Research Article

Analysis of An SEIQRVS Epidemic Model for Corona Virus Infectious Disease

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Abstract: In this paper, a SEIQRVS epidemic infectious disease model is proposed and can simulate the process of COVID-19. The effect of the corona virus on infected individuals is shown. It is a well-known concept that the circulation of infectious diseases may be the reason of growing virus in the susceptible population. The increase in the death rate of the virus is one of the strategies to control infectious diseases. The proposed model system shall be explored to explain the growth and death rate of the virus in the susceptible population. It is shown that the model exhibits two equilibria, namely, the disease-free equilibrium and the endemic equilibrium. The global dynamics are completely determined by the basic reproduction number. If the basic reproduction number is less than 1, the disease-free equilibrium is globally stable which leads to the eradication of the disease from the population. If the basic reproduction number is greater than one, an endemic equilibrium exists and is globally stable in the feasible region under certain conditions. Finally, taking biologically relevant parametric values, numerical simulations are performed to illustrate and verify the analytical results. Normalized forward sensitivity indices are calculated for effective reproduction number, and state variables at endemic equilibrium on various parameters and respective sensitive parameters are identified.

Keywords: Epidemic model, Corona Virus Infectious Disease (COVID-19), Fundamental reproduction number, Global stability, Local stability, Sensitivity Analysis.

1. Introduction

Corona Virus features a place with a huge group of viruses like the severe acute respiratory syndrome (SARS), Middle East Respiratory Syndrome (MERS), cold, etc. On 31 December 2019, the WHO China Country Office was informed regarding cases of pneumonia obscure etiology (obscure reason) recognized in Wuhan City, Hubei Province of China. From 31 December 2019 through 3 January 2020, a sum of 44 case-patients with pneumonia of obscure etiology were accounted for to WHO by the national authorities in China. During this announced period, the causal specialist was not identified. On 11 and 12 January 2020, WHO got further detailed information from the National Health Commission China that the outbreak is said with exposures in one seafood market in Wuhan City. The Chinese authorities identified a replacement sort of corona virus, which was isolated on 7 January 2020. And now, this novel viral infection, Corona viral infection disease, named as (COVID-19), may be a new strain of viral infection that's causing havoc not only in China but also elsewhere within the world [1, 2, 3, 4, 5].

In human history, there are many other outbreaks and spread of diseases such as dengue fever, malaria, influenza, plague, and HIV/AIDS. How to establish appropriate epidemiological models for these epidemics is a difficult task [6]. Some scientists view disease transmission as a complex network for prediction and modeling. For COVID-19, Bastian designed a web-based model constructed from cities and traffic flows to describe the epidemic situation in Hubei Province [7, 8]. Currently, SIS, SIR and SEIR models provide another method of epidemic simulation. A lot of research work has been reported. The results show that those SIS, SIR and SEIR models can well reflect the dynamics of different epidemics. At the same time, these models have been used to model COVID-19 [9, 10, 11, 12, 13, 14, 15].

The purpose of this research is to develop an SEIQRVS compartmental mathematical model for prediction of COVID-19 epidemic trend considering different factors. However, it is different in the following aspects: (1) The compartment model is different; (2) A compartment has been added to the virus to allow non-linear interaction between humans and the environment; (3) Thorough simulation studies have been conducted carried out. This research includes natural recovery, so it is more realistic, and it has never been emphasized before. Driven by Capasso and Serio [16], this paper considers the SEIQRVS epidemic model with nonlinear saturation incidence. Usually, the model contains disease-free equilibrium and an endemic equilibrium. The stability of disease-free homeostasis and the existence of other non-trivial equilibrium can use the so-called basic reproduction number, which quantifies how many secondary infections in susceptible people are exposed to one infection. When the basic reproduction number is less than 1, the disease-free equilibrium is locally asymptotically stable, so the disease disappears after a period. Similarly, when the equilibrium point of an epidemic is an overall attraction, epidemiology means that the disease will prevail and persist in the population.

The structure of this article is as follows. In Section 2 We proposed a mathematical model as the ODE system and defined all the parameters used in the model. In Section 3, we calculate all possible steady state and basic reproduction numbers. In Section 4, numerical simulations are performed to verify the results, in the analysis, biologically relevant parameter values are used. In Section 5, sensitivity analysis and found highly sensitive parameters. Finally, in Section 6, the results are discussed.

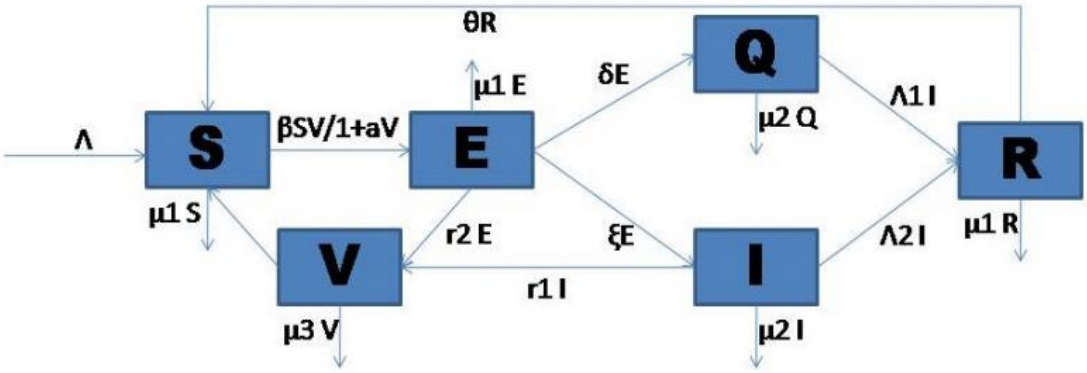

Figure.1 Schematic flow of proposed an SEIQRVS model system.

