A Comparative study on epidemiological characteristics, transmissibility, and pathogenicity of three COVID-19 outbreaks caused by different variants

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Text

Abstract

Objectives: The Omicron BA.2 variant is probably the main epidemic strain worldwide at present. Comparing the epidemiological characteristics, transmissibility, and influencing factors of SARS-CoV-2, the results obtained in this paper will help to provide theoretical support for disease control. **Methods:** This study was a historical information analysis, using the R programming language and SPSS 24.0 for statistical analysis. The Geoda and Arc GIS were used for spatial autocorrelation analysis. **Results:** Local spatial autocorrelations of incidence rate were observed in Delta and Omicron BA.1 outbreaks, while Omicron BA.2 outbreaks showed a random distribution in incidence rate. The R_t of Delta, Omicron BA.1, and Omicron BA.2 were 3.21, 4.29, and 2.96, respectively, and correspondingly, the mean serial interval were 4.29 days (95%CI: 0.37-8.21), 3.84 days (95%CI: 0-8.37), 2.77 days (95%CI: 0-5.83). The asymptomatic infection rate of cases in Delta, Omicron BA.1, and Omicron BA.2 outbreaks were 21.71%, 6.25%, and 4.35%, respectively. **Conclusions:** Omicron BA.2 had the greatest serial interval, transmissibility, and transmission speed, followed by BA.1 and then Delta. Compared to Delta and Omicron BA.1 variants, Omicron BA.2 variants may be less pathogenic and more difficult to control than Omicron BA.1 and Delta.

Keywords: Delta, Omicron BA.1, Omicron BA.2, COVID-19, Variants, Transmissibility, Pathogenicity

Background

Since Corona Virus Disease 2019 (COVID-19) has been declared a global pandemic by the World Health Organization in March 2020[1], various variants had been identified, with 512 million

confirmed cases and more than 6.2 million deaths worldwide as of May 3rd, 2022[2]. During the worldwide pandemic, five variants with substantial global public health implications are now available: Alpha, Beta, Gamma, Delta, and Omicron [3]. The Delta variant, one of them, has become the main variant of the global pandemic in June 2021 since it was officially named in May 2021 and by September 2021, it had swept 185 countries and territories[4]. The Omicron BA.2 variant is likely to be the current major global epidemic strain [5].

Previous studies have shown that Omicron variant could be more than 10 times more infectious than the original variant, and about twice as infectious as Delta variant[6]. The transmissibility of Omicron BA.2 was 1.4 times that of Omicron BA.1[7]. When compared to older wild-type strains and other COVID-19 Variants of Concern (VOCs), Omicron variants have the highest number of mutations that affect their biological properties, such as enhancing transmissibility and causing immune escape[8]. According to a pre-print study from the National Institute for Communicable Diseases of South Africa, the proportion of Omicron patients in the spike was more than three times higher than in Delta outbreaks[9]. The study also found that, in contrast, Omicron transmission was associated with an increased risk of reinfection and a decreased risk of primary infection. These findings imply that Omicron variant cause immunological escape and are more likely to re-infect than Beta or Delta variants.

According to the 2022 WHO monthly report in February, a total of 130 million persons were diagnosed with Omicron in the two and a half months following the identification of the Omicron variant in November 2021[10]. There have been several epidemics of the Omicron variant in China. From 1st March to 22nd April 2022, more than 500,000 local Omicron infections have been reported in almost all provinces across China[11]. Due to the emergence of variants, several countries and

areas have experienced multiple epidemics caused by various variants of the virus [3, 12].

Three outbreaks separately caused by Delta, Omicron BA.1, and Omicron BA.2 occurred in Shenzhen city from January to February 2022, successively. The findings of this study will aid in understanding the epidemiological characteristics, transmissibility, and virulence of various variants in China's current epidemic prevention program. Analyzing various variants, the epidemiological characteristics and transmissibility and their influencing factors would be attributed to providing theoretical support in epidemic prevention and control.

Method

Study site

Shenzhen city (22°27′ to 22°52′ N, 113°46′ to 114°37′ E) is a major economic center and transportation hub in China, with frequent international trade transactions and activities. It is located in the south of Guangdong province, and adjacent to the Hong Kong special administrative region. Shenzhen city has a total area of 1997.47 square kilometers, including nine municipal districts, and a permanent population of 17.5681 million in 2021.

Data collection

From January 1st to March 26th, 2022, local COVID-19 cases were reported in Shenzhen city. According to the epidemiological investigation and gene sequencing results, 16 cases of Delta strain transmission, 34 cases of Omicron BA.1, and 1064 cases of Omicron BA.2 transmission were discovered.

