

1 **Assessing changes in incubation period, serial interval, and generation time of**  
2 **SARS-CoV-2 variants of concern: a systematic review and meta-analysis**

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## 1 **Abstract**

2 **Background:** After the first COVID-19 wave caused by the ancestral lineage, the pandemic has been  
3 fueled from the continuous emergence of new SARS-CoV-2 variants. Understanding key time-to-event  
4 periods for each emerging variant of concern is critical as it can provide insights into the future trajectory  
5 of the virus and help inform outbreak preparedness and response planning. Here, we aim to examine how  
6 the incubation period, serial interval, and generation time have changed from the ancestral SARS-CoV-2  
7 lineage to different variants of concern.

8 **Methods:** We conducted a systematic review and meta-analysis that synthesized the estimates of  
9 incubation period, serial interval, and generation time (both realized and intrinsic) for the ancestral lineage,  
10 Alpha, Beta, and Omicron variants of SARS-CoV-2.

11 **Results:** Our study included 274 records obtained from 147 household studies, contact tracing studies or  
12 studies where epidemiological links were known. With each emerging variant, we found a progressive  
13 shortening of each of the analyzed key time-to-event periods. Specifically, we found that Omicron had the  
14 shortest pooled estimates for the incubation period (3.63 days, 95%CI: 3.25-4.02 days), serial interval  
15 (3.19 days, 95%CI: 2.95-3.43 days), and realized generation time (2.96 days, 95%CI: 2.54-3.38 days)  
16 whereas the ancestral lineage had the highest pooled estimates for each of them. We also observed shorter  
17 pooled estimates for the serial interval compared to the incubation period across the virus lineages. We  
18 found considerable heterogeneities ( $I^2 > 80\%$ ) when pooling the estimates across different virus lineages,  
19 indicating potential unmeasured confounding from population factors (e.g., social behavior, deployed  
20 interventions).

21 **Conclusion:** Our study supports the importance of conducting contact tracing and epidemiological  
22 investigations to monitor changes in SARS-CoV-2 transmission patterns. Our findings highlight a  
23 progressive shortening of the incubation period, serial interval, and generation time, which can lead to  
24 epidemics that spread faster, with larger peak incidence, and harder to control. We also consistently found a  
25 shorter serial interval than incubation period, suggesting that a key feature of SARS-CoV-2 is the potential  
26 for pre-symptomatic transmission. These observations are instrumental to plan for future COVID-19 waves.

1 **Keywords:** COVID-19, variants of concern, incubation period, serial interval, realized generation time,  
2 intrinsic generation time, systematic review, meta-analysis

3  
4 **Introduction**

5 As of April 12, 2023, the COVID-19 pandemic has resulted in more than 762 million reported cases and  
6 6.8 million reported deaths [1]. Since the first detection of SARS-CoV-2 (the virus causing COVID-19) in  
7 Wuhan, China, in December 2020 the virus has started to evolve, and several variants of SARS-CoV-2  
8 have been identified. Five of them were classified as variants of concern (VOCs): Alpha (B.1.1.7), Beta  
9 (B.1.351), Gamma (P.1), Delta (B.1.617.2), and Omicron (B.1.1.529) [2]. Alpha and Delta were  
10 particularly successful at spreading around the globe, causing major waves of infections and associated  
11 hospitalizations since late 2020 and early 2021[3] [4]. In late 2021, Omicron was first detected in South  
12 Africa and spread more rapidly than all other VOCs, causing massive outbreaks worldwide albeit with a  
13 lower associated burden due to high vaccination levels [2, 5, 6]. As of March 2023, Omicron is the  
14 dominant variant worldwide.

15  
16 Knowledge of the transmission dynamics of SARS-CoV-2 VOCs is vital for understanding the  
17 epidemiology of COVID-19 and establishing effective control measures. In this context, three key  
18 indicators are the incubation period, serial interval, and generation time. The incubation period is the  
19 interval between an individual's time of infection and symptom onset [7]; the serial interval is the interval  
20 between symptom onset of the infector and symptom onset of the infectee(s) [7]; the generation time is the  
21 interval between the infector's time of infection and the infectee(s)'s time of infection [8]. For example,  
22 these three indicators are instrumental for defining the duration of quarantine and which contacts need to  
23 be traced as well as providing insights into pre-symptomatic transmission. Moreover, in combination with  
24 the reproduction number, they are key for properly interpreting epidemic growth and forecasting epidemic  
25 timing [9].

26  
27 While many epidemiological investigations have estimated the incubation period, serial interval, and  
28 generation time for the VOCs, these indicators can be affected by a variety of factors related to the specific

1 epidemiological situation of each study as well as deployed interventions [10-14]. For this reason, it is  
2 essential to combine these estimates to provide a more comprehensive picture of these indicators for the  
3 different VOCs. However, previous reviews and meta-analyses on the incubation period, serial interval,  
4 and generation time for SARS-CoV-2 have not examined the evolution of these three indicators across the  
5 different VOCs [13, 15-23]. This information is essential for outbreak preparedness and response planning  
6 as SARS-CoV-2 continues to mutate and systematically comparing changes in these indicators can provide  
7 insights into their possible future trajectory. Therefore, our objective in the present review is to  
8 quantitatively synthesize estimates for the incubation period, serial interval, and generation time and  
9 examine how these indicators have evolved over time from the ancestral lineage to the different VOCs.

10

## 11 **Methods**

### 12 **Search Strategy**

13 We conducted a systematic search following the Preferred Reporting Items for Systematic Reviews and  
14 Meta-Analyses (PRISMA) guideline (see PRISMA checklist) [24]. We searched for studies published in  
15 English on three peer-reviewed databases (PubMed, Embase, and Web of Science) and five preprint servers  
16 (medRxiv, bioRxiv, Europe PMC, SSRN, and arXiv) using predefined search terms (Supplementary Table  
17 S1). All searches were conducted on March 28, 2023.

18

### 19 **Inclusion and exclusion criteria**

20 Studies were included if they satisfied the following criteria: (1) provided at least one summarized statistic  
21 (e.g., central tendency and dispersion) for the incubation period, serial interval, or generation time; (2)  
22 relied on data from a contact tracing study, a household study or a study where epidemiological links were  
23 known.

24

25 We excluded studies that: (1) were meta-analyses and reviews, study protocols, media news, commentaries,  
26 or the full text was unavailable (e.g., conference abstract); (2) SARS-CoV-2 variant/sub-variant or study  
27 period not reported; (3) carried out analysis with sample size less than five; (4) were non-human studies; (5)

1 methods were not described.

2

### 3 **Outcome measures**

4 The outcome variables were incubation period, serial interval, and generation time. We further divided the  
5 generation time into two categories: intrinsic and realized. The intrinsic generation time represents the  
6 generation time that would be observed in a fully connected infinitely large susceptible population in the  
7 absence of interventions and behavioral change. The realized generation time refers to the generation time  
8 that is observed in field condition and is thus affected by specific features of the study population (e.g.,  
9 interventions, individual behaviors, analyzed social settings) [17, 25, 26].

10

### 11 **Data extraction**

12 Study screening and data extraction were performed independently by authors YP.W. and X.X., and  
13 inconsistencies were reconciled together with a third author, Y.Z. For eligible studies, we extracted all  
14 summary statistics related to the outcomes of interest, including mean, median, interquartile range (IQR),  
15 range, standard deviation, quantiles, 95% confidence interval (CI), and 95% credible interval (CrI). In  
16 addition, we collected descriptive data on the authors, article's title, journal, date of publication, study  
17 location (country or region), date of the study period, total number of study subjects, variant type, and  
18 methods used for estimating key time-to-event intervals.

19

### 20 **Quality assessment**

21 Two authors (Z.H. and Y.Z.) independently carried out the quality assessment of the included literature.  
22 The quality assessment scale was adapted from the Newcastle-Ottawa quality assessment questions  
23 (detailed in the Supplementary Table S2) [16]. Disagreements between the two reviewers were resolved  
24 together with a third author, X.X.

25

### 26 **Data analysis**

27 We described the central tendency (mean or median) and dispersion measure (range, IQR, 95%CI, or  
28 95%CrI) for incubation period, serial interval, and generation time for the different VOCs via a forest plot.

1 For studies reporting both mean and median, we preferred the mean estimates since most studies reported  
2 mean. For dispersion measures, we preferred standard deviation, followed by 95% CI/CrI, IQR, and range.

3

4 Next, we conducted a meta-analysis for different SARS-CoV-2 variants. The random- or fixed-effects  
5 models were employed for the pooling analysis according to the heterogeneity test. Notably, if standard  
6 deviation was not available but the parametric distribution of estimates was provided, we derived the  
7 standard deviation from the parametric distribution. Otherwise, we used the 95% CI, if available, to derive  
8 the standard deviation using the formula  $95\% \text{ CI} = \text{mean} \pm 1.96 \times \frac{sd}{\sqrt{n}}$

9

10 For studies reporting only the median and its associated dispersion measure, the corresponding mean,  
11 standard deviation, and 95% CI were approximated using methods described in Luo et al. [27]. If a study  
12 did not include a measure of central tendency or dispersion, the study was included in the review, but not  
13 in the meta-analysis. These methods were implemented using R function *metagen* from package *meta*. The  
14 pooled average estimates with 95% CI were shown in forest plots.

15

16 We used a weighted t-test to assess the significance of the difference between the incubation periods, serial  
17 intervals, and generation times of the ancestral lineage and the Alpha, Delta, and Omicron variants.  
18 Weights were estimated as the inverse of the standard error, and a 2-sided p-value was calculated from a t-  
19 distribution using a bootstrap procedure to account for non-normality [28] [29].

20

21 Publication bias was assessed using a funnel plot and Egger's test. A 2-sided P <0.05 was considered  
22 statistically significant. All analyses were performed in R (version 4.1.0.). This review was not registered.

23

## 24 **Results**

### 25 **Search results**

26 A total of 25,929 studies were identified based on our search strategy. After excluding 3,259 duplicated

1 studies and an additional 22,424 articles via screening titles and abstracts, 246 articles were assessed for  
2 eligibility through a meticulous review of the full article. As per the inclusion/exclusion criteria, 147  
3 studies were included in our analysis [7, 8, 17, 26, 30-172], 7 of which were from preprint platforms.  
4 Among the included studies, 92 studies provided incubation period estimates, 98 studies provided serial  
5 interval estimates, and 21 studies provided generation time estimates. Sixty-three studies reported more  
6 than one outcome; 18 studies provided estimates for more than one virus lineage (Figure 1).

7

## 8 **Study characteristics**

9 We extracted 274 records for the focus key time-to-event periods from 147 included studies. Each record  
10 contained at least one summary statistic of central tendency and dispersion measure of the outcome  
11 variable(s) (Table S4-S7 in the Supplement).

12

13 We identified 109 (39.8%) records for incubation period from 92 studies; the majority of which were based  
14 on COVID-19 data from China (66 [60.6%]). Sixty-nine (63.3%) studies focused on the ancestral lineage,  
15 2 (1.8%) on the Alpha variant, 1 (0.9%) on the Beta variant, 20 (18.3%) on the Delta variant, and 17  
16 (15.6%) on the Omicron variant.

17

18 For serial interval, we obtained 133 (48.5%) records from 99 studies. Nearly half of the records were from  
19 China (46 [34.6%]) and South Korea (14 [10.5%]). Seventy-one (53.4%) studies included focused on the  
20 ancestral lineage, 4 (3.0%) on the Alpha variant, 29 (21.8%) on the Delta variant, and 29 (21.8%) on the  
21 Omicron variant.

22

23 For the generation time, 32 (11.7%) records from 21 studies were included in our analysis, among them  
24 were 27 records for the realized generation time and 5 records for intrinsic generation time. These records  
25 were from China (12 [37.5%]), Italy (7 [21.9%]), UK (5 [15.6%]), Netherlands (4 [12.5%]), Singapore (2  
26 [6.3%]), Germany (1 [3.1%]), and multiple countries (1 [3.1%]). Eleven (34.4%) studies focused on the  
27 ancestral lineage, 5 (15.6%) on the Alpha variant, 10 (31.3%) on the Delta variant, and 6 (18.8%) on the

1 Omicron variant.

2

3 Quality assessment (Table S3 in the Supplement) indicated that 1 study provided a precise exposure  
4 window for cases and identification of the potential infector(s). Sixty-eight studies included a well-  
5 characterized cohort of individuals that were comparable with the population and provided precise  
6 estimates for the symptom onset window for themselves and their potential infector(s).

