

Estimation of the basic reproduction number of novel coronavirus (COVID-19) in Bangladesh: A 65-day outbreak data-driven analysis

Md. Hasan

Bangabandhu Sheikh Mujib Medical University

Akhtar Hossain (✉ akhtar_sbi@du.ac.bd)

Dhaka University

Wasimul Bari

Dhaka University

Syed Shariful Islam

Bangabandhu Sheikh Mujib Medical University

Research article

Keywords: SARS-COV-2; COVID-19; Outbreak; Basic Reproduction Number; Bangladesh

Posted Date: June 8th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-32412/v1>

License:  This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

1 **Estimation of the basic reproduction number of novel coronavirus (COVID-19) in Bangladesh:**
2 **A 65-day outbreak data-driven analysis**

3 Md. Hasan¹, Akhtar Hossain^{2*}, Wasimul Bari², Syed Shariful Islam¹

4

5 ¹Department of Public Health and Informatics, Bangabandhu Sheikh Mujib Medical University, Dhaka,
6 Bangladesh

7 ²Department of Statistics, University of Dhaka, Bangladesh

8

9

10 ***Correspondence author:**

11 Akhtar Hossain

12 Department of Statistics, University of Dhaka, Bangladesh

13 Phone: +8801717812444

14 Email: akhtar_sbi@du.ac.bd

15

16

17

18

19

20

21

22

23

24

25

26

27 **Abstract**

28 **Background:** The outbreak of novel coronavirus disease (COVID-19), started from Wuhan, China, at
29 the end of December 2019, hits almost the entire world. In Bangladesh, the first case was officially
30 reported on March 8, 2020. We estimated the basic reproductive number, R_0 , of COVID-19 for
31 Bangladesh using the first 65-day data of the outbreak.

32 **Methods:** With time-varying disease reporting rate, epidemic curves were estimated using the
33 exponential growth model utilizing daily COVID-19 diagnosis data in Bangladesh from March 8 to
34 May 11, 2020. We estimated R_0 using the estimated intrinsic growth rate (γ). Serial intervals (SI) have
35 been used from two well-known coronaviruses' outbreaks, SARS and MERS; and the early estimate of
36 SI of COVID-19 in Wuhan, China.

37 **Results:** The COVID-19 epidemic in Bangladesh followed an exponential growth model. We found
38 the R_0 to be 1.84 [95% CI: 1.82 – 1.86], 1.82 [95% CI: 1.81 – 1.84], and 1.94 [95% CI: 1.92 – 1.96],
39 for MERS, COVID-19, and SARS SI respectively without adjusting reporting rate. With the adjusted
40 reporting rate, R_0 reduced to 1.63 [95% CI: 1.62 – 1.65], 1.62 [95% CI: 1.61 – 1.64], and 1.71 [95%
41 CI: 1.70 – 1.73] for a five-fold increase. Inverse association between the reporting rate and the basic
42 reproduction number was observed.

43 **Conclusion:** The R_0 was found to be 1.87 for existing cases and was reduced to 1.65 for the five-fold
44 increase of the early reporting rate. Findings suggest a continued COVID-19 outbreak in Bangladesh
45 and immediate steps need to be taken to control.

46 **Keywords:** SARS-COV-2; COVID-19; Outbreak; Basic Reproduction Number; Bangladesh.

