Modelling and projections of the COVID-19 epidemic and the potential impact of social distancing in Cameroon

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Abstract

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) disease (COVID-19) pandemic continues to be a global health problem with a significant impact in Cameroon. The aim of this study was to improve the understanding of the spread of COVID-19 and enhance disease control strategies. We assessed the SIRD (susceptible, infected, recovered and death) model to describe COVID-19 reported cases in Cameroon from March 7 to May 31, 2020, and study the impact of social distancing. We assessed changes in the basic reproduction number (R_0) on a phase-adjusted process and forecasted the long-term epidemic trend. Daily incidence data was fitted to a log-linear model before each peak of the epidemic with the purpose of studying the effective mechanism of variation of the reproduction number R_e. Before the first peak of the epidemic, R_0 was estimated as 6.8. Social distancing and restricted measures contributed to reduce the value to 3.24 by April 30 but remained greater than 1 (R_0=2.43) by May 22 when the initial measures implemented by the government to control the spread of the disease were relaxed. The estimated number of infections ranged 13,703-18,456 by May 31, and will continue increasing throughout June 2020 with more than 20,000 cases expected by the end of June 2020, suggesting that the pandemic is still in the growth phase. Long-

term prediction showed a flattened curve towards April 2021. Preventive measures initially implemented by the government of Cameroon should be strictly maintained and reinforced to reduce R_e to 0.5.

Introduction

The 2019 Novel coronavirus (2019-nCoV/SARS — CoV-2), named by the World Health Organization (WHO) as the Coronavirus Disease 2019 (COVID-19), has given rise to an outbreak of viral pneumonia in Wuhan, China since December 2019.[1-3] It has been found to have similar characteristics with the Middle East respiratory syndrome coronavirus (MERS-Cov).[4] Despite the drastic, large-scale containment measures promptly implemented by the Chinese government, the disease had spread well outside China, reaching countries in all parts of the globe, thus the declaration as a pandemic by the WHO on March 11, 2020 (https://www.who.int/news-room/detail/08-04-2020-who-timeline—-covid-19). COVID-19's incubation period varied greatly among patients and was reported to be 3-7 days, at most 14 days.[5] The Basic reproduction number R_0 is the average number of people who may catch an infection from one contagious person known as the number of secondary infections one infected person can generate, R_0 is known to be time-dynamic and can help control the level of transmission, together with the effective reproduction number R_e.[6-8]

Acknowledging the weak health systems in sub-Saharan Africa (SSA), the Africa Centers for Disease Control (CDC) predicted a worst case scenario of up to 3 million deaths (https://www.dw.com/en/coronavirus-in-africa-how-deadly-could-covid-19-become/a-53230519) within the region. Cameroon identified its first, imported cases on March 7, 2020. Since then, the trend has been rising bringing the country among the top five seriously affected in SSA.[9] On March 17, 11 days after the first case was identified, Cameroon established a response strategy focusing on closing the country's borders, reinforcing hygiene and social distancing, associated with contact tracing, quarantine and screening test targeting all recent air travellers.[10] Other measures in the strategy included closure of worship places, restaurants, bars, schools, and universities, to limit spreading of the disease. Contact tracing and isolation were introduced, since identified in other countries such as Thailand,[11] as means to control the epidemic when there is an increase of the basic reproduction number.[12] The epidemic starts in the two main cities of

Cameroon: Douala and Yaoundé, and has been spreading in the whole country.

However, before the disease reached a controlled level, the government relaxed certain measures by opening bars, restaurants, and leisure facilities on April 30th, 2020, then scheduled to reopen schools and universities on June 1st, 2020. These changes in the epidemic control strategy spurge the daily number of infected cases to an exponential rise.

Several modelling and forecasting approaches have been used on the epidemic data in different countries to study the severity of the disease. These included deterministic models like Susceptible-

Infected-Removed (SIR), Susceptible-Exposed-Infected-Recovered (SEIR) with the daily number of confirmed infections as the main data source.[13-19] Numerous research groups around the world (London School of Tropical Medicine, WHO, and Imperial Colleague teams) have provided scientific evidence to governments and decision-makers using diverse modelling approaches of the evolution of COVID-19 morbidity and mortality.[20-23]

Some authors claimed that COVID-19 has reared features: the epidemic has an infectious probability during the incubation (pre-symptomatic) period; various measures are available to control the development of the epidemic. Existing data source is affected by detection method delay like Polymerase Chain Reaction (PCR) that has a time lag between the real infected and confirmed infected number. These variation in data collection provide challenges to analyse the outbreak but, provide an accurate prediction of the disease trends.[24]

