

viruses from 2022 had doubled ($\chi^2 = 55.3$; $p < 0.0001$) (Appendix Figure). Those considerable changes in substitutions most likely reflect the editing activity of the human APOBEC3G enzyme (apolipoprotein B mRNA editing enzyme, catalytic subunit 3G), which catalyzes strand-specific C>U deamination, resulting in G>A substitutions in the complementary strand of viral genomes (A. O'Toole, unpub. data, <https://virological.org/t/initial-observations-about-putative-apobec3-deaminase-editing-driving-short-term-evolution-of-mpxv-since-2017/830>; [9]).

In conclusion, our analyses of MPXV genome sequences indicate that the virus has been circulating silently and undetected for about 2 decades, probably in multiple non-MPXV-endemic countries outside of Africa. Also, a clear genomic signature of a recent change in hosts is evidenced by major changes in its nucleotide substitution pattern. Our observations have major public health implications; the changing epidemiology of MPXV infections and human circulation of the virus in non-MPXV-endemic countries call for increased surveillance (1). The public health crisis caused by the COVID-19 pandemic may have favored the spread of MPXV under the radar in the past few years; however, the existence of asymptomatic carriers cannot be ruled out and may have contributed to the undetected spread of MPXV.

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References

- Bunge EM, Hoet B, Chen L, Lienert F, Weidenthaler H, Baer LR, et al. The changing epidemiology of human monkeypox – a potential threat? A systematic review. *PLoS Negl Trop Dis*. 2022;16:e0010141. <https://doi.org/10.1371/journal.pntd.0010141>
- Antinori A, Mazzotta V, Vita S, Carletti F, Tacconi D, Lapini LE, et al.; INMI Monkeypox Group. Epidemiological, clinical and virological characteristics of four cases of monkeypox support transmission through sexual contact, Italy, May 2022. *Euro Surveill*. 2022;27:2200421. <https://doi.org/10.2807/1560-7917.ES.2022.27.22.2200421>
- Isidro J, Borges V, Pinto M, Sobral D, Santos JD, Nunes A, et al. Phylogenomic characterization and signs of microevolution in the 2022 multi-country outbreak of monkeypox virus. *Nat Med*. 2022;28:1569–72. <https://doi.org/10.1038/s41591-022-01907-y>
- Saxena SK, Ansari S, Maurya VK, Kumar S, Jain A, Paweska JT, et al. Re-emerging human monkeypox: a major public-health debacle. *J Med Virol*. 2022;95:e27902. <https://doi.org/10.1002/jmv.27902>
- Gigante CM, Korber B, Seabolt MH, Wilkins K, Davidson W, Rao AK, et al. Multiple lineages of monkeypox virus detected in the United States, 2021–2022. *Science*. 2022;378:560–5. <https://doi.org/10.1126/science.add4153> PMID: 36264825
- Alakunle E, Moens U, Nchinda G, Okeke MI. Monkeypox virus in Nigeria: infection biology, epidemiology, and evolution. *Viruses*. 2020;12:1257. <https://doi.org/10.3390/v12111257>
- Shackelton LA, Parrish CR, Holmes EC. Evolutionary basis of codon usage and nucleotide composition bias in vertebrate DNA viruses. *J Mol Evol*. 2006;62:551–63. <https://doi.org/10.1007/s00239-005-0221-1>
- Bailey SF, Alonso Morales LA, Kassen R. Effects of synonymous mutations beyond codon bias: the evidence for adaptive synonymous substitutions from microbial evolution experiments. *Genome Biol Evol*. 2021;13:evab141. <https://doi.org/10.1093/gbe/evab141>
- Yu Q, König R, Pillai S, Chiles K, Kearney M, Palmer S, et al. Single-strand specificity of APOBEC3G accounts for minus-strand deamination of the HIV genome. *Nat Struct Mol Biol*. 2004;11:435–42. <https://doi.org/10.1038/nsmb758>

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Epidemiology of SARS-CoV-2 Omicron BA.5 Infections, Macau, June–July 2022

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A SARS-CoV-2 Omicron BA.5 outbreak occurred in Macau from mid-June through July 2022. Out of >1,800 laboratory-confirmed cases, most were mild or asymptomatic; only 6 deaths were recorded. The outbreak was controlled through stringent public health and social measures, such as repeated universal testing and a stay-at-home order lasting 2 weeks.

The SARS-CoV-2 Omicron subvariant BA.5 has spread rapidly worldwide. A recent outbreak of BA.5 occurred in Macau during June 18–July 31, 2022. The outbreak resulted in 1,821 confirmed cases and 6 deaths but was promptly controlled. We describe the basic epidemiology of this outbreak.