2. Formulation of Mathematical Model

In this section, we use the saturation incidence of the virus to establish an epidemic model system. Many researchers have discussed the role of viruses in the transmission dynamics of infectious diseases. The incidence of non-linearity is given in the form of $\frac{\beta S(t)V(t)}{\rho(V)}$, where $\rho(0) = 1$ and $\dot{\rho}(V) \geq 0$. To control infectious diseases, the growth rate of the virus should depend on the level of exposure and infection.

Here, we propose a SEIQRVS mathematical model and a schematic diagram of the hypothetical situation shown in the figure 1, which is controlled by the following ordinary differential equations:

$$\frac{dS}{dt} = \Lambda - \frac{\beta SV}{1+aV} - \mu_1 S + \theta R, \tag{1}$$

$$\frac{dE}{dt} = \frac{\beta SV}{1+aV} - \delta E - \xi E - \mu_1 E, \tag{2}$$

$$\frac{dI}{dt} = \xi E - \mu_2 I - \Lambda_1 I, \tag{3}$$

$$\frac{dQ}{dt} = \delta E - \mu_2 Q - \Lambda_2 Q, \tag{4}$$

$$\frac{dR}{dt} = \Lambda_1 I + \Lambda_2 Q - \mu_1 R - \theta R, \tag{5}$$

$$\frac{dV}{dt} = r_1 I + r_2 E - \mu_3 V, \tag{6}$$

with the following initial conditions:

$$S(0) = S_0 > 0, E(0) = E_0 > 0, I(0) = I_0 > 0, Q(0) = Q_0 > 0, R(0) = R_0 > 0, V(0) = V_0 > 0.$$

Where N is the entire population at time t, and $N = S + E + I + Q + R + V$. All parameters have positive identity. The definitions of all parameters are summarized in the table 1.

Table.1. Descriptions of the parameters used in this proposed model system (1)-(6)**.**

Parameters	**Definition**	**Dimension**
Λ	Susceptible recruitment rate	$days^{-1}$
β	Coefficient of transmission for exposed individuals	$days^{-1}$
$\frac{1}{a}$	Constant of half-saturation for infected individuals	—
μ	Natural death rate	$days^{-1}$

θ	Transfer rate for recovered individuals to susceptible	$days^{-1}$
ξ	Rate of infectious for exposed individuals	$days^{-1}$
δ	Rate of quarantine for exposed individuals	$days^{-1}$
Λ_1	Rate of recovery for infectious individuals	$days^{-1}$
Λ_2	Rate of recovery for quarantine individuals	$days^{-1}$
r_1	Rate of birth of virus from infectious individuals	$days^{-1}$
r_2	Rate of birth of virus from exposed individuals	$days^{-1}$

3. Analysis of The Model

In this part, we will analyze the basic reproduction number of R_0,(inspired by [17]) the equilibrium of all feasible states, and the local and global stability of these two states (disease-free and endemic).

Assuming that the size of the entire population is N, verify that $\frac{dN}{dt} = \Lambda - \mu N$, thus $N(t) \to \frac{\Lambda}{\mu}$, is $t \to \infty$. Therefore, the viable biological state

$$\Omega = \left\{(S,\ E,\ I,\ Q,\ R,\ V): 0 \le S,\ E,\ I,\ Q,\ R,\ V,\ S + E + I + Q + R + V \le \frac{\Lambda}{\mu}\right\},$$

unchanged to the model system (1)-(6).

3.1. Basic Reproduction Number

The basic reproduction number R_0 is defined as the expected number of secondary cases resulting from a (typical) infection in a fully susceptible population. Similar to [17], we calculate the basic reproduction number. Let $x = (E,\ I,\ Q,\ V)$, then from model (1)-(6), it follows:

$$\frac{dx}{dt} = F - V, \quad \text{where,} \quad F = \begin{bmatrix} \frac{\beta SV}{1+aV} \\ 0 \\ 0 \\ 0 \end{bmatrix} and\ V = \begin{bmatrix} (-\xi - \delta - \mu_1)E \\ \xi E - \mu_2 I - \Lambda_1 I \\ \delta E - \mu_2 Q - \Lambda_2 Q \\ r_1 I + r_2 E - \mu_3 V \end{bmatrix}.$$

