (40.8)	52 (46.4)	59 (46.1)	51 (46.4)
Female	77 (59.2)	60 (53.6)	69 (53.9)	59 (53.6)
Underlying medical comorbidities*, *n* (%)				
No underlying disease	122 (93.8)	73 (65.2)	27 (21.1)	13 (11.8)
One condition	3 (2.3)	16 (14.3)	43 (33.6)	34 (30.9)
Two conditions	4 (3.1)	15 (13.4)	32 (25.0)	29 (26.4)
Three and more conditions	1 (0.8)	8 (7.1)	26 (20.3)	34 (30.9)

* The underlying medical comorbidities included coronary heart disease, high blood pressure, diabetes, thyroid disease, and so on.

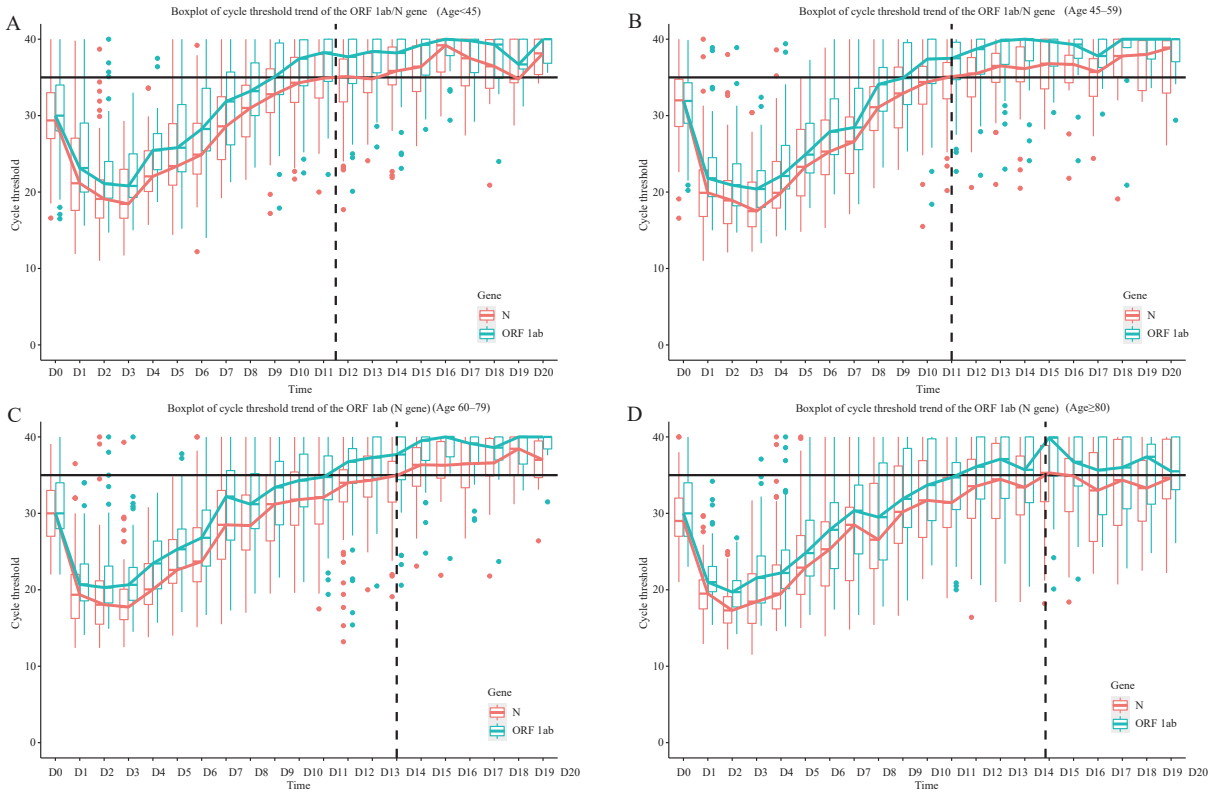

FIGURE 1. Dynamic trends in cycle threshold (Ct) for ORF1ab and N RNA amplification in patients with COVID-19 in different age groups. (A) <45-year-old group, (B) 45–59-year-old group, (C) 60–79-year-old group, and (D) ≥80-year-old group.
Note: Blue boxes and lines represent the ORF1ab gene. The red boxes and lines represent the N gene. Day 0 represents the first positive test for nucleic acid, based on onset date of the disease.
Abbreviation: COVID-19=coronavirus disease 2019; ORF1ab=open reading frames 1ab; N=nucleocapsid.

