Dynamical Behavior of Cholera Epidemic Model with Non-linear Incidence Rate

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Abstract

Cholera is an infection of the small intestine caused by the bacterium Vibrio cholera. In this work, we consider a mathematical model SIRB which represents the dynamics of cholera. To understand the dynamics of the model, the disease free and endemic stability are discussed. The disease free equilibrium is stable locally as well as globally when the basic reproduction less than 1, otherwise an unstable equilibrium exist. If the basic reproduction number exceeds than unity, then the endemic equilibrium is stable locally as well as globally with some sufficient conditions. The numerical solution of the model illustrates the analytical results.
Keywords: Cholera, Reproduction Number, Local Stability, Global Stability, Numerical Solution

1 Introduction

Cholera is a small intestine infection caused by the bacterium Vibrio cholera. The cause also contains the contaminated water and ingestion of food with bacterium Vibrio cholera. Among the 200 serogroups of Vibrio cholera, it is only Vibrio cholera o1and o139 that are known to be the cause of the cholera disease[1]. The etiological agent,Vibrio cholera o1 (and more recently vibrio cholera o139), passes through and survives the gastric acid barrier of the stomach and then penetrates the mucus lining that coats the intestinal epithelial[2]. The main symptoms are watery diarrhea and vomiting. This may result in dehydration and in severe cases grayish-bluish skin. Transmission occurs primarily by drinking water or eating food that has been contaminated by the feces (waste product) of an infected person, including one with no apparent symptoms [3].

The severity of the diarrhea and vomiting can lead to rapid dehydration and electrolyte imbalance, and death in some cases. The primary treatment is oral rehydration therapy, typically with oral rehydration solution, to replace water and electrolytes. If this is not tolerated or does not provide improvement fast enough, intravenous fluids can also be used. Antibacterial drugs are beneficial in those with severe disease to shorten its duration and severity. If the severe diarrhea is not treated, it can result in life-threatening dehydration and electrolyte imbalances. Fever is rare and should raise suspicion for secondary infection. Patients can be lethargic, and might have sunken eyes, dry mouth, cold clammy skin, decreased skin turgor, or wrinkled hands and feet. Kussmaul breathing, a deep and labored breathing pattern, can occur because of acidosis from stool bicarbonate losses and lactic acidosis associated with poor perfusion. Blood pressure drops due to dehydration, peripheral pulse is rapid and thready, and urine output decreases with time. Muscle cramping and weakness, altered consciousness, seizures, or even coma due to electrolyte losses and ion shifts are common, especially in children [4].

Several mathematical models have been modeled on cholera as well as different infectious diseases, such as [5, 6, 7, 8, 10, 12]. In this work, we formulated a mathematical model of cholera in the form of SEIR mathematical model. The model consist four state variable, i.e. susceptible $S(t)$, infected $I(t)$ and recovered $R(t)$ and pathogen population $B(t)$. The mathematical model and their descriptions are presented in section 2. The fundamental properties of the model are discussed in section 3. The stability results are discussed in section 4, and 5. The brief discussion is presented in section 6.
2 Model Formulation

The human population is divided into three subgroups, \(S(t)\)-Susceptible, \(I(t)\)-Infected and \(R(t)\)-Recovered or removed, with \(N(t) = S(t) + I(t) + R(t)\). The term \(B(t)\) represent the pathogen population at time \(t\). The basic governing differential equation consist a system of differential equation is given by

\[
\begin{align*}
\frac{dS}{dt} &= \Lambda - \mu S(t) - \frac{\beta_b S(t)B(t)}{1 + a_1 B(t)} - \frac{\beta_s S(t)I(t)}{1 + a_2 I(t)}, \\
\frac{dI}{dt} &= \frac{\beta_b S(t)B(t)}{1 + a_1 B(t)} + \frac{\beta_s S(t)I(t)}{1 + a_2 I(t)} - (\mu_0 + \mu + \phi)I(t), \\
\frac{dR}{dt} &= \phi I(t) - \mu R(t), \\
\frac{dB}{dt} &= \xi I(t) - dB(t),
\end{align*}
\]

