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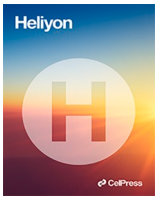

Research article

Clinical characteristics of COVID-19 clusters in three schools in Beijing, China: A retrospective study

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ABSTRACT

Background: This retrospective analysis aims to investigate the clinical characteristics of students infected with the SARS-CoV-2 Omicron variant in three Beijing schools. Additionally, we explore the dynamic trends of nucleic acid cycle threshold values (Ct values) and serum antibody titers throughout the disease course.

Methods: Demographic, clinical, nucleic acid Ct values, and antibody titer data were collected from cases in a COVID-19 cluster in Beijing Ditan Hospital, Capital Medical University, spanning from September 6 to October 1, 2022.

Results: A total of 107 students infected with Omicron (BA.5.2 and BA.2.76) were identified across three schools. Primary clinical manifestations included fever and upper respiratory symptoms (85/107, 79.4 %), with the majority being classified as mild cases (96/107, 89.7 %). Notably, middle school students in the second school exhibited a higher peak body temperature compared to college students in the first and third schools (39.5 °C vs. 38.4 °C, adjusted $P = 0.005$; 39.5 °C vs. 38.6 °C, adjusted $P = 0.002$). Analysis of dynamic changes in Ct values revealed the lowest median Ct value in nasopharyngeal swabs on the third day of illness, reaching 35 after 9–11 days. Oropharyngeal swab nucleic acid median Ct value reached 35 approximately 3–5 days post-onset. Serum antibody detection showed continuous negativity of IgM antibody titers from days 1–10, while IgG antibody titers were positive on the first day and increased rapidly after one week.

Conclusions: The three COVID-19 cluster school outbreaks primarily resulted from Omicron infections, with no severe or fatal cases observed. Clinically, the selection of different types of SARS-CoV-2 nucleic acid swabs for virus detection can be tailored based on the infection's course.

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1. Introduction

SARS-CoV-2 infection is associated with acute respiratory infectious diseases, posing a significant threat to public health [1]. The primary modes of transmission are through air droplets and close contact, both of which have serious implications for human health [1]. Since the identification of SARS-CoV-2, its evolutionary trajectory and mutation rates have been relentless, notably exemplified by the emergence of the Omicron variant and its subsequent subvariants, including BA.1, BA.2, BA.4, BA.5, BA.2.75, and BA.2.76 [1–3].

To a large extent, previous research has focused on the clinical differences between Omicron and non-Omicron. The clinical subtypes of adult infected individuals with Omicron variant in Zhuhai are relatively mild, with a lower incidence of pneumonia, but the duration of nucleic acid positivity is longer [4].The clinical characteristics of pediatric infections are non-specific, but the infection rate in children is significantly increased [4]. In Shanghai, the clinical characteristics and prognostic factors of patients with the Omicron variant were studied [5]. It was found that most of the patients with Omicron infection were 18–30 years old and mild, with fever and upper respiratory symptoms as the main clinical manifestations [5]. At the time of admission, those who were IgG positive for the new coronavirus antibody and those without fever had shorter hospital stay and faster virus clearance [5]. It can be seen that the clinical characteristics of infection with Omicron variant strains are clearly different from those of non Omicron strains.

The above comparative research methods may help to preliminarily understand the characteristics of Omicron, but with the continuous evolution of Omicron and the emergence of new subtypes, subtypes also exhibit their own characteristics under high mutation rates. Compared to the Omicron variant BA. 2 subtype, BA. 5 subtype has a higher proportion of asymptomatic and mild infections, shorter days of negative conversion, and higher viral load [6]. These data emphasize that even within the same variant, different subtypes may exhibit different clinical manifestations, which may have significant impacts on disease transmission patterns, clinical management, and public health strategies.