7

### 8 **Incubation period**

9 The ancestral lineage had the largest pooled mean incubation period (6.46 days, 95%CI: 5.86-7.07 days),  
10 followed by the Alpha variant (4.92 days, 95%CI: 4.53-5.30 days), the Delta variant (4.63, 95%CI: 4.11-  
11 5.15 days), and the Omicron variant (3.63 days, 95%CI: 3.25-4.02 days) (Figure 2, Figure S1). Only one  
12 study reported an estimate for the incubation period of the Beta variant (median: 4.5 days, IQR: 2-7 days).  
13 Each VOC had a significantly shorter incubation period than the ancestral lineage (p-values: <0.001,  
14 <0.001, <0.001 for Alpha, Delta, and Omicron, respectively). Over the course of the pandemic, the central  
15 tendency of the incubation period decreased by 23.8% from the ancestral lineage to Alpha (p-value:  
16 <0.001), 21.5% from Delta to Omicron (p-value: 0.006), and there was no significant difference between  
17 Alpha and Delta (p-value: 0.321). Our results suggested no potential publication bias in the included  
18 studies (p-value: 0.0769) (Figure S5 in the Supplement).

19

### 20 **Serial interval**

21 The ancestral lineage had the largest pooled mean serial interval (4.80 days, 95%CI: 4.48-5.11 days),  
22 followed by the Alpha variant (3.47 days, 95%CI: 2.52-4.41 days), the Delta variant (3.59 days, 95%CI:  
23 3.26-3.92 days) and the Omicron variant (3.19 days, 95%CI: 2.95-3.43 days) (Figure 3, Figure S2). A  
24 significantly shorter serial interval was found for each VOC compared to the ancestral lineage (p-values:  
25 0.032, <0.001, <0.001 for Alpha, Delta, and Omicron, respectively). Likewise, the central tendency of the  
26 serial interval subsequently decreased by 27.7% from the ancestral lineage to Alpha (p-value: 0.032), 11.1%  
27 from the Delta to Omicron (p-value: 0.024). And the differences between Alpha and Delta (p-value: 0.602)



1 was not significant. Our results suggested no potential publication bias in the included studies (p-value:  
2 0.764) (Figure S6 in the Supplement).

3

#### 4 **Generation time**

5 For the realized generation time, the ancestral lineage had the largest pooled mean generation time (4.94  
6 days, 95%CI: 4.29-5.58 days), followed by the Alpha variant (4.36 days, 95%CI: 3.91-4.80 days), the  
7 Delta variant (3.65 days, 95%CI: 3.25-4.05 days), and the Omicron variant (2.96 days, 95%CI: 2.54-3.38  
8 days) (Figure 4, Figure S3). The realized generation times for the Delta and Omicron variants were  
9 significantly shorter than the ancestral lineage (p-values: 0.005, <0.001 for Delta and Omicron,  
10 respectively). The central tendency of the generation time subsequently decreased by 16.3% from Alpha to  
11 Delta (p-value: 0.028), 18.9% from Delta to Omicron (p-value: 0.043), and there was no significant  
12 difference between ancestral lineage and Alpha (p-value: 0.193). Our results suggested no potential  
13 publication bias in the included studies (p-value: 0.709) (Figure S7 in the Supplement).

14

15 For the intrinsic generation time, we obtained a pooled mean estimate of 5.86 days (95%CI: 5.47-6.26 days)  
16 for the Alpha variant based on two studies and 5.67 days (95%CI: 3.79-7.55 days) for the Delta variant  
17 based on two studies (Figure 5, Figure S4). Only one study (for Italy) reported an estimate for the Omicron  
18 variant: 6.84 days (95%CrI: 5.72-8.60 days).

19

#### 20 **Discussion**

21 Our study revealed that Omicron had the shortest pooled estimates for the incubation period (3.63 days,  
22 95%CI: 3.25-4.02 days), serial interval (3.19 days, 95%CI: 2.95-3.43 days), and realized generation time  
23 (2.96 days, 95%CI: 2.54-3.38 days) compared to previous variants. Our results were comparable to those  
24 of Galmiche, S., et al., who reported SARS-CoV-2 incubation period was notably reduced in omicron cases  
25 compared with all other variants of concern [173]. The ancestral lineage had the highest pooled estimates  
26 for each of the three indicators, followed by Alpha and Delta. These finding suggest that the incubation  
27 period, serial interval, and realized generation times of COVID-19 became shorter over the course of the

1 pandemic.

2

3 The majority of the studies included in our analysis provided estimates for the incubation period (92  
4 studies) and serial interval (99 studies), while only 21 studies provided estimates for the generation time.  
5 This suggests that estimates for serial interval and incubation period are easier to obtain as they can more  
6 easily inferred from contact tracing and household studies than estimates for generation time, which  
7 requires more complex Bayesian analyses as the date of infection of the infector and their infectees are  
8 both generally unknown [26, 32]. Furthermore, China provided more records of estimates for incubation  
9 period (60.6%), serial interval (34.6%), and generation time (37.5%) than any other country. This may be  
10 due to the smaller outbreak size of COVID-19 outbreaks in China before the rise of Omicron as compared  
11 to countries with widespread COVID-19 transmission, which made contact tracing and household studies  
12 easier to be conducted. This further support the importance of contact tracing not only as a tool for  
13 monitoring and controlling infectious disease spread, but also for understanding transmission patterns.

14

15 Examining the intrinsic generation time is done using recently developed Bayesian methods, which may  
16 explain why only two studies have provided estimates for this indicator [17, 32]. Between these studies,  
17 there were only 5 records: 2 for Alpha, 2 the Delta, and 1 for Omicron. Given the small sample size, a  
18 pooled mean estimate was not warranted, and we could not compare possible differences between  
19 subsequent VOCs.

20 The incubation period of the ancestral lineage, and the Alpha, Beta, and Delta variants, is generally longer  
21 than that of other acute respiratory viral infections, such as human coronavirus (3.2 days), influenza A  
22 (1.43-1.64 days), parainfluenza (2.6 days), respiratory syncytial virus (4.4 days), and rhinovirus (1.4 days)  
23 [174]. Our findings produced similar mean incubation period estimates to those reported by Du, Z., et al.,  
24 for Delta (4.8 days 95% CI: 3.9-5.6) and Omicron (3.6 days, 95% CI: 2.3-4.9) [175] and those reported by  
25 Wu et. al., for Alpha (5.00 days, 95% CI: 4.94-5.06 days), Delta (4.41 days, 95% CI: 3.76-5.05 days), and  
26 Omicron (3.42 days, 95% CI: 2.88-3.96 days) [23].

27

1 Our study showed that the serial interval of COVID-19 ranged from 1.7 to 7.5 days. These estimates are  
2 longer than those of influenza A(H3N2) (2.2 days) and pandemic influenza A(H1N1)pdm09 (2.8 days), but  
3 shorter than those of the respiratory syncytial virus (RSV, 7.5 days), measles (11.7 days), varicella (14.0  
4 days), smallpox (17.7 days), mumps (18.0 days), rubella (18.3 days), pertussis (22.8 days), and Middle  
5 East respiratory syndrome (MERS, 7.6 days) [176] [177]. Our results were comparable to those of Du, Z.,  
6 et al., who reported an average serial interval of 3.4 days (95% CI, 3.0-3.7) for the Delta variant and 3.1  
7 days (95% CI, 2.9-3.2) for the Omicron variant, respectively [175].

8

9 The mean generation time of COVID-19 ranged from 2.36 to 6.84 days, longer than those of influenza A  
10 (H1N1) (2 days) and pandemic influenza A(H1N1)pdm09 (2.92 days) [178], but shorter than those of the  
11 MERS (10.7 days) [179, 180].

12

13 Overall, the serial interval maintained a shorter pooled mean estimate compared to the incubation period  
14 across different virus lineages, indicating that a large proportion of SARS-CoV-2 transmission occurs prior  
15 to symptom onset [181-183]. Pre-symptomatic transmission was a critical factor facilitating SARS-CoV-2  
16 spread [184], highlighting the importance of obtaining timely estimates of these indicators and keep  
17 monitoring their possible changes over the course of an epidemic.

18

19 The current study provides scientific evidence that the incubation period of COVID-19 has shortened as  
20 the virus has evolved, which has important implications for the formulation of effective epidemic control  
21 strategies such as isolation and quarantine. It is still unclear whether the increase of immunity levels in the  
22 population has contributed to this trend, as prior infection or vaccination can affect the incubation period  
23 by altering the viral load and shedding [185]. Similarly, it is unclear whether the diverse immunological  
24 landscape in different countries has contributed to the substantial heterogeneity of the incubation period  
25 observed for the same variant across different studies.

26

27 Our findings also demonstrated that the serial intervals of COVID-19 shortened with each new VOC.

1 Previous studies have attributed decreased serial intervals to preventive measures that target the duration of  
2 potential transmission, such as isolation, contact tracing, quarantine, and other non-pharmaceutical  
3 interventions (NPIs) [10-12, 49, 186], which is further supported by the fact that longer serial intervals are  
4 often censored due to case isolations [35]. The highly heterogeneous implementation of NPIs between  
5 countries, within country, and time frame has probably contributed to heterogeneous estimates of the serial  
6 interval that we observed between studies. This applies also for estimates of the realized generation time.

7 We acknowledge some limitations in this study. First, results of the included studies revealed considerable  
8 heterogeneities ( $I^2 > 80\%$ ) when pooling the estimates across different virus lineages, indicating potential  
9 unmeasured confounding from population factors (e.g., social behavior). Specifically, heterogeneities for  
10 the incubation period may be due to heterogeneities in the age structure and presence of pre-existing  
11 conditions in the host population [187, 188], whereas diversity in contact settings and the strength of NPIs  
12 may be responsible for heterogeneity of the estimates for the serial interval and realized generation time.  
13 However, these data were rarely available from the included published literature and preprints, thus  
14 preventing further exploration in our study. As per the inclusion criteria, we only used data collected from  
15 studies published in English potentially subjecting our study to reporting bias, which may impact our  
16 results. This study may be limited by recall bias as many studies included in the analysis rely on  
17 retrospective data collection for exposure and symptom onset, which would influence the obtained  
18 estimates. The incubation period for the Beta variant and the intrinsic generation time for Omicron were  
19 each included in only one study, and thus it was not possible to produce pooled estimates.

20

21 In conclusion, our findings suggest that the incubation period, serial interval, and generation time of  
22 SARS-CoV-2 have evolved to shorter intervals with the emergence of each new VOC. Identifying the  
23 length of each of these indicators is critical for understanding the epidemiology of different SARS-CoV-2  
24 variants and developing control measures for mitigating the spread of COVID-19. Moreover,  
25 understanding trends in these indicators can be instrumental for preparedness planning for future COVID-  
26 19 outbreaks.

27

1 **Declarations**

2 **Authors' contributions**

3 M.A., YP.W., Y.W., H.L. conceived and designed the study. H.Y., and M.A. supervised the study. X.X.,  
4 YP.W., Y.Z. and Z.H. participated in data collection. X.X. and YP.W. participated in statistical analysis.  
5 X.X. and Y.Z. prepared the tables and figures. YP.W., A.G.K. and X.X. drafted the manuscript. M.A.,  
6 A.G.K. and YP.W. revised the content critically. All authors contributed to review and revision and  
7 approved the final manuscript as submitted and agree to be accountable for all aspects of the work.

8

9 **Competing interests**

10 H.Y. has received research funding from Sanofi Pasteur, GlaxoSmithKline, Yichang HEC Changjiang  
11 Pharmaceutical Company, Shanghai Roche Pharmaceutical Company, and SINOVAC Biotech Ltd. M.A.  
12 has received research funding from Seqirus. None of those funding is related to this research. All other  
13 authors report no competing interests.