We get, $F = Jacobianof\ \ F\ \ atDFE = \begin{bmatrix} 0 & 0 & 0 & \beta S^0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$

$$\mathrm{V} = Jacobianof\ \ V\ \ atDFE = \begin{bmatrix} -(\xi + \delta + \mu_1) & 0 & 0 & 0 \\ \xi & -(\mu_2 + \Lambda_1) & 0 & 0 \\ \delta & 0 & -(\mu_2 + \Lambda_2) & 0 \\ r_2 & r_1 & 0 & -\mu_3 \end{bmatrix}.$$

$$\mathrm{V}^{-1} = \begin{bmatrix} \frac{1}{\xi+\delta+\mu_1} & 0 & 0 & 0 \\ \frac{\xi}{(\xi+\delta+\mu_1)(\mu_2+\Lambda_1)} & \frac{1}{\mu_2+\Lambda_1} & 0 & 0 \\ \frac{-\delta}{(\xi+\delta+\mu_1)(\mu_2+\Lambda_2)} & 0 & \frac{1}{\mu_2+\Lambda_2} & 0 \\ \frac{\xi r_1 + r_2(\mu_2+\Lambda_1)}{(\xi+\delta+\mu_1)(\mu_2+\Lambda_1)\mu_3} & \frac{r_1}{(\mu_2+\Lambda_1)\mu_3} & 0 & \frac{1}{\mu_3} \end{bmatrix}.$$

Hence, next generation matrix for the model is

$$K = \mathrm{FV}^{-1} = \begin{bmatrix} \frac{\beta S^0[\xi r_1 + r_2(\mu_2+\Lambda_1)]}{(\xi+\delta+\mu_1)(\mu_2+\Lambda_1)\mu_3} & \frac{\beta S^0 r_1}{(\mu_2+\Lambda_1)\mu_3} & 0 & \frac{\beta S^0}{\mu_3} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}.$$

Further, the radius of spectral R_0 of matrix $K = \mathrm{FV}^{-1}$, is R_0 of the system model, which is, $R_0 = \rho(\mathrm{FV}^{-1})$, thus

$$R_0 = \frac{\beta S^0[\xi r_1 + r_2(\mu_2+\Lambda_1)]}{(\xi+\delta+\mu_1)(\mu_2+\Lambda_1)\mu_3}. \quad (7)$$

Since, $$S_0 = \frac{\Lambda}{\mu_1}, \quad (8)$$

$$R_0 = \frac{\beta\Lambda[\xi r_1 + r_2(\mu_2+\Lambda_1)]}{\mu_1\mu_3(\xi+\delta+\mu_1)(\mu_2+\Lambda_1)}. \quad (9)$$

3.2. Interior Equilibrium Points

Here, we analyze that the system (1)-(6) also have endemic equilibrium called interior equilibrium given as,

$\bar{E} = (S^*,\ E^*,\ I^*,\ Q^*,\ R^*,\ V^*)$,

where,

$$E^* = \frac{R_0(\mu_2+\Lambda_1)\mu_3}{\mu_3(\mu_2+\Lambda_1)+a[\xi r_1 + r_2(\mu_2+\Lambda_1)]}, \quad (10)$$

$$S^* = \frac{\Lambda}{\mu_1} + (\frac{1}{\mu_1})[(\frac{\theta(\mu_2+\Lambda_2)\Lambda_1\xi + (\mu_2+\Lambda_1)\Lambda_2\delta}{(\mu_1+\theta)(\mu_2+\Lambda_1)(\mu_2+\Lambda_2)}) - (\frac{\beta S^0(\xi r_1 + r_2(\mu_2+\Lambda_1))}{R_0(\mu_2+\Lambda_1)\mu_3})]E^*, \quad (11)$$

$$I^* = (\frac{\xi}{\mu_2+\Lambda_1})E^*, \quad (12)$$

$$Q^* = (\frac{\delta}{\mu_2+\Lambda_2})E^*, \quad (13)$$

$$R^* = (\frac{1}{\mu_1+\theta})[(\frac{\Lambda_1\xi}{\mu_2+\Lambda_1}) + (\frac{\Lambda_2\delta}{\mu_2+\Lambda_2})]E^*, \quad (14)$$

$$V^* = (\frac{1}{\mu_3})[(\frac{r_1\xi}{\mu_2+\Lambda_1}) + r_2]E^*. \quad (15)$$

From the above discussion, this is observed that equilibrium points for endemic state are exist if and only if $R_0 > 1$.

3.3. Local Stability Analysis of Disease-free and Endemic Equilibrium

Here, we analyze the local asymptotic stability of disease-free equilibrium and endemic equilibrium both. We can explore analytical results by considering the limiting system of (1)-(6) in which the total population is assumed to be constant $N = N^0 = \frac{\Lambda}{\mu}$. Then, the reduced limiting dynamical system is given by

$$\frac{dS}{dt} = \Lambda(1 + \frac{\theta}{\mu_1}) - (\mu_1 + \theta)S - \frac{\beta SV}{1+aV} - \theta E - \theta I - \theta Q, \quad (16)$$

$$\frac{dE}{dt} = \frac{\beta SV}{1+aV} - \xi E - \delta E - \mu_1 E, \quad (17)$$

$$\frac{dI}{dt} = \xi E - \mu_2 I - \Lambda_1 I, \quad (18)$$

$$\frac{dQ}{dt} = \delta E - \mu_2 Q - \Lambda_2 Q, \quad (19)$$

$$\frac{dV}{dt} = r_1 + r_2 - \mu_3 V. \quad (20)$$

with the initial conditions: $S(0) = S_0 > 0,\ E(0) = E_0 > 0,\ I(0) = I_0 > 0,\ Q(0) = Q_0 > 0,\ V(0) = V_0 > 0$.

