# Transmission dynamics of SARS-CoV-2 Omicron variant infections in Hangzhou, Zhejiang, China, January to February 2022

Hualei Xin , Zhe Wang , Shuang Feng , Zhou Sun , Lele Yu , Benjamin J Cowling , Qingxin Kong , Peng Wu

PII: S1201-9712(22)00571-9
DOI: https://doi.org/10.1016/j.ijid.2022.10.033
Reference: IJID 6470

To appear in: *International Journal of Infectious Diseases*

Received date: 5 July 2022
Revised date: 22 September 2022
Accepted date: 23 October 2022

Please cite this article as: Hualei Xin , Zhe Wang , Shuang Feng , Zhou Sun , Lele Yu , Benjamin J Cowling , Qingxin Kong , Peng Wu , Transmission dynamics of SARS-CoV-2 Omicron variant infections in Hangzhou, Zhejiang, China, January to February 2022, *International Journal of Infectious Diseases* (2022), doi: https://doi.org/10.1016/j.ijid.2022.10.033

# Transmission dynamics of SARS-CoV-2 Omicron variant infections in Hangzhou, Zhejiang, China, January to February 2022

Hualei Xin[2*], Zhe Wang[1*], Shuang Feng[1], Zhou Sun[1], Lele Yu[4], Benjamin J Cowling[2,3], Qingxin Kong[1**], Peng Wu[2,3**]

1. Hangzhou Center for Disease Control and Prevention, Hangzhou, Zhejiang, China

2. WHO Collaborating Centre for Infectious Disease Epidemiology and Control, School of Public Health, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong Special Administrative Region, China

3. Laboratory of Data Discovery for Health Limited, Hong Kong Science Park, New Territories, Hong Kong Special Administrative Region, China

4. Xixi Hospital of Hangzhou, Hangzhou, Zhejiang, China

* These authors contributed equally to this article and share first authorship.

** These authors contributed equally as senior authors.

**Correspondence:** Qingxin Kong (kqx79@sina.com)

**Alternate correspondence:** Benjamin J Cowling (bcowling@hku.hk)

**Running head:** Transmission dynamics of Omicron

**Word count (abstract):** 192

**Word count (main text):** 2,367

## Abstract

**Objectives:** We aimed to explore the transmission dynamics of the Omicron BA.1.1 variant in an outbreak in China.

**Methods:** We constructed 113 transmission pairs based on the time of exposure and symptom onset for identified infectors and infectees, using the epidemiological data collected during an outbreak in Hangzhou, Zhejiang province, China, between January and February 2022. Key epidemiological parameters were estimated.

**Results:** The mean estimates of the incubation period and latent period distributions were 3.8 days (95% credible interval: 3.5, 4.1) and 3.1 days (2.8, 3.5), respectively. The overall transmission risk peaked at symptom onset, and we estimated that 33.6% (24.8, 42.5) of transmission occurred before symptom onset. The forward generation time decreased from 5.2 days (4.7, 5.7) at the start of the outbreak to 2.2 days (2.0, 2.5) by the end. Allowing for this variation over time in the generation time distribution, we estimated the $R_t$ dropped rapidly from 9.5 (3.5, 18.4) to 0.8 (0.3, 1.5) over the outbreak.

**Conclusions:** Shorter incubation period and latent period were estimated for the Omicron BA.1.1 variant. Stringent public health measures prevented a large epidemic by reducing transmission as indicated by the shortened generation time.



**Keywords:** SARS-CoV-2; China; Omicron; Transmission

## Introduction

From the end of 2020, multiple variants of concern (VOC) have emerged during the COVID-19 pandemic. Most recently, the Omicron variant has become dominant worldwide over other strains, with a potential of emergence of other new variants or subvariants in the future. Omicron variants have demonstrated increasing transmissibility and therefore are more challenging to control (Kraemer et al., 2021, WHO., 2022). In general, increased transmissibility for a variant indicates an increased transmission strength or a higher transmission speed, or both. The transmission strength refers to the intrinsic transmission ability of a variant, potentially measured by the reproduction number, while the transmission speed can be measured by the exponential growth rate (Hart et al., 2022). Time-delay parameters, i.e., generation time and serial interval, can determine the relationship between a variant's strength and speed of transmission (Hart et al., 2022). Accurate estimation of disease parameters, i.e., incubation period, latent period, infectiousness profile, generation time, and serial interval, allow us to assess the role and effectiveness of control measures like mass testing, isolation and contact tracing on transmission (Kraemer et al., 2021, Park et al., 2021). Some studies of the Omicron variant suggested that it has a shorter incubation period, generation time, and serial interval than previous variants (Backer et al., 2022, Mefsin et al., 2022).

