Short Communication

Effective Reproductive Number estimation for initial stage of COVID-19 pandemic in Latin American Countries

Yaset Caicedo-Ochoa[a,b], David E. Rebellón-Sánchez[a,c], Marcela Peñaloza-Rallón[a], Hector F. Cortés-Motta[a], Yardany R. Méndez-Fandiño[a,*]

[a] Escuela de Medicina. Universidad Pedagógica y Tecnológica de Colombia. Tunja, Colombia
[b] Fundación Valle del Lili, Centro de Investigaciones Clínicas, Cra 98 No. 18 - 49, Cali 760032, Colombia
[c] Centro Internacional de Entrenamiento e Investigaciones Médicas, CIDEIM, Cali, Colombia

A B S T R A C T

Objectives: The coronavirus disease 2019 (COVID-19) has become pandemic and turn in a challenge for Latin America. Understanding the dynamics of the epidemic is essential for decision making, and to reduce the health, economic, and social impacts of the pandemic. The present study aimed to estimate the effective reproductive number (R_t) of Severe Acute Respiratory Syndrome coronavirus 2 (SARS-Cov2) infection during the first 10 days of the outbreak in seven Latin American countries with the highest incidence of cases as of March 23, 2020. Furthermore, we chose to compare the seven countries with Spain and Italy given their history with the virus.

Methods: Incidence data retrieved from the COVID-19 data repository by Johns Hopkins University were analyzed. The R_t was calculated for the first 10 days of the epidemic in Brazil, Ecuador, Chile, Colombia, Panama, Mexico, and Peru. R_t estimations were compared with Spain and Italy values for the same interval.

Results: The median R_t for the first 10 days of the COVID-19 epidemic were 2.90 (2.67-3.14) for Spain and 2.83 (2.7-2.96) for Italy. Latin American R_t estimations were higher in Ecuador (3.95(3.7-4.21)), Panama (3.95(3.7-4.21)), and Brazil (3.95(3.7-4.21)). The smallest one was observed in Peru (2.36(2.11-2.63)). All Latin American countries had R_t greater than 2.

Conclusions: The initial stages of the COVID-19 epidemic in Latin America suggested a high Rt. Interventions such as domestic and international travel restrictions, educational institutions closure, social distancing, and intensified case surveillance should be adopted to prevent the collapse of the health systems.

1. Introduction

In December 2019, Severe Acute Respiratory Syndrome (SARS) with an unknown etiology was reported in Wuhan City, Hubei Province, China. A novel coronavirus disease 2019 (COVID-19) was rapidly identified and characterized (Zhu et al., 2020). In a three-month lapse and despite intense containment measures, COVID-19 cases worldwide have continually increased. On March 11, 2020, the WHO declared the coronavirus a pandemic. At present, more than two million people have been infected worldwide, with the highest incidences appearing in Asia, Europe, and North America. Health systems around the world have collapsed, and mortality rates have reached overwhelming numbers in high income countries (World Health Organization, 2020).

The first COVID-19 case in Latin America was detected in Brazil on February 26, 2020 (Rodriguez-Morales et al., 2020). Since then, more cases have been showing up all around Latin America. In order to mitigate the effects of COVID-19 and make appropriate decisions related to the health, economic, and social system, it is crucial to understand the nature of the outbreak.

Modeling studies are useful in understanding epidemics and evaluating the potential impact of interventions in the early stages of pandemics. The Effective Reproductive number (Rt) is a parameter that can be used to follow-up the epidemics (de Silva et al., 2009; Nishiura et al., 2016; Koo et al., 2020). R_t is different from the basic reproductive number (R_0). The R_0 is the expected number of secondary cases from a primary case in a population where everyone is susceptible. During the course of the epidemic,

* Corresponding author. Universidad Pedagógica y Tecnológica de Colombia. Avenida Central del Norte 39-115, Tunja 150003, Colombia. Tel.: +57 300 600 4649.
E-mail addresses: edgar.caicedo@fvl.org.co (Y. Caicedo-Ochoa), derebellon@cideim.org.co (D.E. Rebellón-Sánchez), marcela.penaloza@uptc.edu.co (M. Peñaloza-Rallón), hefacor@gmail.com (H.F. Cortés-Motta), yardany.mendez@uptc.edu.co (Y.R. Méndez-Fandiño).

some individuals become infected or immune and are no longer susceptible; therefore, the estimation of Rt is more appropriate. R_t is calculated as a function of time and is the actual average number of secondary cases per primary case (Wallinga, 2004). The R_t number will usually be smaller than the R_o number because it takes into account the impact of control measures and non-susceptible individuals in the population (de Silva et al., 2009; Cori et al., 2013; Delamater et al., 2019).