amplification to reach >35 were 11.5 (range: 6 to 39) and 15 days (range: 6 to 39), respectively, which were the longest times in the study (Figure 1). These results indicated that the time required for a negative result (Ct>35) based on the presence of N RNA in COVID-19 infections was longer than that for ORF1ab RNA. Furthermore, the time required for detection of the N and ORF1ab Ct values to reach >35 in people ≥60 years old was longer than that in people <60 years old.

CONCLUSIONS

In this study, we analyzed the dynamic change of ORF1ab and N RNA in patients with COVID-19 over time. We found that the time to a negative result varied among different age groups, with viral nucleic acid shedding persisting for longer in the older age groups than in the younger groups. This may be due to underlying medical comorbidities in the older age groups. We also observed that it took longer for the N gene Ct value to rise to 35 than for the ORF 1ab gene, indicating that the N gene is more sensitive than the ORF 1ab gene in diagnosis.

Early studies of the COVID-19 outbreak reported the viral load of SARS-CoV-2 in different types of clinical specimens from infected patients (*8*–*10*). These studies suggested that the infectious period of Omicron was shorter than the previous strain (*8*). However, the sample size was small and patients were not always continuously sampled for testing. In our study, we collected samples from hospitalized patients on a daily basis and graphically depicted the changing trend of ORF1ab and N RNA detection via their Ct values.

Our study has several limitations. We only collected oropharyngeal swab samples from patients, so we were unable to assess the trend of viral load in other sample types. Additionally, the assignment of people with very mild symptoms to makeshift hospitals instead of designated hospitals for treatment may have introduced selection bias. Furthermore, some patients did not have detailed clinical information, so we were unable to determine whether Ct values changed with

different severity of disease in these patients. Treatment of different cases may have impacted on the change of Ct values.

In conclusion, we examined the natural history and dynamic changes of ORF1ab and N RNA in patients with COVID-19 across different age groups. Patients in the older age group took longer to test negative compared to those in the younger age group, indicating that the time to resolution of Omicron infection increased with age.

Conflicts of interest: No conflicts of interest.

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SUPPLEMENTARY TABLE S1. Changes of Ct values for N and ORF1ab genes from Day 0 to 20 in each age group of COVID-19 patients in Beijing.

