Communications

Reproduction Number of the Omicron Variant Triples That of the Delta Variant

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Abstract: COVID-19 remains a persistent threat, especially with the predominant Omicron variant emerging in early 2022, presenting with high transmissibility, immune escape, and waning. There is a need to rapidly ramp up global vaccine coverage while enhancing public health and social measures. Timely and reliable estimation of the reproduction number throughout a pandemic is critical for assessing the impact of mitigation efforts and the potential need to adjust for control measures. We conducted a systematic review on the reproduction numbers of the Omicron variant and gave the pooled estimates. We identified six studies by searching PubMed, Embase, Web of Science, and Google Scholar for articles published between 1 January 2020 and 6 March 2022. We estimate that the effective reproduction number ranges from 2.43 to 5.11, with a pooled estimate of 4.20 (95% CI: 2.05, 6.35). The Omicron variant has an effective reproduction number which is triple (2.71 (95% CI: 1.86, 3.56)) that of the Delta variant.

Keywords: COVID-19; SARS-CoV-2; reproduction number; Omicron; systematic review; meta-analysis

1. Introduction

COVID-19 remains a persistent threat, especially with the predominant Omicron variant emerging in early 2022, presenting with high transmissibility, immune escape, and waning. There is a need to rapidly ramp up global vaccine coverage while enhancing public health and social measures. Timely and reliable estimation of the reproduction number throughout a pandemic is critical for assessing the impact of mitigation efforts and the potential need to adjust for control measures.

Five SARS-CoV-2 variants of concern (VOC)—the Alpha, Beta, Gamma, Delta, and Omicron variants—have been identified as of 6 March 2022 [1]. The most recent, Omicron, was first identified in November 2021 and has since been reported in 194 countries and territories [2]. The basic reproduction number (R0) and the effective reproduction number (Re) are two key epidemiological metrics used to (i) estimate the average number of secondary infections caused by each infected case in a fully susceptible population and (ii) estimate the average number of secondary infections at a given time point during an epidemic, respectively. Accurate estimates of R0 and Re of SARS-CoV-2 variants are essential for tracking pandemic progress, and for determining the need for and strength of control measures, such as social distancing, to mitigate transmission. Here, we performed
a systematic review and meta-analysis of the published estimates of $R_0$ and $R_e$ for the SARS-CoV-2 Omicron variant.

2. Methods

2.1. Search Strategy and Selection Criteria

All searches were carried out on 6 March 2022 in PubMed, Embase, Web of Science, and Google Scholar for articles published from 1 January 2020 to 6 March 2022. Our search terms for reproduction numbers of SARS-CoV-2 variant included (#1) “COVID-19” or “SARS-CoV-2” or “2019-nCoV” or “coronavirus”; (#2) “reproduct* number” or “reproduct* ratio” or “reproduct* rate” or “transmissibility”; and (#3) Omicron or “B.1.1.529”. Our final search term was #1 and #2 and #3. After reading the abstract and full text, we included the studies that provided information about the estimated reproduction numbers of the Omicron variant and the relative ratio of the Omicron variant to the Delta variant.

2.2. Data Extraction

All data were extracted independently and entered in a standardized form by 3 co-authors (Z.D., H.H., and S.W.). Conflicts over inclusion of the studies and retrieving the estimates of these variables were resolved by Z.D. Information was extracted on the estimates of reproduction number of COVID-19 variants coupled with the corresponding 95% confidence interval (CI) or the 95% credible interval (CrI). Other information, such as the study location and the estimation methods, were also extracted for each selected study. For studies that estimated the ratio, $R_e/R_\delta$, in the reproduction number, for the Omicron variant versus the Delta variant, we calculated the effective reproduction number of the Omicron variant by adopting the values of $R_e$ of the Delta variant, estimated from other studies.

2.3. Statistical Analysis

A random effects model was further used to perform a meta-analysis in this study. Analyses were conducted in R version 4.1.1 (R Foundation for Statistical Computing, Vienna, Austria). Specifically, for studies providing the mean and with 95% confidence intervals, we use R function metagen of the meta package to estimate the pooled estimates of effective reproduction numbers using the random effects model. Our R codes are publicly available upon publication at github (https://github.com/ZhanweiDU/R_Omicron/, accessed on 10 April 2022).

