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

Md. Hasan¹, Akhtar Hossain²*, Wasimul Bari², Syed Shariful Islam¹

¹Department of Public Health and Informatics, Bangabandhu Sheikh Mujib Medical University, Dhaka, Bangladesh
²Department of Statistics, University of Dhaka, Bangladesh

*Correspondence author:

Akhtar Hossain
Department of Statistics, University of Dhaka, Bangladesh
Phone: +8801717812444
Email: akhtar_sbi@du.ac.bd

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
Abstract

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

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

Results: The COVID-19 epidemic in Bangladesh followed an exponential growth model. We found 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], for MERS, COVID-19, and SARS SI respectively without adjusting reporting rate. With the adjusted 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% CI: 1.70 – 1.73] for a five-fold increase. Inverse association between the reporting rate and the basic reproduction number was observed.

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

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

Atypical pneumonia cases with unknown etiology were first detected in Wuhan, China, at the end of December 2019 (1). This disease subsequently found to be caused by a virus, and the World Health Organization (WHO) named this virus as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (2). The disease itself was named as a coronavirus (COVID-19) (2). Evidence suggested that the likelihood of spreading this disease for cross border travelling (3) is very high and hence indicated the global spreading (4). On March 11, 2020, the WHO declared that COVID-19 disease outbreak is a global pandemic (5, 6). As of May 11, 2020 (10.00 GMT+ 6), there have been 4,137,591 confirmed cases found in 187 affected countries, among which 17,07,756 (41%) have been closed. Among the closed cases, 14,24,230 (83%) have recovered from the infection while 2,83,526 (17%) cases were closed as death (7) by COVID-19. The most affected country was the United States of America (13,32,609 cases and 79,607 death) which was followed by Spain (2,24,350 cases and 26,621 death), and United Kingdom (2,24,327 cases and 32,140 death) based on the data up to May 11 2020 (7). In Bangladesh, the first three cases were detected on March 8, and the first death reported on March 18, 2020, from COVID-19 disease (8). A total of 15,691 cases were detected by May 11 while only 7,667 cases reported from the March 8 to April 30, 2020, implying an about 2-fold increase of the cases in 11 days, May 1st to 11th (8). In this regards, it is very urgent to estimate the epidemiological determinants of COVID-19 for assessing the epidemic transmissibility, the prediction of the future trend of epidemic spreading, as well as the planning for control measure. The most important parameter to determine the intrinsic transmissibility of infectious disease is the basic reproduction number ($R_0$) measuring the average number of secondary infectious cases caused by an index case in a 100% susceptible population (9). China and Korea estimated the basic productive number at the early stage of the outbreak and found different estimates in different states. In Wuhan, the $R_0$ was estimated to be 2.68 [95% CI: 2.47 – 2.86] (10), in Hubei province, 6.49 [95% CI: 6.31 – 6.66] (11), in China and overseas,2.90 [95% CI: 2.32 – 2.63] (12), and in Korea, the initial $R_0$ was estimated to be 0.555 and the later estimate revealed $R_0$ between 3.47 and 3.54 (13).
During an epidemic situation, imposing different control measures by the government such as changing personal behaviour (wearing masks, washing hands, maintaining social distance, and sterilizing etc.), and reducing the susceptible populations play a vital role in reducing the reproduction number. An epidemic is considered to be under control when \( R_0 < 1 \) \((14)\).

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

**Methodology**

**Data Source**

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

**Data Management**

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

To account for the effect of increasing surveillance, and to offset the underreported case diagnosis in the early days; we adopted an adjustment mechanism for the daily number of diagnosed cases by a time-
varying reporting rate, motivated by previous studies (14, 18). We assumed that the reporting rate reached at the maximum level on the day the country started testing 2,000 individuals per day. We adjusted the daily number of diagnosed cases before this point in time using a series of reporting rate increments time-varied by the daily number of tests performed. Let \( c(t) \) be the daily diagnosed new cases on the day \( t \); \( T(t) \) be the number of people tested, and \( r(t) \) be the fold change of reporting rate. Then, the adjusted number of daily diagnosed cases, denoted by \( c'(t) \), is obtained as