Time	Age group, <45 years		Age group, 45–59 years		Age group, 60–79 years		Age group, ≥80 years	
	N, Ct, M* (Q_1, Q_3)	ORF1ab, Ct, M (Q_1, Q_3)	N, Ct, M (Q_1, Q_3)	ORF1ab, Ct, M (Q_1, Q_3)	N, Ct, M (Q_1, Q_3)	ORF1ab, Ct, M (Q_1, Q_3)	N, Ct, M (Q_1, Q_3)	ORF1ab, Ct, M (Q_1, Q_3)
Day0	29.4 (27.0, 33.0)	30.0 (28.0, 34.0)	32.0 (28.6, 34.8)	31.9 (29.0, 34.3)	30.0 (27.0, 33.0)	30.0 (28.0, 34.0)	29.0 (27.0, 32.0)	30.0 (27.3, 34.0)
Day1	21.2 (17.6, 27.1)	23.1 (20.0, 29.2)	19.9 (16.8, 22.9)	21.8 (19.4, 24.5)	19.4 (16.3, 22.0)	20.5 (18.5, 23.5)	19.5 (17.5, 21.3)	21.0 (19.7, 22.6)
Day2	19.1 (16.6, 21.6)	21.1 (19.2, 24.1)	18.9 (15.9, 21.5)	20.9 (18.2, 23.7)	18.3 (15.5, 21.4)	20.3 (18.3, 23.1)	17.3 (15.7, 19.1)	19.7 (17.8, 21.2)
Day3	18.5 (16.6, 23.0)	20.8 (19.3, 25.0)	17.5 (15.5, 21.3)	20.4 (18.0, 22.8)	17.8 (16.1, 20.1)	20.7 (18.6, 23.0)	18.5 (15.6, 22.1)	21.6 (18.3, 24.4)
Day4	22.1 (20.1, 25.4)	25.5 (22.9, 27.7)	19.9 (17.9, 24.0)	22.1 (20.4, 26.1)	20.1 (18.1, 23.4)	23.5 (20.4, 26.5)	19.5 (17.5, 23.1)	22.2 (20.2, 25.2)
Day5	23.4 (20.9, 29.0)	25.8 (22.7, 31.5)	23.3 (19.5, 28.2)	24.9 (22.5, 29.0)	22.6 (20.9, 26.6)	25.3 (22.8, 27.8)	22.9 (19.4, 27.1)	24.8 (21.8, 29.1)
Day6	25.0 (22.5, 29.2)	28.3 (25.4, 33.6)	25.3 (22.3, 29.4)	28.0 (25.0, 32.4)	23.7 (21.1, 28.1)	27.0 (23.3, 30.6)	25.3 (20.5, 28.9)	27.9 (22.8, 32.3)
Day7	28.6 (24.3, 32.5)	31.9 (26.4, 35.8)	26.6 (22.4, 29.8)	28.6 (25.3, 33.7)	28.5 (24.0, 33.0)	32.1 (26.5, 35.5)	28.5 (21.2, 30.8)	30.4 (24.8, 33.7)
Day8	31.0 (27.2, 34.0)	33.3 (30.0, 37.0)	31.1 (28.1, 33.8)	34.4 (30.7, 37.1)	28.4 (25.2, 32.4)	31.2 (28.0, 35.2)	26.6 (22.8, 33.9)	29.5 (23.9, 36.6)
Day9	32.9 (30.4, 36.3)	35.7 (32.8, 40.0)	32.9 (28.4, 36.4)	34.9 (31.5, 39.6)	31.2 (26.4, 35.0)	33.7 (29.1, 38.1)	30.5 (26.3, 36.9)	33.0 (28.6, 39.6)
Day10	34.3 (31.7, 37.6)	37.5 (34.2, 40.0)	34.4 (31.5, 36.5)	37.5 (34.3, 40.0)	31.8 (28.5, 35.4)	34.3 (30.9, 37.8)	31.7 (26.9, 36.9)	33.7 (29.1, 39.8)
Day11	35.0 (32.4, 38.1)	38.6 (34.8, 40.0)	35.1 (32.2, 37.0)	37.5 (34.7, 40.0)	32.1 (28.5, 34.8)	35.0 (32.2, 37.6)	31.4 (28.2, 34.7)	34.7 (30.5, 36.7)
Day12	35.1 (31.8, 37.5)	38.3 (35.0, 40.0)	35.4 (32.4, 37.5)	39.0 (35.5, 40.0)	34.0 (31.5, 35.7)	36.8 (34.0, 38.7)	33.6 (29.4, 37.1)	36.7 (32.0, 40.0)
Day13	35.0 (33.1, 38.6)	38.5 (36.0, 40.0)	36.5 (34.4, 38.2)	39.8 (37.1, 40.0)	34.4 (32.1, 37.5)	37.4 (35.1, 40.0)	34.5 (29.3, 39.2)	37.4 (32.0, 40.0)
Day14	35.9 (34.0, 39.0)	38.4 (35.9, 40.0)	36.2 (34.4, 39.0)	40.0 (37.6, 40.0)	35.1 (31.5, 37.1)	37.8 (34.4, 40.0)	33.4 (29.8, 37.5)	35.9 (31.6, 40.0)
Day15	36.3 (33.0, 39.1)	40.0 (36.0, 40.0)	37.0 (33.6, 40.0)	40.0 (36.3, 40.0)	36.5 (33.8, 38.6)	39.9 (37.0, 40.0)	35.3 (31.5, 38.9)	39.9 (34.9, 40.0)
Day16	39.2 (35.7, 40.0)	40.0 (38.0, 40.0)	36.7 (34.3, 37.9)	39.6 (37.7, 40.0)	36.3 (34.6, 39.4)	40.0 (37.6, 40.0)	34.9 (30.2, 37.2)	36.8 (33.6, 40.0)
Day17	37.5 (33.9, 40.0)	40.0 (36.2, 40.0)	35.7 (32.5, 37.5)	39.5 (36.7, 40.0)	36.5 (33.4, 39.3)	39.2 (36.4, 40.0)	33.0 (26.3, 38.0)	36.5 (29.8, 40.0)
Day18	36.5 (33.6, 40.0)	39.3 (34.9, 40.0)	38.5 (35.2, 40.0)	40.0 (38.9, 40.0)	36.6 (34.9, 39.8)	39.2 (37.6, 40.0)	34.4 (28.4, 39.7)	37.2 (30.8, 40.0)
Day19	34.8 (34.3, 40.0)	36.7 (36.1, 40.0)	38.0 (33.3, 39.8)	40.0 (37.4, 40.0)	38.5 (35.1, 40.0)	40.0 (36.5, 40.0)	33.3 (29.0, 36.9)	37.4 (29.8, 39.1)
Day20	38.2 (35.4, 40.0)	40.0 (37.4, 40.0)	39.3 (33.9, 40.0)	40.0 (38.5, 40.0)	37.0 (34.7, 39.5)	40.0 (38.4, 40.0)	34.7 (31.9, 39.7)	36.7 (33.8, 40.0)

