GSJ: Volume 13, Issue 2, February 2025, Online: ISSN 2320-9186

www.globalscientificjournal.com

STABILITY ANALYSIS OF DELAYED MATHEMATICAL MODEL FOR CHOLERA AND EPIDEMIC – ENDEMIC DISEASE.

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Abstract: Cholera is a potentially life-threatening bacterial infection caused by the bacterium *Vibrio cholerae*, with the primary site of infection being the small intestine. The disease typically spreads through contaminated water and food and becomes more pronounced in areas with poor sanitation and inadequate access to clean drinking water. Cholera infection can lead to severe diarrhea, dehydration, and death if left untreated. Individuals with low personal hygiene have higher chances of spreading and/or contracting the disease. A nonlinear delayed mathematical model with environmental factor for the spread of cholera is proposed and analyzed. We prove that the delayed cholera model is biologically meaningful and analyze the local asymptotic stability of the equilibrium points for positive time delays. Both the disease-free (DFE) and endemic equilibria are found and their stability investigated using the Routh Hurwitz stability criterion method. Next Generation Matrix (NGM) method was used to get the basic reproductive number R_0. The disease-free equilibrium point is locally asymptotically stable if $R_0 < 1$, while the endemic equilibrium point is locally asymptotically stable if $R_0 > 1$. Numerical simulations are also carried out to investigate the influence of certain parameters on the spread of disease, to support the analytical results of the model.

Keywords: Stability Analysis, delayed model, Cholera, Infectious Disease,

1.0 Introduction

Mathematical models of disease transmission have provided researchers with critical insights into the progression, control and prevention of disease spread[31]. The most fundamental of these models is the SIR (Susceptible, Infectious and Recovered) differential equation model. Infectious disease can spread and turn into epidemics, taking thousands of lives within a matter of days and one of such diseases is cholera.

Cholera is an acute diarrhea infection of the intestine caused by the ingestion of food or water contaminated with the toxigenic bacterium vibro cholera. Water-borne carriers or bacteria are responsible for the spread of this disease. This disease is transmitted through drinking water which is contaminated from improper treatment of sewage, shaking hands with infected people and eating food cooked by infected people or with contaminated water. Its dynamics are complicated by the multiple interactions between the human host, the pathogen and the environment which contribute to both direct human-to-human and indirect environment-to-human transmission pathways[20,21]. Its symptom is severe acute watery diarrhea that last for three to seven days. Treatments are usually quite effective when administered promptly.

According to [10], Once cholera arrives into a new region, either carried by an infected person or by contaminated water and food, we may expect one of three possible outcomes: no outbreak, an outbreak possibly followed by few waves; or a cholera outbreak followed by subsequent outbreaks that may assume a persistent seasonal pattern. Humans throughout the world can contract cholera. The majority has few or no symptoms but can still spread the disease.

In Nigeria, outbreaks of the disease have been taking place with ever-increasing occurrence ever since the earliest outbreak in 1970 [15]. The United Nation (UN) unit reports: more than 70% of the country's population live below the poverty line and cholera outbreaks are common in poor urban areas which lack proper sanitation and clean drinking water [15]..

In the fight against cholera, it is therefore necessary to design effective control strategies and doing this requires a better understanding of the dynamic of cholera in its initiation, spread and evolution. Preventative measures include vaccination, drinking clean water and washing hand well all of which assume that people have easy access to these resources [14]. According to [22], Developing Countries are most affected by cholera disease due to inadequate sanitation, improper treatment of reservoirs and lack of safe water supply. Many people across the globe live with inadequate sanitation and clean water. 71% or 5.2 billion people use a safely managed drinking water service, 263 million people spent over 30 minutes per round trip to collect water from an improved source; 844 million people still

lack even a basic drinking water service. For sanitation, the situation is even worse; only 39%, or 2.9 billion people, used a safely managed sanitation service in which excreta are safely disposed of in treated off-site; 2.3 billion people still lacked even a basic sanitation service; 600 million people shared improved facilities with other households; 892 million people worldwide still practiced open defecation; more than 2 billion drink water from sources that are faecally contaminated, and 2.4 billion are without basic sanitation facilities, exposing them to a range of water-related diseases including cholera [22].

Over the years, many researchers have widely studied the transmission dynamics of cholera. Mathematicians have developed tools known as model to understand the global dynamics of cholera epidemiology and analyze the complex epidemic and endemic behaviour of cholera disease. Some of the mathematical model of cholera can be found in the typical works of [11,17,18,23].

Recently [33] have analyzed a Cholera model by considering general incidence function for multiple transmissions and a general growth rate function for pathogens.

This paper aims to explore a unified cholera model and conduct a careful mathematical study of the complex cholera dynamics for better understanding of the fundamental disease transmission mechanism using the Routh-Hurwitz criterion and the Rouche's theorem to investigate its stability property.

2.0 Model Assumptions and Formulation

The assumptions used in the process of modeling the spread of cholera are as follows:

a. The value of the birth rate equals Λ.

b. The value of the death rate equals μ.

c. The two ways of transmission are from human to human and environment to human.

d. The populations of susceptible individuals rise due to the natural birth at a constant rate of Λ.

e. The susceptible individuals reduce due to interactions with vibrio cholera, the transmission rate is β_e and the interactions with infected individuals, the transmission rate is β_h.

f. Infected individuals rise due to contact between susceptible individual and vibrio cholera and as well as interactions with already infected individuals.

g. Recoveries and natural deaths contribute to a declined in the number of Infected individuals.

2.1 Model Parameters and Variables

The model considers a total human population size $N(t)$ and is sub-divided into three compartments of susceptible $S(t)$ infected $I(t)$ and recovered $R(t)$. Thus;

$$N(t) = S(t) + I(t) + R(t)$$

The concentration of vibrio cholerae in the environment (contaminated water reservoir) is denoted by B. μ denotes the natural death rate, β_e is the rate of ingestion of vibrio cholerae from environment, while β_h is the rate of human to human transmission. k is the pathogen concentration that yields 50% chance of contracting cholera, γ is the rate of recovery from cholera, δ is the rate of human contribution to vibrio cholerae and ξ is the death rate of vibrio cholerae.

Table 1: Variables of the Cholera Model

Symbol	Description
$\boldsymbol{S(t)}$	Susceptible human population at time t.
$\boldsymbol{I(t)}$	Infected human population at time t.
$\boldsymbol{R(t)}$	Recovered human population at time t.
$\boldsymbol{B(t)}$	Concentration of vibrio cholera in the population at time t.
$\boldsymbol{N}$	Total human population.

Table 2: Parameters of Cholera Model

Symbol	Description
$\boldsymbol{\Lambda}$	Human birth rate
$\boldsymbol{\mu}$	Human death rate
$\boldsymbol{\beta_e}$	Rate of exposure to contaminated water.
$\boldsymbol{\beta_h}$	Rate of human to human transmission.
$\boldsymbol{k}$	The concentration of pathogen that yields 50% chance of contracting cholera
$\boldsymbol{\gamma}$	Recovery rate from cholera.
$\boldsymbol{\delta}$	Rate of contribution of each infected persons to the population of vibrio cholera in the aquatic environment.
$\boldsymbol{\xi}$	Growth rate of vibrio cholerae in the aquatic environment.
$\boldsymbol{\omega}$	Immunity waning rate

τ	Delay in the time in which a person is infected and when he gives off the pathogen bacteria of vibro cholerae to the acquatic environment.

