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From the Research Laboratories

MODELLING THE IMPACT OF VACCINATION ON THE TRANSMISSION DYNAMICS OF COVID-19 IN THE PRESENCE OF ENVIRONMENTAL FACTOR

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Abstract. The emergence of the Coronavirus Disease 2019 (COVID-19) pandemic, as reported by the World Health Organisation (WHO), originating from Wuhan, China in late 2019, poses a significant and formidable challenge to worldwide public health. As a result, more than 20 nations experienced the impact of this lethal illness. This research introduces a mathematical model, namely SEIQRV, which incorporates the SEIR model to analyse the ongoing COVID-19 epidemic in Nigeria. The model incorporates nonlinear forces of infection. The present model takes into account the many modes of transmission involved in the dynamics of infection, as well as the influence of the environmental reservoir on the dissemination of this particular illness to human populations. The establishment of the area in which the model is epidemiologically viable has been confirmed. A comprehensive numerical simulation of the model was performed using the data given by the Nigeria Centre for Disease Control (NCDC). The findings from our analysis and simulation suggest that administering an inadequate dose of vaccination will result in an elevated number of persons who are exposed to and infected by the virus. Additionally, this incomplete dosage is also likely to contribute to an increase in the concentration of the virus within the environmental reservoir. Hence, the need for effective vaccination with a zero-wane-off vaccine and compliance with vaccination dose, which can be achieved through educational campaign and public awareness of the need to be vaccinated, and not to be vaccinated alone but to complete the dose as incomplete dosage is dangerous to the community and the country at large. This will help a great deal in eradicating the spread of the COVID-19.

Keywords: COVID-19; Vaccination; Infection dynamics; Mathematical model; SEIQRV model; Transmission; Basic reproduction number

1. Introduction

Coronaviruses are zoonotic pathogens that may infect both people and animals, exhibiting a diverse spectrum of clinical manifestations, ranging from asymptomatic cases to severe illness requiring hospitalisation in critical care units. These viruses can cause infections in several systems of the body, including the respiratory, gastrointestinal, hepatic, and neurologic systems. The perception of their path-

ogenicity in humans did not reach significant levels until their association with the outbreak of severe acute respiratory syndrome (SARS) in Guangdong, China, between the years 2000 and 2003.According to Weiss and Navas-Martin (2005), these viruses are prevalent among animals on a global scale; nevertheless, their impact on humans has been limited, with just a small number of documented instances.

The 2019 new coronavirus, as designated by the World Health Organisation (WHO), is a kind of coronavirus that specifically impacts the lower respiratory tract of individuals diagnosed with pneumonia in Wuhan, China on December 29, 2019 (Li et al., 2019). The World Health Organisation (WHO) has officially designated the name of the illness caused by the 2019 new coronavirus as COVID-19. This disease has garnered significant worldwide interest since it is associated with a pneumonia epidemic of uncertain origin (Zhu et al., 2019). The virus is now referred to as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). According to Zhu et al. (2019), there was a documented association between a group of individuals suffering from pneumonia of uncertain aetiology and the Huanan South China Seafood Market located in Wuhan, during the month of December in the year 2019.

Prior to the onset of the COVID-19 pandemic, two prominent strains of coronavirus, namely CoV OC43 and CoV 229E, were responsible for mostly inducing mild illnesses in individuals with a robust immune system. Nearly a decade after the emergence of the Severe Acute Respiratory Syndrome (SARS), a new highly contagious coronavirus known as the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) has emerged in urban areas of the Middle East.

In addition to SARS-CoV-2, there are six documented coronaviruses that infect humans, namely HCoV-229E, HCoV-OC43, SARS-CoV, HCoV-NL63, HCoV-HKU1, and MERS-CoV. The occurrence of two significant pandemics, namely Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS), may be attributed to the coronavirus during the last twenty years (Li et al., 2019).

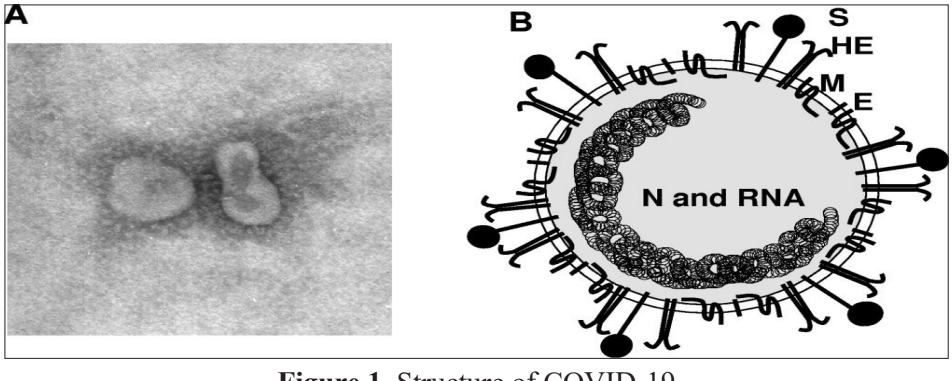

Figure 1. Structure of COVID-19

Various mathematical modelling studies have been undertaken to analyse the dynamics of the propagation of the COVID-19 pandemic. In their work, Okhuese (2020) used the SEIRU model as a tool for examining and forecasting the spread of COVID-19 on a global scale. There is a projected possibility of a reduction in secondary infections if comprehensive preventive measures are universally adhered to. Chen et al. (2020) proposed a mathematical model that aimed to explain a transmission network including bats, hosts, reservoirs, and humans. This model was specifically designed to simulate the possible transmission of infections from the source of infection to humans. To simplify the complexity of the model, it was referred to as the Reservoir-People transmission network model. The calculation of the reproduction number was derived from the Reservoir-People model, using the next-generation matrix as a means to quantify the transmissibility of the virus within the geographical region of Wuhan, China. The predicted value of was found to be 2.30 when considering the transmission from the ambient reservoir to people, and 3.58 when considering transmission from humans to humans. In their study, Yang and Wang (2020) introduced a compartmental model that incorporates many components, including the vulnerable population, the exposed population, the infected population, the recovered population, and the concentration of the pathogen in the environmental reservoir. The reproduction number was determined by using the next-generation matrix methodology to assess the transmissibility of the virus. This analysis focused on the transmission of the virus from individuals who were exposed, infected, or carrying pathogens in the environmental reservoir to vulnerable individuals in Wuhan, China. The projected value of is 4.25, with 1.5 attributed to the indirect transmission route and 2.7 attributed to the direct transmission route. In his study, Daniel (2020) examined the transmission dynamics of infectious diseases in Nigeria, specifically focusing on the transmissibility between individuals and the environmental reservoir. The analysis used nonlinear forces of infection to better understand the spread of the disease throughout the population. According to projections, it is anticipated that Nigeria would have a total of 55,000 confirmed cases by December 25, 2020. Consequently, the implementation of mitigation techniques is recommended, as its efficacy in curtailing the transmission of COVID-19 throughout Nigeria is being emphasised. Previous investigations conducted by Onitilo et al. (2021, 2022) have undertaken rigorous study pertaining to the topic at hand.

However, previous literature did not take into consideration the transmission route from the confirmed cases to the susceptible because, they are isolated and treated. But in a country like Nigeria where it is reported that the clinical practitioners were infected in the process of treating patients with COVID-19. Hence, the need to include this transmission route. Hence, we present a mathematical model for the pandemic COVID-19 to describe the several transmission pathways including

the disease-induced rates for humans, and direct and indirect transmission routes. The direct transmission routes through contact describe the transmission from the exposed individuals to the susceptible individuals; from the infected individuals to the susceptible individuals, and from the quarantine individuals/confirmed cases to susceptible individuals while the indirect transmission routes come from the interaction of the susceptible individuals with these pathogens in the environmental reservoir.