Subject to non-negative initial conditions

\[
S(t) = S_0 \geq 0, \quad I(t) = I_0 \geq 0, \quad R(t) = R_0 \geq 0, \quad B(t) = B_0 \geq 0. \tag{2}
\]

Here in system (1), the human population growth rate is shown by \(\Lambda\). The natural mortality rate of the human population is \(\mu\). The disease contact between \(S(t)\) and \(B(t)\) is shown by \(\beta_b\) while between \(S(t)\) and \(I(t)\) by \(\beta_s\). The term \(a_1\) and \(a_2\) are the saturation constants. The disease death rate at \(I(t)\) is \(\mu_0\) and the rate of recovery from infection is denoted by \(\phi\). The term \(\xi\) represent the human contribution to pathogen and \(d\) is the death rate of the pathogen in the environment.

Since equations \(S, I\) and \(B\) in system (1) are independent of the variable \(R\), so it is reasonable that we reduced the system (1) to the following form:

\[
\begin{align*}
\frac{dS}{dt} &= \Lambda - \mu S(t) - \frac{\beta_b S(t)B(t)}{1 + a_1 B(t)} - \frac{\beta_s S(t)I(t)}{1 + a_2 I(t)}, \\
\frac{dI}{dt} &= \frac{\beta_b S(t)B(t)}{1 + a_1 B(t)} + \frac{\beta_s S(t)I(t)}{1 + a_2 I(t)} - (\mu_0 + \mu + \phi)I(t), \\
\frac{dB}{dt} &= \xi I(t) - dB(t),
\end{align*}
\]

Subject to non-negative initial conditions. The total dynamics of the human population is given by

\[
\frac{d(S + I)}{dt} = \Lambda - \mu S - \mu I - \mu_0 I - \phi I, \\
\leq \Lambda - \mu S - \mu I. \tag{4}
\]
In the absence of $\mu_0$ and $\phi$, the feasible region for the system (3), given by

$$\Pi_1 = \left\{ (S, I) \in R^2_+ : 0 \leq S + I \leq \frac{\Lambda}{\mu} \right\}$$  \hspace{1cm} (5)

and the feasible region for the population of pathogen

$$\Pi_2 = \left\{ B | 0 \leq B \leq \frac{\xi}{d} \right\},$$  \hspace{1cm} (6)

and define $\Theta = \Pi_1 \times \Pi_1$. The feasible region for human and pathogen population, we discuss all the solutions lies inside the region $\Theta$.

3 Fundamental Properties

In this section, we find the fundamental properties of the system (3), which is essential in the proof of the proceeding sections.

**Theorem 2.1**: The associated solutions of the system (3) with initial conditions (2) are non-negative for all $t > 0$.

**Proof**: We can write the system (3) in the matrix form as follows:

$$Y' = M(Y),$$

where $Y = (S, I, B)^T \in R^3$ and $M(Y)$ is given by

$$M(Y) = \begin{pmatrix}
M_1(Y) \\
M_2(Y) \\
M_3(Y)
\end{pmatrix} = \begin{pmatrix}
\Lambda - \mu S(t) - \frac{\beta_b S(t) B(t)}{1 + a_1 B(t)} - \frac{\beta_s S(t) I(t)}{1 + a_2 I(t)} \\
\frac{\beta_b S(t) B(t)}{1 + a_1 B(t)} + \frac{\beta_s S(t) I(t)}{1 + a_2 I(t)} - (\mu_0 + \mu + \phi) I(t) \\
\xi I(t) - dB(t)
\end{pmatrix}.$$  \hspace{1cm} (7)

We have

$$\frac{dS}{dt} |_{S=0} = \Lambda - \mu S \geq 0,$$

$$\frac{dI}{dt} |_{I=0} = \frac{\beta_b S(t) B(t)}{1 + a_1 B(t)} \geq 0,$$

$$\frac{dB}{dt} |_{B=0} = \xi I \geq 0.$$  \hspace{1cm} (8)