2.2 Model Equations

The following differential equations for the cholera dynamics is based on the combination of a regular SIRB model and an environmental component.

$$\frac{dS}{dt} = \Lambda - \beta_e S(t)\frac{B(t)}{k + B(t)} - \beta_h S(t)I(t) + \omega R(t) - \mu S(t) \quad (1)$$

$$\frac{dI}{dt} = \beta_e S(t)\frac{B(t)}{k + B(t)} + \beta_h S(t)I(t) - \gamma I(t) - \mu I(t) \quad (2)$$

$$\frac{dR}{dt} = \gamma I(t) - (\omega + \mu)R(t) \quad (3)$$

$$\frac{dB}{dt} = \delta I(t) - \xi B(t) \quad (4)$$

For simplicity, we let $S(t) = S, I(t) = I, R(t) = R \; and \; B(t) = B,$ so that our new model system becomes: With **Delay;**

$$\frac{dS}{dt} = \Lambda - \beta_e S\frac{B}{k + B} - \beta_h SI + \omega R - \mu S \quad (5)$$

$$\frac{dI}{dt} = \beta_e S\frac{B}{k + B} + \beta_h SI - \gamma I - \mu I \quad (6)$$

$$\frac{dR}{dt} = \gamma I - (\omega + \mu)R \quad (7)$$

$$\frac{dB}{dt} = \delta I(t - \tau) - \xi B \quad (8)$$

2.3 Model Analysis

We first establish the well-posedness of the model by showing that its solutions are positive and bounded.

Well-posedness: in the following Lemma, we can show that the solutions are positive and bounded

Lemma 1: For all $t \geq 0$, the invariant region $\Omega = \{(S, I, R, B) \in \mathbb{R}_+^4 : S(0), I(0), R(0), B(0) > 0, S + I + R = N\}$ then the solutions of $S(t), I(t), R(t), B(t)\}$ of the system equations (1) – (4) exhibits positive invariance.

Proof: Considering equation (5),

$$\frac{dS}{dt} = \Lambda - \beta_e S \frac{B}{k+B} - \beta_h SI + \omega R - \mu S$$

$$\frac{dS}{dt} \geq -\beta_e S \frac{B}{k+B} - \beta_h SI - \mu S$$

$$\frac{dS}{dt} \geq -\left(\beta_e \frac{B}{k+B} + \beta_h I + \mu\right) S \qquad (9)$$

By separation of variables and integrating both sides of equation (9) we have;

$$\frac{dS}{S} \geq -\left(\beta_e \frac{B}{k+B} + \beta_h I + \mu\right) dt$$

$$\int \frac{dS}{S} \geq \int -\left(\beta_e \frac{B}{k+B} + \beta_h I + \mu\right) dt$$

$$\log_e S(t) \geq -\left(\beta_e \frac{B}{k+B} + \beta_h I + \mu\right) t + c_1 \qquad (10)$$

Taking the exponential of both sides of equation (10) we get,

$$S(t) \geq e^{-\left(\beta_e \frac{B}{k+B} + \beta_h I + \mu\right) t} \times e^{c_1}$$

$$S(t) \geq A e^{-\left(\beta_e \frac{B}{k+B} + \beta_h I + \mu\right) t}, \qquad \text{where } A = e^{c_1} \qquad (11)$$

Applying the initial condition at $t = 0$ in equation (11) we have;

$$S(0) = A, \qquad \text{so that,} \qquad S(t) \geq S(0) e^{-\left(\beta_e \frac{B}{k+B} + \beta_h I + \mu\right) t}$$

Therefore, $S(t) \geq 0$ for all $t \geq 0$.

Applying the same method, it is verifiably that $I(0) > 0, R(0) > 0, B(0) > 0$.

It is therefore proven that all state variables are positive for all time t. The solutions are therefore non-negative for $t > 0$.

Next, we show that the system of equation (1) – (4) has solutions which are bounded in the invariant region Ω as contained in the feasible region: $\Omega = \{(S, I, R, B): N < \frac{\Lambda}{\mu}\}$

Lemma 2: The solutions of the model are contained in the feasible region

$$\Omega = \{(S, I, R, B) \in \mathbb{R}_+^4: 0 \leq S, 0 \leq I, 0 \leq R, 0 \leq B; S + I + R \leq \frac{\Lambda}{\mu}\}$$

Proof:

Consider the total population at a time t given by $N(t) = S(t) + I(t) + R(t)$.

Then, taking the time derivative of $N(t)$ from equation (5) – (8), we have;

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \quad (12)$$

From equation (5);

$$\frac{dN}{dt} = \Lambda - \mu S - \gamma I - \mu I + \gamma I + \omega R - (\omega + \mu)R$$

$$\frac{dN}{dt} = \Lambda - \mu S - \mu I - \mu R$$

$$\frac{dN}{dt} \leq \Lambda - (S - I - R)\mu$$

$$\frac{dN}{dt} \leq \Lambda - \mu N$$

$$\frac{dN}{dt} + \mu N \leq \Lambda$$

By using integrating factor method,

$$I.F = e^{\int \mu dt} = e^{\mu t}$$

$$\frac{d}{dt}(e^{\mu t} N) \leq e^{\mu t} \Lambda \quad (13)$$

Integrate both sides of equation (13) we get;

$$\int \frac{d}{dt} e^{\mu t} N dt \leq \int e^{\mu t} \Lambda dt$$

$$e^{\mu t}N(t) \leq \frac{e^{\mu t}\Lambda}{\mu} + c_5$$

$$N(t) \leq \frac{\Lambda}{\mu} + c_5 e^{-\mu t} \quad (14)$$

Taking the initial condition at $t = 0$ in equation (14) we get,

$$N(0) - \frac{\Lambda}{\mu} \leq c_5,$$

Thus,

$$N(t) \leq \frac{\Lambda}{\mu} + (N(0) - \frac{\Lambda}{\mu})e^{-\mu t}$$

Where $N(0)$ is the initial population,

As $t \to \infty$ and taking

$$\lim_{t\to\infty} N(t) \leq \frac{\Lambda}{\mu} + (N(0) - \frac{\Lambda}{\mu})e^{-\mu t}$$

Thus; $0 \leq N < \frac{\Lambda}{\mu}$

The solutions are therefore bounded in the invariant region Ω.

3.1 Stability Analysis of Equilibrium Points

Equilibrium is defined as a constant solution of a model system. The equilibrium point is a condition where there are no changes in each population over time. Epidemiological models are made up of two equilibrium points namely, the Disease-Free Equilibrium and the Endemic Equilibrium.

3.1.1. Disease free Equilibrium point (DFE)

The Disease-Free Equilibrium (DFE) point of a model system is a point where the disease is not present in the population. This means that cholera is absent in the human population and the environment. To find the DFE of the given system (5)-(8), we need to determine the steady-state solution where the infected compartments (I, B) are zero. This is obtained by setting the model equation to zero since there are no infectious individuals in the population and therefore no disease to recover from. This means that;

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = \frac{dB}{dt} = 0 \quad (15)$$

So that,

$$\Lambda - \beta_e S\frac{B}{k+B} - \beta_h SI + \omega R - \mu S = 0 \quad (16)$$

$$\beta_e S\frac{B}{k+B} + \beta_h SI - \gamma I - \mu I = 0 \quad (17)$$

$$\gamma I - (\omega + \mu)R = 0 \quad (18)$$

$$\delta I - \xi B = 0 \quad (19)$$

Since there are no infections at the Disease-Free equilibrium hence, $I = 0$ and substituting this into equation (19) yields;

$$\delta(0) - \xi B = 0$$

Therefore, $B = 0$

Also, we see from equation (18) that:

$$(0)I - (\omega + \mu)R = 0$$

Which implies that; $R = 0$

Furthermore, from equation (17),

$$I = 0$$

Similarly, from equation (16) we get;

$$\Lambda - 0 - 0 - \mu S = 0$$

Therefore, $S = \frac{\Lambda}{\mu}$

Hence, there exists a Disease-Free Equilibrium point given as;

$$(S_0, I_0, R_0, B_0) = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right) \quad (20)$$

3.1.2 Basic Reproduction Number

The basic reproduction number denoted by R_0 is the average number of secondary infections caused by an infectious individual during his/her entire period of infectiousness.

Hence, we calculate the basic reproduction number using the Next Generation Matrix approach.