The local stability of both the equilibria (disease-free and endemic) are established as follows:

3.3.1. Local Stability of Disease-free Equilibrium

The variational matrix at DFE is given by,

$$J_0 = \begin{bmatrix} -(\mu_1+\theta) & -\theta & -\theta & -\theta & \frac{-\beta\Lambda}{\mu_1} \\ 0 & -(\xi+\delta+\mu_1) & 0 & 0 & \frac{\beta\Lambda}{\mu_1} \\ 0 & \xi & -(\mu_2+\Lambda_1) & 0 & 0 \\ 0 & \delta & 0 & -(\mu_2+\Lambda_2) & 0 \\ 0 & r_2 & r_1 & 0 & -\mu_3 \end{bmatrix}.$$

Now, By solving this we get the characteristics equation of J_0 is,

$$(\mu_1+\theta+\lambda)(\mu_2+\Lambda_2+\lambda)[(\xi+\delta+\mu_1+\lambda)(\mu_2+\Lambda_1+\lambda)(-\mu_3-\lambda)+\frac{\beta\Lambda}{\mu_1}(\xi r_1+r_2\lambda+r_2\mu_2+r_2\Lambda_1)]=0. \quad (21)$$

From this we get two roots easily which are, $\lambda=-\theta-\mu_1$ and $\lambda=-\Lambda_2-\mu_2$ For the other three roots of the characteristics equations we have to apply the Routh-Hurwtiz Criterion [17],

$A_1A_2-A_3>0$, where, $A_1>0$, $A_2>0$, $A_3>0$ and $A_1A_2>A_3$.

Now, $$\lambda^3+\lambda^2A_1+\lambda A_2+A_3=0$$

where, $A_1=\Lambda_1+\mu_2+\mu_1+\delta+\xi+\mu_3$,

$$A_2=\xi\mu_3+\mu_1\mu_3+\delta\mu_3+\mu_2\mu_3+\Lambda_1\mu_3+\xi\mu_2+\xi\Lambda_1+\delta\mu_2+\delta\Lambda_1+\mu_1\mu_2+\mu_1\Lambda_1-\frac{-\beta\Lambda r_2}{\mu_1},$$

and $$A_3=\xi\mu_2\mu_3+\xi\mu_3\Lambda_1+\delta\mu_2\mu_3+\delta\Lambda_1\mu_3+\mu_1\mu_2\mu_3+\mu_1\Lambda_1\mu_3-\frac{\beta\Lambda\xi r_1}{\mu_1}-\frac{\beta\Lambda r_2\mu_2}{\mu_1}-\frac{\beta\Lambda r_2\Lambda_1}{\mu_1}.$$

Clearly, $A_1>0$, $A_2>0$, $A_3>0$ and $(A_1A_2-A_3)>0$. Therefore, according to Routh-Hurwitz criteria, disease free equilibria E^0 is Locally Asymptotically Stable.

Hence, by all five roots of the characteristics equation, we can say that the disease-free equilibrium (DFE) is locally asymptotically stable for the system (16)-(20).

3.3.2. Local Stability of Endemic Equilibrium

The matrix of variational at interior equilibria point is given as,

$$J = \begin{bmatrix} -(\mu_1+\theta-\frac{\beta V}{1+aV}-\lambda) & -\theta & -\theta & -\theta & -\frac{\beta S}{1+aV^2} \\ \frac{\beta V}{1+aV} & -(\xi+\delta+\mu_1+\lambda) & 0 & 0 & \frac{\beta S}{1+aV^2} \\ 0 & \xi & -(\mu_2+\Lambda_1+\lambda) & 0 & 0 \\ 0 & \delta & 0 & -(\mu_2+\Lambda_2+\lambda) & 0 \\ 0 & r_2 & r_1 & 0 & -(\mu_3+\lambda) \end{bmatrix}. \quad (22)$$

Now, By solving this we get the characteristics equation of J is,

$\lambda^5+\lambda^4A_1+\lambda^3A_2+\lambda^2A_3+\lambda A_5+A_6=0$,

Now, for the other three roots of the characteristics equations, we have to apply the Routh-Hurwitz Criterion [17],

$$(A_1A_4-A_5)(A_1A_2A_3-A_3^2-A_1^2A_4)-A_5(A_1A_2-A_3)^2+A_1A_5^2>0,$$

where, $A_1>0$, $A_2>0$, $A_3>0$, $A_4>0$, $A_5>0$, and $A_1A_2A_3>A_3^2+A_1^2A_4$.

