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Transmissibility of COVID-19 in Rwanda: Epidemiological Modeling Study

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ABSTRACT

Background: The coronavirus disease 2019 (COVID-19) pandemic has become a public health threat in the 21st century. It contributed to more than 1.5 million deaths, per the report of the World Health Organization. Mathematical models have been used in epidemiology for decades to analyze the dynamism of infectious diseases and their impact on population health.

Objective: This study aimed to investigate the transmissibility of the coronavirus disease 2019 (COVID-19) pandemic in Rwanda from March 2020 to October 2021.

Methods: A mathematical model was proposed with five compartments, and a basic reproduction number (R_0) was computed using the next-generation matrix. Four periods were selected, and each period had 5 months, from March 2020 to October 2021. Four R_0 values showing the dynamism of the pandemic in each period were calculated using Python 3.8, and the disease spread among individuals living in Rwanda. The countrywide data extracted from the Rwanda Biomedical Center website were used to determine the coherence and relevance of diagnosis with case prevalence using STATA 13.1.

Results: There was a significant increase in R_0 across the 4 periods from March 2020 to October 2021. The computed basic reproductive numbers are as follows: March to July 2020: R_0=2.99; August to December 2020: R_0=4.1; January to May 2021: R_0=8.11; June to October 2021: R_0=24.7 There was a statistically significant correlation with mass diagnosis and the number of infected individuals in the population (P=.01).

Conclusion: Since all and continued to increase with respect to the study periods, since the real data showed a positive contribution to mass diagnosis, the pandemic still persisted in the population, and mass diagnosis was key for explaining the rate of infection.

BACKGROUND

The world has been facing an unexpected coronavirus disease 2019 (COVID-19) pandemic. At the end of 2019, the novel coronavirus was first reported in Wuhan city in China. The occurrence of the pandemic was declared from a group of patients admitted to hospitals globally at the end of December 2019.[1] An epidemiological assessment carried out by medical practitioners revealed that this disease was associated with seafood consumption and wet animal market food products in Wuhan.[1] The novel coronavirus was characterized by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) symptoms; therefore, the World Health Organization named it coronavirus disease 2019, which is commonly known as COVID-19, and the pandemic was declared in March 2020.[2] According to statistics from mid-July 2020, the COVID-19 pandemic was declared in more than 213 countries and contributed to 15,969,465 morbidities and 643,390 deaths. In recent years, severe acute respiratory syndrome coronavirus 1 (SARS-CoV-1) and Middle Eastern respiratory syndrome coronavirus (MERS-CoV) have contributed to major outbreaks similar to COVID-19,[3-4] and COVID-19 has been transmitted from humans to humans via direct contact with this virus. However, the inhalation of respiratory droplets from either nonclinical or clinically infected individuals can cause transmission of the infection.[5] The incubation period of COVID-19 ranges from 2 to 14 days, and approximately 97.5% of infected individuals become symptomatic after these days.[6–9]

The worldwide spread, unstopped, and uncontrolled nature of the COVID-19 pandemic compelled China and many nations to institute serious containment measures.[10] As the pandemic became critical, several vaccines, such as AstraZeneca, Johnson and Johnson, Modena, and Pfizer, were manufactured and approved by the WHO for the prevention of the COVID-19 pandemic. Although many low-income countries

have faced a challenge in acquiring a significant number of vaccines to administer a sufficient proportion to their population, efforts have been made to foster preventive measures such as mask-wearing, social distancing, quarantine of suspected cases, and contact tracing.[11] On the other hand, in high-income countries where vaccines are manufactured and available, approximately 60% of their population has received at least the first dose of the COVID-19 vaccine.[12]