Therefore,

$$M_i |_{Y_i=0,Y_i \in C_+^3} \geq 0, \hspace{0.2cm} i = 1, 2, 3.$$  \hspace{1cm} (9)

Thus, the corresponding solutions of system (3) for $Y(t) \in R^3_+$ for all time $t \geq 0$. 
3.1 Basic Reproduction Number $R_0$

In this subsection, we determine the basic reproduction number $R_0$ for the proposed system (3), by using the same procedure developed in [11]. Suppose $x = (I, B)$, where

\[
F = \begin{bmatrix}
\frac{\beta_sSB}{1+a_1B} & \frac{\beta_sSI}{1+a_1I} \\
0 & 0
\end{bmatrix}
\quad \text{and} \quad
V = \begin{bmatrix}
(\mu + \mu_0 + \phi)I \\
-\xi I + dB
\end{bmatrix},
\]

we obtained the matrix $F$ and $V$ as

\[
F = \begin{bmatrix}
\beta_sS^0 & 0 \\
0 & 0
\end{bmatrix}
\quad \text{and} \quad
V = \begin{bmatrix}
(\mu + \mu_0 + \phi) & 0 \\
-\xi & d
\end{bmatrix}.
\]

The matrix $FV^{-1}$ is

\[
FV^{-1} = \begin{bmatrix}
\frac{\beta_sS^0}{\mu(\mu + \mu_0 + \phi)} & \frac{\beta_bS^0}{\xi(\mu + \mu_0 + \phi)} \\
0 & 0
\end{bmatrix}.
\]

The required basic reproduction number $R_0$ of the system is given by

\[
R_0 = \frac{\Lambda\beta_s}{\mu(\mu + \mu_0 + \phi)} + \frac{\Lambda\beta_b\xi}{\mu d(\mu + \mu_0 + \phi)}.
\]

It is obvious that $R_{01} < R_0$ and $R_{02} < R_0$.

3.2 Equilibrium Points

In the proposed subsection, we determine the equilibria of the system (3) at $\mathcal{E}^0 = (S^0, 0, 0)$ and $\mathcal{E}^1 = (S^*, I^*, B^*)$. Taking the right side of the system (3) equal zero, the corresponding equilibria at the point $\mathcal{E}^0 = (S^0, 0, 0)$ and $\mathcal{E}^1 = (S^*, I^*, B^*)$ obtained as follows:

\[
\mathcal{E}^0 = (S^0, 0, 0) = (\frac{\Lambda}{\mu}, 0, 0), \quad \text{Disease Free Equilibrium},
\]

and at $\mathcal{E}^1 = (S^*, I^*, B^*)$

\[
S^* = \frac{\beta_b\xi - (\mu + \mu_0 + \phi)}{(d + a_1\xi I^*)(1 + a_2I^*)},
\]

\[
B^* = \frac{\xi I^*}{d},
\]

called the endemic equilibria.
4 Disease Free stability

In this section, we find out the stability result of the disease free equilibrium at the equilibrium point $E^0$. The local and global stability of the disease free equilibrium is presented in the following:

**Theorem 4.1** The disease free equilibrium of the system at $E^0$ is locally asymptotically stable, if $R_{01} < R_0 < 1$ and $R_{02} < R_0 < 1$, otherwise unstable.

**Proof:** At the equilibrium point $E^0$, the Jacobian matrix $J_1$ is given by

$$J_1 = \begin{pmatrix} -\mu & -\beta_s S^0 & -\beta_b S^0 \\ 0 & \beta_s S^0 - (\mu + \mu_0 + \phi) & \beta_b S^0 \\ 0 & \xi & -d \end{pmatrix}. \tag{10}$$

The characteristics equation of the Jacobian matrix $J_1$ is

$$(\mu + \lambda)[\lambda^2 + a_1 \lambda + a_0 \lambda] = 0,$$

where

$$a_1 = \frac{\Lambda d \beta_s}{\mu} + d(\mu + \mu_0 + \phi)(1 - R_{02}) > 0, \quad a_2 = d + (\mu + \mu_0 + \phi)(1 - R_{01}) > 0.$$

The first eigenvalue of the Jacobian matrix $J_1$ is $-\mu$, the other two eigenvalues are negative if and only if $R_{01} < R_0 < 1$ and $R_{02} < R_0 < 1$. The Routh-Hurtwiz conditions are satisfied i.e., $(a_1 > 0, a_2 > 0)$. All the eigenvalues of the Jacobian matrix $J_1$ have negative real part, so, the disease free equilibrium $E^0$ of the system (3) is locally asymptotically stable. □.