Let's consider the matrix H

Consisting of two $n \times n$ matrices F and V such that;

$H = FV^{-1}$

And

$$F = \left[\frac{\partial \mathcal{F}_i(E_0)}{\partial x_j}\right], \qquad and \qquad V = \left[\frac{\partial \mathcal{V}_i(E_0)}{\partial x_j}\right]$$

Here, F is defined as the Jacobian of $\mathcal{F}_i$ such that, f_i is the rate of appearance of new infections in compartment i. V is the Jacobian of $\mathcal{V}_i$ such that, v_i is the rate of transfer of individuals from compartment i by all other means and E_0 is the disease free equilibrium. The basic reproduction number R_0 is therefore, given as the dominant Eigen-value or the spectral radius of matrix H.

Thus, $R_0 = \text{þ}FV^{-1}$ (21)

Using the system of equations in equation (5 – 8), by considering the infectious compartment to be I and B, identifying the infectious compartment as equation (5) and (6) of the mathematical model.

$$\frac{dI}{dt} = \beta_e S\frac{B}{k+B} + \beta_h SI - (\gamma + \mu)I \quad (22)$$

$$\frac{dB}{dt} = \delta I(t-\tau) - \xi B \quad (23)$$

The linearized system of the equations (22) and (23) about the DFE is given by $F = \begin{bmatrix} \beta_e S\frac{B}{k+B} + \beta_h SI \\ \delta I(t-\tau) \end{bmatrix}$ and $V = \begin{bmatrix} (\gamma+\mu)I \\ \xi B \end{bmatrix}$

By computing the Jacobian matrices and evaluating at DFE, we get

$$F = \begin{bmatrix} \beta_h\frac{\Lambda}{\mu} & \beta_e\frac{\Lambda}{\mu k} \\ \delta & 0 \end{bmatrix} \quad (24)$$

$$V = \begin{bmatrix} \gamma + \mu & 0 \\ 0 & \xi \end{bmatrix} \tag{25}$$

$$FV^{-1} = \begin{bmatrix} \left(\frac{\beta_h \Lambda}{\mu(\gamma+\mu)}\right) & \left(\frac{\beta_e \Lambda}{\mu k \xi}\right) \\ \frac{\delta}{\gamma+\mu} & 0 \end{bmatrix} \tag{26}$$

The characteristics equation is,

$$\lambda^2 - \left(\frac{\beta_h \Lambda}{\mu(\gamma+\mu)}\right)\lambda - \left(\frac{\beta_e \Lambda \delta}{\mu k \xi(\gamma+\mu)}\right) = 0$$

But by the Next Generation Matrix principle, the largest or dominant Eigen value is the Basic Reproduction Number ($R_0 = \text{þ}FV^{-1}$). Therefore, the Basic Reproduction Number becomes;

$$R_0 = \frac{1}{2}\left[\frac{\beta_h \Lambda}{\mu(\gamma+\mu)} + \sqrt{\left(\frac{\beta_h \Lambda}{\mu(\gamma+\mu)}\right)^2 + \frac{4\beta_e \Lambda \delta}{\mu k \xi(\gamma+\mu)}}\right] \tag{27}$$

3.2. Local Stability of the Disease-Free Equilibrium

Theorem 3.1: The Disease-Free Equilibrium, E_0 of the model is locally asymptotically stable if $R_0 < 1$ and is unstable if $R_0 > 1$.

Proof:

The system is linearized by computing the Jacobian matrix of the system at the DFE. The dynamical system's Jacobian matrix J becomes

Let $a_1, a_2, a_3, a_4 \in A$ and

$$a_1(s,i,r,b) = \Lambda - \beta_e S\frac{B}{k+B} - \beta_h SI + \omega R - \mu S$$

$$a_2(s,i,r,b) = \beta_e S\frac{B}{k+B} + \beta_h SI - \gamma I - \mu I$$

$$a_3(s,i,r,b) = \gamma I - (\omega + \mu)R$$

$$a_4(s,i,r,b) = \delta I(t-\tau) - \xi B$$

So that the Jacobian Matrix becomes

$$A=\begin{bmatrix} -\mu & \beta_h\frac{\Lambda}{\mu} & \omega & -\beta_e\frac{\Lambda}{\mu k} \\ 0 & \beta_h\frac{\Lambda}{\mu}-\gamma-\mu & 0 & \beta_e\frac{\Lambda}{\mu k} \\ 0 & \gamma & -(\omega+\mu) & 0 \\ 0 & \delta e^{-\lambda\tau} & 0 & -\xi \end{bmatrix}$$

This is a transcendental equation due to the delay term $e^{-\lambda\tau}$. Solving it analytically is challenging, but we can analyze the stability by considering the no-delay case ($\tau = 0$) and using the Routh-Hurwitz criterion.

Evaluating the Eigen values of A to obtained

$$|A-\lambda I|=\begin{bmatrix} -\mu & \beta_h\frac{\Lambda}{\mu} & \omega & -\beta_e\frac{\Lambda}{\mu k} \\ 0 & \beta_h\frac{\Lambda}{\mu}-\gamma-\mu & 0 & \beta_e\frac{\Lambda}{\mu k} \\ 0 & \gamma & -(\omega+\mu) & 0 \\ 0 & \delta e^{-\lambda\tau} & 0 & -\xi \end{bmatrix}-\lambda\begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

$$=\begin{bmatrix} -(\mu+\lambda) & \beta_h\frac{\Lambda}{\mu} & \omega & -\beta_e\frac{\Lambda}{\mu k} \\ 0 & \beta_h\frac{\Lambda}{\mu}-\gamma-\mu-\lambda & 0 & \beta_e\frac{\Lambda}{\mu k} \\ 0 & \gamma & -(\mu+\omega)-\lambda & 0 \\ 0 & \delta e^{-\lambda\tau} & 0 & -(\xi+\lambda) \end{bmatrix}$$

$$=-(\mu+\lambda)\begin{bmatrix} \beta_h\frac{\Lambda}{\mu}-\gamma-\mu-\lambda & 0 & \beta_e\frac{\Lambda}{\mu k} \\ \gamma & -(\mu+\omega+\lambda) & 0 \\ \delta e^{-\lambda\tau} & 0 & -(\xi+\lambda) \end{bmatrix}$$

$$|A-\lambda I|=(\mu+\lambda)(\mu+\omega+\lambda)\begin{bmatrix} -\beta_h\frac{\Lambda}{\mu}+\gamma+\mu+\lambda & -\beta_e\frac{\Lambda}{\mu k} \\ -\delta e^{-\lambda\tau} & (\xi+\lambda) \end{bmatrix} \quad (28)$$

From equation (24), we see that $\lambda_1 = -\mu,\ \lambda_2 = -(\mu+\omega+\lambda)$. We then proceed to find the other Eigen values of the reduced block matrix given by;

$$A=\begin{bmatrix} -\beta_h\frac{\Lambda}{\mu}+\gamma+\mu & -\beta_e\frac{\Lambda}{\mu k} \\ -\delta e^{-\lambda\tau} & \xi \end{bmatrix} \quad (29)$$

Let Tr be the Trace of A and α be the determinant of A and considering the linear system $x'(t) = Ax(t)$, the following conditions can be shown;

a) If $\alpha < 0$, the characteristic roots of A will have opposite signs.

b) If $\alpha > 0$ and $\Delta = Tr^2 - 4\alpha \geq 0$, the characteristic roots of matrix A will have the same sign. The roots will be negative if $Tr < 0$ and positive if $Tr > 0$.

c) If $\alpha > 0$, $\Delta < 0$ and $Tr \neq 0$ then, the characteristic roots of matrix A will be imaginary with negative real part if $Tr < 0$ and a positive real part if $Tr > 0$.

d) If $\alpha > 0$ and $Tr = 0$ then, matrix A will have purely imaginary roots.

The Eigen values of matrix A are obtained from the characteristic equation;

$$\lambda^2 - (a + d)\lambda + (\mathrm{ad} + \mathrm{bc}) = 0 \quad (30)$$

$$\lambda^2 - Tr\lambda + \alpha = 0$$

$$\lambda = \frac{Tr \pm \sqrt{Tr^2 - 4\alpha}}{2} \quad (31)$$

Thus,

a*) If $\alpha < 0$, there exist two real Eigen values of opposite signs.

b*) If $\alpha > 0$ and $\Delta \geq 0$, there exist two real Eigen values of the same sign as the Trace.

c*) If $\alpha > 0$, $\Delta < 0$ and $Tr \neq 0$, there exist two complex conjugate Eigen values $\lambda = p \pm ir$.

d*) If $\alpha > 0$ and $Tr = 0$, there exist two purely imaginary complex conjugate Eigen values.