The inaugural case of Omicron BA.2.76 infection and localized transmission was documented in Chongqing, China, on August 16, 2022 [2]. Concurrently, the Beijing Center for Disease Control and Prevention (CDC) reported the prevalence of subvariants BA.5.2 and BF.7 in Beijing between November and December 2022 [3]. The advent of the “super mutated strain” Omicron has engendered widespread concern. From September 6 to October 1, 2022, a cluster epidemic of COVID-19 occurred in three schools in Beijing. A total of 107 patients infected with Omicron were admitted to Beijing Ditan Hospital, Capital Medical University. In an effort to delineate the clinical manifestations of Omicron infection and ascertain the dynamic trends of nucleic acid cycle threshold values (Ct values) and serum antibody titers over the course of the disease, a retrospective analysis was conducted across three school clusters in Beijing.

This comprehensive analysis encompassed demographic information, clinical characteristics, laboratory indicators, Ct values, and antibody titers of all infected students during this epidemic. The aim of this study is to furnish clinicians with updated insights, facilitating the optimization of treatment plans. This, in turn, ensures that medical professionals are well-equipped to safeguard themselves and provide optimal care when confronted with new variants. The subsequent sections provide a detailed account of the pertinent findings.

2. Methods

2.1. Study population

Between September 6 and October 1, 2022, three schools in Beijing experienced a cluster of COVID-19 outbreaks, resulting in the admission of 107 Omicron-infected students to Beijing Ditan Hospital, Capital Medical University. These 107 Omicron-infected students had complete demographic, clinical and laboratory data. All of them were included in the following analysis. A retrospective investigation was conducted on the following aspects of the infected students: I) General demographic characteristics and vaccination history, II) Clinical data, encompassing clinical manifestations, types of manifestations, length of hospital stay, and days for nucleic acid negative conversion, and III) Laboratory indicators, including the Ct value of SARS-CoV-2 nucleic acid and antibody titers (Supplementary Fig. 1).

The case definition and clinical classification adhered to the diagnostic criteria outlined in the “Diagnosis and Treatment Plan for COVID-19 (trial version 9)” [7]. Ethical approval for this study was obtained from the Medical Ethics Committee of Beijing Ditan Hospital. Informed consent from patients and their families was exempted, and the study adhered to the principles of the Declaration of Helsinki.

2.2. Strain identification, nucleic acid ct value, and antibody titer determination

Upon whole genome sequencing, the Omicron BA.5.2 and BA.2.76 strains were identified. The virus RNA was extracted using the QIAamp Viral RNA Mini Kit (Qiagen, Germany), yielding a total RNA solution of 60 μL from 140 μL throat swab specimens. The ORF1ab and N genes of the 2019-novel coronavirus (2019-nCoV) were detected through real-time PCR using an ABI7500 instrument. Criteria for interpretation were as follows: positive (Ct value < 35, typical amplification curve), gray area (Ct value < 35), and negative (Ct value ≥ 35 or no amplification curve). Antibodies were detected using chemiluminescence with reagents from Autobio. Antibody results, expressed as S/CO, were deemed negative if S/CO ≤ 0.79, otherwise positive.

2.3. Statistical analysis

Data analysis was performed using SPSS 26.0 and GraphPad Prism 9.1.0. The normality of measurement data was assessed using the Shapiro-Wilk test. Normally distributed measurement data (e.g., length of hospital stay) were presented as mean ± standard deviation, analyzed using the independent sample *t*-test for group comparisons. Non-normally distributed measurement data were expressed as median (quartile) [M (P_{25}, P_{75})] and analyzed using the Mann-Whitney *U* test or Kruskal-Wallis *H* test. *P* values were corrected using the Bonferroni method for pairwise comparisons among multiple groups. Count data were presented as [n (%)] and analyzed using Pearson χ^2 test or Fisher's exact test. A significance level of $P < 0.05$ was applied for statistical significance.

