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Investigating the transmission dynamics of SARS-CoV-2 in Nigeria: A SEIR modelling approach

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ABSTRACT

This study was designed to investigate the transmission dynamics of the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) to inform policy advisory vital for managing the spread of the virus in Nigeria. We applied the Susceptible-Exposed-Infectious-Recovered (SEIR)-type predictive model to discern the transmission dynamics of SARS-CoV-2 at different stages of the pandemic; incidence, during and after the lockdown from 27th March 2020 to 22nd September 2020 in Nigeria. Our model was calibrated with the COVID-19 data (obtained from the Nigeria Centre for Disease Control) using the "lsqcurvefit" package in MATLAB to fit the "cumulative active cases" and "cumulative death" data. We adopted the Latin hypercube sampling with a partial rank correlation coefficient index to determine the measure of uncertainty in our parameter estimation at a 99% confidence interval (CI). At the incidence of SARS-CoV-2 in Nigeria, the basic reproduction number (R_0) was 6.860; 99%CI [6.003, 7.882]. R_0 decreased by half (3.566; 99%CI [3.503, 3.613]) during the lockdown, and R_0 was 1.238; 99%CI [1.215, 1.262] after easing the lockdown. If all parameters are maintained (as in after easing the lockdown), our model forecasted a gradual and perpetual surge through the next 12 months or more. In the light of our results and available data, evidence of human-to-human transmission at higher rates is still very likely. A timely, proactive, and well-articulated effort should help mitigate the transmission of SARS-CoV-2 in Nigeria.

Introduction

The novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) responsible for the coronavirus disease (COVID-19) is a member of the coronavirus family that was first identified and linked to a seafood market in Wuhan, China, in December 2019 [1]. The SARS-CoV-2 is the seventh member of the coronavirus family known to cause disease in humans

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[1–3]. The clinical features of COVID-19 manifest in neurologic, enteric, hepatic and respiratory systems, with varying degrees of severity ranging from asymptomatic to mild and severe diseases and death. The World Health Organization (WHO) declared the SARS-CoV-2 outbreak a public health emergency of international concern due to its global spread and threat of high mortality [4]. Data from the WHO as of 14th October 2020 revealed that the COVID-19 outbreak has accounted for 38,002,699 infected and 1083,234 death cases globally [5].

The first confirmed case of COVID-19 in sub-Saharan Africa was reported in Nigeria on 27th February 2020 [6]. Data used for this study spanned from 27th March 2020 to 22nd September 2020. Also, the number of new cases arising from the community transmission of SARS-CoV-2 in Nigeria has increased to over 57,000 confirmed cases nationwide [7]. Aside daily briefings from the Nigerian Center for Disease Control (NCDC) on COVID-19 cases and mortality in Nigeria, summary estimates on SARS-CoV-2 transmission are mainly lacking, limiting the scope of appropriate epidemiological decisions for the prevention and management of the COVID-19 pandemic in Nigeria.

Developing robust mathematical models are helpful for understanding and predicting disease transmission [8]. Infectious disease model is an analytical tool for making public health decisions during epidemics, particularly in the light of limited data and a weak surveillance system [9]. Some reports [10–15] have applied modelling tools in understanding the dynamics and implications of SARS-CoV-2 transmission. For example, fractal, deterministic and stochastic equations have been applied to predict the behaviour of COVID-19 in Africa and Europe, considering nine human compartments [10]. However, the statistical analysis forecasted daily deaths and infections only and some of the parameters were stochastically perturbed.

On the dynamics of COVID-19 in Nigeria, Ibrahim & Oladipo[13] developed an auto-regressive integrated moving average (applying a non-stationary time series model to data from the NCDC) for time-based forecasting of the COVID-19 outbreak. Similarly, Okuonghae and Omame [15] presented a mathematical model on the influences of non-pharmaceutical intervention on active cases accumulation of COVID-19 and forecasted 160,000 COVID-19 cases by mid-August 2020 in Lagos, Nigeria. Whereas the data provided by the NCDC by mid-August 2020 was lower, revealing only 2751 active cases in Lagos, Nigeria. This is partly because of high error susceptibilities arising from using a singular compartment for model fitting and estimation. Also, these models did not test the significance of symptom manifestations in the understanding of SARS-CoV-2 transmission in Nigeria.

The Susceptible-Exposed-Infectious-Recovered (SEIR) model integrates three categories of infectious population (i.e. symptomatic, asymptomatic and isolated). The model is sturdy with a globally asymptotically stable disease-free equilibrium point (whenever the basic reproduction number is less than unity). Whether the application of the SEIR model could advance understanding the transmission dynamics of SARS-CoV-2 in Nigeria is yet to be clearly understood. The criticality of accurate and valid primary information in ascertaining underlying risk(s), features and severity of the SARS-CoV-2 cannot be underestimated in providing epidemiological evidence vital for the control and management of the SARS-CoV-2 transmission in Nigeria. Such information would help provide sound scientific decision(s) that will inform public health guidelines or advisory in the prevention and control of SARS-CoV-2 transmission in Nigeria.

This report leads the debate on the transmission dynamics and statistical validity of human to human transmission of SARS-CoV-2 in Nigeria using the SEIR model (in the light of limited primary data on the presenting clinical characteristics of SARS-CoV-2) for an initial assessment of SARS-CoV-2 transmission in Nigeria. In our study, the Infectious compartment was split into two (asymptomatic and symptomatic compartments), and the quarantined compartment was also incorporated into the general SEIR model. Our approach was necessitated by poor medical intelligence and surveillance [16], which is usually peculiar to low and middle-income countries. This study relied on publicly profiled data (by the NCDC) of confirmed cases and mortality to provide an SEIR-model assessment of SARS-CoV-2 transmission in Nigeria.