2. Model Analysis and Formulation

2.1. Formulation

To investigate the transmission dynamics of COVID-19 among humans, we utilise the SEIR model framework, which considers a total population size N. We incorporate the presence of quarantined individuals and the concentration of the virus in the environmental reservoir into our model. Consequently, we propose a mathematical model denoted as SEIQRV to examine the ongoing epidemic in Nigeria.

The susceptible compartment, represented by S, comprises persons who are at risk of being infected. The exposed compartment, designated by E, consists of individuals who have been infected but have not yet shown symptoms. The infected population, denoted by I, represents individuals who are displaying complete illness symptoms. The compartments that are exposed and infected consist of individuals who are respectively asymptomatic and symptomatic with the infection. The quarantine compartment, referred to as Q, comprises individuals who have been proven positive for a certain condition, have been placed under quarantine, and have received vaccination. Individuals who decline to undergo therapy or vaccination are reclassified into the susceptible compartment. Following a period of therapy and completion of all necessary observational procedures to ensure the successful recuperation from the aforementioned infectious ailment, individuals are then transferred to the designated recovery compartment, signified by R. Finally, the variable V denotes the concentration of the pathogen in the environmental reservoir. The following diagram illustrates the transmission dynamics of the COVID-19 pandemic using the SEICRV model, under the premise that people who have recovered from the disease develop immunity and are not susceptible to reinfection. In order to study the transmission dynamics of COVID-19 among humans, we adopt the SEIR model framework with total population of human size NN and formulate a model that include the quarantine individuals and the concentration of the virus in the environmental reservoir, hence propose a mathematical model of the form SEIQRV to investigate the present epidemic in Nigeria.

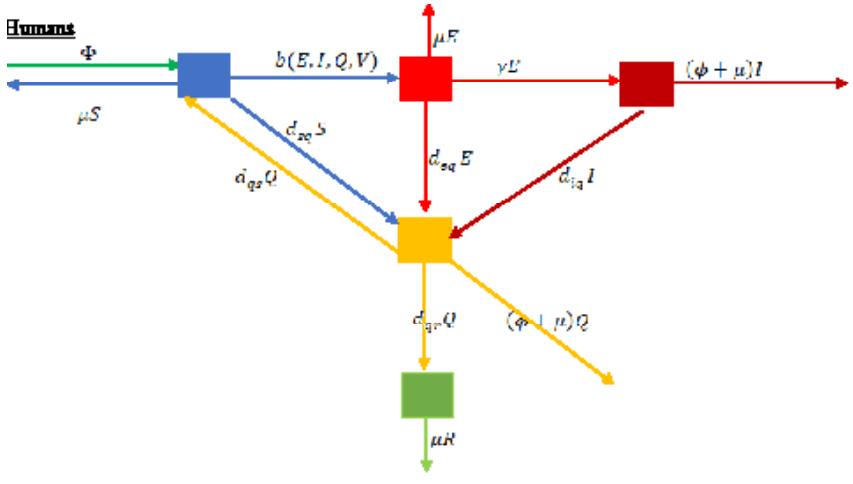

Figure 2. Transmission dynamics of the infectious disease

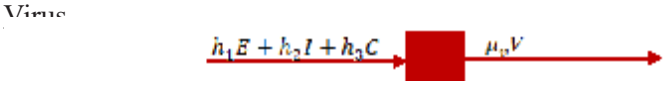

Figure 3. Concentration of the virus in the environmental reservoir

The transmission dynamics of the disease are described by a six-dimensional system of ordinary differential equations, as seen in Figures 1 and 2.

$$\begin{cases} \dfrac{dS}{dt} = \Phi - b(E,I,Q,V) + d_{qs}Q - (d_{sq} + \mu)S \\ \dfrac{dE}{dt} = b(E,I,Q,V) - (\gamma + d_{eq} + \mu)E \\ \dfrac{dI}{dt} = \gamma E - (\phi_i + d_{iq} + \mu)I \\ \dfrac{dQ}{dt} = d_{sq}S + d_{eq}E + d_{iq}I - (d_{qs} + d_{qr} + \phi_q + \mu)Q \\ \dfrac{dR}{dt} = d_{qr}Q - \mu R \\ \dfrac{dV}{dt} = h_1E + h_2I + h_3Q - \mu_v V \end{cases} \tag{1.1}$$

Together with the initial conditions

$$\begin{cases} S(0) = S_0, & E(0) = E_0 \\ I(0) = I_0, & Q(0) = Q_0, \\ R(0) = R_0, & V(0) = V_0, \end{cases} \tag{1.2}$$

The variable Φ denotes the population inflow within the context of the study. The symbol μ represents the fatality rate, where it is assumed that all individuals in the compartment experience natural death. The symbol ϕ represents the rate of death produced by the illness, whereas γ^{-1} represents the duration of the incubation period between the time of infection and the start of symptoms. The variable d_qr represents the rate at which individuals recover from the sickness. The variable d_{iq} represents the rate at which persons who are verified to be infected with the illness are classified as infectious. The variable d_{eq} represents the rate at which people who have been exposed to COVID-19 are tested and provide positive results. The variable d_{sq} represents the rate at which individuals in the susceptible compartment choose to undergo testing and vaccination, resulting in their transition to the recovery compartment. However, if individuals fail to complete their vaccination or if any confirmed cases fail to complete their treatments, they are returned to the susceptible compartment at a rate denoted by d_{qs}. The rates at which the exposed, infected, and quarantined individuals contribute the virus to the environmental reservoir are denoted as h_1, h_2, and h_3, respectively. The removal of the virus from the environmental reservoir is represented by μ_v.

For the infection degree $b(E,I,Q,V)$ of COVID-19 pandemic in the susceptible compartment, the mathematical expression is as follows:

$$b(E,I,Q,V) = \beta_E SE + \beta_I SI + \beta_Q SQ + \beta_v SV$$

The terms $\beta_E SE, \beta_I SI, \beta_Q SQ, \beta_V SV$, bilinear incidences define respectively the transmission rates between susceptible and exposed, susceptible and infected, susceptible and confirmed and from the environment to humans.

2.2. Boundedness of the Solution

It is necessary to demonstrate that the transmission dynamics defined by system exhibit epidemiological and mathematical well-posedness within a viable area denoted by $\mathcal{F}$

$$\mathcal{F}_h = \left\{ (S,E,I,Q,R) \in \mathbb{R}_+^5 : N \le \frac{\Phi}{\mu} \right\}$$

and

$$= \left\{ \quad \in \mathbb{R} \qquad \leq \frac{(\ _1 + \ _2 \quad _3)\Phi}{\mu\mu} \right\}$$

where,

$$N(t) = S(t) + E(t) + I(t) + Q(t) + R(t) + D(t)$$

Theorem 1: There exist a domain $\mathcal{F}$ in which the solution set $\{S, E, I, Q, R, V\}$ is contained and bounded.

