A SEIR Model of COVID-19 to Study the Effect of Vaccination

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Abstract: **In this work, we analyse and suggest a generalized mathematical model to comprehend the effects of vaccination on COVID-19 transmission. Susceptible (*S*), vaccinated (*V*), exposed (*E*), symptomatically infected (I_S), asymptomatically infected (*Ia*), quarantined (*Q*), and recovered (*R*), are the seven compartmental classifications introduced. Using the next-generation matrix technique, the fundamental reproduction number (abbreviated R_0) of the suggested model was calculated. The findings indicate that the disease-free equilibrium (DFE) is globally asymptotically stable for $R_0 < 1$. The model's mathematical analysis is bolsteredby computational modelling. Furthermore, the numerical outcomes demonstrate that proper implementation of vaccination would contribute significantly to limiting the COVID-19 epidemic or any pandemic situation.**

Keywords: Covid-19 Pandemic, Mathematical Modelling, SEIR Model, Vaccination.

INTRODUCTION

The new coronavirus SARS-CoV-2 is the cause of the COVID-19 pandemic, which has become one of the worst worldwide health emergencies of our time. The virus first appeared in late 2019 and has since spread to other continents, causing disease, fatalities, and social unrest in its wake. In addition to immediately endangering public health, the pandemic has spurred an unprecedented amount of study to better understand the virus, the dynamics of its transmission, and the efficacy of several intervention approaches. Mathematical models have proven to be important tools in understanding the disease's transmission, assessing the effectiveness of public health treatments, and projecting possible future scenarios in the face of this unprecedented problem. Compartmental modelling is one such modelling technique that has grown in popularity while discussing the dynamics of infectious diseases. These models employ a series of equations to characterise the transitions between discrete compartments, each of which represents a separate state of health or stage of disease. These models offer a formal framework for researching disease dynamics, forecasting outcomes, and guiding policy choices by including epidemiological parameters. The novel coronavirus disease (COVID-19) is a contagious disease that started spreading throughout the world [1, 2] in December 2019, and still it is showing its fatal effects globally. The world has experienced severe coronavirus attacks many times, caused by SARS-CoV [3], MERS-CoV [4, 5, 6, 7], and SARS-CoV-2 [8]. All coronavirus patients experience the same symptoms, including respiratory issues, fever, dry cough, etc. However, COVID-19 is more contagious than its predecessors [8]. Many countries were affected by this disease. As a high number of people moved from one countryto another, the disease spread mostly through them via air travel [9, 10, 11]. WHO issued warnings to all countries about screening individuals at both ends of the country (at the border) and upon entry (in order to stop the spread of the disease).

After April 5, 2020 Covid 19 had spread in every country and each country has experienced severe suffering by this disease. A number of people got infected by covid 19 and many of them were sent quarantine stage to cease the spread of this virus. Since exposed and asymptomatic persons were not showing the symptoms of the disease therefore they were more responsible for spreading the disease. Due to the limited medical facilities in most countries and a large number of infections the test of confirmation of disease is low. This fact also increases the number of infected populations [12]. The only approach to

stop the transmission of sickness is to reduce social contact and interaction among people because the disease spreads through interaction and there is still no effective treatment of the same. The Chinese government implemented a lockdown program to maintain social distancing and was able to stop the disease's spread. Every country, except for a few, followed the policy until the invention of vaccines and their availability on a large scale.

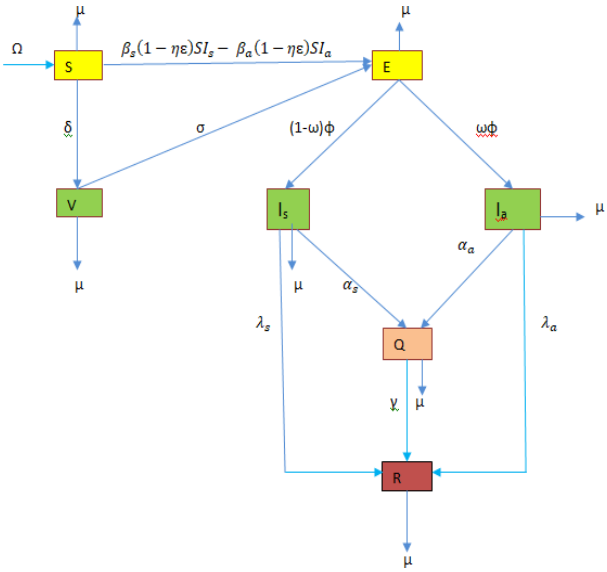

Figure 1. Flowchart related to the Model

Scientists have been looking for ways to lower the transmission and death rates since the outbreak. Herd immunity and vaccination are just two of the many solutions for the disease to disappear over time. It has been claimed that vaccines for viruses significantly improve global health [13]. The most successful method of preventing influenza infection, which shares many similarities with Covid-19, is vaccination [14].