Between 19 January 2022 and 4 February 2022, an COVID-19 outbreak occurred in Hangzhou, Zhejiang province, China. The epidemiological investigation showed that all cases identified in this outbreak could be traced back to an index case, and the gene sequence analysis revealed that all patients were infected with the Omicron variant sublineage of BA.1.1 (or Nextstrain clade 21K). Active case-finding strategies such as daily district-range mass PCR and routine PCR

testing among close contacts were implemented to identify all cases in this outbreak. Cases found were isolated, and detailed epidemiological information was collected, including infection source, exposure time, dates, and results of each time PCR testing, et al. In this study, we investigated the transmission dynamics of the Omicron outbreak.

## Methods

### *Data collection*

We retrospectively collected information on all RT-PCR confirmed COVID-19 cases infected with the Omicron variant (BA.1.1) from the outbreak between 23 January 2022 and 4 February 2022 in Hangzhou, Zhejiang province, China. Demographic information including sex, age, and occupation was collected. Other data such as underlying conditions, severity status, and vaccination status, were also collected. Patients' severity status was categorized as asymptomatic, mild, moderate, severe, and critical (**Supplementary materials**). Vaccination status including vaccine brand and type, dose of vaccination, date of the last dose, was collected for each case. Cases were defined as receiving incomplete vaccination series, complete primary vaccination series, or booster vaccination series if they received one, two or three doses of an inactivated vaccine (BIBP COVID-19, Sinopharm, Beijing, China, or CoronaVac, Sinovac Biotech Ltd, Beijing, China) 14 days or longer before the first day of exposure to an infector, respectively.

To estimate the incubation period distribution (time duration between infection and presenting symptoms), we collected information for each infectee on the first date of exposure (lower bound of infection date) and the last date of exposure (upper bound of infection date) to an infector

along with the date of symptoms onset. The latent period describes the interval from infection to becoming infectious and was measured as the interval between exposure to an infector and the first positive PCR test in this study. The dates of the last negative PCR test (lower bound of the possible start of viral shedding) and first positive PCR test (upper bound of the possible start of viral shedding) were used to inform the start time of viral shedding.

We constructed transmission pairs based on infectors and infectees identified from contact tracing with an available infection time window and symptom onset dates. The generation time distribution (interval of infections between two successive cases in a transmission chain), serial interval distribution (interval of symptoms onset between two successive cases in a transmission chain), and infectiousness profile (transmission risk during the infectious period relative to the symptoms onset of infectors) were estimated based on these transmission pairs. (**Supplementary materials**)

***Statistical analysis***

We estimated the incubation period and latent period distribution in a Bayesian framework. Gamma, lognormal and Weibull distributions were fitted separately, and non-negative flat prior probability distributions were specified for the studied parameters for the three assumed distributions. The distribution with the lowest leave-one-out information criterion (LOO IC) was selected as the final model. Interval censoring of the infection window and viral shedding window were accounted for in estimation of the incubation period and the latent period.

We obtained the infection time for each infectee including some infectors who were also identified as an infectee in the transmission chain based on the estimated incubation period and latent period in every iteration in the model (Supplementary materials). The generation time distribution was then estimated by calculating the time interval between the infection time of infectors and infectees using all iterations in the model. The serial interval distribution was estimated using the time of symptoms onset of infectors and infectees. Since the distribution of generation time and serial interval could change over time during an outbreak, we estimated the time-varying forward distributions of the generation time and serial interval using a series of running time windows with a fixed time window of 4 days (**Supplementary materials**). Using the time-varying mean and standard deviation of the forward generation time and the daily incident case information, we estimated the daily instantaneous reproduction number ($R_t$) by applying the statistical methods used in the EpiEstim package (Cori et al., 2013) (**Supplementary materials**).

We estimated the infectiousness profile for Omicron infections in this outbreak based on individual time intervals between the infection time of the infectee and the symptom onset of the infector from all transmission pairs. The daily cumulative proportions of transmission were estimated in relation to the date of symptom onset of the infector, including the proportion of pre-symptomatic transmission.