Materials and method

Data source

We obtained data from the ongoing daily situation reports on active cases, hospitalizations, recoveries and associated mortality of SARS-CoV-2 provided by the NCDC. The index case of the SARS-CoV-2 was reported on 27th February 2020 [6]. We utilized data comprising three distinct time-point; the initial stage of SARS-CoV-2 incidence (27th February 2020 through 29th March 2020), lockdown period (30th March 2020 through 3rd May 2020) and post lockdown period (4th May 2020 through 22nd September 2020) within the first seven-month window of SARS-CoV-2 outbreak in Nigeria.

Model formulation

The total population was partitioned into six compartments – Susceptible (S), Exposed (E), Infectious with symptoms (I), Infectious but asymptomatic (A), hospitalized-individuals isolated for medical care (H) and recovered (R) compartments [17,18].

Our model was formulated based on the following assumptions;

1 Individuals in H compartments are likely in isolation and therefore assumed unlikely to transmit the disease in the population.
2 Disease transmission only is likely when a susceptible individual comes in contact with discharges from asymptomatic or symptomatic individuals.

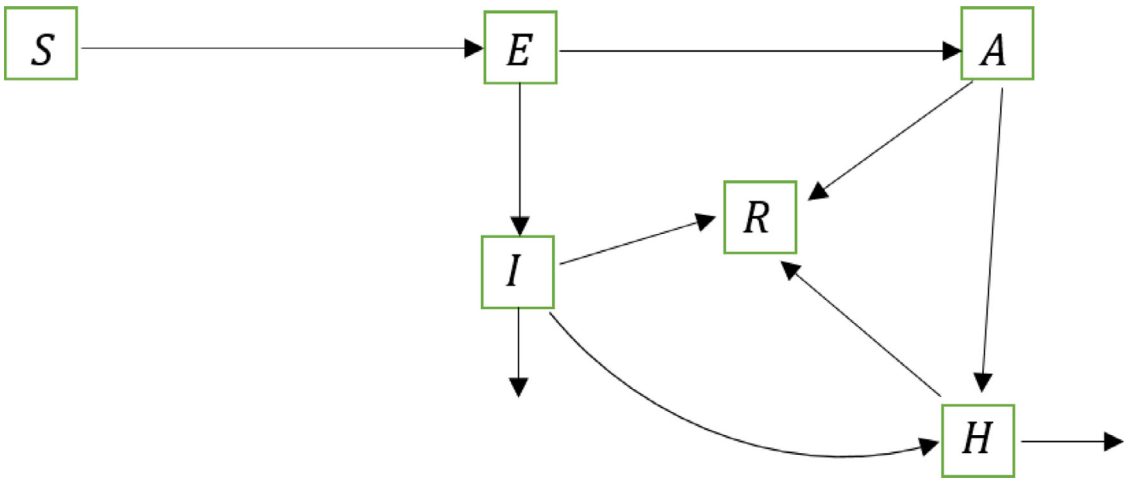

Fig. 1. Flowchart describing the dynamics of SARS-CoV-2 transmission.

Table 1
Summary of parameters.

Parameter	Meaning	Value	Refs.	Default Value
β	Infectious-susceptible transmission rate		Data fitting	
η	Reduction in disease transmission for asymptomatic individual		Data fitting	
$\frac{1}{\sigma_I}$	The incubation period for COVID 19 before becoming symptomatic infected	3 – 14 days	[19,20]	8
$\frac{1}{\sigma_A}$	The incubation period for COVID 19 before becoming asymptomatic infected	3 – 14 days	[19,20]	9
ρ_A	The recovery rate for asymptomatic infected	$\frac{1}{14} - \frac{1}{3}$ day $^{-1}$	[21,22]	$\frac{1}{9}$
ρ_I	The recovery rate for symptomatic infected	$\frac{1}{30} - \frac{1}{3}$ day $^{-1}$	[21,22]	$\frac{1}{15}$
ρ_H	The recovery rate for hospitalized individuals		Data fitting	
h_I	The rate at which symptomatic infected becomes hospitalized		Data fitting	
δ_I	Disease induced death rate for symptomatic infected individuals		Data fitting	
δ_H	Disease induced death rate for hospitalized individuals		Data fitting	
h_A	The rate at which asymptomatic infected becomes hospitalized		Data fitting	

3 The disease is likely to be transmitted faster among the symptomatic population than the asymptomatic population with a variability factor η. However, epidemiologically carriers, i.e. asymptomatic populations, are more efficient transmitters of infection because they are likely to interact more freely with susceptible populations and cause more disease transmission.
4 Recovery rates for symptomatic, asymptomatic and hospitalized are different.
5 We considered SARS-CoV-2-related deaths only for hospitalized and symptomatic populations.

A susceptible individual becomes exposed to the SARS-CoV-2 when in contact with an infectious individual at a transmission rate;

$$\frac{\beta}{S+E+A+I+R}(I+\eta A).$$

An exposed individual progresses to infectious class after an incubation period of $^1/_\sigma$ days. Symptomatic individuals become hospitalized at the rate h_I. Asymptomatic, symptomatic infected and hospitalized individuals recover at the rates ρ_A, ρ_A and ρ_H, respectively. Graphical illustration of the dynamics is shown in Fig. 1, and definitions of parameters are given in Table 1.