Three goals are pursued by this study: first, to improve our comprehension of the dynamics of COVID-19; second, to assess the efficacy of various control approaches; and third, to offer significant insights to help policy and decision-makers. As part of the continuing worldwide effort to contain the epidemic, we aim to participate by building a strong and flexible compartmental model. This study aims to give a clear and complete explanation of the disease's progression within communities by presenting a comprehensive compartmental model for the COVID-19 pandemic. The model allows for the examination of multiple scenarios and their consequences for public health by incorporating a number of significant parameters, such as population characteristics, intervention methods, illness progression rates, and transmission rates. Section 2 of this paper represents the formulation of the mathematical model, section 3 elaborates the analysis of the model, stability analysis is presented in section 4, section 5 focuses on the numerical simulation. Finally, section 6 states the concluding remarks on the present work.

MODEL FORMULATION

The investigations of [15, 16] served as inspiration for the mathematical model of Covid-19 transmission that was developed in this work with the goal of generalisation. In the present study, the total population is divided into seven compartments. The total population is denoted by $N(t)$ at any time, whereas the seven epidemiological compartments are susceptible ($S(t)$) (the individuals who are not infected by the disease but can catch the disease), exposed

population ($E(t)$) (individuals who are infected by the disease but not yet infectious), vaccinated population ($V(t)$) (class of individuals who are vaccinated), infected and symptomatic ($I_s(t)$) (individuals show clinical symptoms of covid-19 infection), infected asymptomatic ($I_a(t)$) (individuals infected but they have no visible clinical symptoms), quarantined ($Q(t)$) (individuals who are quarantined), and recovered compartment ($R(t)$) (individuals recovered from either asymptomatic or symptomatic class). The disease-induced death rate is neglected in this study [17].

$$
\begin{aligned}
\frac{dS}{dt} &= \Omega - \beta_S(1-\eta\varepsilon)SI_S - \beta_a(1-\eta\varepsilon)SI_a - \mu S - \delta S \\
\frac{dS}{dt} &= \beta_S(1-\eta\varepsilon)SI_S - \beta_a(1-\eta\varepsilon)SI_a - \mu E - \omega\phi E - (1-\omega)\phi E + \beta_S\sigma VI_S + \beta_a\sigma VI_a \\
\frac{dI_S}{dt} &= (1-\omega)\phi E - \alpha_S I_S - \lambda_S I_S - \mu I_S \\
\frac{dI_a}{dt} &= \omega\phi E - \alpha_a I_a - \lambda_a I_a - \mu I_a \qquad (1) \\
\frac{dQ}{dt} &= \alpha_S I_S + \alpha_a I_a - \gamma Q - \mu Q \\
\frac{dR}{dt} &= \lambda_S I_S + \lambda_a I_a + \gamma Q - \mu R \\
\frac{dV}{dt} &= \delta S - \beta_S\sigma VI_S - \beta_a\sigma VI_a - \mu V
\end{aligned}
$$

Now since the total population is

$$N(t) = S(t) + E(t) + I_S(t) + I_a(t) + Q(t) + R(t) + V(t)$$

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI_S}{dt} + \frac{dI_a}{dt} + \frac{dQ}{dt} + \frac{dR}{dt} + \frac{dV}{dt}$$

$$\frac{dN}{dt} = \Omega - \mu\left(S + E + I_S + I_a + Q + R + V\right)$$

$$\frac{dN}{dt} = \Omega - \mu N \qquad (2)$$

$$0 \le N \le \frac{\Omega}{\mu}$$

The depicted model represents the interactions between the total population, and hence the variables can be considered to be non-negative for $t \geq 0$ and that the solutions of the demonstrated model will remain positive for $t \geq 0$. Because of this, our model is mathematically well-posed and can be used further to study its dynamics.

$$\Lambda = \left\{S, E, I_S, I_a, Q, R, V \in R_+^7 : S + E + I_S + I_a + Q + R + V \le \frac{\Omega}{\mu}\right\} \quad (3)$$

TABLE 1. Notations are used to indicate compartments and their meanings.