Given that the impact of the pandemic has remained critically grave, many unsolved questions have emerged in the minds of infectious disease scientists. The assumption that the recovered individuals developed protective immunity created disagreement between scientists.[13] The current emergence of SARS-CoV-2 and the limited scale at which SARS-CoV-1 and MERS-CoV epidemics have occurred obscured the availability of data that could act as concrete evidence of reinfection by SARS-CoV-2.[13] According to previously published research on serology tests of seasonal human coronavirus229E (HCoV-229E) to investigate antibody dynamics after viral invasion, findings revealed that approximately 50% of infected individuals lost Nct antibodies within six months following the period of infection.[13] The gain of herd immunity after infection is well understood among scientists and researchers. However, a high reduction of protective immunity poses a challenge to herd immunity among patients. If this short-lived immune system is lost, people can be at risk of infection by new viral variants, such as Omicron and Delta. A significant research question among researchers was, will the reinfection with SARS-CoV-2 impact the dynamism of the COVID-19 pandemic? The combination of asymptomatic cases and reinfections requires further investigative research. Epidemiological models are becoming a significant tool that facilitates understanding the dynamism of infectious disease transmission, specifically during epidemics and outbreaks.[14–18] Since the declaration of the pandemic in March 2020, the transmissibility rate of three was declared, and we believe that the transmission rate changed throughout the pandemic period; however, this information was missing. Therefore, this study aimed to estimate the variation in the basic reproduction number (Ro) of COVID-19 from March 2020 to October 2021 in Rwanda.

MATERIALS AND METHODS

The selected period was based on interventions of the government of Rwanda to curb the pandemic, for instance, period 1 of March to July (3-7) 2020, there was a total lockdown, where in July some activities such as supermarkets were opened. In the period 2 from August to December (8-12)2020, there was free movement within a district. For period 3 of January to May (1-5)2021, there was reinforcement of covid19 vaccine. In period 4 from June to October (6-10)2021, there was a massive vaccination and the target was to provide herd immunity to the population.

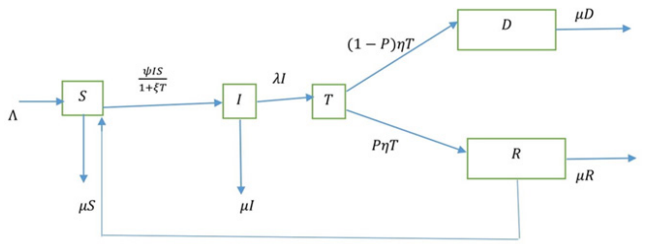
Model Formulation

We studied the contribution of a mathematical model approach to strengthen COVID-19 pandemic diagnosis in Rwanda. To understand this scenario, we formulated a model diagram with five compartments. Furthermore, we analyzed the dynamics of this model using a system of nonlinear differential equations generated from it. The model diagram below describes the human population. At a given time (t), a population N(t) is sub-partitioned into five different compartments. The class of individuals yet to be diagnosed is represented by S(t), and the observed cases are denoted by I(t). Similarly, the individuals who are reated are denoted by T (t), and the class of the recovered population is represented by R(t). Additionally, those who die are denoted by D(t). The total population is then given by:

$$N(t)=S(t)+I(t)+T(t)+R(t)+D(t)$$

The diagram illustrates the formulated model (Figure 1).

FIGURE 1: The Formulated SITRD Model



For description of each variable and parameter used in the mathematical model (see Table 1)

From the first Model, we derived a system of nonlinear differential equations, which were:

$$\begin{cases} \frac{dS}{dt} = \Lambda - \frac{\psi IS}{1+\xi T} - \mu S + \varphi R \\ \frac{dI}{dt} = \frac{\psi IS}{1+\xi T} - \lambda I - \mu I \\ \frac{dT}{dt} = \lambda I - (1-P)\eta T - P\eta T \\ \frac{dR}{dt} = P\eta T - \varphi R - \mu R \\ \frac{dD}{dt} = (1-P)\eta T - \mu D \end{cases} \quad (1)$$

For the above system to be mathematically equipped, we subject it to the following initial conditions:

$$S(0) = S_0 > 0;\ I(0) = I_0 > 0;\ T(0) = T_0 > 0;\ R(0) = R_0 > 0;\ D(0) = D_0 > 0$$

The basic reproduction number

R_0 is defined as the number of secondary infected individuals introduced by only one infected population into individuals to be diagnosed, i.e., the susceptible population,[19] and it is generally a threshold parameter indicating whether the disease stays or dies out in a

system.[20] R_0 is more generally computed using the next generation matrix and is given by $\rho(FV^{(-1)})$, where $\rho(M)$ is the spectral radius of a matrix M and where F $V^{(-1)}$ denotes the matrix product of the new transfer term and the inverse of the remaining transfer terms.[21]

Consider ψIS/(1+ξT) to be a new transfer and *I,T* compartments to be the remaining transfer terms

Then, the following matrices hold:

