Dynamical Analysis on A Model of Cholera Epidemic with Quarantine, Vaccination, and Two Path of Transmissions

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Abstract. This research focus on dynamical analysis of a SIQRVB (Susceptible-Infectious-Quarantined-Recovered-Vaccinated-Bacterial) model. It describe the spread of cholerae with quarantine, vaccination and two transmission paths. As is well-known, there mainly exist two transmission paths for cholerae: environment-to-human transmission and human-to-human transmission. This model has two equilibrium points, that is disease-free equilibrium point which always exists and an endemic equilibrium point that exists with some conditions. The local stability of the equilibrium points is investigated by using Routh-Hurwitz criteria. The method of Next Generation Matrix is applied to get the basic reproduction number $R_0$. It can be shown numerically that disease-free equilibrium point is locally asymptotic stable when $R_0 < 1$, while the endemic equilibrium point exist and locally asymptotic stable when satisfy Routh-Hurwitz criteria. Numerical simulations are given to illustrate the theoretical results.

Keywords: SIQRVB epidemic model, Cholerae, equilibrium point, local stability.

1. Introduction
Cholera is an acute diarrhoea disease caused by infection of the bacteria *Vibrio cholerae*, and kills over 21,000 people each year [9]. *Vibrio cholerae* has two life cycles, which are in the host body (human) and in the water. Therefore, the mechanism of transmission of cholera disease is quite complex. There mainly exist two transmission paths for cholerae: environment-to-human transmission and human-to-human transmission. Human-to-human transmission occurs due to direct contact with contaminated hands, while interactions between susceptible individuals and bacteria can occur due to drinking water that has been contaminated with bacteria, consumption of raw or uncooked seafood perfectly, as well as consumption of fruit and vegetables washed with water contaminated with bacteria *Vibrio cholerae* [4]. Cholera disease is closely related to poverty, poor sanitation, and lack of clean drinking water. An infected person may exhibit symptoms and not. Symptoms experienced by people with cholera disease include watery diarrhoea, vomiting and leg cramps. Between 2007 and 2018, cholera outbreaks in some countries, namely in Angola, Haiti, Zimbabwe and Yemen [5, 6].

In mathematics, there is an epidemic model that can be used to describe the behavior of disease spread. Many researchers have analyzed the epidemic model of cholera spread, such as Wang and Modnak [8], Khan et al. [2], Quan Sun et al. [10], and Lemos et al. [5,6]. Wang and Modnak [8] present and analyze a cholera epidemiological model with control measures incorporated which partitioned a population into three classes, namely susceptible (S), infected (I), and recovered (R). There is also B denote the concentration of the vibrios in the environment. In 2015, the research was continued by Khan et al. [2]...
by modify the bilinear incident rate into saturated incident rate. In 2017, Quan Sun et al. [10] modify the model proposed by Wang and Modnak [8] by adding the vaccination and disinfection parameter, at the same year Lemos et al. [5] propose a mathematical model for cholera with treatment through quarantine (SIQRB). In 2018, Lemos et al. [6] development on the previous model [5] by adding the individual population compartment of the vaccine so that the proposed model became the model of a cholera disease spread with six compartments, namely SITRVB, with T treatment individuals and V is vaccination. The numerical simulation results shows the importance of vaccination to decrease the rate of spread of cholera disease. Based on [6] in this paper, we propose a SIQRVB (Susceptible–Infectious–Quarantined–Recovered–Vaccinated–Bacterial) type model. The paper is organized as follows. In Section 2, we formulate our model for cholera transmission dynamics. In section 3 we investigated the equilibrium point of the model, their local stability analysis and the basic reproduction number. In section 4 we presented the numerical simulations. Finally in section 5 we give conclusion and some discussions.