Infectious disease dynamic model was employed for modelling and prediction of COVID-individuals in Wuhan, China.[13] The model was used to describe different phases of the epidemic enabling the estimation of the reproduction number. A similar modelling using SEIR model was used to describe South African COVID-19 data accounting for social distancing and lockdown date and time parameters.[19] Other authors suggested a SIRD model to analyse and forecast the COVID-19 spreading.[16,21] Each modelling approach proposed an estimation of the basic reproduction number R_0, either as a constant or time-dependent parameter.[25,26] To measure how fast the virus is growing, the reproduction number at time t, denoted R_t is the average number of people who become infected by an infectious person.[27-29] When R_t is above 1, the virus spread quickly and the spreading is reduced when its below 1 and can stop when the value is equal to 0.5. Another critical parameter for the epidemic model is the serial interval (SI). The SI is the duration between onset of symptoms in a primary case of the disease, and the onset of symptoms in any secondary cases resulting from the primary cases.[30,31] This variable is used to, study the variation of the effective reproduction number R_e on a day-by-day basis, and guide the tracking of the effectiveness of public health interventions.

Besides shedding light on the dynamics of the epidemic spreading, the intend of our analysis was to provide government officials with realistic estimates for the time and magnitude of the epidemic peak *i.e.*, the maximum number of infected individuals, as well as gauge the effect of containment measures based on models and forecasting tools. This study also intended to answer the following questions: What information can we learn from the evolution of the pandemic in Cameroon? When could we expect the epidemic curve to reach the highest peak, from which it will start reducing and flattening? In which stage of the epidemic schools will reopen on June 1, 2020?

Materials and Methods

Ethical considerations

This study has used anonymised data set for which no ethics approval or consent to use was required.

Data source and exploration

We extracted COVID-19 data from March 7, 2020 to May 31, 2020. Reported data included the total daily infected, recovered, death, and active cases. All information was obtained from online repository (https://worldometerinfo.com/coronavirus/cameroon) and was provided as Supplementary Table 1 and Figure 1.

On March 7th, 2020, the Cameroon reported its first 2 imported cases of COVID-19, and subsequent cases were confirmed by March 15th, 2020. Intervention measures application began on March 17th, 2020. Supplementary Figure 1 described the active number of cases or the number of infected individuals (equals to cumulated cases per day minus total number recovered minus total number of deaths). The recovered number and the number of deaths were in an increasing trend. Daily reported cases were very sparse. Indeed, twenty dates with incidence of 0 were reported by April 30 (Supplementary Figure 1). As a result, repeated value of cumulative cases was found over more than 3 days. Because of these data gaps, we organised the study in 4 phases. Phase 1 used the data obtained from March 7, 2020 to April 3, 2020, where a peak of 203 cases were reported on April 3. The second phase started on April 4, 2020 and ended on April 30, 2020. During this phase, the number of cases continued to increase, while the control measures described above were reinforced. New measures such as 14-day quarantine were introduced for individuals who had closed contacts with a COVID-19 infected patient. We noticed jumps between some dates of reporting new cases (between March 12 and March 13), probably indicating either an error in the data collection methods, a change in the testing/screening methods, or variation in incubation period for asymptomatic individuals. The second epidemic peak occurred during May 1 and May 22, precisely on May 21 with 555 new cases reported. The period of May 1 to May 22 was considered as the third epidemic phase. Data from May 23 to May 31 (phase 4) were used to predict the epidemic level by the end of June 2020. As of May 31, the total cases of infected, deaths and recovered were 6150, 191, and 3567, respectively.

Table 1. Basic reproduction number and phase-adjusted estimates of the number of individual infected by COVID-19 cases in Cameroon.

Epidemic phases	Description	SIRD R_0	Log-linear R_0	Daily new cases expected by the end**	Range number of infected$
March 7-April 03	First epidemic peak (first phase)	6.80	3.05 (2.36-3.73)+		14-2.782
April 04-April 30	Lockdown and social distance (second phase)	3.24		230	1.620-6.224
May 1-May 22	Second epidemic peak; lockdown released (third phase)	2.43	2.5 (0.18-4.81)+	1.800	4.452-9.971
May 23-May 31	Lockdown released; preparation to return to school (fourth phase)	2.95			13.703-18.456
May 1-May 31*	Whole lockdown released period	3.05			19.130

R_0 estimated by SIRD; + 95% confidence interval; *the period was used to study the long-term projection by June 2020; **estimated using the detected epidemic peaks; $at the end of each period.

The modelling approaches

Two modelling approaches were used: a compartment modelling for cumulative cases, and a log-linear modelling applied on daily incidence data.