**Lemma 4.1:** The global stability of the disease free equilibrium is guaranteed if it is written in the form:

$$\frac{d\mathcal{X}}{dt} = \mathcal{F}(\mathcal{X}, \mathcal{Z}),$$
$$\frac{d\mathcal{Z}}{dt} = \mathcal{G}(\mathcal{X}, \mathcal{Z}), \quad \mathcal{G}(\mathcal{X}, \mathcal{Z}) = 0, \tag{11}$$

where $\mathcal{X} = S \in \mathcal{X}_1$ and $\mathcal{Z} = (I, B) \in \mathcal{X}_2$, repetitively represent the number of uninfected and infected individuals. The disease free equilibrium is now denoted by $U_0 = (\mathcal{X}^0, 0)$. The conditions $\mathcal{P}_1$ and $\mathcal{P}_2$ given below must be satisfied:

$$\mathcal{P}_1 : \quad \text{For } \frac{d\mathcal{X}}{dt} = \mathcal{F}(\mathcal{X}, 0) = 0,$$

$$\mathcal{P}_2 : \quad \mathcal{G}(\mathcal{X}, \mathcal{Z}) = \mathcal{A}\mathcal{Z} - \mathcal{G}(\mathcal{X}, \mathcal{Z}), \quad \text{where } \mathcal{G}(\mathcal{X}, \mathcal{Z}) \geq 0, \text{ for } (\mathcal{X}, \mathcal{Z}) \in \mathcal{A}\mathcal{Z}.$$
the matrix \( A = D_z \mathcal{G}(X, Z) \) is M-matrix, and \( \Theta \) is the biological feasible region. Then, the equilibrium point \( U_0 = (X^0, 0) \) is globally asymptotically stable. □

Now, we prove the global stability of the disease free equilibrium.

**Theorem 4.2:** If \( R_0 < 1 \), the disease free equilibrium of the system (3) at \( \mathcal{E}^0 \) is globally asymptotically stable.

**Proof:** According to Lemma 4.1, the conditions \( P_1 \) and \( P_2 \) for system (3) as follows:

\[
P_1 : \quad \mathcal{F}(X, I) = [\Lambda - \mu S],
\]

\[
P_2 : \quad \mathcal{G}(X, Z) = AZ - \mathcal{G}(X, Z), \quad \text{where} \quad \mathcal{G}(X, Z) \geq 0, \quad \text{for} \quad (X, Z) \in \Theta,
\]

where

\[
A = \begin{bmatrix}
\beta_s S^0 - (\mu + \mu_0 + \phi) & \beta_b S^0 \\
\xi & -d
\end{bmatrix}, \quad Z = \begin{bmatrix}
I \\
B
\end{bmatrix}
\]

\[
\mathcal{G}(X, Z) = \begin{bmatrix}
\beta_s [S^0 - \frac{S}{1+\alpha I}] + \beta_b [S^0 - \frac{S}{1+\alpha B}] \\
\beta_b B^* + \frac{\beta_b I^*}{1+\alpha I} \\
\frac{\beta_b B^*}{1+\alpha I} + \frac{\beta_b I^*}{1+\alpha I} \\
\frac{\beta_b B^*}{1+\alpha I} + \frac{\beta_b I^*}{1+\alpha I} \\
0 \\
\xi \\
-d
\end{bmatrix}
\]

Since \( A \) represents a Metzler matrix and \( \mathcal{G}(X, Z) \geq 0 \) at the point \( \mathcal{E}^0 \). Thus, the system (3) about the disease free equilibrium \( \mathcal{E}^0 \) is globally asymptotically stable.