Now considering condition (b), we can therefore determine the signs of the other Eigen values. For the remaining two Eigen values to be negative then, $\alpha > 0$ and $Tr < 0$. We now proceed to find the conditions that makes the determinant positive and the Trace negative. From the reduced block matrix, the determinant is given by;

$$\alpha = \xi\left(-\beta_h \frac{\Lambda}{\mu} + \gamma + \mu\right) - \delta e^{-\lambda\tau}\left(\beta_e \frac{\Lambda}{\mu k}\right) \quad (32)$$

Let $a = \beta_h \frac{\Lambda}{\mu} - \gamma - \mu$

When $\tau = 0$, equation (30) becomes,

$$\lambda^2 + (\xi - a)\lambda - a\xi - \beta_e \frac{\Lambda\delta}{\mu k} = 0 \quad (33)$$

The dominant eigenvalue of equation (33) can be shown to be positive if and only if,

$$R_0 = \frac{1}{2}\left[\frac{\beta_h \Lambda}{\mu(\gamma+\mu)} + \sqrt{\left(\frac{\beta_h \Lambda}{\mu(\gamma+\mu)}\right)^2 + \frac{4\beta_e \Lambda \delta}{\mu k \xi(\gamma+\mu)}}\right] > 1 \quad (34)$$

Next, the Trace of the reduced block matrix is given by;

$$Tr = \beta_h \frac{\Lambda}{\mu} - \gamma - \mu - \xi$$

$$Tr = \beta_h \frac{\Lambda}{\mu} - \xi - (\gamma+\mu) \quad (35)$$

Making $(\gamma+\mu)$ the subject of formula from equation (27) we get;

$$(\gamma+\mu) = \frac{\Lambda}{\mu R_0}\left(\beta_h + \frac{\beta_e \delta}{\xi k}\right) \quad (36)$$

On substituting equation (36) into equation (35), we have;

$$Tr = \beta_h \frac{\Lambda}{\mu} - \xi - \frac{\Lambda}{\mu R_0}\left(\beta_h + \frac{\beta_e \delta}{\xi k}\right) \quad (36)$$

Since the Trace of the reduced matrix needs to have negative Eigen values, we look for condition under which $\beta_h \frac{\Lambda}{\mu}$ is negative.

$$\beta_h \frac{\Lambda}{\mu} - \frac{\Lambda}{\mu R_0}\beta_h = 0 \quad (37)$$

Simplifying equation (37) gives;

$$\beta_h \frac{\Lambda}{\mu}\left(1 - \frac{1}{R_0}\right) < 0 \quad (38)$$

From equation (38) we see that if $R_0 < 1$ then, the equation becomes negative. Therefore, the Jacobian matrix of the disease-free equilibrium has negative eigen values only when $R_0 < 1$ which implies that the disease-free equilibrium is locally asymptotically stable. The result of the theorem also confirms the conditions for local stability as outlined in [35]

Even when $\tau > 0$ one may show that the delay does not change the threshold, the DFE is locally asymptotically stable if and only if all characteristic roots have negative real part, and this is equivalent to $R_0 < 1$.

3.3 Stability Analysis of the Endemic Equilibrium

Theorem 3.2: Suppose that $R_0 > 1$, then ∃ an Endemic Equilibrium (EE) of the model that is globally stable and is unstable if $R_0 < 1$.

Proof:

The EE (S^*, I^*, R^*, B^*) satisfies:

$$\Lambda - \beta_e S^* \frac{B^*}{k + B^*} - \beta_h S^* I^* + \omega R^* - \mu S^* = 0$$

$$\beta_e S^* \frac{B^*}{k + B^*} + \beta_h S^* I^* - \gamma I^* - \mu I^* = 0$$

$$\gamma I^* - (\omega + \mu) R^* = 0$$

$$\delta I^* - \xi B^* = 0$$

Thus, we obtain

$B^* = \frac{\delta}{\xi} I^*$, and $R^* = \frac{\gamma}{\omega + \mu} I^*$

Because the model has a discrete time delay, the linearization about the endemic equilibrium is a delay-differential equation. Since the delay is only in the term $\delta I(t - \tau)$ then, only the environmental equation is non-instantaneous. Consider the following co-ordinate transformation; $x_1(t) = S(t), x_2(t) = I(t), x_3(t) = R(t),\ x_4(t) = B(t)$ where (S, I, R, B) denotes the equilibrium points of equations (5) – (8) then;

$$\dot{x}(t) = A_0 x(t) + A_1 x(t - \tau) \tag{39}$$

Where,

$$A_0 = \begin{bmatrix} -\beta_e \frac{B^*}{k+B^*} - \beta_h I^* - \mu & -\beta_h S^* & \omega & -\beta_e \frac{S^* k}{(k+B^*)^2} \\ \beta_e \frac{B^*}{k+B^*} + \beta_h I^* & \beta_h S^* - (\gamma + \mu) & 0 & \beta_e \frac{S^* k}{(k+B^*)^2} \\ 0 & \gamma & -(\mu + \omega) & 0 \\ 0 & \delta & 0 & -\xi \end{bmatrix}$$

$$A_1 = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & \delta & 0 & 0 \end{bmatrix}$$

The characteristic equation becomes

$$\Delta(y) = |y I_{4\times 4} - A_0 - A_1 e^{-\tau y}|$$

Since the recovered variable R is decoupled, we may concentrate on the three-dimensional subsystem in the variables S, I, B,

$$x(t) = \begin{pmatrix} s(t) \\ i(t) \\ b(t) \end{pmatrix}$$

We have,

$$\dot{x}(t) = A_0^* x(t) + A_1^* x(t-\tau)$$

With,

$$A_0^* = \begin{pmatrix} J_{11} & J_{12} & J_{14} \\ J_{21} & J_{22} & J_{24} \\ 0 & 0 & -\xi \end{pmatrix} \text{ and } A_1^* = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & \delta & 0 \end{pmatrix}$$

The characteristic equation becomes

$$\Delta(y) = |yI_{4\times 4} - A_0^* - A_1^* e^{-\tau y}|$$

The characteristics equation of the above can be written as,

$$\delta J_{14} e^{-\tau y}[(y - J_{11}) - J_{21}] + (y + \xi)[(y - J_{11})(y - J_{22}) - J_{12}J_{21}] = 0 \qquad (40)$$

Where, $J_{11} = -\beta_e \frac{B^*}{k+B^*} - \beta_h I^* - \mu$, $J_{12} = -\beta_h S^*$, $J_{14} = -\beta_e \frac{S^* k}{(k+B^*)^2}$, $J_{21} = \beta_e \frac{B^*}{k+B^*} + \beta_h I^*$, $J_{22} = \beta_h S^* - (\gamma + \mu)$

Theorem 3.3: if $R_0 > 1$, then the endemic equilibrium is stable for any time-delay $\tau \geq 0$. If $R_0 < 1$, then the endemic equilibrium is unstable for any time-delay $\tau \geq 0$.

Proof:

The characteristic equation is given by;

$$P(y, \tau) = (y + \mu + \omega)(y + \mu)\left(y^2 + \left(\gamma + \mu + \xi - \beta_h \frac{\Lambda}{\mu}\right)y + \Gamma_1 + \Gamma_2\right) = 0 \qquad (41)$$

Where $\Gamma_1 = \delta\beta_e \frac{\Lambda}{\mu} e^{-\tau y}$, $\Gamma_2 = \xi(\gamma + \mu) - \xi\beta_h \frac{\Lambda}{\mu} - \delta\beta_e \frac{\Lambda}{\mu k}$

Case 1: Let $\tau = 0$

Then, equation (41) becomes;

$$P(y,0) = (y+\mu+\omega)(y+\mu)\left(y^2 + \left(\gamma+\mu+\xi-\beta_h\frac{\Lambda}{\mu}\right)y + \delta\beta_e\frac{\Lambda}{\mu} + \Gamma_2\right) = 0 \qquad (42)$$

We need to prove that all roots of the characteristic equation have negative real parts. It is quite easy to see from (42) that $y_1 = -\mu, y_2 = -\omega - \mu$ are roots of (42) and are all negative. Thus, we just need to analyze the third term of (42), here denoted by P_1.