Classical compartment models are used to classify individuals into five types at time t: susceptible (S; at risk of contracting the disease), exposed (E; infected but not yet infectious), infectious (I; capable of transmitting the disease), and removed (R; those who recover or die from the disease). The total population size (N) is given by N=S+E+I+R+D. It is assumed that susceptible individuals who have been infected first enter a latent (exposed) stage during which they may have a low level of infectivity. We employed the SIRD (without the E compartment) model to fit the reported observed data (I, R, D). The model is suitable to demonstrate the spread and forecasting of the new coronavirus. It can account for social distancing and mortality rate, and provides mechanism to describe transition between compartments, as well as estimate values of R_0 on a phase-adjusted basis. It has also been used to analyse and simulate COVID-19 infection for several countries.[32,33]

SIRD model

The differential equations of the SIRD model are given as:[16,25]

$$dS/dt = -\rho*\beta*I*S/N$$
$$dI/dt = \rho*\beta*I*S/N - \gamma*(1-\mu)*I - \mu*I$$
$$dR/dt = \gamma*(1-\mu)*I$$
$$dD/dt = \mu*I$$

The model has four parameters: the transmission rate or the growth rate β, which controls the transition between S and I; the recovery rate γ for hospitalized patients, and the death rate μ. We incorporated social distancing through a constant rate ρ which falls in the interval 0-1. The social distancing parameter is expected to decrease the force of infection during strict application of intervention measures.[19] We expected that ρ will tend to 1, but we acknowledged that perfect social distancing could be difficult to achieve as it is directly linked to human behaviour.

In most exponential models, the value of R_0 is estimated by the expression $\beta/\gamma+\mu$.[25,34] This quantity was used to fit the numbers of infected individuals in each compartment of the SIRD model by the end of each epidemic phase. Precisely, R_0 was used to fit the cumulated reported cases

from March 7 to April 3 (first peak of the epidemic), April 4 to April 30 (before control measures), then from May 1 to May 22 (two weeks after the relaxation of the control measures), and during May 23 and May 31. Each epidemic phase provided an estimate of the values R_0 and R_e whose quantity guided the predictions and provided insight on the level of disease spreading among individuals within the population.

Assumption and initialization of SIRD model's parameters

In the modelling process, S was assumed to represent the population of Cameroon (Total population by 2017, N=24 million). The initial assumed number of cases caused by zoonotic exposure was I=2. Due to data gaps in the reporting dates of infected individuals, challenges occurred in the estimation of hospitalization average period. However, some authors estimated the hospitalization period of 12.39±4.77 days.[35] The median time from disease onset to diagnosis among confirmed cases was set at 5.[36] The parameter γ was set as 1/18 (ceiling of 12.39±5 is 18) as suggested in Wang et al.[13] R_0 was chosen based on a fitted exponential function: it has been estimated
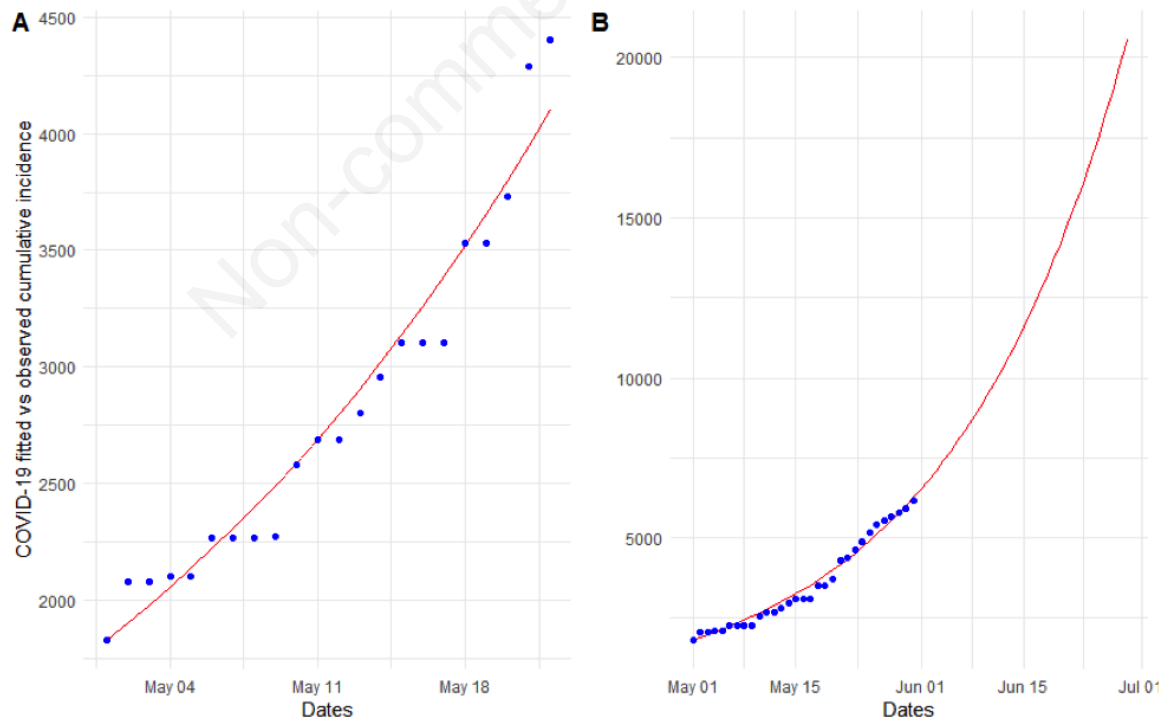
Figure 1. Evolution and projections of cases after the relaxing of preventive measures (May 1 to May 31, 2020). A: Third phase of the epidemic (May 1 to May 22)-adjusted and observed cumulative incidence; R_0 was estimated as 2.43. B: observed data (May 1 to May 31) *versus* fitted cumulative data reported were used to project the epidemic curve by July 1, 2020.: The model predicted a significant increase of cases by July 2020.

