8-2020

Severe Acute Respiratory Syndrome Coronavirus 2 Transmission Potential, Iran, 2020

Kamalich Muniz-Rodriguez
Georgia Southern University, Jiann-Ping Hsu College of Public Health, km11200@georgiasouthern.edu

Isaac Fung
Georgia Southern University, Jiann-Ping Hsu College of Public Health, cfung@georgiasouthern.edu

Shayesteh R. Ferdosi
The Translational Genomics Research Institute

Sylvia Ofori
Georgia Southern University, Jiann-Ping Hsu College of Public Health, so01935@georgiasouthern.edu

Yiseul Lee
Georgia State University

See next page for additional authors

Authors
Kamalich Muniz-Rodriguez, Isaac Fung, Shayesteh R. Ferdosi, Sylvia Ofori, Yiseul Lee, Amna Tariq, and Gerardo Chowell

Severe Acute Respiratory Syndrome Coronavirus 2 Transmission Potential, Iran, 2020

Kamalich Muniz-Rodriguez,[1] Isaac Chun-Hai Fung,[1] Shayesteh R. Ferdosi, Sylvia K. Ofori, Yiseul Lee, Amna Tariq, Gerardo Chowell

Author affiliations: Georgia Southern University, Statesboro, Georgia, USA (K. Muniz-Rodriguez, I.C.-H. Fung, S.K. Ofori); The Translational Genomics Research Institute, Phoenix, Arizona, USA (S.R. Ferdosi); Georgia State University School of Public Health, Atlanta, Georgia, USA (Y. Lee, A. Tariq, G. Chowell)

DOI: https://doi.org/10.3201/eid2608.200536

To determine the transmission potential of severe acute respiratory syndrome coronavirus 2 in Iran in 2020, we estimated the reproduction number as 4.4 (95% CI 3.9–4.9) by using a generalized growth model and 3.5 (95% CI 1.3–8.1) by using epidemic doubling time. The reproduction number decreased to 1.55 after social distancing interventions were implemented.

Since early 2020, Iran has been experiencing a devastating epidemic of coronavirus disease (COVID-19) (*1*). To determine the transmission potential of severe acute respiratory syndrome coronavirus 2 and thereby guide outbreak response efforts, we calculated basic reproduction numbers (R_0). During the early transmission phase, R_0 quantifies the average number of secondary cases generated by a primary case in a completely susceptible population, absent interventions or behavioral changes. $R_0>1$ indicates the possibility of sustained transmission; $R_0<1$ implies that transmission chains cannot sustain epidemic growth. As the epidemic continues, the effective reproduction number (R_e) offers a time-dependent record of the average number of secondary cases per case as the number of susceptible persons becomes depleted and control interventions take effect. We used 2 methods to quantify the reproduction number by using the curve of reported COVID-19 cases in Iran and its 5 regions (Appendix Table 1, https://wwwnc.cdc.gov/EID/article/26/8/20-0536-App1.pdf). The Georgia Southern University Institutional Review Board made a non–human subjects determination for this project (H20364), under the G8 exemption category.

[1]These first authors contributed equally to this article.

For method 1, we used a generalized growth model (*2*) with the growth rate and its scaling factor to characterize the daily reported incidence. Next, we simulated the calibrated generalized growth model by using a discretized probability distribution of the serial interval and assuming a Poisson error structure (Appendix).

We based method 2 on calculation of the epidemic's doubling times, which correspond to the times when the cumulative incidence doubles and are estimated by using the curve of cumulative daily reported cases. To quantify parameter uncertainty, we used parametric bootstrapping with a Poisson error structure around the number of new reported cases to derive 95% CIs (*3*–*5*). Assuming exponential growth, the epidemic growth rate is equal to ln(2)/doubling time. Assuming that the preinfectious and infectious periods follow an exponential distribution, $R_0 \approx (1 + \text{growth rate} \times \text{serial interval})$ (Appendix) (*6*).