Currently, governments in Latin America have taken measures to mitigate the spread of COVID-19 primarily based on world health organization recommendations. However, the potential impact of the virus in Latin America is still unknown. The first cases in Latin America were reported months after the virus spread in China, Italy, Spain, and North America. Given the urgency in these countries, governments need more accurate estimates of what could happen in Latin America in order to make informed decisions. The present study estimated the Rt of SARS-Cov2 during the first 10 days of the outbreak in seven Latin American countries and compared it to the R_t in Spain and Italy.

2. Material and Methods

2.1. Data Source

Time-dependent incidence data were retrieved from the *2019 Novel Coronavirus COVID-19* Johns Hopkins University data repository (Dong et al., 2020). Brazil, Ecuador, Chile, Colombia, Panama, Mexico, and Peru were selected because they had been through 10 days of the outbreak, as well as having the highest incidence of cases in Latin America as of March 23, 2020. We chose to compare the Latin American R_t values with Spain and Italy because they had similar population numbers to the Latin American countries. Additionally, Spain and Italy were among the most affected countries in Europe due to COVID-19 (Yuan et al., 2020)**.**

2.2. Data analysis

To calculate Rt values, we used the same methodology of Cori et al (Cori et al., 2013). R_t was estimated by the ratio of the number of new infections generated in step t, I_t, to the total infectiousness of infected individuals at time t, given by $\sum_{s=1}^{t} I_{t-a} w_s$, the sum of infection incidence up to the time step t - 1, weighted by the infectivity function w_s. R_t values equal or below one indicates that there will be a decline in the number of cases. R_t values higher than one indicate that the number of cases will increase. Contact traces and transmissibility can change over time in regard to the outbreak progression. R_t values can be adjusted to include a serial interval (SI) as the infectivity function, under the assumption of a gamma distribution (Wallinga, 2004; Cori et al., 2013).

We estimated two scenarios: a) An Rt estimated using the SI calculated by (Li et al., 2020) for the early transmission in the Wuhan's outbreak (mean SI of 7.5 days, and standard deviation (SD) of 3.4 days). b) An Rt estimated using the SI calculated by (Nishiura et al., 2020) through Bayesian statistics of exponential growth rate adjusted by the growth of curve during the initial stage of the outbreak (Mean SI: 4.7 days. SD SI: 2.9 days).

Analytical estimates of the R_t were obtained within a Bayesian framework. R_t was estimated in a 10 days interval from the date that a cumulative incidence of 25 or more cases of COVID-19 was reached in each country. The choice of the 25 cases of cumulative incidence is to goal a coefficient of variation of 0.2 in each time window (Cori et al., 2013). We reported the median and 95% credible interval (CI). Additionally, we report how many days it took to reach the incidence of 25 cases in each country. Statistical analysis was performed using R language version 3.6.3 (R Core Team, 2019).

3. Results

The interval of days required to reach 25 cumulative cases was divergent in Latin American countries compared with European referents. While 22 and 25 days were required in Italy and Spain, respectively, the interval in Latin America ranged from 3 days in Panama to 15 days in Mexico.

Rt estimates in the first 10 days after reach the 25 cumulative incidence are described in Table 1. All Latin American countries had R_t greater than 2. Ecuador and Panama had the highest Rt values of Latin America, while Peru had the lowest. Rt estimates for Ecuador, Panama, and Brazil were higher than both European referents. Spain and Italy had higher Rt values than Mexico, Colombia, Peru, and Chile (Fig. 1).

4. Discussion

Important variations were observed when the Rt was calculated using the parameters of (Li et al., 2020) or (Nishiura et al., 2020). The differences between both serial intervals are related to the infectious probability time, which was higher for Li et al. To analyze the initial phases of the outbreak, we preferred to use Nishiuria et al.'s (2020) parameters. The findings using these parameters show more conservative scenarios and less variation than previous studies made in other regions of the world (Yuan et al., 2020; Zhang et al., 2020).