Thus,

$$P_1(y,0) = \left(y^2 + \left(\gamma+\mu+\xi-\beta_h\frac{\Lambda}{\mu}\right)y + \delta\beta_e\frac{\Lambda}{\mu} + \Gamma_2\right) = 0$$

Using the Routh-Hurwitz criterion, we know that all roots of $P_1(y,0)$ have negative real parts if and only if the co-efficient of $P_1(y,0)$ are strictly positive. In this case, we have $\left(\gamma+\mu+\xi-\beta_h\frac{\Lambda}{\mu}\right) > 0$ if and only if $\gamma+\mu+\xi > \beta_h\frac{\Lambda}{\mu}$ and $\Gamma_2 = \xi(\gamma+\mu) - \xi\beta_h\frac{\Lambda}{\mu} - \delta\beta_e\frac{\Lambda}{\mu k} > 0$ if and only if $R_0 < 1$, since;

$$\xi\beta_h\frac{\Lambda}{\mu} - \delta\beta_e\frac{\Lambda}{\mu k} = \frac{\Lambda}{\mu(\gamma+\mu)}\left(\beta_h - \beta_e\frac{\delta}{\xi k}\right)\xi(\gamma+\mu) = R_0\big(\xi(\gamma+\mu)\big)$$

This implies that;

$$\Gamma_2 = \xi(\gamma+\mu) - \xi\beta_h\frac{\Lambda}{\mu} - \delta\beta_e\frac{\Lambda}{\mu k} = \xi(\gamma+\mu) - R_0\big(\xi(\gamma+\mu)\big)$$

$$= \xi(\gamma+\mu)(1-R_0)$$

Clearly, Γ_2 is positive only if $R_0 < 1$.

Case II: Let $\tau > 0$

We use Rouche's theorem to prove that all roots of the characteristic equation (41) cannot intersect the imaginary axis i.e the characteristics equation cannot have pure imaginary roots. Suppose the contrary, that is, suppose there exist $\omega \in \mathbb{R}$ such that $y = \omega i$ is a solution of equation (42). Replacing $y = \omega i$ in the second term of equation (41), we get;

$$-\omega^2 + \left(\gamma+\mu+\xi-\beta_h\frac{\Lambda}{\mu}\right)\omega i + \left(\xi(\gamma+\mu) - \left(\xi\beta_h\frac{\Lambda}{\mu} + \delta\beta_e\frac{\Lambda}{\mu k}\right)\right) + \delta\beta_e\frac{\Lambda}{\mu k}\big(\cos(\tau\omega) - i\sin(\tau\omega)\big) = 0$$

Let $\Gamma_1 = \delta\beta_e\frac{\Lambda}{\mu}e^{-\tau y}$, $\Gamma_2 = \xi(\gamma+\mu) - \left(\xi\beta_h\frac{\Lambda}{\mu} + \delta\beta_e\frac{\Lambda}{\mu k}\right), \Gamma_0 = \left(\gamma+\mu+\xi-\beta_h\frac{\Lambda}{\mu}\right)$

So that we get;

$$-\omega^2 + \Gamma_0\omega i + \Gamma_2 + \Gamma_1\left(\cos(\tau\omega) - i\sin(\tau\omega)\right) = 0$$

Separating the real and imaginary parts gives;

$$\begin{cases} -\omega^2 + \Gamma_2 = -\Gamma_1\cos(\tau\omega) \\ -\Gamma_0\omega = -\Gamma_1\sin(\tau\omega) \end{cases}$$

By adding up the squares of both equations and using the fundamental trigonometric formula, we obtain;

$$\omega^4 + (\Gamma_0{}^2 - 2\Gamma_2)\omega^2 + \Gamma_2{}^2 - \Gamma_1{}^2 = 0 \tag{43}$$

Then,

$$\omega^2 = \frac{1}{2}\left[-(\Gamma_0{}^2 - 2\Gamma_2) \pm \sqrt{(\Gamma_0{}^2 - 2\Gamma_2)^2 - 4(\Gamma_2{}^2 - \Gamma_1{}^2)}\right]$$

This implies that equation (43) has no positive roots when $R_0 > 1$ which shows that equation (41) has no imaginary roots for all $\tau > 0$. Therefore, the endemic equilibrium is locally stable for any $\tau > 0$.

4.1 Model parameters and values

Some of the parameters which are compatible with cholera have been obtained from literature while others have been estimated. The parameter values are shown in Table 3.

Table 3: Parameters of Cholera Model

Symbol	Value	Source
$\boldsymbol{\Lambda}$	4.109 x 10^3 People/day	Omondi et al., 2015
$\boldsymbol{\mu}$	2.537 x 10^{-5} People/day	Omondi et al., 2015
$\boldsymbol{\beta_e}$	Varied day^{-1}	Varied
$\boldsymbol{\beta_h}$	Varied day^{-1}	Varied
$\boldsymbol{k}$	9.5 x 10^{-4} day^{-1}	Estimated
$\boldsymbol{\gamma}$	1.884 x 10^{-3} day^{-1}	Tate et al., 2009
$\boldsymbol{\delta}$	1.0 x 10^{-3} day^{-1}	Assumed
$\boldsymbol{\xi}$	2.3 x 10^{-1} day^{-1}	Mari et al., 2011
$\boldsymbol{\omega}$	2.778 x 10^{-3} day^{-1}	Vesikari et al., 2006