3. Results

3.1. Basic demographics and epidemiological evidence

A total of 107 students from three schools were infected during the COVID-19 outbreaks between September 6 and October 1, 2022. In School No.1, a science university, 51 students were infected with a median age of 20.0 (20.0, 20.0) years, predominantly males (50/51, 98.0 %). In School No.2, a middle school affiliated with a university, 17 students were infected with a median age of 16.0 (16.0, 17.0) years, including 7 boys (7/17, 41.2 %). School No.3, a liberal arts university, had 39 female cases (39/39, 100.0 %) with a median age of 18.0 (18.0, 19.0) years. A total of 6 cases (6/107, 5.6 %) had underlying diseases, including hypertension (2 cases), allergic rhinitis (1 case), sinusitis (1 case), and chronic pharyngitis (1 case). No severe cases were reported among patients with underlying diseases. Significant differences in age, sex, and the number of doses of inactivated vaccine were observed among the three schools (Table 1). All 107 cases did not show severe symptoms (Table 3). The predominant clinical manifestations were fever and upper respiratory symptoms (85/107, 79.4 %), with the majority classified as mild cases (96/107, 89.7 %) (Table 3).

3.2. Clinical differences between two and three doses of inactivated vaccine

All cases were vaccinated for COVID-19 according to the vaccine manufacture's and government recommendations, including one dose, two doses and three doses and comprising of five vaccine brands: Biotech, Sinovac, COVID-19 Vero Vaccine, Zhifei, and CanSino. Biotech, Sinovac, COVID-19 Vero Vaccine are inactivated vaccines, Zhifei is a recombinant protein vaccine, and CanSino is an adenovirus vector vaccine (adenovirus type-5) (Table 1). School No.1 predominantly received three doses of inactivated vaccine (49/50, 98.0 %), while School No.2 exclusively received two doses of inactivated vaccine. School No.3 had 36 cases (36/39, 92.3 %) with varying vaccine doses. In total, 34 cases (34/107, 31.8 %) received two doses, 68 cases (68/107, 63.6 %) received three doses, and 5 cases (5/107, 4.6 %) received other vaccines or only one dose, and were excluded from further analysis. A comparison between the two groups revealed significant differences in the male-to-female ratio and age ($P < 0.001$), with no disparities in other indicators ($P > 0.05$) (Table 2). The median peak body temperature of fever patients with two doses was 39.0 °C (38.0, 39.5), slightly higher than the three-dose group with 38.5 °C (38.0, 39.1) (Fig. 1B), though not statistically significant ($Z = -0.960$, $P = 0.337$).

3.3. Clinical differences between omicron BA.5.2 and BA.2.76 infections

School No.1 reported exclusively BA.5.2 infections, while School No.2 and School No.3 had BA.2.76 infections. Among the 107 infected students, 51 (47.7 %) were infected with BA.5.2, and 56 (52.3 %) with BA.2.76. Significant differences in gender ratio and age were observed between the two groups ($P < 0.001$). Except for cough and expectoration ($P = 0.035$), other indicators showed no statistical significance ($P > 0.05$) (Table 3). Fever patients with BA.5.2 had a median peak temperature of 38.4 °C (38.0, 39.1), slightly lower than BA.2.76 patients with 38.8 °C (38.0, 39.3) during the disease course (Fig. 1A), though not statistically significant ($Z = -1.131$, $P = 0.258$). Further analysis of fever patients across the three schools revealed significant differences in the median peak

Table 1
Basic Demographics and Epidemiological Evidence of infected students in the three schools.

Item	The first school (n = 51)	The second school (n = 17)	The third school (n = 39)	statistic	*P*
Type of School	Science university	Middle school	Liberal arts university		
Male [n (%)]	50 (98.04)	7 (41.18)	0 (0.00)	$\chi^2 = 86.52$[a]	**< 0.001**
Age [*M*(P_{25},P_{75}), years]	20.00 (20.00 , 20.00)	16.00 (16.00 , 17.00)	18.00 (18.00 , 19.00)	$H = 83.01$	**< 0.001**
BMI[*M*(P_{25},P_{75}), kg/m^2]	21.26 (20.07 , 24.33)	23.39 (19.78 , 26.43)	21.48 (19.05 , 23.66)	$H = 1.41$	0.49
Underlying diseases [n(%)]	4 (7.84)	1 (5.88)	1 (2.56)	$\chi^2 = 1.22$[b]	0.54
COVID-19 vaccination [n (%)]	51 (100.00)	17 (100.00)	39 (100.00)		
Inactivated vaccine [n (%)]	50 (98.00)	17 (100.00)	36 (92.30)	$\chi^2 = 68.49$[b]	**< 0.001**
1 dose	0 (0.00)	0 (0.00)	1 (2.79)		
2 dose	1 (2.00)	17 (100.00)	16 (44.44)		
3 dose	49 (98.00)	0 (0.00)	19 (52.78)		

[a] : Pearson χ^2test.
[b] :Fisher's exact probability method,BMI: Body mass index.