In this study, we adopted historical information analysis to compare the epidemiological characteristics, transmissibility, and pathogenicity of three COVID-19 outbreaks caused by different variants. The sample size was determined by outbreak size. Data in our study was from

epidemiological investigations and surveillances, which were updated and managed in the National Infectious Diseases Information Reporting Management System (IDIRMS) and stored in Shenzhen Center for Disease Control and Prevention.

The following case information included: gender, age, Area, occupation, clinical typing, vaccination shots, initial screening positive CT (Cycle threshold) value, onset date, initial exposure date, last exposure date, and initial screening positive date. The preceding cases with a clear transmission relationship were used for the calculation of the serial interval.

Diagnostic criteria

Once a positive case has been identified, an epidemiological investigation and wider nucleic acid detection are in place, for expanding the search to other relative cases. All cases were diagnosed according to the eighth edition of the diagnostic protocol for COVID-19 in China.

Relative index

Moran's index

The Global Moran’s Index is proposed by the Australian statistician Patrick Alfred Pierce Moran to assess the overall pattern and spatial agglomeration whose value range from −1 to +1. The Global Moran's I and the Local Moran's I are calculated for the spatial autocorrelation analysis. The null hypothesis of spatial autocorrelation in this study inferred that the spatial distribution of incidence rate in all districts of Shenzhen city is randomly distributed ($\alpha = 0.05$), implying no spatial autocorrelation.

When Moran's I is greater than zero, the data has a spatial positive correlation, and the larger the value, the more obvious the spatial correlation is. When Moran's I is less than zero, the data has a spatial negative correlation, and the lower the value, the greater the spatial difference. When Moran's

I is 0 or close to 0, the data has a stochastic distribution.

Incubation period and serial interval

The incubation period refers to the time interval between the infection and onset of the disease. Actually, for most infections, the exact date of infection is hard to figure out in a real-world outbreak. But the date range of exposure was available based on the memory of infections, which can be extracted from individual epidemiological investigations. And we assumed that the infection possibility of each day within the exposed date range is equal. Infector-infectee pair is inferred also based on some key information from individual epidemiological investigations, which include physical activity, family structure, and the relationship between infectee and confirmed infections. Because we did not go far enough in inferring all infector-infectee pairs based on the recall of infectee and infector, this study excluded some infections in the estimated serial interval. We simply enumerate all possible infections – infectee pair and estimated respectively to generate the maximum and minimum time, using the R (R Foundation, Vienna, Austria) Epitrix package estimate incubation period by the MASS package of R[13]. We fitted Gamma distribution for estimating incubation periods. For the serial interval estimated in the Epitrix package, we assumed the infection possibility of each day within the exposed date range is equal. Then we fitted the Gamma distribution based on weighted serial interval.

Time-dependent reproduction number

The time-dependent reproduction number (R_t) is the average number of new cases that an infected case can cause at the time (T) in the epidemic process. Through epidemiological investigation, in cases with a clear transmission relationship, the time interval of onset of symptoms between source of infection and second-generation case, namely, the Serial interval could be

obtained. The Epitrix package of R version 4.1.2[14] was used to calculate R_t.

Data analysis

ESRI ArcGIS Desktop, version 10.8 (ESRI Corp., Redlands, C.A., USA)and GeoDa, version 1.180(Luc Anselin, Center for Spatial Data Science, The University of Chicago, I.L. USA, http://geodacenter.github.io/index-cn.html) were used to calculate Moran's I, and R (Version 4.1.2, R Foundation) was used to calculate the incubation period, latent period, and R_t. IBM SPSS Statistics for Windows, version 27.0 (IBM Corp., Armonk, N.Y., USA) was used for statistical analysis of transmissibility and pathogenicity influencing factors by using Chi-square test, Fisher's exact test and T-test.

Result

Epidemiological characteristics

Among the cases in Delta, Omicron BA.1, and Omicron BA.2 outbreaks, the age groups with the largest number of cases were 20-29 years old (37.50%, 6/16), 40-49 years old (39.13%, 9/23) and 30-39 years old (23,97%, 255/1064) respectively. There was a statistical significance in the distribution of the three outbreaks of cases across regions (χ^2=252.94, p<0.001). There were no statistical significance in the occupational composition ratio and vaccination status of patients for three outbreaks. The clinical types of the three outbreak cases had statistical significances, the proportions of asymptomatic infections were 21.71 % (231/1064), 4.35% (1/23), and 6.25 % (1/16), respectively (Table 1). The proportion of symptomatic cases showing symptoms in three outbreaks were Delta: 13/15(86.67%), BA.1:21/22(94.45%), and BA.2:590/833(70.83%), respectively.