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

(1)

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

Reproductive Number

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

\[
R_0 = \frac{1}{M(-\gamma)} = \frac{1}{\int_{0}^{\infty} e^{-\gamma h(k)} dk}
\]  

(2)

where \( h(\cdot) \) is the probability density function of serial (or generation) interval of disease defined as the time from infection of an individual to the infection of a secondary case by that individual (22).
function $M(\cdot)$ is the Laplace transform of $h(\cdot)$ known as the moment generating function of serial interval. A deviance based statistic ($R^2$) (21) has also been computed to test the goodness of fit of the epidemic curve (21, 23).

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

**Results**

The estimated exponential epidemic curves are presented in Figure 1 (b), (d), (f), (h), (j), (l), and (n) for the number of diagnosed cases as observed and 0.5, 1, 2, 3, 4, and 5-fold increased reporting rate adjusted number of cases. These figures, for each scenario, depicted the actual cumulative number of diagnosed cases, the cumulative adjusted number of cases, and estimated epidemic curve. The goodness-of-fit deviance $R^2$ of the estimated epidemic curves, maximum (0.89) for the model of actual case numbers and minimum (0.85) for the model of case numbers adjusted for a 5-fold increase in reporting rate, indicated that the epidemic data satisfactorily followed the exponential growth as we assumed. Figure 2 presents the estimated $R_0$ and 95% confidence interval [CI] for all scenarios presented by the actual and fold increased reporting rates adjusted cases under the three SI’s discussed previously. For MERS SI, the estimated $R_0$ ranges from 1.84 [95% CI: 1.82 – 1.86] to 1.63 [95% CI: 1.62 – 1.65] associated with the actual number of cases to 5-fold increase of the early reporting rate.

Similarly, for SARS SI the estimated $R_0$ varied between 1.94 [95% CI: 1.92 – 1.96] and 1.71 [95% CI: 1.70 – 1.73]. Following the estimated SI of COVID-19, estimated $R_0$ showed 1.82 [95% CI: 1.81 – 1.84] for an actual case number to 1.62 [95% CI: 1.61 – 1.64] for case numbers adjusted for a 5-fold increase in early reporting rate. In all the scenarios, the estimated $R_0$ was found to be significantly higher than 1, indicating that size of the outbreak is increasing in Bangladesh, and each of the primary cases
continues infecting 1.87 new individuals on average based on the reporting rate as observed. The average number of new infection from each primary infected cases could be down to 1.65 if the reporting rate is increased to 5-fold to adjust the case numbers in the early phase of the outbreak.

**Discussion**

With the ever-growing number of COVID-19 cases, the world is currently in a pandemic situation (5, 6). It is already established that COVID-19 transmitted from human-to-human (27). The basic transmissibility parameter, reproduction number $R_0$, is an important epidemiologic factor evaluating the level of the epidemics and selecting the appropriate prevention and intervention policies. However, in the case of COVID-19, epidemiological information including $R_0$ was not well known as it is a new strain of the virus, and a country must do a quick review and change plan accordingly to the situation of the epidemic (13). In this regards, we estimated the basic reproduction number for Bangladesh based on the SI of SARS (26), MERS (25), and COVID-19 estimated from data on diagnosed cases in Wuhan, China (24) under a broad spectrum of observed and adjusted reporting rates. The findings of this investigation were a little bit lower than the WHO declared reproductive number, for the human to human (direct) transmission, interval 2 – 2.5 for China (28) and also slightly lower than the other similar pathogens like as SARS ($R_0$: 2 – 5) (26, 29), and MERS ($R_0$: 2.0 – 6.7) (30). We found Bangladesh to be in a slightly better position, in terms of transmissibility of COVID-19 infection, than the two neighbouring countries India and Pakistan having estimated $R_0$ 2.56 and 2.65, respectively. (31, 32).