Hence, we have

$(A_1A_4-A_5)(A_1A_2A_3-A_3^2-A_1^2A_4)-A_5(A_1A_2-A_3)^2+A_1A_5^2=\delta\Lambda_1\mu_3+\delta\mu_2\mu_3+\Lambda_1\mu_1\mu_3+\mu_1\mu_2\mu_3+\Lambda_1\mu_3\xi+\mu_2\mu_3\xi+\frac{\beta V}{1+aV}+(\theta\Lambda_2+\Lambda_2\mu_1+\theta\mu_2+\mu_1\mu_2)(\delta+\Lambda_1+\mu_1+\mu_2+\mu_3+\xi)+\frac{\beta S}{(1+aV)^2}(\xi r_1+r_2\mu_2+r_2\Lambda_1)+\frac{\beta V}{1+aV}(2\delta\theta+\delta\Lambda_1+\theta\Lambda_2+\Lambda_1\Lambda_2+\theta\mu_1+\Lambda_1\mu_1+\Lambda_2\mu_1+\delta\mu_2+\theta\mu_2+\Lambda_1\mu_2+\Lambda_2\mu_2+2\mu_1\mu_2+\mu_2^2+\theta\xi+\Lambda_1\xi+\Lambda_2\xi+2\mu_2\xi)+(\theta+\Lambda_2+\mu_1+\mu_2)(\frac{\beta S}{(1+aV)^2}+\delta\Lambda_1+\Lambda_1\mu_1+\delta\mu_2+\mu_1\mu_2+\delta\mu_3+\Lambda_1\mu_3+\mu_1\mu_3+\mu_2\mu_3+\Lambda_1\xi+\mu_2\xi+\mu_3\xi)+(\frac{\beta V}{1+aV}+\delta+\xi+\Lambda_1+\mu_1+\mu_2+\mu_3)(\frac{\beta Sr_1}{(1+aV)^2}+\delta\theta+\delta\Lambda_1+\delta\Lambda_2+\delta\mu_1+\theta\mu_1+2\Lambda_1\mu_1+\Lambda_2\mu_1+\mu_1^2+2\delta\mu_2+3\mu_1\mu_2+\delta\mu_3+\Lambda_1\mu_3+2\mu_1\mu_3+\mu_2\mu_3+\theta\xi+\Lambda_1\xi+\Lambda_2\xi+\mu_1\xi+2\mu_2\xi+\mu_3\xi+\frac{\beta V}{1+aV}(\xi+2\delta+2\mu_2+\mu_1+\Lambda_1+\Lambda_2))\mu_3>0.$

Clearly $A_1 > 0$, $A_2 > 0$, $A_3 > 0$, $A_4 > 0$, $A_5 > 0$, and $A_1A_2A_3 > A_3^2 + A_1^2A_4$. Therefore, by Routh-Hurwitz criteria, interior equilibria point $\bar{E}$ is Locally Asymptotically Stable for model system (16)-(20).

3.4. Global Stability of Disease-free and Endemic Equilibrium

In this part, we explore the global stability for both the disease-free and endemic equilibrium,

3.4.1. Global Stability of Disease-free Equilibrium

Let $Z = (E,\ I)$ and $X = (S)$, and $Q_0 = (X^0,\ 0), where \quad X^0 = \frac{\Lambda}{\mu_1}$. (23)

Then, $$\frac{dX}{dt} = F(X,\ Z) = \Lambda(1 + \frac{\theta}{\mu_1}) - (\mu_1 + \theta)S - \frac{\beta SV}{1+aV} - \theta E - \theta I - \theta Q.$$

At $S = S^0$, $G(X,\ 0) = 0$ and $\frac{dX}{dt} = F(X,\ 0) = \Lambda(1 + \frac{\theta}{\mu_1}) - (\mu_1 + \theta)X$.

As $X \to X^0$, $t \to \infty$. Therefore, $X = X^0 (= S^0)$ is g.a.s.

Now, $$G(X,Z) = \begin{bmatrix} -(\mu_1 + \xi + \delta) & 0 & 0 & \beta S^0 \\ \xi & -(\mu_2 + \Lambda_1) & 0 & 0 \\ \delta & 0 & -(\mu_2 + \Lambda_2) & 0 \\ r_2 & r_1 & 0 & -\mu_3 \end{bmatrix} \begin{bmatrix} \mathrm{E} \\ I \\ Q \\ V \end{bmatrix} - \begin{bmatrix} \beta S^0 V - \frac{\beta SV}{1+aV} \\ 0 \\ 0 \\ 0 \end{bmatrix},$$

$$G(X, \quad Z) = BZ - \hat{G}(X, \quad Z),$$

where,

$$B = \begin{bmatrix} -(\mu_1 + \xi + \delta) & 0 & 0 & \beta S^0 \\ \xi & -(\mu_2 + \Lambda_1) & 0 & 0 \\ \delta & 0 & -(\mu_2 + \Lambda_2) & 0 \\ r_2 & r_1 & 0 & -\mu_3 \end{bmatrix} \quad and \quad \hat{G}(X, \quad Z) = \begin{bmatrix} \beta S^0 V - \frac{\beta SV}{1 + aV} \\ 0 \\ 0 \\ 0 \end{bmatrix}.$$

Thus both the conditions are satisfied, therefore the DFE E^0 is globally asymptotically stable if $R_0 < 1$.

3.4.1. Global Stability of Endemic Equilibrium

For the global stability of endemic equilibrium of the system (16)-(20) we use the Lyapunov's Direct Method of Stability, Consider a positive definite function:

$$V_1 = \frac{1}{2}(D_1S^2 + D_2E^2 + D_3I^2 + D_4Q^2 + D_5V^2), \qquad (24)$$

Then using the system (16)-(20) in $\frac{dV_1}{dt}$, we get,

$$\frac{dV_1}{dt} = (D_1S)(\Lambda(1 + \frac{\theta}{\mu}) - \mu_1S - \theta S - \frac{\beta SV}{1+aV} - \theta E - \theta I - \theta Q) + (D_2E)(\frac{\beta SV}{1+aV} - \xi E - \delta E - \mu_1 E) + (D_3I)(\xi E - \mu_2 I - \Lambda_1 I) + (D_4Q)(\delta E - \mu_2 Q - \Lambda_2 Q) + (D_5V)(r_1 I + r_2 E - \mu_3 V), \qquad (25)$$

$$\frac{dV_1}{dt} = D_1(\Lambda S + \frac{\theta \Lambda S}{\mu_1} - \mu_1 S^2 - \theta S^2 - \theta SE - \theta SI - \theta SQ) + D_2(-\xi E^2 - \delta E^2 - \mu_1 E^2) + D_3(\xi EI - \mu_2 I^2 - \Lambda_1 I^2) + D_4(\delta EQ - \mu_2 Q^2 - \Lambda_2 Q^2) + D_5(r_1 IV + r_2 EV - \mu_3 V^2), \qquad (26)$$