2. Model Formulation
This section describe a modified the model of Lemos et al. [6] by considering the human-to-human transmission and disinfection parameter. We propose a SIRQV (Susceptible–Infectious–Quarantined–Recovered–Vaccinated) type model and consider a class of bacterial concentration for the dynamics of cholera. The total population $N(t)$ is divided into five classes: susceptible $S(t)$, infectious with symptoms $I(t)$, in treatment through quarantine $Q(t)$, recovered $R(t)$ and vaccinated $V(t)$ at time $t$, for $t ≥ 0$. Furthermore, we consider a class $B(t)$ that reflects the bacterial concentration at time $t$. Assumed that there is a positive recruitment rate $\Lambda$ into the susceptible class $S(t)$ and a positive natural death rate $\mu$. $\varphi$ is the rate of vaccination of susceptible individuals. The cholera model developed in this paper is a combined system of human populations and the environmental component (SIQRB-B), with the environment-to-human transmission represented by saturated incident rate $\frac{\beta_1}{k+B}S$ and human-to-human transmission by bilinear incident rate $\beta_2SI$. $\omega_1$ and $\omega_2$ is the rate of decrease in the immunity of recovered and vaccinated individual, respectively and therefore becomes susceptible again. During quarantine, infected individual are isolated and subject to a proper medication, at rate $\gamma$. And then, $\eta$ is the rate of recovered individuals. The disease-related death rates associated with the individuals that are infected and in quarantine are $\delta_1$ and $\delta_2$, respectively. Bacterial concentration increase at rate $\epsilon$. On the other hand, the bacterial concentration can decrease at mortality rate $d$ and disinfection rate $c$. These assumptions are translated in the following mathematical model:

$$\frac{dS}{dt} = \Lambda - \frac{\beta_1 B}{k+B}S - \beta_2 SI + \omega_1 R + \omega_2 V - (\varphi + \mu)S,$$

$$\frac{dI}{dt} = \frac{\beta_1 B}{k+B}S + \beta_2 SI - (\gamma + \mu + \delta_1)I,$$

$$\frac{dQ}{dt} = \gamma I - (\eta + \mu + \delta_2)Q,$$

$$\frac{dR}{dt} = \eta Q - (\omega_1 + \mu)R,$$

$$\frac{dV}{dt} = \varphi S - (\omega_2 + \mu)V,$$

$$\frac{dB}{dt} = \epsilon I - (c + d)B.$$

(2.1)
with initial condition:
\[ S(0) \geq 0, \ I(0) \geq 0, \ Q(0) \geq 0, \ R(0) \geq 0, \ V(0) \geq 0, \text{ and } B(0) \geq 0. \]

3. Model Analysis
3.1 Basic Reproduction Number
Basic reproduction number \((R_0)\), is the threshold for the spread of disease. The basic reproduction number investigated by using Next Generation Matrix \([3]\) that can be formed based on compartment \(I\) and \(B\).

So, we can define matrix \(F\) and \(V\) from those compartment as follows:
\[
F = \begin{bmatrix}
\frac{\beta_2 \Lambda k_4}{k_0 k_4 - \omega_2 \varphi} & \frac{\beta_1 \Lambda k_4}{(k_0 k_4 - \omega_2 \varphi)k} \\
0 & 0
\end{bmatrix}
\]
and
\[
V = \begin{bmatrix}
k_1 \\
-\epsilon \\
k_5
\end{bmatrix}.
\]

The next generation matrix \((H)\) stated with
\[
H = FV^{-1}.
\]

Basic reproduction number is the spectral radius of next generation matrix \((H)\), we have:
\[
R_0 = \frac{\Lambda k_4 (\beta_2 k k_5 + \beta_1 \epsilon)}{k k_1 k_5 (k_0 k_4 - \varphi \omega_2)}.
\]