47

48

49

50

51 **Introduction**

52 Atypical pneumonia cases with unknown aetiology were first detected in Wuhan, China, at the end of
53 December 2019 (1). This disease subsequently found to be caused by a virus, and the World Health
54 Organization (WHO) named this virus as severe acute respiratory syndrome coronavirus 2 (SARS-
55 COV-2) (2). The disease itself was named as a coronavirus (COVID-19) (2). Evidence suggested that
56 the likelihood of spreading this disease for cross border travelling (3) is very high and hence indicated
57 the global spreading (4). On March 11, 2020, the WHO declared that COVID-19 disease outbreaks a
58 global pandemic (5, 6). As of May 11, 2020 (10.00 GMT+ 6), there have been 4,137,591 confirmed
59 cases found in 187 affected countries, among which 17,07,756 (41%) have been closed. Among the
60 closed cases, 14,24,230 (83%) have recovered from the infection while 2,83,526 (17%) cases were
61 closed as death (7) by COVID-19. The most affected country was the United States of America
62 (13,32,609 cases and 79,607 death) which was followed by Spain (2,24,350 cases and 26,621 death),
63 and United Kingdom (2,24,327 cases and 32,140 death) based on the data up to May 11 2020 (7). In
64 Bangladesh, the first three cases were detected on March 8, and the first death reported on March 18,
65 2020, from COVID-19 disease (8). A total of 15,691 cases were detected by May 11 while only 7,667
66 cases reported from the March 8 to April 30, 2020, implying an about 2-fold increase of the cases in 11
67 days, May 1st to 11th (8). In this regards, it is very urgent to estimate the epidemiological determinants
68 of COVID-19 for assessing the epidemic transmissibility, the prediction of the future trend of epidemic
69 spreading, as well as the planning for control measure. The most important parameter to determine the
70 intrinsic transmissibility of infectious disease is the basic reproduction number (R_0) measuring the
71 average number of secondary infectious cases caused by an index case in a 100% susceptible population
72 (9). China and Korea estimated the basic productive number at the early stage of the outbreak and found
73 different estimates in different states. In Wuhan, the R_0 was estimated to be 2.68 [95% CI: 2.47 – 2.86]
74 (10), in Hubei province, 6.49 [95% CI: 6.31 – 6.66] (11), in China and overseas, 2.90 [95% CI: 2.32 –
75 2.63] (12), and in Korea, the initial R_0 was estimated to be 0.555 and the later estimate revealed R_0
76 between 3.47 and 3.54 (13).

77 During an epidemic situation, imposing different control measures by the government such as changing
78 personal behaviour (wearing masks, washing hands, maintaining social distance, and sterilizing etc.),
79 and reducing the susceptible populations play a vital role in reducing the reproduction number. An
80 epidemic is considered to be under control when $R_0 < 1$ (14).

81 To the best of our knowledge, there was no existing research quantifying the transmissibility of COVID-
82 19 in Bangladesh. In this study, we attempt to estimate the transmissibility of COVID-19 using the basic
83 reproductive number, R_0 utilizing the publicly available daily reported data in Bangladesh.

84 **Methodology**

85 **Data Source**

86 Time series data on COVID-19 diagnosis were collected from the daily reported cases published in the
87 website of Institution of Epidemiology, Disease Control and Research (IEDCR) (15) and Corona info,
88 Directorate General of Health Service (DGHS), Ministry of Health and Family Welfare (MoHFW),
89 Bangladesh (8). All cases were laboratory-confirmed following the suspected case definition of the
90 World Health Organization (WHO) (16) and the National guidelines on clinical management of
91 coronavirus disease 2019 (COVID-19) (17).

92 **Data Management**

93 Data have been captured from March 8, the date of first cases detected in Bangladesh, up to May 11,
94 2020, as of the submission date of this manuscript was May 12, 2020. In the beginning, the number of
95 the diagnosed cases was very low due to the low volume of testing, and the number of diagnosed cases
96 gradually increased with the increasing number of tests, indicating a direct link between the number of
97 case diagnosed and the number of people tested. The increasing daily number of tests were governed
98 by the growing level of public awareness and government surveillance, including enhancement of test
99 and treatment facilities.

100 To account for the effect of increasing surveillance, and to offset the underreported case diagnosis in
101 the early days; we adopted an adjustment mechanism for the daily number of diagnosed cases by a time-

102 varying reporting rate, motivated by previous studies (14, 18). We assumed that the reporting rate
 103 reached at the maximum level on the day the country started testing 2,000 individuals per day. We
 104 adjusted the daily number of diagnosed cases before this point in time using a series of reporting rate
 105 increments time-varied by the daily number of tests performed. Let $c(t)$ be the daily diagnosed new
 106 cases on the day t ; $T(t)$ be the number of people tested, and $r(t)$ be the fold change of reporting rate,
 107 Then, the adjusted number of daily diagnosed cases, denoted by $c'(t)$, is obtained as

$$c'(t) = \begin{cases} c(t) \times [1 + r(t) \times 1.00]; & \text{if } T(t) < 100 \\ c(t) \times [1 + r(t) \times 0.75]; & \text{if } 100 \leq T(t) < 500 \\ c(t) \times [1 + r(t) \times 0.50]; & \text{if } 500 \leq T(t) < 1000 \\ c(t) \times [1 + r(t) \times 0.25]; & \text{if } 1000 \leq T(t) < 2000 \\ c(t) \times [1 + r(t) \times 0.00]; & \text{if } T(t) \geq 2000 \end{cases} \quad (1)$$