For both methods, the serial interval was assumed to follow a gamma distribution; mean (± SD) = 4.41 (± 3.17) days (*7*; C. You et al., unpub. data, https://www.medrxiv.org/content/10.1101/2020.02.08.20021253v2). We used MATLAB version R2019b (https://www.mathworks.com) and R version 3.6.2 (https://www.r-project.org) for data analyses and creating figures. We determined that a priori $\alpha = 0.05$.

Using Wikipedia as a starting point, we double-checked the daily reported new cases during February 19–March 19, 2020 (the day before the Iranian New Year) against official Iran press releases and other credible news sources and corrected the data according to official data (Appendix Tables 2, 3, Figure 1). Incident cases for the 5 regions were missing for 2 days (March 2–3), which we excluded from our analysis. Because the reported national number of new cases did not match the sum of new cases reported in Iran's 5 regions on March 5, we treated each time series as independent and used the data as reported. Using method 1, we estimated R_0 data for February 19–March 1, 2020. Using method 2, we estimated R_0 from the early transmission phase (February 19–March 1, 2020) and R_e based on the growth rate estimated during March 6–19, 2020, when the epidemic slowed, probably reflecting the effect of social distancing.

Using method 1, we estimated an R_0 of 4.4 (95% CI 3.9–4.9) for COVID-19 in Iran. We estimated a growth rate of 0.65 (95% CI 0.56–0.75) and a scaling parameter of 0.96 (95% CI 0.93–1.00) (Appendix Table 4). The scaling parameter indicated near-exponential epidemic growth (Figure). Using method 2, we found