that the reproduction number for COVID-19 could vary from 2.7 (with β close to 0.54 and γ close to 0.2) to 5.31; 95% CI (3.99-6.96).[8] Thus, β was set to 0.15; μ was the proportion of death in the Cameroon population by April 30 and was initialized as 61/1832=0.033%. We took ρ=0.45 as estimated in Nyabadza *et al.*,[19] considering R_0 to be time-dependent and fitted the model for different phases of the epidemic accordingly.

In the second modelling approach, a log-linear model was used to estimate the growth in the different phases of the epidemic peak characterized by the growth-phase and the decay phase. Daily records of the incidence cases were used to estimate the basic reproduction number and evaluate the change in the effective reproduction number R_e, to an extend of tracking the effectiveness of public health interventions on a day-to-day basis, and possibly predict at the earliest instance when the curve of infection during an outbreak will change its direction. To study the time-dependent of the effective reproduction number Re distribution, Serial Intervals (SI) were parametrized using a discrete *gamma* distribution with mean, and standard deviation.[37] Several authors estimated the serial interval distribution to have a mean of 7.5 days with a standard deviation (SD) of 3.4 days.[30,31,38-40] This values were found very closed to the *serial interval* parameters for the MERS virus, with a mean of 7.6 and a SD of 3.4.[36,37] We studied three scenarios of the R_e the onset of the disease to April 30; the first, second and third scenario used a mean of 7.5, and SD=3.4; 2.3 days and SD of 1.4; 2 and SD of 1, respectively. The fourth scenario was stretched until the month of May 2020.

Available estimation techniques

Ordinary differential equations were solved using numerical methods. We fitted parameter values that minimised the residual sum of squares between the observed cumulative incidence and the predicted cumulative incidence. Optimization was carried out using the L-BFGS-B algorithm.

For log-linear modelling, the analysis was carried out with R Epidemics Consortium (RECON) packages (RECON - R Epidemics Consortium/United Kingdom/London) developed to fit log-linear models to epidemic data (https://www.repidemicsconsortium.org/), as well as implementing the serial distributions of R_e. The free statistical software R (R Core team 2020, Vienna, Austria, version 3.6.3) was applied for all the calculations and estimations found in the current study.[41]

Results

Using the SIRD model

Estimation of the epidemic trend using a multi-phases analysis

Results from phase-to-phase analysis are summarized in Table 1. During the primary phase (March 7 to March 16) of the epidemic, R_0 was estimated at 2.21. After extending this primary phase to April 3rd, 2020, the date of the first peak of the epidemic R_0 yielded 6.80. The number of infections by the end of this first phase (April 3) varied between 14 and 2,782. During the second phase (April 4-April 30), with the initial values of I=529, D=8, R=17, S=N-I-R-D, the model estimated the values of R_0 at 3.24, thus resulting in a decrease of R_0 and a decline in the total infections from 1,620 to 6,224. This reduction of R_0 suggested an impact of the social distancing including local and national lockdown, and other non-pharmaceutical interventions such as individual isolation, closure of schools and universities, banning of mass gatherings and/or public events. Supplementary Figure 2 showed the fitted versus observed cumulative incidence for the first and second phases, suggesting SIRD model as an appropriate tool to describe the epidemic.

With the model initial conditions after the end of lockdown (May 1 to May 22, before the second peak of the epidemic) set at S=N-1832-837-61, I=1832, R=837, D =61, R_0 was estimated as 2.43, with the number of infected individuals ranging from 4,452 to 9,971. Figure 1 shows how correlated are the observed and the fitted values despite repeated number of cases.

From May 23 to May 31, the number of infected people reached 18,000 cases with R_0=2.95 (Table 1).

Long-term forecasting of the COVID-19 in Cameroon

COVID-19's projection during the month of July 2020 revealed an ascending epidemic curve (Figure 1).

In the context where COVID-19 preventive measures are not respected during the reopening of schools, projections could reach more than 20,000 individuals infected by 30th of June 2020 (Figure 1).

