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Review Article

Estimate of the Basic Reproduction Number for Delta variant of SARS-CoV-2: A Systematic Review and Meta-analysis

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ABSTRACT

Introduction: An essential concept in assessing the extent to which an infectious outbreak spread is the concept of basic reproductive number (R_0). The current systematic review and meta-analysis aimed to estimate the R_0 of the Delta variant of SARS-CoV-2 based on studies published from 1 January 2021 to 23 September 2021.
Methods: International databases (including Google Scholar, Science Direct, PubMed, and Scopus) were searched using keywords: "Basic reproduction number, R_0, COVID-19, SARS-COV-2, Severe Acute Respiratory Syndrome Coronavirus, NCOV, 2019 NCOV, coronavirus, Delta variant, B.1.617.2". Due to significant heterogeneity, DerSimonian-Laird random-effects model was used to estimate the pooled value of R_0.
Results: A total of 245 reports were identified. After assessing the inclusion criteria, three studies were selected. The pooled R_0 for the Delta variant was estimated as 5.10 (95% CI, 3.04 to 7.17), (I^2 =86.77%, T^2:2.68, p-value from the chi-square test for heterogeneity was<0.001).
Conclusion: Considering the estimated value of R_0 for the Delta variant of SARS-CoV-2, the amount of vaccine coverage required to achieve herd immunity appears to be higher than previous variants of the virus.

Introduction

To date, Several SARS-CoV-2 variants have been recognized, four of which (Alpha, Beta, Gamma, and Delta) are of specific concern due to higher transmissibility and mortality.[1] Delta (B.1.617.2) variant is estimated to increase the risk of hospitalization by about 85%.[2] This variant was first observed in India, and nowadays, it is found in different parts of the world and has become a global challenge.[3] A key concept in judging the extent to which an infectious epidemic tends to vanish or spread is the concept of basic reproductive number

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(R_0).[4] The origin of this concept is demography and later entered the field of epidemiology. R_0 represents the average number of infections generated by an infected person in a susceptible population without any vaccination.[5] The conceptual model of the R_0 is $D \times C \times P = R_0$. In this model, P is the probability of transmission in each contact, C is the number of daily contacts by a contagious individual, and D is the number of days a person is contagious. Therefore, D depends mainly on the biological features of the disease, while C and P depend on the social characteristics of the population. An $R_0 > 1$ means that the epidemic will propagate, and an $R_0 < 1$, means the epidemic will disappear. The rate at which an epidemic disappears or spreads depends on how far away R_0 is from one.[5] To date, published studies reporting an R_0 for the Delta variant of SARS-CoV-2 are rare. The present paper reviews the R_0 of the Delta variant based on a few available studies that exist through the literature and aims to estimate the pooled R_0 for the Delta (B.1.617.2) variant of SARS-CoV-2, using original articles published during 2021.

Methods

This systematic review and meta-analysis were performed to estimate the pooled R_0 of Delta (B.1.617.2) variant of SARS-CoV-2 in articles published from 1 January 2021 to 23 September 2021. We searched international databases (including Google Scholar, Science Direct, PubMed, and Scopus) to obtain studies on the R_0 of the Delta variant of SARS-CoV-2. The keywords were as follows:
Basic reproduction number, R_0, COVID-19, SARS-COV-2, Severe Acute Respiratory Syndrome Coronavirus, NCOV, 2019 NCOV, coronavirus, Delta variant, B.1.617.2.

Study Selection and Data Extraction

In the current study, all papers and preprints published in 2021 that estimated R_0 for the Delta variant of SARS-COV-2 were entered into the meta-analysis. The first author's name, country, model used to calculate R_0, and the estimated R_0 value (with a 95% confidence interval, CI) were extracted from the articles.

Risk of bias assessment

The critical appraisal of included manuscripts was assessed using the modified risk-of-bias (ROB) operational criteria.[6]

Statistical Analysis

Heterogeneity between studies was considered using the I^2 index, the Cochran Q test, and T^2. Because of the high I^2 value (>75%), as well as the significance of the Cochran Q test ($p<0.001$) DerSimonian-Laird random-effects model was used to estimate the pooled value of R_0 in this study. The procedure suggested by DerSimonian and Laird is the simplest and most commonly used method to fitting the random-effects model for meta-analysis.[7]
According to the Cochrane criteria and I^2 index, the amount of heterogeneity was divided into four categories: 0 to 40% (no important), 30 to 60% (moderate heterogeneity), 50 to 90% (substantial heterogeneity), and finally 75% and above (considerable heterogeneity).[8, 9] A classical measure of heterogeneity is Cochran's Q, which has long been used to assess statistical heterogeneity in meta-analysis and calculated as the weighted sum of squared differences

between individual study estimations and the pooled estimation across studies. Q is distributed as a chi-square statistic with k (number of studies) minus 1 degree of freedom (10). Data were analyzed using Stata version 16 (Stata Corp., College Station, TX, USA).