Now using the inequality $\pm 2ab \leq (a^2 + b^2)$ and also using region Ω on the right hand side of the above equation, we get:

$$\frac{dV_1}{dt} \leq -[(\frac{b_{11}S^2}{3} - b_{12}SE + \frac{b_{22}E^2}{4}) + (\frac{b_{22}E^2}{4} - b_{23}EI + \frac{b_{33}I^2}{2}) + (\frac{b_{22}E^2}{4} - b_{24}EQ + \frac{b_{44}Q^2}{2}) + (\frac{b_{22}E^2}{4} - b_{25}EV + \frac{b_{55}V^2}{2}) + (\frac{b_{33}I^2}{2} - b_{35}IV + \frac{b_{55}V^2}{2}) + (\frac{b_{11}S^2}{2} - b_{13}SI + \frac{b_{33}I^2}{3}) + (\frac{b_{11}S^2}{2} - b_{14}SQ + \frac{b_{44}Q^2}{2}), \qquad (27)$$

where, $b_{11} = D_1(\mu_1 + \theta - \frac{\beta\Lambda}{2\mu_1})$, $b_{22} = D_2(\mu_1 + \xi + \delta - \frac{\beta\Lambda}{2\mu_1})$, $b_{33} = D_3(\mu_2 + \Lambda_1)$, $b_{44} = D_4(\mu_2 + \Lambda_2), b_{55} = D_5\mu_3$, $b_{12} = D_1\theta$, $b_{13} = D_1\theta$, $b_{14} = D_1\theta$, $b_{23} = D_3\xi$, $b_{24} = D_4\delta$, $b_{25} = D_5r_2$, $b_{35} = D_5r_1$.

Hence by Lyapunov's direct method of stability, we find that the endemic equilibrium is globally stable or non-linearly stable if following conditions are satisfied.

- $$[\mu_1 + \theta - \frac{\beta\Lambda}{2\mu_1}] > 0.$$

- $[\mu_1 + \xi + \delta - \frac{\beta\Lambda}{2\mu_1}] > 0.$
- $[\mu_1 + \theta - \frac{\beta\Lambda}{2\mu_1}][\mu_1 + \xi + \delta - \frac{\beta\Lambda}{2\mu_1}] > [\theta^2].$

Hence, we show that endemic equilibrium point $\bar{E}$ is globally asymptotically stable under the above-mentioned conditions.

4. Numerical Simulation

Under this part, we do numerous numerical simulation to explain the previous established result with the parametric values given in Table 2.

Table.2. Parametric values which are used for the numerical simulation in this model system (16)-(20)**.**

Parameters	**Values**	**Dimensions**
Rate of recruitment for susceptible (Λ)	0.4	$days^{-1}$
Coefficient of transmission for exposed individuals (β)	0.008	$days^{-1}$
Constant of half-saturation for infected individuals ($1/a$)	10	—
Natural death rate for susceptible and exposed individuals (μ_1)	0.005	$days^{-1}$
Natural death rate for infectious and quarantine individuals (μ_2)	0.008	$days^{-1}$
Natural death rate for virus (μ_3)	0.8	$days^{-1}$
Transfer rate from recovered individuals to susceptible individuals (θ)	0.01	$days^{-1}$
Rate of infectious for exposed individuals (ξ)	1/10	$days^{-1}$
Rate of quarantine for exposed individuals (δ)	1/10	$days^{-1}$
Rate of recovery for infectious individuals (Λ_1)	variable	$days^{-1}$
Rate of recovery for quarantine individuals (Λ_2)	0.04	$days^{-1}$
Birth rate of virus from infectious individuals (r_1)	variable	$days^{-1}$
Birth rate of virus from exposed individuals (r_2)	0.1	$days^{-1}$

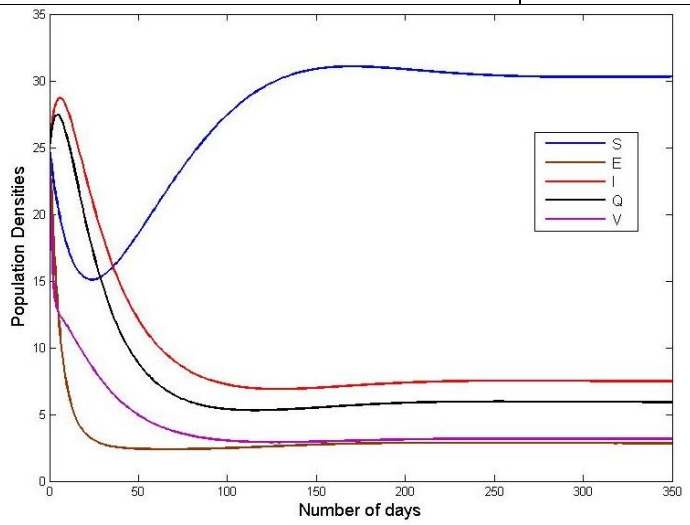

Figure.2 Population densities at virus rate $r_1 = 0.3$.