* M indicates the median age in each age group. Q1 and Q3 represent the lower quartile and upper quartile, respectively.Abbreviation: Ct=cycle threshold; N=nucleocapsid; ORF1ab=open reading frames 1ab;COVID-19=coronavirus disease 2019.

Perspectives

Developmental Gerontology and Active Population Aging in China

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ABSTRACT

Population aging is an irreversible process in the development of modern society, which brings challenges to comprehensive modernized social governance. Population aging is a "dualistic" development issue that not only leads to aging of the labor force structure but also creates new demographic dividends. This study describes the core thoughts of developmental gerontology (DG), which provides new insight into the relationship between active aging and comprehensive governance for modernized society. The development of DG will provide a feasible and sustainable path to integrate and coordinate the relationship between population aging, society, and economy.

Population aging is an irreversible trend in demographic transition and the development process of the global population and modern society. According to World Population Prospects 2022, the proportion of the population aged 60 years and older has exceeded 10% in the 21st century and will increase rapidly in the future. By the middle of this century, 70% of older adults will be concentrated in developing areas (*1*). China has the largest population of older adults in the world, and the proportion of older adults aged above 60 years old increased from 13.32% in 2010 to 18.73% in 2020 (*2*). The rapid speed and large scale of aging population pose severe challenges to social development. Thus, the task of renewing the relationship between population aging and modernized social governance is urgent and challenging.

THE DUALITY OF POPULATION AGING

Human Aging Omics (HAO), a theory of aging, argues that the aging process in lifecourse is highly related to the systematic identification, manifestation, and quantification of all sets of health conditions as well as the complex relationships with internal biomolecules and the external environment throughout the life course (*3*). Although internal biomolecules interact with the external environment over the life course, unhealthy risks continue to increase (*3*), and the aging process does not have a single timeline. It is the process of gradual expansion of health diversity. Therefore, the period of aging is not a cumulation of aging, illness, disability, and dependency but, rather, a process of highly differentiating health status. This awareness of "healthy diversity" provides opportunities for the development and achievement of active aging.

Population aging is not simply a "unitary" social burden problem but a "dualistic" development issue. Although the intensification of population aging inevitably leads to aging of the labor force structure and further increases the cost of China's labor force, this adversity can be eliminated to some extent. With the improvement and development of living quality and technology, the overall health of older adults has greatly improved and life expectancy with disabilities has been compressed. It is fully demonstrated that most of older adults, defined by calendar age, are no longer dependents but persons with great potential to participate in socioeconomic activities and create new demographic dividends. In that case, the definition of older adults should be transformed from the calendar age definition to the perspective of "active aging," which is based on health development.

ACTIVELY AGING THROUGHOUT THE LIFE COURSE TO CONSTRUCT DEVELOPMENTAL GERONTOLOGY

Developmental gerontology (DG) is a new interdisciplinary branch of natural and social science that focuses on the relationship between the aging process, population aging patterns and comprehensive modernized social governance. It defines "aging" from the perspectives of technological, social, and economic

development. It breaks through the traditional definition of aging — the biological process of human aging. DG aims to fully explore the potential of humans in the process of aging and release new demographic dividends for older adults.