14

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19 Epidemiologists (CSTE) (NU38OT000297). The study does not necessarily represent the views of CDC  
20 and CSTE. The funders had no role in the design and conduct of the study; collection, management,  
21 analysis, and interpretation of the data; preparation, review, or approval of the manuscript; and decision to  
22 submit the manuscript for publication.

23

24 **Availability of data**

25 All data are collected from open source with detailed description in Supplemental Information.

26

27 **Ethics approval and consent to participate**

1 Not applicable.

2

3 **Acknowledgements**

4 Not applicable.

5

6 **Consent for publication**

7 Not applicable.

8

## 1 References

- 2 1. WHO Coronavirus (COVID-19) Dashboard [<https://covid19.who.int/>]
- 3 2. Tracking SARS-CoV-2 variants [<https://www.who.int/activities/tracking-SARS-CoV-2-variants/>]
- 4 3. Salvatore M, Purkayastha S, Ganapathi L, Bhattacharyya R, Kundu R, Zimmermann L, Ray D, Hazra  
5 A, Kleinsasser M, Solomon S et al. Lessons from SARS-CoV-2 in India: A data-driven framework for  
6 pandemic resilience. *Sci Adv.* 2022; 8(24):eabp8621.
- 7 4. Bolze A, Luo S, White S, Cirulli ET, Wyman D, Dei Rossi A, Machado H, Cassens T, Jacobs S,  
8 Schiabor Barrett KM et al. SARS-CoV-2 variant Delta rapidly displaced variant Alpha in the United  
9 States and led to higher viral loads. *Cell Reports Medicine.* 2022; 3(3):100564.
- 10 5. Aleem A, Akbar Samad AB, Vaqar S. Emerging Variants of SARS-CoV-2 And Novel Therapeutics  
11 Against Coronavirus (COVID-19): StatPearls Publishing, Treasure Island (FL); 2023.
- 12 6. Zhang L, Li Q, Liang Z, Li T, Liu S, Cui Q, Nie J, Wu Q, Qu X, Huang W et al. The significant  
13 immune escape of pseudotyped SARS-CoV-2 variant Omicron. *Emerg Microbes Infect.* 2022; 11(1):1-  
14 5.
- 15 7. Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, Ren R, Leung KSM, Lau EHY, Wong JY et al. Early  
16 transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia. *New England*  
17 *Journal of Medicine.* 2020; 382(13):1199-1207.
- 18 8. Ferretti L, Wymant C, Kendall M, Zhao L, Nurtay A, Abeler-Dorner L, Parker M, Bonsall D, Fraser C.  
19 Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing.  
20 *SCIENCE.* 2020; 368(6491).
- 21 9. Nelson KE, Williams CFM, Graham NMH, Balows A. *Infectious Disease Epidemiology: Theory and*  
22 *Practice*, 3rd ed; 2007.
- 23 10. Zeng K, Santhya S, Soong A, Malhotra N, Pushparajah D, Thoon KC, Yeo B, Ho ZJM, Cheng MCI.  
24 Serial Intervals and Incubation Periods of SARS-CoV-2 Omicron and Delta Variants, Singapore. *Emerg*  
25 *Infect Dis.* 2023; 29(4):814-817.
- 26 11. Ahlers M, Aralis H, Tang W, Sussman JB, Fonarow GC, Ziaieian B. Non-pharmaceutical interventions  
27 and covid-19 burden in the United States: retrospective, observational cohort study. *BMJ Med.* 2022;  
28 1(1):e000030.
- 29 12. Ali ST, Wang L, Lau EHY, Xu XK, Du Z, Wu Y, Leung GM, Cowling BJ. Serial interval of SARS-  
30 CoV-2 was shortened over time by nonpharmaceutical interventions. *Science.* 2020; 369(6507):1106-  
31 1109.
- 32 13. Ali ST, Yeung A, Shan S, Wang L, Gao H, Du Z, Xu XK, Wu P, Lau EHY, Cowling BJ. Serial Intervals  
33 and Case Isolation Delays for Coronavirus Disease 2019: A Systematic Review and Meta-Analysis.  
34 *Clin Infect Dis.* 2022; 74(4):685-694.
- 35 14. Pung R, Mak TM, Kucharski AJ, Lee VJ. Serial intervals in SARS-CoV-2 B.1.617.2 variant cases.  
36 *Lancet.* 2021; 398(10303):837-838.
- 37 15. Alene M, Yismaw L, Assemie MA, Ketema DB, Gietaneh W, Birhan TY. Serial interval and incubation  
38 period of COVID-19: a systematic review and meta-analysis. *BMC Infect Dis.* 2021; 21(1):257.
- 39 16. Conor M, Áine C, Kevin H, Ann B, Andrew WB, Francis B, Miriam C, John G, Elizabeth L, David M  
40 et al. Incubation period of COVID-19: a rapid systematic review and meta-analysis of observational  
41 research. *BMJ Open.* 2020; 10(8):e039652.
- 42 17. Hart WS, Miller E, Andrews NJ, Waight P, Maini PK, Funk S, Thompson RN. Generation time of the  
43 alpha and delta SARS-CoV-2 variants: an epidemiological analysis. *The Lancet Infectious Diseases.*  
44 2022; 22(5):603-610.
- 45 18. Hussein M, Toraih E, Elshazli R, Fawzy M, Houghton A, Tatum D, Killackey M, Kandil E, Duchesne J.  
46 Meta-analysis on Serial Intervals and Reproductive Rates for SARS-CoV-2. *Ann Surg.* 2021;  
47 273(3):416-423.
- 48 19. John G, Miriam C, Áine C, Kevin H, David M, Andrew B, Conor M, Ann B, Elizabeth Ann L, Simon  
49 M. Rapid review of available evidence on the serial interval and generation time of COVID-19. *BMJ*  
50 *Open.* 2020; 10(11):e040263.
- 51 20. Manica M, Litvinova M, De Bellis A, Guzzetta G, Mancuso P, Vicentini M, Venturelli F, Bisaccia E,  
52 Bento AI, Poletti P et al. Estimation of the incubation period and generation time of SARS-CoV-2  
53 Alpha and Delta variants from contact tracing data. *Epidemiology & Infection.* 2023; 151:e5.
- 54 21. Rai B, Shukla A, Dwivedi LK. Estimates of serial interval for COVID-19: A systematic review and  
55 meta-analysis. *Clin Epidemiol Glob Health.* 2021; 9:157-161.
- 56 22. Vink MA, Bootsma MCJ, Wallinga J. Serial Intervals of Respiratory Infectious Diseases: A Systematic  
57 Review and Analysis. *American Journal of Epidemiology.* 2014; 180(9):865-875.
- 58 23. Wu Y, Kang L, Guo Z, Liu J, Liu M, Liang W. Incubation Period of COVID-19 Caused by Unique

- 1 SARS-CoV-2 Strains: A Systematic Review and Meta-analysis. *JAMA Network Open*. 2022;  
2 5(8):e2228008-e2228008.
- 3 24. Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, Shamseer L, Tetzlaff JM,  
4 Akl EA, Brennan SE et al. The PRISMA 2020 statement: an updated guideline for reporting systematic  
5 reviews. *Bmj*. 2021; 372:n71.
- 6 25. Champredon D, Dushoff J. Intrinsic and realized generation intervals in infectious-disease transmission.  
7 *Proc Biol Sci*. 2015; 282(1821):20152026.
- 8 26. Manica M, Litvinova M, De Bellis A, Guzzetta G, Mancuso P, Vicentini M, Venturelli F, Bisaccia E,  
9 Bento AI, Poletti P et al. Estimation of the incubation period and generation time of SARS-CoV-2  
10 Alpha and Delta variants from contact tracing data. *Epidemiol Infect*. 2022; 151:e5.
- 11 27. Luo D, Wan X, Liu J, Tong T. Optimally estimating the sample mean from the sample size, median,  
12 mid-range, and/or mid-quartile range. *Stat Methods Med Res*. 2018; 27(6):1785-1805.
- 13 28. Watkins Bruner D, Moore D, Parlanti A, Dorgan J, Engstrom P. Relative risk of prostate cancer for men  
14 with affected relatives: Systematic review and meta-analysis. *International Journal of Cancer*. 2003;  
15 107(5):797-803.
- 16 29. Efron B, Tibshirani R. *An Introduction to the Bootstrap*; 1994.
- 17 30. Shen Y, Xu W, Li C, Handel A, Martinez L, Ling F, Ebell M, Fu X, Pan J, Ren J et al. A cluster of novel  
18 coronavirus disease 2019 infections indicating person-to-person transmission among casual contacts  
19 from social gatherings: An outbreak case-contact investigation. *Open Forum Infectious Diseases*. 2020;  
20 7(6).
- 21 31. Song JS, Lee J, Kim M, Jeong HS, Kim MS, Kim SG, Yoo HN, Lee JJ, Lee HY, Lee SE et al. Serial  
22 Intervals and Household Transmission of SARS-CoV-2 Omicron Variant, South Korea, 2021.  
23 *Emerging Infectious Diseases*. 2022; 28(3):756-759.
- 24 32. Manica M, De Bellis A, Guzzetta G, Mancuso P, Vicentini M, Venturelli F, Zerbini A, Bisaccia E,  
25 Litvinova M, Menegale F et al. Intrinsic generation time of the SARS-CoV-2 Omicron variant: An  
26 observational study of household transmission. *Lancet Reg Health Eur*. 2022; 19:100446.
- 27 33. Vazirinejad R, Khalili P, Jafarzadeh A, Shabani Z, Jamalizadeh A, Rezaei B, Ahmadnia H, Rezayati M-  
28 t, Ebrahimian M, Mehralinasab G et al. A contact tracing prospective cohort retrieving epidemiological  
29 facts on SARS-CoV-2 transmission aspects; a serological analysis. *Research Square*. 2020.
- 30 34. Mefsin YM, Chen D, Bond HS, Lin Y, Cheung JK, Wong JY, Ali ST, Lau EHY, Wu P, Leung GM et al.  
31 Epidemiology of Infections with SARS-CoV-2 Omicron BA.2 Variant, Hong Kong, January-March  
32 2022. *Emerging infectious diseases*. 2022; 28(9):1856-1858.
- 33 35. Li L, Han ZG, Qin PZ, Liu WH, Yang Z, Chen ZQ, Li K, Xie CJ, Ma Y, Wang H et al. Transmission  
34 and containment of the SARS-CoV-2 Delta variant of concern in Guangzhou, China: A population-  
35 based study. *PLoS neglected tropical diseases*. 2022; 16(1):e0010048.
- 36 36. Bender JK, Brandl M, Höhle M, Buchholz U, Zeitlmann N. Analysis of Asymptomatic and  
37 Presymptomatic Transmission in SARS-CoV-2 Outbreak, Germany, 2020. *Emerging infectious  
38 diseases*. 2021; 27(4).
- 39 37. Ma X, Wu K, Li Y, Li S, Cao L, Xie H, Zheng J, Zhou R, Yuan Z, Huang Z et al. Contact tracing period  
40 and epidemiological characteristics of an outbreak of the SARS-CoV-2 Delta variant in Guangzhou.  
41 *International Journal of Infectious Diseases*. 2022; 117:18-23.
- 42 38. Liu JY, Chen TJ, Hwang SJ. Analysis of community-acquired COVID-19 cases in Taiwan. *Journal of  
43 the Chinese Medical Association*. 2020:1087-1092.
- 44 39. Del Águila-Mejía J, Wallmann R, Calvo-Montes J, Rodríguez-Lozano J, Valle-Madrado T, Aginagalde-  
45 Llorente A. Secondary Attack Rate, Transmission and Incubation Periods, and Serial Interval of SARS-  
46 CoV-2 Omicron Variant, Spain. *Emerging infectious diseases*. 2022; 28(6).
- 47 40. Homma Y, Katsuta T, Oka H, Inoue K, Toyoshima C, Iwaki H, Yamashita Y, Shinomiya H. The  
48 incubation period of the SARS-CoV-2 B.1.1.7 variant is shorter than that of other strains. *J Infect*. 2021;  
49 83(2):e15-e17.
- 50 41. Haddad N, Clapham HE, Abou Naja H, Saleh M, Farah Z, Ghosn N, Mrad P, Howard N. Calculating  
51 the serial interval of SARS-CoV-2 in Lebanon using 2020 contact-tracing data. *BMC Infectious  
52 Diseases*. 2021; 21(1).
- 53 42. Shi P, Gao Y, Shen Y, Chen E, Chen H, Liu J, Chen Y, Xiao Y, Wang K, Shi C et al. Characteristics and  
54 evaluation of the effectiveness of monitoring and control measures for the first 69 Patients with  
55 COVID-19 from 18 January 2020 to 2 March in Wuxi, China. *Sustain Cities Soc*. 2021; 64:102559.
- 56 43. Kang M, Xin H, Yuan J, Taslim Ali S, Liang Z, Zhang J, Hu T, Lau EHY, Zhang Y, Zhang M et al.  
57 Transmission dynamics and epidemiological characteristics of SARS-CoV-2 Delta variant infections in  
58 Guangdong, China, May to June 2021. *Eurosurveillance*. 2022; 27(10).
- 59 44. Ogata T, Tanaka H, Irie F, Hirayama A, Takahashi Y. Shorter Incubation Period among Unvaccinated  
60 Delta Variant Coronavirus Disease 2019 Patients in Japan. *International Journal of Environmental*