Moran's index

The Global Moran's I of Delta outbreaks is -0.083, (p=0.267, z=-0.340), and the Global Moran's

I of Omicron BA.1 outbreak is -0.141 (p=0.253, z=-0.340). This result means the incidence rates in Omicron BA.1 outbreak and Delta outbreaks did not have global spatial autocorrelation. The Global Moran's I of the Omicron BA.2 outbreak is 0.048, (p<0.05, z>1.96), since the value of Global Moran's I is close to 0, it is considered that the incidence rate in Omicron BA.2 outbreak shows a weak positive spatial correlation (Supplementary Materials, Table S1).

In the Delta outbreak, the Longhua district and Yantian district have low-high clusters of incident rates (p=0.001). That means the incidence rate in Longhua and Yantian districts were low, and the incidence rates in their adjacent areas may be high. Similarly, in the Omicron BA.1 outbreak, Guangming district and Longhua district (p=0.05) showed a low-high cluster. The incidence rate of Bao'an district (p=0.001) showed a high-low cluster, meaning the that incidence rate in Bao'an district was low, and the incidence rates in adjacent areas may be high (Fig.1). The incidence the rates in Delta outbreak and the Omicron BA.1 outbreak had local spatial autocorrelation. Although the Moran's I of the Omicron BA.2 outbreak is 0.048, (p<0.05, z>1.96), since the value of Global Moran's I is close to 0, it is considered that the incidence rate in Omicron BA.2 outbreak shows a weak positive spatial correlation, but the local autocorrelation analysis results found that there is no local spatial correlation, so it is considered that there is no spatial autocorrelation globally. Therefore, the incidence rate in Omicron BA.2 outbreak was considered to be randomly distributed.

Incubation period

The mean incubation period and its standard deviation of the Delta, Omicron BA.1, and Omicron BA.2 outbreaks were 4.16±2.03 days, 4.85±2.37 days, and 4.17±1.94 days, respectively, and the 95%CI were (0.18, 8.14), (0, 9.51), (0, 7.97), respectively (Supplementary Materials, Fig. S1).

Public health and social measures

Public health and social measures WHO defines public health and social measures (PHSM) as actions performed by individuals, institutions, communities, local and national governments, and international organizations to slow or stop the spread of infectious diseases like COVID-19[15]. PHSM includes non-pharmaceutical interventions, physical distancing measures, pre-and post-exposure prophylaxis, and vaccines. Among them, social distancing measures can significantly reduce the frequency of contact, vaccination and wearing masks can reduce the probability of infection, and surveillance measures focus on finding and controlling the source of infection and key contact groups, which played an important role in preventing the spread of the epidemic.

Similar social distancing measures and monitoring measures were taken in three outbreaks. Omicron BA.2 outbreak was widely involved and lasted for a long time with stronger social distancing measures and quarantine management of people. Detailed interventions for three outbreaks were shown in (Supplementary Materials, Table S2).

Transmissibility

Time-dependent reproduction number

Serial interval refers to the time interval between the source of infection and the onset of symptoms in secondary cases. The mean serial interval of Delta, Omicron BA.1, and Omicron BA.2 were 4.15days (95%CI: 0.37-8.21), 3.84 days (95%CI: 0-8.37), 2.77 days (95%CI: 0-5.83), respectively (Fig.2a). Serial intervals of the three variants showed a clear trend of shortening . The R_t of the Delta strain on January 5th was 3.21(95%CI: 1.04-5.87). The Omicron BA.1 outbreak had an R_t of 4.29 (95%CI:2.05, 7.32) on January 30th, The R_t of the Omicron BA.2 outbreak showed obvious shocks and fluctuations. On February 15th, the R_t was 2.96 (95%CI: 1.85, 4.31). On March 1st, the

mean of R_t dropped below 1. After March 6th, the R_t gradually recovered. The average R_t. fell back below 1 again on March 20th. (Fig2.b)

Cycle threshold value

The nucleic acid detection of the COVID-19 virus usually adopts the method of real-time fluorescent reverse transcription PCR (Reverse transcription-polymerase chain reaction, RT-PCR). In this study, the CT (Cycle threshold**)** value of the first recorded case was selected as the CT value.

CT value can be obtained by detecting the O gene or N gene. After the normality test (Kolmogorov-Smirnov Test and Shapiro-Wilk Test), the CT value of Delta and Omicron BA.1 coincided with normal distribution (p>0.05) while the CT value of Omicron BA.2 did not (p<0.05). However, the normality of the outcome variable was met by invocation of the central limit theorem (n= 1064). After two independent sample t-tests, the difference in the mean CT value of cases detected by the O gene and N gene in the three outbreaks was not statistically significant (p>0.05). By analyzing the variance, it was found that there was no significant difference in the mean values of CT values among the three variants (Supplementary Materials, Fig.S2).