108 Finally, the adjusted cumulative number of cases were computed $C(t) = \sum_{\tau \leq t} c'(\tau)$. Alongside
 109 analyzing the originally diagnosed number of cases, we considered analyzing multiple other scenarios
 110 defined by 0.5, 1, 2, 3, 4, and 5-fold increasing of reporting rate. As it is very difficult to assess the
 111 exact reporting rate due to unavailability of required data, we considered analyzing these seven scenario
 112 covering a broad spectrum of variation in the reporting rate. Figure 1 provides further detail on each of
 113 these scenarios that we have investigated for COVID-19 SI. Other scenarios for MERS and SARS SI
 114 was given in the supplemental file Figure S1 and Figure S2, respectively.

115 **Reproductive Number**

116 Following previous studies (14, 19, 20), exponential epidemic curves have been fitted to the data on the
 117 daily diagnosed number of cases, both original and adjusted, using the equation (1) for the different
 118 reporting rate increase. The main parameter of this curve is the intrinsic growth rate (γ), indicating the
 119 change in the number of new cases in a given period. This parameter was estimated using the Poisson
 120 regression (21). The basic reproductive number was estimated using the following equation (2) (20).

$$R_0 = \frac{1}{M(-\gamma)} = \frac{1}{\int_0^{\infty} e^{-\gamma k} h(k) dk} \quad (2)$$

121 where $h(\cdot)$ is the probability density function of serial (or generation) interval of disease defined as the
 122 time from infection of an individual to the infection of a secondary case by that individual (22). The

123 function $M(\cdot)$ is the Laplace transform of $h(\cdot)$ known as the moment generating function of serial
124 interval. A deviance based statistic (R^2) (21) has also been computed to test the goodness of fit of the
125 epidemic curve (21, 23).

126 We employed the Gamma distribution as the distribution of serial interval. We used the serial interval
127 (SI) information reported for COVID-19 cases of Wuhan, China using 425 cases (24). We also have
128 conducted our analyses using the SI information for Middle East Respiratory Syndrome (MERS), and
129 the Severe Acute Respiratory Syndrome (SARS) as these two viruses share the same pathogen as
130 COVID-19. The mean \pm SD for Gamma distribution was considered as 7.6 ± 3.4 days for MERS (25),
131 7.5 ± 3.4 days for COVID-19 (24); and 8.4 ± 3.8 days for SARS (26). All the data were analyzed using
132 statistical software R using the package R0 (21).

133 **Results**

134 The estimated exponential epidemic curves are presented in Figure 1 (b), (d), (f), (h), (j), (l), and (n) for
135 the number of diagnosed cases as observed and 0.5, 1, 2, 3, 4, and 5-fold increased reporting rate
136 adjusted number of cases. These figures, for each scenario, depicted the actual cumulative number of
137 diagnosed cases, the cumulative adjusted number of cases, and estimated epidemic curve. The
138 goodness-of-fit deviance R^2 of the estimated epidemic curves, maximum (0.89) for the model of actual
139 case numbers and minimum (0.85) for the model of case numbers adjusted for a 5-fold increase in
140 reporting rate, indicated that the epidemic data satisfactorily followed the exponential growth as we
141 assumed. Figure 2 presents the estimated R_0 and 95% confidence interval [CI] for all scenarios
142 presented by the actual and fold increased reporting rates adjusted cases under the three SI's discussed
143 previously. For MERS SI, the estimated R_0 ranges from 1.84 [95% CI: 1.82 – 1.86] to 1.63 [95% CI:
144 1.62 – 1.65] associated with the actual number of cases to 5-fold increase of the early reporting rate.
145 Similarly, for SARS SI the estimated R_0 varied between 1.94 [95% CI: 1.92 – 1.96] and 1.71 [95% CI:
146 1.70 – 1.73]. Following the estimated SI of COVID-19, estimated R_0 showed 1.82 [95% CI: 1.81 –
147 1.84] for an actual case number to 1.62 [95% CI: 1.61 – 1.64] for case numbers adjusted for a 5-fold
148 increase in early reporting rate. In all the scenarios, the estimated R_0 was found to be significantly higher
149 than 1, indicating that size of the outbreak is increasing in Bangladesh, and each of the primary cases