Let

$$a = \begin{bmatrix} \frac{\psi IS}{1+\xi T} \\ 0 \end{bmatrix}; F = J(a) = \begin{bmatrix} \frac{\partial I}{\partial t} & \frac{\partial T}{\partial t} \\ 0 & 0 \end{bmatrix}$$

$$F = \begin{bmatrix} \frac{\psi S}{1+\xi T} & \frac{-(\psi IS)(1+\xi T)'}{(1+\xi T)^2} \\ 0 & 0 \end{bmatrix} = \begin{bmatrix} \frac{\psi S}{1+\xi T} & \frac{-\psi I \xi S}{(1+\xi T)^2} \\ 0 & 0 \end{bmatrix}$$

$$F_{E_0} = \begin{bmatrix} \frac{\psi \Lambda}{\mu} & 0 \\ 0 & 0 \end{bmatrix}$$

$$b = \begin{bmatrix} \lambda I + \mu I \\ -\lambda I + (1-P)\eta T + P\eta T \end{bmatrix}; V = J(b) = \begin{bmatrix} \frac{\partial I}{\partial t} & \frac{\partial T}{\partial t} \\ \frac{\partial I}{\partial t} & \frac{\partial T}{\partial t} \end{bmatrix}$$

$$V = \begin{bmatrix} \lambda+\mu & 0 \\ -\lambda & \eta \end{bmatrix}$$

$$V_{E_0} = \begin{bmatrix} \lambda+\mu & 0 \\ -\lambda & \eta \end{bmatrix}$$

$$V_{E_0}^{-1} = \frac{1}{\det(V_{E_0})}\begin{bmatrix} \eta & 0 \\ \lambda & \lambda+\mu \end{bmatrix} = \frac{1}{\eta(\lambda+\mu)}\begin{bmatrix} \eta & 0 \\ \lambda & \lambda+\mu \end{bmatrix}$$

$$V_{E_0}^{-1} = \begin{bmatrix} \frac{1}{\lambda+\mu} & 0 \\ \frac{\lambda}{\eta(\lambda+\mu)} & \frac{1}{\eta} \end{bmatrix}$$

$$M = F_{E_0} V_{E_0}^{-1} = \begin{bmatrix} \frac{\psi\Lambda}{\mu} & 0 \\ 0 & 0 \end{bmatrix}\begin{bmatrix} \frac{1}{\lambda+\mu} & 0 \\ \frac{\lambda}{\eta(\lambda+\mu)} & \frac{1}{\eta} \end{bmatrix} = \begin{bmatrix} \frac{\psi\Lambda}{\mu(\lambda+\mu)} & 0 \\ 0 & 0 \end{bmatrix}$$

$$R_0 = \frac{\psi\Lambda}{\mu(\lambda+\mu)}$$

which is the leading eigenvalue of the next generation matrix *M*.

SIMULATION RESULTS

Numerical simulation

In this section, we simulate the model (1) using variable and parameter values. With five compartmental models, the real data of each variable is known. Since the total population is given by

$$S(0) = S_0 > 0; I(0) = I_0 > 0; T(0) = T_0 > 0; R(0) = R_0 > 0; D(0) = D_0 > 0$$

With real numbers of the remaining variables, *S(t)* can be obtained by the following equation:

$$S(t) = N(t) - \big(I(t) + T(t) + R(t) + D(t)\big)$$

As previously mentioned, the study is subjected to a period of COVID-19 in months. The current population of Rwanda is 13,381,897 as of Friday, November 5, 2021, on the basis of the Worldometer elaboration of the latest United Nations data.