Based on this description, we obtained the following system of equations:

$$\frac{dS}{dt} = -\frac{\beta S}{N-H}(I+\eta A), \tag{2.1}$$

$$\frac{dE}{dt} = \frac{\beta S}{N-H}(I+\eta A) - \sigma_A E - \sigma_I E, \tag{2.2}$$

$$\frac{dA}{dt} = \sigma_A E - (\rho_A + h_A)A, \tag{2.3}$$

$$\frac{dI}{dt} = \sigma_I E - (\rho_I + h_I + \delta_I)I, \tag{2.4}$$

$$\frac{dH}{dt} = h_A A + h_I I - (\rho_H + \delta_H)H, \tag{2.5}$$

$$\frac{dR}{dt} = \rho_A A + \rho_I I + \rho_H H, \tag{2.6}$$

where $N(t) = S(t) + E(t) + A(t) + I(t) + H(t) + R(t)$.

For data fitting and parameter estimation, we included the "Death" compartment (D) to keep track of the death cases.

$$\frac{dD}{dt} = \delta_I I + \delta_H H. \tag{2.7}$$

Basic reproduction number

The basic reproduction number ($\Re_0$) is a parameter that refers to the average number of secondary infections by a single primary infectious individual during the person's infectious period. For example, if $\Re_0 = 2$, an infectious individual will infect two susceptible individuals during the person's infectious period (assuming everyone around the infectious person is susceptible). On the other hand, if $\Re_0 < 1$, the number of infected individuals decreases with time, implying the pandemic is likely under control. The disease remains endemic when $\Re_0 = 1$ [23].

Using the next-generation operator approach;

System (2.1)–(2.6) has a disease-free equilibrium (DFE) given by;

$$\varepsilon_0 = (S_0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0).$$

Where $S_0 = S(0)$ and $R_0 = R(0)$.

Using the next-generation operator approach of [23], we obtained;

$$F = \begin{pmatrix} 0 & \beta\eta & \beta \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix},$$

and

$$V = \begin{pmatrix} \frac{\beta\sigma_I}{(\sigma_A+\sigma_I)(\rho_I+\delta_I+h_I)} + \frac{\beta\eta\sigma_A}{(\rho_A+h_A)(\sigma_A+\sigma_I)} & \frac{\beta\eta}{\rho_A+h_A} & \frac{\beta}{\rho_I+\delta_I+h_I} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

The $\Re_0$ associated with DFE ε_0 is the spectral radius of the matrix FV^{-1} was obtained as;

$$\Re_0 = \frac{\beta\sigma_I}{(\sigma_A+\sigma_I)(\rho_I+\delta_I+h_I)} + \frac{\beta\eta\sigma_A}{(\rho_A+h_A)(\sigma_A+\sigma_I)}.$$

The term $\frac{\beta\sigma_I}{(\sigma_A+\sigma_I)(\rho_I+\delta_I+h_I)}$ gives the contribution of symptomatic infected class to the spread of the virus while $\frac{\beta\eta\sigma_A}{(\rho_A+h_A)(\sigma_A+\sigma_I)}$ gives the contribution of asymptomatic infected class.

Data fitting

We used the COVID-19 data provided by the NCDC [7] from 27th March 2020 through 22nd September 2020 to estimate the transmission rate (β), which symptomatic infected becomes hospitalized (h_I), hospitalization rate for a symptomatic individuals (h_A),recovery rate for hospitalized individuals (ρ_H), disease induced death rates (δ_H & δ_I) and reduction in disease transmission for asymptomatic individual (η). Details of parameter for the data fitting are presented in Table 1. Nigeria is roughly about 200,000,000 population country [24,25], we therefore set $S(0) = 199,999,998$, $I(0) = 1$, $H(0) = 1$, and other variables are set to zero initially.

We used the "lsqcurvefit" package in MATLAB to model fit the "cumulative active cases" and "cumulative death" data to H and D compartments of our model, respectively. The "lsqcurvefit" package by MATLAB solves nonlinear data-fitting problems in the least-square sense. That is, given input data "$t$data" (which could be matrices or vectors) and the observed output data "$y$data" (which could be matrices or vectors), we find coefficients x that best fit the equation.

$$\min_x \| G(x, tdata) - ydata \|_2^2 = \min_x \sum_i (G(x, tdata_i) - ydata_i)^2.$$

Where $G(x, tdata)$ is a matrix-valued or vector-valued function of the same size as $y$data [26].

Uncertainty and sensitivity analysis

Uncertainty analysis (UA) was applied to determine the significance of uncertainties arising from the model inputs to the ambiguity in the outcomes of a model [27]. Sensitivity analysis (SA) tests the stability of important parameters in the dynamics of SARS-CoV-2 transmission in our report [23]. UA and SA were applied to determine the response of model outputs to parameter variation by; identifying and isolating major sources of parametric uncertainty, identifying parameters with the most significant influence on the model, prioritizing additional data collection and estimating possible variation in model forecasts arising from variations in model parameters. Details of the significance and method of UA&SA has been reported elsewhere [28,29].

There are different techniques for executing SA [30]. The focus of this study is to quantify the impact of each parameter on the ($\Re_0$) and determine which parameters are important in contributing uncertainty to the predictions of our model. Therefore, we adopted Latin hypercube sampling with a partial rank correlation coefficient index (LHS-PRCC). Details of the method have been reported elsewhere [31,32].