A long-term forecast using SIRD revealed that, if intervention is not strictly applied in a context of re-opening of schools and Universities, the epidemic will continue to grow and could show a downwards by late October 2020 (Figure 2). On the other hand, since infected persons would have increased, the health system

may not be able to manage all the cases. As a result, the number of deaths will increase, as will the number of recovered individuals (Figure 2). In addition, the epidemic will continue growing until January 2021 when, we expect a reduction in the number of total cases (Figure 2). Figure 2 brought up the persistence of the pandemic until January 2021 and demonstrated that the epidemic will continue despite the downwards curve predicted towards April 2021.

Modelling the epidemic trajectory using incidence data and a log-linear model. What can be learn from that?

The daily incidence data were described on Figure 3. As zero-cases were reported in 2 or 3 consecutive days, as a result, dates with zero-values were ignored.

We fitted two log-linear models: firstly, on the growth phase *i.e.*, before the peak (April 3, 2020 with 203 observed new cases); then secondly during the phase after the peak (April 4 to April 30). Fitted values from the model with confidence limits, as well as observed incidence data, were displayed on Figure 3A. The Figure revealed a probability of imported cases in the country at the beginning of the epidemic. Parameters of interest extracted from the model were: growth rate prior to the peak estimated as 0.185 (95% CI= 0.14-0.23); growth and decay rates were equivalent to a doubling time of 3.74 days (95% CI 3.0 – 4.95 days), and a halving time of 16.77 days (95% CI 6.72 – 33.89 days).

Estimating changes in the effective and basic reproduction number by April 30

We studied the basic reproductive number for the growth phase (Figure 3B). The values of R_0 ranged from 2 to 4.10 with mean value of 3.05 (95% CI=2.36-3.73). This value was smaller than the value estimated by the SIRD model at the same period. After the peak observed from April 3 to April 30, R_0 mean value was estimated as 1.31 with 95% CI=0.95-3.02, thus resulting in a decrease in the value of R_0 although still above 1, and an upsurge of the epidemic. However, little decrease was observed on the number of infected individuals traducing a positive effect of the implementation of preventive measures during the second phase of the epidemic.