$N = 13{,}381{,}897$ (Nations, 2021), $\sum_{i=3}^{7} S_i = 13{,}381{,}897 - (1{,}994 + 1{,}994 + 1{,}542 + 5) = 13{,}376{,}362$, $\sum_{i=3}^{7} I_i = 1{,}994, \sum_{i=3}^{7} T_i = 1{,}994, \sum_{i=3}^{7} R_i = 1{,}542, \sum_{i=3}^{7} D_i = 5$, Diagnosed= 4,257,445 for the first period, $\sum_{i=8}^{12} S_i = 13{,}381{,}897 - (6{,}256 + 6{,}256 + 5{,}556 + 81) = 13{,}363{,}748$, $\sum_{i=8}^{12} I_i = 6{,}256, \sum_{i=8}^{12} T_i = 6{,}256, \sum_{i=8}^{12} R_i = 5{,}556, \sum_{i=8}^{12} D_i = 81$, Diagnosed= 6,011,045 for the second period in 2020. In 2021, the same procedure applies, that is, $\sum_{i=3}^{7} S_i = 13{,}381{,}897 - (15{,}131 + 15{,}131 + 10{,}012 + 115) = 13{,}225{,}682, \sum_{i=1}^{5} I_i = 15{,}131, \sum_{i=1}^{5} T_i = 15{,}131, \sum_{i=1}^{5} R_i = 10{,}012, \sum_{i=1}^{5} D_i = 115$, diagnosed= 1,002,025 for the first period; $\sum_{i=6}^{10} S_i = 13{,}381{,}897 - (42{,}190 + 42{,}190 + 19{,}825 + 941) = 13{,}276{,}751, \sum_{i=6}^{10} I_i = 42{,}190, \sum_{i=6}^{10} T_i = 42{,}190, \sum_{i=6}^{10} R_i = 19{,}825, \sum_{i=6}^{10} D_i = 941$, diagnosed= 1,615,667 for the second period in 2021 (rbc, 2021)

TABLE 1: Description of First Model's Variables and Parameters

Variables & Parameters	Description
S	Individuals to be diagnosed
I	Observed cases
T	Treated individuals
R	Recovered population
D	Class of deaths
Λ	Recruitment rate of individuals who join S
ξ	Education adjustment to reduce new cases by applying possible treatments
ψ	Contact rate of S and I
λ	Rate of infected individuals
η	Rate at which T can either join R and/or D
P	Corresponding probability of T joining R or D
φ	Rate at which R move back to S if not D
μ	Natural death in all compartments

Table 2. Description of Second Model's Variables and Parameters

Transmissibility of COVID-19 For Periods 1 and 2

Figure 2 shows that the number of cases started to increase after the registration of the first case on March 14, 2020. In this regard, the basic reproduction number (R_0) was computed from the above parameters and variable values extracted from the Rwanda biomedical center website. As per period (1) from March to July 2020, the computed basic reproductive number (R_0) was 2.99. The inference is that one infected person had to transmit COVID-19 to 3 people in the population. However, Figure 3 shows that COVID-19 has dramatically increased with respect to time, with R_0 continuing to increase from 3 to 4. From the statistics above, the first period, i.e., from March to July 2020, shows that the total number of screening tests was 4,257,445, with total positive cases of 1,994. Similarly,

for the second period from August to December 2020, the total number of screened individuals was 6,011,045, with positive COVID-19 cases at 6,256. Clearly, the greater the number of individuals screened for COVID-19 was, the greater the number of cases that were diagnosed. This finding provides insight into the COVID-19 pandemic situation in a population so that preventive measures against infectious disease can be reinforced to reduce morbidity and mortality (Table 2).

TABLE 2: Model's Variable and Parameter Values According to Period

Period 1	Values
S_1=13,376,362	Calculated
I_1=1,994	(rbc, 2021)
T_1=1,994	(rbc, 2021)
R_1=1,542	(rbc, 2021)
D_1=5	(rbc, 2021)
Λ_1=13	From (rbc, 2021) Data
Period 2	
S_2=13,363,748	(rbc, 2021)
I_2=6,256	(rbc, 2021)
T_2=6,256	(rbc, 2021)
R_2=5,556	(rbc, 2021)
D_2=81	(rbc, 2021)
Λ_2=41	From (rbc, 2021) Data
Period 3	
S_3=13,225,682	(rbc, 2021)
I_3=15,131	(rbc, 2021)
T_3=15,131	(rbc, 2021)
R_3=10,012	(rbc, 2021)
D_3=115	(rbc, 2021)
Λ_3=152	Estimated from (rbc, 2021) Data
Period 4	
S_4=13,276,751	(rbc, 2021)
I_4=42,190	(rbc, 2021)
T_4=42,190	(rbc, 2021)
R_4=19,825	(rbc, 2021)
D_4=941	(rbc, 2021)
Λ_4=285	From (rbc, 2021) Data
Parameter values	
ξ=0.6	Estimated
ψ=0.9	Estimated
λ=0.3	Estimated
η=0.15	Estimated
P=0.25	Estimated
φ=0.22	Estimated
μ=0.12	Estimated

