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A Between-Host Cholera Mathematical Model Incorporating Temperature Dependence

Owade Kennedy Jackob[1]
Okaka Akinyi[2]
Frankline Tireito[3]

[1,2,3] Department of Mathematics, Masinde Muliro University of Science and Technology, P.O Box 190-50100, Kakamega (Kenya).

*kowade@mmust.ac.ke

Abstract

This paper establishes a between-host cholera model with temperature dependent parameter. This is done using system of $ODEs$ to analyse the effect of temperature change on cholera disease. The model analysis reveals that when $R_0 < 1$, the disease free equilibrium point is locally and globally asymptotically stable. It is also noticed that if $R_0 > 1$, the endemic equilibrium point is locally asymptotically stable. The sensitivity analysis of model parameters shows that R_0 depends intensively on infection rate of pathogen α_1 normalized with temperature. An increase in infection rate of pathogen α_1 that is dependent on temperature by 10% would increase R_0 by 10% and decreasing it by 10% reduces R_0 by 10%; hence, increasing the temperature of the environment where the pathogen lives would help reduce the rate of infection of the pathogen, thus reducing the reproduction number R_0. We conducted numerical simulation of the model in response to temperature changes, and the results indicate that $Vibrio\ cholerae$ pathogens multiply faster at 23^0C but between $23^0C < T \leq 43^0C$ the pathogen multiplication is hindered, therefore, at 23^0C, more pathogens active to cause infection compared to high temperatures.

Keywords: Between-Host Cholera Model; Temperature dependent Parameter

1 Introduction

Cholera is one of the acute diarrhoeal disease that results when people take food/water contaminated with cholera pathogen known as *Vibrio cholerae*. Cholera continues to threaten human life and, therefore, is a pointer to social and human development. In order to extend efforts in the fight against cholera, governments worldwide and healthcare organizations have included specific measures in a set of controls, such as use of clean water, food quality, sanitation and vaccination.

Even with vaccination against cholera, *Vibrio cholerae* is still found in the human small intestine and is either defecated or transferred between people [17]. From research [18], the typical standard state environmental temperature is, on average 20.0^0C to 25.0^0C, and the average axillary body temperature is 37.0^0C, the upper limit of which is regarded as 38.0^0C. The study done in [1] concludes that temperature influences the rate of disease transmission through various characteristics that affects the vector population, including the reproduction rate, development period, mortality rate, and the period with which the vector bites. As theoretical work has also pointed out, many other functions and most life history characters are temperature sensitive, and these traits generally exhibit non-linear temperature slopes [1]. From the cross-sectional research, it has been evidenced that cholera incidence has been more dominant when there is interchange of seasons persistently involving the human population and cholera disease [4].

Impacts on the quality of drinking waters can be related to changes in environmental conditions such as climate. Flooding can worsen waste-water treatment plants or septic systems or cause combined sewerage systems to overflow and pollute nearby water surfaces or wells. In addition, attention is being paid to the presence of pathogens in storm waters[4]. Also, sanitary water conditions are another problem during drought, as the available water has concentrated contamination. Besides, multiple uses of water from the same water body, for example, cleaning, bathing, and drawing water during drought, may raise the risk of water contamination and, therefore exposure to cholera disease.

A study by Arquam *et al* [8] formulated an SIR model given by;

$$\begin{aligned}
\frac{dS_{hk(t)}}{dt} &= -\beta_h(k)S_{hk}(t)I_{hk}(t) - \beta_{vh}b(T)S_{hk}(t)I_n(t) \\
\frac{dI_{hk(t)}}{dt} &= \beta_h(k)S_{hk}(t)I_{hk}(t) + \beta_{vh}b(T)S_{hk}(t)I_v(t) - \mu_h I_{hk}(t) \\
\frac{dR_{hk(t)}}{dt} &= \mu_h I_{hk}(t) \qquad (1)
\end{aligned}$$

where $b(T)$ is the bitting rate that is a function of temperature. The study aimed to find a correlation between temperature and the spread of vector diseases. Since the research found that favourable temperature enhance the transfer of the disease from vector to host, consequently, to the host population. The study additionally demonstrates that the disease's spread rate escalates as the threshold value $b(T)$ is squared and is dependent on temperature and this shows that temperature increases the critical threshold value of the spreading rate of the disease.

Population migration frequently influences malaria prevalence in relation to temperature fluctuations; therefore, Eunice *et al*[13] formulated a model to predict the effect of these factors in Nigeria. A new deterministic model analyzes the effect of temperature fluctuations and immigration on malaria incidence in Nigeria at the population level. There is also the transmission of disease by immigrants into the community. However, this demonstrates the scenario of backward bifurcation in the absence of immigration. The analysis of DFE of the model proved that the steady-state of prevalence rate of the disease is locally asymptotically stable when there are no infective immigrants. However, the outcome demonstrates that the model possesses an endemic equilibrium stage if the immigration parameter is positive. When there is no disease induced death, it is possible to demonstrate that the endemic equilibrium point is globally attractive. Hence, numerical studies of the model reveal that in Nigeria, the risk of malaria rises with mean temperatures in the range $(22 \text{ to } 28)^0C$.

Salisu and Danbaba [9] formulated a model on the impact of temperature fluctuations on controlling malaria. It rises with births because new individuals who are wholly susceptible to the disease are continuously added to the population. This population strengthens through the depreciation of vaccinated-acquired immunity by wholly vaccinated people and weakens through vaccination. From this, it can be deduced that a proportion of these individuals get infected with malaria after effective interaction with ineffective mosquitoes at a temperature dependent rate $\lambda H(T)$, given by;

$$\lambda H(T) = \frac{\beta_{VH} M_I(t)}{N_V(t)}(1 - \epsilon_B \alpha_B)\alpha_M(T)$$

The study constructs and discusses both a non-autonomous and autonomous models for malaria transmission in a population. We use it to forecast the effect of temperature fluctuations on the spread of cholera disease.