Parameters and their uncertainties were estimated from posterior distributions using the *rstan* package in R software (R Foundation for Statistical Computing, Vienna, Austria).

## Results

### *The outbreak*

As of 4 February 2022, in total 114 cases infected with the Omicron variant (BA.1.1) were reported in the outbreak in Hangzhou (Figure 1A), with cases numbers increasing from 19 January 2020, peaking on 31 January 2022, and declining rapidly thereafter. One half (45.6%) of the cases were male. The median age was 33.0 years (Interquartile range [IQR]: 25.3, 48.8), with 91 cases (79.8%) aged between 15-64 years. Seventeen cases (14.9%) had underlying conditions before infection with COVID-19. The majority of the cases showed mild symptoms (107, 93.9%), and the remaining were moderate infections (7, 6.1%). There were 4 (3.5%), 70 (61.4%), and 22 (19.3%) cases with incomplete vaccination series, complete primary vaccination series, and booster vaccination series, respectively. Among the 92 cases with complete primary or booster vaccination series, 27 (29.3%) had their first exposure to a confirmed case occurred within 90 days after the last vaccination dose, and 65 (70.7%) beyond 90 days.

### *Parameter estimation*

Information on infection, symptoms onset, and laboratory testing were available for all 114 cases for estimation of the incubation period and the latent period. Using the gamma distribution, we estimated the mean incubation period was 3.8 days (95% credible interval [95% CrI]: 3.5, 4.1), with 95% of the cases developing symptoms within 6.2 days (5.7, 6.9) after exposure (Figure S1A, Table S1). Cumulative frequency distribution showed that 98.0% (95.5, 99.3) of cases had symptom onset within 7 days, and 100.0% (99.8, 100.0) within 10 days after exposure (Table S2). The mean latent period was estimated to be 3.1 days (2.8, 3.5), with the 95$^{th}$ percentile of

5.9 days (5.3, 6.8) (Figure S1B, Table S1). There were 98.2% (95.7, 99.4) and 99.9% (99.6, 100.0) of the cases start shedding virus within 7 days and 10 days, respectively (Table S2).

We constructed 113 transmission pairs with infection and symptoms onset information for both infectors and infectees (Figure S2), with 46 (40.7%), 47 (41.6%), and 20 (17.7%) pairs identified in households, workplace, and public areas, respectively. The mean estimates of the time-varying forward generation time were gradually dropped from 5.2 days (4.7, 5.7) to 2.2 days (2.0, 2.5) over the study period (Figure 1B). The time-varying mean serial intervals decreased from 6.0 days (5.5, 6.5) between 19 January 2022 and 22 January 2022 to 1.7 days (1.3, 2.0) between 28 January 2022 and 31 January 2022 (Figure 1B). The estimated $R_t$ declined rapidly from 9.5 (3.5, 18.4) on 22 January 2022 to 0.8 (0.3, 1.5) on 4 February 2022 (Figure 1C). We estimated that 4.4% (0.9, 8.0) of the transmissions occurred $\geq$ 4 days before symptom onset of infectors, 33.6% (24.8, 42.5) of the transmission occurred before symptoms onset, with the transmission risk peaking at onset, and all of the observed transmission events occurring within five days following infectors' symptoms onset (Figure 1D).

**Discussion**

In this study, we retrospectively collected detailed information on laboratory-confirmed COVID-19 cases infected with Omicron variant with the lineage of BA.1.1. The characterized transmission pairs allowed us to estimate the transmission parameters of this variant. We showed that compared with the Delta variant of SARS-CoV-2, the Omicron variant had a shorter incubation period and latent period.

We estimated that the mean incubation period for the Omicron variant was 3.8 days (95% CrI: 3.5, 4.1), similar to the previously reported 3.5 days in Italy (Manica et al., 2022), but was almost two days shorter than the Delta variant (Kang et al., 2022). Along with the infectiousness peak at the day of symptom onset, a quicker coverage of outbreak control measures needs to be facilitated to suppress transmission. In the outbreak we studied, interventions including district-range lockdown and daily screening using PCR testing were implemented immediately after identifying the index case; all cases found were treated and isolated in the designated hospital, and close contacts were quarantined in hotels. The measures implemented were proven effective, with the $R_t$ decreasing rapidly from 9.5 to 0.8 within 14 days.