- 1 Research and Public Health. 2022; 19(3).
- 2 45. Zhang L, Zhu J, Wang X, Yang J, Liu XF, Xu X-K. Characterizing COVID-19 Transmission:  
3 Incubation Period, Reproduction Rate, and Multiple-Generation Spreading. *FRONTIERS IN PHYSICS*.  
4 2021; 8.
- 5 46. Song R, Han B, Song M, Wang L, Conlon CP, Dong T, Tian D, Zhang W, Chen Z, Zhang F et al.  
6 Clinical and epidemiological features of COVID-19 family clusters in Beijing, China. *Journal of*  
7 *Infection*. 2020; 81(2):e26-e30.
- 8 47. Brandal LT, MacDonald E, Veneti L, Ravlo T, Lange H, Naseer U, Feruglio S, Bragstad K, Hungnes O,  
9 Ødeskaug LE et al. Outbreak caused by the SARS-CoV-2 Omicron variant in Norway, November to  
10 December 2021. *Euro surveillance*. 2021; 26(50).
- 11 48. Geismar C, Fragaszy E, Nguyen V, Fong WLE, Shrotri M, Beale S, Rodger A, Lamos V, Byrne T,  
12 Kovar J et al. Serial interval of COVID-19 and the effect of Variant B.1.1.7: analyses from prospective  
13 community cohort study (Virus Watch). *Wellcome open research*. 2021; 6:224-224.
- 14 49. Pung R, Mak TM, Kucharski AJ, Lee VJ. Serial intervals in SARS-CoV-2 B.1.617.2 variant cases. *The*  
15 *Lancet*. 2021; 398(10303):837-838.
- 16 50. Ryu S, Kim D, Lim JS, Ali ST, Cowling BJ. Serial Interval and Transmission Dynamics during SARS-  
17 CoV-2 Delta Variant Predominance, South Korea. *Emerging infectious diseases*. 2022; 28(2):407-410.
- 18 51. Kremer C, Braeye T, Proesmans K, André E, Torneri A, Hens N. Serial Intervals for SARS-CoV-2  
19 Omicron and Delta Variants, Belgium, November 19-December 31, 2021. *Emerging infectious diseases*.  
20 2022; 28(8):1699-1702.
- 21 52. Backer JA, Eggink D, Andeweg SP, Veldhuijzen IK, van Maarseveen N, Vermaas K, Vlaemynck B,  
22 Schepers R, van den Hof S, Reusken CBEM et al. Shorter serial intervals in SARS-CoV-2 cases with  
23 Omicron BA.1 variant compared with Delta variant, the Netherlands, 13 to 26 December 2021.  
24 *Eurosurveillance*. 2022; 27(6).
- 25 53. Kim D, Ali ST, Kim S, Jo J, Lim JS, Lee S, Ryu S. Estimation of Serial Interval and Reproduction  
26 Number to Quantify the Transmissibility of SARS-CoV-2 Omicron Variant in South Korea. *Viruses*.  
27 2022; 14(3).
- 28 54. Gupta M, Parameswaran GG, Sra MS, Mohanta R, Patel D, Gupta A, Bansal B, Jain V, Mazumder A,  
29 Arora M et al. Contact tracing of COVID-19 in Karnataka, India: Superspreading and determinants of  
30 infectiousness and symptomatic infection. *PLoS One*. 2022; 17(7 July).
- 31 55. Hwang H, Lim JS, Song SA, Achangwa C, Sim W, Kim G, Ryu S. Transmission Dynamics of the Delta  
32 Variant of SARS-CoV-2 Infections in South Korea. *Journal of Infectious Diseases*. 2022; 225(5):793-  
33 799.
- 34 56. Li D, Li AE, Li ZQ, Bao Y, Liu T, Qin XR, Yu XJ. SARS-CoV-2 Delta Variant in Jingmen City, Hubei  
35 Province, China, 2021: Children Susceptible and Vaccination Breakthrough Infection. *Frontiers in*  
36 *Microbiology*. 2022; 13:856757.
- 37 57. Tanaka H, Ogata T, Shibata T, Nagai H, Takahashi Y, Kinoshita M, Matsubayashi K, Hattori S,  
38 Taniguchi C. Shorter Incubation Period among COVID-19 Cases with the BA.1 Omicron Variant.  
39 *INTERNATIONAL JOURNAL OF ENVIRONMENTAL RESEARCH AND PUBLIC HEALTH*. 2022;  
40 19(10).
- 41 58. Bao C, Pan E, Ai J, Dai Q, Xu K, Shi N, Gao Q, Hu J, Peng Z, Huang H et al. COVID-19 outbreak  
42 following a single patient exposure at an entertainment site: An epidemiological study. *Transboundary*  
43 *and Emerging Diseases*. 2021; 68(2):773-781.
- 44 59. Shim E, Choi W, Kwon D, Kim T, Song Y. Transmission Potential of the Omicron Variant of Severe  
45 Acute Respiratory Syndrome Coronavirus 2 in South Korea, 25 November 2021-8 January 2022. *Open*  
46 *forum infectious diseases*. 2022; 9(7):ofac248.
- 47 60. Amato L, Candeloro L, Di Girolamo A, Savini L, Puglia I, Marcacci M, Caporale M, Mangone I,  
48 Cammà C, Conte A et al. Epidemiological and genomic findings of the first documented Italian  
49 outbreak of SARS-CoV-2 Alpha variant of concern. *Epidemics*. 2022; 39:100578.
- 50 61. Du Z, Xu X, Wu Y, Wang L, Cowling BJ, Meyers LA. Serial Interval of COVID-19 among Publicly  
51 Reported Confirmed Cases. *Emerg Infect Dis*. 2020; 26(6):1341-1343.
- 52 62. Song Y, Shim E. Proportion of Pre-Symptomatic Transmission Events Associated with COVID-19 in  
53 South Korea. *Journal of Clinical Medicine*. 2022; 11(14).
- 54 63. McAlevey P, Rainey E, McKaig C, Richardson C, Anderson C, Tilley C, Kmiecik ED, Dallat M,  
55 Stevens H, Sheridan P et al. Outbreak of SARS-CoV-2 in a teenage discotheque in Northern Ireland-  
56 November 2021. *Public Health*. 2022; 211:81-84.
- 57 64. Sang Woo Park KS. Inferring the differences in incubation-period and generation-interval distributions  
58 of the Delta and Omicron variants of SARS-CoV-2. *medRxiv*. 2022.
- 59 65. Zhu W, Zhang M, Pan J, Yao Y, Wang W. Effects of prolonged incubation period and centralized  
60 quarantine on the COVID-19 outbreak in Shijiazhuang, China: a modeling study. *BMC Medicine*. 2021;

- 19(1).
66. Allen H, Tessier E, Turner C, Anderson C, Blomquist P, Simons D, Løchen A, Jarvis CI, Groves N, Capelastegui F et al. Comparative transmission of SARS-CoV-2 Omicron (B.1.1.529) and Delta (B.1.617.2) variants and the impact of vaccination: national cohort study, England. *medRxiv*. 2022.
67. Helmsdal G, Hansen OK, Møller LF, Christiansen DH, Petersen MS, Kristiansen MF. Omicron outbreak at a private gathering in the Faroe Islands, infecting 21 of 33 triple-vaccinated healthcare workers. *Clin Infect Dis*. 2022.
68. Zhang M, Xiao J, Deng A, Zhang Y, Zhuang Y, Hu T, Li J, Tu H, Li B, Zhou Y et al. Transmission Dynamics of an Outbreak of the COVID-19 Delta Variant B.1.617.2 - Guangdong Province, China, May-June 2021. *China CDC Wkly*. 2021; 3(27):584-586.
69. Ping K, Lei M, Gou Y, Tao Z, Yao G, Hu C, Tao Q, Zou Z, Wang D, Li S et al. Epidemiologic characteristics of covid-19 in guizhou province, China. *Journal of Infection in Developing Countries*. 2021; 15(3):389-397.
70. Liu Y, Zhao S, Ryu S, Ran J, Fan J, He D. Estimating the incubation period of SARS-CoV-2 Omicron BA.1 variant in comparison with that during the Delta variant dominance in South Korea. *One Health*. 2022; 15:100425.
71. Deng B, Liu W, Guo Z, Luo L, Yang T, Huang J, Abudunaibi B, Zhang Y, Ouyang X, Wang D et al. Natural history and cycle threshold values analysis of COVID-19 in Xiamen City, China. *Infectious Disease Modelling*. 2022; 7(3):486-497.
72. Ki M. Epidemiologic characteristics of early cases with 2019 novel coronavirus (2019-nCoV) disease in Korea. *Epidemiol Health*. 2020; 42:e2020007.
73. Buchholz U, An Der Heiden M. Serial interval in households infected with SARS-CoV-2 variant B.1.1.529 (Omicron) are even shorter compared to Delta. *Epidemiology and Infection*. 2022; 150:e165.
74. team TS-C-vwlBci. Linked transmission chains of imported SARS-CoV-2 variant B.1.351 across mainland France, January 2021. *Euro Surveill*. 2021; 26(13).
75. Mao S, Huang T, Yuan H, Li M, Huang X, Yang C, Zhou X, Cheng X, Su Q, Wu X. Epidemiological analysis of 67 local COVID-19 clusters in Sichuan Province, China. *BMC Public Health*. 2020; 20(1):1525.
76. Ali ST, Chen D, Lim WW, Yeung A, Adam DC, Lau YC, Lau EHY, Wong JY, Xiao J, Ho F et al. Insights into COVID-19 epidemiology and control from temporal changes in serial interval distributions in Hong Kong. *medRxiv*. 2022.
77. Zeng K, Santhya S, Soong A, Malhotra N, Pushparajah D, Thoon KC, Yeo B, Ho ZJM, Cheng MCI. Serial Intervals and Incubation Periods of SARS-CoV-2 Omicron and Delta Variants, Singapore. *Emerging infectious diseases*. 2023; 29(4).
78. Yan X, Xiao W, Zhou S, Wang X, Wang Z, Zhao M, Li T, Jia Z, Zhang B, Shui T. A four-generation family transmission chain of COVID-19 along the China-Myanmar border in October to November 2021. *Frontiers in public health*. 2022; 10:1004817.
79. Zhang X, Wang H, Wang Y, Lei Y, Xu K, Zhang J, Han Y, Zeng J, Deng S, Wang Y. Epidemiological and clinical based study on four passages of COVID-19 patients: intervention at asymptomatic period contributes to early recovery. *BMC Infectious Diseases*. 2020; 20(1).
80. Xiong W, Peng L, Tsang TK, Cowling BJ. Epidemiology of SARS-CoV-2 Omicron BA.5 Infections, Macau, June-July 2022. *Emerging infectious diseases*. 2023; 29(2):453-456.
81. Wright E, Pollard G, Robertson H, Anuradha S. Household transmission of the Delta COVID-19 variant in Queensland, Australia: A case series. *Epidemiology and Infection*. 2022; 150.
82. Wei Z, Ma W, Wang Z, Li J, Fu X, Chang H, Qiu Y, Tian H, Zhu Y, Xia A et al. Household transmission of SARS-CoV-2 during the Omicron wave in Shanghai, China: A case-ascertained study. *Influenza Other Respir Viruses*. 2023; 17(2):e13097.
83. Yu X, Sun X, Cui P, Pan H, Lin S, Han R, Jiang C, Fang Q, Kong D, Zhu Y et al. Epidemiological and clinical characteristics of 333 confirmed cases with coronavirus disease 2019 in Shanghai, China. *Transboundary and Emerging Diseases*. 2020; 67(4):1697-1707.
84. Wang K, Guo Z, Zeng T, Sun S, Lu Y, Wang J, Li S, Luan Z, Li H, Zhang J et al. Transmission Characteristics and Inactivated Vaccine Effectiveness Against Transmission of SARS-CoV-2 Omicron BA.5 Variants in Urumqi, China. *JAMA Netw Open*. 2023; 6(3):e235755-e235755.
85. Wang J, Ma T, Ding S, Xu K, Zhang M, Zhang Z, Dai Q, Tao S, Wang H, Cheng X et al. Dynamic characteristics of a COVID-19 outbreak in Nanjing, Jiangsu province, China. *Frontiers in public health*. 2022; 10:933075.
86. Ogata T, Tanaka H. SARS-CoV-2 Incubation Period during the Omicron BA.5- Dominant Period in Japan. *Emerging Infectious Diseases*. 2023; 29(3):595-598.
87. Luo K, Wu Y, Wang Y, Liu Z, Yi L, Zhao S, Yan X, Yang H, Sun K, Ajelli M et al. Transmission Dynamics and Epidemiological Characteristics of the SARS-CoV-2 Delta Variant - Hunan Province,