### 5 Stability of Endemic Equilibrium

This section investigates the local and global stability of endemic equilibrium of the system (3).

**Theorem 5.1:** If the basic reproduction number \( R_0 > 1 \) and \( \beta_b \xi < (\mu + \mu_0 + \phi) \), then the endemic equilibrium \( \mathcal{E}^1 \) of the system (3) is locally asymptotically stable.

**Proof:** The Jacobian matrix \( J_2 \) of the system (3) at the endemic equilibrium \( \mathcal{E}^1 \), is given by

\[
J_2 = \begin{bmatrix}
-\mu - \frac{\beta_b B^*}{1+\alpha_1 B^*} - \frac{\beta_b I^*}{1+\alpha_2 I^*} & -\frac{a_2 \beta_s S^* I^*}{(1+\alpha_1 I^*)^2} & -\frac{a_1 \beta_b S^* B^*}{(1+\alpha_1 B^*)^2} \\
\frac{\beta_b B^*}{1+\alpha_1 B^*} + \frac{\beta_b I^*}{1+\alpha_2 I^*} & \frac{a_2 \beta_s S^* I^*}{(1+\alpha_1 I^*)^2} - (\mu + \mu_0 + \phi) & \frac{a_1 \beta_b S^* B^*}{(1+\alpha_1 B^*)^2} \\
0 & \xi & -d
\end{bmatrix}
\]

One of the eigenvalue of the Jacobian matrix \( J_1 \) is \( -\mu - \frac{\beta_b B^*}{1+\alpha_1 B^*} - \frac{\beta_b I^*}{1+\alpha_2 I^*} < 0 \), has negative real part. To find the other two eigenvalues, we follow Routh-Hurtwiz Criteria, i.e. \( \text{trace}J_2 < 0 \) and \( \text{det}J_2 > 0 \). From the Jacobian matrix
\( J_2 \), we have

\[
\text{det} J_2 = \left( \frac{a_2 \beta_s}{(1 + a_2 I^*)^2} + \frac{\xi^2 a_1 \beta_b}{(d + a_1 \xi)} \right) \left( \frac{(\mu + \mu_0 + \phi) - \beta_b \xi}{(d + a_1 \xi I^*)(1 + a_2 I^*)} \right) dI^* + (\mu + \mu_0 + \phi) > 0,
\]

and

\[
\text{trace} J_2 = -\frac{a_2 \beta_s I^*}{(1 + a_2 I^*)^3(d + a_1 \xi I^*)} (\mu + \mu_0 + \phi) - (\mu + \mu_0 + \phi) - d < 0.
\]

Trace \( J_2 < 0 \) and \( \text{det} J_2 > 0 \) if \( \beta_b \xi < (\mu + \mu_0 + \phi) \). Thus, the Jacobian matrix \( J_2 \) has negative real part if \( \beta_b \xi < (\mu + \mu_0 + \phi) \) and \( R_0 > 1 \). So the endemic equilibrium \( E_1 \) of the system (3) is stable locally asymptotically.

**Theorem 5.2:** If \( R_0 > 1 \), then the system is stable globally asymptotically.

**Proof:** Consider the following lyapunov function

\[
\mathcal{L} = (S - S^* - S^* \ln \frac{S}{S^*}) C_1 + (I - I^* - I^* \ln \frac{I}{I^*}) C_2 + C_3 B,
\]

(14)

taking the time derivative of \( \mathcal{L} \), we obtain

\[
\mathcal{L}' = C_1 (1 - S \frac{dS}{dt}) + C_2 (1 - I \frac{dI}{dt}) + C_3 \frac{dB}{dt},
\]

(15)

using system (3), we obtain

\[
\mathcal{L}' = C_1 (1 - S \frac{dS}{dt}) \left[ \Lambda - \mu S(t) - \beta_b S(t) B(t) - \beta_s S(t) I(t) \right] + C_2 (1 - I \frac{dI}{dt}) \left[ \beta_b S(t) B(t) \right] \left[ 1 + a_1 B(t) \right] + C_2 (1 - I \frac{dI}{dt}) \left[ \beta_s S(t) I(t) \right] \left[ 1 + a_2 I(t) \right] + C_3 \left[ \phi I(t) - \mu R(t) \right].
\]