Proof:

Let

$$U_1(S, E, I, Q, R) = S(t) + E(t) + I(t) + Q(t) + R(t) + D(t)$$

and

$$U_1(V) = V(t)$$

Then the time derivatives $U_1^{'}$ and $U_2^{'}$ along solutions of the system are:

$$U_1^{'} = \frac{\partial U_1}{\partial S}\frac{dS}{dt} + \frac{\partial U_1}{\partial E}\frac{dE}{dt} + \frac{\partial U_1}{\partial I}\frac{dI}{dt} + \frac{\partial U_1}{\partial Q}\frac{dQ}{dt} + \frac{\partial U_1}{\partial R}\frac{dR}{dt} + \frac{\partial U_1}{\partial D}\frac{dD}{dt}$$

and

$$U_2^{'} = \frac{\partial U_2}{\partial V}\frac{dV}{dt}$$

It follows that

$$U_1^{'} \leq \Phi - \mu U_1 \text{ and } U_2^{'} \leq (h_1 + h_2 + h_3)\Phi - \mu\mu_v U_2 \qquad (1.3)$$

Solving the differential equations yield

$$U_1 \leq \frac{\Phi}{\mu}(1 - \exp(-\mu t)) + U_1(S_0, E_0, I_0, Q_0, R_0)\exp(-\mu t)$$

and

$$U_2 \leq \frac{(h_1 + h_2 + h_3)\Phi}{\mu\mu_v}(1 - \exp(-\mu\mu_v t)) + U_2(V_0)\exp(-\mu\mu_v t)$$

Therefore, taking the limits as $t \to \infty$ yields

$$U_1 \leq \frac{\Phi}{\mu} \text{ and } U_2 \leq \frac{(h_1 + h_2 + h_3)\Phi}{\mu\mu_v}$$

Hence, every possible solution of the population belongs inside the feasible zone, indicating the existence and definition of the feasible region for the specified model in equation and is defined by

$$\mathcal{D} = \left\{ (S, E, I, Q, R, V) \in \mathbb{R}_+^6 : N \leq \frac{\Phi}{\mu}, V \leq \frac{(h_1 + h_2 + h_3)\Phi}{\mu\mu_v} \right\}$$

2.3. Equilibrium Point

2.3.1. Existence of Disease-free Equilibrium Point (DFE)

The DFE point are equilibrium point where no infection of COVID-19 occurred. Let

$$E_0 = (S^*, E^*, I^*, Q^*, R^*, V^*).$$

Thus at DFE point $E_0, E^*, I^*, Q^*, R^*, V^* = 0$. In respect of this, solving , the resulting DFE point obtained is

$$E_0 = (S_0, 0, 0, 0, 0, 0, 0)$$

$$= \left(\frac{\Phi}{\mu + d_{sq}}, 0, 0, 0, 0, 0, 0 \right)$$

2.3.2. Stability of the Free Disease Equilibrium Point

Here, we show that the disease free state E_0 is asymptotically stable if $J(E_0)$ is negative and unstable if $J(E_0)$ is positive.

To start with, we find the Jacobian matrix of the system at the disease-free equilibrium point E_0 which is obtained as

$$J(E_0) = \begin{pmatrix} -(\mu + d_{sc}) & -\beta_E S_0 & -\beta_I S_0 & -\beta_Q S_0 + d_{qs} & 0 & -\beta_V S_0 \\ 0 & -w_1 & 0 & 0 & 0 & 0 \\ 0 & \gamma & -w_2 & 0 & 0 & 0 \\ d_{sq} & d_{eq} & d_{iq} & -w_3 & 0 & 0 \\ 0 & 0 & 0 & d_{qr} & -\mu & 0 \\ 0 & h_1 & h_2 & h_3 & 0 & -\mu_v \end{pmatrix}$$

Where, $w_1 = \gamma + d_{eq} + \mu, \quad w_2 = \phi + \mu + d_{iq}$, and $w_3 = \phi + \mu + d_{qr} + d_{qs}$

The column(s) or row(s) with diagonal terms forms the first set of eigenvalue(s), the remaining eigenvalues are then obtained from the sub-matrix $J_n(E_0), n \in \mathbb{N}$ which is formed by excluding the column(s) and row(s) of the associated eigenvalue(s). For matrix $J(E_0)$, the eigenvalues are $-\mu$ and $-w_1$, for sub-matrix $_1(\ _0)$, we have $-w_2$. The remaining three eigenvalues are obtained from the sub-matrix

$$J_2(E_0) = \begin{pmatrix} -(\mu + d_{sq}) & -\beta_Q S_0 + d_{qs} & -\beta_v S_0 \\ d_{sq} & -w_3 & 0 \\ 0 & h_3 & -\mu_v \end{pmatrix}$$

The eigenvalues of the matrix $J_2(E_0)$ are the roots of the characteristics equation

$$\lambda^3 + (\mu + d_{sq} + w_3 + \mu_v)\lambda^2 + (d_{sq}w_3 + d_{sq}\mu_v + w_3\mu + \mu\mu_v + w_3\mu_v + \beta_C S_0 d_{sq} - d_{qs}d_{sq})\lambda + w_3\mu_v(d_{sq} + \mu) + d_{sq}S_0(\beta_V h_3 + \beta_Q \mu_v) - d_{sq}\mu_v = 0 \quad (1.4)$$

Where

$$\begin{aligned} A_3 &= 1 \\ A_2 &= \mu + d_{sq} + w_3 + \mu_v \\ A_1 &= d_{sq}w_3 + d_{sq}\mu_v + w_3\mu + \mu\mu_v + w_3\mu_v + \beta_Q S_0 d_{sq} - d_{qs}d_{sq} \\ A_0 &= w_3\mu_v(d_{sq} + \mu) + d_{sq}S_0(\beta_V h_3 + \beta_Q \mu_v) - d_{sq}\mu_v \end{aligned} \quad (1.5)$$

Employing the Routh-Hurwitz criterion (Murray, 2001) which states that all roots of the polynomial has negative real parts if and only if the coefficient $A_i > 0$ and matrices $H_i > 0$ for $i = 0,1,2,3$. From equation , we have that $A_0 > 0, A_2 > 0, A_3 > 0$. Also, $A_1 > 0$ provided $w_3, \mu_v, > d_{cs}$. Also, the Hurwitz matrices for the polynomial are positive i.e

$$H_1 = A_2 > 0, H_2 = \begin{vmatrix} A_2 & A_3 \\ A_0 & A_1 \end{vmatrix} > 0, H_3 = \begin{vmatrix} A_2 & A_3 & 0 \\ A_0 & A_1 & A_2 \\ 0 & 0 & A_0 \end{vmatrix} > 0$$

Hence, it follows that the eigenvalues of the Jacobian matrix J(E_0) possess a negative real component, so establishing the local or asymptotic stability of the disease-free equilibrium point. This suggests that in order for a state to achieve freedom from the virus, the rate of individuals transitioning from the confirmed cases category to the recovered category must exceed the rate at which individuals transition back from the confirmed cases category to the susceptible category, while also ensuring effective removal of the virus from the environmental reservoir. The attainment of a disease-free condition may be ensured by eliminating pathogens from the environmental reservoir and ensuring a higher number of individuals who have received treatment compared to those who have declined it.

Otherwise, if $w_3, \mu_v, < d_{qs}$, we see that $A_1 < 0$ and by Descarte's rule of sign, there is at least one sign change in the sequence A_3, A_2, A_1, A_0 of the coefficient of the polynomial . So, there is at least one eigenvalue with positive real part and the disease-free equilibrium point is unstable.