We referred to the criteria in other references which were set CT value < 25 as high infectivity[16-18], and CT value > 25 as low infectivity. The proportion of cases with a CT value of >25 in three outbreaks were not significantly different in gender, age, occupation, and vaccine doses. Among the Omicron BA.2 outbreaks, the proportion of male cases with CT value <25 (33.45%, 188/562) was lower than that of female cases (40.64%, 204/502). The proportion of symptomatic patients with CT value <25 was higher than that of asymptomatic patients, the proportion of symptomatic patients with CT value <25 was 38.90% (324/833), and the proportion of asymptomatic patients with CT <25 was 29.44% (68/231) (Table 2).

Pathogenicity

The highest proportion of asymptomatic infections in Omicron BA.2 was 21.71% (231/1064), which was significantly higher than that of Delta (6.25%, 1/16) and Omicron BA.1 (4.35%, 1/23). Compared with Delta and Omicron BA.1, Omicron BA.2 is more likely to produce asymptomatic infections, and its pathogenicity is weakened to a certain extent compared with Omicron BA.1 and Delta variant (Table 3). There were no significant differences in the proportion of asymptomatic infections in Delta and Omicron BA.1 cases with age, gender, occupation, number of vaccinations, and CT values. In Omicron BA.2 outbreak, the proportion of asymptomatic infections in the group with CT value <25 (29.44%) was lower than that in the group with CT value ≥25 (38.90%), with statistically significant. There is a significant difference in the proportion of asymptomatic infections in the 0-9 years (30.00%, 33/110) and 20-29 years age groups (10.36%,20/193).

Discussion

The age groups of 20-29 years, 30-39 years, and 40-49 years accounted for the most cases among the three outbreaks. The 20-49 years age group may be more susceptible to infection owing to their frequent social activities. Three outbreaks differ in terms of regional dispersion and spatial aggregation. Because both the Delta and Omicron BA.1 outbreaks were infrequent and resulted from the importation of a single source of illness. The imported outbreak from a single source of infection might be controlled locally in a short amount of time due to their small scope; the Omicron BA.2 outbreak is caused by the continual intake of several infectious sources. The outbreak of Omicron BA.2 was linked to similar entry cases at multiple ports, indicating clear cross-regional transmission.

In practice, because secondary case exposure and infection source are not a single occurrence, there are continuous multiple exposures, making it impossible to determine which exposure caused

the infection. When the interval between the last exposure time and the case's onset time is used as the incubation period, the calculated incubation period is shorter than when the continuous exposure time is used. Because it is difficult to determine the time of initial exposure in epidemiological studies, the last exposure time is more commonly used in practical applications to calculate the incubation period, but this method may underestimate the values of the incubation period. Both incubation period was calculated using continuous exposure time. The serial intervals of Delta, Omicron BA.1, and Omicron BA.2 were significantly shortened, but all were lower than the incubation period, especially in Omicron BA.2 variant. This may suggest that a substantial portion of the contagion occurred before the onset of symptoms in cases[19].

It seems that the transmissibility of the three variants, Omicron BA.1>Delta>Omicron BA.2. Compared with the Delta variant, the transmissibility of Omicron BA.1 and BA.2 increased by 33.64%. However, Omicron BA.2 are more infectious than Delta and Omicron BA.1 variants[20, 21]. The Delta outbreak and Omicron BA.1 outbreak were of limited size, and the limitation of the outbreaks scale may increase systemic error to some extent.

Although CT value was considered as an index that may be related to the infectivity of the patient[22], the clear criteria for dividing high or low infectivity was still not confirmed. Therefore, we referred to the criteria in other references which were set CT value < 25 as high infectivity, and CT value > 25 as low infectivity[16-18]. Some research found that PCR result was relative to CT value: It can be observed that 70% of the cases can cultivate the virus in vitro when their CT values were below 25 [16]. Several studies have found that patients with CT values < 25 have higher severity of symptoms [17, 18]. Therefore, patients' CT values were classified into two categories in this study:<25 and≥25. The proportion of female patients with CT values under 25 was considerably

higher than that of male patients in the Omicron BA.2 outbreak, implying those female patients may have a larger viral load than male patients. Asymptomatic infected people with higher CT values may be more infectious, being difficult to detect because they do not exhibit symptoms, making transmission stealthy. More research should determine whether there is a clear relationship between CT value and transmissibility[22]. This study showed that there was no statistical significance in the CT values of the cases caused by the three variants. Due to the large scale of the Omicron BA.2 outbreak in Shenzhen city, detection reagents produced by several different manufacturers were used, and the limitation of data collection made it impossible to distinguish CT values of reagents from different manufacturers, which may have affected the results of our statistical analysis.