FIGURE 2: Transmissibility For Period 1

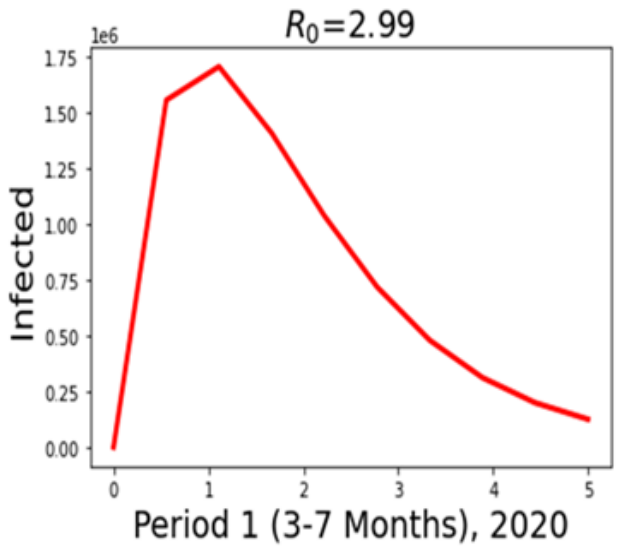
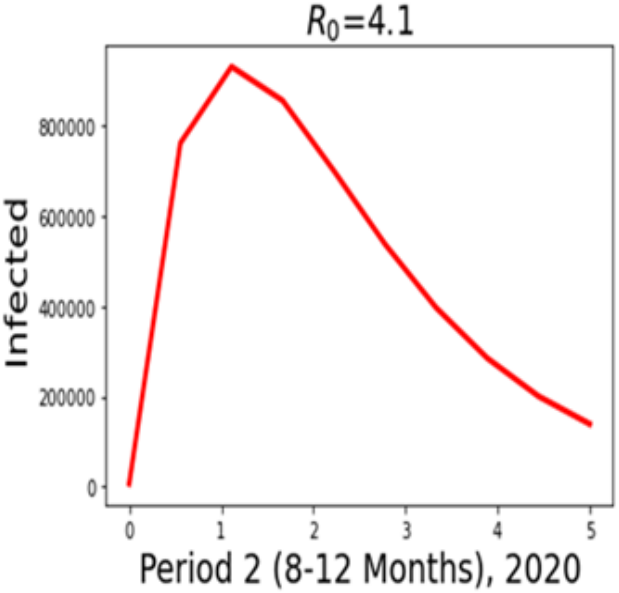


FIGURE 3: Transmissibility For Period 2



Transmissibility of COVID-19 For Period 3 and 4

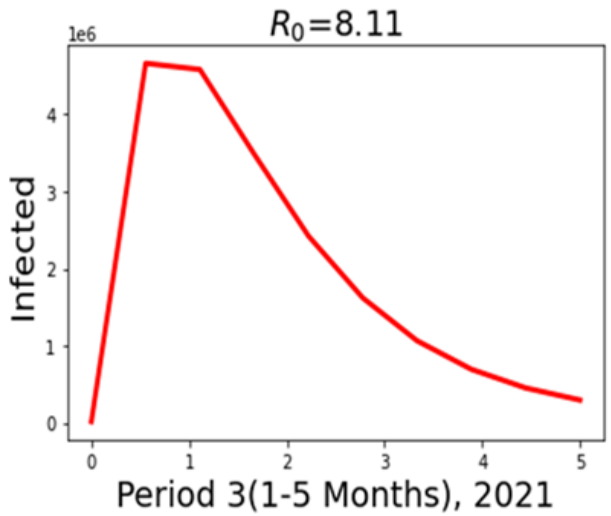
Figures 4 and 5 show the morbidity of COVID-19 in individuals. Figure 4 shows that in the period from January to May 2021, the basic reproduction number was 8.11, which reflects the high spread of the COVID-19 pandemic in individuals living in Rwanda. COVID-19 has been spreading quickly due to contact among gatherings

and incoming and outgoing travelers, which has led to a high rate of reported mortality. A typical example can be observed in Figure 5 during the period from June to October 2021, where 941 people died due to COVID-19-related complications from 42,190 positive cases. It has been shown that there is a linear association between increased cases and deaths if no serious control measures are taken, leading to worsened pandemic impacts in a country and globally. Figure 4 shows an increase in cases and Figure 5 a dramatic increase in a population at a given time (t); thus, the four basic reproduction numbers and respective figures show the instability of Covid-19 viral infection with respect to time since all R_0 values are greater than 1.