150 continues infecting 1.87 new individuals on average based on the reporting rate as observed. The
151 average number of new infection from each primary infected cases could be down to 1.65 if the
152 reporting rate is increased to 5-fold to adjust the case numbers in the early phase of the outbreak.

153 **Discussion**

154 With the ever-growing number of COVID-19 cases, the world is currently in a pandemic situation (5,
155 6). It is already established that COVID-19 transmitted from human-to-human (27). The basic
156 transmissibility parameter, reproduction number R_0 , is an important epidemiologic factor evaluating
157 the level of the epidemics and selecting the appropriate prevention and intervention policies. However,
158 in the case of COVID-19, epidemiological information including R_0 was not well known as it is a new
159 strain of the virus, and a country must do a quick review and change plan accordingly to the situation
160 of the epidemic (13). In this regards, we estimated the basic reproduction number for Bangladesh based
161 on the SI of SARS (26), MERS (25), and COVID-19 estimated from data on diagnosed cases in Wuhan,
162 China (24) under a broad spectrum of observed and adjusted reporting rates. The findings of this
163 investigation were a little bit lower than the WHO declared reproductive number, for the human to
164 human (direct) transmission, interval 2 – 2.5 for China (28) and also slightly lower than the other similar
165 pathogens like as SARS (R_0 : 2 – 5) (26, 29), and MERS (R_0 : 2.0 – 6.7) (30). We found Bangladesh to
166 be in a slightly better position, in terms of transmissibility of COVID-19 infection, than the two
167 neighbouring countries India and Pakistan having estimated R_0 2.56 and 2.65, respectively. (31, 32).
168 Besides these, the basic reproduction number estimated in different provinces of China at different
169 period ranged between 1.5 and 6.49 (33). In Korea, this figure was 3.54 (data using between February
170 18-March 1, 2020) (13), which was higher than that in Bangladesh. In Italy, in the early phase (February
171 25-March 12, 2020) of the outbreak, the estimated R_0 was 2.43 to 3.10 (34), and in Algeria, it was found
172 to be 2.55 [95% CI: 2.15 – 2.94] using the actual incidence data of first 25 days of the outbreak (35).

173 The accuracy of the basic reproduction number relies on the selection of the SI of COVID-19; however,
174 as of yet, there is no consistent evidence regarding this interval. Determining the SI requires sufficient
175 information of the chain of the disease transmission with a long period of follow up study with a

176 sufficient number of patients(36). Following the literature (14) we have used the SI of SARS and MERS
177 that approximately gave a similar insight of COVID-19 at the early stage of the outbreak. We also have
178 considered using an early phase estimate of SI for COVID-19 from Wuhan, China (24) which is similar
179 to the SI of MERS and yielded a similar estimate of the basic reproduction number for Bangladesh. As
180 we are currently in the middle of the pandemic and uncertain as to when Bangladesh will reach the
181 plateau of new infections, our exercise is merely inferential and aimed to aid the timely public health
182 interventions by the Government of Bangladesh.

183 **Conclusion**

184 Using a series of 65 days daily diagnosed case numbers in Bangladesh, we estimated the basic
185 reproduction number R_0 of COVID-19 as 1.84 [95% CI: 1.82 – 1.86], 1.82 [95% CI: 1.81 – 1.84], and
186 1.94 [95% CI: 1.92 – 1.96], for MERS, COVID-19, and SARS SI respectively. The reproduction
187 exhibited a downward trend with adjustments in case numbers for increasing reporting rate and reached
188 to 1.63 [95% CI: 1.62 – 1.65], 1.62 [95% CI: 1.61 – 1.64], and 1.71 [95% CI: 1.70 – 1.73] for a five-
189 fold increase. The basic reproduction number staying significantly higher than 1, even after an
190 adjustment for a five-fold increase in reporting rate, is an indicator of a still-growing outbreak of
191 COVID-19 in Bangladesh. The observed inverse relationship between the increase in reporting rate and
192 basic reproduction number insinuate a better control of the outbreak in Bangladesh conditional on taking
193 advantages of the higher reporting rate, e.g., by ensuring expanded testing coverages.