3.2 Equilibrium point and their local stability analysis
Suppose that \(k_0 = \varphi + \mu, \ k_1 = \gamma + \mu + \delta_1, \ k_2 = \eta + \mu + \delta_2, \ k_3 = \omega_1 + \mu, \ k_4 = \omega_2 + \mu, \text{ and } k_5 = c + d\). System (2.1) has two equilibrium points that is disease-free equilibrium point \(E_0 = (S_0, I_0, Q_0, R_0, V_0, B_0) = (\frac{\xi}{k_6}, 0, 0, 0, \frac{\varphi \xi}{k_4 k_6}, 0)\) and endemic equilibrium point \(E^* = (S^*, I^*, Q^*, R^*, V^*, B^*)\), where \(S^* = \frac{\Lambda}{k_6} + k_7 I^*, \ Q^* = \frac{\gamma I^*}{k_2}, \ R^* = \frac{\eta I^*}{k_2 k_3}, \ V^* = \frac{\varphi}{k_4} (k_6 + k_7 I^*), \ B^* = \frac{\epsilon I^*}{k_5}\) and \(I^*\) is positive root of the quadratic equation \(KI^* + LI^* + M\), where:
\[
K = \beta_2 \epsilon k_6 k_7
\]
\[
L = \beta_2 \epsilon k_6 k_7 + \beta_2 k k_5 k_7 + \beta_2 \epsilon \Lambda - k_1 k_6 \epsilon
\]
\[
M = \beta_1 \epsilon \Lambda + \beta_2 k k_5 \Lambda - k k_1 k_5 k_6
\]
\[
k_6 = k_0 - \frac{\omega_2 \varphi}{k_4}
\]
\[
k_7 = \frac{\omega_1 \gamma k_2 k_3}{k_2 k_3 k_6}
\]
Furthermore, from the above equation can be obtained some possibilities that \( I^* \) is a positive real number if and only if \( D \geq 0 \), or \( L^2 - 4KM \geq 0 \).

The local stability of equilibrium point will be analyzed by linearizing system [1] resulting Jacobian matrix as follows

\[
J = \begin{bmatrix}
- \frac{\beta_1 B}{k + B} - \frac{\beta_2 L}{k + B} - k_0 - \beta_2 S & 0 & \omega_1 & \omega_2 & 0 & 0 & - \frac{\beta_1 S}{k + B} + \frac{\beta_1 BS}{(k + B)^2} \\
\frac{\beta_1 B}{k + B} + \frac{\beta_2 L}{k + B} - k_1 & 0 & 0 & 0 & - \frac{\beta_1 S}{k + B} & 0 & \frac{\beta_1 BS}{(k + B)^2} \\
0 & \gamma & - k_2 & 0 & 0 & 0 & 0 \\
0 & 0 & \eta & - k_3 & 0 & 0 & 0 \\
\phi & 0 & 0 & 0 & - k_4 & 0 & 0 \\
0 & \epsilon & 0 & 0 & 0 & - k_5 & 0
\end{bmatrix}
\]

When the real part of all of eigenvalues of the Jacobian matrix are negative then the equilibrium point is stable otherwise, it is unstable.

3.2.1 Behaviour of disease free equilibrium point

Substituted the disease free equilibrium point \( E_0 \) into the Jacobian matrix, we have

\[
J(E_0) = \begin{bmatrix}
- k_0 - \frac{\beta_2 L}{k_6} & 0 & \omega_1 & \omega_2 & 0 & - \frac{\beta_1 \Lambda}{kk_6} \\
0 & - \frac{\beta_2 L}{k_6} & 0 & 0 & 0 & \beta_1 \Lambda & 0 \\
0 & \gamma & - k_2 & 0 & 0 & 0 & 0 \\
0 & 0 & \eta & - k_3 & 0 & 0 & 0 \\
\phi & 0 & 0 & 0 & - k_4 & 0 & 0 \\
0 & \epsilon & 0 & 0 & 0 & - k_5 & 0
\end{bmatrix}
\]