τ	Varied day^{-1}	Parashar et al., 2003

4.1 Numerical Simulation

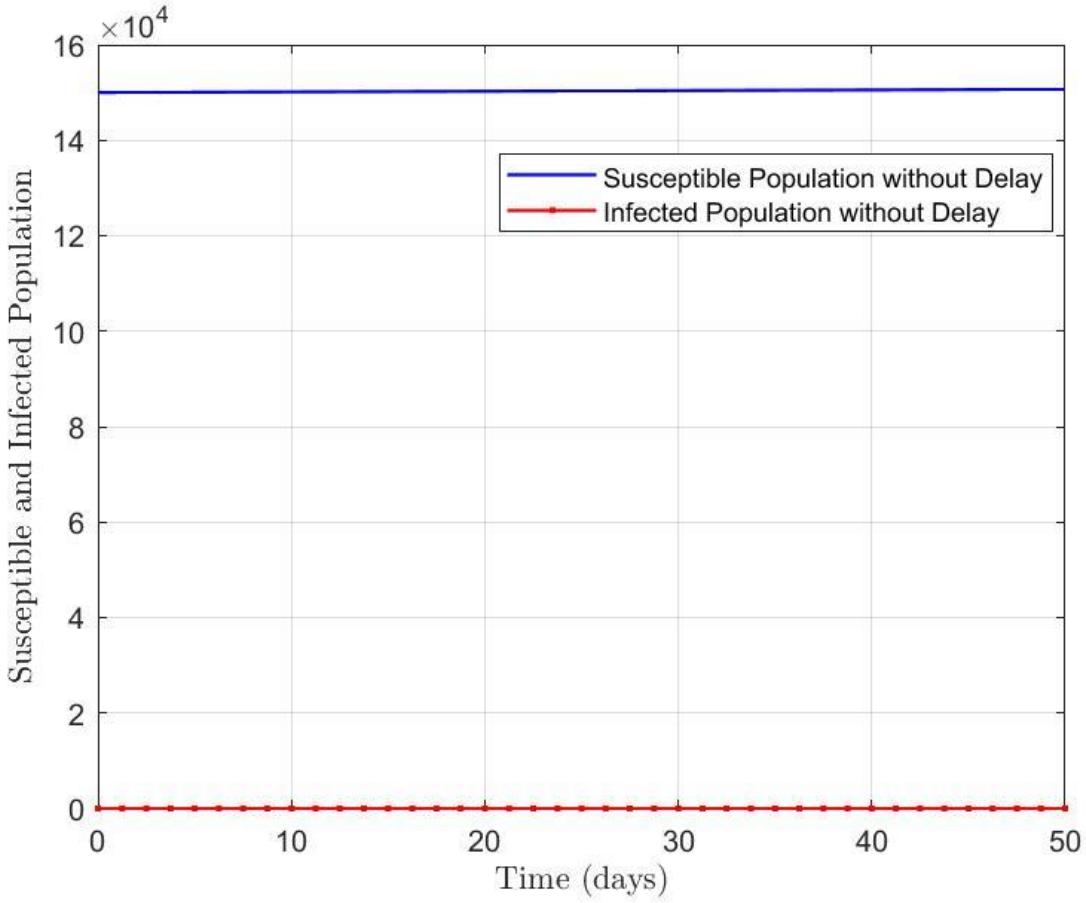

Figure 4.1: Dynamics of Susceptible and Infected Population with Delay

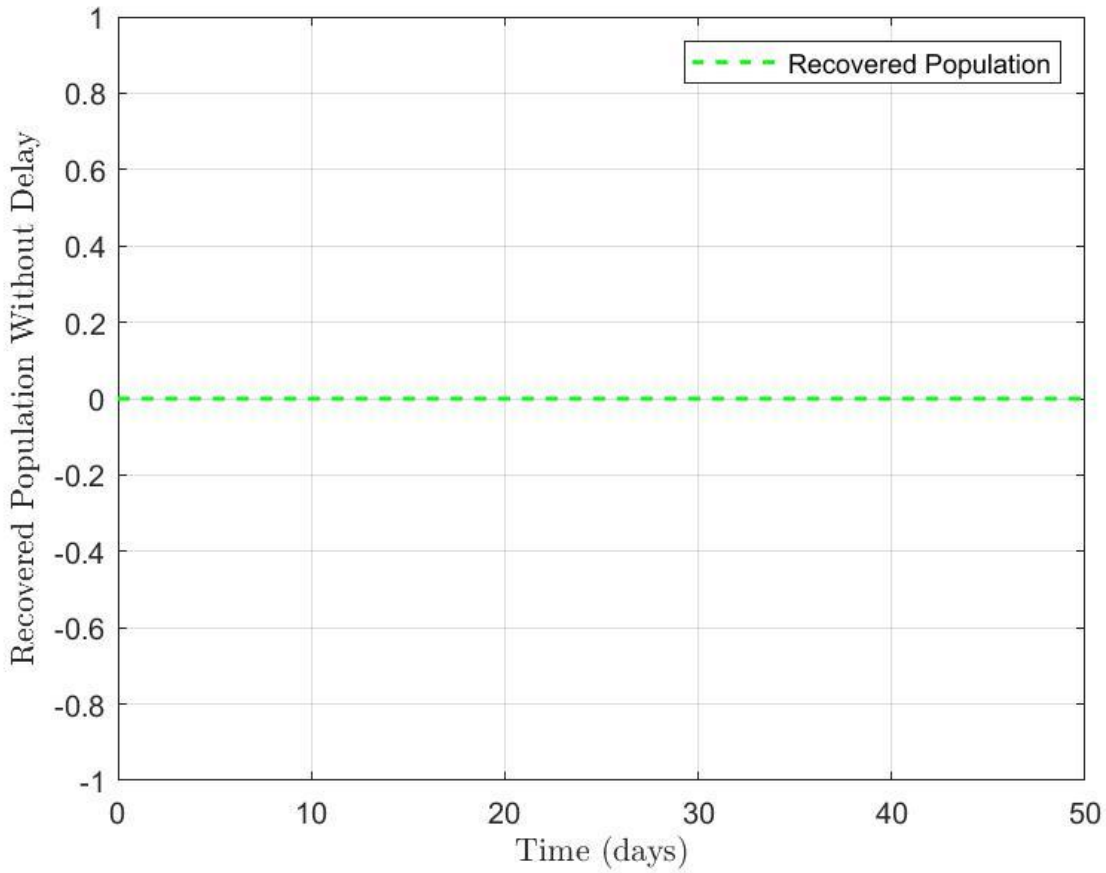

Figure 4.2: Dynamics of Recovered Population with Delay

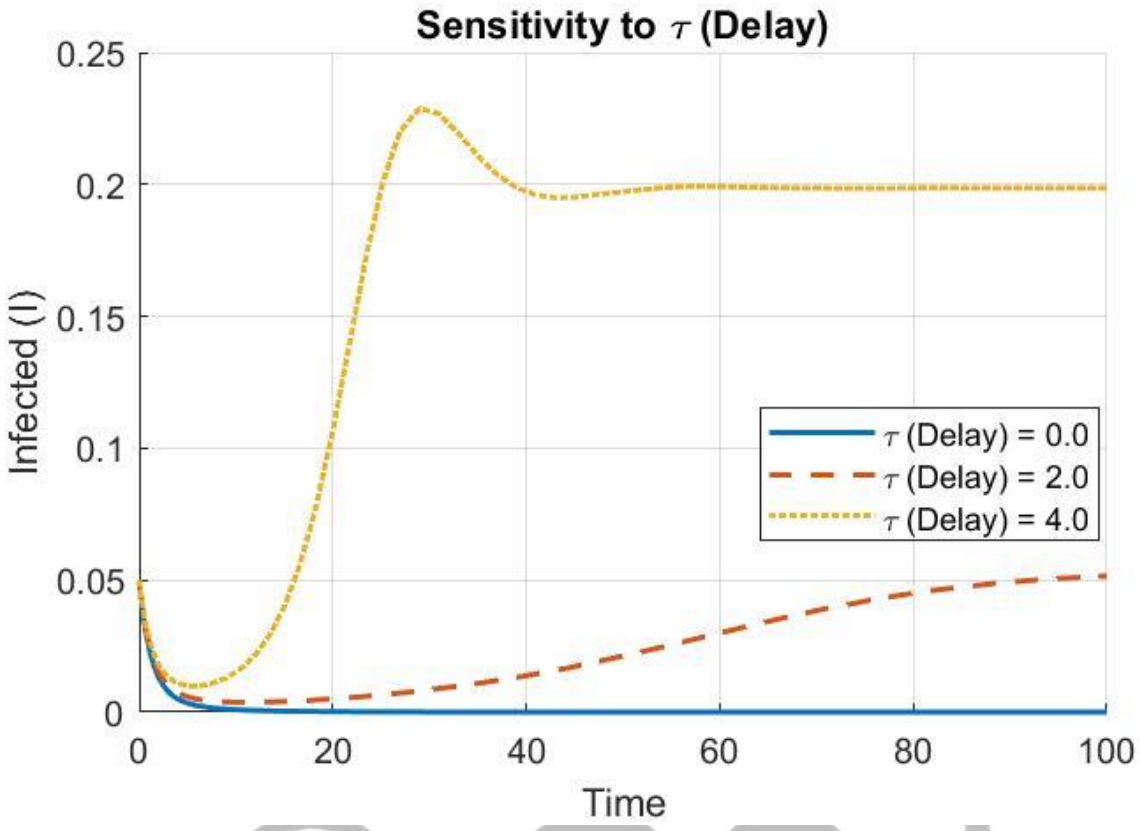

Figure 4.3: Plot of the Sensitivity of Delay in the Infected Population

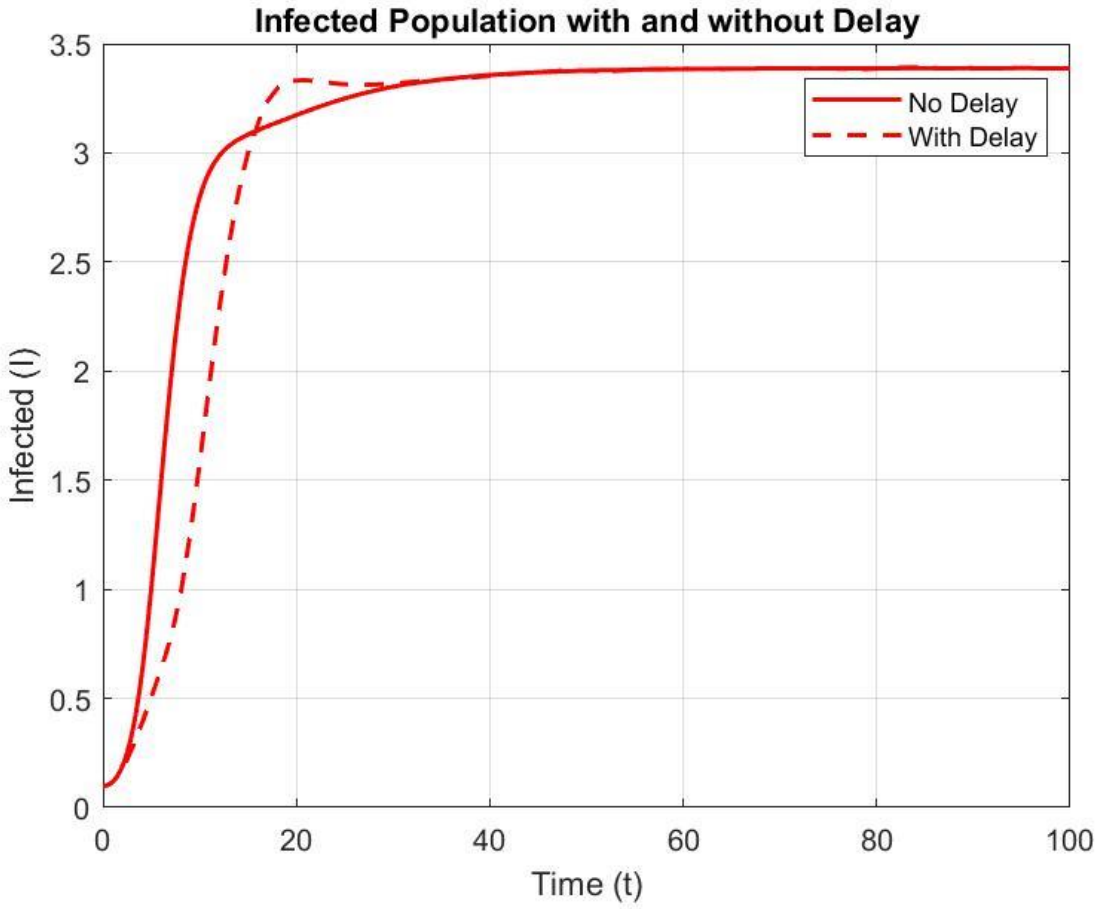

Figure 4.4: Dynamics of Infected Population with and without Delay

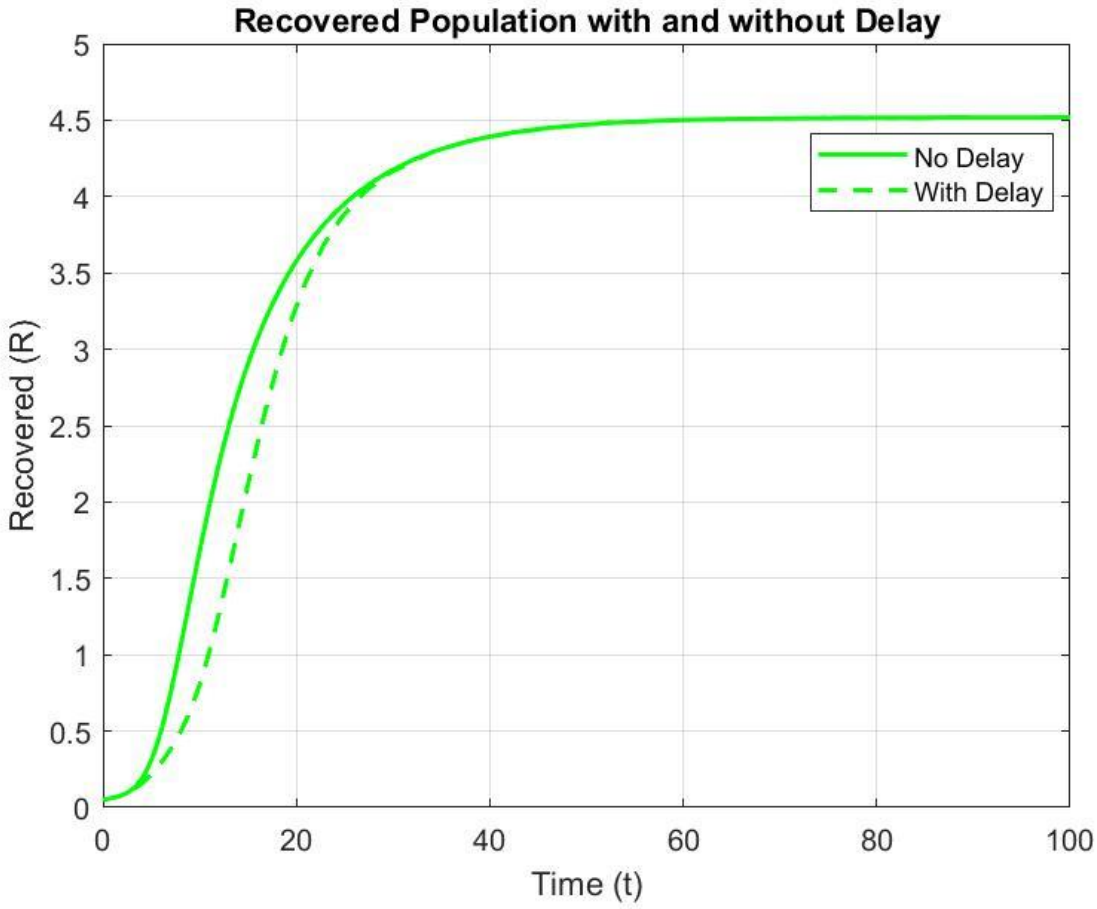

Figure 4.5: Dynamics of Recovered Population with and without Delay

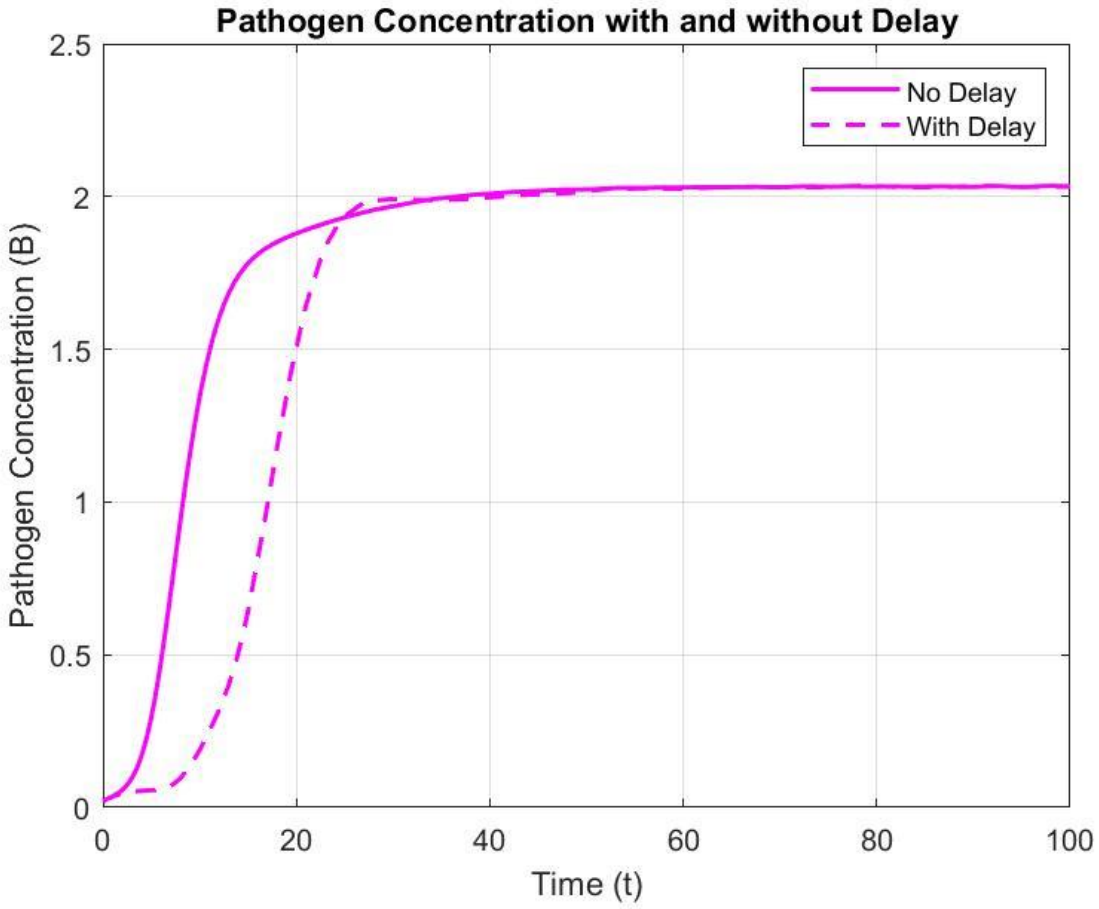

Figure 4.6: Dynamics of Pathogen Concentration with and without Delay

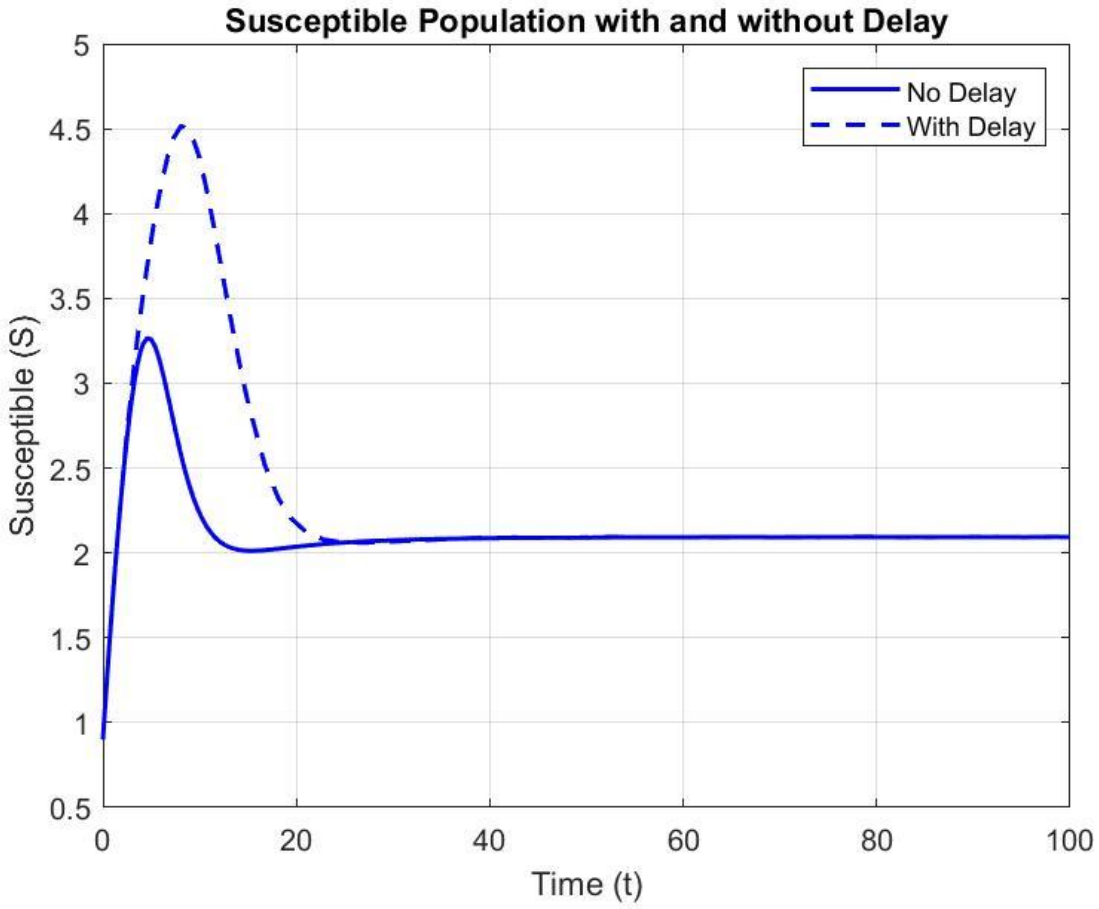

Figure 4.7: Dynamics of Susceptible Population with and without Delay

In this section, we present the numerical simulation of the proposed model (5-8). The given system is solved numerically by using MATLAB. The parameter value and their description has been presented in Table 4.3.

To be able to illustrate the behaviour of solutions with time, there must be a susceptible human population and *Vibrios* in the environment therefore, $S(t) > 0, B(t) > 0, I(t) \geq 0$ and $R(t) \geq 0$. With these conditions in mind, we consider the following initial values $S(t) = 100, I(t) = 1, R(t) = 1 \; and \; B(t) = 8$. When we calculate R_0 from the values shown in Table 4.3, we get its value to be $0.8329 < 1$. A numerical simulation of the cholera model using the original system variables before normalization was conducted using MATLAB's ode45.