(a) For virus growth rate of infectious individuals $\Lambda_1 = 0.03$ and $r_1 = 0.3$ we obtain effective reproduction number $R_0 = 3.47112 > 1$. The system (16)-(20) has an endemic equilibrium $\bar{E}(30.3302,\ 2.84208,\ 7.47915,\ 5.92099,\ 3.15994)$. Also the conditions for global stability $[\mu_1 + \theta - \frac{\beta\Lambda}{2\mu_1}] > 0.$ $[\mu_1 + \xi + \delta - \frac{\beta\Lambda}{2\mu_1}] > 0.$ and

$[\mu_1 + \theta - \frac{\beta\Lambda}{2\mu_1}][\mu_1 + \xi + \delta - \frac{\beta\Lambda}{2\mu_1}] > [\theta^2]$. hold good and hence, the conditions are satisfied. Hence the pandemic equilibria $\bar{E}$ is Globally Asymptotically Stable (Figure2).

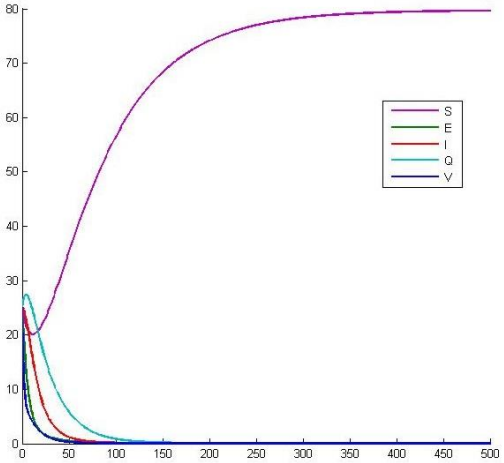

Figure.3 Population densities at virus rate $r_1 = 0.15$.

(b) For virus growth rate $\Lambda_1 = 0.09$ and $r_1 = 0.15$, we obtain effective reproduction number $R_0 = 0.987556 < 1$. The disease-free equilibrium $E^0(80,\ 0,\ 0,\ 0,\ 0)$ is globally asymptotically stable (See Figure3).

5. Sensitivity Analysis

In this part, we analyze R_0 for the the sensitivity analysis and endemic steady state by taking parametric values given in Table 2.

Since we have the expression for R_0, we evaluate the expressions for the sensitivity index of R_0 with respect to all eight parameters. The effective reproduction number R_0 is a function of eight parameters $\Lambda, \mu_1, \mu_2, \mu_3, \beta, \delta, \Lambda_1, \xi,\ r_1$ and r_2. The normalized sensitivity indices for eight parameters are obtained as:

$$\Upsilon_{\Lambda}^{R_0} = \frac{\partial R_0}{\partial \Lambda}\frac{\Lambda}{R_0} = 1,\quad \Upsilon_{\mu_1}^{R_0} = \frac{\partial R_0}{\partial \mu_1}\frac{\mu_1}{R_0} = \frac{-(\xi+\delta+2\mu_1)}{\xi+\delta+\mu_1},\quad \Upsilon_{\mu_2}^{R_0} = \frac{\partial R_0}{\partial \mu_2}\frac{\mu_2}{R_0} = \frac{-\xi\ r_1\mu_2}{(\Lambda_1+\mu_2)(\xi\ r_1+\ r_2\Lambda_1+\ r_2\mu_2)},\quad \Upsilon_{\mu_3}^{R_0} = \frac{\partial R_0}{\partial \mu_3}\frac{\mu_3}{R_0} = (-1),$$

$$\Upsilon_{\beta}^{R_0} = \frac{\partial R_0}{\partial \beta}\frac{\beta}{R_0} = 1,\ \Upsilon_{\delta}^{R_0} = \frac{\partial R_0}{\partial \delta}\frac{\delta}{R_0} = \frac{-\delta}{\delta+\xi+\mu_1},\ \Upsilon_{\Lambda_1}^{R_0} = \frac{\partial R_0}{\partial \Lambda_1}\frac{\Lambda_1}{R_0} = \frac{-\xi\ r_1\Lambda_1}{(\Lambda_1+\mu_2)(\xi\ r_1+\ r_2\Lambda_1+\ r_2\mu_2)},$$

$$\Upsilon_{\xi}^{R_0} = \frac{\partial R_0}{\partial \xi}\frac{\xi}{R_0} = \frac{\xi(\delta\ r_1+\ r_1\mu_1-\ r_2\Lambda_1-\ r_2\mu_2)}{(\xi+\delta+\mu_1)(\xi\ r_1+\ r_2\Lambda_1+\ r_2\mu_2)},\ \Upsilon_{r_1}^{R_0} = \frac{\partial R_0}{\partial\ r_1}\frac{r_1}{R_0} = \frac{r_1\xi}{\xi\ r_1+\ r_2\Lambda_1+\ r_2\mu_2},\ \Upsilon_{r_2}^{R_0} = \frac{\partial R_0}{\partial\ r_2}\frac{r_2}{R_0} = \frac{r_2(\Lambda_1+\mu_2)}{\xi\ r_1+\ r_2\Lambda_1+\ r_2\mu_2}.$$

by using the value of parameters of Table 2, the sensitivity indices of effective R_0 for ten various parameters are shown in Table 3. We explore that β and Λ are highly sensitive, μ_1, μ_3, Λ_1 are sensitive and $\xi,\ r_1,\ r_2, \mu_2, \delta$ are less sensitive to R_0.