Macau, a special administrative region of China with 683,000 persons, has been applying intensive public health and social measures to reduce SARS-CoV-2 variant importation and prevent community outbreaks as part of China’s dynamic zero COVID strategy. In Macau, this strategy has included stringent travel restrictions and up to 28-day on-arrival quarantines (1) to avoid infections within communities. As in China, all SARS-CoV-2-infected persons are strictly isolated in special facilities, and contact tracing expedites timely quarantine of close contacts outside the home. Throughout the pandemic before June 2022, only 17 domestic confirmed cases (2.5

cases/100,000 population) and no deaths were reported in Macau. Since early 2021, inactivated virus (Sinopharm, <http://www.sinopharm.com>) and mRNA (Pfizer-BioNTech, <https://www.pfizer.com>) vaccines have been available in Macau. By June 19, 2022, vaccine coverage within the entire population was 85.6% for ≥2 doses and 40.5% for 3 doses.

In mid-June 2022, a SARS-CoV-2 Omicron BA.5 outbreak began in Macau (2). The first case was detected in a person with symptoms who sought treatment at a hospital on June 18, 2022. The source of infection remains unknown (3). Identification of a community outbreak prompted the government of Macau to impose a series of domestic public health and social measures to control local transmission (Appendix Table 1, <https://wwwnc.cdc.gov/EID/article/29/2/22-1243-App1.pdf>). Macau entered an immediate prevention state at 1:00 AM on June 19, 2022. Multiple rounds of universal PCR testing were