Besides these, the basic reproduction number estimated in different provinces of China at different period ranged between 1.5 and 6.49 (33). In Korea, this figure was 3.54 (data using between February 18-March 1, 2020) (13), which was higher than that in Bangladesh. In Italy, in the early phase (February 25-March 12, 2020) of the outbreak, the estimated $R_0$ was 2.43 to 3.10 (34), and in Algeria, it was found to be 2.55 [95% CI: 2.15 – 2.94] using the actual incidence data of first 25 days of the outbreak (35).

The accuracy of the basic reproduction number relies on the selection of the SI of COVID-19; however, as of yet, there is no consistent evidence regarding this interval. Determining the SI requires sufficient information of the chain of the disease transmission with a long period of follow up study with a
sufficient number of patients (36). Following the literature (14) we have used the SI of SARS and MERS that approximately gave a similar insight of COVID-19 at the early stage of the outbreak. We also have considered using an early phase estimate of SI for COVID-19 from Wuhan, China (24) which is similar to the SI of MERS and yielded a similar estimate of the basic reproduction number for Bangladesh. As we are currently in the middle of the pandemic and uncertain as to when Bangladesh will reach the plateau of new infections, our exercise is merely inferential and aimed to aid the timely public health interventions by the Government of Bangladesh.

**Conclusion**

Using a series of 65 days daily diagnosed case numbers in Bangladesh, we estimated the basic 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 $1.94$ [95% CI: $1.92 – 1.96$], for MERS, COVID-19, and SARS SI respectively. The reproduction exhibited a downward trend with adjustments in case numbers for increasing reporting rate and reached 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-fold increase. The basic reproduction number staying significantly higher than 1, even after an adjustment for a five-fold increase in reporting rate, is an indicator of a still-growing outbreak of COVID-19 in Bangladesh. The observed inverse relationship between the increase in reporting rate and basic reproduction number insinuate a better control of the outbreak in Bangladesh conditional on taking advantages of the higher reporting rate, e.g., by ensuring expanded testing coverages.

**Abbreviations**

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

**Ethics approval and consent to participate**

The ethical approval or individual consent was not applicable.

**Availability of data and materials**

All data and materials used in this work were publicly available.
Consent for publication

Not applicable

Funding

There is no funding source for this study

Conflict of interests

The authors declare no competing interests.

Author's contributions

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

Acknowledgements

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

References

1. Wuhan Municipal Health Commission. Wuhan Municipal Health Commission briefing on the pneumonia epidemic situation (31 Dec 2019, in Chinese) 2019 [Available from: http://wjw.wuhan.gov.cn/front/web/showDetail/2019123108989

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

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

4. Leung K, Wu J, Leung G. Nowcasting and forecasting the Wuhan 2019-nCoV outbreak2020.
5. Cucinotta D, Vanelli M. WHO Declares COVID-19 a Pandemic. Acta bio-medica : Atenei Parmensis. 2020;91(1):157-60.

6. WHO Timeline - COVID-19. This statement is updated on an ongoing basis, in response to evolving events and common media queries 2020 [Available from: https://www.who.int/news-room/detail/08-04-2020-who-timeline---covid-19.

7. Coronavirus resource center; Johns Hopkins University & Medicine 2020 [Available from: https://coronavirus.jhu.edu/.

8. Directorate general of Health Services (DGHS), Ministry of Health and Family Welfare, Government of the People's Republic of bangladesh: Corona info 2020 [Available from: http://covid19tracker.gov.bd/.

9. Anderson RM, Anderson B, May RM. Infectious diseases of humans: dynamics and control: Oxford university press; 1992.

10. Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. Lancet (London, England). 2020;395(10225):689-97.

11. Shen M, Peng Z, Xiao Y, Zhang L. Modelling the epidemic trend of the 2019 novel coronavirus outbreak in China. bioRxiv. 2020:2020.01.23.916726.

12. Liu T, Hu J, Kang M, Lin L, Zhong H, Xiao J, et al. Transmission dynamics of 2019 novel coronavirus (2019-nCoV). bioRxiv. 2020:2020.01.25.919787.

13. Choi S, Ki M. Estimating the reproductive number and the outbreak size of COVID-19 in Korea. Epidemiology and health. 2020;42:e2020011.