However, some studies reported that there is no significant correlation between CT value and the severity of illness[22, 23]. In this study, this difference only showed statistical significance in Omicron BA.2 outbreak. Patients with lower CT values may be more likely to develop symptoms in Omicron BA.2, resulting in more insidious transmission and thus greater spread potential. The vaccinated patients in the three outbreaks were all ordinary, mild, and asymptomatic infected patients, no severe and critical patient. Vaccination might have a positive impact on the emergence of severe and critical patients.

In Omicron BA.2 outbreaks, we discovered that none of the patients in the 0-9 years age group had received their booster immunization, whereas greater than two third of the patients in the 20-29 years age group had. Due to the lack of booster doses, there may be more asymptomatic infections in the 0-9 years age group than in the 20-29 years age group.

The limitation of our study can be summarized in four parts. First of all, the Delta outbreak and Omicron BA.1 outbreak were of limited size, and the limitation of the outbreak scale may increase

systemic error to some extent, such as transmissibility. For the comparison of transmissibility, the R_t of the Omicron BA.1 variant was higher than that of the Delta variant, while that of Omicron BA.2 was lower than both Delta and Omicron BA.1 variants and this phenomenon might be interpreted by insufficient sample size for Delta and Omicron BA.1 outbreaks. Secondly, the CT value in different outbreaks showed no statistical difference might be owing to detection reagents from different companies used in outbreaks. On account of various detection reagents from different companies might have different detection result, CT value should be analyzed with in various detection reagents while these CT value we had could not be distinguished by their detection reagents. The result of analysis of CT value might be affected by different detection reagents. Thirdly, we just used the proportion of asymptomatic cases to compare the pathogenicity of three variants, which might be improved in further research. Fourthly, for such parameters, incubation period and serial interval, we were unable to consider the proportion of secondary transmission that occurred before symptom onset and compare these parameters in different age groups and gender groups, owing to the limitation of the accessibility of data and the small sample size.

Conclusion

The transmissibility of the three strains was Omicron BA.2>Omicron BA.1>Delta. Compared with the Delta variant, the transmissibility of Omicron BA.1 increased by 33.64%. The diminishing serial interval from the three variants suggests that the transmissibility and spread speed of the three strains was Omicron BA.2>Omicron BA.1>Delta. Omicron variants caused less symptomatic infections may indicate that the Omicron BA.2 variant might be weaker than Omicron BA.1 and Delta in pathogenicity. Therefore, Omicron BA.2 might be harder to control and prevent compared with Delta and Omicron BA.1 variants.

List of abbreviations

Corona Virus Disease 2019, (COVID-19), Variants of concern, (VOCs), Time-dependent reproduction number (R_t), PCR (Reverse transcription-polymerase chain reaction, RT-PCR), Cycle threshold(CT), Public health and social measures (PHSM), The National Infectious Diseases Information Reporting Management System (IDIRMS)

Declarations

Ethics approval and consent to participate

This work was done in support of ongoing public health response and hence was determined not to be human subjects research after consultation with the School of Public Health institutional review board at Xiamen University. Data collection is part of the continuing public health investigation of an emerging outbreak and therefore the individual informed consent was waived. The study was approved by the ethics committees of Shenzhen Center for Disease Control and Prevention. Analytical datasets were constructed in an anonymised manner, and all analyses of personally identifiable data took place onsite at the Shenzhen Center for Disease Control and Prevention. Therefore, no human subjects were involved in this work and therefore ethical approvals might be not required for the development of this manuscript.

Consent for publication

Not applicable.

Availability of data and materials

The data that support the findings of this study are available from Shenzhen Centre for Disease Control and Prevention but restrictions apply to the availability of these data, which were used under license for the current study, and so are not publicly available. However, data are available from the

authors upon reasonable request and with the permission of Dr. Lu (Email: 25430557@qq.com).

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

XZ and TC designed this study. SF and JL collected all required data. CL, TC, and JL contributed to the conception of the study. CL, PL, YG, and KG analyzed data and draw tables. CL and PL calculated the transmissibility of each outbreak, BZ and YS draw all figures and CL and JL were major contributors to write the manuscript. JL was contributed significantly to analysis and manuscript preparation. XZ, and TC helped perform the analysis with constructive discussions. YM and CL provided language help. All authors read and approved the final manuscript.