The Rt estimates in the first ten days of the COVID-19 pandemic were higher in some of the Latin American countries compared to the European referents. The aggressive dynamics of the outbreak in countries such as Brazil, Ecuador and Panama should be considered by surveillance systems in order to provide a quick response and stricter containment strategies. Despite the fact that the estimated Rt for Colombia, Peru, Chile and Mexico were lower than the European ones, the variation with respect to them is minimal. All

Table 1
Effective reproductive number (R_t) estimates for Latin American countries, Italy and Spain.

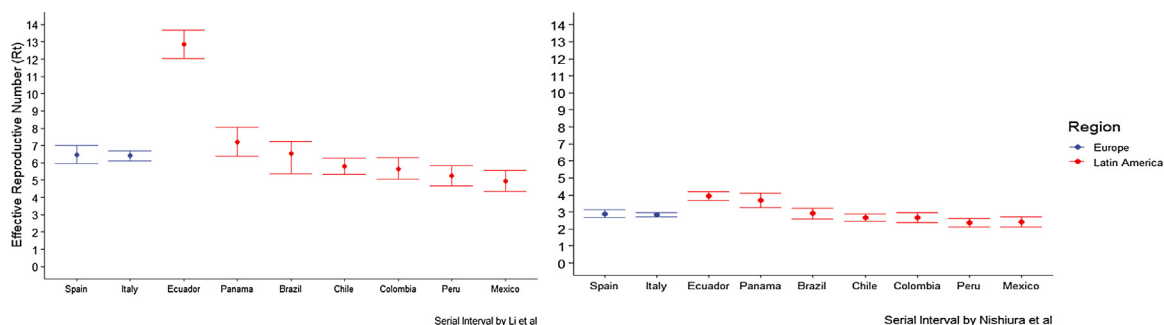| Country	Date in which each country completes at least 25 cases of cumulative incidence	The interval between the start of the outbreak and the cumulative incidence > - 25 cases (days)	Rt in the first 10-day using SI of Li et al Median (95% Credible Interval)	Rt in the first 10-day using SI of Nishiura et al Median (95% Credible Interval)
Spain	26-February	25	6.48(5.97-7.02)	2.90(2.67-3.14)
Italy	22-February	22	6.41(6.11-6.71)	2.83(2.70-2.96)
Ecuador	14-March	13	12.86 (12.05-13.69)	3.95 (3.70-4.21)
Panama	13-March	3	7.19(6.37-8.08)	3.67(3.25-4.13)
Brazil	09-March	12	6.53(5.85-7.25)	2.91(2.60-3.23)
Chile	13-March	10	5.79(5.32-6.28)	2.67(2.45-2.89)
Colombia	15-March	9	5.65(5.04-6.29)	2.67(2.38-2.98)
Peru	13-March	7	5.24(4.68-5.83)	2.36(2.11-2.63)
Mexico	12-March	15	4.94(4.37-5.56)	2.42(2.14-2.72)

Fig. 1. Comparison of Rt estimates for Latin American countries, Italy and Spain using two different serial intervals.

Latin American countries had R_t greater than 2, indicating an exponential growth. There is a high probability that the capacity of the Latin American healthcare systems is overwhelmed. Furthermore, the COVID-19 pandemic could have serious repercussions in the region, given the context of politically divided countries, social inequality, economic limitations, internal conflicts, and social protests (Rodriguez-Morales et al., 2020).

Although containment strategies have been implemented in some countries to mitigate the impact of the pandemic, additional interventions should be prioritized to attenuate the consequences of the outbreak and prevent similar scenarios observed in Spain and Italy. Domestic and international travel restrictions, educational institutions closure, elderly isolation, compulsory social distancing, and intensified case surveillance are strategies that may attenuate the consequences of COVID-19 (Koo et al., 2020).

Potential limitations in interpreting our results are associated with underestimation or overestimation of Rt measurements. These may vary based on available diagnostic tests, the inclusion of imported cases in the early stages of the outbreak, and delays in reporting cases by health institutes (de Silva et al., 2009; Cori et al., 2013). Under ideal conditions, Rt should be calculated using the date of the onset of symptoms and not the diagnostic report date. However, none real-time available data sources have this information for the region. In the current scenario, calculating an approximate Rt using the date of diagnostic report is a useful tool, and provides valuable information on the dynamics of the outbreak in its initial stages.

In conclusion, the COVID-19 outbreak represents a real threat to low-income countries like those in Latin America. Rt estimation for initial stage of COVID-19 pandemic in Latin American countries shows an aggressive dynamic of outbreak and suggest a grim scenario. Capacity development, intensified surveillance, and human, financial and infrastructure resources must be prioritized urgently.