Figure 4.1 and figure 4.2 shows that when $R_0 < 1$ all the trajectories of infectives and recovered converge to zero regardless of the parameter values. Also, the susceptible population remain stable in the DFE. Consequently, our cholera free state can only be asymptotically stable.

Using the values in Table 4.3 and varying some parameter values, to get $R_0 > 1$, we compute the value of $R_0 = 3.214 > 1$. When $R_0 > 1$, the cholera free equilibrium becomes unstable and the endemic equilibrium becomes stable. Consequently, the endemic equilibrium is asymptotically stable.

Comparing the system with and without delay, it can be seen that there is a significant difference in the susceptible infected, recovered and pathogen population with and without delay. The analysis of figure 4 – figure 7 clearly shows stability at $R_0 > 1$ for this combined human-environment epidemiological model. We also see from figure 4.3, varying the value of the delay term significantly affects the growth rate of the infectives. The higher the delay term, the more infected individuals are increased in the system, while a lower delay term also reduces the number of infected individuals in the environment.

5.0 Conclusion

This paper is devoted to the formulation and analysis of a time-delayed mathematical model for cholera. We also added time delay, which represents the time between the instant at which an individual becomes infected and the instant at which he begins to have symptoms of cholera infection by the bacterium Vibrio cholerae. The considered model is a $SIRB$ (Susceptible, Infectious, Recovered, Bacteria Concentration) system, where an additional class B (a class of bacterial concentration in the dynamics of cholera) is considered. The formulated model is analyzed, providing the non-negativity of the solutions for non-negative initial conditions, as well as the disease-free equilibrium, basic reproduction number, and endemic equilibrium. Through the analysis of the model, it has been found that in the absence of delay, the disease-free equilibrium E_0 is unstable whenever the endemic equilibrium EE exists. However, the endemic equilibrium is locally stable and remains stable for all $t > 0$ each time under $R_0 > 0$. Our analysis shows that the ingestion rate of the bacteria through contaminated sources β has an important influence on the stability of the endemic equilibrium. Finally, the main contributions and novelties of this paper are, (i) a more realistic cholera model with time delay; (ii) inclusion of pathogen concentration compartment (iii) considering multiple transmission pathways. For future work, we suggest that an investigation of how inclusion of a control measure in terms of vaccine will affect this model should be done. We also propose that future researchers should try and implement this model in a multi-group framework with multiple delay.

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