Variables in the model	Meaning
S	Susceptible population
E	Exposed population
I_S	Symptomatically infectious population
I_a	Asymptomatic but infectious population
Q	Quarantined population
R	Recovered compartment
V	Vaccinated Population

ANALYSIS OF MODEL

In this section, we presented the qualitative study of the above-described model (1).

TABLE 2. Parameters used in the study and their meanings.

Model Parameters	Meaning of the notations
Ω	The inclusion rate into the compartment of a susceptible population
β_S	The effective contact rate of S with I_S
β_a	Effect of social distancing
η	The proportion of the population who use mask
ε	Efficacy of masks
$1-\omega$	A fraction of the exposed population shows clinical symptoms
φ	Rate of progression from exposed to infectious compartment
α_S	Isolation rate for individuals in the symptomatically infected compartment
α_a	The isolation rate of asymptomatically infectious
δ	Rate of vaccination
σ	Vaccine's inefficacy
γ	Average days until recovery
μ	Natural death rate
λ_a	Rate of recovery of asymptomatically infectious population
λ_S	Rate of recovery of symptomatically infectious

Positivity and boundedness of solution:

Theorem 1. If S(0), E(0), I_s(0), I_a(0), Q(0), R(0), and V (0) > 0, then the solutions (S(t), E(t), I_s(t), I_a(t), Q(t), R(t), and V (t)) of the model (1) are all positive for t > 0.

Proof. From the first equation of the group of equations (1), we have

$$\frac{dS}{dt} = \Omega - \beta_S\left(1-\eta\varepsilon\right)SI_S - \beta_a\left(1-\eta\varepsilon\right)SI_a - \mu S - \delta S$$

$$\frac{dS}{dt} \ge \beta_S\left(1-\eta\varepsilon\right)SI_S - \beta_a\left(1-\eta\varepsilon\right)SI_a - \mu S - \delta S \quad (4)$$

Using the variable separable method we get,

$$S\left(t\right) \ge S_0 e^{-\int_0^t \left(\beta_S\left(1-\eta\varepsilon\right)I_S - \beta_a\left(1-\eta\varepsilon\right)I_a - \mu - \delta\right)ds} > 0 \quad (5)$$

Since the initial value S_0 and the exponential functions in the above equation are always positive. Hence $S(t)$ is positive. Using the same idea to check other equations of the model (1), we get

$$E(t)>0, I_S(t)>0, I_a(t)>0, Q(t)>0, R(t)>0, and V(t)>0$$

Theorem 2. All positive solutions described in theorem 1 are also bounded.

Proof. By adding all the sub-equations of equation (1) we get

$$\frac{dN}{dt}=\Omega-\mu\left(S+E+I_S+I_a+Q+R+V\right)$$

$$\frac{dN}{dt}=\Omega-\mu N(t) \qquad (6)$$

Which can be written as

$$N(t)=\frac{\Omega}{\mu}-\left[\frac{\Omega-\mu N_0}{\mu}\right]e^{-\mu t} \qquad (7)$$

from above equation $N(t)\to\frac{\Omega}{\mu}$ as $t\to\infty$. Hence, solutions of model (1) are bounded.

Equilibrium points of the depicted Model:

By setting the right-hand side of all equations of the model (1) to zero, the equilibrium points are obtained as

$$\begin{aligned}
&\Omega-\beta_S(1-\eta\varepsilon)SI_S-\beta_a(1-\eta\varepsilon)SI_a-\mu S-\delta S=0\\
&\beta_S(1-\eta\varepsilon)SI_S-\beta_a(1-\eta\varepsilon)SI_a-\mu E-\omega\phi E-(1-\omega)\phi E+\beta_S\sigma VI_S+\beta_a\sigma VI_a=0\\
&(1-\omega)\phi E-\alpha_S I_S-\lambda_S I_S-\mu I_S=0\\
&\omega\phi E-\alpha_a I_a-\lambda_a I_a-\mu I_a=0 \qquad (8)\\
&\alpha_S I_S+\alpha_a I_a-\gamma Q-\mu Q=0\\
&\lambda_S I_S+\lambda_a I_a+\gamma Q-\mu R=0\\
&\delta S-\beta_S\sigma VI_S-\beta_a\sigma VI_a-\mu V=0
\end{aligned}$$

In the preceding sections, we consider the studies of disease-free equilibrium (DFEP) points and endemic equilibrium points (EEP).

Disease Free Equilibrium point (DFEP):

The disease-free state is introduced by the nonexistence of disease nodes. We denote DFEP by

$$X^0=\left(S^0,E^0,I_S^0,I_a^0,Q^0,R^0,V^0\right)$$

Where

$$S^0=\frac{\Omega}{(\mu+\delta)}$$

$$E^0=0$$

$$I_S{}^0=0$$

$$I_a{}^0=0$$

$$Q^0=0$$

$$R^0=0$$

$$V^0=\frac{\delta\Omega}{\mu(\mu=\delta)}$$

Endemic equilibrium point (EEP):

The endemic equilibrium point is considered based on the existence of the disease and is denoted by

$$X^*=\left(S^*,E^*,I_S^*,I_a^*,Q^*,R^*,V^*\right)$$

Where

$$S^*=\frac{\Omega}{\beta_S(1-\eta\varepsilon)I_S-\beta_a(1-\eta\varepsilon)I_a-\mu-\delta}$$

$$E^*=\frac{\beta_S(1-\eta\varepsilon)SI_S-\beta_a(1-\eta\varepsilon)SI_a+\beta_S\sigma VI_S+\beta_a\sigma VI_a}{(\phi+\mu)}$$

$$I_S^*=\frac{(1-\omega)\phi E}{(\alpha_S+\lambda_S+\mu)}$$

$$I_a^*=\frac{\omega\phi E}{(\alpha_a+\lambda_a+\mu)}$$

$$Q^*=\frac{\alpha_S I_S+\alpha_a I_a}{(\gamma+\mu)}$$

$$R^*=\frac{\lambda_S I_S+\lambda_a I_a+\gamma Q}{\mu}$$

$$V^*=\frac{\delta_S}{(\mu+\beta_S\sigma VI_S+\beta_a\sigma VI_a)}$$

The Basic Reproduction number:

The fundamental reproduction number of the described model is calculated using the next-generation matrix method. In this work, we provide the fundamental reproduction number of the model (1), which is referred to as the quantity of COVID-19 infections that result from a single COVID-19 disease infection. The vectors F (signifies a new infection) and V (signifies the movement of individuals between compartments) are provided as:

$$F=\begin{pmatrix}\beta_S(1-\eta\varepsilon)SI_S-\beta_a(1-\eta\varepsilon)SI_a+\beta_S\sigma VI_S+\beta_a\sigma VI_a\\0\\0\end{pmatrix}$$

$$V=\begin{pmatrix}(\phi+\mu)E\\-(1-\omega)\phi E+(\alpha_S+\lambda_S+\mu)I_S\\-\omega\phi E+(\alpha_a+\lambda_a+\mu)I_a\end{pmatrix}$$

Jacobians F and V are computed below:

$$F=\begin{pmatrix}0&\beta_S(1-\eta\varepsilon)S+\beta_S\sigma V&\beta_a(1-\eta\varepsilon)S+\beta_a\sigma V\\0&0&0\\0&0&0\end{pmatrix}$$

$$V=\begin{pmatrix}(\phi+\mu)&0&0\\-(1-\omega)\phi&(\alpha_s+\lambda_s+\mu)&0\\-\omega\phi&0&(\alpha_a+\lambda_a+\mu)\end{pmatrix}$$

Now, for DFEP (disease-free equilibrium point)

$$F=\begin{pmatrix}0&\beta_S(1-\eta\varepsilon)\frac{\Omega}{(\mu+\delta)}+\beta_S\sigma\frac{\delta\Omega}{\mu(\mu+\delta)}&\beta_a(1-\eta\varepsilon)\frac{\Omega}{(\mu+\delta)}+\beta_a\sigma\frac{\delta\Omega}{\mu(\mu+\delta)}\\0&0&0\\0&0&0\end{pmatrix}$$

$$V=\begin{pmatrix}(\phi+\mu)&0&0\\-(1-\omega)\phi&(\alpha_s+\lambda_s+\mu)&0\\-\omega\phi&0&(\alpha_a+\lambda_a+\mu)\end{pmatrix}$$

Hence computing the Jacobian matrices F and V, the basic reproduction number of the model is given by

$$R_0=\rho\left(FV^{-1}\right)=\frac{\phi S^0}{(\phi+\mu)}\left[\frac{\beta_S(1-\eta\varepsilon)(1-\omega)}{(\alpha_s+\lambda_s+\mu)}+\frac{\beta_a(1-\eta\varepsilon)\omega}{(\alpha_a+\lambda_a+\mu)}\right]$$

$$+\frac{\sigma\phi V^0}{(\phi+\mu)}\left[\frac{\beta_s(1-\omega)}{(\alpha_s+\lambda_s+\mu)}+\frac{\beta_a\omega}{(\alpha_a+\lambda_a+\mu)}\right]$$

$$=\frac{\beta_S\phi(1-\omega)}{(\alpha_s+\lambda_s+\mu)(\phi+\mu)}\left((1-\eta\varepsilon)S^0+\sigma V^0\right)$$

$$+\frac{\beta_a\omega\phi}{(\alpha_a+\lambda_a+\mu)(\phi+\mu)}\left((1-\eta\varepsilon)S^0+\sigma V^0\right)$$

$$=\left((1-\eta\varepsilon)S^0+\sigma V^0\right)\left[\frac{\beta_S\phi(1-\omega)}{(\alpha_s+\lambda_s+\mu)(\phi+\mu)}+\frac{\beta_a\omega\phi}{(\alpha_a+\lambda_a+\mu)(\phi+\mu)}\right] \quad (9)$$

STABILITY ANALYSIS

Local Stability

(Disease Free Equilibrium Point DFEP)

Theorem 3. If $R_0 < 1$, the disease-free equilibrium $\left(S^0=\frac{\Omega}{(\delta+\mu)},0,0,0,0,0,V^0=\frac{\delta\Omega}{\mu(\delta+\mu)}\right)$ of the system 1 is locally asymptotically stable in the region F.

Proof. At the disease-free equilibrium point $\left(S^0=\frac{\Omega}{(\delta+\mu)},0,0,0,0,0,V^0=\frac{\delta\Omega}{\mu(\delta+\mu)}\right)$, the Jacobian matrix is

$$\begin{pmatrix}-\mu-\delta&0&-\beta_S(1-\eta\varepsilon)\frac{\Omega}{(\mu+\delta)}&-\beta_a(1-\eta\varepsilon)\frac{\Omega}{(\mu+\delta)}&0&0&0\\0&-\phi-\mu&\beta_S(1-\eta\varepsilon)\frac{\Omega}{(\mu+\delta)}+\beta_S\sigma\frac{\delta\Omega}{\mu(\mu+\delta)}&\beta_a(1-\eta\varepsilon)\frac{\Omega}{(\mu+\delta)}+\beta_a\sigma\frac{\delta\Omega}{\mu(\mu+\delta)}&0&0&0\\0&(1-\omega\phi)&-(\alpha_s+\lambda_s+\mu)&0&0&0&0\\0&\omega\phi&0&-(\alpha_a+\lambda_a+\mu)&0&0&0\\0&0&\alpha_S&\alpha_a&-\gamma-\mu&0&0\\0&0&\lambda_S&\lambda_a&\gamma&-\mu&0\\\delta&0&-\beta_S\sigma\frac{\delta\Omega}{\mu(\mu+\delta)}&-\beta_a\sigma\frac{\delta\Omega}{\mu(\mu+\delta)}&0&0&-\mu\end{pmatrix}$$

where the eigenvalues are given by

$$\lambda_1=-\mu-\delta,$$
$$\lambda_2=-\phi-\mu,$$
$$\lambda_3=-\alpha_S-\lambda_S-\mu,$$
$$\lambda_4=-\alpha_a-\lambda_a-\mu,$$
$$\lambda_5=-\gamma-\mu,$$
$$\lambda_6=-\mu,$$
$$\lambda_7=-\mu,$$

Thus, all Eigenvalues have negative real parts. Therefore, by Routh-Hurwitz's criterion of stability, system 1 is locally asymptotically stable at disease-free equilibrium points.

Global Stability Analysis of DFEP

To prove the global stability of the disease-free equilibrium, the Lyapunov function below is constructed:

$$L = B_1E + B_2I_S + B_3I_a$$

where

$$B_1 = (\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)$$

$$B_2 = (\alpha_a + \lambda_a + \mu)\beta_S(1-\eta\varepsilon)S$$

$$B_3 = (\alpha_s + \lambda_s + \mu)\beta_a(1-\eta\varepsilon)S$$

$$\frac{dL}{dt} = B_1\frac{dE}{dt} + B_2\frac{dI_s}{dt} + B_3\frac{dI_a}{dt}$$

$$\frac{dL}{dt} = B_1\left[\beta_S(1-\eta\varepsilon)SI_S - \beta_a(1-\eta\varepsilon)SI_a - (\phi+\mu)E + \beta_S\sigma VI_S + \beta_a\sigma VI_a\right]$$

$$+B_2\left[(1-\omega)\phi E - (\alpha_s + \lambda_s + \mu)I_S\right]$$

$$+B_3\left[\omega\phi E - (\alpha_a + \lambda_a + \mu)I_a\right]$$

$$\frac{dL}{dt} = (\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)$$

$$\left[\beta_S(1-\eta\varepsilon)SI_S - \beta_a(1-\eta\varepsilon)SI_a - (\phi+\mu)E + \beta_S\sigma VI_S + \beta_a\sigma VI_a\right]$$

$$+(\alpha_a + \lambda_a + \mu)\beta_S(1-\eta\varepsilon)S\left[(1-\omega)\phi E - (\alpha_s + \lambda_s + \mu)I_S\right]$$

$$+(\alpha_s + \lambda_s + \mu)\beta_a(1-\eta\varepsilon)S\left[\omega\phi E - (\alpha_a + \lambda_a + \mu)I_a\right]$$

$$\frac{dL}{dt} = (\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)\beta_S(1-\eta\varepsilon)SI_S$$

$$+(\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)\beta_a(1-\eta\varepsilon)SI_a$$

$$-(\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)(\phi+\mu)E$$

$$+(\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)\beta_S\sigma VI_S$$

$$+(\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)\beta_a\sigma VI_a$$

$$+(\alpha_a + \lambda_a + \mu)\beta_S(1-\eta\varepsilon)S(1-\omega)\phi E$$

$$-(\alpha_a + \lambda_a + \mu)\beta_S(1-\eta\varepsilon)(\alpha_s + \lambda_s + \mu)SI_S$$

$$+(\alpha_s + \lambda_s + \mu)\beta_a(1-\eta\varepsilon)S\omega\phi E$$

$$-(\alpha_s + \lambda_s + \mu)\beta_a(1-\eta\varepsilon)(\alpha_a + \lambda_a + \mu)SI_a$$

$$\frac{dL}{dt} = (\alpha_a + \lambda_a + \mu)\beta_S(1-\eta\varepsilon)S(1-\omega)\phi E$$

$$+(\alpha_s + \lambda_s + \mu)\beta_a(1-\eta\varepsilon)S\omega\phi E$$

$$-(\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)(\phi+\mu)E$$

$$(\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)\frac{(1-\omega)\phi E}{(\alpha_s + \lambda_s + \mu)}\beta_S\sigma V$$

$$+(\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)\frac{\omega\phi E}{(\alpha_a + \lambda_a + \mu)}\beta_a\sigma V$$

$$\frac{dL}{dt} \le (\alpha_a + \lambda_a + \mu)(\alpha_s + \lambda_s + \mu)(\phi+\mu)[R_0 - 1]E \quad (10)$$

where R_0 is given by (9). Hence, $\frac{\partial L}{dt} \le 0$ if $R_0 \le 1$ and, $\frac{\partial L}{dt} = 0$ if E = 0. With the help of LaSalle's Principal, we can conclude the global asymptotic stability of the DFEP of model 1 provided $R_0 \le 1$.

RESULTS AND DISCUSSIONS

Numerical calculations are carried out to establish the analysis of model 1. The simulation is divided into three parts. The purpose of the first and second parts is to provide an example of the numerical interpretation of the endemic equilibrium and disease-free equilibrium points respectively. In the third part, we will examine how well model 1 fits actual data.

Below mentioned initial conditions are used in the simulation for endemic equilibrium points. Here we collected the data from March 2021 to July 2021 Covid19 cases in Madhya Pradesh, India from (http://www.covid19india. org)

$S(0) =$	72626809,
$I_s(0) =$	200,
$E(0) =$	0,
$I_a(0) =$	100,
$Q(0) =$	50,
$R(0) =$	0,
$V(0) =$	0

(11)

Values of each parameter used for the numerical calculations are provided in Table 3. Derived results are presented in Figures 2 - 4.

For a disease-free equilibrium situation, the infected population is missing in the whole population to outspread the infection to other classes of population (I_a = 0 and I_s = 0). So, no changes were observed in the exposed, quarantined and recovered population. As a result, 2 gives only significant results for the susceptible population.

Sub-figures of Figure 4 show the number of individuals in each compartment. We can observe an initial increase and then a gradual decrease in the number of the infected class when vaccination affects significantly reduces the spread of the pandemic and to reduce the number of infected populations drastically.

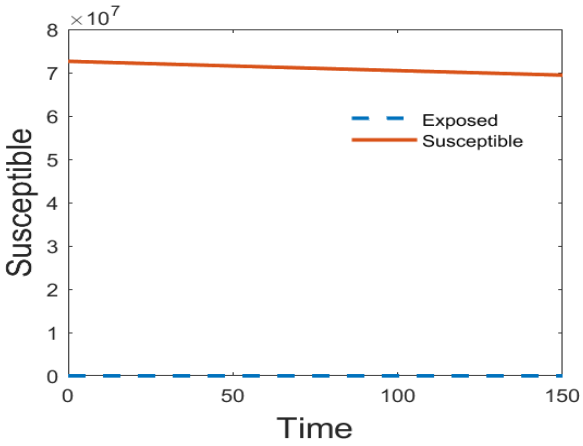

FIGURE 2. Results related to DFEP

In addition, the number of COVID-19 pandemic patients who have recovered and are in quarantine has increased. The image also shows that the pandemic's progress can be slowed down if the interventions are adhered to closely.

Three sub-figures of Figure 4 show how the change in vaccination rate will affect the susceptible and infected population. We have taken four different values of the vaccination rate (δ = 0, 0.005, 0.01, 0.05 and 0.1) into consideration and depicted the graphs for depicting the effect of the same of symptomatic, total infected and susceptible populations, respectively. We can observe that the number of susceptible and infected individuals decreases gradually with the increase in vaccination rate.

Parameters	Parametric values for EEP	Parametric values for DFEP	Source
Ω	4796.36	4796.36	[18]
βs	858×10^{-10}	150×10^{-13}	assumed
βa	343×10^{-10}	120×10^{-13}	assumed
η	0.1	0.1	[19]
ε	0.5	0.5	[19]
ω	0.5	0.5	[20]
φ	1/6	1/6	[21]
μ	178×10^{-7}	178×10^{-7}	[22]
αs	0.2	0.2	[23]
αa	0.2	0.2	[23]
γ	1/5.5	1/5.5	[24]
λa	1/10	1/10	[20]
λs	1/10	1/10	[20]
δ	0.00035	0.00035	[25]

TABLE 3. Parametric values used for numerical simulation of the DFEP and EEP

CONCLUSION

In order to comprehend the dynamics of the COVID-19 pandemic (or any pandemic caused by infectious diseases),a generalised nonlinear mathematical model was put out and examined in this work. It was calculated what the equilibrium points for the developed model are. The fundamental reproduction number indicated as pertaining to the model was also estimated using the next generation matrix technique. Additionally, this investigation demonstrated that the pandemic will end if the BRN is designated as $R_0 < 1$. On the other hand, the pandemic will persist in the population if $R_0 > 1$. Furthermore, it has been demonstrated that the equilibrium point for the disease-free states are globally asymptotically stable, the global asymptotic stability of EEP can also be proved using Lyapunov asymptotic stability theorem.

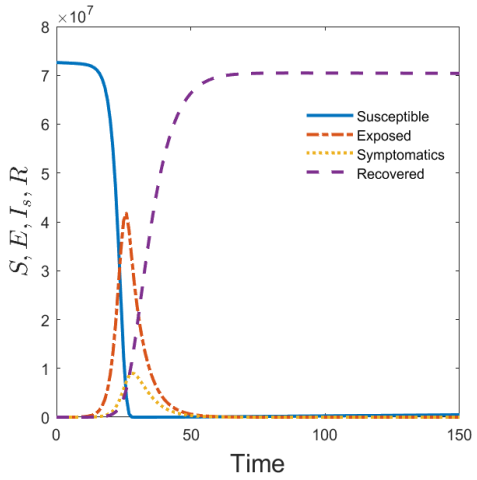

FIGURE 3(a). Numerical results related to the EEP

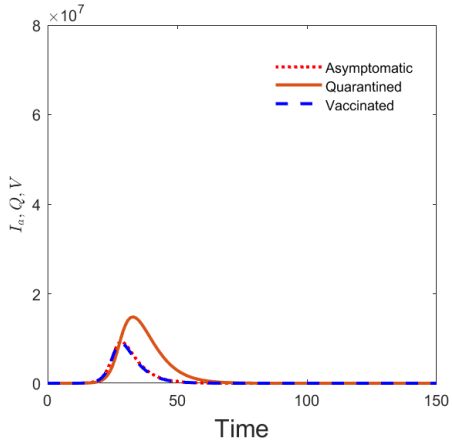

FIGURE 3(b). Numerical results related to the EEP

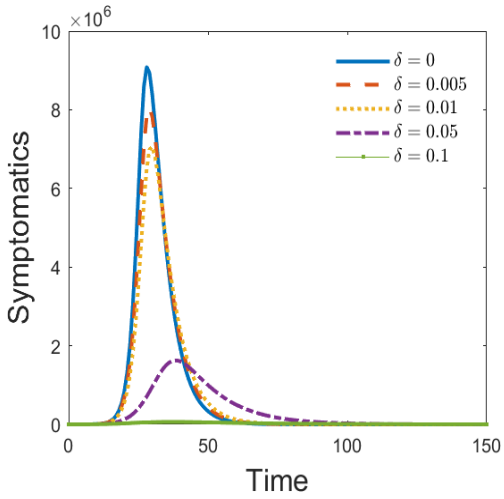

FIGURE 4 (a). Numerical results of the predicted cases of Symptomatic individuals,

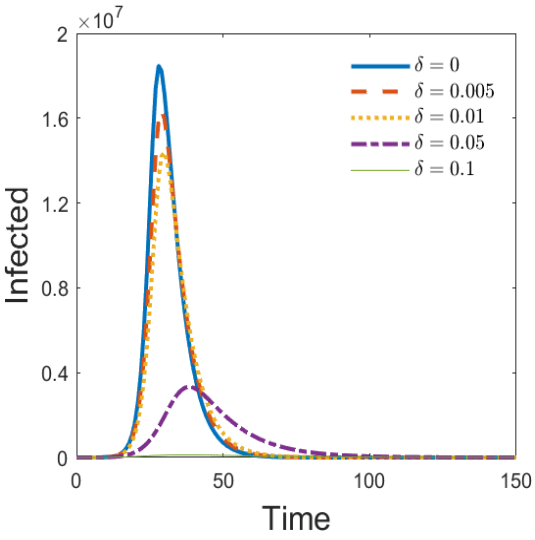

FIGURE 4 (b). Numerical results of the predicted cases of total Infected population

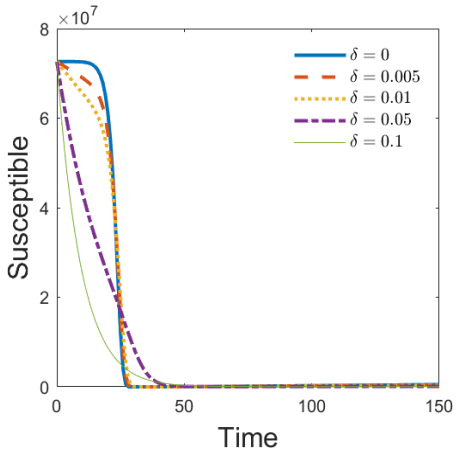

FIGURE 4 (c). Numerical results of the predicted cases of Susceptiblepopulation.

The model study was supported by numerical simulations. The model was also fitted to actual data in order to forecast real-world cases of infection in the community. This study also examined the various consequences of vaccination, and it concluded that sufficient rate of vaccination consistently and appropriately can stop the COVID- 19 pandemic or any such pandemic situation due to infectious disease from spreading. Research into a vaccine to stop the COVID-19 pandemic is producing very positive results. However, in any pandemic scenario, it takes a longtime for vaccines to be widely available in every

country on the earth. Therefore, using additional precautions (such wearing a mask) should be beneficial until immunisations are made available to everyone.

DATA AVAILABILITY

The data used to support the finding of this study are included within the article.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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