Table 2
Clinical differences between two and three doses of inactivated vaccine.

Item	two doses (n = 34)	Three doses (n = 68)	statistic	*P*
Male [n(%)]	7 (20.59)	49 (72.06)	$\chi^2 = 24.25$[a]	**< 0.001**
Age [$M(P_{25},P_{75})$, years]	17.00 (16.00,18.00)	20.00 (19.00,20.00)	$Z = -7.67$	**< 0.001**
Underlying diseases [n (%)]	1 (2.94)	5 (7.35)	$\chi^2 = 0.20$[a]	0.65
BMI[$M(P_{25},P_{75})$, kg/m^2]	21.37 (19.41,25.54)	21.88 (20.07, 24.28)	$Z = -0.26$	0.79
Clinical manifestations [n (%)]				
fever	29 (85.29)	53 (77.94)	$\chi^2 = 0.78$[a]	0.38
Chills	2 (5.88)	9 (13.24)	$\chi^2 = 0.62$[b]	0.43
fatigue	3 (8.82)	9 (13.24)	$\chi^2 = 0.11$[b]	0.74
Headache	5 (14.71)	9 (13.24)	$\chi^2 = 0.00$[b]	1.00
Dizziness	3 (8.82)	1 (1.47)	$\chi^2 = 1.60$[b]	0.21
Muscle soreness	1 (2.94)	9 (13.24)	$\chi^2 = 1.68$[b]	0.19
Upper Respiratory Symptoms	29 (85.29)	54 (79.41)	$\chi^2 = 0.52$[a]	0.47
Nasal obstruction	1 (2.94)	9 (13.24)	$\chi^2 = 1.68$[b]	0.19
Runny nose	1 (2.94)	6 (8.82)	$\chi^2 = 0.48$[b]	0.49
Cough and expectoration	19 (55.88)	27 (39.71)	$\chi^2 = 2.40$[a]	0.12
Discomfort in the pharynx	22 (64.71)	37 (54.41)	$\chi^2 = 0.98$[a]	0.32
Clinical classification [n (%)]			$\chi^2 = 0.99$[c]	0.73
Asymptomatic	1 (2.94)	4 (5.88)		
Mild	31 (91.18)	62 (91.18)		
Common	2 (5.88)	2 (2.94)		
Length of hospitalization ($\bar{x} \pm s$, days)	13.12 ± 0.48	12.38 ± 0.41	$t = 1.09$	0.28
Days of nucleic acid negative conversion [$M(P_{25},P_{75})$, days]	13.50 (11.00,15.00)	12.00 (10.00, 14.00)	$Z = -1.61$	0.11
Duration of fever [$M(P_{25},P_{75})$, days]	2.00 (1.00, 3.00)	1.00 (0.00, 2.00)	$Z = -1.30$	0.19

[a] : Pearson χ^2 test.
[b] : Continuous correction χ^2test.
[c] :Fisher's exact probability method,BMI: Body mass index.

Table 3
Clinical differences in cases infected with Omicron BA.5.2 and BA2.76 strains.

Item	BA.5.2 (n = 51)	BA.2.76 (n = 56)	statistic	*P*
Male [n(%)]	50 (98.04)	7 (12.50)	$\chi^2 = 78.46$[a]	**< 0.001**
Age [$M(P_{25},P_{75})$, years]	20.00 (20.00, 20.00)	18.00 (17.00, 18.75)	$Z = -8.43$	**< 0.001**
Underlying diseases [n (%)]	4 (7.84)	2 (3.57)	$\chi^2 = 0.29$[b]	0.59
BMI[$M(P_{25},P_{75})$, kg/m^2]	21.26(20.07,24.33)	21.66 (19.58, 25.15)	$Z = -0.11$	0.92
Clinical manifestations [n (%)]				
fever	41 (80.39)	44 (78.57)	$\chi^2 = 0.05$[a]	0.82
Chills	7 (13.73)	4 (7.14)	$\chi^2 = 1.25$[a]	0.26
fatigue	7 (13.73)	5 (8.93)	$\chi^2 = 0.62$[a]	0.43
Headache	7 (13.73)	7 (12.50)	$\chi^2 = 0.03$[a]	0.85
Dizziness	1 (1.96)	3 (5.36)	$\chi^2 = 0.17$[b]	0.68
Muscle soreness	7 (13.73)	3 (5.36)	$\chi^2 = 1.33$[b]	0.25
Upper Respiratory Symptoms	40 (78.43)	45 (80.36)	$\chi^2 = 0.06$[a]	0.81
Nasal obstruction	6 (11.76)	4 (7.14)	$\chi^2 = 0.24$[b]	0.63
Runny nose	5 (9.80)	2 (3.57)	$\chi^2 = 0.83$[b]	0.36
Cough and expectoration	17 (33.33)	30 (53.57)	$\chi^2 = 4.44$[a]	**0.03**
Discomfort in the pharynx	30 (58.82)	30 (53.57)	$\chi^2 = 0.30$[a]	0.58
Clinical classification [n(%)]			$\chi^2 = 0.26$[c]	1.00
Asymptomatic	3 (5.88)	4 (7.14)		
Mild	46 (90.20)	50 (89.29)		
Common	2 (3.92)	2 (3.57)		
Length of hospitalization ($\bar{x} \pm s$, days)	12.00 (10.00 , 14.00)	13.50 (11.00, 15.00)	$Z = -1.50$	0.13
Days of nucleic acid negative conversion [$M(P_{25},P_{75})$,days]	11.00 (9.00 , 13.00)	13.00 (11.00, 15.00)	$Z = -1.86$	0.06
Duration of fever [$M(P_{25},P_{75})$,days]	1.00 (0.00, 2.00)	1.00 (0.25, 2.00)	$Z = -0.10$	0.92

[a] : Pearson χ^2test.
[b] : Continuous correction χ^2test.
[c] :Fisher's exact probability method,BMI: Body mass index.

temperature ($H = 12.264$, $P = 0.002$). School No.1 and School No.3 had lower temperatures compared to School No.2 (adjusted $P = 0.005$ and $P = 0.002$, respectively) (Fig. 1C).

3.4. Dynamic changes trend of nucleic acid ct value and antibody titer

Changes in SARS-CoV-2 nucleic acid Ct value and antibody titer were monitored throughout the disease course on all patients.

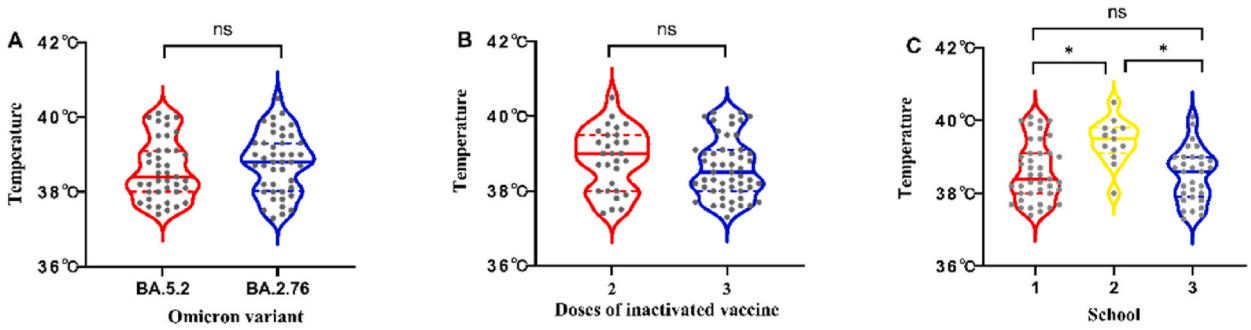

Fig. 1. Peak body temperature distribution of febrile patients in different groups during hospitalization
A. Peak body temperature in students infected with BA.5.2 (n = 41) or BA.2.76 (n = 44) omicron strains.
B. Peak body temperature in students with Two (n = 29) or Three doses (n = 53) of inactivated vaccine;
C. Peak body temperature in students from School No.1 (n = 41), No.2 (n = 13) or No.3 (n = 31).