The eigenvalues are obtained \( \lambda_1 = - k_3 \), \( \lambda_2 = - k_2 \) and the other are the eigenvalue of the matrix

\[
A = \begin{bmatrix}
- k_0 & \omega_2 \\
\phi & - k_4
\end{bmatrix}
\]

and

\[
B = \begin{bmatrix}
\frac{\beta_2 L}{k_6} - k_1 & \frac{\beta_1 \Lambda}{kk_6} \\
\beta_1 \Lambda & k_6
\end{bmatrix}
\]

Based on matrix A, we obtained \( \lambda^2 + (k_0 + k_4)\lambda + k_0 k_4 - \omega_2 \phi = 0 \) thus acquired negative eigenvalue \( \lambda_{3,4} = -\frac{b \pm \sqrt{b^2 - 4ac}}{2a} < 0 \). The equilibrium is asymptotic stable if \( \det(B) > 0 \) and \( \text{trace}(B) < 0 \) [7]. So that it can be concluded that the disease-free equilibrium is locally asymptotic stable, if \( R_0 < 1 \).

3.2.2 Behaviour of endemic equilibrium point

The Jacobian matrix at \( E^* \) is given by

\[
J(E^*) = \begin{bmatrix}
E_1 & E_3 & 0 & \omega_1 & \omega_2 & E_5 \\
E_2 & E_4 & 0 & 0 & 0 & E_6 \\
0 & \gamma & - k_2 & 0 & 0 & 0 \\
0 & 0 & \eta & - k_3 & 0 & 0 \\
\phi & 0 & 0 & 0 & - k_4 & 0 \\
0 & \epsilon & 0 & 0 & 0 & - k_5
\end{bmatrix}
\]
where,
\[ E_1 = \frac{-\beta_1 B^*}{k + B^*} - \beta_2 I^* - k_0 \]
\[ E_2 = \frac{\beta_1 B^*}{k + B^*} + \beta_2 I^* \]
\[ E_3 = -\beta_2 S^* \]

The characteristic equation of \( \mathbb{J}(E^*) \) is
\[ a_0 \lambda^5 + a_1 \lambda^4 + a_2 \lambda^3 + a_3 \lambda^2 + a_4 \lambda + a_5 = 0, \]
where
\[ a_0 = 1 \]
\[ a_1 = k_3 - E_1 - E_4 + k_5 + \omega_2 \varphi \]
\[ a_2 = k_2 k_3 - E_1 k_3 - E_4 k_3 + k_3 k_5 + k_3 \omega_2 \varphi + E_1 E_4 - E_1 E_5 - E_4 E_5 - E_6 \epsilon - E_2 E_3 - E_4 \omega_2 \varphi + k_5 \omega_2 \varphi \]
\[ a_3 = k_2 k_3 k_5 - E_1 k_2 k_3 - E_4 k_2 k_3 + k_2 k_3 \omega_2 \varphi + E_1 E_4 k_3 - E_1 k_3 k_5 - E_6 k_3 \epsilon - E_2 E_3 k_5 - E_4 k_3 \omega_2 \varphi + E_1 E_4 k_5 + E_1 E_4 \epsilon - E_2 E_3 k_5 - E_2 E_5 \epsilon - E_4 E_5 \omega_2 \varphi - E_6 \omega_2 \varphi \epsilon \]
\[ a_4 = E_1 E_4 k_2 k_5 - E_1 k_2 k_3 k_5 - E_4 k_2 k_3 k_5 - E_6 k_2 k_3 \epsilon - E_2 E_3 k_2 k_3 - E_4 k_2 k_3 \omega_2 \varphi + k_2 k_3 k_5 \omega_2 \varphi + E_1 E_4 k_5 + E_1 E_4 \epsilon - E_2 E_3 k_5 - E_2 E_5 k_3 \epsilon - E_4 E_5 k_3 \omega_2 \varphi + E_6 k_3 \omega_2 \varphi \epsilon - E_2 k_5 \omega_1 \eta \gamma^2 \]
\[ a_5 = E_1 E_4 k_2 k_3 k_5 + E_1 E_5 k_2 k_3 \epsilon - E_2 E_3 k_2 k_3 - E_2 E_5 k_2 k_3 \epsilon - E_4 E_5 k_2 k_3 \omega_2 \varphi - E_6 k_2 k_3 \omega_2 \varphi \epsilon \]