HAO is one of the foundations of DG, and its cores include dynamic measurement and continuous evaluation of health, disease, aging, disability, and mortality through the life course. It is a useful tool to effectively identify the cumulation of exposures from birth to the end of life. For a long time, the methods of life science have been used to distinguish the differences in calendar age, biological age, and social age. As previous studies with animal experiments have shown, an association between aging and dynamic changes in deoxyribonucleic acid (DNA) methylation was found (*4*). DNA methylation was used to measure the age of human cells, referred to as the biological age, which was shown to be correlated with breast cancer risk (*5*). Moreover, the potential reasons for differentiation in trajectories of human physiological function through the life course were detected in previous studies. For example, evidence has demonstrated that the level of cognition in childhood determines the ceiling of the adult cognition level, its starting point of decline (*6*), and that the level of risk exposure in early life has a strong impact on mental and cognitive health in adulthood, which further explains the interactions of health status in the corresponding period of "gestational age-aging process-old age" (*7*–*8*). Optimistically, the development of life science and technology, as well as medical innovation, was expected to lead to the gradual maturation of technologies in the fields of storage, repair and regeneration of cells, etc. However, the important role of artificial intelligence (AI) technology in compensating and expanding human physiological functions cannot be ignored. All these factors contribute to the increase in population health reserves in the "life bank" and provide opportunities for expanding the length and width of life. Undoubtedly, these are important conjunctions for developmental gerontology to combine thoughts of natural science, social science and economic science (*5*).

According to DG, it is important to not only treat the relationship between population aging and comprehensive modernized social governance from the perspectives of aging, disease, disability, etc. but also combine the rules of population development and the characteristics of socioeconomic development. The positive and dynamic perspective and population structure stratified thinking are essential to re-examine issues of population aging and the development of older adults' human capital. In addition, the keys to realizing active and healthy aging with expanded dividends are 1) to scientifically and rationally develop older adults' human capital on the basis of the achievement of both social significance and life significance in later life and 2) to rethink the relationships of the chain of population structure, social development and population aging on account of the contexts of social development, the population aging process, systematic demographic change, historical change, and changes in fertility, family structure and mobility.

Based on the rules of human life development, DG provides new insight into the relationship between active aging and comprehensive modernized social governance. It analyzes the feasibility of developing human capital of older adults and believes that the health dividends for older adults will bring new vitality to social and economic development. Older adults not only accumulate a large amount of intellectual capital and social wealth but also contribute to social and cultural development, family cohesion strengthening and social harmony. As such, they have great potential in re-employment, continuing education, social management, volunteering, and scientific and technological innovation. Thus, with the improvement of health conditions, an increasing number of healthy older adults will become the potential labor force, increase the overall reserves of the labor force, and expand effective labor resources (*9*). The improvement of the health condition of older adults means the extension of the demographic dividend. By fully developing the potential abilities of older adults in the active phase and the population health dividend in older age, China can obtain the new demographic dividend once again, which provides a new impetus for social and economic development.

Furthermore, DG explores the relationship between population aging, the changes in macroeconomic structure, and the growth of the regional economy based on system analysis, which is under the background of the changes in consumption structure from the development of human capital in later life. DG regards older adults as not only an important productive and support force for comprehensive modernized social governance but also the driving forces for industrial restructuring and increasing total factor productivity. Population aging will promote the upgrading of the consumption structure and drive

enterprises to replace the labor force with capital and technology, further upgrading and rationalizing China's industrial structure. As the quality of the labor force increases, technology advances, infrastructure improves, the total factor productivity of society rises significantly, and the disadvantages brought about by increasing labor costs under population aging gets compensated to some extent (*10*). These factors provide a good opportunity for China to complete the transformation of its industrial structure, respond actively to population aging and improve comprehensive modernized social governance.