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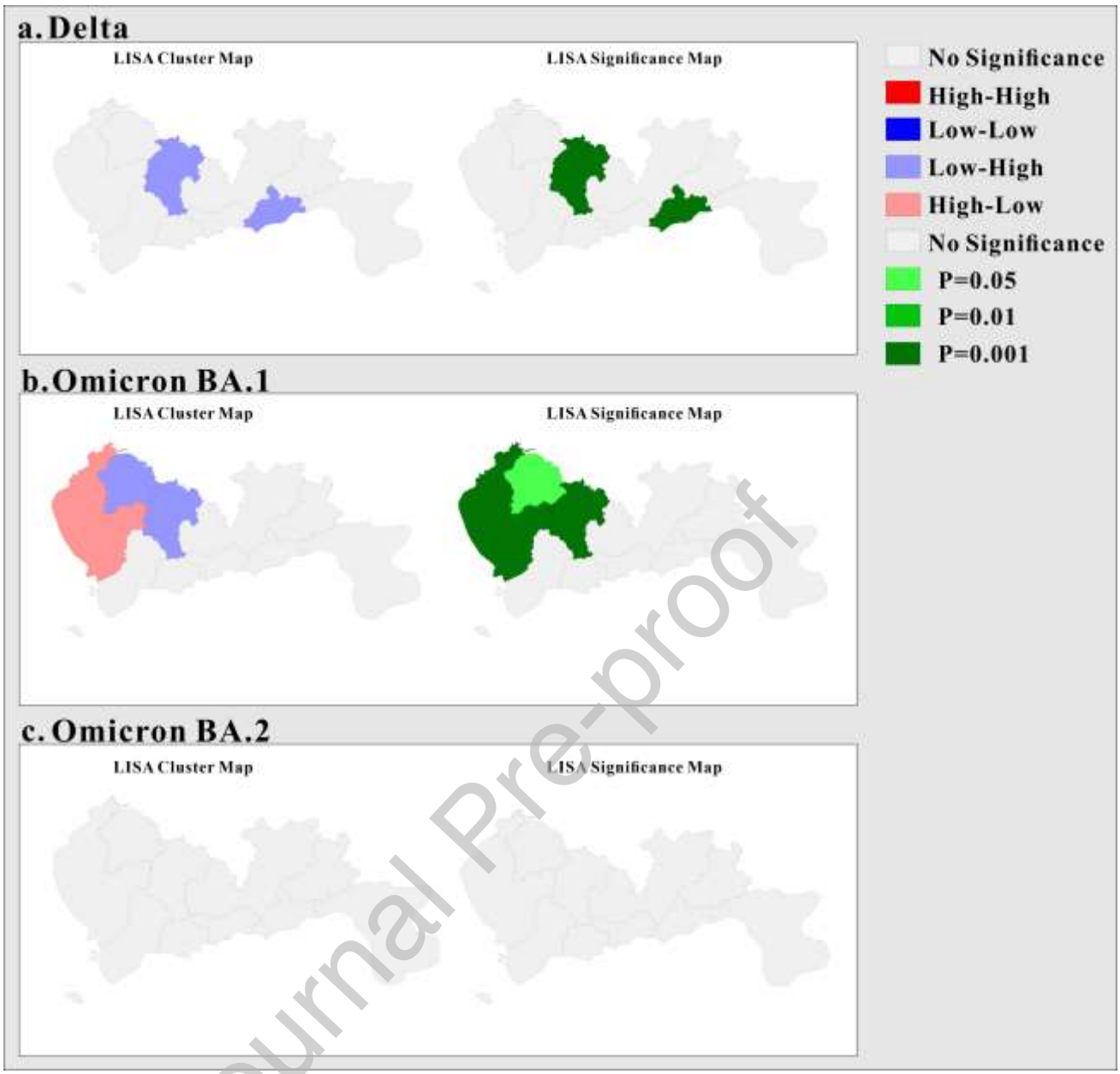
Figure Legend

Figure.1 The local spatial autocorrelation result from three outbreaks (a. Delta outbreak, b. Omicron BA.1 outbreak, c. Omicron BA.2 outbreak)

Figure 2. Serial intervals and the variation tendency in Time-dependent reproduction number of three outbreaks (a. Serial intervals, b. the variation tendency in Time-dependent reproduction number)