Hospitalization days ranged from 6 to 21 days, with a median of 13.0 days (11.0, 15.0). A total of 1285 nasopharyngeal swab samples, 1001 oropharyngeal swab samples, and 468 serum antibody samples were collected. Ct values of nucleic acid in nasopharyngeal swabs were lowest on day 3 [ORF = 21.8 (20.36, 28.2), N = 19.6 (16.98, 26.14)], reaching 35 approximately 9–11 days after onset (Fig. 2A). Oropharyngeal swab Ct values reached 35 around 3–5 days after onset, with a shorter detection window compared to nasopharyngeal swabs (Fig. 2B). The mean IgM antibody titer remained negative after 10 days of illness [negative threshold: ≤Log0.79 (−0.102372909), Fig. 3A], while IgG antibody titers turned positive around day 1, increasing rapidly after approximately a week [positive threshold: ≥Log1.21 (0.08278537), Fig. 3B].

4. Discussion

Since the discovery of SARS-CoV-2 in late 2019, the continuous emergence of mutant strains has prompted the World Health Organization (WHO) to classify them into different genotypes, such as Alpha, Beta, Gamma, Delta, and Omicron strains, with the last five listed as "Variants of Concern (VOC)" [8,9]. The Omicron strains, particularly BA.5.2 and BA.2.76, represent the most diverse and challenging variants to date, exhibiting enhanced immune evasion and increased transmissibility [8,9]. Several investigations have scrutinized the clinical attributes of individuals afflicted with Delta and Omicron strains [10,11], revealing distinct clinical profiles associated with different viral genotypes. Our study adds to the limited comparative research on the clinical characteristics of patients infected with different Omicron subtype strains, shedding light on the diverse clinical manifestations, Ct values, and serum antibody titers. Our results deepen the clinical understanding of COVID-19 infection with circulating strains supporting the adjustment of epidemiological and treatment strategies.

The most common initial symptoms post-COVID-19 infection include upper respiratory tract symptoms and fever, posing a higher risk for severe outcomes in older individuals with underlying conditions, those with compromised immune systems, and unvaccinated individuals [12]. Despite vaccination, COVID-19 infections can still occur [13,14], particularly in cases involving Omicron BA.4 and BA.5 subvariants, which exhibit enhanced serum immune escape and low neutralizing antibody titers, potentially contributing to breakthrough infections [15,16]. Even with 100 % vaccination rate among the student cases, our findings align with these previous reports indicating a mild clinical classification in Omicron-infected patients after vaccination, with no severe cases or deaths observed [12,17]. The predominance of mild cases reinforces the crucial role of vaccination in preventing severe outcomes.

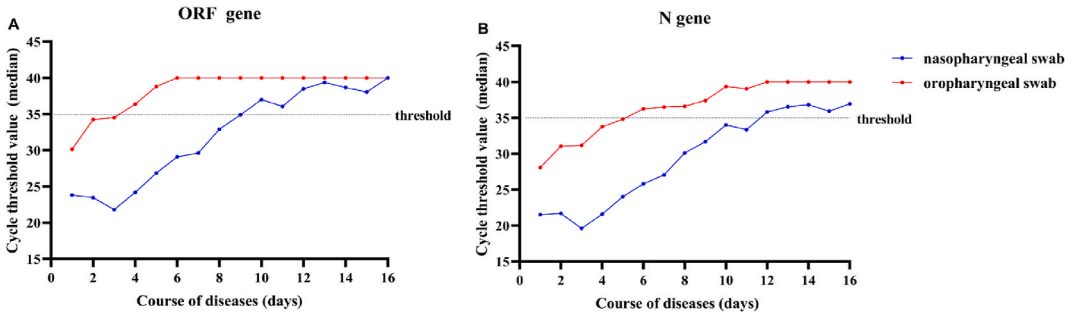

Fig. 2. Molecular diagnostics (Ct values) results of novel coronavirus nucleic acid detection in nasopharyngeal swabs and oropharyngeal swabs
Ct value of the ORF gene (A) and N gene (B) on the 1st to 16th day after onset. If the Ct value reaches negative and the value cannot be detected, use Ct = 40 instead;
The Ct value that meets discharge criteria is ≥ 35.

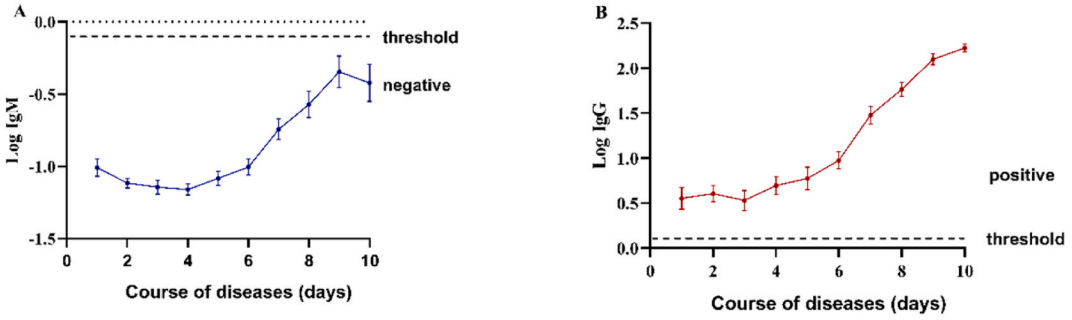

Fig. 3. Dynamic trends of specific IgM and IgG antibody titers in patients
Serological IgM (A) and IgG (B) antibody titer against SARS-CoV-2 throughout disease course. Antibody titer were transformed to logarithm scale. Criteria: Negative: ≤Log0.79(-0.102372909); Positive: ≥Log1.21(0.08278537); Suspicious: ≥ Log 0.8 (−0.096910013) and ≤ Log 1.2 (0.079181246).

Upper respiratory symptoms, such as cough (47/107, 43.9 %) and sore throat (60/107, 56.1 %), along with fever (85/107, 79.4%), were the predominant clinical manifestations in our study, consistent with other reports on Omicron-infected patients [18–21]. Notably, the age differences among the schools influenced the peak body temperature, as peak body temperature among students from School No.1 and School No.3, a science and liberal arts university, respectively (age≥18 years old), were lower than students from School No.2, a middle school affiliated with a university (age < 18 years old). This aligns with existing research indicating higher proportions of fever in younger Omicron-infected patients [22]. Different temperature measurement methods and techniques may affect the accuracy and consistency of the obtained data. In this study, the timing of the occurrence of cases was during the epidemic prevention and control period in China, and the management standards for all hospitalized cases were unified. We measured the patient's body temperature using an infrared thermometer on the day of admission and collected data for subsequent analysis. Children (age < 18 years old) are susceptible to pathogen invasion due to incomplete physiological and immune development, and common symptoms such as cough and fever are common in the early stages. The body is actively activating defense mechanisms to fight against pathogens and strive to restore health. However, the influence of age on symptoms and nucleic acid conversion time in mild Omicron cases remains controversial [23].

According to our research results, there was no statistically significant difference in the clinical characteristics of students infected with BA. 5.2 and BA. 2.76, except for cough and sputum. In fact, the clinical differences between Omicron subtype strains have an extremely important impact on public health interventions, including vaccination strategies and treatment methods. Different subtype strains may have varying degrees of escape ability against existing vaccines, which means that regular evaluations of the vaccine's protective efficacy against emerging subtypes are necessary. For example, the upgraded protein subunit COVID-19 vaccine ZF2001 has stronger neutralizing activity against the prevalent sub variants BF.7, BQ.1, BQ.1.1 and XBB [24]. At the same time, the emergence of subtype strains requires us to evaluate the effectiveness of antiviral drugs, adjust treatment plans, and even implement more personalized treatment strategies. In addition, strengthening virus monitoring and genetic sequencing capabilities, updating public health guidance, and continuous public education are all important steps in addressing the challenges of subtype strains. In summary, facing the diversity of Omicron subtypes, public health strategies must maintain flexibility and adaptability to effectively control the development of the epidemic.