2.3.3. Computation of Basic Reproduction Number

The reproduction number $\mathcal{R}_0$ refers to the anticipated number of cases that arise from a single case within a community in which all people are vulnerable to infection. If $\mathcal{R}_0 > 1$ implies that certain measures are implemented, as such, there would

be a decrease in the number of cases. Conversely, if $\mathcal{R}_0 > 1$ such measures are not implemented, there would be a rise in the number of cases, perhaps leading to the declaration of an epidemic. The magnitude of is directly proportional to the level of difficulty in managing the epidemic. Consequently, it becomes essential to forecast the potential spread of an illness within the population.

To get $\mathcal{R}_0$ for the model in equation (1.1), the next generation matrix approach is used. The components pertaining to infection in this model are E, I, Q, V. The derivatives at the disease-free equilibrium point are to be determined. The infection matrix and the transition matrix are denoted as $\mathcal{F}$ and $\mathcal{V}$, respectively.

$$F = \begin{pmatrix} \beta_E S_0 & \beta_I S_0 & \beta_Q S_0 & \beta_V S_0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

$$\mathcal{V} = \begin{pmatrix} w_1 & 0 & 0 & 0 \\ -\gamma & w_2 & 0 & 0 \\ -d_{eq} & -d_{iq} & w_3 & 0 \\ -h_1 & -h_2 & -h_3 & \mu_v \end{pmatrix}$$

Where $w_1 = \gamma + d_{eq} + \mu, \quad w_2 = \phi + \mu + d_{iq}$, and $w_3 = \phi + \mu + d_{qr} + d_{qs}$.

Hence, the reproduction number for the model is

$$\mathcal{R}_0 = \rho(FV^{-1}) = \frac{\beta_E S_0}{w_1} + \frac{\gamma \beta_I S_0}{w_1 w_2} + \frac{\beta_Q S_0}{w_1 w_2 w_3}(d_{eq} w_2 + d_{iq}\gamma) + \frac{\beta_V S_0}{\mu_v w_1 w_2 w_3}(d_{eq} h_2 w_2 + h_1 w_2 w_3 + \gamma d_{iq} h_3 + \gamma h_2 w_3) \tag{1.6}$$

$$\mathcal{R}_0 = \mathcal{R}_E + \mathcal{R}_I + \mathcal{R}_Q + \mathcal{R}_V \tag{1.7}$$

The first three components $\mathcal{R}_0$ in equation (1.7), namely $\mathcal{R}_E, \mathcal{R}_I$ and $\mathcal{R}_Q$, quantify the impact of human-to-human transmission channels, namely the exposure of susceptible individuals to diseased individuals, and the transfer from infected individuals to susceptible individuals. The fourth component $\mathcal{R}_V$, quantifies the contribution of the environment to the human transmission route. The four transmission pathways described include the comprehensive assessment of the infection risk associated with the Covid-19 outbreak in Nigeria. The subsequent elucidation delineates each of the components of the fundamental reproductive number.

The first component $\mathcal{R}_E$ quantifies the multiplication of the contact rate between susceptible people and exposed individuals in close proximity to the disease-free equilibrium β_E, divided by the average length spent in the exposed class $\frac{1}{w_1}$.

Additionally, $\mathcal{R}_I$ quantifies the multiplication of the rate at which susceptible people come into contact with infected persons in close proximity to the disease-free equilibrium (DFE) β_I, and the time between infection and the appearance of symptoms γ, relative to the average duration within the combined exposed and infected population $\frac{1}{w_1 + w_2}$. In a similar vein, $\mathcal{R}_Q$ quantifies the combined effect of the contact rate between susceptible individuals and confirmed cases in close proximity to a DFE β_Q. It also takes into account the multiplication of two factors: the rate at which individuals transition from the infected class to the removed class, and the rate at which exposed individuals become confirmed cases. Additionally, it considers the multiplication of the number of infected individuals who test positive for the disease after the incubation period $\left(d_{ec} w_2 + d_{ic} \gamma\right)$, and the average duration of individuals in the exposed, infected, and quarantine class $\left(\frac{1}{w_1 w_2 w_3}\right)$. Lastly, $\mathcal{R}_V$ measures the product of contact rate of susceptible individuals from the concentration of the virus in the environment near DFE β_V and the sum of the product of the following: rate at which individuals are confirmed, removal from the infected class and the contribution of the confirmed cases in the environmental reservoir to the removal of the virus from the environmental reservoir; removal from exposed class, infected class and the ratio of the contribution of the exposed individuals in the environmental reservoir to the removal of the virus from the environmental reservoir; rate at which infected individuals are positive with the infectious disease after the incubation period and the ratio of the contribution of the confirmed cases in the environmental reservoir to the removal of the virus from the environmental reservoir; removal of infected individuals after the incubation period and the ratio of the contribution of the infected individual in the environmental reservoir to the removal of the virus from the environmental reservoir $(d_{eq} w_2 h_3 / \mu_v + w_2 w_3 h_1 / \mu_v + \gamma d_{iq} h_3 h_3 / \mu_v + \gamma w_2 h_2 / \mu_v)$, over the average duration in the product of exposed, infected and quarantine population $\left(\frac{1}{w_1 w_2 w_3}\right)$.

Sensitivity Analysis

The present research incorporates sensitivity analysis to assess the individual impact of each parameter on the basic reproduction number. The purpose of this

analysis is to assess the extent to which each parameter value contributes to the reproduction number.

The calculation of the basic reproduction number is calculated as follows:

$$\mathcal{R}_0 = \rho(F\mathcal{V}^{-1}) = \frac{\beta_E S_0}{w_1} + \frac{\gamma\beta_I S_0}{w_1 w_2} + \frac{\beta_Q S_0}{w_1 w_2 w_3}(d_{eq} w_2 + d_{iq}\gamma) + \frac{\beta_V S_0}{\mu_v w_1 w_2 w_3}(d_{eq} h_3 w_2 + h_1 w_2 w_3 + \gamma d_{iq} h_3 + \gamma h_2 w_2) \tag{1.8}$$

Sensitivity index of the model parameter is provided as:

$$S_X^{R_0} = \frac{\partial R_0}{\partial X} \times \frac{X}{R_0} \tag{1.9}$$

Where X denotes any parameter in the model.

The estimation of the sensitivity index for each of the parameters is presented in Table 1.

Table 1. The estimation of the sensitivity index for each of the parameters

SYMBOL	VALUE	SOURCE	SENSITIVITY INDEX			
			R_0	R_E	R_I	R_C
			0.036402	0.0334	7.01E-05	0.000538
Φ	22655	Daniel (2020)	1	1	1	1
$1/\gamma$	1/7	Yang and Wang (2020)	-0.13257	-0.139	0.861001	-0.00845
d_{qr}	1/14	Onitilo and Daniel (2022)	-0.01737	0	0	-0.71469
μ_V	1	Yang and Wang (2020)	-0.06576	0	0	0
μ	0.0182	Daniel (2020)	-0.06583	-0.06123	-0.08771	-0.24679
d_{eq}	4.103e-5	Daniel (2020)	-0.82216	-0.84329	-0.84329	0.026159
d_{iq}	0.626	Daniel (2020)	-0.00269	0	-0.91094	0.011626
β_E	3.366e-8	Daniel (2020)	0.917541	1	0	0
β_I	6.396e-9	Daniel (2020)	0.001925	0	1	0
β_Q	1.023e-9	Assumed	0.014775	0	0	1
β_V	1.886e-8	Daniel (2020)	0.065759	0	0	0
h_1	2.010	Daniel (2020)	0.054892	0	0	0
h_2	0.235	Daniel (2020)	0.001334	0	0	0
h_3	0.035	Assumed	0.009533	0	0	0

d_{sq}	0.4	Assumed	-0.95648	-0.95648	-0.95648	-0.95648
d_{qs}	0.8667	Daniel (2020)	-3.6E-06	0	0	-0.00015
ϕ_I	0.043	Iboi et al. (2020)	-0.0004	0	-0.06257	-0.00817
ϕ_Q	0.103	Iboi et al. (2020)	-0.00251	0	0	-0.10306