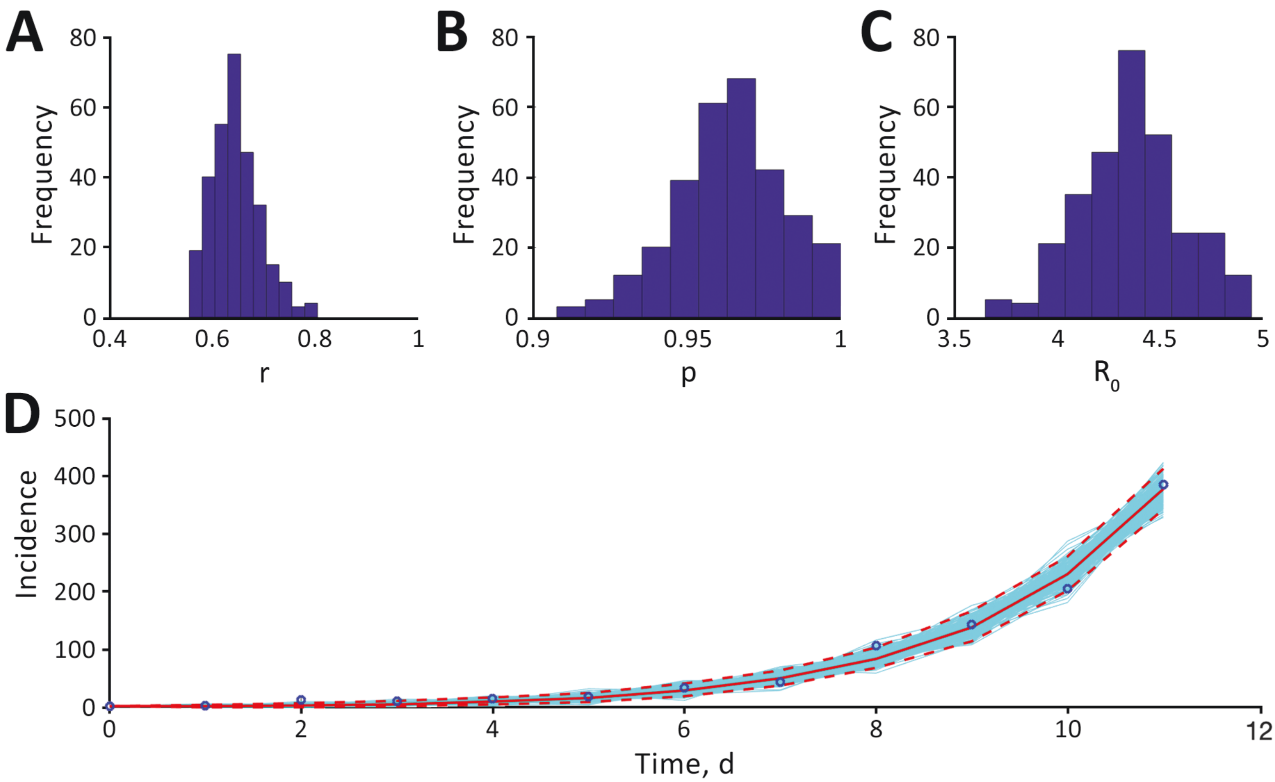

Figure. Estimates of transmission potential for severe acute respiratory syndrome coronavirus 2 in Iran, 2020. A) Growth rate, r; B) scaling of the growth rate parameter, p; C) mean basic reproduction number, R_0; and D) fit of the generalized growth model (method 1) to the Iran data, assuming Poisson error structure as of March 1, 2020. Dashed lines indicate 95% CIs.

that during February 19–March 1, the cumulative incidence of confirmed cases in Iran had doubled 8 times. The estimated epidemic doubling time was 1.20 (95% CI 1.05–1.45) days, and the corresponding R_0 estimate was 3.50 (95% CI 1.28–8.14). During March 6–19, the cumulative incidence of confirmed cases doubled 1 time; doubling time was 5.46 (95% CI 5.29–5.65) days. The corresponding R_e estimate was 1.55 (95% CI 1.06–2.57) (Appendix Table 5, Figures 7, 8). Our results are robust and consistent with Iran's COVID-19 R_0 estimates of 4.7 (A. Ahmadi et al., unpub. data, https://www.medrxiv.org/content/10.1101/2020.03.17.20037671v3) and 4.86 (E. Sahafizadeh, unpub. data, https://www.medrxiv.org/content/10.1101/2020.03.20.20038422v2) but higher than the R_0 of 2.72 estimated by N. Ghaffarzadegan and H. Rahmandad (unpub. data, https://www.medrxiv.org/content/10.1101/2020.03.22.20040956v1).

Our study has limitations. Our analysis is based on the number of daily reported cases, whereas it would be ideal to analyze case counts by dates of symptoms onset, which were not available. Case counts could be underreported because of underdiagnosis, given subclinical or asymptomatic cases or limited testing capacity to test persons with mild illness. The rapid increase in case counts might represent a belated realization of epidemic severity and rapid catching up and testing many persons with suspected cases. If the reporting ratio remains constant over the study period, and given the near-exponential growth of the epidemic's trajectory, our estimates would remain reliable. Although data are not stratified according to imported and local cases, we assumed that persons were infected locally because transmission has probably been ongoing in Iran for some time (*8*).

Although the COVID-19 epidemic in Iran has slowed substantially, the situation remains dire. Tighter social distancing interventions are needed to bring this epidemic under control.

G.C. received support from NSF grant 1414374 as part of the joint NSF-NIH-USDA Ecology and Evolution of Infectious Diseases program. I.C.-H.F. received salary support from the Centers for Disease Control and Prevention (CDC) (19IPA1908208). This article is not part of I.C.-H.F's CDC-sponsored projects.

About the Authors

Ms. Muniz-Rodriguez is a doctoral student in epidemiology and Dr. Fung is an associate professor of epidemiology at Jiann-Ping Hsu College of Public Health, Georgia Southern University. Their research interests include infectious disease epidemiology, digital health, and disaster emergency responses.