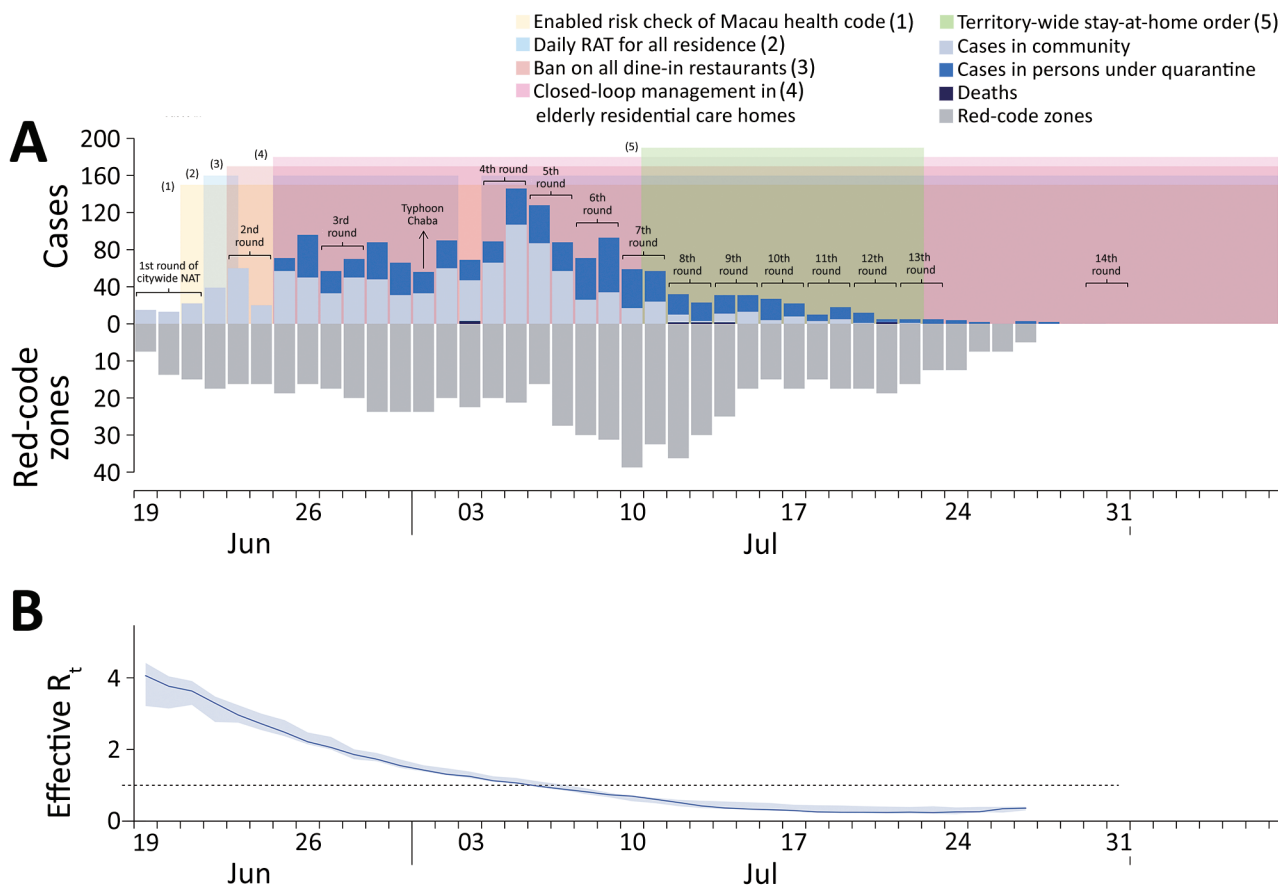


Figure. Number of PCR-positive COVID-19 cases and time-varying reproductive number in study of epidemiology of SARS-CoV-2 Omicron BA.5 infections, Macau, June–July 2022. A) PCR-confirmed COVID-19 cases and deaths in Macau during June and July 2022. Light blue bars indicate daily numbers of COVID-19 cases confirmed by PCR in the community; dark blue bars indicate persons under quarantine; black bars indicate number of reported deaths. Gray bars under the x-axis indicate the number of real-time red-code zones (areas with movement restrictions in place) in Macau. Shaded areas indicate when public health and social measures (indicated by numbers 1–5) were implemented to control COVID-19 transmission. B) Estimates of time-varying R_t to quantify real-time transmissibility of SARS-CoV-2 Omicron BA.5 in Macau. Dotted line indicates R_t of 1. RAT, rapid antigen test; R_t , effective reproductive number

Table. Estimated incubation periods for SARS-CoV-2 Omicron BA.5 variant according to population percentiles using lognormal, gamma, or Weibull probability distributions in study of epidemiology of SARS-CoV-2 Omicron BA.5 infections, Macau, June–July 2022*

Percentile	Incubation, d (95% CI)		
	Lognormal	Gamma	Weibull
Mean	3.27 (3.07–3.45)	3.00 (2.83–3.16)	3.26 (3.07–3.40)
2.5th	1.46 (1.17–1.74)	1.87 (1.74–2.00)	1.10 (0.93–1.25)
5th	1.64 (1.37–1.90)	2.02 (1.89–2.16)	1.38 (1.20–1.52)
50th	3.04 (2.87–3.18)	2.95 (2.79–3.12)	3.23 (3.03–3.38)
95th	5.67 (4.97–6.67)	4.13 (3.94–4.33)	5.24 (4.74–5.52)
97.5th	6.39 (5.49–7.77)	4.39 (4.19–4.59)	5.61 (5.05–5.94)
99th	7.34 (6.16–9.29)	4.70 (4.49–4.91)	6.03 (5.40–6.44)
AIC value†	360.80	377.57	370.45

*Mean number of days was estimated after adjusting for exponential growth. AIC, Akaike information criterion.

†AIC values were calculated to compare the fit of each model.

scheduled; and 14 rounds of citywide PCR testing were conducted for all persons in Macau. To identify infected persons, PCR testing was performed on June 22 and 25 for specific groups that included persons with Myanmar passports and those who sought care at places visited by persons who had SARS-CoV-2-positive tests (4,5). On June 23, schools, entertainment venues, public dining, and other nonessential businesses were closed, and residents were encouraged to stay at home. Closed-loop management was implemented in residential care homes beginning on June 25. Beginning on June 27, all persons were asked to conduct daily rapid antigen tests and report test results to an online platform (Appendix Tables 1, 2). The government enabled the risk check function of the Macau health code and implemented a district-specific epidemic prevention plan. Yellow- and red-code zones with movement restrictions were announced daily. As the daily case numbers grew, the government issued static management instructions comparable to a complete stay-at-home order beginning after midnight on July 11 and lasting until midnight on July 23; essential workers were excluded.

Among 1,821 cases that included 937 female and 884 male persons (3 months to 100 years of age), a total of 1,116 were classified as asymptomatic. The daily number of new positive cases peaked on July 5, 2022, at 146 PCR-positive cases (Figure 1, panel A). We estimated the time-varying reproductive number (Figure 1, panel B) to quantify real-time transmissibility (Appendix). The estimated time-varying reproductive number was <1 after July 7, 2022. In the final (14th) round of universal PCR testing on July 30–31, SARS-CoV-2 RNA was not found in specimens from persons in the community, confirming that the outbreak was contained.

Using information on 500 case-patients with known exposure and symptom onset reported during the early outbreak phase, we estimated that the mean incubation period for Omicron BA.5 was 3.27 days (SD \pm 1.05 days), after adjusting for exponential

growth (6) (Table; Appendix Figure). The BA.5 incubation period was similar to 3.2 days for Omicron BA.1 (7) and 4.5 days for BA.2 (8) and shorter than that for other SARS-CoV-2 variants (9).

Among 572 PCR-confirmed cases reported by June 30, a total of 23 case-patients had received 1 SARS-CoV-2 vaccine dose, 216 had received 2 vaccine doses, 224 had received 3 vaccine doses, and 109 were unvaccinated (Appendix Table 3). Although only 10% of the population was unvaccinated, 19% of the SARS-CoV-2-infected persons were unvaccinated.

Among the 1,821 locally infected case-patients, 6 deaths occurred (Appendix Table 4). Therefore, the case-fatality risk for Omicron-infected persons in Macau was 0.33% (95% CI 0.13%–0.76%). Persons who died of COVID-19 were 86–100 (mean 92.5, SD \pm 5.0) years of age. Among the 6 case-patients who died, 3 had received 2 doses of vaccine, and the other 3 were unvaccinated.