Results

Details of the theoretical results are presented below;

The total human population:

$$N(t) = S(t) + E(t) + A(t) + I(t) + H(t) + R(t). \tag{3.1}$$

If $N(0) = N_0$, then from (2.1)–(2.6), we have $N(t) \leq N_0$.

The following result gives the feasible region of Eqs. (2.1)–(2.6):

Theorem 3.1 *Let the initial data for* (2.1)–(2.6) *be* $S(0) > 0$, $E(0) \geq 0$, $A(0) \geq 0$, $I(0) \geq 0$, $H(0) \geq 0$, $R(0) \geq 0$. *Then the solution* $(S(t), E(t), A(t), I(t), H(t), R(t))$ *of the model will remain non-negative for all time* $t > 0$. *Furthermore, the feasible region of the solution is given by:*

$$\begin{aligned}\Gamma = \Big\{&(S(t), E(t), A(t), I(t), H(t), R(t)) \in \mathbb{R}^6_+ : \\ &S(t) + E(t) + A(t) + I(t) + H(t) + R(t) \leq N_0\Big\}.\end{aligned} \tag{3.2}$$

Proof. It follows from the first line of (2.1) that;

$$S(t) = S(0) \exp\left(\int_0^t -\frac{\beta(I(s) + \eta A(s))}{N(s) - H(s)}\, ds\right) > 0 \quad \text{for } t > 0.$$

A similar expression can be obtained for $E(t)$, $A(t)$, $I(t)$, $H(t)$, $R(t)$ (3.2) follows by adding (2.1) through (2.6) [17].

Theorem 3.2 The disease-free equilibrium ε_0 of (2.1)–(2.6) is globally asymptotically stable in Γ if $\Re_0 < 1$.

Proof We define a Lyapunov function

$$L = \left(\frac{\beta\sigma_I}{(\sigma_A + \sigma_I)(\rho_I + \delta_I + h_I)} + \frac{\beta\eta\sigma_A}{(\rho_A + h_A)(\sigma_A + \sigma_I)}\right)E + \frac{I}{\rho_I + \delta_I + h_I} + \frac{A}{\rho_A + h_A}. \tag{3.3}$$

The time derivative of (3.2) along the solution path of the COVID-19 model (2.1)–(2.6) is given as;

$$\begin{aligned}\dot{L} &= \left(\tfrac{\beta\sigma_I}{(\sigma_A+\sigma_I)(\rho_I+\delta_I+h_I)} + \tfrac{\beta\eta\sigma_A}{(\rho_A+h_A)(\sigma_A+\sigma_I)}\right)\left(\tfrac{\beta S}{N-H}(I + \eta A) - \sigma_A E - \sigma_I E\right) \\ &+ \tfrac{\sigma_I E - (\rho_I + h_I + \delta_I)I}{\rho_I+\delta_I+h_I} + \tfrac{\sigma_A E - (\rho_A + h_A)A}{\rho_A + h_A}, \\ &= \tfrac{\Re_0 S}{N-H}(I + \eta A) - (I + \eta A), \\ &\leq (\Re_0 - 1)(I + \eta A)\end{aligned}$$

It follows that $\dot{L} \leq 0$ if $\Re_0 < 1$ with $\dot{L} = 0$, if and only if $I = A = 0$. Therefore, it can be concluded from LaSalle's Invariance Principle that the disease-free equilibrium is globally asymptotically stable whenever $\Re_0 < 1$.

Remark 3.3 Theorem 3.3 implies that backward bifurcation and reinfection are ruled out provided there is no importation of infected individuals. Thus the condition R0 < 1 is sufficient for the disease eradication provided there is no immigration of infected individuals.

Details of the parameter estimates for our model curve fit is presented in Table 2 and Fig. 2. At the outbreak of SARS-CoV-2 in Nigeria (27th February 2020 through 29th March 2020), we estimated $\beta = 0.716$, $\eta = 0.859$, $h_A = 0.136$, $h_I = 0.000$, $\rho_H = 0.06$, $\delta_H = 0.000$, $\delta_I = 0.000$, and $\Re_0 = 6.860$ 99% CI [6.003, 7.882].

Lock-down was initiated from 30th March 2020 to 3rd May 2020, and the average $\Re_0 = 3.566$ 99%CI [3.503, 3.613] decreased by half during this period. The effect of the lockdown was simulated in Fig. 3. The average basic reproduction number throughout this period was 3.566. The rapidity of SARS-CoV-2 transmission and death cases reduced during this period, but this was not enough to prevent the transmission and eradication of the disease in Nigeria. This is probably due to the high number of individuals already with the diseases before lockdown initiation. During the lockdown, markets with perishable and basic household necessities remained open, health workers and other essential service providers (such as law enforcement agencies, emergency services, etc.) kept operating. This might also account for the insignificant decline in

Table 2
Estimated parameters for the transmission dynamics of SARS-CoV-2 stratified by the different stages of the Infection outbreak in Nigeria.