14. Zhao S, Lin Q, Ran J, Musa SS, Yang G, Wang W, et al. Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak. International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases. 2020;92:214-7.
15. Institute of Epidemiology, Disease Control and Research (IEDCR) 2020 [Available from: https://www.iedcr.gov.bd/]

16. Laboratory testing for 2019 novel coronavirus (2019-nCoV) in suspected human cases; Interim guidance 2020 [Available from: https://www.who.int/publications-detail/laboratory-testing-for-2019-novel-coronavirus-in-suspected-human-cases-20200117]

17. National Guidelines on Clinical Management of Coronavirus Disease 2019 (Covid-19); Directorate General of Health Services Ministry of Health & Family Welfare Government of the People's Republic of Bangladesh 2020 [ ]

18. Wu JT, Cowling BJ, Lau EH, Ip DK, Ho LM, Tsang T, et al. School closure and mitigation of pandemic (H1N1) 2009, Hong Kong. Emerging infectious diseases. 2010;16(3):538-41.

19. de Silva UC, Warachit J, Waicharoen S, Chittaganpitch M. A preliminary analysis of the epidemiology of influenza A(H1N1)v virus infection in Thailand from early outbreak data, June-July 2009. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin. 2009;14(31).

20. Zhao S, Musa SS, Fu H, He D, Qin J. Simple framework for real-time forecast in a data-limited situation: the Zika virus (ZIKV) outbreaks in Brazil from 2015 to 2016 as an example. Parasites & Vectors. 2019;12(1):344.

21. Obadia T, Haneef R, Boëlle PY. The R0 package: a toolbox to estimate reproduction numbers for epidemic outbreaks. BMC medical informatics and decision making. 2012;12:147.

22. Wallinga J, Lipsitch M. How generation intervals shape the relationship between growth rates and reproductive numbers. Proc Biol Sci. 2007;274(1609):599-604.

23. Cameron AC, Windmeijer FAG. Deviance Based R-squared Measures of Goodness of Fit for Generalized Linear Models: Australian National University, Faculty of Economics and Depts. of Economics, Research School of Pacific Studies, Research School of Social Sciences; 1993.
24. Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, et al. Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia. The New England journal of medicine. 2020;382(13):1199-207.

25. Assiri A, McGeer A, Perl TM, Price CS, Al Rabeeah AA, Cummings DA, et al. Hospital outbreak of Middle East respiratory syndrome coronavirus. The New England journal of medicine. 2013;369(5):407-16.

26. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and control of severe acute respiratory syndrome. Science (New York, NY). 2003;300(5627):1966-70.

27. Mission summary: WHO Field Visit to Wuhan, China 20-21 January 2020 2020. 

28. Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19). 2020.

29. Wallinga J, Teunis P. Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures. American journal of epidemiology. 2004;160(6):509-16.

30. Majumder MS, Rivers C, Lofgren E, Fisman D. Estimation of MERS-Coronavirus Reproductive Number and Case Fatality Rate for the Spring 2014 Saudi Arabia Outbreak: Insights from Publicly Available Data. PLoS currents. 2014;6.

31. Rai B, Shukla A, Dwivedi LK. COVID-19 in India: Predictions, Reproduction Number and Public Health Preparedness. medRxiv. 2020:2020.04.09.20059261.

32. Syed F, Sibgatullah S. Estimation of the Final Size of the COVID-19 Epidemic in Pakistan. medRxiv. 2020:2020.04.01.20050369.

33. Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. Journal of travel medicine. 2020;27(2):taaa021.

34. D’Arienzo M, Coniglio A. Assessment of the SARS-CoV-2 basic reproduction number, R0, based on the early phase of COVID-19 outbreak in Italy. Biosafety and Health. 2020.

35. Hamidouche M. COVID-19 outbreak in Algeria: A mathematical Model to predict cumulative cases. medRxiv. 2020:2020.03.20.20039891.
Cowling BJ, Fang VJ, Riley S, Malik Peiris JS, Leung GM. Estimation of the serial interval of influenza. Epidemiology. 2009;20(3):344-7.

Figure Legends

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.