A limitation of our study is that we could not separate the effects of each public health and social measure because they were implemented as a package. High compliance with those stringent measures during the outbreak might have maximized the effectiveness of the interventions (10), although those measures might not be easily applicable to other locations outside of China. In conclusion, our study indicates that SARS-CoV-2 outbreaks can be controlled through stringent public health and social measures, such as repeated universal PCR testing and stay-at-home orders lasting at least 2 weeks.

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References

1. Macao Government. Novel Coronavirus Response and Coordination Center of Macau. New epidemic prevention measures will be implemented from midnight on January 6. 2021 Dec 30 [cited 2022 Nov 14]. <https://www.gcs.gov.mo/detail/zh-hans/N21LdGxjb9?8>
2. Macao Government. Novel Coronavirus Response and Coordination Center of Macau. The virus in this outbreak is identified as Omicron BA.5. 2022 Jul 8 [cited 2022 Nov 14]. <https://www.gcs.gov.mo/detail/zh-hans/N22GHgyjUI?4>
3. Macao Government. Novel Coronavirus Response and Coordination Center of Macau. So far (20th) at 4 p.m., there have been 36 nucleic acid positive cases, and the two confirmed groups are related. 2022 Jun 20 [cited 2022 Nov 14]. <https://www.gcs.gov.mo/detail/zh-hant/N22FTpK7To?30>
4. Macao Government. Novel Coronavirus Response and Coordination Center of Macau. Novel Coronavirus Response and Coordination Centre announces nucleic acid testing arrangements in key areas and for key groups on June 22. 2022 June 22 [cited 2022 Nov 14]. <https://www.gcs.gov.mo/detail/en/N22FU62sfT>
5. Macao Government. Novel Coronavirus Response and Coordination Center of Macau. The Response and Coordination Centre announces the arrangements of the NAT for key areas tomorrow (25 June). 2022 June 25 [cited 2022 Nov 14]. <https://www.gcs.gov.mo/detail/en/N22FYNcgqW>
6. Verity R, Okell LC, Dorigatti I, Winskill P, Whittaker C, Imai N, et al. Estimates of the severity of coronavirus disease 2019: a model-based analysis. *Lancet Infect Dis.* 2020;20:669–77. [https://doi.org/10.1016/S1473-3099\(20\)30243-7](https://doi.org/10.1016/S1473-3099(20)30243-7)
7. 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. <https://doi.org/10.2807/1560-7917.ES.2022.27.6.2200042>
8. Mefsin YM, Chen D, Bond HS, Lin Y, Cheung JK, Wong JY, et al. Epidemiology of infections with SARS-CoV-2 Omicron BA.2 variant, Hong Kong, January–March 2022. *Emerg Infect Dis.* 2022;28:1856–8. <https://doi.org/10.3201/eid2809.220613>
9. Wu Y, Kang L, Guo Z, Liu J, Liu M, Liang W. Incubation period of COVID-19 caused by unique SARS-CoV-2 strains: a systematic review and meta-analysis. *JAMA Netw Open.* 2022;5:e2228008. PubMed <https://doi.org/10.1001/jamanetworkopen.2022.28008>
10. Zhou L, Wu Z, Li Z, Zhang Y, McGoogan JM, Li Q, et al. One hundred days of coronavirus disease 2019 prevention and control in China. *Clin Infect Dis.* 2021;72:332–9. <https://doi.org/10.1093/cid/ciaa725>

Serologic Evidence of *Orientia* Infection among Rural Population, Cauca Department, Colombia

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We assessed serum samples collected in Cauca Department, Colombia, from 486 persons for *Orientia* seroreactivity. Overall, 13.8% showed reactive IgG by indirect immunofluorescence antibody assay and ELISA. Of those samples, 30% (20/67) were confirmed to be positive by Western blot, showing ≥ 1 reactive band to *Orientia* 56-kD or 47-kD antigens.

Scrub typhus, caused by species in the genus *Orientia*, is a reemerging mite-borne rickettsiosis and a major cause of acute undifferentiated febrile illness (AUI) (1). Classically, scrub typhus was believed to be strictly endemic to the so-called tsutsugamushi triangle, which ranges from southeastern Siberia in the North to the Kamchatka Peninsula in the East, northern Australia in the South, and Pakistan in the West (1). However, scrub typhus outside the tsutsugamushi triangle was suggested 70 years ago because

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Appendix

Materials and Methods

Incubation Period Estimation

We obtained person-level data for the first 500 COVID-19 cases diagnosed in Macau during June 18–29, 2022 (<https://www.ssm.gov.mo/apps1/PreventCOVID-19/en.aspx#clg22916>). We used symptom keywords (feel unwell, fever, fatigue, sore throat, cough, stuffy nose, runny nose, diarrhea, headache, chills) to filter cases for onset date information. For each case, we assumed the following behaviors as possible exposure periods: having contact with persons with confirmed COVID-19, visiting red or yellow code zone(s), and dining outside of the home. If none of those high-risk behaviors were mentioned in the case report, we assumed that the person was infected during other lower-risk outdoor activities, such as shopping or walking, and the periods of lower-risk outdoor activities were treated as potential exposure periods. For each case, we recorded the start and end time of the exposure period. For cases with >1 possible exposure period, we processed each possible exposure time identically. Those data were considered as interval-censored data in the estimation.