Previous studies suggested that the faster epidemic growth identified for the Omicron variant was attributed to three epidemiological factors: immune evasion, higher intrinsic transmission potential (measured by reproduction number), and a shorter serial interval or generation time (Backer et al., 2022, Mefsin et al., 2022). Our analysis of a small outbreak in Hangzhou showed the instantaneous reproduction number for the Omicron outbreak was 9.5 in the early stage of the outbreak and dropped to 0.8 at the end of the outbreak, no obvious increasing was identified compared to the values in a Delta outbreak (Kang et al., 2022). Although the sample size was limited our study, we could still conclude that higher intrinsic transmissibility of the Omicron variant may not be the only driver of the fast spread of Omicron.

We found the proportion of pre-symptomatic transmission was 33.6%, lower than the proportions identified for the ancestral strain (Ren et al., 2021). As shown in our study, the time difference between the mean estimate of the latent period (3.1 days) and incubation period (3.8

days) was only 0.7 days, significantly shorter than the time difference among wild-type of SARS-CoV-2 (1.4 days) (Xin et al., 2022) and the Delta variant (1.9 days) (Kang et al., 2022). Therefore, a short infectious period before symptom onset might exist for the Omicron infections, limiting the potential for pre-symptomatic transmission compared to earlier strains with longer incubation periods.

The decreasing trend of time-varying generation time and serial interval identified in this study was likely caused by earlier isolation of cases as the epidemic progressed, which reduced the later effective infectious period of SARS-CoV-2-infected individuals by preventing contacts with susceptible individuals later in the infectious period. An overall shorter generation time than the serial interval identified in this study indicated that the incubation period was shorter among infectors than infectees in the transmission pairs. When estimating the time-varying forward generation time and serial interval (as in our study), the forward-looking incubation period of infectees should remain constant throughout an epidemic; however, the backward-looking incubation period of infectors tends to be shorter in the increasing phase of an outbreak and longer in the decreasing phase of an epidemic (Park et al., 2021). This is because the difference between forward generation time and the serial interval is the difference between incubation period of infectors and infectee (Park et al., 2021), that leads to a shorter and longer generation time than serial interval in the increasing phase of the epidemic and decreasing phase of the epidemic, respectively. This explains the difference between time-varying generation time and serial interval shown in figure 1B. The generation time was shorter than the serial interval in the first nine running time windows, then reversed in the last one running time windows. The more

extended period of the increasing epidemic phase than the decreasing phase identified in the epidemic curve leads to an overall shorter generation time than the serial interval.

Some limitations exist in this study. First, the sample size was relatively small, decreasing the precision of the estimated parameters. Second, we used the time interval between infection and the first time of the positive PCR test (Ct < 40) as a proxy for estimation of the latent period. However, there is possibility that transmission would not occur until the viral load of the case reached a certain level. Thus, our approach might underestimate the latent period. Third, we did not consider the impact of vaccination on the transmission dynamics of the Omicron outbreak. Future studies are needed to explore the relationship between vaccination and risk of transmission. In addition, all individuals used to estimate the generation time and serial interval were symptomatic, which might result in an underestimation of the parameters because symptomatic cases tend to be isolated or self-isolated quicker than asymptomatic cases. Finally, the use of household transmission pairs might underestimate the generation time and serial interval given the possibility of multi-introduction of infection into the household.

In conclusion, our study revealed a shorter incubation period and latent period time for Omicron BA.1.1 infections compared with earlier variants of concern. Enhanced capacity in rapid testing, contact tracing, isolation of cases and quarantine of close contacts is needed to interrupt chains of transmission.

## Conflicts of interest

BJC consults for AstraZeneca, Fosun Pharma, GSK, Moderna, Pfizer, Roche and Sanofi Pasteur. The authors report no other potential conflicts of interest.

## Author contributions

QK, BC conceived the study. Data collection and cleaning were conducted by ZW, SF, ZS, LY. Data analyses were done by HX, ZW and PW. HX wrote the first draft of the manuscript. All authors critically reviewed and revised the manuscript and approved the final version.