On the other hand, R_e values oscillated between 2.5 and 10 during the first 15 days of the epidemic and tended to 1 on April 30 (Supplementary Figure 3). This observation was in favour of the successfulness of mitigation efforts towards the reduction of COVID-19's transmission in Cameroon. However, because the reproduction number
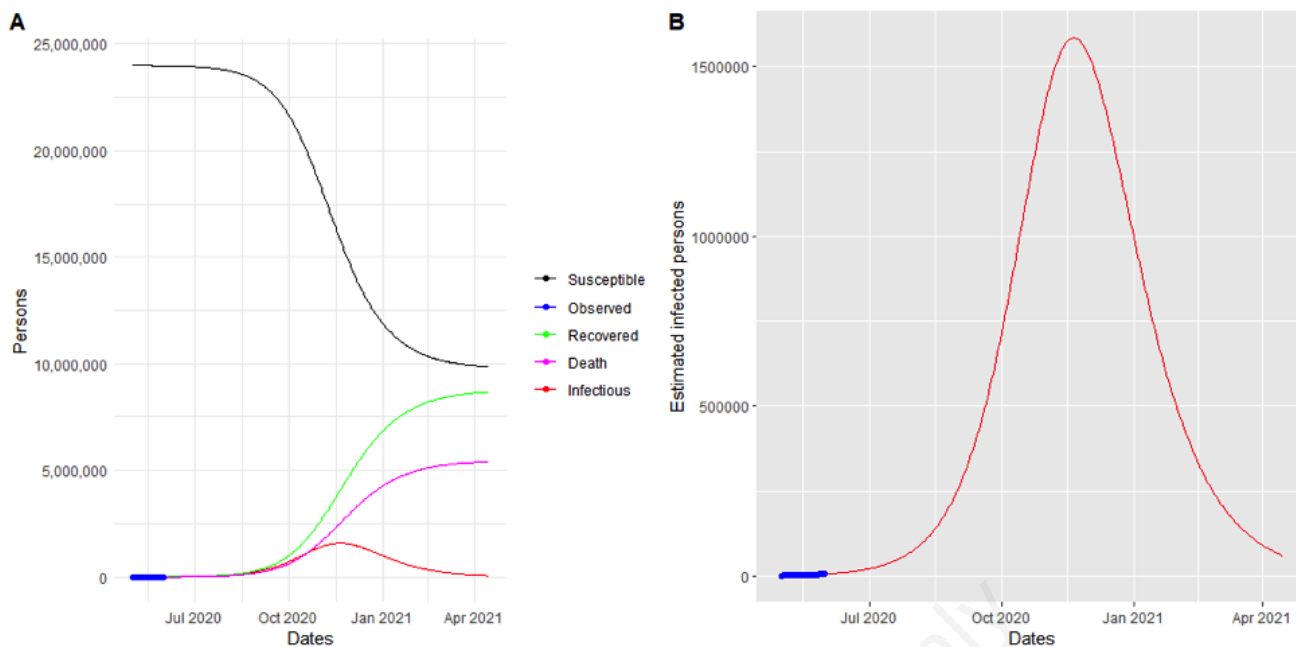
Figure 2. SIRD model by April 2021, COVID-19 estimates infected, recovered, and deaths in Cameroon. A: Cameroon long-term prediction of the epidemic using the whole data from May 1 to May 31, 2020. B: Projected curve of the infected persons by April 2021 showed a possible downwards by January 2021 under the conditions that social distancing had positively affected the disease trend, suggesting seriousness in the respect of preventive measures. According to this curve, total infected cases included severe mild disease condition, unquarantined and quarantined infected were estimated to more than 2 million by December 2020.
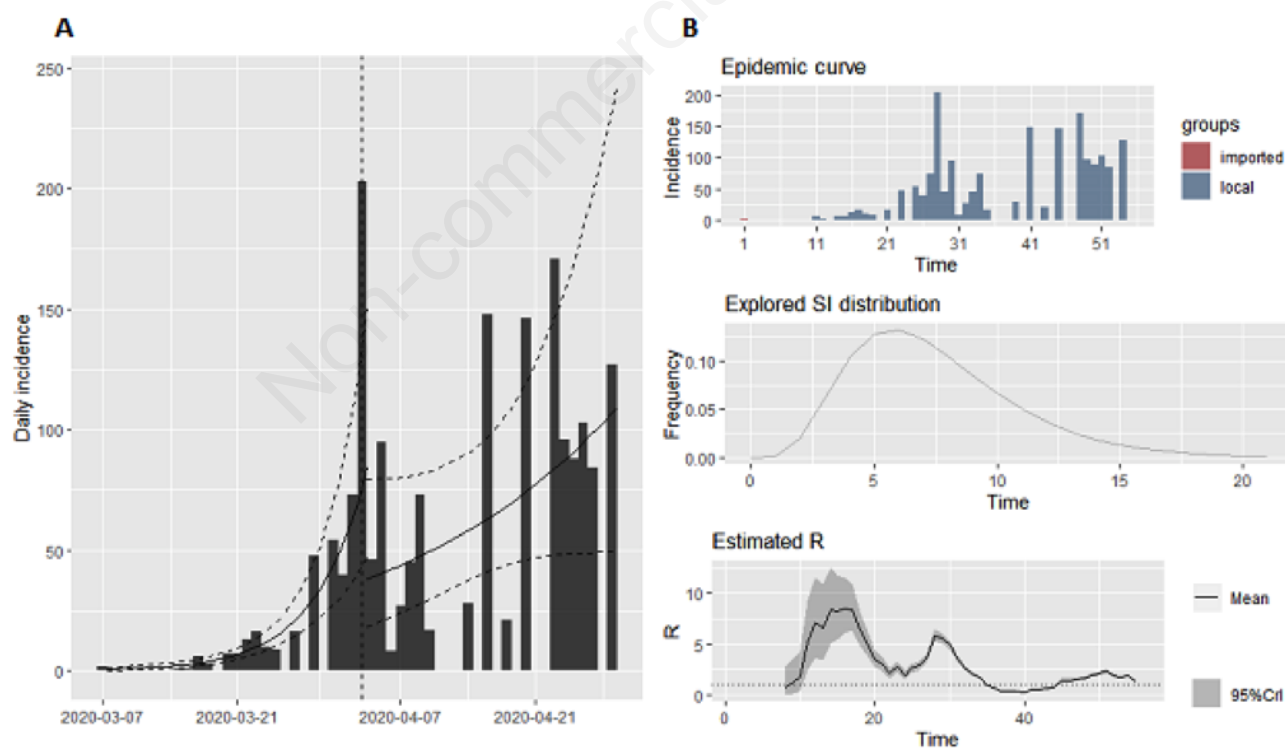

Figure 3. Log-linear modelling of daily incidence by April 30 and the variation in the effective reproduction number Re. A: Daily incidence of lab-confirmed cases by April 30; empty spaces between bars represented 0-incidence data; first epidemic peak in the growth phase (vertical dotted line); log-linear model adjusted before and after the peak suggested an epidemic in the exponential phase; over 230 new cases were expected by April 30. B: The data source lacked information on imported cases; the serial interval distribution and the variation of the reproductive number were sampled from a gamma distribution with mean=7.5 days and sigma=3.4; high values of the R_e were estimated for the first 20 days; R=Re tended to decrease by the end of the second phase.

was still greater than 1, the outbreak was yet to be under control in the country (Supplementary Figure 3).

Projection using early phase

Following the epidemic peak that occurred on April 3, 2020, we projected the incidence data for the first section of the growth phase to assess the trend of the epidemic curve. This analysis used incidence data from March 7 to March 24, which corresponded to 14 days before the peak, and comparison was made between projected and observed data. It was found that the highest peak of the epidemic was yet to be reached as the projected daily cases were increasing continuously (Supplementary Figure 4).