We fitted lognormal, gamma, and Weibull parametric probability distribution models to the data to estimate incubation periods by using the maximum likelihood method (*1*). The best fitted model was determined by the smallest value of the Akaike information criterion. We derived estimates of means, SD, medians, and 95% percentiles for incubation period distribution from the models. We determined the corresponding 95% CIs for each estimate by using the parametric bootstrap method with 1,000 bootstrapped samples. In our calculations, we corrected sampling bias according to the computed exponential growth rate ($r = 0.18$) of the Omicron BA.5 variant by using data collected from the first 500 COVID-19 cases during June 18–29, 2022.

Estimate of Time-Varying Reproductive Number

Model details

We estimated the time-varying reproductive number (R_t) from real data as previously described (2). In brief, the R_t assumes that the distribution of infectiousness through time is independent of calendar time. Transmission is then modeled by using a Poisson process. The probability distribution $w(s)$ denotes the infectiousness profile since infection; therefore, the rate for infection at time step $t-s$ generates new infections in time step t that are equal to $R(t)w(s)$, where $R(t)$ is the instantaneous reproductive number at time t . The actual number of new local infection cases at time t was denoted as $Y(t)$; the infection incidence at time t has Poisson distribution with mean $R(t) \sum_{s=1}^t Y(t-s)w(s)$.

The true number of infection cases was unobserved because we only observed new local cases reported on day k [$Y(k)$]. To overcome this challenge, we used:

$$Y(t) \sim \text{Poisson} \left\{ R(t) \sum_{k=1}^{t-1} Y(k)w(t-k) \right\}$$

where $R(t)$ is the time-varying effective reproductive number at time t .

Likelihood function

We used the smoothing method as previously described (2), assuming that the transmissibility was constant over a time period $[t-\tau+1, t]$, where τ is the smoothing parameter. Hence, likelihood of infection incidence during this time period was:

$$P(Y(t), \dots, Y(t-\tau+1) | Y(1), \dots, Y(t-\tau)) = \prod_{s=t-\tau+1}^t \frac{(R^\tau(t)\phi(s))^{Y(s)} e^{-R^\tau(t)\phi(s)}}{Y(s)!}$$

where $\phi(s) = \sum_{k=1}^{s-1} Y(k)w(s-k)$. The total likelihood is the product of the individual likelihood at each time t in the observed data. The first $\tau-1$ days were excluded because of τ -day smoothing.

Prior Probability Distribution

We assumed the prior probability distribution for $R(t)$ was a gamma distribution (parameters 1, 5) (mean 5, SD ± 5).

Estimate of Model Parameters

We conducted our analysis in a Bayesian framework and used the Markov chain Monte Carlo method (3) to estimate model parameters. At each step k , we updated the model parameters θ by using the random walk Metropolis-Hastings algorithm (3). The step size of the proposal was adjusted to have an acceptance rate of 20%–30%.

Assumptions for Input Parameters

For incubation period distribution, we use the estimated distribution mean of 3.2 days. The empirical distribution of delay from disease onset to report was set as follows: 50% probability delayed by day 1, 40% by day 2, and 8% by day 3, then the remaining 2% probability was equally distributed over days 4–20. According to those distributions, we constructed the distribution for delay from initial infection to report by convoluting the incubation period distribution and empirical distribution of delay from onset to report. We then used a deconvolution approach (4) to obtain the epidemic curve by infection time, which was achieved by using the fit incidence function in the incidental package in R (The R Project for Statistical Computing, <https://www.r-project.org>).

The infectiousness since infection w_t was a convolution of incubation period and infectiousness relative to onset (allowed to be presymptomatic) according to viral shedding data with a shifted gamma distribution (mean 12.3 days, SD ± 8 days) (5); therefore, the shift parameter c was 12.3 days. Peak infectiousness was on day 0. We proposed an infectiousness profile $g_c(t_1 - t_{s1})$ that described the probability of a transmission event occurring at time t_1 after illness onset t_{s1} . We assumed a gamma distribution $g(t)$ with a time shift to determine the start of infectiousness c days before symptom onset; therefore, $g_c(t) = g(t + c)$ determined presymptomatic transmission. We analyzed the epidemic curve until July 31, 2022, and used $\tau = 7$ in our analysis to avoid unstable estimates for time-varying reproductive numbers.