- 1 China, 2021. *China CDC Wkly.* 2023; 5(3):56-62.
- 2 88. Guo Z, Zhao S, Yam CHK, Li C, Jiang X, Chow TY, Chong KC, Yeoh EK. Estimating the serial  
3 intervals of SARS-CoV-2 Omicron BA.4, BA.5, and BA.2.12.1 variants in Hong Kong. *Influenza  
4 Other Respir Viruses.* 2023; 17(2).
- 5 89. Guo Z, Zhao S, Mok CKP, So RTY, Yam CHK, Chow TY, Chan TCP, Wei Y, Min KJ, Wang MH et al.  
6 Comparing the incubation period, serial interval, and infectiousness profile between SARS-CoV-2  
7 Omicron and Delta variants. *Journal of medical virology.* 2023; 95(3):e28648.
- 8 90. Geismar C, Nguyen V, Fragaszy E, Shrotri M, Navaratnam AMD, Beale S, Byrne TE, Fong WLE,  
9 Yavlinsky A, Kovar J et al. Bayesian reconstruction of household transmissions to infer the serial  
10 interval of COVID-19 by variants of concern: analysis from a prospective community cohort study  
11 (Virus Watch). *The Lancet.* 2022; 400:S40.
- 12 91. Guo CX, He L, Yin JY, Meng XG, Tan W, Yang GP, Bo T, Liu JP, Lin XJ, Chen X. Epidemiological  
13 and clinical features of pediatric COVID-19. *BMC Medicine.* 2020; 18(1).
- 14 92. Nie X, Fan L, Mu G, Tan Q, Wang M, Xie Y, Cao L, Zhou M, Zhang Z, Chen W. Epidemiological  
15 characteristics and incubation period of 7015 confirmed cases with coronavirus disease 2019 outside  
16 Hubei Province in China. *Journal of Infectious Diseases.* 2020; 222(1):26-35.
- 17 93. Yu S, Cui S, Rui J, Zhao Z, Deng B, Liu C, Li K, Wang Y, Yang Z, Li Q et al. Epidemiological  
18 Characteristics and Transmissibility for SARS-CoV-2 of Population Level and Cluster Level in a  
19 Chinese City. *Frontiers in public health.* 2021; 9:799536.
- 20 94. Wang P, Lu JA, Jin Y, Zhu M, Wang L, Chen S. Statistical and network analysis of 1212 COVID-19  
21 patients in Henan, China. *Int J Infect Dis.* 2020; 95:391-398.
- 22 95. Son H, Lee H, Lee M, Eun Y, Park K, Kim S, Park W, Kwon S, Ahn B, Kim D et al. Epidemiological  
23 characteristics of and containment measures for COVID-19 in Busan, Korea. *Epidemiol Health.* 2020;  
24 42:e2020035.
- 25 96. Baskaradoss JK, Alsumait A, Malik S, Ariga J, Geevarghese A, Francis R, Vazhiyodan A, Alexander R,  
26 Menon P, Behzadi S et al. Epidemiological characteristics of COVID-19 cases among indians residing  
27 in Kuwait. *Eastern Mediterranean Health Journal.* 2021; 27(8):745-754.
- 28 97. Bae S, Kim H, Jung TY, Lim JA, Jo DH, Kang GS, Jeong SH, Choi DK, Kim HJ, Cheon YH et al.  
29 Epidemiological Characteristics of COVID-19 Outbreak at Fitness Centers in Cheonan, Korea. *Journal  
30 of Korean medical science.* 2020; 35(31):e288.
- 31 98. Du S, Lu H, Su Y, Wang X, Bi S, Wu J, Wang W, Yu X, Yang M. Epidemiological Characteristics of  
32 COVID-19 under Government-mandated Control Measures during January-February 2020 in Inner  
33 Mongolia, China. *Japanese journal of infectious diseases.* 2021; 75(4):361-367.
- 34 99. Thway AM, Teza H, Win TT, Htun YM, Aung MM, Win YN, Tun KM. Epidemiological characteristics  
35 of SARS-COV-2 in Myanmar. *medRxiv.* 2020.
- 36 100. Kwok KO, Wong VWY, Wei WI, Wong SYS, Tang JWT. Epidemiological characteristics of the first 53  
37 laboratory-confirmed cases of COVID-19 epidemic in Hong Kong, 13 February 2020. *Euro Surveill.*  
38 2020; 25(16).
- 39 101. Lai CKC, Ng RWY, Wong MCS, Chong KC, Yeoh YK, Chen Z, Chan PKS. Epidemiological  
40 characteristics of the first 100 cases of coronavirus disease 2019 (COVID-19) in Hong Kong Special  
41 Administrative Region, China, a city with a stringent containment policy. *Int J Epidemiol.* 2020;  
42 49(4):1096-1105.
- 43 102. Jia J, Hu X, Yang F, Song X, Dong L, Zhang J, Jiang F, Gao R. Epidemiological Characteristics on the  
44 Clustering Nature of COVID-19 in Qingdao City, 2020: A Descriptive Analysis. *Disaster medicine and  
45 public health preparedness.* 2020; 14(5):643-647.
- 46 103. Hua CZ, Miao ZP, Zheng JS, Huang Q, Sun QF, Lu HP, Su FF, Wang WH, Huang LP, Chen DQ et al.  
47 Epidemiological features and viral shedding in children with SARS-CoV-2 infection. *Journal of  
48 Medical Virology.* 2020; 92(11):2804-2812.
- 49 104. Wong J, Chaw L, Koh WC, Alikhan MF, Jamaludin SA, Poh WWP, Naing L. Epidemiological  
50 investigation of the first 135 COVID-19 cases in Brunei: Implications for surveillance, control, and  
51 travel restrictions. *American Journal of Tropical Medicine and Hygiene.* 2020; 103(4):1608-1613.
- 52 105. Haw NJL, Uy J, Sy KTL, Abrigo MRM. Epidemiological profile and transmission dynamics of  
53 COVID-19 in the Philippines. *Epidemiology and infection.* 2020; 148:e204.
- 54 106. Zhang Q, Zhu J, Jia C, Xu S, Jiang T, Wang S. Epidemiology and Clinical Outcomes of COVID-19  
55 Patients in Northwestern China Who Had a History of Exposure in Wuhan City: Departure Time-  
56 Originated Pinpoint Surveillance. *Frontiers in Medicine.* 2021; 8.
- 57 107. Ganyani T, Kremer C, Chen D, Torneri A, Faes C, Wallinga J, Hens N. Estimating the generation  
58 interval for coronavirus disease (COVID-19) based on symptom onset data, March 2020.  
59 *Eurosurveillance.* 2020; 25(17).
- 60 108. Hart WS, Abbott S, Endo A, Hellewell J, Miller E, Andrews N, Maini PK, Funk S, Thompson RN.