Estimating changes in the effective reproduction number from May 1 to May 22, 2020

According to the Supplementary Figure 5, the basic reproduction number ranged from 0.33 to 7, with a mean of value of 2.5 (95% CI=0.18-4.81). When we compared these values of R_0 before and after the first peak, the reproductive number showed a significant increase to the extent that an infected individual could generate more than 6 new infections. The model also predicted over 1750 new cases per day by 22 May (Figure 4A), and the effective reproduction number R_e also increased to more than 2 by May 22 (Figure 4B).

Discussion

Phase-to-phase analysis of the epidemic has demonstrated that the coronavirus epidemic is up surging rapidly in Cameroon and may take time before the number of newly infected individuals start to reduce. The reproduction number was increasing despite the effort of the government to contain the disease and its value was higher than WHO estimates at the initial phase of the epidemic (2 to 2.5). Despite the increase of cases, social measures taking by the government has played a role in the decrease of the basic reproduction number between the first phase and the second phase. However, phase-adjusted estimation of the number of coronaviruses revealed a high number of infected individuals in the population who were not quarantined. Indeed, the distribution of R_0 reached its peak when the government declared the end of the lockdown, i.e., when relaxation was observed in the communities, which probably led to an increase in the number of secondary infections. Predicted trends suggested that everyone is at risk of infection.

The trend of the number of cumulated cases in Cameroon revealed that, the number of newly reported cases start increasing around March/ 17/2020, which likely implied more infections not diagnosed and recorded in the early phase. In addition, the
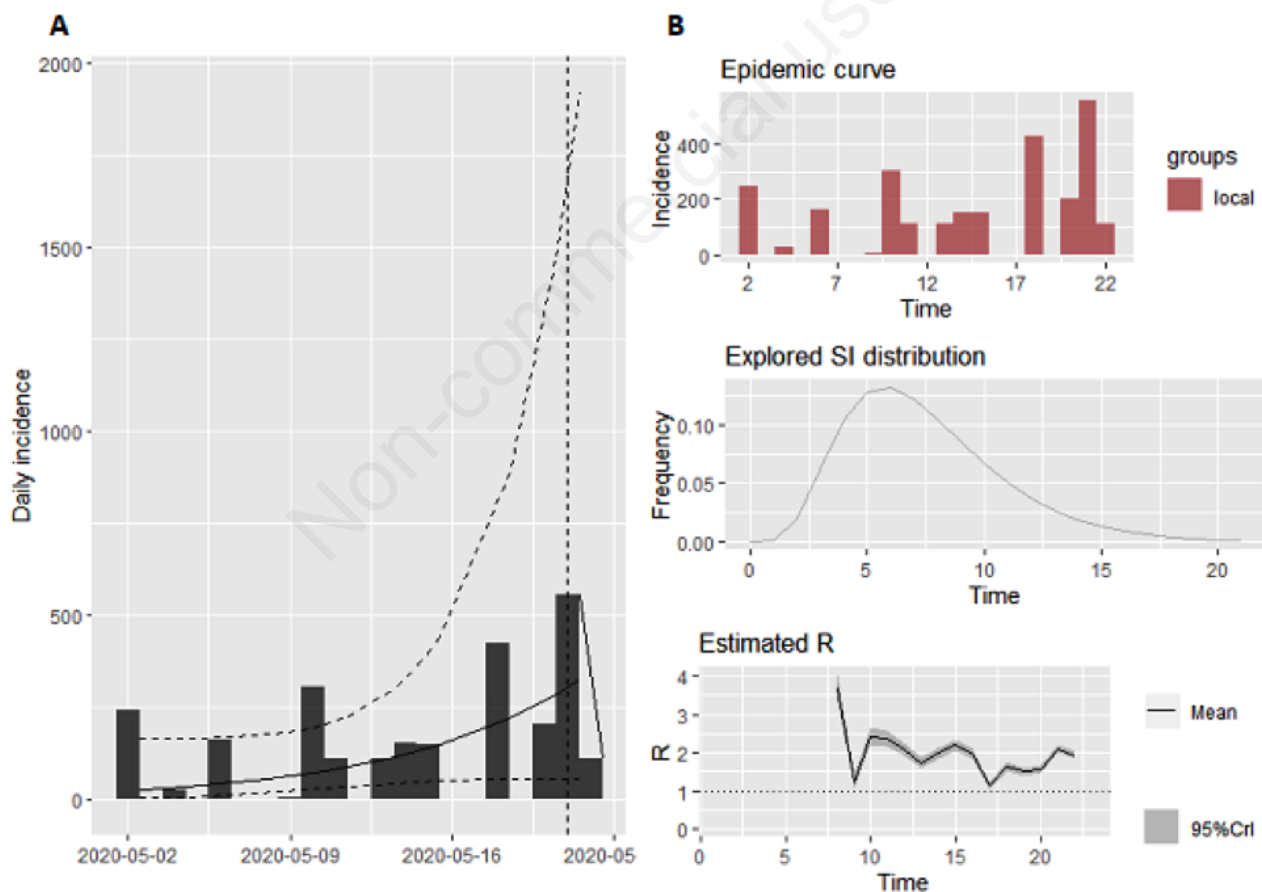