194 **Abbreviations**

195 WHO: World Health Organization; MERS: Middle East Respiratory Syndrome; SARS: Severe Acute
196 Respiratory Syndrome; COVID-19: Coronavirus Disease-2019.

197 **Ethics approval and consent to participate**

198 The ethical approval or individual consent was not applicable

199 **Availability of data and materials**

200 All data and materials used in this work were publicly available.

201

202 **Consent for publication**

203 Not applicable

204 **Funding**

205 There is no funding source for this study

206 **Conflict of interests**

207 The authors declare no competing interests.

208 **Author's contributions**

209 MH and AH developed the study concepts and finalized the data analysis. MH wrote the first draft of
210 this manuscript with the substantial input from all co-authors. MH, AH, WB and SSI critically reviewed
211 the manuscript. All authors read and approved the final manuscript.

212 **Acknowledgements**

213 We thank IEDCR and the Health Ministry of Bangladesh for making this data in public.

214

215 **References**

216 1. Wuhan Municipal Health Commission. Wuhan Municipal Health Commission briefing on the
217 pneumonia epidemic situation (31 Dec 2019, in Chinese) 2019 [Available from:

218 <http://wjw.wuhan.gov.cn/front/web/showDetail/2019123108989>

219 2. Naming the coronavirus disease (COVID-19) and the virus that causes it 2019 [Available
220 from: [https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-](https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-(covid-2019)-and-the-virus-that-causes-it)

221 [guidance/naming-the-coronavirus-disease-\(covid-2019\)-and-the-virus-that-causes-it](https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-(covid-2019)-and-the-virus-that-causes-it).

222 3. Bogoch, II, Watts A, Thomas-Bachli A, Huber C, Kraemer MUG, Khan K. Pneumonia of
223 unknown aetiology in Wuhan, China: potential for international spread via commercial air travel.
224 Journal of travel medicine. 2020;27(2).

225 4. Leung K, Wu J, Leung G. Nowcasting and forecasting the Wuhan 2019-nCoV outbreak2020.

- 226 5. Cucinotta D, Vanelli M. WHO Declares COVID-19 a Pandemic. *Acta bio-medica : Atenei*
227 *Parmensis*. 2020;91(1):157-60.
- 228 6. WHO Timeline - COVID-19. This statement is updated on an ongoing basis, in response to
229 evolving events and common media queries 2020 [Available from: [https://www.who.int/news-](https://www.who.int/news-room/detail/08-04-2020-who-timeline---covid-19)
230 [room/detail/08-04-2020-who-timeline---covid-19](https://www.who.int/news-room/detail/08-04-2020-who-timeline---covid-19)].
- 231 7. Coronavirus resource center; Johns Hopkins University & Medicine 2020 [Available from:
232 <https://coronavirus.jhu.edu/>].
- 233 8. Directorate general of Health Services (DGHS), Ministry of Health and Family Welfare,
234 Government of the People's Republic of bangladesh: Corona info 2020 [Available from:
235 <http://covid19tracker.gov.bd/>].
- 236 9. Anderson RM, Anderson B, May RM. *Infectious diseases of humans: dynamics and control*:
237 Oxford university press; 1992.
- 238 10. Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and
239 international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study.
240 *Lancet (London, England)*. 2020;395(10225):689-97.
- 241 11. Shen M, Peng Z, Xiao Y, Zhang L. Modelling the epidemic trend of the 2019 novel coronavirus
242 outbreak in China. *bioRxiv*. 2020:2020.01.23.916726.
- 243 12. Liu T, Hu J, Kang M, Lin L, Zhong H, Xiao J, et al. Transmission dynamics of 2019 novel
244 coronavirus (2019-nCoV). *bioRxiv*. 2020:2020.01.25.919787.
- 245 13. Choi S, Ki M. Estimating the reproductive number and the outbreak size of COVID-19 in
246 Korea. *Epidemiology and health*. 2020;42:e2020011.
- 247 14. Zhao S, Lin Q, Ran J, Musa SS, Yang G, Wang W, et al. Preliminary estimation of the basic
248 reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven
249 analysis in the early phase of the outbreak. *International journal of infectious diseases : IJID : official*
250 *publication of the International Society for Infectious Diseases*. 2020;92:214-7.