Funding sources

Ethical Approval

This research does not involve human subjects. It is not required to obtain Institutional Review Board (IRB) approval.

5. Conflict of interest

The authors declare not to have any conflict of interest.

References

Cori A, Ferguson NM, Fraser C, Cauchemez S. A new framework and software to estimate time-varying reproduction numbers during epidemics. Am J Epidemiol [Internet]. 2013;178(9)1505–12 Nov 1 [cited 2020 Apr 2]. Available from: http://www.ncbi.nlm.nih.gov/pubmed/24043437.

Delamater PL, Street EJ, Leslie TF, Yang YT, Jacobsen KH. Complexity of the basic reproduction number (R0). Emerg Infect Dis. Jan 1 2019;25(1)1–4 Available from: https://wwwnc.cdc.gov/eid/article/25/1/17-1901_article.

Dong E, Du H, Gardner L. An interactive web-based dashboard to track COVID-19 in real time. Lancet Infect Dis. 2020;0(0) Available from: https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30120-1/fulltext.

Koo JR, Cook AR, Park M, Sun Y, Sun H, Lim JT, et al. Interventions to mitigate early spread of SARS-CoV-2 in Singapore: a modelling study. Lancet Infect Dis [Internet]. 2020; Mar [cited 2020 Mar 24];0(0). Available from: https://linkinghub.elsevier.com/retrieve/pii/S1473309920301626.

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. N Engl J Med. 2020; Jan 29 Available from: https://www.nejm.org/doi/full/10.1056/NEJMoa2001316.

Nishiura H, Kinoshita R, Mizumoto K, Yasuda Y, Nah K. Transmission potential of Zika virus infection in the South Pacific. Int J Infect Dis [Internet]. 2016;45:95–7 Apr 1 [cited 2020 Apr 2]. Available from: http://www.ncbi.nlm.nih.gov/pubmed/26923081.

Nishiura H, Linton NM, Akhmetzhanov AR. Serial interval of novel coronavirus (COVID-19) infections. Int J Infect Dis [Internet]. 2020;93:284–6 Mar 4 [cited 2020 Mar 24]. Available from: http://www.ncbi.nlm.nih.gov/pubmed/32145466.

R Core Team. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing; 2019.

Rodriguez-Morales AJ, Gallego V, Escalera-Antezana JP, Mendez CA, Zambrano LI, Franco-Paredes C, et al. COVID-19 in Latin America: The implications of the first confirmed case in Brazil. Travel Med Infect Dis [Internet]. 2020;101613 Feb 29 [cited 2020 Mar 23]. Available from: http://www.ncbi.nlm.nih.gov/pubmed/32126292.

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. Eurosurveillance [Internet]. 2009;14(31)19292 Aug 6 [cited 2020 Mar 23]. Available from: http://www.eurosurveillance.org/content/10.2807/ese.14.31.19292-en.

Wallinga J, Teunis P. Different Epidemic Curves for Severe Acute Respiratory Syndrome Reveal Similar Impacts of Control Measures. Am J Epidemiol 2004;160(6)509–16 Sep Available from: https://academic.oup.com/aje/article/160/6/509/79472.

World Health Organization. Coronavirus (COVID-19) events as they happen [Internet]. 2020 [cited 2020 Mar 22]. Available from: https://www.who.int/emergencies/diseases/novel-coronavirus-2019/events-as-they-happen.

Yuan J, Li M, Lv G, Lu ZK. Monitoring Transmissibility and Mortality of COVID-19 in Europe. Int J Infect Dis 2020; Available from: https://www.ijidonline.com/article/S1201-9712(20)30182-X/fulltext.

Zhang S, Diao MY, Yu W, Pei L, Lin Z, Chen D. Estimation of the reproductive number of novel coronavirus (COVID-19) and the probable outbreak size on the Diamond Princess cruise ship: A data-driven analysis. Int J Infect Dis. Apr 1 2020;93:201–4 Available from: https://www.ijidonline.com/article/S1201-9712(20)30091-6/pdf.

Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, et al. A novel coronavirus from patients with pneumonia in China, 2019. N Engl J Med [Internet]. 2020;382(8)727–33 Feb 20 [cited 2020 Mar 22]. Available from: http://www.nejm.org/doi/10.1056/NEJMoa2001017.