## Funding

This project was supported by a commissioned grant under the Health and Medical Research Fund from the Food and Health Bureau of the Hong Kong SAR Government (grant no. CID-HKU2), AIR@InnoHK administered by Innovation and Technology Commission, and Health Technology Programme (project no. A20220843) of the Hangzhou Health Commission. BJC is supported by a RGC Senior Research Fellow Scheme grant (HKU SRFS2021-7S03) from the Research Grants Council of the Hong Kong Special Administrative Region, China.

## Ethical approval statement

This study was approved by the institutional ethics committee of the Hangzhou Center for Disease Control and Prevention (HZCDC).

## Acknowledgments

The authors thank Julie Au for technical support.

## References

Backer JA, Eggink D, Andeweg SP, Veldhuijzen IK, van Maarseveen N, Vermaas K, et al. Shorter serial intervals in SARS-CoV-2 cases with Omicron BA.1 variant compared with Delta variant, the Netherlands, 13 to 26 December 2021. Euro Surveill 2022;27:2200042.

Cori A, Ferguson NM, Fraser C, Cauchemez S. A new framework and software to estimate time-varying reproduction numbers during epidemics. Am J Epidemiol 2013;178:1505-12.

Hart WS, Miller E, Andrews NJ, Waight P, Maini PK, Funk S, et al. Generation time of the alpha and delta SARS-CoV-2 variants: an epidemiological analysis. Lancet Infect Dis 2022;22:603-10.

Kang M, Xin H, Yuan J, Ali ST, Liang Z, Zhang J, et al. Transmission dynamics and epidemiological characteristics of SARS-CoV-2 Delta variant infections in Guangdong, China, May to June 2021. Euro Surveill 2022;27:2100815.

Kraemer MUG, Pybus OG, Fraser C, Cauchemez S, Rambaut A, Cowling BJ. Monitoring key epidemiological parameters of SARS-CoV-2 transmission. Nat Med 2021;27:1854-5.

Manica M, De Bellis A, Guzzetta G, Mancuso P, Vicentini M, Venturelli F, et al. Intrinsic generation time of the SARS-CoV-2 Omicron variant: An observational study of household transmission. Lancet Reg Health Eur 2022;19:100446.

Mefsin Y, Chen D, Bond HS, Lin Y, Cheung JK, Wong JY, et al. Epidemiology of infections with SARS-CoV-2 Omicron BA.2 variant in Hong Kong, January-March 2022. medRxiv 2022:2022.04.07.22273595.

Park SW, Sun K, Champredon D, Li M, Bolker BM, Earn DJD, et al. Forward-looking serial intervals correctly link epidemic growth to reproduction numbers. Proc Natl Acad Sci U S A 2021;118.

Ren X, Li Y, Yang X, Li Z, Cui J, Zhu A, et al. Evidence for pre-symptomatic transmission of coronavirus disease 2019 (COVID-19) in China. Influenza Other Respir Viruses 2021;15:19-26.

WHO. Enhancing response to Omicron SARS-CoV-2 variant.; 2022. Available from: https://www.who.int/publications/m/item/enhancing-readiness-for-omicron-(b.1.1.529)-technical-brief-and-priority-actions-for-member-states. [Accessed 17 April 2022].

Xin H, Li Y, Wu P, Li Z, Lau EHY, Qin Y, et al. Estimating the Latent Period of Coronavirus Disease 2019 (COVID-19). Clin Infect Dis 2022;74:1678-81.

**FIGURE LEGENDS**

**Figure 1. The forward estimates of generation time, serial intervals and instantaneous reproduction numbers, and cumulative distribution of infectiousness profile during the SARS-CoV-2 Omicron outbreak in Hangzhou, Zhejiang, China, January–February 2022.** **A)** Epidemic curve based on symptom onset dates of all cases in the Omicron outbreak in Hangzhou. **B)** Estimated time-varying forward mean estimates of the generation time and serial interval for a series of running time windows with fixed lengths of 7 days. The horizontal axis represents the last date for each time window. Points (generation time) and triangles (serial interval) represent the point estimates. Vertical error bars represent the 95% credible intervals (95% CrI). **C)** Daily estimates of $R_t$ by using the time-varying forward mean and standard deviation of generation time and daily case incidence data. The red solid line and pink area represents the point estimates and 95% CrI, respectively. The dashed line represents $R_t = 1$. **D)** Cumulative frequency distribution of the infectiousness profile (transmission risk) relative to symptom onset of infectors. Points represent the point estimates. Vertical error bars represent the 95% CrI.