- 251 15. Institute of Epidemiology, Disease Control and Research (IEDCR) 2020 [Available from:
252 <https://www.iedcr.gov.bd/>.
- 253 16. Laboratory testing for 2019 novel coronavirus (2019-nCoV) in suspected human cases;
254 Interim guidance 2020 [Available from: [https://www.who.int/publications-detail/laboratory-testing-](https://www.who.int/publications-detail/laboratory-testing-for-2019-novel-coronavirus-in-suspected-human-cases-20200117)
255 [for-2019-novel-coronavirus-in-suspected-human-cases-20200117](https://www.who.int/publications-detail/laboratory-testing-for-2019-novel-coronavirus-in-suspected-human-cases-20200117).
- 256 17. National Guidelines on Clinical Management of Coronavirus Disease 2019 (Covid-19):
257 Directorate General of Health Services Ministry of Health & Family Welfare Government of the
258 People's Republic of Bangladesh 2020 [
- 259 18. Wu JT, Cowling BJ, Lau EH, Ip DK, Ho LM, Tsang T, et al. School closure and mitigation of
260 pandemic (H1N1) 2009, Hong Kong. *Emerging infectious diseases*. 2010;16(3):538-41.
- 261 19. de Silva UC, Warachit J, Waicharoen S, Chittaganpitch M. A preliminary analysis of the
262 epidemiology of influenza A(H1N1)v virus infection in Thailand from early outbreak data, June-July
263 2009. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European*
264 *communicable disease bulletin*. 2009;14(31).
- 265 20. Zhao S, Musa SS, Fu H, He D, Qin J. Simple framework for real-time forecast in a data-limited
266 situation: the Zika virus (ZIKV) outbreaks in Brazil from 2015 to 2016 as an example. *Parasites &*
267 *Vectors*. 2019;12(1):344.
- 268 21. Obadia T, Haneef R, Boëlle PY. The R0 package: a toolbox to estimate reproduction numbers
269 for epidemic outbreaks. *BMC medical informatics and decision making*. 2012;12:147.
- 270 22. Wallinga J, Lipsitch M. How generation intervals shape the relationship between growth
271 rates and reproductive numbers. *Proc Biol Sci*. 2007;274(1609):599-604.
- 272 23. Cameron AC, Windmeijer FAG. *Deviance Based R-squared Measures of Goodness of Fit for*
273 *Generalized Linear Models: Australian National University, Faculty of Economics and Depts. of*
274 *Economics, Research School of Pacific Studies, Research School of Social Sciences; 1993.*

- 275 24. Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, et al. Early Transmission Dynamics in Wuhan,
276 China, of Novel Coronavirus-Infected Pneumonia. *The New England journal of medicine*.
277 2020;382(13):1199-207.
- 278 25. Assiri A, McGeer A, Perl TM, Price CS, Al Rabeeah AA, Cummings DA, et al. Hospital outbreak
279 of Middle East respiratory syndrome coronavirus. *The New England journal of medicine*.
280 2013;369(5):407-16.
- 281 26. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and
282 control of severe acute respiratory syndrome. *Science (New York, NY)*. 2003;300(5627):1966-70.
- 283 27. Mission summary: WHO Field Visit to Wuhan, China 20-21 January 2020 2020 [
- 284 28. Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19). 2020.
- 285 29. Wallinga J, Teunis P. Different epidemic curves for severe acute respiratory syndrome reveal
286 similar impacts of control measures. *American journal of epidemiology*. 2004;160(6):509-16.
- 287 30. Majumder MS, Rivers C, Lofgren E, Fisman D. Estimation of MERS-Coronavirus Reproductive
288 Number and Case Fatality Rate for the Spring 2014 Saudi Arabia Outbreak: Insights from Publicly
289 Available Data. *PLoS currents*. 2014;6.
- 290 31. Rai B, Shukla A, Dwivedi LK. COVID-19 in India: Predictions, Reproduction Number and Public
291 Health Preparedness. *medRxiv*. 2020:2020.04.09.20059261.
- 292 32. Syed F, Sibgatullah S. Estimation of the Final Size of the COVID-19 Epidemic in Pakistan.
293 *medRxiv*. 2020:2020.04.01.20050369.
- 294 33. Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher
295 compared to SARS coronavirus. *Journal of travel medicine*. 2020;27(2):taaa021.
- 296 34. D'Arienzo M, Coniglio A. Assessment of the SARS-CoV-2 basic reproduction number, R_0 ,
297 based on the early phase of COVID-19 outbreak in Italy. *Biosafety and Health*. 2020.
- 298 35. Hamidouche M. COVID-19 outbreak in Algeria: A mathematical Model to predict cumulative
299 cases. *medRxiv*. 2020:2020.03.20.20039891.

