The reproductive number of COVID-19 is higher compared to SARS coronavirus

Ying Liu[1], Albert A Gayle[2], Annelies Wilder-Smith[2,3], Joacim Rocklöv[2]*

1 School of International Business, Xiamen University Tan Kah Kee College, Zhangzhou, China.

2 Department of Public Health and Clinical Medicine, Section of Sustainable Health, Umeå University, Umeå, Sweden.

3 Heidelberg Institute of Public Health, Heidelberg, Germany

* Correspondence: joacim.rocklov@umu.se; Tel.: +46706361635

Teaser: Our review found the average R0 for 2019-nCoV to be 3.28, which exceeds WHO estimates of 1.4 to 2.5.

Keywords: Coronavirus, Wuhan, China, SARS, public health emergency of international concern, 2019-nCoV, epidemic potential, R_0

Introduction

In Wuhan, China, a novel and alarmingly contagious primary atypical (viral) pneumonia broke out in December 2019. It has since been identified as a zoonotic coronavirus, similar to SARS coronavirus and MERS coronavirus, and named 2019-nCoV. As of 8th February, 2020, 33,738 confirmed cases and 811 deaths have been reported in China.

Here we review the basic reproduction number (R_0) of the 2019-nCoV virus. R_0 is an indication of the transmissibility of a virus, representing the average number of new infections generated by an infectious person in a totally naïve population. For R_0 greater than one the number infected is likely to increase, and for R_0 less than one transmission is likely to die out. The basic reproduction number is a central concept in infectious disease epidemiology, indicating the risk of an infectious agent with respect to epidemic spread.

Methods and Results

PubMed, bioRxiv and Google Scholar were accessed to search for eligible studies. The term "2019-nCoV & basic reproduction number" was used. The time period covered was from January 1, 2020 to 7 February 2020. For this time period, we identified 12 studies which estimated the basic reproductive number for 2019-nCoV

from China and overseas. Table 1 shows that the estimates ranged from 1.4 to 6.49, with a mean of 3.28, a median of 2.79 and IQR of 1.16.

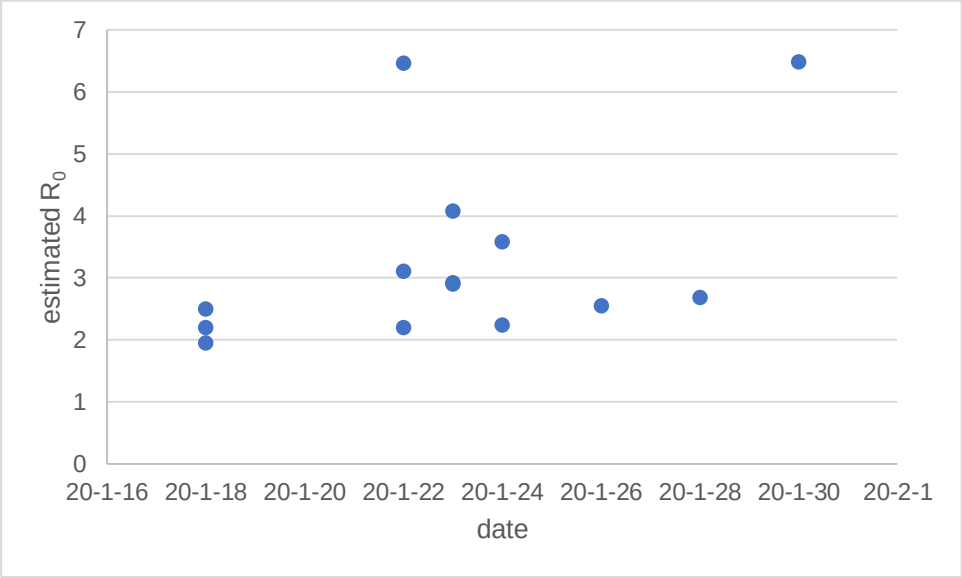

Fig 1. Timeline of the R_0 estimates for the 2019-nCoV virus in China

The first studies initially reported estimates of R_0 with lower values. Estimations subsequently increased and then again returned in the most recent estimates to the levels initially reported. A closer look reveals that the estimation method used played a role.