	Incidence		Lockdown		Post – lockdown		Current situation	
	Estimate	99% Confidence Interval	Estimate	99% Confidence Interval	Estimate	99% Confidence Interval	Estimate	99% Confidence Interval
β	0.716	[0.713, 0.719]	0.389	[0.387, 0.391]	0.128	[0.127, 0.129]	0.118	[0.110, 0.126]
η	0.859	[0.844, 0.874]	0.370	[0.359, 0.382]	0.664	[0.650, 0.679]	0.500	[0.364, 0.636]
h_A	0.136	[0.127, 0.145]	2.811×10^{-2}	$[2.752, 2.870] \times 10^{-2}$	1.397×10^{-3}	$[0.\ 919, 1.875] \times 10^{-3}$	0.004	$[1.932, 7.391] \times 10^{-3}$
h_I	9.160×10^{-8}	$[0, 9.288] \times 10^{-3}$	7.361×10^{-9}	$[0, 3.822] \times 10^{-4}$	1.046×10^{-2}	$[1.006, 1.086] \times 10^{-2}$	0.013	$[1.187, 1.597] \times 10^{-2}$
ρ_H	6.659×10^{-2}	$[5.986, 7.332] \times 10^{-2}$	8.053×10^{-2}	$[7.731, 8.376] \times 10^{-2}$	3.281×10^{-2}	$[3.156, 3.405] \times 10^{-2}$	0.177	[0.163, 0.191]
δ_H	2.536×10^{-3}	$[0, 6.601] \times 10^{-3}$	1.122×10^{-3}	$[0, 2.733] \times 10^{-3}$	9.283×10^{-8}	$[0, 5.513] \times 10^{-4}$	3.201×10^{-4}	$[0, 2.776] \times 10^{-3}$
δ_I	6.048×10^{-8}	$[0, 1.126] \times 10^{-3}$	3.013×10^{-4}	$[1.187, 4.839] \times 10^{-4}$	1.850×10^{-3}	$[0.\ 609, 3.091] \times 10^{-4}$	4.087×10^{-6}	$[0, 2.984] \times 10^{-4}$
$\Re_0$	6.860	[6.003, 7.882]	3.566	[3.503, 3.613]	1.238	[1.215, 1.262]	1.018	[0.866, 1.183]

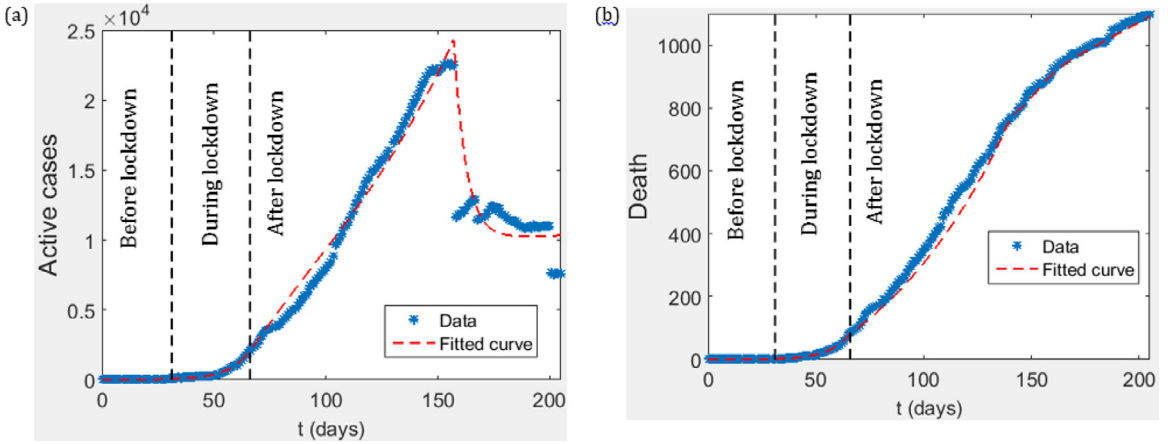

Fig. 2. Curve fittings of the H compartment to the cumulative "active cases" data (a) and (b) the D compartment to the cumulative "death" data.

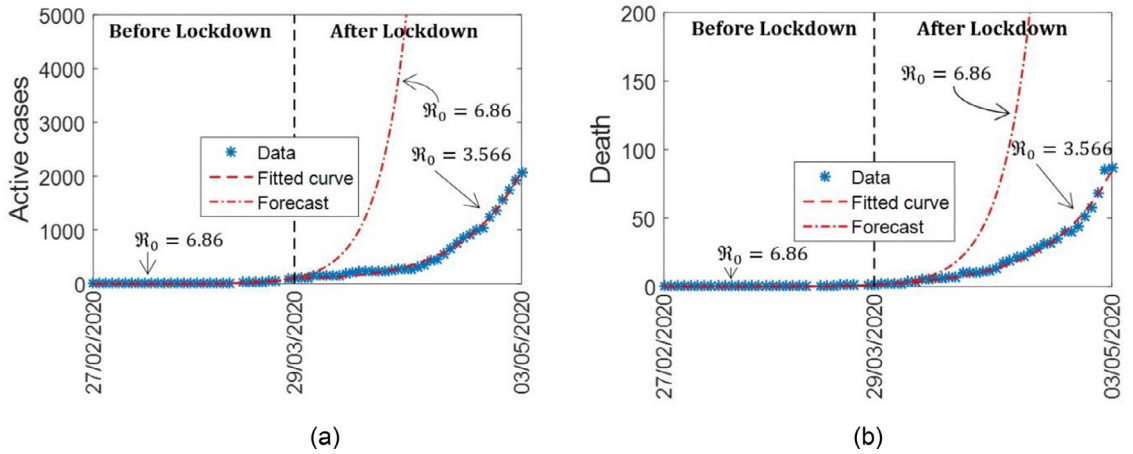

Fig. 3. Effect of lockdown on the transmission of the virus; number of active cases (a) and deaths (b).

the reported cases of the virus during the lockdown. After easing the lockdown (4th May 2020 through 22nd September 2020), $\Re_0$ was 1.238 99%CI [1.215, 1.262].