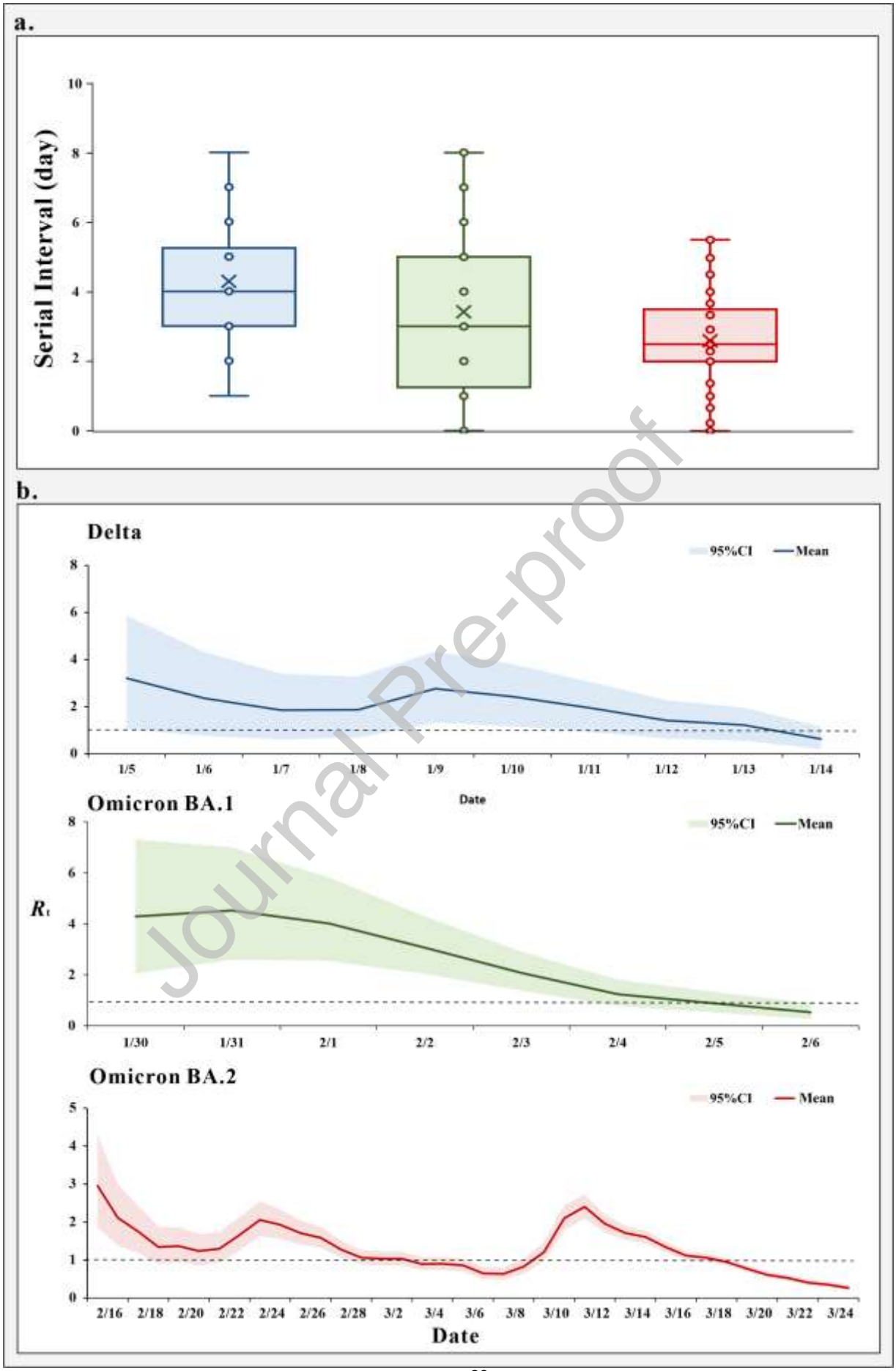


Table1. Epidemiological characteristics of three outbreaks in Shenzhen city

	Delta	Omicron BA.1	Omicron BA.2	P-value	Statistic
Age group				0.811	H=0.42
0~9	1	1	110		
10~19	0	1	77		
20~29	6	6	193		
30~39	2	3	255		
40~49	4	9	193		
50~59	1	1	159		
60~69	0	1	50		
70~	2	1	27		
Gender				0.200	χ^2=3.36
Male	5	11	562		
Female	11	12	502		
District	*	*		<0.001	χ^2=252.94
Futian	0	0	622		
Nanshan	0	0	160		
Luohu	9	0	65		
Baoan	0	22	136		

Longgang	7		1	49	
Longhua	0		0	22	
Yantian	0		0	5	
Dapeng	0		0	1	
Pingshan	0		0	0	
Guangming	0		0	4	
Occupation				0.887	χ^2=11.43
Cadre or clerk	5		5	207	
Worker	3		6	144	
Household	3		3	157	
Teacher	0		0	12	
Retiree	0		2	58	
Other	0		0	47	
Scatter Children	1		0	43	
Business service	4		5	249	
Unknown	0		0	4	
Student	0		2	131	
Medical service	0		0	12	
Clinical Type		* **	* *	<0.001	χ^2=244.15
Normal	2		10	12	