Inference

After obtaining the epidemic curve by infection time, we used the Markov chain Monte Carlo approach (3) to estimate R_t . We accounted for the uncertainty of input parameters, including incubation period and infectiousness profile, to obtain the final estimates of R_t as follows. We used the bootstrap approach (6,7) to account for input parameter uncertainty and obtain final estimates of R_t . In each iteration, we used the deconvolution approach described

previously to reconstruct the epidemic curve by infection dates and estimate R_t . We determined the mean and 2.5% and 97.5% quantiles for those R_t estimates for each time point across the 200 bootstrap iterations.

References

1. Verity R, Okell LC, Dorigatti I, Winskill P, Whittaker C, Imai N, et al. Estimates of the severity of coronavirus disease 2019: a model-based analysis. *Lancet Infect Dis.* 2020;20:669–77. [PubMed https://doi.org/10.1016/S1473-3099\(20\)30243-7](https://doi.org/10.1016/S1473-3099(20)30243-7)
2. 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. [PubMed https://doi.org/10.1093/aje/kwt133](https://doi.org/10.1093/aje/kwt133)
3. Bennet JE, Berzuini C, Best NG, Buck C, Carlin BP, Clayton DG, et al. Markov chain Monte Carlo in Practice. In: Gilks WR, Richardson S, Spiegelhalter DJ, editors. London: Chapman & Hall; 1996. p. 1–512.
4. Miller AC, Hannah LA, Futoma J, Foti NJ, Fox EB, D'Amour A, et al. Statistical deconvolution for inference of infection time series. *Epidemiology.* 2022;33:470–9. [PubMed https://doi.org/10.1097/EDE.0000000000001495](https://doi.org/10.1097/EDE.0000000000001495)
5. He X, Lau EHY, Wu P, Deng X, Wang J, Hao X, et al. Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nat Med.* 2020;26:672–5. [PubMed https://doi.org/10.1038/s41591-020-0869-5](https://doi.org/10.1038/s41591-020-0869-5)
6. Salje H, Cummings DAT, Rodriguez-Barrquer I, Katzelnick LC, Lessler J, Klungthong C, et al. Reconstruction of antibody dynamics and infection histories to evaluate dengue risk. *Nature.* 2018;557:719–23. [PubMed https://doi.org/10.1038/s41586-018-0157-4](https://doi.org/10.1038/s41586-018-0157-4)
7. Tsang TK, Wu P, Lau EHY, Cowling BJ. Accounting for imported cases in estimating the time-varying reproductive number of coronavirus disease 2019 in Hong Kong. *J Infect Dis.* 2021;224:783–7. [PubMed https://doi.org/10.1093/infdis/jiab299](https://doi.org/10.1093/infdis/jiab299)

Appendix Table 1. Public health and social measures implemented during June–July 2022 in Macau in study of epidemiology of SARS-CoV-2 Omicron BA.5 infections*