3. Results

We identified 123 studies by searching PubMed, Embase, Web of Science, and Google Scholar for articles published between 1 January 2020 and 6 March 2022, and additionally included 3 studies from our own reference list. Of these, 2 duplicates were removed, and 98 studies were excluded through title and abstract screening, leaving 28 studies for full-text assessment. Six of them were finally included in this study, providing one $R_0$ estimate and six $R_e$ estimates. The detailed selection process is illustrated in Figure 1. The reported substrains include BA.1, BA.2, and BA.1.1, among which BA.1 was the most studied. The final six selected studies were conducted in South Africa, Denmark, South Africa, China, England, and India, respectively (Table 1).
Estimates of reproduction numbers were reported for South Africa, Denmark, China, England, and India, with mean estimates of $R_e$ ranging from 2.43 to 5.11 (Tables 1 and S1), together with the reported reproduction numbers of the Delta variant over countries [2]). After excluding one study [8] where the 95% CI was not reported, the pooled estimate of $R_e$ was 4.20 (95% CI: 2.05, 6.35). Overall, the Omicron variant has a higher reproduction
number than that of the Delta variant. The ratio of the reproduction numbers between the Omicron and the Delta variant ranges from 1.60 to 4.20, with a pooled estimate of 2.71 (95% CI: 1.86, 3.56), denoting that the Omicron variant has a higher transmission potential compared with other earlier variants (Alpha, Beta, Delta, Epsilon, Eta, Gamma, Iota, Kappa, Zeta, R.1 (a Pango lineage not labeled by the WHO), B.1.1.519, B.1.1.222, N501Y, and D514G (lineages not labeled by the WHO)) [10].

4. Discussion

Given the ongoing appearance of new variations, the pandemic’s future is bleak [11]. Throughout the pandemic, governments resorted mostly to mass vaccination to decrease transmission and reduce mortality [12]. To prevent the spread of variants with a higher transmissibility, more drastic interventions may be required. It is thus necessary to guide control measures in reducing the propagation of viruses by accurately estimating the reproduction number for various wild-type genetic variants. This systematic review may provide epidemiologists with practical guidelines of the range of effective reproduction numbers across countries to fit transmission rates in epidemic simulation, perhaps for estimates of importation risks from regions with Omicron outbreaks to a susceptible region. As more specific estimates for Omicron substrains are available, further updates should be made to inform epidemic simulation.

A few caveats need to be discussed. First, we did not include factors potentially correlated with estimates of the reproduction number, such as contact patterns and climatic factors, because of data availability. Second, we only studied basic and effective reproduction numbers to assess the transmissibility of SARS-CoV-2 variants, rather than that of transmission advantage using other metrics apart from reproduction numbers. Third, most of the eligible studies in our review did not account for waning of immunity and re-infection, which could impact the comparison of effective reproduction numbers. Fourth, some studies estimate reproductive numbers in the early period of outbreaks, which may provide lower values. We use the reported estimates of reproduction numbers directly without any adjustment. Fifth, there are three substrains (e.g., BA.1, BA.2, and BA.1.1) of the Omicron variant in our studies. BA.2 is expected to be more transmissible than BA.1 [13]. The effective reproduction number in the study period with the substrain mixing of BA.2 and others may be underestimated when BA.2 has been the prevalent Omicron substrain globally since January 2022 [14].

In conclusion, multiple estimates of the effective reproduction number of the Omicron variant have been reported, tripling that of the Delta variant. COVID-19 remains a persistent threat, especially with the predominant Omicron variant presenting in early 2022 with high transmissibility, immune escape, and waning. There is a need to rapidly ramp up global vaccine coverage while enhancing public health and social measures.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/v14040821/s1, Table S1. Description of studies included for the Omicron variant of SARS-CoV-2. References [3–10] are cited in the supplementary materials.

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