Results

After searching, 245 relevant articles were identified; 40 were removed due to duplication. Of the remaining 205 articles, 190 articles were excluded after screening based on title and abstract. Finally, 15 full texts passed the eligibility assessment. Moreover, we excluded seven records due to reporting of reproductive number for the previous variant instead of delta variant and insufficient data. Finally, we included eight studies in this systematic review, and three studies were selected to estimate the pooled value of R_0 for delta variant (Figure 1 and Table1). All of the studies were included without considering the quality. The included studies were from China (4 studies), Australia (1 study), England (1 study), United Kingdom (1 study), and the United States (1 study). The mean R_0 calculated based on eight studies as 5.27±1.16, with a range of 4.3 to 6.4. More information is depicted in Table 1. According to the results of the random-effects model, the pooled R_0 for delta variant of SARS-COV-2 was estimated as 5.10 (95% CI, 3.04 to 7.17) (Figure 2). (I^2 =86.77%, T^2:2.68, p from the chi-square test for heterogeneity was<0.001).

Discussion

In the present paper, we have combined the R_0 reported from the literature to estimate R_0 for Delta variant SARS-CoV-2. Our meta-analysis found that the overall R_0 was 5.10 (95% CI, 3.04 to 7.17), which is higher than previous estimates of 3.32[17] and 2.79[18] for the first SARS-CoV-2. This figure is much higher even compared to SARS, MERS, and Ebola.[19] Such a high R_0 means that an infected person infects at least almost six susceptible people. On the other hand, some characteristics of the Delta variant such as high hospitalization, ICU admission, and case fatality rate,[2, 20]

Table 1. Descriptive characteristics of the studies that estimated R_0 for Delta variant of SARS-COV-2

First author	Country	Model	Basic Reproduction Number(R_0)	95% CI**	ROB**
Sheryl L, et al[11]	Australia	Re-calibrated agent-based model	5.97	5.93-6	Low
Min Kang, et al[12]	China	-	6.4	3.7-9.3	Low
Meng Zhang, et al[3]	China	Maximum Likelihood	3.2	2-4.8	Low
Hengkong Lee, et al[1]	China	-	6	-	Low
Qingfeng Shi[13]	China	-	4.04-5	-	Low
Jennifer R[14]	USA	-	4.6	-	Low
*SPI-M-O[15]	England	-	5 -8	-	-
David Mackie, et al[16]	UK	-	5.2	-	Low

*Pandemic Influenza Group on Modelling, Operational sub-group (SPI-M-O)
**Confidence Interval
***Risk of Bias

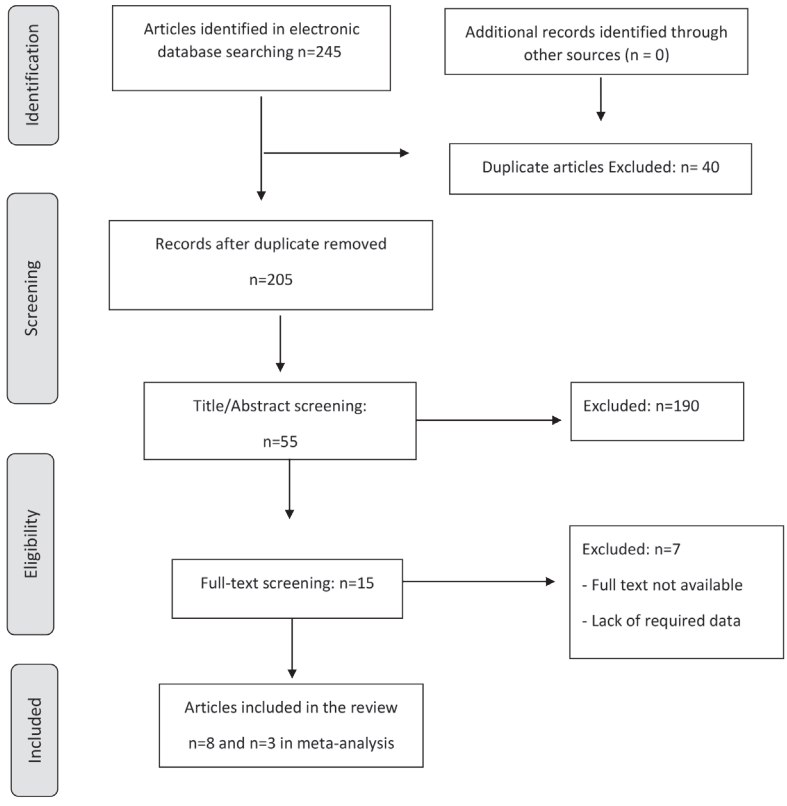

Figure 1. PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) flow diagram for the studies included in the current meta-analysis.

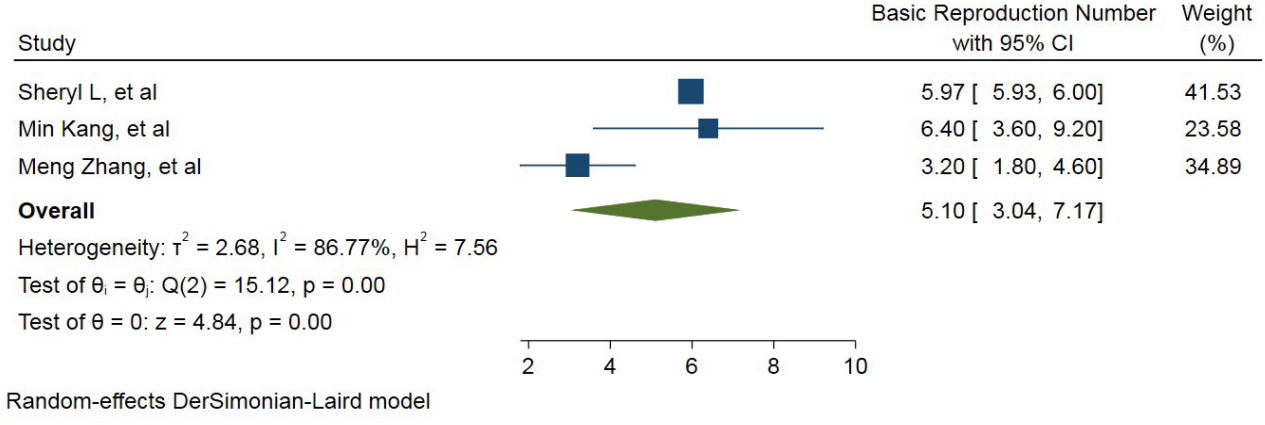

Figure 2. Forest plot of the estimated Basic reproduction number (R0) of delta variant of SARS-COV-2.

lower vaccine effectiveness,[21, 22] shorter key transmission parameters including,[3] the incubation period (4.4 days), generation time (2.9 days) and serial interval (2.3 days), suggest that controlling the spread of this variant may be harder compared to the SARS-CoV-2 strains. Therefore, strengthening public health measures to combat this type of SARS-CoV-2 is inevitable. For this purpose, a 70% vaccine coverage is required. A reproductive number

of 5.10 would imply a vaccine coverage rate above 80%, assuming a 100% vaccine efficacy. Korean studies showed that herd immunity is unlikely to be achieved with the potential emergence of the Delta variant;[23] therefore, controlling SARS-CoV-2 transmission in South Korea would be more difficult.[24]

Another noteworthy point is that R_0 may vary from one population to another or even in subgroups of a single population because the pattern of contacts among individuals may be different.[25] Also, R_0 varies due to factors influencing the disease contact rate and the biological characteristics of the virus, and the actual reproductive number may be even higher than the estimated one.[25, 26] However, with decreasing vaccine effectiveness associated with the Delta variant,[21, 22] maybe even an 80% vaccine coverage rate would be insufficient to prevent Delta outbreaks.

Our study has some limitations. The meta-analysis was based on only three papers and should be interpreted with caution. Estimated R_0 depends on the validity of the assumptions of models, and due to lack of studies, we were not able to subgroup the studies according to the method of calculation. In addition, data insufficiency and the shortness of the study period may affect the estimates of R_0. Our results indicated significant heterogeneity among the included studies. The variation among reported R_0 studies implies that precisely estimating R_0 is relatively difficult.

Conclusion

Considering the estimated R_0 for the Delta variant of SARS-CoV-2, the amount of vaccine coverage required to achieve herd immunity appears to be higher than previous variants of the virus. Also, pay close attention to the incidence of the variant strains, and reducing the number of contacts within the population via non-pharmaceutical interventions must be maintained even after the ongoing coverage rate of vaccination to almost 100%.

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Conflicts of interest

The authors have no conflicts of interest associated with the material presented in this paper.

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Author contribution

MS, carried out the search and data analysis and was responsible for the manuscript writing. YA, carried out the search, data analysis and was responsible for the manuscript writing. FE contributed to searching and selection and the manuscript writing.

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