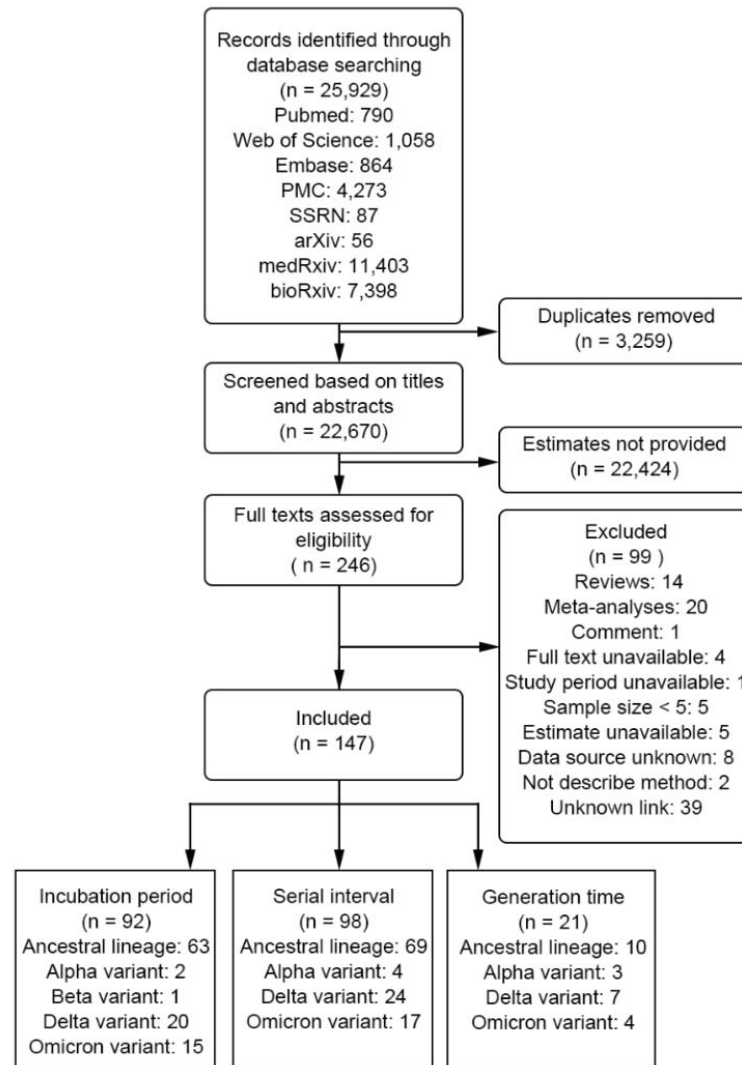
- 1 Inference of the SARS-CoV-2 generation time using UK household data. *Elife*. 2022; 11:e70767.
- 2 109. Hu S, Wang W, Wang Y, Litvinova M, Luo K, Ren L, Sun Q, Chen X, Zeng G, Li J et al. Infectivity,  
3 susceptibility, and risk factors associated with SARS-CoV-2 transmission under intensive contact  
4 tracing in Hunan, China. *Nature Communications*. 2021; 12(1):1533.
- 5 110. Zhao S, Tang B, Musa SS, Ma S, Zhang J, Zeng M, Yun Q, Guo W, Zheng Y, Yang Z et al. Estimating  
6 the generation interval and inferring the latent period of COVID-19 from the contact tracing data.  
7 *Epidemics*. 2021; 36.
- 8 111. Lau YC, Tsang TK, Kennedy-Shaffer L, Kahn R, Lau EHY, Chen D, Wong JY, Ali ST, Wu P, Cowling  
9 BJ. Joint Estimation Of Generation Time And Incubation Period For Coronavirus Disease (Covid-19). *J*  
10 *Infect Dis*. 2021; 224(10):1664-1671.
- 11 112. Deng Y, You C, Liu Y, Qin J, Zhou XH. Estimation of incubation period and generation time based on  
12 observed length-biased epidemic cohort with censoring for COVID-19 outbreak in China. *Biometrics*.  
13 2021; 77(3):929-941.
- 14 113. Böhm S, Woudenberg T, Chen D, Marosevic DV, Böhmer MM, Hansen L, Wallinga J, Sing A, Katz K.  
15 Epidemiology and transmission characteristics of early COVID-19 cases, 20 January-19 March 2020,  
16 in Bavaria, Germany. *Epidemiology and infection*. 2021; 149:e65.
- 17 114. Böhmer MM, Buchholz U, Corman VM, Hoch M, Katz K, Marosevic DV, Böhm S, Woudenberg T,  
18 Ackermann N, Konrad R et al. Investigation of a COVID-19 outbreak in Germany resulting from a  
19 single travel-associated primary case: a case series. *The Lancet Infectious Diseases*. 2020; 20(8):920-  
20 928.
- 21 115. Wu J, Huang Y, Tu C, Bi C, Chen Z, Luo L, Huang M, Chen M, Tan C, Wang Z et al. Household  
22 Transmission of SARS-CoV-2, Zhuhai, China, 2020. *Clinical Infectious Diseases*. 2020; 71(16):2099-  
23 2108.
- 24 116. Yang L, Dai J, Zhao J, Wang Y, Deng P, Wang J. Estimation of incubation period and serial interval of  
25 COVID-19: Analysis of 178 cases and 131 transmission chains in Hubei province, China.  
26 *Epidemiology and Infection*. 2020; 148:e117.
- 27 117. Zhang J, Litvinova M, Wang W, Wang Y, Deng X, Chen X, Li M, Zheng W, Yi L, Chen X et al.  
28 Evolving epidemiology and transmission dynamics of coronavirus disease 2019 outside Hubei province,  
29 China: a descriptive and modelling study. *The Lancet Infectious Diseases*. 2020; 20(7):793-802.
- 30 118. Backer JA, Klinkenberg D, Wallinga J. Incubation period of 2019 novel coronavirus (2019-nCoV)  
31 infections among travellers from Wuhan, China, 20 28 January 2020. *Eurosurveillance*. 2020; 25(5).
- 32 119. Bui LV, Nguyen HT, Levine H, Nguyen HN, Nguyen TA, Nguyen TP, Nguyen TT, Do TTT, Pham NT,  
33 Bui MH. Estimation of the incubation period of COVID-19 in Vietnam. *PLoS One*. 2020;  
34 15(12):e0243889.
- 35 120. Cheng C, Zhang D, Dang D, Geng J, Zhu P, Yuan M, Liang R, Yang H, Jin Y, Xie J et al. Incubation  
36 Period of COVID-19 From 11545 Patients in Observation Study. *Research Square*. 2021.
- 37 121. Han T. Outbreak investigation: transmission of COVID-19 started from a spa facility in a local  
38 community in Korea. *Epidemiol Health*. 2020; 42:e2020056.
- 39 122. Kong TK. Longer incubation period of coronavirus disease 2019 (COVID-19) in older adults. *Aging*  
40 *Medicine*. 2020; 3(2):102-109.
- 41 123. Men K, Wang X, Yihao L, Zhang G, Hu J, Gao Y, Han H. Estimate the incubation period of  
42 coronavirus 2019 (COVID-19). *medRxiv*. 2020.
- 43 124. Xiao Z, Guo W, Luo Z, Liao J, Wen F, Lin Y. Examining geographical disparities in the incubation  
44 period of the COVID-19 infected cases in Shenzhen and Hefei, China. *Environmental Health and*  
45 *Preventive Medicine*. 2021; 26(1).
- 46 125. Xiao Z, Xie X, Guo W, Luo Z, Liao J, Wen F, Zhou Q, Han L, Zheng T. Examining the incubation  
47 period distributions of COVID-19 on Chinese patients with different travel histories. *Journal of*  
48 *Infection in Developing Countries*. 2020; 14(4):323-327.
- 49 126. Ratovoson R, Razafimahatratra R, Randriamanantsoa L, Raberahona M, Rabarison HJ,  
50 Rahaingovahoaka FN, Andriamasy EH, Herindrainy P, Razanajatovo N, Andriamandimby SF et al.  
51 Household transmission of COVID-19 among the earliest cases in Antananarivo, Madagascar.  
52 *Influenza Other Respir Viruses*. 2022; 16(1):48-55.
- 53 127. Aghaali M, Kolifarhood G, Nikbakht R, Saadati HM, Hashemi Nazari SS. Estimation of the serial  
54 interval and basic reproduction number of COVID-19 in Qom, Iran, and three other countries: A data-  
55 driven analysis in the early phase of the outbreak. *Transboundary and emerging diseases*. 2020;  
56 67(6):2860-2868.
- 57 128. Bi Q, Wu Y, Mei S, Ye C, Zou X, Zhang Z, Liu X, Wei L, Truelove SA, Zhang T et al. Epidemiology  
58 and transmission of COVID-19 in 391 cases and 1286 of their close contacts in Shenzhen, China: a  
59 retrospective cohort study. *The Lancet Infectious Diseases*. 2020; 20(8):911-919.
- 60 129. Chu VT, Yousaf AR, Chang K, Schwartz NG, McDaniel CJ, Lee SH, Szablewski CM, Brown M,

- 1 Drenzek CL, Dirlikov E et al. Household Transmission of SARS-CoV-2 from Children and  
2 Adolescents. *N Engl J Med.* 2021; 385(10):954-956.
- 3 130. Expert Taskforce for the C-CSO. Epidemiology of COVID-19 Outbreak on Cruise Ship Quarantined at  
4 Yokohama, Japan, February 2020. *Emerging infectious diseases.* 2020; 26(11):2591-2597.
- 5 131. McAloon CG, Wall P, Griffin J, Casey M, Barber A, Codd M, Gormley E, Butler F, Mc VMLL, Walsh  
6 C et al. Estimation of the serial interval and proportion of pre-symptomatic transmission events of  
7 COVID-19 in Ireland using contact tracing data. *BMC Public Health.* 2021; 21(1):805.
- 8 132. Ng SH-X, Kaur P, Kremer C, Tan WS, Tan AL, Hens N, Toh MP, Teow KL, Kannapiran P. Estimating  
9 Transmission Parameters for COVID-19 Clusters by Using Symptom Onset Data, Singapore, January-  
10 April 2020. *Emerging infectious diseases.* 2021; 27(2):582-585.
- 11 133. Talmoudi K, Safer M, Letaief H, Hchaichi A, Harizi C, Dhaouadi S, Derouiche S, Bouaziz I, Gharbi D,  
12 Najar N et al. Estimating transmission dynamics and serial interval of the first wave of COVID-19  
13 infections under different control measures: a statistical analysis in Tunisia from February 29 to May 5,  
14 2020. *BMC Infectious Diseases.* 2020; 20(1):914.
- 15 134. Wang K, Zhao S, Liao Y, Zhao T, Wang X, Zhang X, Jiao H, Li H, Yin Y, Wang MH et al. Estimating  
16 the serial interval of the novel coronavirus disease (COVID-19) based on the public surveillance data in  
17 Shenzhen, China, from 19 January to 22 February 2020. *Transboundary and emerging diseases.* 2020;  
18 67(6):2818-2822.
- 19 135. Kwok KO, Wei WI, Huang Y, Kam KM, Chan EYY, Riley S, Chan HHH, Hui DSC, Wong SYS, Yeoh  
20 EK. Evolving Epidemiological Characteristics of COVID-19 in Hong Kong From January to August  
21 2020: Retrospective Study. *Journal of medical Internet research.* 2021; 23(4):e26645.
- 22 136. Chong DWQ, Jayaraj VJ, Ng CW, Sam IC, Said MA, Ahmad Zaki R, Hairi NN, Nik Farid ND, Hoe  
23 VCW, Isahak M et al. Propagation of a hospital-associated cluster of COVID-19 in Malaysia. *BMC  
24 Infectious Diseases.* 2021; 21(1).
- 25 137. Dai J, Yang L, Zhao J. Probable longer incubation period for elderly covid-19 cases: Analysis of 180  
26 contact tracing data in hubei province, china. *Risk Management and Healthcare Policy.* 2020; 13:1111-  
27 1117.
- 28 138. Huang L, Zhang X, Zhang X, Wei Z, Zhang L, Xu J, Liang P, Xu Y, Zhang C, Xu A. Rapid  
29 asymptomatic transmission of COVID-19 during the incubation period demonstrating strong infectivity  
30 in a cluster of youngsters aged 16-23 years outside Wuhan and characteristics of young patients with  
31 COVID-19: A prospective contact-tracing study. *Journal of Infection.* 2020; 80(6):e1-e13.
- 32 139. Li M, Chen P, Yuan Q, Song B, Ma J. Transmission characteristics of the COVID-19 outbreak in China:  
33 a study driven by data. *medRxiv.* 2020.
- 34 140. Areekal B, Vijayan SM, Suseela MS, Andrews MA, Ravi RK, Sukumaran ST, Jose R, Edappanatt FTT.  
35 Risk factors, epidemiological and clinical outcome of close contacts of covid-19 cases in a tertiary  
36 hospital in southern india. *Journal of Clinical and Diagnostic Research.* 2021; 15(3):LC34-LC37.
- 37 141. Cao Y, Wang Y, Das A, Pan CQ, Xie W. Transmission dynamics of COVID-19 among index case  
38 family clusters in Beijing, China. *Epidemiology and Infection.* 2020.
- 39 142. Chun JY, Baek G, Kim Y. Transmission onset distribution of COVID-19. *International Journal of  
40 Infectious Diseases.* 2020; 99:403-407.
- 41 143. Tindale LC, Stockdale JE, Coombe M, Garlock ES, Lau WYV, Saraswat M, Zhang L, Chen D,  
42 Wallinga J, Colijn C. Evidence for transmission of COVID-19 prior to symptom onset. *Elife.* 2020; 9.
- 43 144. Won YS, Kim JH, Ahn CY, Lee H. Subcritical transmission in the early stage of covid-19 in korea.  
44 *International Journal of Environmental Research and Public Health.* 2021; 18(3):1-10.
- 45 145. Xia W, Liao J, Li C, Li Y, Qian X, Sun X, Xu H, Mahai G, Zhao X, Shi L et al. Transmission of corona  
46 virus disease 2019 during the incubation period may lead to a quarantine loophole. *medRxiv.* 2020.
- 47 146. Zhao H, Zhang Z, Lun W, Chen Z, Lu X, Li J, Qiu F, Li S, Mao C, Lu Y et al. Transmission dynamics  
48 and successful control measures of SARS-CoV-2 in the mega-size city of Guangzhou, China. *Medicine  
49 (United States).* 2021; 100(48).
- 50 147. Lauer SA, Grantz KH, Bi Q, Jones FK, Zheng Q, Meredith HR, Azman AS, Reich NG, Lessler J. The  
51 incubation period of coronavirus disease 2019 (CoVID-19) from publicly reported confirmed cases:  
52 Estimation and application. *Annals of Internal Medicine.* 2020; 172(9):577-582.
- 53 148. Emecen AN, Basoglu Sensoy E, Sezgin E, Yildirim Ustuner B, Keskin S, Siyve N, Celik SG, Bayrak G,  
54 Senturk Durukan N, Coskun Beyan A et al. Transmission dynamics and timing of key events for  
55 SARS-CoV-2 infection in healthcare workers. *Infect Dis.* 2021; 53(7):531-537.
- 56 149. Li M, Liu K, Song Y, Wang M, Wu J. Serial Interval and Generation Interval for Imported and Local  
57 Infectors, Respectively, Estimated Using Reported Contact-Tracing Data of COVID-19 in China.  
58 *Frontiers in public health.* 2020; 8:577431.
- 59 150. Ali ST, Wang L, Lau EHY, Xu X-K, Du Z, Wu Y, Leung GM, Cowling BJ. Serial interval of SARS-  
60 CoV-2 was shortened over time by nonpharmaceutical interventions. *Science.* 2020; 369(6507):1106-