Date	Type	Subtype	Measure	Date announced	Source
2022 Jun 15	Travel	Border control	Period of centralized medical observation in isolation for arrivals shortened to 10 d beginning at 0:00 AM on June 15	2022 Jun 10	https://www.gcs.gov.mo/detail/en/N22FK5iS6F?14
2022 Jun 19	Community	Quarantine	Zone-specific, multi-level focused approach to epidemic prevention and control activated. Closure and control measures implemented for living areas of persons with confirmed cases. Nucleic acid tests will temporarily be conducted on days 1–3, 5, and 7. Only entry into but no exit from the zone will be permitted with the exception of staff for red-coded zones. No person can leave the zone until the first test is concluded for yellow-coded zones.	2022 Jun 19	https://www.gcs.gov.mo/detail/en/N22FSgsvrf?6
2022 Jun 19	Clinical	Citywide NAT	Launch of first round of citywide NATs from 12:00 AM on June 19 to 12:00 PM on June 21	2022 Jun 19	https://www.gcs.gov.mo/detail/en/N22FSulQCY?8
2022 Jun 21	Community	Health code application	Enabled the risk check function of Macau Health Code	2022 Jun 21	https://www.gcs.gov.mo/detail/en/N22FUNLza4?30
2022 Jun 22	Clinical	RAT	All residents in Macau were required to conduct RATs.	2022 Jun 22	https://www.gcs.gov.mo/detail/en/N22FUAMVEq?39
2022 Jun 22	Clinical	Focused NAT	Launch of NATs in key areas for key groups. Inspection focus of key groups included persons who work or live in Macao with Myanmar passports and those who had the same action tracking as positive cases during the last citywide NAT program. Inspection focus in key areas on June 22 included persons who live, work, or have activities in area surrounded by Avenida de Horta e Costa, Rua do Almirante Costa Cabral, Estrada Do Repouso, and Avenida do Almirante Lacerda. The focus of NATs for key areas on June 25 included persons who worked or stayed at the following place(s) for >30 min after June 18: Luis de Camões Park, Lou Lim Ioc Park, shops at Rua da Emenda, shops along Bairro Iao Hon 1st Street to Bairro Iao Hon 8th Street, Fu Tai Industrial Building on Avenida de Venceslau de Morais, and San Kin Yip Commercial Centre on Avenida da Amizade.	2022 Jun 22	https://www.gcs.gov.mo/detail/en/N22FU62sft?4
2022 Jun 23	Clinical	Citywide NAT	Launch of second round of citywide NATs from 9:00 AM on June 23 to 12:00 PM on June 24	2022 Jun 22	https://www.gcs.gov.mo/detail/en-hans/N22FVAAHVa?17
2022 Jun 23	Community	Restaurant	Certain recreational facilities and dining-in at restaurants suspended beginning at 5 PM on June 23	2022 Jun 23	https://www.gcs.gov.mo/detail/en/N22FWwg05w?9
2022 Jun 25	Clinical	Focused NAT	Launch of NAT for key areas. Focus of NATs for key areas included persons who worked or stayed at the following place(s) for >30 min after June 18: Luis de Camões Park, Lou Lim Ioc Park, shops at Rua da Emenda and Bairro Iao Hon 1st Street to Bairro Iao Hon 8th Street, Fu Tai Industrial Building on Avenida de Venceslau de Morais, and San Kin Yip Commercial Centre on Avenida da Amizade.	2022 Jun 25	https://www.gcs.gov.mo/detail/en/N22FYncgqW?keyword=key+areas+nucleic
2022 Jun 25	Community	Elderly residential care home	Implemented a preventive closed-loop management in elderly residential care homes	2022 Jun 24	https://www.gcs.gov.mo/detail/zh-hans/N22FX5iTTD?6
2022 Jun 27	Clinical	RAT	Beginning on June 27, citizens must perform a self-rapid antigen test and declare before going to the inspection station. If the test result was negative, they could go to the inspection station for a NAT and show the certificate; otherwise, they could not enter the station.	2022 Jun 26	https://www.gcs.gov.mo/detail/zh-hans/N22FZ0BVyB?3
2022 Jun 27	Clinical	Citywide NAT	Launch of citywide NATs from 9:00 AM on June 27 to 12:00 PM on 28 June 28. The 3rd round of NAT was June 27–28.	2022 Jun 26	https://www.gcs.gov.mo/detail/en/N22FSulQCY?8
2022 Jun 29	Clinical	RAT	Announced that RAT results affect the health code and launched requirement for RATs for 2 consecutive days starting on June 29–30. If citizens did not complete the declaration of RAT results as required, their Macau health code would be converted to a yellow code at 0:00 AM the next day, and citizens must complete the test on the	2022 Jun 28	https://www.gcs.gov.mo/detail/en/N22FblvTVG?5

Date	Type	Subtype	Measure	Date announced	Source
			same day before they could be converted back to a green code. If the RAT was not done for 2 consecutive days, the code would be changed to red, and NAT would be required. The code could be changed back to green after a negative NAT.		
2022 Jul 4	Clinical	Citywide NAT	Launch of citywide NAT from 9:00 AM July 4 to 6:00 PM on July 9. The 4th round of NAT was July 4-5, 5th round was July 6-7, and 6th round was July 8-9.	2022 Jul 3	https://www.gcs.gov.mo/detail/en/N22GCad4aM?9
2022 Jul 9	Community	Relatively static management	Macao suspended all non-essential industrial and commercial activities from 0:00 AM on July 11 to 0:00 AM on July 18 and called on residents to minimize movement to reduce risk of virus transmission, except for those persons whose activity was deemed essential to the community and day-to-day lives of the public.	2022 Jul 9	https://www.gcs.gov.mo/detail/zh-hans/N22G1kjA4P?10
2022 Jul 10	Clinical	Citywide NAT	Launched 4 more rounds of citywide NATs from 9:00 AM on July 10 to 6:00 PM on July 17. The 7th round of NAT was July 10-11, 8th round was July 12-13, 9th round was July 14-15, and 10th round was July 16-17.	2022 Jul 8	https://www.gcs.gov.mo/detail/zh-hans/N22GHvwnRa?7
2022 Jul 18	Clinical	Citywide NAT	Launched 3 more rounds of citywide NATs from 9:00 AM on July 18 to 6:00 PM on July 23. The 11th round of NAT was July 18-19, 12th round was July 20-21, and 13th round was July 22-23.	2022 Jul 16	https://www.gcs.gov.mo/detail/zh-hans/N22GPkhUgx?8
2022 Jul 30	Clinical	Citywide NAT	Launched 14th round of citywide NAT from 9:00 AM on July 30 to 6:00 PM on 31 July 31	2022 Jul 20	https://www.gcs.gov.mo/detail/zh-hans/N22GTdO030?11

*NAT, nucleic acid test; RAT, rapid antigen test.