Key laboratory indicators for confirming COVID-19 include nasopharyngeal or oropharyngeal viral nucleic acid levels (generally based in molecular diagnostics tests) and serum IgG and IgM levels (based on chemistry Luminescent immunoassay technology). Our study, in agreement with previous research, found that nasopharyngeal swabs had higher accuracy than oropharyngeal swabs in detecting viral nucleic acid [25–28]. The earlier reaching of Ct value 35 in oropharyngeal swabs highlights the suitability of nasopharyngeal samples for monitoring new coronavirus infections. Others have reported that the median time for IgM antibody conversion in patients diagnosed with COVID-19 is 10–12 days after onset [29,30]. Our study was limited by late testing, and therefore we could not observe IgM changes 10 days post-onset. IgG positivity early in the disease course indicates previous COVID-19 vaccination and/or potential longer-lasting protection post-infection [31]. The retrospective nature of our study collected data (e.g. IgG levels) up one week after hospitalization, but long-term follow-up after discharge was not possible.

This study has limitations. Firstly, as a retrospective analysis, this study only focused on the data of 107 patients in the Beijing area, with a relatively limited sample size and a single geographical representation. The conclusions drawn from this can only map the characteristics of specific clinical cohorts, weakening the universality and influence of the research results. Secondly, this study did not fully explore antibody dynamics, specifically due to the lack of continuous monitoring of antibody levels in patients during the rehabilitation stage. The change in antibody levels is a key indicator for evaluating an individual's immune status and disease progression, but this deficiency means that we were unable to capture the dynamic changes in antibody titers on and after the 10th day of onset. Given the above limitations, future research designs should focus on expanding sample size, increasing geographical diversity, and enhancing the representativeness and broad applicability of research results. At the same time, establishing a sound long-term follow-up mechanism, especially continuous tracking of immune markers, will help deepen our understanding of the natural history of diseases and immune regulation processes, and provide scientific basis for making more accurate clinical decisions.

5. Conclusion

This study analyzed a COVID-19 outbreak in three Beijing schools caused by Omicron variants BA.5.2 and BA.2.76. Predominant clinical features included fever and upper respiratory symptoms (85/107, 79.4 %), with the majority classified as mild cases (96/107, 89.7 %). Nasopharyngeal samples proved more suitable for monitoring the infection course, suggesting medical staff can tailor SARS-CoV-2 nucleic acid swab choices based on the disease's progression. This study preliminarily revealed the clinical characteristics and response patterns of the target population of Omicron under specific conditions. However, due to the limitations of the sample size, the universality and depth of the current conclusions are limited, and there is an need to carry out larger scale, prospective design research projects to enhance the representativeness and reliability of the research results.

Human subjects/informed consent statement

Ethical approval for this study was obtained from the Medical Ethics Committee of Beijing Ditan Hospital (number: 2020-003-01). Informed consent from patients and their families was exempted, and the study adhered to the principles of the Declaration of Helsinki.

Consent for publication

Not applicable.

Data availability statement

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

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CRediT authorship contribution statement

Zhixia Gu: Writing – original draft, Methodology, Investigation, Data curation. **Rui Song:** Writing – original draft, Methodology, Investigation, Data curation. **Yuanyuan Zhang:** Conceptualization. **Yiwei Hao:** Investigation. **Shugui Sheng:** Investigation. **Xiaoyou Chen:** Writing – review & editing, Investigation, Conceptualization. **Ronghua Jin:** Writing – review & editing, Investigation, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.heliyon.2024.e35425.

List of abbreviations

Ct	values cycle threshold values
CDC	center for disease control and prevention
2019-nCoV	the 2019-novel coronavirus
WHO	the World Health Organization
VOC	variants of concern

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