Furthermore, we estimated transmission rate (β), the rate at which symptomatic infected become hospitalized(h_I), the hospitalization rate for asymptomatic individuals(h_A), the recovery rate for hospitalized individuals (ρ_H), disease-induced death rates (δ_H & δ_I) and reduction in disease transmission for asymptomatic individual (η) for the period under review (Table 2). We fitted the curve for data at different phases of the SARS-CoV-2 pandemic to forecast the transmission dynamics. If all parameters are maintained (as in after easing the lockdown), our model forecasted a gradual and perpetual surge through the next 12 months or more, suggesting about 1.5million active cases (representing about 900,000 asymptomatic infections and 800,000 symptomatic infections) in Nigeria (Fig. 4). Also, our model suggested that 32,000 cases are likely to be in isolation for medical care, 280,000 cases for unconfirmed asymptomatic individuals and 400,000 unconfirmed symptomatic individuals (Fig. 4a,c and d). The number of death cases from the COVID-19 pandemic will likely rise to ≈1900 (Fig. 4b).

Using the LHS/PRCC technique, sensitivity indices relative to the model were derived. We generated 5000 samples from a uniform distribution of each parameter and used them as simulation inputs (Fig. 5). The recovery rates for symptomatic infection(ρ_I), asymptomatic infection(ρ_A), infectious-susceptible transmission rate(β), and reduction in disease transmission for an asymptomatic individual(η) are critical for the precise estimation of SARS-CoV-2 transmission in Nigeria.

Uncertainties in any of these four parameters is an important contributor to uncertainty in the prevalence of the disease. Of vital significance in the sensitivity of our model are two critical parameters; recovery rates for symptomatic infection(ρ_I) and asymptomatic infection(ρ_A). These parameters are likely to exert significant weight in de-escalating SARS-CoV-2 transmission in Nigeria. Also, the high PRCC value of the reduction in disease transmission for an asymptomatic individual(η) indicated the significance of asymptomatic infected individuals to the spread of SARS-CoV-2 in Nigeria (Fig. 6).

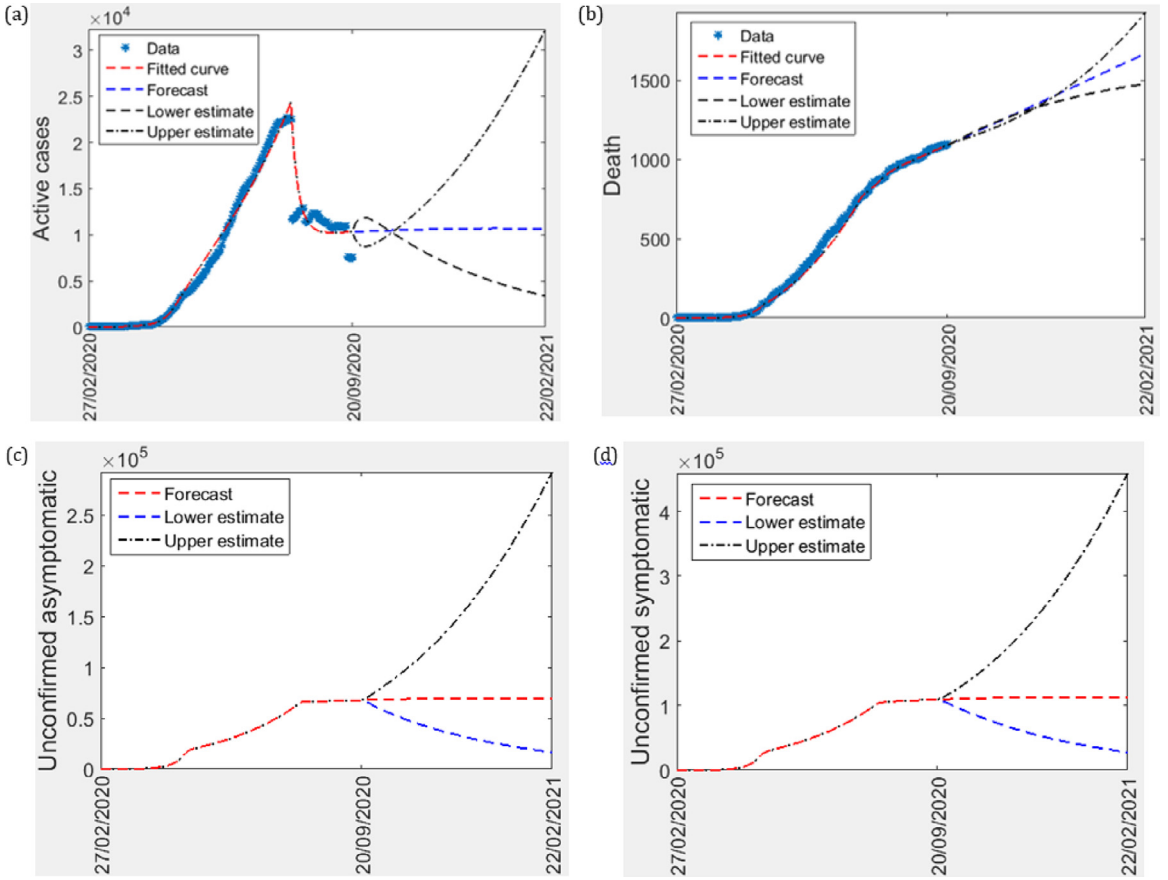

Fig. 4. Forecast for the active cases (a), cumulative death (b), unconfirmed asymptomatic cases (c) and unconfirmed symptomatic cases (d).