300 36. Cowling BJ, Fang VJ, Riley S, Malik Peiris JS, Leung GM. Estimation of the serial interval of
301 influenza. *Epidemiology*. 2009;20(3):344-7.

302

303

304

305

306

307 **Figure Legends**

308 **Figure 1:** The scenarios of the change in the reporting rate (top panels) and the exponential
309 growth fitting (bottom panels) based on the COVID-19 SI. The top panels, i.e., (a), (c), (e),
310 (g), (i), (k), and (m) show the assumed change in the reporting rate. The bottom panels, i.e.,
311 (b), (d), (f), (h), (j), (l), and (n) show the reported (or observed, black circles), adjusted (green
312 dots) and fitted (blue curve) the number of COVID-19 infections. The vertical grey line
313 represents the date when the number of tests reached 100, 500, 1000, and 2000. Panels (a)
314 and (b) show the scenarios that the reporting rate was unchanged. Panels (c) and (d) show the
315 scenarios that the reporting rate increased by 0.5-fold. Panels (e) and (f) show the scenarios
316 that the reporting rate increased by 1-fold. Panels (g) and (h) show the scenarios that the
317 reporting rate increased by 2-fold. Panels (i) and (j) show the scenarios that the reporting rate
318 increased by 3-fold. Panels (k) and (l) show the scenarios that the reporting rate increased by
319 4-fold. Panels (m) and (n) show the scenarios that the reporting rate increased by 5-fold.

320

321 **Figure 2:** This figure depicted the estimated basic reproduction number, R_0 , under different
322 reporting rate fold increase. The estimated R_0 is shown with the number and (95% CI)
323 format. Three figure was presented considering three SI of MERS, COVID-19, and SARS.