Table 1. Published estimates of R_0 for 2019-nCoV

Study (study year)	Location	Study date	Methods	Approaches	R_0 estimates (average)	95% CI
Joseph T Wu et al (2020)[1]	Wuhan	December 31, 2019, to January 28, 2020	Stochastic Markov Chain Monte Carlo methods (MCMC)	MCMC methods with Gibbs sampling and non-informative flat prior, using posterior distribution	2.68	2.47-2.86
Mingwang Shen et al. (2020)[2]	Hubei province	January12-22, 2020	Mathematical model, dynamic compartmental model with population divided into five compartments: susceptible individuals, asymptomatic individuals during the incubation period, infectious individuals with symptoms, isolated individuals with treatment,	$R_0 = \beta/\alpha$ β= mean person-to-person transmission rate/day in the absence of control interventions, using nonlinear least squares method to get its point estimate α=isolation rate=6	6.49	6.31-6.66

			recovered individuals			
Tao Liu et al (2020)[3]	China and overseas	January 23, 2020,	Statistical exponential Growth, using SARS generation time=8.4 days, SD=3.8 days	Applies Poisson regression to fit the exponential growth rate $R_0 = 1/M(-r)$ M=moment generating function of the generation time distribution r=fitted exponential growth rate	2.90	2.32-3.63
Tao Liu et al (2020)[3]	China and overseas	January 23, 2020	Statistical maximum likelihood estimation, using SARS generation time=8.4 days, SD=3.8 days	Maximize log-likelihood to estimate R_0 by using surveillance data during a disease epidemic, and assuming the secondary case is Poisson distribution with expected value R_0	2.92	2.28-3.67
Jonathan M. Read et al (2020)[4]	China	January 1 to 22, 2020	Mathematical transmission model assuming latent period=4 days and near to the incubation period	Assumes daily time increments with Poisson-distribution and apply a deterministic SEIR metapopulation transmission model, transmission rate=1.94, infectious period =1.61 days	3.11	2.39-4.13
Maimuna Majumder et al (2020)[5]	Wuhan	December 8, 2019 and January 26, 2020	Mathematical Incidence Decay and Exponential Adjustment (IDEA) model	Adopted mean serial interval lengths from SARS and MERS ranging from 6 to 10 days to fit the IDEA model ,	2.0-3.1 (2.55)	/
WHO	China	January 18, 2020	/	/	1.4-2.5 (1.95)	/
Zhidong Cao et al (2020)[6]	China	January 23, 2020	Mathematical model including compartments Susceptible-Exposed-Infectious-Recovered-Death-Cumulative (SEIRDC)	$R = K\,2\,(L \times D) + K(L + D) + 1$ L=average latent period=7, D=average latent infectious period=9, K=logarithmic growth rate of the case counts	4.08	/
Shi Zhao et al (2020)[7]	China	January 10 to 24, 2020	Statistical exponential growth model method adopting serial interval from SARS (mean=8.4 days, SD=3.8	Corresponding to 8-fold increase in the reporting rate $R_0 = 1/M(-r)$ r =intrinsic growth rate M= moment generating function	2.24	1.96-2.55

			days) and MERS (mean=7.6 days, SD=3.4 days)			
Shi Zhao et al (2020)[7]	China	January 10 to 24, 2020	Statistical exponential growth model method adopting serial interval from SARS (mean=8.4 days, SD=3.8 days) and MERS (mean=7.6 days, SD=3.4 days)	Corresponding to 2-fold increase in the reporting rate $R_0 = 1/M(-r)$ r =intrinsic growth rate M= moment generating function	3.58	2.89-4.39
Natsuko Imai (2020)[8]	Wuhan	January 18, 2020	Mathematical model, computational modelling of potential epidemic trajectories	Assume SARS-like levels of case-to-case variability in the numbers of secondary cases and a SARS-like generation time with 8.4 days, and set number of cases caused by zoonotic exposure and assumed total number of cases to estimate R_0 values for best-case, median and worst-case.	1.5-3.5 (2.5)	/
Julien Riou and Christian L. Althaus (2020)[9]	China and overseas	January 18, 2020	Stochastic simulations of early outbreak trajectories	Stochastic simulations of early outbreak trajectories were performed that are consistent with the epidemiological findings to date	2.2	
Tang, Biao et al. (2020)[10]	China	January 22, 2020	Mathematical SEIR-type epidemiological model incorporates appropriate compartments corresponding to interventions	Method-based method and Likelihood-based method	6.47	5.71-7.23
Qun Li et al.(2020)	China	January 22, 2020	Statistical exponential growth model	Mean incubation period=5.2 days, mean serial interval=7.5 days	2.2	1.4-3.9
Averaged						*3.28*