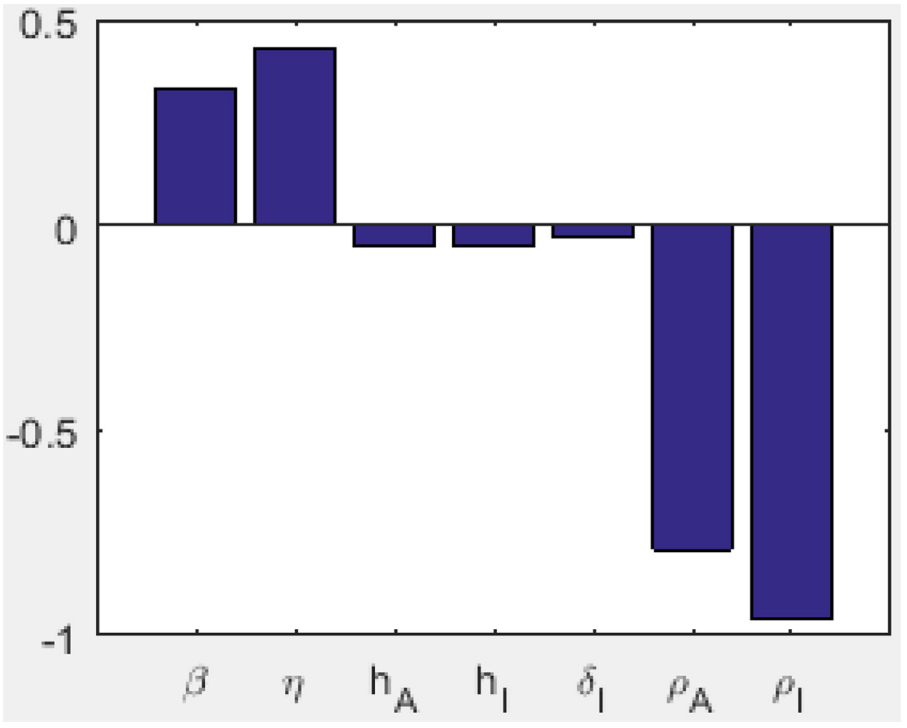

Fig. 5. PRCC of the impacts of the parameters on the disease dynamics.