Disease Screening Situation Analysis For Real Data

Figure 6 shows the contribution of mass screening to gathering information on the COVID-19 situation. Therefore, there is a strong correlation and linear relationship between mass screening and cases. The data were extracted from the Rwanda Biomedical Centre (RBC) during the study period.

FIGURE 4: Transmissibility For Period 3



Correlation Between Screening and Case Findings

Table 3 shows the correlations between individuals diagnosed in April 2020 and the corresponding cases. According to data from the RBC website, the number of diagnosed cases was 159,559, with 3257 COVID-19-positive cases in April 2020. However, the individuals diagnosed in May were 195,951 with 12083 cases. The same table shows that the correlation of the number of cases with a small population is low, that is, 0.3, and it is not statistically significant since the *P* value of .1168 is greater than .05 for the situation in April 2020. For the situation in May 2020, the statistics show a strong correlation if a greater number of screenings is performed with a corresponding increase in positive cases. This difference was statistically significant, with a *P* value of .0001, which was less than the set significance level. Therefore, a strong correlation of 0.9 was observed in May 2020. Notably, from the RBC data, the number of individuals diagnosed with COVID-19 in May was greater than that in April, and the number of cases differed from each other. Therefore, mass screening within populations provides a greater number of cases.

FIGURE 5: Transmissibility For Period 4

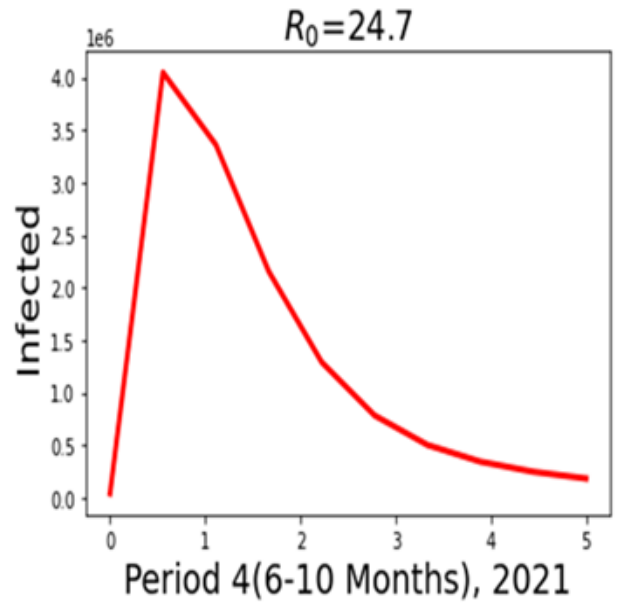


FIGURE 6: Disease Screening Situation Analysis for Real Data

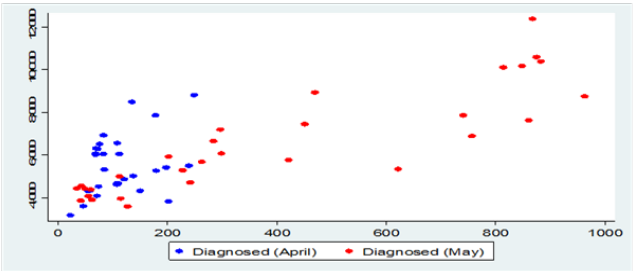


TABLE 3: Correlation Between Screening and Case Finding

April 2020	May 2020
Screened number: 159,559	Screened number: 195,951
Active cases: 3,257	Active cases:12,083
Number of obs=29	Number of obs=30
Spearman's rho=0.2976	Spearman's rho=0.8945
Test of H0: Diagnosed April & cases are independent	Test of H0: Diagnosed May & cases are independent
Prob> |t|= 0.1168	Prob> |t|= 0.0001