References

1. Wood G. Coronavirus could break Iranian society [cited 2020 Feb 29]. https://www.theatlantic.com/ideas/archive/2020/02/iran-cannot-handle-coronavirus/607150/
2. Viboud C, Simonsen L, Chowell G. A generalized-growth model to characterize the early ascending phase of infectious disease outbreaks. Epidemics. 2016;15:27–37. https://doi.org/10.1016/j.epidem.2016.01.002
3. Banks HT, Hu S, Thompson WC. Modeling and inverse problems in the presence of uncertainty: CRC Press; 2014.
4. Chowell G, Ammon CE, Hengartner NW, Hyman JM. Transmission dynamics of the great influenza pandemic of 1918 in Geneva, Switzerland: assessing the effects of hypothetical interventions. J Theor Biol. 2006;241:193–204. https://doi.org/10.1016/j.jtbi.2005.11.026
5. Chowell G, Shim E, Brauer F, Diaz-Dueñas P, Hyman JM, Castillo-Chavez C. Modelling the transmission dynamics of acute haemorrhagic conjunctivitis: application to the 2003 outbreak in Mexico. Stat Med. 2006;25:1840–57. https://doi.org/10.1002/sim.2352
6. Vynnycky E, White RG. An introduction to infectious disease modelling. Oxford (UK): Oxford University Press; 2010.
7. Nishiura H, Linton NM, Akhmetzhanov AR. Serial interval of novel coronavirus (COVID-19) infections. Int J Infect Dis. 2020;93:284–6. https://doi.org/10.1016/j.ijid.2020.02.060
8. Tuite AR, Bogoch II, Sherbo R, Watts A, Fisman D, Khan K. Estimation of coronavirus disease 2019 (COVID-19) burden and potential for international dissemination of infection from Iran. Ann Intern Med. 2020. https://doi.org/10.7326/M20-0696

Address for correspondence: Isaac Chun-Hai Fung, Department of Biostatistics, Epidemiology and Environmental Health Sciences, Jiann-Ping Hsu College of Public Health, Georgia Southern University, PO Box 7989, Statesboro, GA 30460-7989 USA; email: cfung@georgiasouthern.edu; or Gerardo Chowell, Department of Population Health Sciences, School of Public Health, Georgia State University, Suite 662, Office 640B, Atlanta, GA 30303, USA; email: gchowell@gsu.edu.

Cluster of Coronavirus Disease Associated with Fitness Dance Classes, South Korea

Sukbin Jang, Si Hyun Han, Ji-Young Rhee

Author affiliation: Dankook University Hospital, Dankook University College of Medicine, Cheonan, South Korea

DOI: https://doi.org/10.3201/eid2608.200633

During 24 days in Cheonan, South Korea, 112 persons were infected with severe acute respiratory syndrome coronavirus 2 associated with fitness dance classes at 12 sports facilities. Intense physical exercise in densely populated sports facilities could increase risk for infection. Vigorous exercise in confined spaces should be minimized during outbreaks.

By April 30, 2020, South Korea had reported 10,765 cases of coronavirus disease (COVID-19) (*1*); ≈76.2% of cases were from Daegu and North Gyeongsang provinces. On February 25, a COVID-19 case was detected in Cheonan, a city ≈200 km from Daegu. In response, public health and government officials from Cheonan and South Chungcheong Province activated the emergency response system. We began active surveillance and focused on identifying possible COVID-19 cases and contacts. We interviewed consecutive confirmed cases and found all had participated in a fitness dance class. We traced contacts back to a nationwide fitness dance instructor workshop that was held on February 15 in Cheonan.

Fitness dance classes set to Latin rhythms have gained popularity in South Korea because of the high aerobic intensity (*2*). At the February 15 workshop, instructors trained intensely for 4 hours. Among 27 instructors who participated in the workshop, 8 had positive real-time reverse transcription PCR (RT-PCR) results for severe acute respiratory syndrome coronavirus 2, which causes COVID-19; 6 were from Cheonan and 1 was from Daegu, which had the most reported COVID-19 cases in South Korea. All were asymptomatic on the day of the workshop.

By March 9, we identified 112 COVID-19 cases associated with fitness dance classes in 12 different sports facilities in Cheonan (Figure). All cases were confirmed by RT-PCR; 82 (73.2%) were symptomatic and 30 (26.8%) were asymptomatic at the time of laboratory confirmation. Instructors with very mild symptoms, such as coughs, taught classes for ≈1 week after attending the workshop