The two studies using stochastic methods to estimate R_0, report a range of 2.2-2.68 with an average of 2.44.[1, 9] The six studies that used mathematical methods to estimate R_0 produced a range from 1.5 to 6.49, with an average of 4.2.[2, 4-6, 8, 10] The three studies using statistical methods such as exponential growth estimated an R_0 ranging from 2.2 to 3.58, with an average of 2.67.[3, 7]

Discussion

Our review found the average R_0 to be 3.28 and median to be 2.79, which exceed WHO estimates of 1.4 to 2.5. The studies using stochastic and statistical methods for deriving R_0 provide estimates that are reasonably comparable. However, the studies using mathematical methods produce estimates that are, on average, higher. Some of the mathematically derived estimates fall within the range produced the statistical and stochastic estimates. It is important to further assess the reason for the higher R_0 values estimated by some the mathematical studies. For example, modelling assumptions may have played a role. In more recent studies, R_0 seems to have stabilized at around 2-3. R_0 estimations produced at later stages can be expected to be more reliable, as they build upon more case data and include the effect of awareness and intervention. It is worthy to note that the WHO point estimates are consistently below all published estimates, although the higher end of the WHO range includes the lower end of the estimates reviewed here.

R_0 estimates for SARS have been reported to range between 2-5, which is within the range of the mean R_0 for 2019-nCoV found in this review. Due to similarities of both pathogen and region of exposure, this is expected. On the other hand, despite the heightened public awareness and impressively strong interventional response, the 2019-nCoV is already more widespread than SARS, indicating it may be more transmissible.

Conclusions

This review found that the estimated mean R_0 for 2019-nCoV is around 3.28, with a median of 2.79 and IQR of 1.16, which is considerably higher than the WHO estimate at 1.95. These estimates of R_0 depend on the estimation method used as well as the validity of the underlying assumptions. Due to insufficient data and short onset time, current estimates of R_0 for 2019-nCoV are possibly biased. However, as more data is accumulated, estimation error can be expected to decrease, and a clearer picture should form. Based on these considerations, R_0 for 2019-nCoV is expected to be around 2-3, which is broadly consistent with the WHO estimate.

Author contributions: JR and AWS had the idea, YL did the literature search and created the table and figure. YL and AWS wrote the first draft; AAG drafted the final manuscript. All authors contributed to the final manuscript.

Conflict of interest: None declared.

References

[1] Joseph T Wu et al. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study.
[2] 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. doi: 10.1101/2020.01.23.916726.
[3] 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. doi: 10.1101/2020.01.25.919787.
[4] Read JM, Bridgen JRE, Cummings DAT, Ho A, Jewell CP. Novel coronavirus 2019-nCoV: early estimation of epidemiological parameters and epidemic predictions. medRxiv. 2020:2020.01.23.20018549. doi: 10.1101/2020.01.23.20018549.
[5] Majumder, M. and Mandl, K. D. (2020) 'Early Transmissibility Assessment of a Novel Coronavirus in Wuhan, China'. Available at: https://papers.ssrn.com/abstract=3524675 (Accessed: 27 January 2020).
[6] Zhidong Cao et al. Estimating the effective reproduction number of the 2019-nCoV in China Jan. 29, 2020
[7] Zhao S, Ran J, Musa SS, Yang G, Lou Y, Gao D, et al. Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A datadriven analysis in the early phase of the outbreak. bioRxiv. 2020:2020.01.23.916395. doi: 10.1101/2020.01.23.916395.
[8] Imai N, Cori A, Dorigatti I, Baguelin M, Donnelly CA, Riley S, et al. Report 3: Transmissibility of 2019-nCoV. 2020.
[9] Riou, J. and Althaus, C. L. (2020) Pattern of early human-to-human transmission of Wuhan 2019-nCoV, bioRxiv 2020.01.23.917351. Available at: https://www.biorxiv.org/content/10.1101/2020.01.23.917351v1.full.pdf (Accessed: 27 January 2020).
[10] Tang, Biao and Wang, Xia and Li, Qian and Bragazzi, Nicola Luigi and Tang, Sanyi and Xiao, Yanni and Wu, Jianhong, Estimation of the Transmission Risk of 2019-nCov and Its Implication for Public Health Interventions (January 24, 2020). Available at SSRN: https://ssrn.com/abstract=3525558 or http://dx.doi.org/10.2139/ssrn.3525558