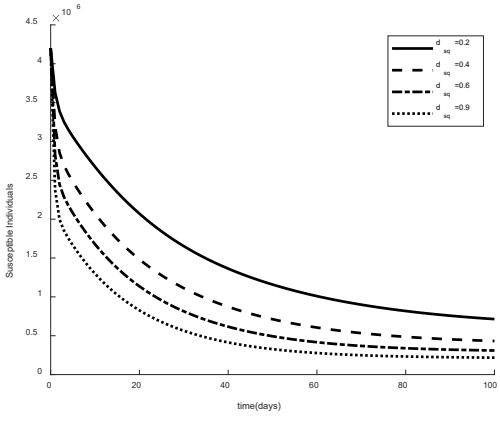

Figure 4. Simulation showing the impact of vaccination on the susceptible individuals

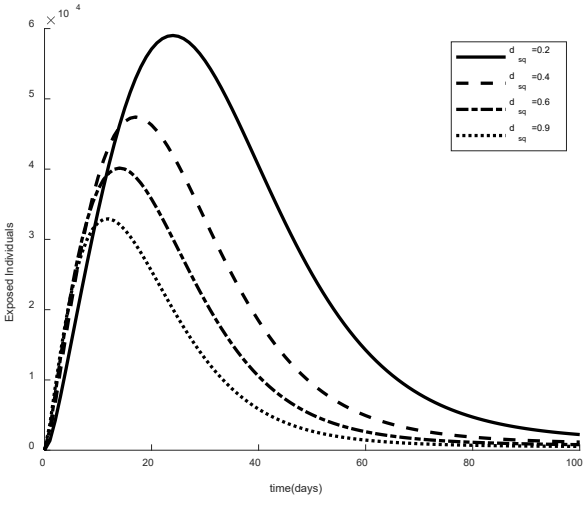

Figure 5. Simulation showing the impact of vaccination on the exposed individuals

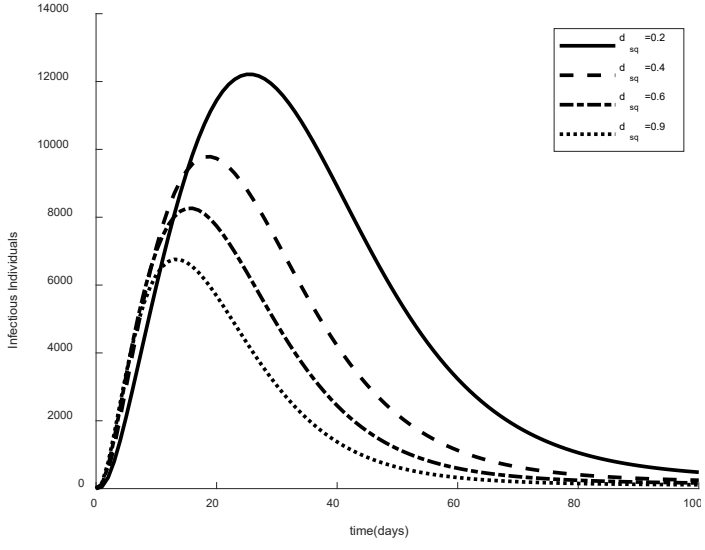

Figure 6. Simulation showing the impact of vaccination on the infectious individuals

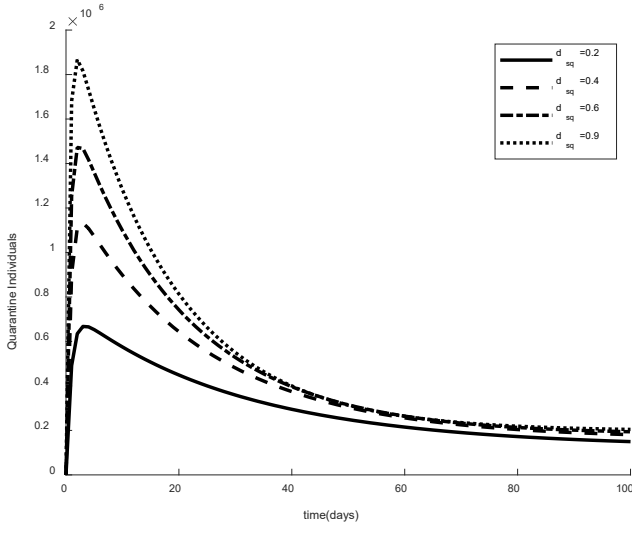

Figure 7. Simulation showing the impact of vaccination on the quarantine individuals

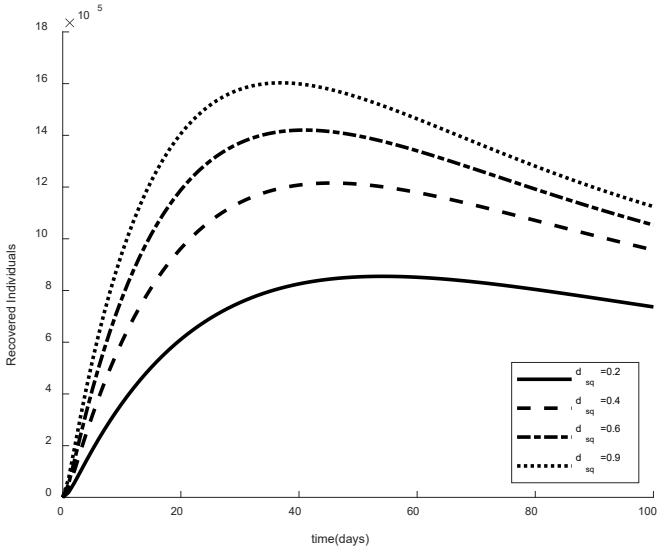

Figure 8. Simulation showing the impact of vaccination on the recovered individuals

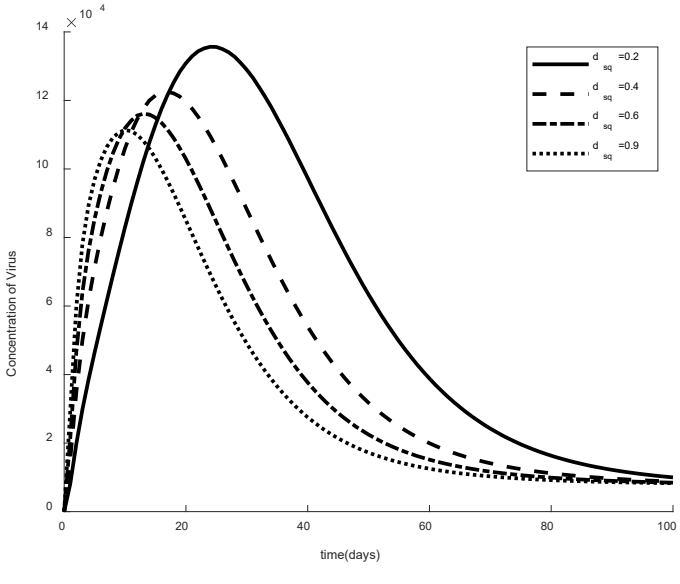

Figure 9. Simulation showing the impact of vaccination on the environment reservoir

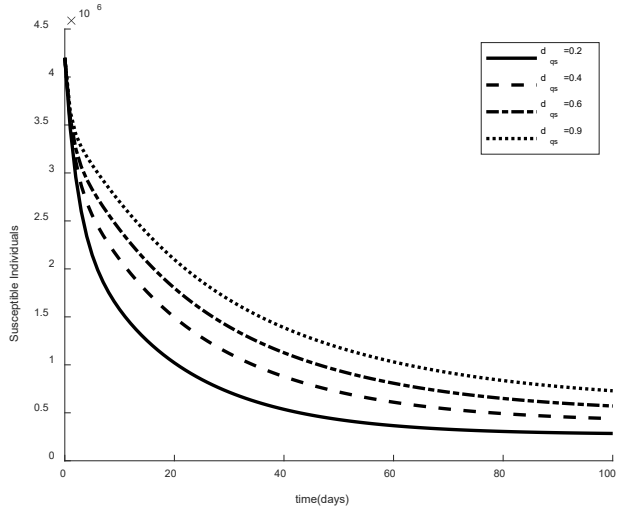

Figure 10. Simulation showing the impact of incomplete vaccination on the susceptible individuals

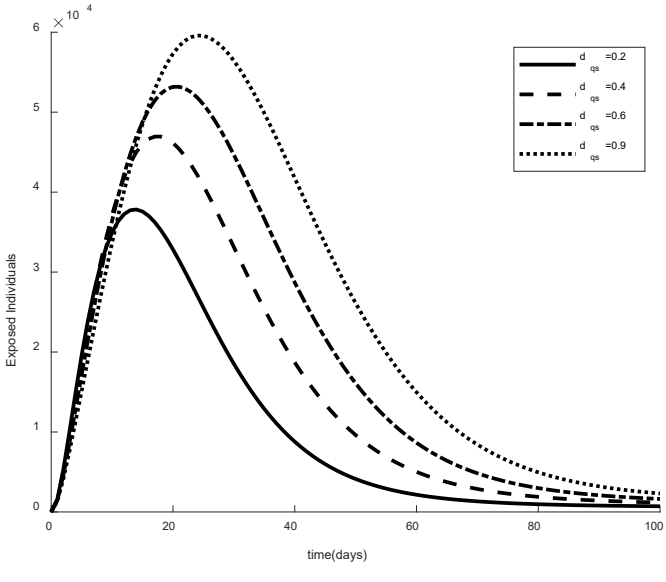

Figure 11. Simulation showing the impact of incomplete vaccination on the exposed individuals

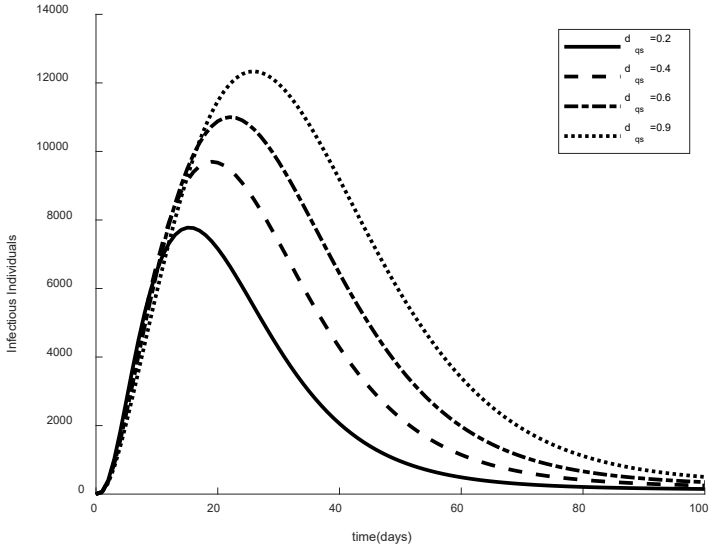

Figure 12. Simulation showing the impact of incomplete vaccination on the infectious individuals

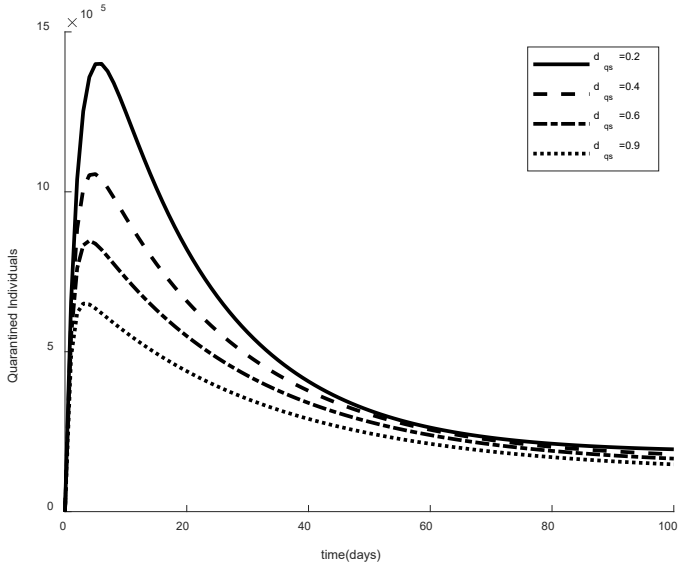

Figure 13. Simulation showing the impact of incomplete vaccination on the quarantine individuals

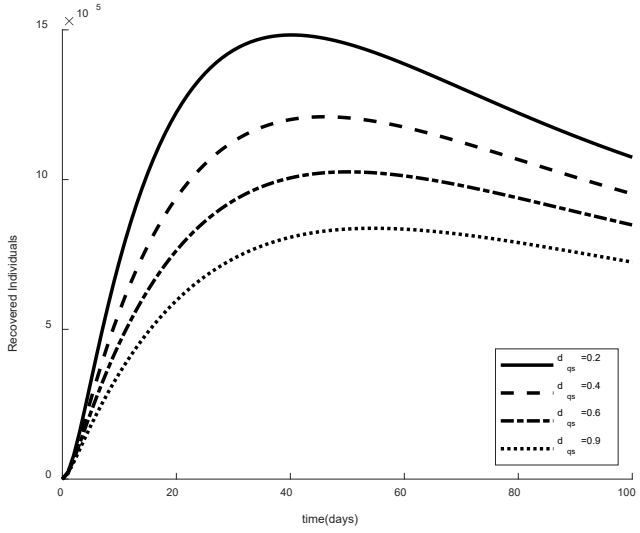

Figure 14. Simulation showing the impact of incomplete vaccination on the recovered individuals

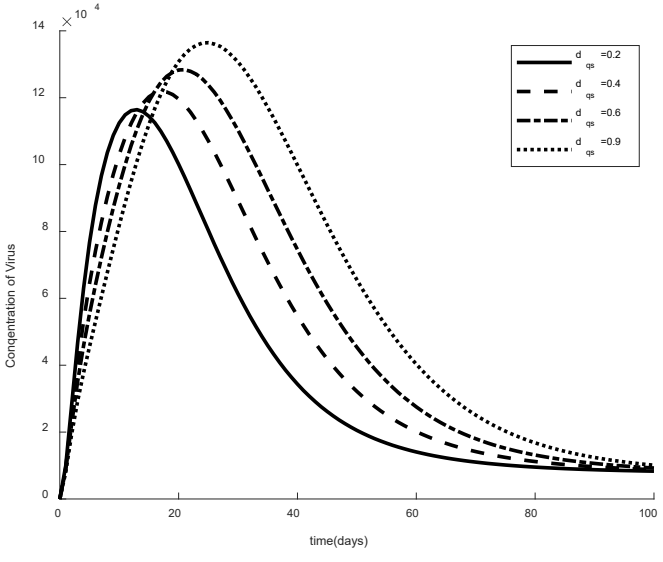

Figure 15. Simulation showing the impact of incomplete vaccination in the environmental reservoir

Results and Discussion

In the present study, we have introduced the SEIQRV transmission model, which incorporates the pathways of transmission from the environment to humans and from humans to humans. In order to simulate the model, data from Nigeria was used, as seen in Table 1. The rates used in this study are 0.2, 0.4, 0.6, and 0.9, which correspond to percentages of 20%, 40%, 60%, and 90% respectively. Figure 4 illustrates a simulation plot that depicts the effect of vaccination on susceptible people at several vaccination rates, namely $d_{sq} = 0.2, 0.4, 0.6,$ and 0.9. There is a correlation between the rate of vaccination and the number of persons exiting the compartment for the purpose of vaccination. Consequently, there is a decrease in the population size inside the compartment. However, a reversal of this trend is noticed in Figure 10. Figure 10 depicts a simulation plot that showcases the impact of incomplete COVID-19 dosage with rates (d_{qs}) at various levels: 0.2, 0.4, 0.6, and 0.9. It has been noticed that the number of persons increases when people fail to complete their prescribed dose.

Figures 5 and 6 depict the simulation plot illustrating the influence of vaccination on the populations of exposed and infectious individuals, with varying vaccination rates of $d_{sq} = 0.2, 0.4, 0.6,$ and $0.90.9$, respectively. Similarly, Figures 11 and 12 present the impact of incomplete vaccination on the populations of exposed and infectious individuals, with rates of $d_{qs} = 0.2, 0.4, 0.6$, and 0.9, respectively. Figures 5 and 6 illustrate a decline in the population inside these compartments, which may be attributed to an increase in the vaccination rate among people. This demonstrates that the implementation of vaccinations may significantly decrease the frequency of interactions between susceptible persons and those who are exposed or infectious, resulting in a notable reduction in infection rates. However, the phenomenon described in Figures 11 and 12, which illustrate an increase in the population of exposed and infected persons due to a corresponding increase in infection rates.

Figures 7 and 8 depict the simulation plot illustrating the influence of vaccination on the populations of quarantined and recovered individuals, with varying vaccination rates $(d_{sq} = 0.2, 0.4, 0.6, 0.9)$. Similarly, Figures 13 and 14 provide a description of the impact of incomplete vaccination on the populations of quarantined and recovered individuals, also considering the rates $(d_{qs} = 0.2, 0.4, 0.6, 0.9)$. The observed data in Figures 7 and 8 indicate a notable rise in the population size inside these compartments. This increase is attributed to a corresponding increase in the rate of vaccination among people. Due to the observed rise in vaccination rates, there has been a corresponding increase in the population of vaccinated persons inside the quarantine compartment, thereby leading to an upsurge in the number of individuals who have successfully recovered from the illness. A reversal of

the aforementioned trend is seen in Figures 13 and 14, whereby a decrease in the population sizes of the quarantine and recovered compartments is noted. This suggests that a significant proportion of people die prior entering these compartments. Nevertheless, it is shown in Figure 9 that an increase in vaccination rates leads to a decrease in pathogen concentration inside environmental reservoirs. Conversely, Figure 15 demonstrates that insufficient dose of the COVID-19 vaccine tends to increase the number of pathogens present in these reservoirs. The presence of a significant population of persons with inadequate dose has been identified as a contributing factor to the proliferation of these diseases in environmental reservoirs.

Table 1 presents the basic reproduction number and the respective contributions from persons who are exposed, infected, and quarantined. The data indicates that persons who are exposed demonstrate a higher level of contribution, followed by those who are isolated, and lastly, individuals who are infectious. Persons who are asymptomatic yet infected with the illness have the potential to spread it in public settings. Despite being without symptoms, these persons may freely move about in their surroundings. The primary determinant for the impact of the basic reproduction number on persons in quarantine compartment is the medical practitioner. The healthcare professional becomes infected by a confirmed patient and then transmits the infection to additional patients with unrelated conditions, either via negligence or unintentionally. Finally, the persons who are infected but not yet showing symptoms contribute more than those who are unwell and unable to move about due to their illness.

Table 1 presents the sensitivity analysis results for the parameters in the model. The primary objective is to investigate the degree of sensitivity shown by a model in response to variations in both its parameter values and structural configuration. According to the data shown in Table 1, it can be seen that the sensitivity index for $\Phi = +1$ indicates a positive relationship between Φ and R_0. Specifically, a rise in Φ will result in a proportional increase in R_0. Likewise, a reduction in the value of Φ will result in a corresponding drop in the value of R_0. Therefore, the variable Φ exhibits a direct relationship with the values of R_0, R_E, R_I, and R_C. Similarly, it can be noted from Table 1 that the variables $\beta_E, \beta_I, \beta_Q, h_1, h_2$, and h_3 exhibit a direct proportionality with R_0. Additionally, the sensitivity index for d_{sq} is calculated to be -0.95648. This indicates that an increase in d_{sq} will result in a proportional drop in the basic reproduction number (R_0). Likewise, an augmentation in the value of d_{sq} will result in a reduction in the value of R_0. Therefore, the variable d_{sq} exhibits an inverse relationship with the variables R_0, R_E, R_I, and R_C. The variables $d_{eq}, \gamma, \mu, \mu_v, d_{qr}, d_{iq}, \phi_Q, \phi_I$, and $d_{qs}d_{qs}$ exhibit an inverse relationship with R_0, as shown by the data presented in Table 1.

Conclusion

The present study investigated the transmission dynamics of COVID-19 by the use of a deterministic model consisting of systems of ordinary differential equations. The model incorporates persons who are susceptible, exposed, infectious, quarantined, and recovered, as well as the concentration of pathogens in the environmental reservoir. The efficacy of COVID-19 vaccination in mitigating the transmission of the virus was further examined by the use of numerical simulation. The impact of the model's parameters on the basic reproduction number, as well as the evaluation of the parameters' sensitivity, was also conducted. Based on the research results, a high vaccination rate has the potential to decrease the rate of interactions between suusceptible individuals and those who are exposed or infectious. Consequently, this reduction in contact rates would contribute to a decrease in the overall infection rate. As a result, there is a decrease in the population's exposure and infection rates, leading to a rise in the number of persons undergoing quarantine and seeking medical care. Therefore, the synergistic impact of implementing a successful vaccination strategy using a non-waning vaccine and ensuring full completion of COVID-19 vaccination will provide a more substantial outcome. This approach would effectively decrease infection rates among the human population and mitigate the contribution of people to the environmental reservoir. This will result in the expeditious elimination of COVID-19. This study highlights the importance of implementing a robust vaccination strategy that includes the use of a long-lasting vaccine with no waning efficacy. Additionally, it emphasises the significance of ensuring compliance with the recommended vaccination schedule. This can be accomplished through the implementation of educational campaigns and raising public awareness regarding the necessity of receiving the complete vaccine dosage. It is crucial to emphasise that incomplete vaccination poses a significant risk to both the community and the nation as a whole. This intervention will significantly contribute to mitigating the transmission of the COVID-19 virus.

REFERENCES

CHEN, T., RUI, J., WANG, Q., ZHAO, Z., CUI, J., & YIN, L., 2020. A mathematical model for simulating the phase-based transmissibility of a novel coronavirus. *Infectious Diseases of Poverty.* vol. 9, no. 24. https://doi.org/10.1186/s40249-020-00640-3.

COUNTRYMETERS. Nigeria Population 2020 live. Online: https://countrymeters.info/en/Nigeria.

DANIEL, D. O., 2020. Mathematical Model for the Transmission of COVID-19 with Nonlinear Forces of Infection and the Need for Prevention Measure in Nigeria. *Journal of Infectious Diseases and Epidemiology.* vol. 6, no. 5, p. 158.

EMORINKEN, M., 2020. "BREAKING: COVID-19: NCDC confirms one new case in FCT" (https://thenationonlineng.net/breaking-covid-19-ncdc-confirms-one-new-case-in-fct). *The Nation Newspaper*. Retrieved 22 September 2020.

EMORINKEN, M., 2020. "UPDATED: Nigeria records 10 new positive cases of COVID-19" (https://thenationonlineng.net/updated-nigeria-records-10-new-positive-cases-of-covid-19). *The Nation Newspaper.* Retrieved 21 September 2023.

European Centre for Disease Prevention and Control 2020. Disease background of COVID-19. www.ecdc.europa.eu/en/2019-ncov-background-disease. (accessed 12.09.23)

IBOI, E. A., SHAROMI, O. O., NGONGHALA, C. N., & GUMEL, A. B., 2020. Mathematical Modeling and Analysis of COVID-19 Pandemic in Nigeria. *Mathematical Biosciences and Engineering*. vol. 17, pp. 7192 – 7220. https://doi.org/10.3934/mbe.2020369.

INDEX MUNDI. Nigeria death rate- Demography. www.indexmundi.com/nigeria/death_rate.html (accessed 12.09.23)

KUCHARSKI, A.J., RUSSELL, T.W., DIAMOND, C., LIU, Y., | EDMUNDS, J., FUNK, S., & EGGO, R.M., 2020. Early dynamics of transmission and control of COVID-19: a mathematical modelling study. *Lancert Infect Dis*. https://doi.org/10.1016/s1473-3099(20)30144-4.

MURRAY, J.D., 2001. Mathematical Biology I: An introduction. 3rd Edition. Berlin, Heidelberg: Springer-Verla.

LI, Q., GUAN, X., WU, P., WANG, X., ZHOU, L., & TONG, Y. 2020. Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia. *New England Journal of Medicine* https://doi.org/10.1056/NEJMoa2001316.

LIN, Q., ZHAO, S., GAO, D., LOU, Y., YANG, S., MUSA, SS, WANG, M. H., CAI, Y., WANG, W., YANG, L., & HE, D., 2020. A conceptual model for the coronavirus disease 2019 (COVID-10) outbreak in Wuhan, China with individual reaction and governmental action. *International Journal of Infectious Diseases.* vol. 93, pp. 211 – 216. https://doi.org/10.1016/j.ijid.2020.02.058.

NIGERIA CENTRE FOR DISEASE CONTROL, 2020. First case of Corona virus disease in Nigeria. Accessed 12th Sept., 2023. Online: http://covid19.ncdc.gov.ng/news/227/first-case-of-corona-virus-disease-confirmed-in-nigera (accessed 12.09.23).

NIGERIA CENTRE FOR DISEASE CONTROL, 2020. NCDC Coronavirus COVID-19 Microsite, 2020. Online: http://covid19.ncdc.gov.ng (accessed 14.09.23).

OHIA, C., BAKAREY, A.S., & AHMAD, T., 2020. COVID-19 and Nigeria: Putting the realities in context, *International Journal of Infectious Diseases*. vol. 95, pp. 279 – 289. http://doi.org/10.1016/j.ijid.2020.04.062.

OKHUESE V.A., 2020. Mathematical predictions for COVID-19 as a global pandemic. medRxiv. https://doi.org/10.1101/2020.03.19.20038794.

ONITILO, S. A., USMAN, M. A., ODETUNDE, O. S., HAMMED, F. A., OGUNWOBI, Z. O., HARUNA, H. A., & DANIEL, D O., 2020. Mathematical modeling of 2019 novel Coronavirus (2019 – NCOV) Pandemic in Nigeria. *Chemistry: Bulgarian Journal of Science Education*. vol. 29, no. 3, pp. 398 – 413.

ONITILO, S. A., DANIEL, D. O., & HARUNA, H. A., 2021. Modeling analysis of coronavirus epidemic in Nigeria using Lyapunov functions. *FUW Trends in Science & Technology Journal*. vol. 6, no 2, pp. 627 – 632.

ONITILO, S. A., & DANIEL, D. O., 2022. Mathematical Modeling and Simulation of Coronavirus (COVID-19) in Lagos State, Nigeria. *Çankaya University Journal of Science and Engineering*, vol. 19, no. 2, pp. 078 – 094.

ONYEDIKA-UGOEZE, N., 2023. "Nigeria's coronavirus cases now 40" (https://guardian.ng/breakingnews/nigerias-coronavirus-toll-cases-now-40). *The Guardian Newspaper.* Retrieved 24 September 2023.

OYELEKE, S., 2020. "UPDATED: 10 dead as Nigeria's coronavirus cases rise to 318" (https://punchng.com/breaking-nige ria-records-13-new-cases-total-now-318). *The Punch Newspaper.* Retrieved 11 September, 2023

OYELEKE, S., 2020. "UPDATED: Italian who brought coronavirus to Nigeria discharged" (https://punchng.com/breaking- italian-who-brought-coronavirus-to-nigeria-discharged). *The Punch Newspaper*. Retrieved 21 September 2023.

TUITE, A.R., FISMAN, D. N., & GREER, A. L., 2020. Mathematical modeling of COVID-19 transmission and mitigation strategies in the population of Ontario. Canada. *medRxiv*. https://doi.org/10.1101/2020.03.24 .20042705.

WEISS, S. & NAVAS-MARTIN, S., 2005. Coronavirus pathogenesis and the emerging pathogen severe acute respiratory syndrome Coronavirus. *Microbiology and Molecular Biology Reviews*. vol. 69, no. 4, pp. 635 – 664. https://doi.org/10.1128/mmbr.69.4.635-664.2005

World Health Organization, 2020 Q&A: Influenza and COVID-19-similarities and differences. Online: https://www.who.int/emergencies//diseases/novel-coronavirus-2019/question-and-answers-hub/q-a-detail/q-a-similarities-and-differences-covid-19-and-influenza (accessed 12.09.2023).

World Health Organization, 2020. Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19). Online: https:www.who.int/publications-detail/report-of-the-who-china-joint-mission-on-coronavirus-disease-2019-(covid-19) (accessed 12.09.23).

World Health Organization, 2020. WHO characterized COVID-19 as a pandemic. Online: http://www.who.int/dg/speeces/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---11-march-2020 (accessed 12.09.2023).

YANG, C., & WANG, J. A., 2020. Mathematical model for the novel coronavirus epidemic in Wuhan, China. *AIMS Mathematical Biosciences and Engineering*. http://www.aimspress.com/journal/MBE.

ZHU, N., ZHANG, D., WANG, W., LI, X., YANG, B., & SONG, J., 2019. A novel coronavirus from patients with pneumonia in China. *New England Journal of Medicine.* https://doi.org/10.1056/nejmoa2001017

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