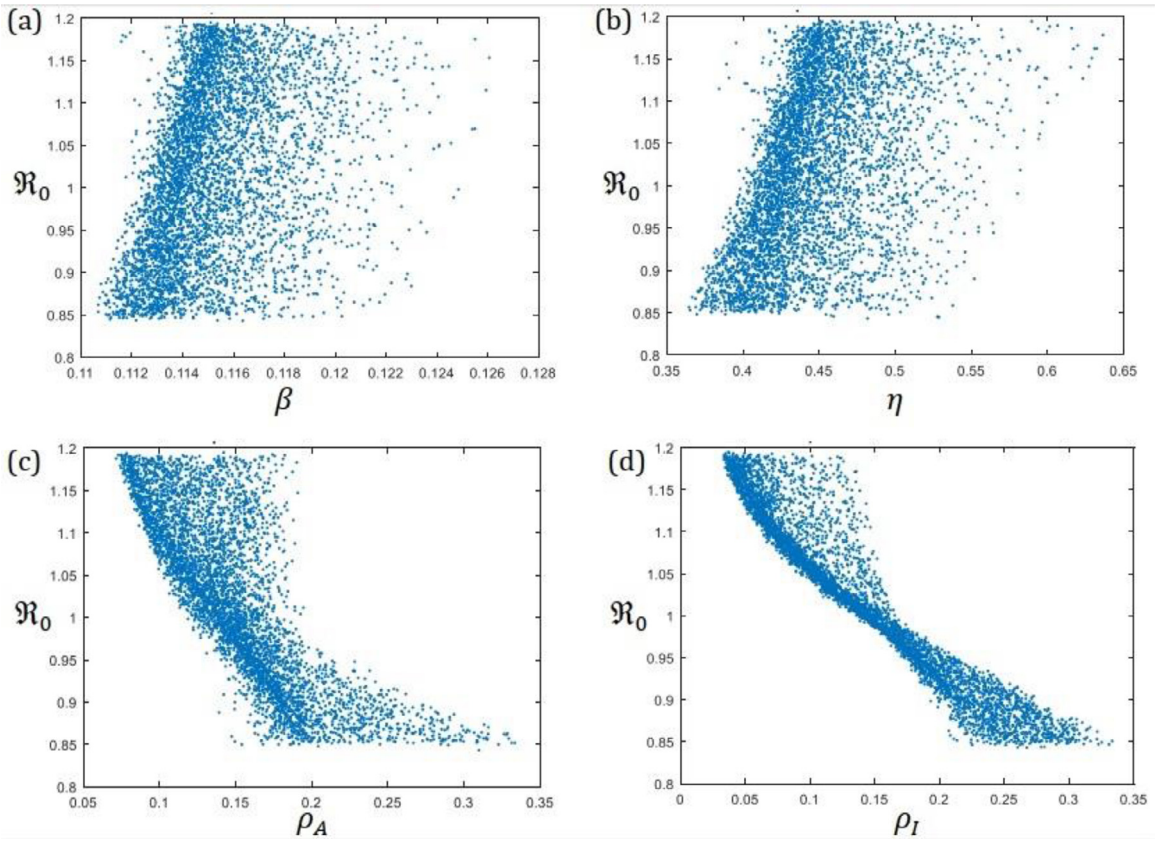

Fig. 6. Scatter plots illustrating the relationship between the basic reproduction number, $\Re_0$, and parameters with the greatest PRCC magnitudes (using values in Tables 1&5 and 5000 simulations per run); (a) Infectious-susceptible transmission rate, β, (b) Reduction in disease transmission for asymptomatic individual, η, (c) Recovery rate for asymptomatic infected, ρ_A and (d) Recovery rate for symptomatic infected, ρ_I.

Our sensitivity analysis suggests an increase in recovery rates for symptomatic infection(ρ_I) and asymptomatic infection(ρ_A), but a decrease in infectious-susceptible transmission rate (β) and disease transmission for asymptomatic individual (η)would significantly curtail SARS-CoV-2 transmission in Nigeria.

Discussion

Our report is the first (to the best of our knowledge) to model fit SARS-CoV-2 transmission using the SEIR technique in Nigeria. Using the "active cases" data provided by NCDC from March and April 2020, Okuonghae and Omame [15] predicted cumulative active cases of the disease in Lagos would be 160,000 in mid-August 2020. In contrast, the data provided by NCDC showed 2751 active cases in Lagos as of 11/08/2020. Two compartments were fitted to real-life data to provide a more accurate parameter estimate in our report. Thus, our model was all-inclusive, sturdy and conservative, considering the significance of non-pharmaceutical interventions at different stages of the COVID-19 outbreak to predict the dynamics of SARS-CoV-2 transmission in Nigeria.

At the initial phase of the outbreak (before lockdown), the R_0 was high and comparable to another study from China [33]. At that time, the disease was novel to the Nigerian population with zero immunity to infection, making the entire population susceptible to its rapid spread. By the period of the lockdown, R_0 was reduced by half. This observation was in tandem with the average R_0 of 3.28 reported in another study from China [34], which was obtained later when the population might have acquired some level of immune resistance. Control measures and non-pharmaceutical interventions (such as the rational use of face masks, rigorous public awareness, contact tracing, immediate isolation and prompt treatment [35–38]) likely promoted a significant increase in risk perception of the virus and behaviour change [39], but not sufficient to significantly reduce the community transmission of SARS-CoV-2. It is also worth noting that R_0 estimates can be affected by several factors such as; genetic, behavioural, environmental, etc.

After easing the lockdown, the R_0 was still greater than 1 ($R_0 = 1.018$), implying the COVID-19 pandemic is not entirely under control in Nigeria, and higher transmission rates are plausible in Nigeria. In this study, If all parameters are maintained (as in after easing the lockdown), our model forecasted a perpetual surge in cases and mortality arising from SARS-CoV-2 transmission in Nigeria from October 2020 through the next 12 months or more. Several efforts are in place and ongoing in

managing the spread of SARS-CoV-2 in Nigeria [40,41], but the effectiveness of such efforts are largely unclear. More studies assessing the impact of these control measures on the SARS-CoV-2 transmission in Nigeria are necessary.

There are several issues worth itemizing. First, the testing rate for SARS-CoV-2 is in Nigeria is largely unknown and likely to be relatively low. Less than a million of the over 200 million population has been tested for the virus [42]. However, a recent seroprevalence study of SARS-CoV-2 antibodies in Anambra State, Nigeria, revealed that one in every six persons had been infected and developed antibodies [43], implying more susceptibility to the virus. Second, the implementation and compliance level to non-pharmaceutical intervention is poor and low, respectively. Third, the case report of SARS-CoV-2 has been predominantly limited to urban areas with limited data from the rural settings. Also, the highly strained health systems and poor surveillance infrastructure limit the validity and representativeness of the data provided by the NCDC.

Our study (like any other) is limited because SARS-CoV-2 is an emerging pathogen. Also, the model fit is as good as its assumptions. Our findings must be interpreted with caution in light of the sparse reliability of phenomenological models. Because the testing rate in this population appears relatively low and thus the number of people with the virus but not down with the disease is largely unknown. The necessity of a country-wide serosurvey cannot be underestimated in elucidating the holistic perspective of SARS-CoV-2 transmission in Nigeria. A few strengths of our study are worth mentioning. Our study is the first to model fit SARS-CoV-2 transmission using the SEIR technique in Nigeria. Second, compared to earlier studies [15,44], our report presented conservative and realistic estimates considering multiple compartments and time points in the outbreak of the disease. Third, our model suggests context-specific information vital to inform public health decisions for managing and preventing SARS-CoV-2 transmission in Nigeria.

Conclusion

In this study, the SEIR model was applied in predicting the spread of SARS-CoV-2 in Nigeria, taking into account time-point scenarios. Though we observed a reduction in the transmission rate of the virus, the likelihood of human to human transmission of the virus is still likely ongoing in significant proportions. The imperative of a timely and well-articulated long-term strategy would be golden in preventing an uncontrolled pandemic situation in Nigeria.

Declaration of Competing Interest

The authors declare they have no competing interests.

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