Appendix Table 2. Number of persons tested during multiple rounds of citywide nucleic acid testing in study of epidemiology of SARS-CoV-2 Omicron BA.5 infections, Macau, June–July 2022*

Round	Dates	No. tested	Proportion, %
1	Jun 19–21	677,586	99.21
2	Jun 23–24	667,144	97.68
3	Jun 27–28	652,544	95.54
4	Jul 4–5	637,349	93.32
5	Jul 6–7	667,597	97.74
6	Jul 8–9	658,906	96.47
7	Jul 10–11	658,879	96.47
8	Jul 12–13	665,385	97.42
9	Jul 14–15	664,532	97.30
10	Jul 16–17	667,342	97.71
11	Jul 18–19	666,849	97.64
12	Jul 20–21	669,234	97.98
13	Jul 22–23	722,335	105.76
14	Jul 30–31	707,277	103.55

*Dates for 14 rounds of testing by PCR and numbers and percentages of persons tested during each round.

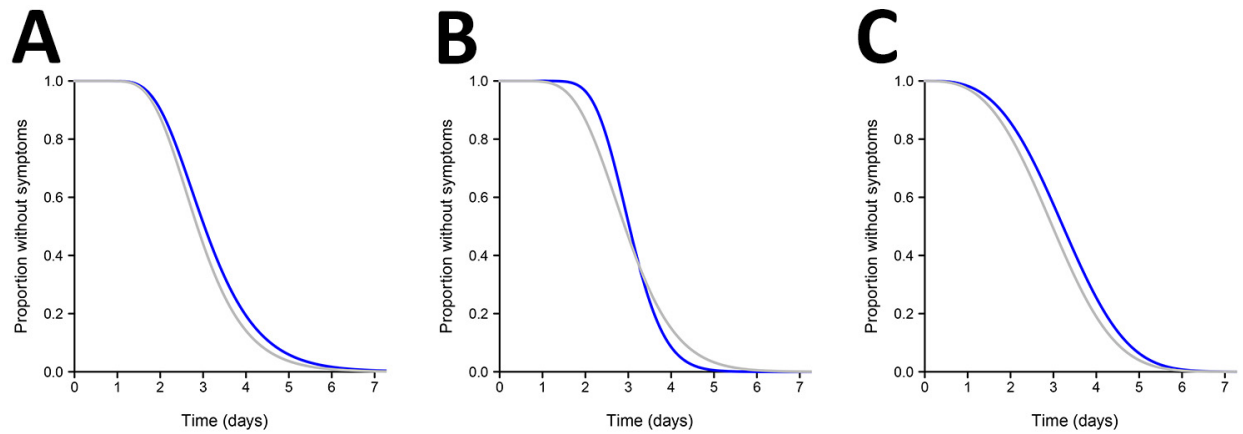
Appendix Table 3. Vaccination status among general population and persons with confirmed COVID-19 cases in June 2022 in study of epidemiology of SARS-CoV-2 Omicron BA.5 infections, Macau, June–July 2022

Type	General population on 2022 Jun 19		Confirmed cases during 2022 Jun 19–30	
	No. persons (%)		No. persons (%)	
Unvaccinated	70,923 (10.38)		109 (19.06)	
Received only the 1st dose	27,701 (4.05)		23 (4.02)	
Completed the 2nd dose	307,851 (45.06)		216 (37.76)	
Completed the 3rd dose	276,725 (40.50)		224 (39.16)	
Received at least 1 dose	612,277 (89.62)		463 (80.94)	
Received at least 2 doses	584,576 (85.56)		440 (76.92)	
Total	683,200		572	

Appendix Table 4. Characteristics of the 6 patients who died of COVID-19 in Macau in study of epidemiology of SARS-CoV-2 Omicron BA.5 infections, Macau, June–July 2022

Date of hospital admission	Date of death	Age, y/sex	Vaccination status	Chronic disease history
2022 Jun 29	2022 Jul 3	94/F	2 doses of inactivated virus vaccine	Hypertension, hyperlipidemia, stroke
2022 Jun 30	2022 Jul 3	100/F	None	Hypertension, brain degeneration, fractures
2022 Jul 6*	2022 Jul 12	88/F	Unknown	Severe diabetes, heart disease, aortic dissection tear
2022 Jul 3*	2022 Jul 13	94/F	Unknown	Chronic heart failure, respiratory failure
2022 Jul 5	2022 Jul 14	86/F	2 doses of inactivated vaccine	Chronic kidney disease, dementia
2022 Jul 9	2022 Jul 21	93/M	None	Chronic heart disease, chronic lung disease

*Macau Health Bureau did not report detailed vaccination status for these 2 patients. One patient received 2 vaccine doses, the other was unvaccinated.



Appendix Figure. Estimated incubation period distributions for SARS-CoV-2 infections in study of epidemiology of SARS-CoV-2 Omicron BA.5 infections, Macau, June–July 2022. Gray lines show the cumulative probability for each distribution; blue lines show the cumulative probability after adjusting for integrations for each distribution. Data were fitted to (A) lognormal, (B) gamma, and (C) Weibull parametric probability distribution models to estimate incubation periods by using the maximum likelihood method.