THOUGHTS ON PROMOTING ACTIVE POPULATION AGING FROM THE PERSPECTIVE OF DG

The key to active population aging is to realize that older adults are an important, productive support and driving force for social and economic development. It is also the key to treating aging, diseases, and disabilities throughout the life course and for society. It is fair to say that giving full play to the health values of older adults, actively developing their potential human capital and maximizing the health dividends from older adults, have almost become the only feasible way to integrate and coordinate the development of population aging and society and economy in a sustainable way to some extent. Below are some thoughts about how to adopt DG in promoting active population aging:

Increasing the Health Reserves and Developing the Health Dividends of Older Adults

First, it is important to fully understand the significance of the health dividends of older adults in the comprehensive governance of modernized society. DG advances that the negative impact of population aging on economic growth can be mitigated or even eliminated under consideration for population health factors (*9*). The combined impact of the health dividends of older adults and the labor force health dividends on the national savings rate can be expressed as follows:

$$s = 1 - \frac{c_L}{y} - \frac{c_R}{y}\frac{R - \beta R}{\alpha L + \beta R} \quad (1)$$

where s denotes the national savings rate, L denotes the number of workers, and y denotes the output level per capita of the workforce. c_L denotes the per capita consumption level, c_R denotes the per capita consumption level for the elderly population, R denotes the number of the elderly population, and β is assumed to be the proportion of the elderly population among the healthy elderly population.

Furthermore, from the perspective of labor productivity, the per capita output level of the labor force is influenced by the health level of the labor force, so the actual labor productivity can be expressed as follows:

$$y = y(\beta_L L + \beta_R R) \quad (2)$$

where β_L denotes the health coefficient of the labor force, and β_R denotes the health coefficient of older adults. Thus, in terms of economic growth, health improvement can generate health dividends for older adults.

Equation (*2*) shows that with the increasing number of older adults in China, health promotion through technological development and social support is one of the important ways to explore the "health dividend of older age" and respond actively to population aging.

Second, the investment in the development of health science and technology and the establishment of health support systems should be increased. During the process of population aging, it is important to identify and control health risks exposed to gestational age- aging process- old age to minimize the occurrence of diseases and disabilities from birth to old age during life and prevent the accumulation and outbreaks of disease, disability and even death in older age. This is also important for improving the health condition, productivity and efficiency of the labor force and extending the labor health dividend to achieve economic growth.

Third, it is important to strengthen the systems and mechanisms to promote population health at all levels of governance. To actively respond to population aging, the use of the following is essential: 1) multidimensional health-related indicators to measure the development conditions of a region or a unit; 2) a life course approach to promote active aging and construction of suitable systems to promoting the health of children, the labor force and older adults.

Accelerating the Construction of Aged-friendly Cities and Society

First, it is necessary to promote the construction of an age-friendly society by building a healthy environment, renovating a supportive environment,

and establishing an age-friendly basic, sociocultural, and social supporting environment. Meanwhile, a sound system providing health services for older adults led by the government, integrated into and supported by society, should be formed to encourage older adults to create a supportive and inclusive social environment. In addition, providing rich and diverse opportunities for older adults to actively participate in various social affairs can help to realize self-achievement, provide elderly a sense of competence and promote active aging.

Establishing the View of Active Aging in Active Participation, Contribution and Sharing of Society by Older Adults

DG highlights that older adults are the precious wealth and resources of society and the social labor forces that cannot be ignored. With a comprehensive definition of old age, a sound and effective system should be established to improve the participation, contribution and sharing of society by older adults to form a new pattern of modern governance of the aging society. First, the permanent mechanism for developing the human capital of older adults should be established. It is beneficial to give a full role to the market economy, gradually establish a competitive and orderly labor market system for older adults, fully mobilize the enthusiasm of elderly workers to re-employment, promote ways for flexible employment for older adults, activate the stock of human capital, and further improve the efficiency and level of social production. Second, it is important to actively develop the aging industry and cultivate new economic growth drivers for an aging society. Older adults in China have huge consumption potential. Thus, efforts should be made to overcome the current conflict between overcapacity and unmeet diverse demands of older adults, actively adjust the social industrial structure to adapt to population aging and promote the upgrading and transformation of the industrial structure. Driven by the health and demand of older adults, the proportion of the elderly health industry in the entire economy should be increased. In-depth application of the new generation information technology such as fifth generation technology (5G), AI, and big data in the field of population aging and health should be explored to cultivate new driving forces for social economic development.

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