Therefore, a between-host cholera model that has temperature dependent parameter is developed in this paper, the infection rate of the pathogen α_1 that is dependent on temperature is incorporated both on long and short cycle transmission roots. This will help us understand the dynamics of cholera disease with temperature change.

2 Model Description, Formulation and Analysis

We divide the human population into three categories: Susceptible individuals $S(t)$, Infected individuals $I(t)$ and the Recovered individuals $R(t)$. $B(t)$ is incorporated in the model which indicates the *Vibrio cholerae* concentration as a function of time. The system enlists vulnerable people being recruited at a constant rate β. Through interaction, the following factors reduce the population of the susceptible individuals: infection resulting from interaction with the *Vibrio cholerae* in the environment (long cycle) at the rate θ and in the house-hold (short cycle) at a rate θ_1. Notably, the transmission rates through the long and short cycle is regulated through ω and ϕ. Susceptible individuals are reduced through oral vaccination at the rate v. Interaction with the cholera pathogen *Vibrio cholerae* creates the infected population the rate δA

In formulation of this model, the environment's temperature is considered as a determining factor in the multiplication of *Vibrio cholerae* and its ability to cause infection; hence, the temperature dependent parameter $\alpha_1(T)$ is incorporated into both the long and short cycle transmission routes. The number of infected people produced owing to the route time generated by the interaction of the susceptible individuals with the pathogen in the environment is given by $\omega\theta\frac{SB\alpha_1(T)}{K+B}$.

$\phi\theta_1 SI\alpha_1(T)$ is the rate at which people are infected by the short route, as a result of infected individuals interacting with the susceptible. The rate of infection-related death, natural death, and infection recovery reduces the infected population at the rates σ, μ and γ respectively. K is carrying capacity of vibrios. Additionally, susceptible individuals receive vaccination at the rate v. The natural death contribute to this population's reduction at a rate μ. The concentration of the vibrio is generated into the population at a rate ϵ through the action of the infected individuals [15] and is cleared by natural death at the rate μ_1.

The system of $ODEs$ based on the description above is:

$$\begin{aligned}
\frac{dS}{dt} &= (1-\delta)A + \beta S - \frac{\omega\theta SB\alpha_1(T)}{K+B} - \phi\theta_1 SI\alpha_1(T) - (v+\mu)S \\
\frac{dI}{dt} &= \delta A + \frac{\omega\theta SB\alpha_1(T)}{K+B} + \phi\theta_1 SI\alpha_1(T) - (\gamma+\epsilon+\mu+\sigma)I \\
\frac{dR}{dt} &= \gamma I + vS - \mu R \\
\frac{dB}{dt} &= \epsilon I - \mu_1 B
\end{aligned} \tag{2}$$

2.1 Positivity and Boundedness of the Model

Proposition 1. *Solutions of model (2) are positive in the region defined as* $\psi = (S, I, R) \in \mathbb{R}^3_+ \times \mathbb{R}$

Proof. Considering the first equation of (2), we see that

$$\begin{aligned}
\frac{dS}{dt} &= (1-\delta)A + \beta S - \frac{\omega\theta SB\alpha_1(T)}{K+B} - \phi\theta_1 SI\alpha_1(T) - (v+\mu)S \\
&= -\{\frac{\omega\theta B\alpha_1(T)}{K+B} + \phi\theta_1 I\alpha_1(T) + (v+\mu)\}S
\end{aligned} \tag{3}$$

This implies that $S(t) > S_0 e^{-\int_0^t \frac{\omega\theta B\alpha_1(T)}{K+B} + \phi\theta_1 I\alpha_1(T) + (v+\mu)dt} > 0$

This implies that $S(t) > 0$.

From the second equation of model (2) given by;

$$\frac{dI}{dt} = \delta A + \frac{\omega\theta SB\alpha_1(T)}{K+B} + \phi\theta_1 SI\alpha_1(T) - (\gamma + \epsilon + \mu + \sigma)I$$

$$> -(\gamma + \epsilon + \mu + \sigma)I$$

In a similar manner it results in $I(t) > I_0 e^{-\int_0^t (\gamma+\epsilon+\mu+\sigma)dt} > 0$

This implies that $I(t) > 0$.

Also from the third equation of model (2) given by;

$$\frac{dR}{dt} = \gamma I + vS - \mu R$$

Which results in $R(t) = R_0 e^{-\int_0^t (\mu)dt} > 0$
This implies that $R(t) > 0$.

Therefore the region $\psi = (S, I, R) \in \mathbb{R}^3_+$ is a positive invariant set for the system of equation (2). Hence, the solutions of model (2) are all positive. □

Since model (2) formulated describes human population, the population will always remain bounded. We use *Proposition* (2) to prove for boundedness of the model as follows;

Proposition 2. *Solutions of model (2) are bounded for* $t \geq 0$ *in the region* $\psi \in \mathbb{R}^3_+$

Proof. Given $N(t) := S(t) + I(t) + R(t)$ as the total number of human population. From the system of equation (2);

$$N'(t) \leq \delta A - \mu(S + I + R) \leq \delta A - \mu N(t)$$
$$N'(t) \leq \delta A - \mu N(t)$$

Integrating both sides of $N'(t) \leq \delta A - \mu N(t)$ with respect to (t) given by;

$$\int N'(t)dt \leq \int (\delta A - \mu N(t))dt$$

$$N(t)e^{\mu t} \leq \int \frac{\delta A}{\mu} e^{\mu t} dt$$

Integrating the right side of $N(t)e^{\mu t} \leq \int \frac{\delta A}{\mu} e^{\mu t} dt$ with respect to (t) yields

$$N(t)e^{\mu t} \leq \frac{\delta A}{\mu^2} e^{\mu t} + C$$

$$N(t) \leq \frac{\delta A}{\mu^2} + Ce^{-\mu t}$$

$$\lim_{t\to\infty} N(t) \leq \frac{\delta A}{\mu^2}$$

Therefore, $N(t)$ is bounded. From *Proposition* (1) and (2), solutions of model (2) are positive and bounded provided $t \geq 0$. Hence, system (2) is epidemiologically meaningful for its solutions to be considered in ψ. □

3 Basic Reproduction Number, R_0.

Definition 3.1. *The basic reproduction number* (R_0) *is the number of secondary infections resulting from the introduction of an infective individual into a population of susceptible individuals.*

Applying the method of next generation matrix approach given by Van den and Watmough [14] to determine the basic reproduction number R_0, consider the matrix formed by;

$$R_0 = FV^{-1}.$$

Where F is the Jacobian of $\mathcal{F}$ which refers to the rate of new infection and V is the Jacobian of $\mathcal{V}$ which is the matrix for the transition terms. From model (2) the associated matrices are;

$$\mathcal{F} = \begin{pmatrix} \frac{\omega\theta SB\alpha_1(T)}{K+B} + \phi\theta_1 SI\alpha_1(T) \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{4}$$

$$\mathcal{V} = \begin{pmatrix} (\gamma+\epsilon+\mu+\sigma)I \\ 0 \\ -(\gamma I + vS) + \mu R \\ -\epsilon I + \mu_1 B \end{pmatrix} \tag{5}$$

The reproduction number $R_0 = \rho(FV^{-1})$ is the spectral radius of the matrix FV^{-1}. Therefore;

$$R_0 = \frac{(1-\delta)A\phi\theta_1\alpha_1(T)}{(v+\mu-\beta)(\gamma+\epsilon+\mu+\sigma)} \tag{6}$$

Since R_0 is a measure of the severity of an epidemic, it determines whether the disease will invade in a population. Epidemiologically, this implies that if $R_0 < 1$ the infection dies out and if $R_0 > 1$ the disease persist in the population which may result to occurrence of the disease.

3.1 Existence of DFE point

This is a state in which there is no cholera disease, hence $I = B = 0$.

Proposition 3. *For the model (2) there always exists a DFE point denoted* (S^0, I^0, R^0, B^0).

Proof. Since at disease free equilibrium point, the rate of change of the model equation (2) are assumed to be zero. Therefore

$$(1-\delta)A + \beta S - \frac{\omega\theta SB\alpha_1(T)}{K+B} - \phi\theta_1 SI\alpha_1(T) - vS - \mu S = 0$$

$$\delta A + \frac{\omega\theta SB\alpha_1(T)}{K+B} + \phi\theta_1 SI\alpha_1(T) - (\gamma+\epsilon+\mu+\sigma)I = 0$$

$$\gamma I + vS - \mu R = 0$$

$$\epsilon I - \mu_1 B = 0$$

Since at DFE the infection compartments are zero, let $I = 0$ and $B = 0$, by substituting $I = 0$, $B = 0$ into equations 2 yield;

$$(1-\delta)A + \beta S - vS - \mu S = 0$$
$$\delta A = 0$$

$$vS - \mu R = 0$$

Solving the above equation yields

$$S = \frac{(1-\delta)A}{(v+\mu-\beta)}$$
$$I = 0$$
$$B = 0$$
$$R = \frac{v(1-\delta)A}{\mu(v+\mu-\beta)}$$

Therefore the DFE of model (2) is;

$$(S^0, I^0, R^0, B^0) = (\frac{(1-\delta)A}{(v+\mu-\beta)}, 0, \frac{v(1-\delta)A}{\mu(v+\mu-\beta)}, 0)$$

Hence the DFE point of model (2). This means that there is no infection in the DFE of the model (2). □

3.2 Local Stability of the Disease Free Equilibrium (DFE)

Theorem 3.1. *The DFE of model (2) is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$ For any time $t \geq 0$*

Proof. Substituting the DFE points in the jacobian matrix of (2) yields;

$$J_{DFE} = \begin{pmatrix} \beta-(v+\mu) & \frac{-\phi\theta_1(1-\delta)A\alpha_1(T)}{v+\mu-\beta} & 0 & -\frac{\omega\theta(1-\delta)A\alpha_1(T)}{K(v+\mu-\beta)} \\ 0 & \frac{\phi\theta_1(1-\delta)A\alpha_1(T)}{v+\mu-\beta} - (\gamma+\epsilon+\mu+\sigma) & 0 & \frac{\omega\theta(1-\delta)A\alpha_1(T)}{K(v+\mu-\beta)} \\ v & \gamma & -\mu & 0 \\ 0 & \epsilon & 0 & -\mu_1 \end{pmatrix} \tag{7}$$

Consider the equation

$$\mid J_{DFE} - \lambda I \mid = 0$$

yielding;

$$\begin{vmatrix} \beta-(v+\mu)-\lambda & \frac{-\phi\theta_1(1-\delta)A\alpha_1(T)}{v+\mu-\beta} & 0 & -\frac{\omega\theta(1-\delta)A\alpha_1(T)}{K(v+\mu-\beta)} \\ 0 & \frac{\phi\theta_1(1-\delta)A\alpha_1(T)}{v+\mu-\beta} - (\gamma+\epsilon+\mu+\sigma)-\lambda & 0 & \frac{\omega\theta(1-\delta)A\alpha_1(T)}{K(v+\mu-\beta)} \\ v & \gamma & -\mu-\lambda & 0 \\ 0 & \epsilon & 0 & -\mu_1-\lambda \end{vmatrix} = 0 \tag{8}$$

Since the eigenvalues are strictly real and negative, this confirms local asymptotic stability as it can be seen clearly that $\lambda_1 = -\mu$ and $\lambda_2 = -\mu_1$. For the next two eigenvalues, consider Jordan 2×2 block matrix

$$A_2 = \begin{vmatrix} \beta-(v+\mu)-\lambda & -\phi\theta_1 S\alpha_1(T) \\ 0 & \phi\theta_1 S\alpha_1(T) - (\gamma+\epsilon+\mu+\sigma)-\lambda \end{vmatrix} \tag{9}$$

To find the eigenvalues we find the determinant of (A_2) yield:

$$[\beta-(v+\mu)-\lambda][\phi\theta_1 S\alpha_1(T) - (\gamma+\epsilon+\mu+\sigma)-\lambda] - [0 \times (-\phi\theta_1 S\alpha_1(T))] = 0$$
$$\lambda^2 - \lambda[(v+\mu-\beta) - (\gamma+\epsilon+\mu+\sigma) + \phi\theta_1 S\alpha_1(T)] -$$
$$(v+\mu-\beta)[(v+\mu-\beta)(\gamma+\epsilon+\mu+\sigma)] + \phi\theta_1 S = 0$$

Let

$$a = 1$$

$$b = -[(v+\mu-\beta)-(\gamma+\epsilon+\mu+\sigma)+\phi\theta_1 S\alpha_1(T)]$$
$$c = (v+\mu-\beta)[(v+\mu-\beta)(\gamma+\epsilon+\mu+\sigma)]+\phi\theta_1 S\alpha_1(T)$$

Solving quadratically the previous equation gives;

$$\lambda_{3,4} = \frac{-b \pm \sqrt{b^2-4ac}}{2a}$$

Substituting a, b and c;

$$\lambda_{3,4} = \frac{-b \pm \sqrt{b^2-4ac}}{2}$$

Whenever $R_0 < 1$, $\phi\theta_1 \frac{(1-\delta)A}{(v+\mu-\beta)}\alpha_1(T) < (\gamma+\epsilon+\mu+\sigma)$ and $\beta < (v+\mu)$ then $\lambda_3 < 0$, $\lambda_4 < 0$. Hence all the four roots are real and negative, it implies that DFE is locally asymptotically stable if $R_0 < 1$, otherwise unstable.

This means that even if there is a slight variation in the DFE, model (2) solutions will end up in DFE if $R_0 < 1$.

Epidemiologically, if a few infectious individuals are placed in a fully susceptible population, then there is a high chance of infecting less than one individual in its entire period of infectivity, this means cholera disease would die out if $R_0 < 1$; otherwise the disease may spread. □

3.3 Global Stability of the Disease Free Equilibrium (DFE)

In this section, the global asymptotic stability of the DFE of the model (2) is explored. Using the Matrix theoretic method; let

$$f(x,y) = (F-V)x - \mathcal{F}(x,y) + \mathcal{V}(x,y)$$

Then $x^{'} = (F-V)x - f(x,y)$

Now let $f(0,y) = 0$ and $\omega^T \geq 0$ be the left eigenvector of the nonnegative $V^{-1}F$ corresponding to the eigenvalue $\rho V^{-1}F = \rho F V^{-1} = R_0$. Therefore the following results provide a general method to construct Lyapunov function for $x^{'} = (F-V)x - f(x,y)$. This type of Lyapunov function was used to determine the global dynamics for disease models for instance [6] [7].

Theorem 3.2. *From a study [16], let F, V and $f(x,y)$ be defined as in $f(x,y) = (F-V)x - \mathcal{F}(x,y) + \mathcal{V}(x,y)$ and $F = [\frac{\partial F_i}{\partial x_j}(0,y_0)]$ and $V = [\frac{\partial V_i}{\partial x_j}(0,y_0)]$ respectively. If $f(x,y) \geq 0$ in $\Gamma \subset \mathbb{R}_+^{n+m}$, $F \geq 0$, $V^{-1} \geq 0$ and $R_0 \leq 1$, then the function $C = \omega^T V^{-1} x$ is a Lyapunov function on Γ.*

Proof. From model (2)

$$\mathcal{F} = \begin{pmatrix} \frac{\omega\theta SB\alpha_1(T)}{K+B} + \phi\theta_1 SI\alpha_1(T) \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{10}$$

And

$$\mathcal{V} = \begin{pmatrix} (\gamma+\epsilon+\mu+\sigma)I \\ 0 \\ -(\gamma I + vS) + \mu R \\ -\epsilon I + \mu_1 B \end{pmatrix} \tag{11}$$

Differentiating C along solution of

$$x^{'} = \mathcal{F}(x,y) - \mathcal{V}(x,y), y^{'} = g(x,y)$$

Gives;

$$C^{'} = C^{'}|_{(x'=\mathcal{F}(x,y)-\mathcal{V}(x,y),y'=g(x,y))} = \omega^T V^{-1} x^{'} = \omega^T V^{-1}(F-V)x - \omega^T V^{-1} f(x,y)$$
$$= (R_0 - 1)\omega^T x - \omega^T V^{-1} f(x,y)$$

Since $\omega^T \geq 0$, $V^{-1} \geq 0$ and $f(x,y) \geq 0$ in Γ, then the last term is nonpositive.

If $R_0 \leq 1$, then $C^{'} \leq 0$ in Γ and therefore C is a Lyapunov function for $x^{'} = \mathcal{F}(x,y) - \mathcal{V}(x,y)$. □

Theorem 3.3. *Let F, V and $f(x,y)$ be defined as in $f(x,y) = (F-V)x - \mathcal{F}(x,y) + \mathcal{V}(x,y)$ and $F = [\frac{\partial F_i}{\partial x_j}(0,y_0)]$ and $V = [\frac{\partial V_i}{\partial x_j}(0,y_0)]$ respectively. Suppose that $f(x,y) \geq 0$ with $f(x,y_0) = 0$ in Γ, $F \geq 0$, $V^{-1} \geq 0$ and $V^{-1}F$ is irreducible. Assuming that the DFE system $y^{'} = g(0,y)$ has a unique equilibrium $y = y_0 > 0$ that is globally asymptotically stable in $\mathbb{R}^m_+$. Then the following results holds for $x^{'} = \mathcal{F}(x,y) - \mathcal{V}(x,y), y^{'} = g(x,y)$.*

(i) Provided $R_0 < 1$, DFE is GAS in Γ

(ii) Provided $R_0 > 1$, DFE is unstable and the system $x^{'} = \mathcal{F}(x,y) - \mathcal{V}(x,y), y^{'} = g(x,y)$ is uniformly persistent and there exists at least one EE

Proof. Since $C = \omega^T V^{-1} x$ is a Lyapunov function for $x^{'} = \mathcal{F}(x,y) - \mathcal{V}(x,y), y^{'} = g(x,y)$ provided $R_0 < 1$. Since $V^{-1}F$ is irreducible , it follows that $\omega > 0$.

Hence by $(R_0 - 1)\omega^T x - \omega^T V^{-1} f(x,y)$, $C^{'} = 0$ implying that $\omega^T x = 0$ and thus $x = 0$.

If $R_0 > 1$, then by $(R_0 - 1)\omega^T x - \omega^T V^{-1} f(x,y)$, $C^{'} = (R_0 - 1)\omega^T x > 0$ provided $x > 0$ and $y = y_0$. By continuity $C^{'} > 0$ in a neighborhood of P_0. Therefore, solutions in the positive cone sufficiently close to P_0 move away from P_0, this implies that P_0 is unstable.

Epidemiologically implying that if a large number of infectious individuals are introduced into a fully susceptible population, the disease would die off if there are no secondary infections produced whenever $R_0 < 1$, otherwise the disease would spread. □

3.4 Local Stability of the Endemic Equilibrium (EE) Points

This is a state in which an infection persists in the population. To obtain EE points, the model (2) is solved simultaneously.

Theorem 3.4. *The endemic equilibrium point $EE^*(S^*, I^*, R^*, B^*)$ of model (2) is locally asymptotically stable whenever $R_0 > 1$.*

Proof. When the system of equations in model system (2) is equated to zero

$$(1-\delta)A + \beta S - \frac{\omega\theta SB\alpha_1(T)}{K+B} - \phi\theta_1 SI\alpha_1(T) - vS - \mu S = 0$$

$$\delta A + \frac{\omega\theta SB\alpha_1(T)}{K+B} + \phi\theta_1 SI\alpha_1(T) - (\gamma + \epsilon + \mu + \sigma)I = 0$$

$$\gamma I + vS - \mu R = 0$$

$$\epsilon I - \mu_1 B = 0$$

Adding the equations above and solving for I Yields;

$$I^* = \frac{\mu + \sigma}{A}$$

When I^* is substituted into $\epsilon I - \mu_1 B = 0$ yields

$$\epsilon(\frac{\mu + \sigma}{A}) - \mu_1 B = 0$$

Hence

$$B^* = \epsilon(\frac{\mu + \sigma}{\mu_1 A})$$

Substituting I^* and B^* into

$$\delta A + \beta S - \frac{\omega\theta S B^* \alpha_1(T)}{K + B^*} - \phi\theta_1 S I^* \alpha_1(T) - vS - \mu S = 0$$

$$S^* = \frac{[\frac{\phi\theta_1\alpha_1(T)(\mu+\sigma)}{A} + \frac{\omega\theta\alpha_1(T)}{\tau A} + v + \mu - \beta]}{\delta A}$$

Substituting I^* and S^* into $\gamma I + vS - \mu R = 0$ yields

$$R^* = [\frac{\gamma(\mu + \sigma)}{A} + \frac{v}{\mu\delta A}(\frac{\phi\theta_1\alpha_1(T)(\mu + \sigma)}{A} + \frac{\omega\theta\alpha_1(T)}{\mu_1 A} + v + \mu - \beta)]$$

Let

$$g = (v + \mu) + \beta - \frac{\omega\theta B^* \alpha_1(T)}{K + B^*}$$

$$h = \frac{\omega\theta B^* \alpha_1(T)}{K + B^*} + \phi\theta_1 I^* \alpha_1(T)$$

The jacobian matrix of (2) is given by

$$J_{EE^*} = \begin{pmatrix} -g - \phi\theta_1 I^* \alpha_1(T) & -\phi\theta_1 S^* \alpha_1(T) & 0 & -\frac{\omega\theta S^* K \alpha_1(T)}{(K+B^*)^2} \\ h & \phi\theta_1 S^* - (\gamma + \epsilon + \mu + \sigma) & 0 & \frac{\omega\theta S^* K \alpha_1(T)}{(K+B^*)^2} \\ v & \gamma & -\mu & 0 \\ 0 & \epsilon & 0 & -\mu_1 \end{pmatrix} \tag{12}$$

To find the eigenvalues, consider the characteristics equation

$$| \lambda I - J_{EE^*} | = 0$$

Yields;

$$\begin{vmatrix} -g - \lambda & -\phi\theta_1 S^* & 0 & -\frac{\omega\theta S^* K \alpha_1(T)}{(K+B^*)^2} \\ h & \phi\theta_1 S^* \alpha_1(T) - (\gamma + \epsilon + \mu + \sigma) - \lambda & 0 & \frac{\omega\theta S^* K \alpha_1(T)}{(K+B^*)^2} \\ v & \gamma & -\mu - \lambda & 0 \\ 0 & \epsilon & 0 & -\mu_1 - \lambda \end{vmatrix} = 0 \tag{13}$$

From (13) which can be written as $(\lambda + \mu)(\lambda + \mu_1)(\lambda^2 + b\lambda + c) = 0$
Where

$$b = [(v + \mu - \beta) + \frac{\omega\theta B^* \alpha_1(T)}{K + B^*} + \phi\theta_1 I^* \alpha_1(T)] + ((\gamma + \epsilon + \mu + \sigma) - \phi\theta_1 S^* \alpha_1(T))$$

And

$$c = [(v + \mu - \beta) + \frac{\omega\theta B^* \alpha_1(T)}{K + B^*} + \phi\theta_1 I^* \alpha_1(T)]((\gamma + \epsilon + \mu + \sigma) - \phi\theta_1 S^* \alpha_1(T)) -$$
$$[\frac{\omega\theta B^* \alpha_1(T)}{K + B^*} - \phi\theta_1 I^* \alpha_1(T)]\phi\theta_1 S^* \alpha_1(T)$$

It implies that $\lambda_1 = -\mu$ and $\lambda_2 = -\mu_1$. Hence it can clearly see that $\lambda_1 = -\mu$, $\lambda_2 = -\mu_1$ are negative.

To find the remaining eigenvalues of (13), let $\lambda^2 + b\lambda + c = 0$ such that
When $\lambda^2 + b\lambda + c = 0$ is solved yield $b = \lambda_3 + \lambda_4$ and $c = \lambda_3\lambda_4$. Hence whenever $R_0 < 1$, then $2(\frac{\omega\theta B^* \alpha_1(T)}{K+B^*}) + (v+\mu-\beta) < (\gamma+\epsilon+\mu+\sigma)\frac{I^*}{S^*}$. If $\beta < v+\mu$ then $b > 0$, $c > 0$. Therefore, $\lambda_3 < 0$, $\lambda_4 < 0$. Therefore all the roots are real and negative and EE^* is locally asymptotically stable whenever $R_0 > 1$, otherwise unstable.

This means that a small perturbation of the EE, the solutions of the model (2) will always converge to the EE whenever $R_0 > 1$.

Epidemiologically it implies that if a few infectious individuals are introduced into a fully susceptible population and there are new secondary infections produced whenever $R_0 > 1$, then the disease would persist in the population. □

4 Sensitivity Analysis

Sensitivity analysis is the responsiveness of a model to an input variable or parameter. We conduct this analysis to understand the impact of changing a parameter's value on the models's compartment. These parameters are useful in determining the pattern of the spread of an infection [11]. This is done by employing the normalized forward sensitivity index of the variable to the parameter, which represents the ratio of the relative change in the parameter [11]. This is why this index is defined using partial derivatives.

Definition 4.1. *The normalized forward sensitivity index of a variable R_0 that depend differentiability on a parameter p is defined by;*

$$\theta_p^{R_0} = \frac{\partial R_0}{\partial p}\frac{p}{R_0}$$

p is the parameter whose sensitivity index is to be measured [11].

Hence, to understand the dynamics of the disease spread, the sensitivity indices of this primary reproduction number R_0 regarding the parameters should be ascertained. The R_0 of model 2 is given by;

$$R_0 = \frac{(1-\delta)A\phi\theta_1\alpha_1(T)}{(v+\mu-\beta)(\gamma+\epsilon+\mu+\sigma)}$$

Let $c_1 = (\mu-\beta)$, $c_2 = (\epsilon+\mu+\sigma)$, $c_3 = (\gamma+\mu+\sigma)$, $c_4 = (v+\mu)$, $c_5 = (v-\beta)$, $c_6 = (\gamma+\epsilon+\sigma)$, $c_7 = (v+\mu-\beta)$ and $c_8 = (\gamma+\epsilon+\mu)$. We now analyze the sensitivity indices of the parameter R_0 yields
For ϕ;

$$\frac{\partial R_0}{\partial \phi} \times (\frac{\phi}{R_0}) = \frac{\theta_1(1-\delta)A\alpha_1(T)}{(v+c_1)(\gamma+c_2)} \times \frac{\phi(v+c_1)(\gamma+c_2)}{\phi\theta_1(1-\delta)A\alpha_1(T)} = 1$$

For θ_1

$$\frac{\partial R_0}{\partial \theta_1} \times (\frac{\theta_1}{R_0}) = \frac{\phi(1-\delta)A\alpha_1(T)}{(v+c_1)(\gamma+c_2)} \times \frac{\theta_1(v+c_1)(\gamma+c_2)}{\phi\theta_1(1-\delta)A\alpha_1(T)} = 1$$

For $\alpha_1(T)$

$$\frac{\partial R_0}{\partial \alpha_1(T)} \times (\frac{\alpha_1(T)}{R_0}) = \frac{\phi\theta_1(1-\delta)A}{(v+c_1)(\gamma+c_2)} \times \frac{\alpha_1(T)(v+c_1)(\gamma+c_2)}{\phi\theta_1(1-\delta)A\alpha_1(T)} = 1$$

For v

$$\frac{\partial R_0}{\partial v} \times (\frac{v}{R_0}) = \frac{\phi\theta_1(1-\delta)A\alpha_1(T)}{(\gamma+c_2)} \times [-(v+c_1)^{-2} \times \frac{v(v+c_1)(\gamma+c_2)}{\phi\theta_1(1-\delta)A\alpha_1(T)}] = -\frac{v}{v+\mu-\beta}$$

For μ

$$\frac{\partial R_0}{\partial \mu} \times (\frac{\mu}{R_0}) = \frac{\phi\theta_1(1-\delta)A\alpha_1(T)}{(\mu^2+\mu c_6+\mu c_5+c_5c_6)^2} \times \frac{(2\mu+c_6+c_5)\mu(\mu+c_5)(\mu+c_6)}{\phi\theta_1(1-\delta)A\alpha_1(T)}$$

$$= -\frac{\mu(2\mu+c_6+c_5)}{(\mu^2+\mu c_6+\mu c_5+c_5c_6)}$$

For β

$$\frac{\partial R_0}{\partial \beta} \times (\frac{\beta}{R_0}) = \frac{\phi\theta_1(1-\delta)A\alpha_1(T)}{(\gamma+c_2)}[-(c_4-\beta)^{-2}]\frac{-\beta(c_4-\beta)(\gamma+c_2)}{(\phi\theta_1(1-\delta)A\alpha_1(T))} = \frac{\beta}{v+\mu-\beta}$$

For γ

$$\frac{\partial R_0}{\partial \gamma} \times (\frac{\gamma}{R_0}) = \frac{\phi\theta_1(1-\delta)A\alpha_1(T)}{(v+c_1)} \times [-(\gamma+c_2)^{-2}] \times \frac{\gamma}{\phi\theta_1(1-\delta)A\alpha_1(T)} = -\frac{\gamma}{(\gamma+\mu+\sigma)}$$

For ϵ

$$\frac{\partial R_0}{\partial \epsilon} \times (\frac{\epsilon}{R_0}) = \frac{\phi\theta_1(1-\delta)A\alpha_1(T)}{(v+c_1)} \times [-(\epsilon+c_3)^{-2}] \times \frac{\epsilon(v+c_1)(\epsilon+c_3)}{(\phi\theta_1(1-\delta)A\alpha_1(T))} = -\frac{\epsilon}{\epsilon+\mu+\gamma+\sigma}$$

For σ

$$\frac{\partial R_0}{\partial \sigma} \times (\frac{\sigma}{R_0}) = \frac{\phi\theta_1(1-\delta)A\alpha_1(T)}{(c_7)}[-(c_8+\sigma)^{-2}] \times \frac{\sigma c_7(c_8+\sigma)}{\phi\theta_1(1-\delta)A\alpha_1(T)} = -\frac{\sigma}{\gamma+\mu+\sigma+\epsilon}$$

Using parameter values in Table 2 the sensitivity indices of R_0 in Table 1 are obtained.

These indices measures the relative change in R_0 with the parameter change. Thus, by employing these indices, therefore, using these indices, we identify the parameters that significantly influences R_0 and necessitate focussing on them for intervention strategies.

Table 1. Sensitivity indices of R_0 with respect to the model parameter

Parameters	Sensitivity indices
ϕ	1
θ_1	1
γ	-0.45454545
α_1	1
β	0.0714285714
ϵ	-0.083333
σ	-0.25
v	-0.8333333
μ	-0.34375

From Table 1 we discuss these parameters and how they affect the R_0 of our $SIRB$ cholera temperature dependent disease transmission model.

From the sensitivity analysis of the parameters of model (2), it is revealed that R_0 is much more sensitive to the infection rate of pathogen α_1 that is dependent on temperature. An increase in infection rate of pathogen α_1 that is dependent on temperature by 10% would increase R_0 by 10% and decreasing it by 10% reduces R_0 by 10%.

Sensitivity analysis also reveals that R_0 is also sensitive to the control through the short cycle ϕ, which decreases R_0 by 10%, recovery rate of humans from the infection γ that reduces R_0 by 8.6538% and by 4.454545% due to vaccination of susceptible and increase in environmental temperature by 10% respectively.

As well, if the rate of recovery of infected individuals γ is raised by 10%, then there shall be decline in R_0 by 8.6538%

By doing this sensitivity analysis, the study now recommends that the temperature of the environment should be raised because the infection rate of the pathogen is known to be reliant on temperature, as evidenced by the lesser R_0 in the event that there is a rise in the temperature of the environment.

5 Numerical Simulation

In this section, we use the temperature-dependent $SIRB$ between-host cholera model to numerically solve the model system (2), substantiating the theoretical findings. This is done by first plugging in the initial values obtained from relevant literature, as shown in $Table$ 2.

Subsequently, we obtain the results in section (5.2) by fitting the model equations (2) in the MATLAB software, using the parameter values in Table 2.

5.1 Parameter Values

Values of the parameters in Table (2) are derived from literature, and others through estimation.

Table 2. Parameter values for the Between-Host Cholera Model

Description	Parameters	Initial value	Source
Susceptible	S	1000	Estimated
Pathogens	B	100000	[19]
Temperature(T_0 - Average room temperature and T - Possible max temperature of a human body due to an infection)		$T_0 = 23^0C$ and $T = 43^0C$	Estimated
Natural death rate	μ	0.06 day^{-1}	[19]
death due to infection	σ	0.7	[20]
vaccination rate	v	0.2	[19]
Rate of recovery	γ	0.1	[20]
Rate of recruitment of S	β	0.02	Estimated
Natural death rate of B	μ_1	0.06	Estimated

5.2 Simulation Results and Discussion

Simulation results presented in this paper is based on the $SIR - B$ model that is related to fluctuations with regard to the dynamics of cholera disease, this results are concentrated on this aspect as described in *Fig* (1), *Fig* (2), *Fig* (3) and *Fig* (4). Our simulation results is focused on the effect of temperature on the dynamics of cholera disease. The key focus is in *Fig* (2) which shows the behaviour in population of *Vibrio cholerae* for different values of temperature.

A study [21] that analyzes water quality in wet and dry seasons under climate change recommends the discovery that a large number of polluting substances usually get into the water basin. This is due to there being no collection systems for sewage and refineries; the waste water from the surrounding villages also drops into the water basin; in turn, they dump a lot of pollutants into the basin. The findings of this study established that, during the dry season, when the temperature is high, there is little clean water for use, and this leads to water pollution. This means that cholera disease will still prevail in the dry season, and this implies that appropriate measures should be taken to curb it. The simulation results demonstrate this for the between-host cholera model with temperature dependent parameter as shown in the figures: *Fig* (1), *Fig* (2), *Fig* (3) and *Fig* (4) respectively.

In *Figure* (1), is a graph of B when $T = 43^0C$ and $T = 23^0C$. The population of B at $T = 43^0C$ is reduced at a faster rate but when $T = 23^0C$ the population of B is high, this is an indication that vibrios spread and multiply faster at $T = 23^0C$ but they spread and multiply at lower rate when the temperature is high. This is clearly seen in *Figure* (2)

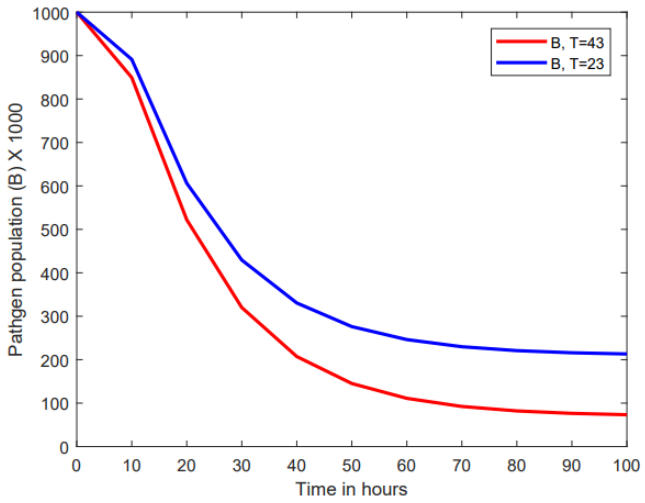

Figure 1: B against time for $T = 43^0C$ and $T = 23^0C$

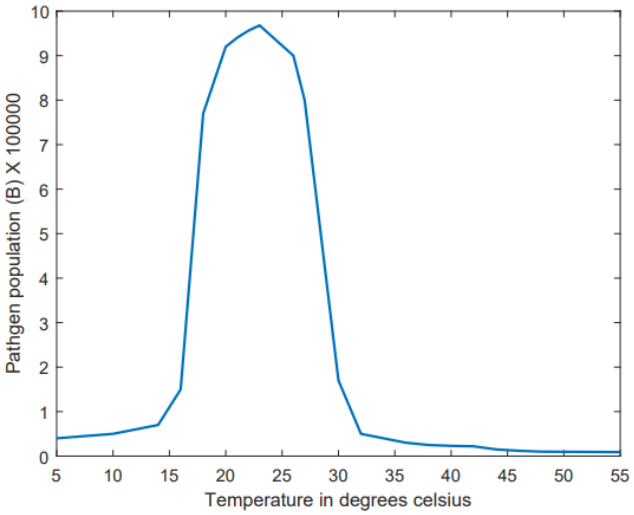

Figure 2: B against temperature in degree Celsius

In *Figure* (3), is a graph of susceptible population when $T = 43^0C$, $T = 30^0C$ up-to $T = 23^0C$. The population of susceptible reduces at a faster rate when the temperature is $T = 23^0C$ and at a lower rate when the temperature is high ($T = 43^0C$). This implies that at $T = 23^0C$ there are more pathogens present to cause infection hence more susceptible individuals are being infected.

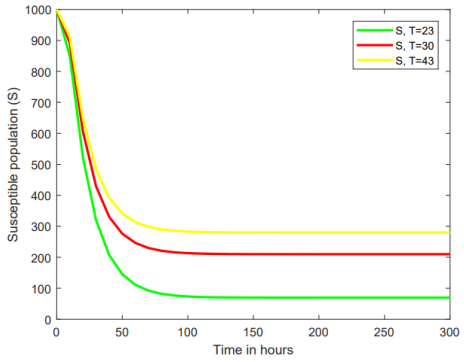

Figure 3: S against time when $T = 43^0C$, $T = 30^0C$ and $T = 23^0C$

In *Figure* (4), when $T = 23^0C$ the population of the infected individuals increases at a higher rate compared to when the temperature is $T = 30^0C$ and $T = 43^0C$ respectively. This shows that at $T = 23^0C$ there are more pathogens active to cause infections which leads to many individuals being infected, after sometimes this population decreases. Despite the differences in environmental temperature where the pathogens live(food or water), there will still be infected individuals which shows persistence in cholera disease.

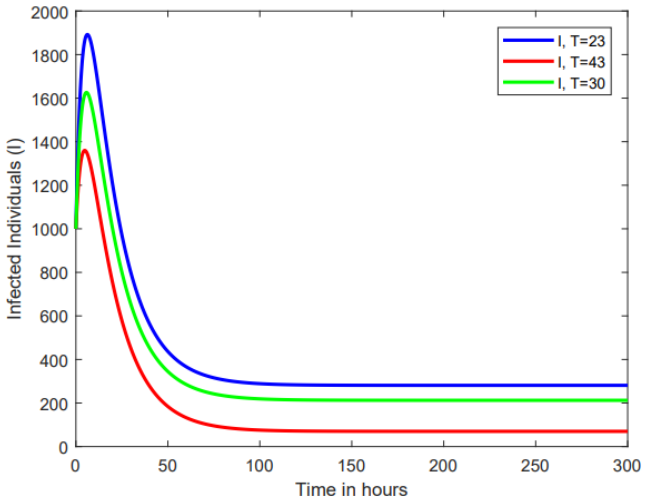

Figure 4: I against time when $T = 43^0C$ and $T = 23^0C$

6 Conclusion

We have developed a between-host cholera model with temperature dependent parameter. The model's equilibrium points, both local and global DFE, remain stable when $R_0 < 1$, indicating the pathogen's extinction in an individual. On the other hand, when $R_0 > 1$, the DFE becomes unstable. The model also has endemic equilibrium point which is locally asymptotically stable when $R_0 > 1$, which means that there is persistent infection. We conducted a numerical analysis to visually depict the model's analytic solutions, and the simulation outcome reveals that *Vibrio cholerae* pathogens can multiply and spread more quickly at 23^0C. However, their multiplication slows down between $23^0C < T \leq 43^0C$. Consequently at 23^0C, the number of pathogens active to cause infection is higher than at higher temperatures. Therefore, due to changes in climatic conditions, most areas experience temperature intervals between 23^0C to 43^0C , which explains why, despite the use of cholera vaccines, cholera epidemics persist. Sensitivity analysis of model (2) parameters is done to find how sensitive the parameters of model (2) are, we look at the infection rate of pathogen α_1 which changes with temperature. This lowers R_0 by 10%. Recovery rate of humans from the infection γ will also reduce R_0 by 4.454545%. Through sensitivity analysis, the study suggest that increasing the temperature of the food or water would help reduce the infection rate of the pathogen that depends on temperature since this would help reduce the reproduction number R_0.

7 Recommendations

This study recommends that the movement of individuals should be considered for further study to investigate the dynamics of the model as individuals move from dry areas to wet areas.

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Competing Interests

Authors have declared that no competing interests exist.

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