Figures

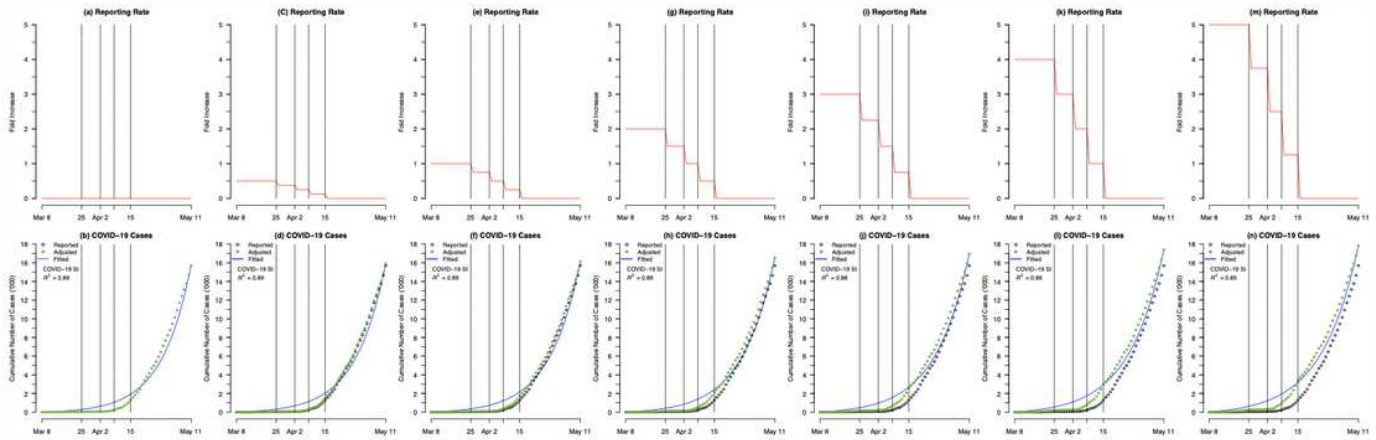


Figure 1

The scenarios of the change in the reporting rate (top panels) and the exponential growth fitting (bottom panels) based on the COVID-19 SI. The top panels, i.e., (a), (c), (e), (g), (i), (k), and (m) show the assumed change in the reporting rate. The bottom panels, i.e., (b), (d), (f), (h), (j), (l), and (n) show the reported (or observed, black circles), adjusted (green dots) and fitted (blue curve) the number of COVID-19 infections. The vertical grey line represents the date when the number of tests reached 100, 500, 1000, and 2000. Panels (a) and (b) show the scenarios that the reporting rate was unchanged. Panels (c) and (d) show the scenarios that the reporting rate increased by 0.5-fold. Panels (e) and (f) show the scenarios that the reporting rate increased by 1-fold. Panels (g) and (h) show the scenarios that the reporting rate increased by 2-fold. Panels (i) and (j) show the scenarios that the reporting rate increased by 3-fold. Panels (k) and (l) show the scenarios that the reporting rate increased by 4-fold. Panels (m) and (n) show the scenarios that the reporting rate increased by 5-fold.

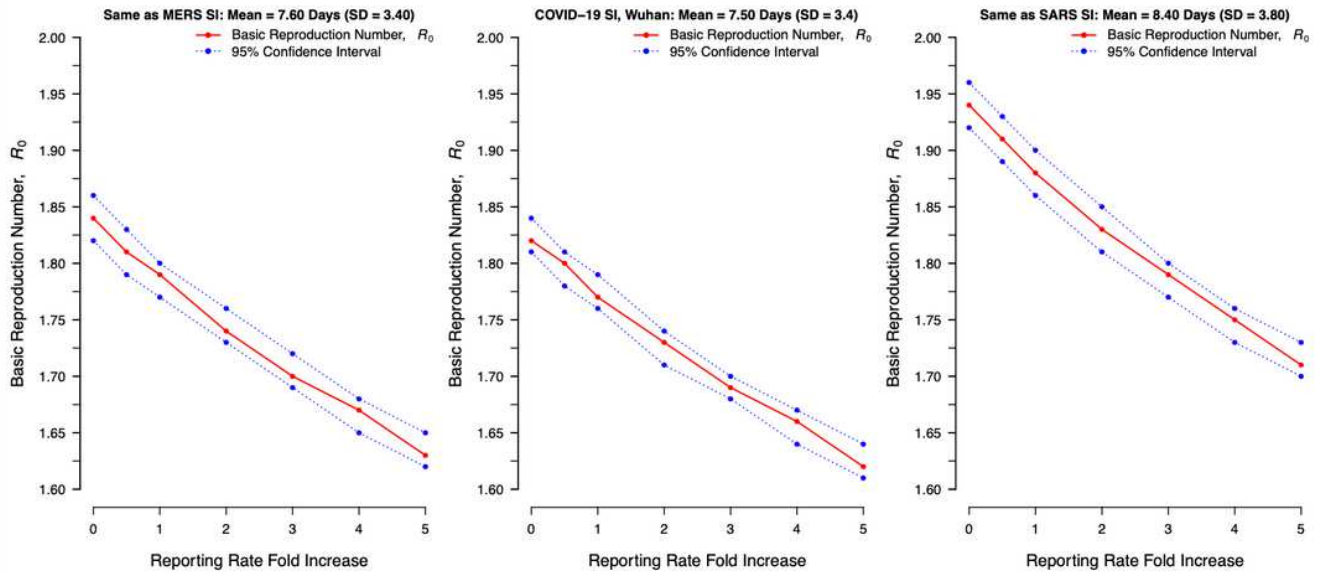


Figure 2

This figure depicted the estimated basic reproduction number, R_0 , under different reporting rate fold increase. The estimated R_0 is shown with the number and (95% CI) format. Three figure was presented considering three SI of MERS, COVID-19, and SARS.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [SupplementalMaterials.docx](#)