- 1 1109.
- 2 151. Bernal Lopez J, Panagiotopoulos N, Byers C, Vilaplana TG, Boddington N, Zhang XS, Charlett A,  
3 Elgohari S, Coughlan L, Whillock R et al. Transmission dynamics of COVID-19 in household and  
4 community settings in the United Kingdom, January to March 2020. *Eurosurveillance*. 2022; 27(15).
- 5 152. Cereda D, Manica M, Tirani M, Rovida F, Demicheli V, Ajelli M, Poletti P, Trentini F, Guzzetta G,  
6 Marziano V et al. The early phase of the COVID-19 epidemic in Lombardy, Italy. *Epidemics*. 2021; 37.
- 7 153. Hong K, Yum S, Kim J, Chun BC. The Serial Interval of COVID-19 in Korea: 1,567 Pairs of  
8 Symptomatic Cases from Contact Tracing. *Journal of Korean medical science*. 2020; 35(50):e435.
- 9 154. Lavezzo E, Franchin E, Ciavarella C, Cuomo-Dannenburg G, Barzon L, Del Vecchio C, Rossi L,  
10 Manganelli R, Loregian A, Navarin N et al. Suppression of a SARS-CoV-2 outbreak in the Italian  
11 municipality of Vo'. *Nature*. 2020; 584(7821):425-429.
- 12 155. Liu T, Qi L, Yao M, Tian K, Lin M, Jiang H, Zeng M, Huang J. Serial Interval and Reproductive  
13 Number of COVID-19 Among 116 Infector-infectee Pairs - Jingzhou City, Hubei Province, China,  
14 2020. *China CDC Wkly*. 2020; 2(27):491-495.
- 15 156. Najafi F, Izadi N, Hashemi-Nazari SS, Khosravi-Shadmani F, Nikbakht R, Shakiba E. Serial interval  
16 and time-varying reproduction number estimation for COVID-19 in western Iran. *New Microbes and  
17 New Infections*. 2020; 36.
- 18 157. Prete CA, Buss L, Dighe A, Porto VB, da Silva Candido D, Ghilardi F, Pybus OG, de Oliveira WK,  
19 Croda JHR, Sabino EC et al. Serial interval distribution of SARS-CoV-2 infection in Brazil. *J Travel  
20 Med*. 2021; 28(2).
- 21 158. Reed IG, Walker ES, Landguth EL. SARS-CoV-2 Serial Interval Variation, Montana, USA, March 1-  
22 July 31, 2020. *Emerging infectious diseases*. 2021; 27(5):1486-1491.
- 23 159. Ryu S, Ali ST, Noh E, Kim D, Lau EHY, Cowling BJ. Transmission dynamics and control of two  
24 epidemic waves of SARS-CoV-2 in South Korea. *BMC Infectious Diseases*. 2021; 21(1).
- 25 160. Saurabh S, Verma MK, Gautam V, Kumar N, Goel AD, Gupta MK, Bhardwaj P, Misra S. Transmission  
26 Dynamics of the COVID-19 Epidemic at the District Level in India: Prospective Observational Study.  
27 *JMIR public health and surveillance*. 2020; 6(4):e22678.
- 28 161. Thai PQ, Rabaa MA, Luong DH, Tan DQ, Quang TD, Quach HL, Hoang Thi NA, Dinh PC, Nghia ND,  
29 Tu TA et al. The First 100 Days of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)  
30 Control in Vietnam. *Clinical Infectious Diseases*. 2021; 72(9):E334-E342.
- 31 162. Wang Y, Siesel C, Chen Y, Lopman B, Edison L, Thomas M, Adams C, Lau M, Teunis PFM. Severe  
32 Acute Respiratory Syndrome Coronavirus 2 Transmission in Georgia, USA, February 1-July 13, 2020.  
33 *Emerg Infect Dis*. 2021; 27(10):2578-2587.
- 34 163. Qin J, You C, Lin Q, Hu T, Yu S, Zhou XH. Estimation of incubation period distribution of COVID-19  
35 using disease onset forward time: A novel cross-sectional and forward follow-up study. *Science  
36 advances*. 2020; 6(33):eabc1202.
- 37 164. Ren X, Li Y, Yang X, Li Z, Cui J, Zhu A, Zhao H, Yu J, Nie T, Ren M et al. Evidence for pre-  
38 symptomatic transmission of coronavirus disease 2019 (COVID-19) in China. *Influenza Other Respir  
39 Viruses*. 2021; 15(1):19-26.
- 40 165. Zhao S, Gao D, Zhuang Z, Chong MKC, Cai Y, Ran J, Cao P, Wang K, Lou Y, Wang W et al.  
41 Estimating the Serial Interval of the Novel Coronavirus Disease (COVID-19): A Statistical Analysis  
42 Using the Public Data in Hong Kong From January 16 to February 15, 2020. *FRONTIERS IN  
43 PHYSICS*. 2020; 8.
- 44 166. Adam DC, Wu P, Wong JY, Lau EHY, Tsang TK, Cauchemez S, Leung GM, Cowling BJ. Clustering  
45 and superspreading potential of SARS-CoV-2 infections in Hong Kong. *Nat Med*. 2020; 26(11):1714-  
46 1719.
- 47 167. Althobaity Y, Wu J, Tildesley MJ. A comparative analysis of epidemiological characteristics of MERS-  
48 CoV and SARS-CoV-2 in Saudi Arabia. *Infectious Disease Modelling*. 2022; 7(3):473-485.
- 49 168. Wang Y, Sun K, Pan Y, Yi L, Huo D, Wu Y, Dong S, Guo J, Dou X, Wang W et al. SARS-CoV-2  
50 containment was achievable during the early stage of the pandemic: a retrospective modelling study of  
51 the Xinfadi outbreak in Beijing. *medRxiv*. 2022.
- 52 169. Achangwa C, Park H, Ryu S. Incubation period of wild type of SARS-CoV-2 infections by age, gender,  
53 and epidemic periods. *Frontiers in public health*. 2022; 10:905020.
- 54 170. Zhao Q, Zhang Y, Li M, Tian R, Zhao Y, Cao B, Yao L, Sheng X, Yu Y. Epidemiological clustered  
55 characteristics of coronavirus disease 2019 (COVID-19) in three phases of transmission in Jilin  
56 Province, China. *PLoS One*. 2023; 18(1):e0279879.
- 57 171. Somda SMA, Ouedraogo B, Pare CB, Kouanda S. Estimation of the Serial Interval and the Effective  
58 Reproductive Number of COVID-19 Outbreak Using Contact Data in Burkina Faso, a Sub-Saharan  
59 African Country. *Comput Math Methods Med*. 2022; 2022:8239915.
- 60 172. Hammond V, Butchard M, Stablein H, Jack S. COVID-19 in one region of New Zealand: a descriptive

- 1 epidemiological study. *Aust N Z J Public Health*. 2022; 46(6):745-750.
- 2 173. Galmiche S, Cortier T, Charmet T, Schaeffer L, Chény O, von Platen C, Lévy A, Martin S, Omar F,  
3 David C et al. SARS-CoV-2 incubation period across variants of concern, individual factors, and  
4 circumstances of infection in France: a case series analysis from the ComCor study. *Lancet Microbe*.  
5 2023.
- 6 174. Lessler J, Reich NG, Brookmeyer R, Perl TM, Nelson KE, Cummings DA. Incubation periods of acute  
7 respiratory viral infections: a systematic review. *Lancet Infect Dis*. 2009; 9(5):291-300.
- 8 175. Du Z, Liu C, Wang L, Bai Y, Lau EHY, Wu P, Cowling BJ. Shorter serial intervals and incubation  
9 periods in SARS-CoV-2 variants than the SARS-CoV-2 ancestral strain. *Journal of travel medicine*.  
10 2022.
- 11 176. Vink MA, Bootsma MC, Wallinga J. Serial intervals of respiratory infectious diseases: a systematic  
12 review and analysis. *Am J Epidemiol*. 2014; 180(9):865-875.
- 13 177. Assiri A, McGeer A, Perl TM, Price CS, Al Rabeeah AA, Cummings DA, Alabdullatif ZN, Assad M,  
14 Almulhim A, Makhdoom H et al. Hospital outbreak of Middle East respiratory syndrome coronavirus.  
15 *N Engl J Med*. 2013; 369(5):407-416.
- 16 178. Roll U, Yaari R, Katriel G, Barnea O, Stone L, Mendelson E, Mandelboim M, Huppert A. Onset of a  
17 pandemic: characterizing the initial phase of the swine flu (H1N1) epidemic in Israel. *BMC Infect Dis*.  
18 2011; 11:92.
- 19 179. Cauchemez S, Fraser C, Van Kerkhove MD, Donnelly CA, Riley S, Rambaut A, Enouf V, van der Werf  
20 S, Ferguson NM. Middle East respiratory syndrome coronavirus: quantification of the extent of the  
21 epidemic, surveillance biases, and transmissibility. *Lancet Infect Dis*. 2014; 14(1):50-56.
- 22 180. Asiedu-Bekoe F, Adu DA, Offei A. Mass oseltamivir prophylaxis halts pandemic influenza A H1N1  
23 2009 outbreak in a secondary school in Ashanti Region, Ghana. *Ghana Med J*. 2012; 46(4):219-224.
- 24 181. Viego V, Geri M, Castiglia J, Jouglard E. Período de incubación e intervalo serial para COVID-19 en  
25 una cadena de transmisión en Bahía Blanca (Argentina). *Ciencia & Saúde Coletiva*. 2020; 25.
- 26 182. Nishiura H, Linton NM, Akhmetzhanov AR. Serial interval of novel coronavirus (COVID-19)  
27 infections. *International Journal of Infectious Diseases*. 2020; 93:284-286.
- 28 183. Alene M, Yismaw L, Assemie MA, Ketema DB, Gietaneh W, Birhan TY. Serial interval and incubation  
29 period of COVID-19: a systematic review and meta-analysis. *BMC Infectious Diseases*. 2021;  
30 21(1):257.
- 31 184. Sun K, Wang W, Gao L, Wang Y, Luo K, Ren L, Zhan Z, Chen X, Zhao S, Huang Y et al. Transmission  
32 heterogeneities, kinetics, and controllability of SARS-CoV-2. *Science*. 2021; 371(6526):eabe2424.
- 33 185. Puhach O, Meyer B, Eckerle I. SARS-CoV-2 viral load and shedding kinetics. *Nat Rev Microbiol*.  
34 2022.
- 35 186. Ali ST, Yeung A, Shan S, Wang L, Gao H, Du Z, Xu X-K, Wu P, Lau EHY, Cowling BJ. Serial  
36 Intervals and Case Isolation Delays for Coronavirus Disease 2019: A Systematic Review and Meta-  
37 Analysis. *Clinical Infectious Diseases*. 2021; 74(4):685-694.
- 38 187. Jiehao C, Jin X, Daojiong L, Zhi Y, Lei X, Zhenghai Q, Yuehua Z, Hua Z, Ran J, Pengcheng L et al. A  
39 Case Series of Children With 2019 Novel Coronavirus Infection: Clinical and Epidemiological  
40 Features. *Clin Infect Dis*. 2020; 71(6):1547-1551.
- 41 188. Han YN, Feng ZW, Sun LN, Ren XX, Wang H, Xue YM, Wang Y, Fang Y. A comparative-descriptive  
42 analysis of clinical characteristics in 2019-coronavirus-infected children and adults. *Journal of Medical  
43 Virology*. 2020; 92(9):1596-1602.
- 44
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1 **Figures**

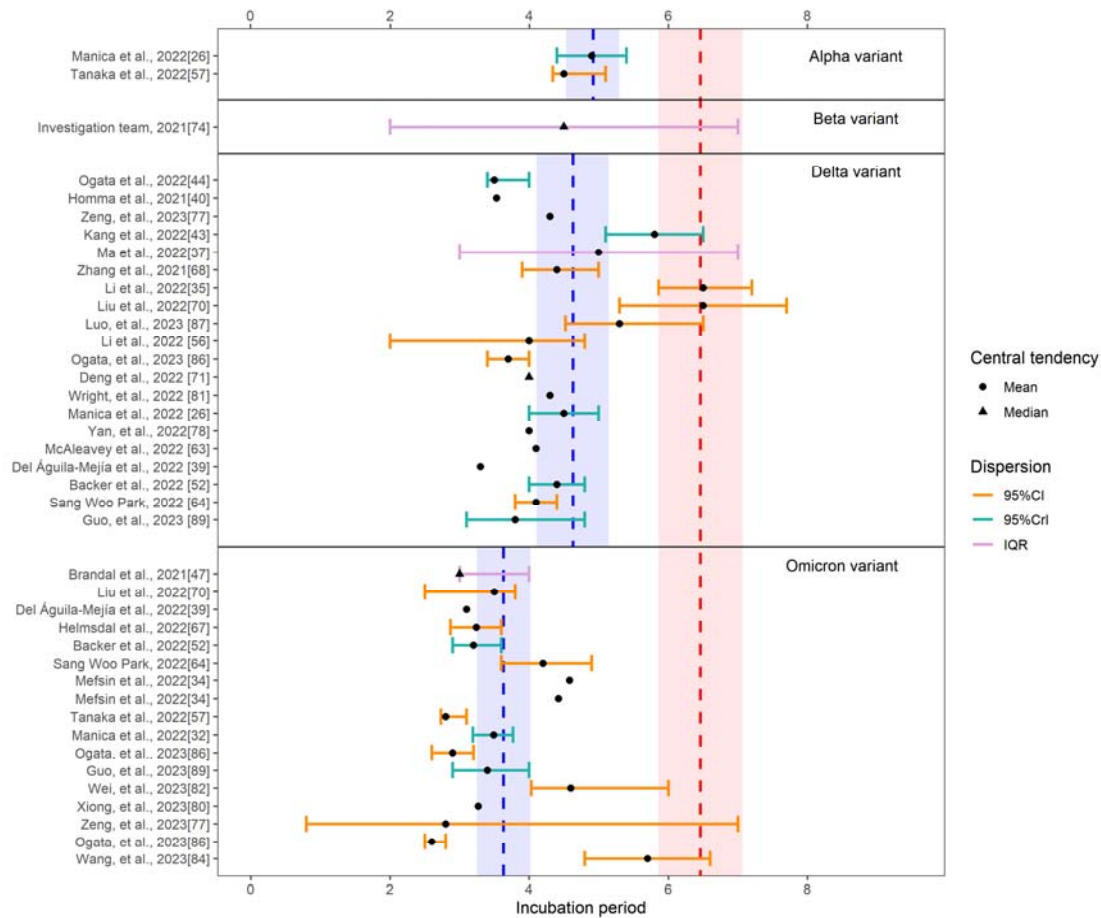


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3 **Figure 1. Study Flow Diagram.**

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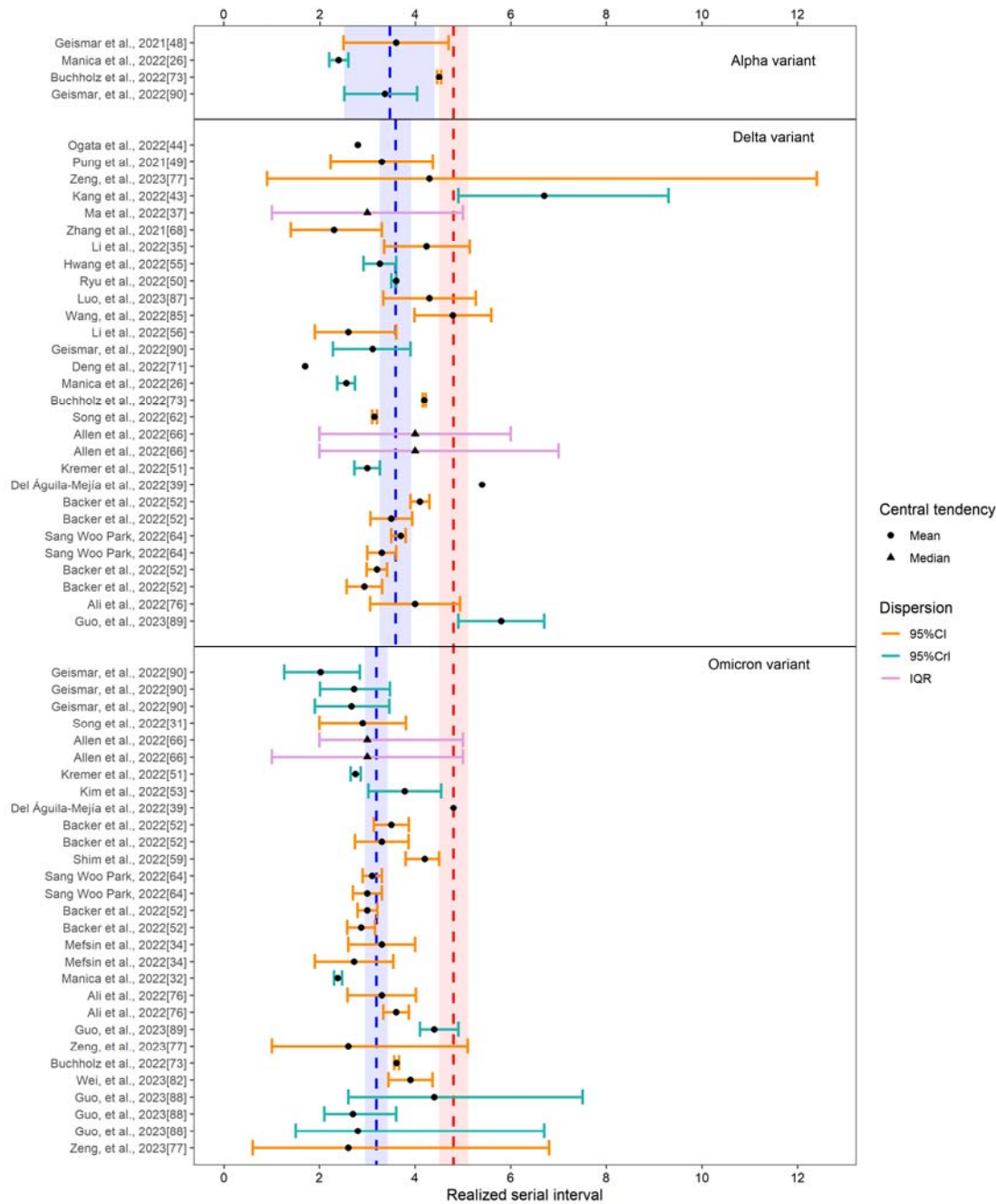




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2 **Figure 2. The reported estimates of the incubation period.** The red vertical dotted line and rectangle  
3 correspond to the pooled mean estimate and its 95% CI of the ancestral lineage, respectively. The blue  
4 vertical dotted line and rectangle in different strata denote the pooled mean estimates and their 95% CI of  
5 corresponding variants, respectively. Black points and triangles represent mean estimates and median  
6 estimates, respectively. The horizontal segments indicate CI (orange), CrI (green), and IQR (purple).

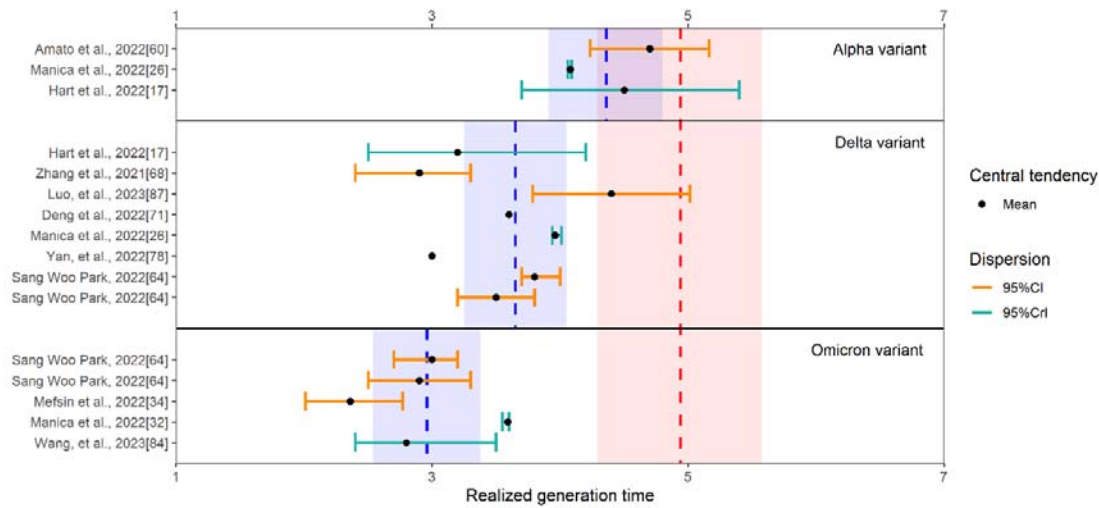
7 Abbreviations: CI, confidence interval; CrI, credible interval; IQR, interquartile range.



1

2 **Figure 3. The reported estimates of the realized serial interval.** The red vertical dotted line and  
 3 rectangle correspond to the pooled mean estimate and its 95%CI of the ancestral lineage, respectively. The  
 4 blue vertical dotted line and rectangle in different strata denote the pooled mean estimates and their 95%CI  
 5 of corresponding variants, respectively. Black points and triangles represent mean estimates and median  
 6 estimates, respectively. The horizontal segments indicate CI (orange), CrI (green), and IQR (purple).  
 7 Abbreviations: CI, confidence interval; CrI, credible interval; IQR, interquartile range.

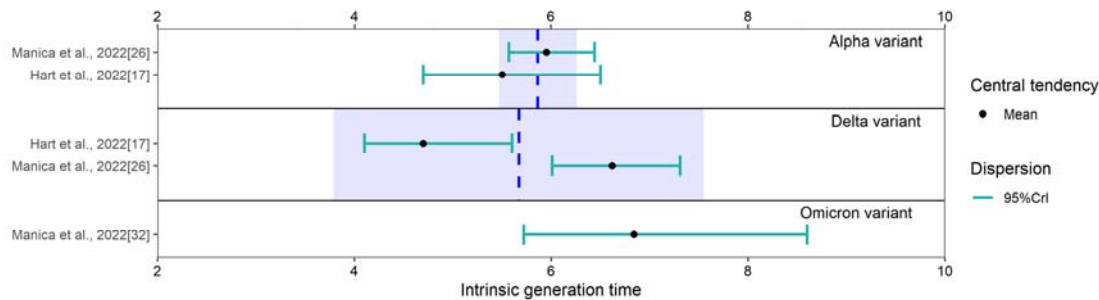
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3 **Figure 4. The reported estimates of the realized generation time.** The red vertical dotted line and  
 4 rectangle correspond to the pooled mean estimate and its 95%CI of the ancestral lineage, respectively. The  
 5 blue vertical dotted line and rectangle in different strata denote the pooled mean estimates and their 95%CI  
 6 of corresponding variants, respectively. Black points and triangles represent mean estimates and median  
 7 estimates, respectively. The horizontal segments indicate CI (orange), CrI (green), and IQR (purple).  
 8 Abbreviations: CI, confidence interval; CrI, credible interval; IQR, interquartile range.

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11 **Figure 5. The reported estimates of the intrinsic generation time.** The blue vertical dotted line and  
 12 rectangle in different strata denote the pooled mean estimates and their 95%CI of corresponding variants,  
 13 respectively. Black points and triangles represent mean estimates and median estimates, respectively. The  
 14 horizontal segments indicate CI (orange), CrI (green), and IQR (purple). Abbreviations: CI, confidence  
 15 interval; CrI, credible interval; IQR, interquartile range.

16