Hence, according to the Routh-Hurwitz criteria, the roots of the characteristic equation of \( \mathbb{J}(E^*) \) have negative real part if and only if
i. \( a_1 > 0 \)
ii. \( a_1 a_2 - a_3 > 0 \)
iii. \( a_1 a_2 a_3 - a_2^2 - a_1^2 - 4a_4 > 0 \)
iv. \( a_1 a_2 a_3 a_4 + 2a_1 a_4 a_5 + a_2 a_3 a_5 - a_1^2 a_4 - a_1 a_2^2 - a_1 a_4^2 - a_4^2 a_5 - a_2^2 a_5 - a_2 a_5^2 - a_2 a_5^2 - a_2 a_5^2 > 0 \)
v. \( a_5(a_1 a_2 a_3 a_4 + 2a_1 a_4 a_5 + a_2 a_3 a_5 - a_1^2 a_4 - a_1 a_2^2 - a_1 a_4^2 - a_4^2 a_5 - a_2^2 a_5 - a_2 a_5^2) > 0 \)

4. Numerical Simulation
In this section, the dynamics models (2.1) is studied numerically using the parameters values that set as follows: \( \Lambda = 0.3980273973, \beta_1 = 0.03, \beta_2 = 0.0001, k = 100000, \omega_1 = 0.10958904, \omega_2 = 0.5, \mu = 0.00022493, \varphi = 0.15, \delta_1 = 0.0015, \delta_2 = 0.0002, \eta = 0.2, \gamma = 0.15, \epsilon = 0.97, c = 0.4, d = 0.3. \) The disease free equilibrium point \( E_0 = (1361.3,0,0,0,408.2,0) \) is locally asymptotic stable because \( R_0 = 0.9010 < 1 \) according to the previous analysis, and an endemic equilibrium point \( E^* \) does not exist.
Figure 1. Numerical simulations of system (2.1) when $R_0 < 1$.

Figure 1. show a numerical simulations when $R_0 < 1$ with three different initial conditions, that is $NA_1 = (90, 45, 20, 15, 10, 27500), NA_2 = (170, 130, 140, 110, 130, 8500)$ and $NA_3 = (250, 215, 260, 220, 220, 17500)$. From this simulation results can be noted that the solution of system (2.1) converge to the disease free equilibrium point. Then, we consider the same parameters value except $\beta_1 = 0.59$ dan $\beta_2 = 0.001$. 
Figure 2. Numerical simulations of system (2.1) when $R_0 > 1$.

The numerical simulation in Figure 2 confirm that endemic equilibrium point is locally asymptotic stable because $R_0 = 9.0458 > 1$ while the disease free equilibrium point is not stable. By using some different initial conditions, that is $NA_1 = (90,45,20,15,10,27500)$, $NA_2 = (170,130,140,110,130,8500)$ and $NA_3 = (250, 215,260,220,220,17500)$, the solution of system (2.1) converge to the endemic equilibrium point which means that there is a spread of cholera.
5. Conclusion

In this paper, we proposed analytically and numerically, a SIQRVB model for cholera transmission dynamics. Based on the results of the analysis, there are two equilibrium points, which are the disease free equilibrium points that always exist and endemic equilibrium points that exist with certain conditions. The disease-free equilibrium points is locally asymptotic stable, if $R_0 < 1$ while endemic equilibrium points exist if $R_0 > 1$ and locally asymptotic stable, then it follows from Routh-Hurwitz criteria. Simulations of our mathematical model, with vaccination and quarantined show conformance with analytically results.

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