DISCUSSION

The transmissibility rate of the COVID-19 pandemic in Rwanda has changed over time. In the first 5 months of the pandemic, Rwanda fostered preventive measures early at the beginning of the pandemic, and the transmissibility rate was based not only on the number of infected individuals but also on measures that were put in place.[22] We observed a transmissibility rate (R_0) of Ro=2.99 in the first period considered in our study, which reflects the growth of the pandemic since the calculated basic reproductive number was greater than 1 (Figure 2). In a modeling study conducted in China, a transmissibility rate of Ro=2.33 was observed before early February, but it subsequently decreased to approximately R_o= 0.04. This was associated with the prevention measures put in place on January.[23] A decrease in transmissibility rate was observed in a study carried out in Japan, and a negative association between lockdown and pandemic dynamism was observed; the average transmissibility rate was R_o=3.44, which declined to Ro=1.68 in early February. Despite the negative association between prevention measures and the transmissibility of COVID-19, the findings revealed the significant role of nonpharmaceutical prevention measures in preventing the spread of the pandemic in Wuhan [24]. During the first 10 days of the pandemic, the basic reproductive number was observed and varied by country. The median Rt calculated values were in Spain (2.90), Italy (2.83), Ecuador (3.95), Panama (3.95), Brazil (3.95), and Peru (2.36).[25- 26] The transmissibility of the mentioned countries in the first 10 days of the COVID-19 pandemic seemed to be greater than that of Rwanda in the first 5 months of the pandemic. The second period considered was from August 2020 to December 2020. Although a short reduction in the susceptible population was observed, there was a significant increase in the rates of infection and recovery. During this period, we observed an increased rate of transmissibility (Ro) from the first period to the second period. It varied from 2.99 to 4.11, which was almost double that of the first period (Figure 2&3). There is a strong relationship between passengers traveling by air, car drivers, walking, transit mobility and the dynamism of the COVID-19 pandemic.[27] These findings contrast with the results observed in India, where the significant decline in transmissibility of COVID-19 over a longitudinal phase of time was considered. With respect to the nonintervention period and partial and total lockdowns, the transmissibility of infection varied from 4.46 (7.1), 1.47 (2.33), and 0.817 (1.29), respectively.[28] A study carried out in Saudi Arabia divided the COVID-19 pandemic phase on the basis of lockdowns reported that there were no significant differences in the mean reproductive number. However, Ro was less than 1 within the considered intervals, which is hypothetically an impact of lockdowns on the transmissibility of the pandemic.[29] In our study, we did not consider intervals based on prevention measures; however, the data were collected in various ways on the basis of preventive measures extracted from the Rwanda Biomedical Center website. The rigorous implementation of coronavirus disease 2019 was associated with a reduction in the transmissibility rate of the pandemic worldwide.[30] Our study revealed a high growth curve of transmissibility from March 2020 to October 2021. We observed sudden growth in transmissibility periods 3 and 4, which occurred from January to May 2021 and June to October 2022 (Figures 4 and 5). This was associated with a reduction in preventive measures taken to curb the spread of the pandemic. Mass screening of the disease was considered in the present study, and we observed that the infection rate was associated with the number of diagnosed individuals. The more people are screened, the more the infectivity rate increases. However, other factors, such as treatment and mortality, can affect the infectivity rate (Figure 6). During the period between April 2021 and May 2021, a significant correlation between mass screening and the infection rate increased, as observed in May 2021, when more people were diagnosed. Different reports in Rwanda revealed that the mass screening of SARS-CoV-2 was significantly related to the infectivity rate among susceptible populations. This correlation allows healthcare stakeholders to identify unrecognized asymptomatic or mild cases and compare them with other countries on the continent.[31] In Saudi Arabia, the basic reproductive Ro was associated with preventive measures, including the expansion of the screening process, where the measures and strategies put in place to curb the transmission of the pandemic affected the growth curve of COVID-19 dynamism.[32] Another study reported that the reduction in COVID-19 dynamism is significantly associated with isolation and tracing strategies rather than other prevention measures put in place to curb the spread of the pandemic.[33]

CONCLUSION

We developed a model to estimate the variation in the basic reproduction number (Ro) of COVID-19 from March 2020 to October 2021 in Rwanda. The four basic reproduction numbers (R_0) were greater than 1 and continued to increase with respect to time in the periods proposed. The actual data revealed a positive effect, from which we can make inferences. With respect to COVID-19 when screening a large population, mathematical models can be useful tools for accurately predicting disease behavior, especially with the support of R_0 and figures drawn from the model. We therefore recommend that the government of Rwanda increase tests on a mass population to obtain accurate information concerning other infectious diseases with pandemic potential.

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