Next, we will evaluate the sensitivity indices for the interior equilibrium $\bar{E} = (S^*,\ E^*,\ I^*,\ Q^*,\ R^*,\ V^*)$ which is the function of ten parameters which are $\Lambda, \mu_1, \mu_2, \mu_3, \beta, \xi, \theta, \delta, \Lambda_1,\ \Lambda_2, a,\ r_1$, and r_2. Sensitivity indices of endemic equilibrium at $r_1 = 0.3$ is given in Table 4 calculated by using parameters as in Table 2 at $r_1 = 0.3$.

From Table 4, we observe that S^* is highly sensitive to parameters $\Lambda, \mu_1, \mu_3, \beta$ and r_1. E^* is highly sensitive to parameters $\Lambda, \mu_1, \mu_3, \Lambda_1, \beta$ and r_1. I^* is highly sensitive to parameters $\Lambda, \mu_1, \mu_3, \Lambda_1, \beta$ and r_1. Q^* is highly sensitive to parameters $\Lambda, \mu_1, \mu_3, \Lambda_1, \beta$ and r_1. R^* is highly sensitive to parameters $\Lambda, \mu_1, \mu_3, \Lambda_1, \beta$ and r_1. Similarly, V^* is highly sensitive to parameters $\Lambda, \mu_1, \mu_3, \Lambda_1, \beta$ and r_1.

Table.3. The sensitivity indices, $\Upsilon_{y_j}^{R_0} = \frac{\partial R0V}{\partial y_j} \times \frac{y_j}{R_0}$, of effective R_0 to parameters, y_j for parametric values shown in Table 2 at $r_1 = 0.3$

Parameter (y_j)	**Sensitivity index of R_0 w.r.t. y_j ($\Upsilon_{y_j}^{R_0}$)**
Λ	1.000
μ_1	-1.02439
μ_2	-0.186858
μ_3	-1
Λ_1	-0.700716
β	+1.000
ξ	0.399769
δ	-0.487805
r_1	0.887574
r_2	0.112426

Table.4. The sensitivity indices, $\Upsilon_{y_j}^{x_i} = \frac{\partial x_i}{\partial y_j} \times \frac{y_j}{x_i}$, of the state variables at endemic equilibrium, x_i, to the parameters, y_j for parameter values given in Table 2

y_j	$\Upsilon_{y_j}^{S^*}$	$\Upsilon_{y_j}^{E^*}$	$\Upsilon_{y_j}^{I^*}$	$\Upsilon_{y_j}^{Q^*}$	$\Upsilon_{y_j}^{R^*}$	$\Upsilon_{y_j}^{V^*}$
Λ	+0.314776	+1.40468	+1.40468	+1.40468	+1.40468	+1.40468
μ_1	-0.179274	-0.908841	-0.908841	-0.908841	-1.24217	-0.908841
μ_2	0.0864619	-0.261154	-0.47168	-0.427821	-0.449158	-0.448012
μ_3	0.685224	-0.404675	-0.404675	-0.404675	-0.404675	-1.40468
Λ_1	0.502797	-0.182488	-0.971962	-0.182488	-0.0800699	-0.883204
Λ_2	0.0189274	0.0844627	0.0844627	-0.748871	0.170048	0.0844627
β	-0.883125	0.521551	0.521551	0.521551	0.521551	0.521551
ξ	-0.274223	-0.327329	0.672671	-0.327329	0.159157	0.560245
δ	0.339941	-0.659836	-0.659836	0.340164	-0.146323	-0.659836
r_1	-0.608187	0.359179	0.359179	0.359179	0.359179	1.24675
r_2	-0.077037	0.045496	0.045496	0.045496	0.045496	0.157922
θ	0.0145887	-0.0384473	-0.0384473	-0.0384473	0.0394696	-0.0384473
a	0.0145887	-0.0384473	-0.0384473	-0.0384473	0.0394696	-0.0384473

6. Conclusion

In this study, a SEIQRVS epidemic infectious disease model with nonlinear saturation incidence rate is proposed and analyzed the effects of the virus which are generated by exposed and infectious class both by using the stability theory of ordinary differential equations. The conclusions of this study are given as follows:

- The proposed model has considered with virus class (V) and the critical rate of virus is derived which are r_1 and r_2.
- The basic reproduction number R_0 is calculated for the system which is the most important threshold for the epidemic dynamics, also the model exists in two biologically feasible states which are, the disease-free equilibrium and endemic equilibrium.
- By the observation of the analysis we get that the rate of affecting viruses r_1 and r_2 affects the basic reproduction number R_0 and therefore, the features which are qualitative of the model system has been moderated.

- Since there are usually errors in data collection and presumed parameter values, sensitivity analysis is very important to discover highly sensitive parameters. Normalized forward sensitivity indices are calculated for effective reproduction number, and state variables at endemic equilibrium on various parameters and respective sensitive parameters are identified.
- Considering the significance of this ongoing global public health emergency, although our conclusions are limited by the small sample size, we believe that the findings reported here are important for understanding the transmission potential of COVID-19 infection.

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