(16)

After some arrangements, we obtain

\[
\mathcal{L}' = -\frac{(S - S^*)^2}{S} \mu \xi - \xi \beta_b \xi \left( \frac{\beta_s}{(d + a_1 \xi I)} \right) \left[ I^* - \frac{S^*}{I} \right] < 0.
\]

(17)

The positive constants are \( C_1 = C_2 = \xi \) and \( C_3 = (\mu + \mu_0 + \phi) \). \( \mathcal{L}' < 0 \), if and only if \( \frac{E}{S} > \frac{S^*}{T} \), with \( R_0 > 1 \). Thus, the endemic equilibrium \( E_1 \) of the system (3) is globally asymptotically stable.

### 6 Discussion

The dynamical behavior of cholera epidemic model with non-linear incidence rate is investigated. The model construction and basic results are derived and discussed. The threshold quantity that examine the stability of the equilibrium is obtained. The disease free and endemic equilibrium obtained and discussed.
For the threshold quantity $R_0$, we obtained the stability analysis of the model. The reduced model (3), is stable locally as well as globally when the threshold quantity, less than unity, is derived. If the threshold exceeds than unity, the persistence occur and the disease permanently exists in the community. For, this, we proved that the model (3) is stable both locally and globally. For the values of the parameters for which the threshold quantity are less than unity is presented in Figure 1. Figure 2 represents the dynamical behavior of the human population, with the baseline $S(0) = 200$, $I(0) = 03$ and $R(0) = 1$. Figure 3, represents the dynamical behavior of pathogen population, with the baseline $B(0) = 20$. Figure 4 is the combined graph of the human with pathogen. The detail of the parameters values used in simulation is presented in Table 1.

Table 1: Parameter values used in Numerical simulations.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Value</th>
<th>Dimension</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\Lambda$</td>
<td>Population growth rate of human</td>
<td>0.6</td>
<td>Per day$^{-1}$</td>
</tr>
<tr>
<td>$\beta_b$</td>
<td>The contact rate between susceptible $S$ and Pathogen $B$</td>
<td>0.05</td>
<td>Per day$^{-1}$</td>
</tr>
<tr>
<td>$\beta_s$</td>
<td>The contact rate between susceptible $S$ and infected $I$</td>
<td>0.05</td>
<td>Per day$^{-1}$</td>
</tr>
<tr>
<td>$a_1$ and $a_2$</td>
<td>The saturation constants</td>
<td>0.02, 0.03</td>
<td>—</td>
</tr>
<tr>
<td>$\mu$</td>
<td>Natural death rate of human</td>
<td>0.1</td>
<td>Per day$^{-1}$</td>
</tr>
<tr>
<td>$\mu_0$</td>
<td>Disease related death rate</td>
<td>0.01</td>
<td>Per day$^{-1}$</td>
</tr>
<tr>
<td>$\phi$</td>
<td>The rate at which the individuals recovered</td>
<td>0.03</td>
<td>Per day$^{-1}$</td>
</tr>
<tr>
<td>$\xi$</td>
<td>The contribution of human to the pathogen</td>
<td>0.1</td>
<td>Per day$^{-1}$</td>
</tr>
<tr>
<td>$d$</td>
<td>The death rate at pathogen population</td>
<td>0.3</td>
<td>Per day$^{-1}$</td>
</tr>
</tbody>
</table>

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References


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Figure 1: The plot represents $R_0 < 1$, when $\Lambda = 0.6, \beta_1 = 0.04, \beta_2 = 0.05, \mu = 0.2, \mu_0 = 0.01, \phi = 0.01, d = 0.02, \xi = 0.01$. 
Figure 2: The plot represents the population behavior of human.
Figure 3: The plot represents the population behavior of Pathogen.
Figure 4: The plot represents the population behavior of human with pathogen.