Figure 4. Log-linear modelling of the epidemic after lockdown easing (May 1 to May 22). A: Prediction was made on very sketchy data; over 1800 new cases per day by 22 May. This was probably an overestimate, due to potential reporting-date-not-onset-date bias, but nevertheless the result illustrated the exponential nature of typical epidemic behaviour. B: Tt was likely that new cases were only from the local population; the change in the effective reproductive number was studied with a serial interval (SI) of mean 7.5 and standard deviation of 3.4, and is showing a R_e significantly greater than 1.

country experienced almost 2 weeks of underreporting which likely had been a period during which more contacts from infected people occurred including many mild and asymptomatic cases. The number of infections will continue to increase throughout June 2020 with no indication of a decline. If control measures were continuing uninterrupted, the estimated number of infections could reach a peak in October 2020 (additional figure 6) allowing for a decline in the rate of infection.

In the early phase of the epidemic, R_0's estimate value was 6.80, then decreased to 3.24 in the second phase of the epidemic while R_e got close to 1 suggesting an impact of the measures that were implemented by the government. Unfortunately, the softening of these measures have led to an increase of R_e to more than 1. Some authors provide a preliminary estimation of the basic reproductive number through exponential growth of the infected individuals.[42] They found the values of R_0 ranging from 2.24 to 3.58 were associated with the reporting rate.[42] Our estimates of R_0 differed with the value reported in the early phase of the epidemic by the LSTMH (2.35; 95% CI=1.15-4.77).[21] In the present work, the effective reproduction number R_e was not below 1. Thus, it might be very difficult to contain or control the spreading of this virus especially in the context of relaxing measures and reopening of schools. For instance, after the relaxation of the control measures, the number of cases were almost 2-fold than in the previous phase, suggesting an increase of zoonotic sources of infection. This further suggests the importance and effectiveness of enhancing public health measures in an outbreak context such as COVID-19.

A projection by the Center for Disease Dynamics, Economics & Policy revealed, over 30,000 severe infections will occur without implementation of measures to contain the disease in Cameroon during the months of June and July 2020.[43] As a result, these severe infections could increase the risk of death in the country.

Due to unavailable data like mild condition cases, critical and severe cases, some considerations were not made on the model in terms of new components, thus suggesting that our model could have underestimated the true total number of infected individuals. In addition, there were probably quarantined and un-quarantined infected individuals in the population with the latter constituting a source of infection to susceptible persons.[14] Widespread screening tests in the population could become a useful means to obtain a reliable estimate of the number of infected individuals, being asymptomatic or not. Projection under a moderated implementation of mitigation measures resulted in up to 2 million total infections (asymptomatic, symptomatic, and severe) in Cameroon between June and Mid-July 2020.[43] In addition, a study used a stochastic approach based on Markov chain to provide an estimate that more than 8 million individuals may be infected in the country.[23]

However, these estimates may not be sustained if unforeseeable factors occurred; for example, if some infections were caused by other source of exposures such as animals. This work has demonstrated that the epidemic will evolve during a long period of time in Cameroon if strict prevention measures are not applied. It is expected that by December 2020 and all over the 2021 year, the epidemic will still be on the exponential growth phase.

Limitations

Difficulties occurred during the implementation of the log-linear modelling approach, as zero- daily reported incidence points were found in the datasets. Although these observations were ignored in the analysis, such gap in the time series may have reduced the accuracy of the model's estimates, which would have led to a significant discrepancy between the real number of cases and the number of cases observed.[6] Indeed, some authors compared R_0 in different scenarios and found that when the daily ratio increases to more than 5 times, the basic reproductive number decreased; when it remained unchanged, R_0 remains very high.[6]

In Cameroon, the number of infections began to increase around March 17 implying that, more people had not been diagnosed at the beginning of the epidemic, of which probably imported cases of COVID-19 were occurring, but were not recordedDespite these limitations, the current study has provided a contribution to the understanding of COVID-19 infection in Cameroon. As a result, a pandemic such as covid-19 calls on everyone to show a high level of responsibility to others.

Conclusions

The epidemic of COVID-19 is in the exponential phase in Cameroon and has not yet show a downwards trend. With the reopening of schools and leisure activities, the country must implement large screening tests, quarantine suspected cases while improving healthcare systems, and maintain the application of preventive measures.

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