Light	13	12	821		
Asymptomatic	1	1	231		
Vaccination Dose				0.258	H=2.71
0	2	2	120		
1	1	1	25		
2	9	8	427		
3	4	12	492		
CT Value				0.275	χ^2=2.58
<25	9	9	392		
>=25	7	14	672		
Average of CT Value	26.00	28.43	27.32	0.647	F=0.44

Table 2. The analysis of Cycle threshold (CT) Value in three outbreaks in Shenzhen city

	Delta outbreak				Omicron BA.1 outbreak				Omicron BA.2 outbreak			
	CT value <25	**CT value ≥25**	**Statistics**	**P value**	**CT value <25**	**CT value ≥25**	**Statistics**	**P value**	**CT value <25**	**CT value ≥25**	**Statistics**	**P value**
Gender			Fisher	0.308			Fisher	1			$\chi2$= 5.885	<0.05
Male	4	1			4	7			188	374		
Female	5	6			5	7			204	298		
Age group			Fisher	0.693			Fisher	0.690			$\chi2$= 13.62	0.058
0~9	1	0			0	1			35	75		
10~19	0	0			1	0			28	49		
20~29	4	2			2	4			64	129		
30~39	1	1			2	1			102	153		
40~49	2	2			3	6			60	133		
50~59	1	0			1	0			75	84		
60~69	0	0			0	1			19	31		

70~	0	2		0	1		9	18		
Occupation		Fisher	0.811		Fisher	0.433			$\chi2$= 7.36	0.697
Cadre or clerk	2	3		3	2		71	136		
Worker	2	1		3	3		54	90		
Household	1	2		1	2		64	93		
Teacher	0	0					3	9		
Retiree	0	0		1	1		18	40		
Other	0	0					19	28		
Scatter Children	1	0					15	28		
Business service	3	1		0	5		97	152		
Unknown	0	0					1	3		
Student	0	0		1	1		43	88		
Medical service	0	0					7	5		
Clinical		Fisher	1		Fisher	0.5			$\chi2$=	<0.

Type			er			er	08		6.99	05
Normal	6	6		4	6		5	7		
Light	2	1		4	8		319	502	*	
Asymptomatic	1	0		1	0		68	163	*	
Pathogenicity			1			Fisher	0.319		χ^2= 6.95	<0.01
Symptomatic	8	7		8	14		324	509	*	
Asymptomatic	0	1		1	0		68	163	*	
Vaccination dose			Fisher 1			Fisher 1			χ^2= 1.641	0.651
0	1	1		1	1		45	75		
1	0	1		0	1		8	17		
2	5	4		3	5		149	278		
3	3	1		5	7		190	302		

* The difference was statistically significant.

Table 3. The analysis of Pathogenicity in three outbreaks in Shenzhen city

	Delta				Omicron BA.1				Omicron BA.2			
	Symptomatic	Asymptomatic	Statistics	P Value	Symptomatic	Asymptomatic	Statistics	P Value	Symptomatic	Asymptomatic	Statistics	P Value
Gender			Fisher	1			Fisher	0.478			χ^2= 1.421	0.234
Male	5	0			4	7			432	130		
Female	10	1			5	7			401	101		
Age group			Fisher	0.438			Fisher				χ^2= 27.41	<0.001
0~9	1	0			0	0			77	33	*	
10~19	0	0			1	0			60	17		
20~29	5	1			2	0			173	20	*	
30~39	2	0			2	0			205	50		
40~49	4	0			3	1			141	52		
50~59	1	0			1	0			120	39		

60~69	0	0		0	0		40	10	
70~	2	0		0	0		17	10	
								χ^2=	
Occupation		Fisher	0.438		Fisher	1		13.31	0.182
Cadre or clerk	5			5	0		169	38	
Worker	3			5	1		105	39	
Household	2	1		3	0		121	36	
Teacher				0	0		10	2	
Retiree				2	0		45	13	
Other				0	0		42	5	
Scatter Children	1			0	0		34	9	
Business service	4			5	0		200	49	
Unknown	0			0	0		3	1	
Student	0			2	0		93	38	
Medical service	0			0	0		11	1	

CT			Fish			Fish	0.3		χ^2=	<0.
Value			er	1		er	918		6.95	01
<25	8	0		8	1		324	68	*	
>=25	7	1		14	0		509	163	*	
Vaccina										
tion			Fish	0.4		Fish			χ^2=	0.6
dose			er	37		er	1		1.49	85
0	2	0		2	0		89	31		
1	1	0		1	0		19	6		
2	9	0		8	0		336	91		
3	3	1		11	1		389	103		

* The difference was statistically significant.

Declaration of interests

☒ 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.

☐The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: