



A mathematical Analysis for the Control of Cholera Dynamic in a Population

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ABSTRACT

In this paper, a new mathematical model for the cholera transmission dynamics was developed and thoroughly analyzed to better understand the spread of the disease. Our model incorporates some infected humans that recovered from infection, after the immunity wanes and individual still alive return to susceptible class again, vital (births and deaths) dynamics and disease induced deaths. The basic reproduction number R_0 was obtained which can be used to control the transmission dynamics of the disease and therefore the conditions for local and global stability of the disease free equilibrium was established.

Keywords: *Vibrio cholera*, Equilibria states, Basic reproduction number, Stability

INTRODUCTION

Cholera has become a worldwide health problem. It is an acute intestinal infectious disease caused by the bacterium *Vibrio cholera* (Colwell and Huq 1994; Hartley et al. 2006), is endemic in many parts of the world, especially the Indian sub-continent, parts of Asia, Africa, and Latin America. There have been seven cholera pandemics since 1816, with the first occurring in India causing the death of hundreds of thousands of people (World Health Organization 2013). The last cholera pandemic, which started from Indonesia in 1961, swept across Bangladesh in 1963, India in 1964, Africa in 1971, Japan in the late 1970s, and reached the Americas in 1991 (World Health Organization 2013). Recent outbreaks of cholera have been recorded in India (2007), Congo (2008), Iraq (2008), Zimbabwe (2009), Vietnam (2009), Haiti (2010), and Nigeria (2010) (Tian and Wang 2011). It is estimated that, in the year 2010, cholera affects 3–5 million people and causes 100,000–130,000 deaths globally (Tian and Wang 2011).

Cholera is primarily transmitted to humans from the environment (by ingesting water or food contaminated with the bacteria *Vibrio cholerae*) (Colwell and Huq 1994; Hartley et al. 2006). It has short incubation period, ranges from a few hours to 5 days. The symptoms of

cholera include severe diarrhea, vomiting, loss of skin elasticity, thirst, and muscle cramps (Zuckerman et al. 2007) (although it should be stated that most people (nearly 80 %) infected with cholera do not show symptoms, carrying the bacteria for weeks and slowly excreting them to the water supply Zhou and Cui 2010). People infected with cholera are treated using fluid replacement therapy and antibiotics (this is known to reduce the number of cholera-induced deaths to 1 % of the diagnosed cases, in addition to decreasing the severity of illness, (Sanchez et al. 2011).

In order to find an efficient way to control an infection, it is of great importance to establish its transmission dynamics. One main goal of mathematical epidemiology is to understand how to control and eradicate diseases (Ma and Ma, 2006). Mathematical models are used extensively in the study of ecological and epidemiological phenomena (Kaplan and Brandeau, 1994). They are particularly helpful as experimental tools with which to evaluate and compare control procedures and preventive strategies, and to investigate the

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relative effects of various sociological, biological and environmental factors on the spread of diseases. This is so because they can help in figuring out decisions that are of significance importance on the outcomes and provide comprehensive examinations that enter into decisions in a way that human reasoning and debate cannot.

A mathematical model for cholera disease was developed by (Codeco., 2001) with three compartments of susceptible humans (S), infected human (I) and the concentration of toxigenic *V. Cholera* in water (B). He explicitly incorporated the environmental component, i.e., *V. Cholerae* concentration in water supply (denoted by B), in to a regular SIR system to form a combined human-environment. They obtained the basic reproduction number, R_o and established conditions for local stability of both the disease and endemic equilibria. In a similar development (Hartley et al., 2006) extended this model to include the hyperinfectious state of the bacterium. Hove-Musek et.al 2010 investigated the effects of malnutrition on the spread of endemic cholera. In this study, we therefore complement and extend the works of the aforementioned authors by having four (4) compartment of Susceptible class (S), infected class (I), Recovery class (R) and the concentration of toxigenic *V. Cholera* in water (B). We also incorporated some infected humans that recovered from infection, after the immunity wanes and individual still alive return to susceptible class again ,vital dynamics, recovery due to treatment and disease induced death.

MODEL FORMULATIONS

The susceptible human population is generated via recruitment of humans (through birth or immigration) in to the community at the constant rate, bN respectively. This population is decreased following infection, which can be acquired via infection at the rate given by $\lambda = \frac{aB}{K+B}$ where a is the exposure to contaminated sources (mostly water or food), K is the concentration of *V. Cholera* in water that yields a 50% chance of catching cholera and $\lambda(B) = \frac{B}{K+B}$ is used to account for the

probability that a susceptible individual acquires cholera infection after coming in contact with a contaminated source (see also Codeco 2001). Natural death occurs in S, I and R classes at a rate μ and individual in I compartment suffers additional death due to diseases at the rate δ . Recovery class increased due to the arrival of new immune individuals that recovered of the infection at the rate η and τ , respectively. Similarly the *Vibrio cholerae* concentration (B) is generated through the excretion of *V. cholerae* particles to the environment, by infectious individuals without cholera symptoms at the rate (e). This population is increased by the growth rate of *V. cholera* in the aquatic environment at the rate (m).

The corresponding mathematical equations of the above description are given by a system of ordinary differential equations below

$$\frac{dS}{dt} = bN - a\lambda BS - \mu S + \omega R \quad (1)$$

$$\frac{dI}{dt} = a\lambda BS - (\gamma + \mu + \delta)I \quad (2)$$

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

$$\frac{dB}{dt} = mB + eI \quad (4)$$

Where

$$N = S + I + R \quad (5)$$

and

$$\frac{dN}{dt} = (b - \mu)N - \delta I \quad (6)$$

in the biological - feasible region:

$$\Omega = \{(S, I, R, B) \in \mathbb{R}_+^4 : S + I + R = 1 \text{ and } S \geq 0, I \geq 0, R \geq 0, B \geq 0\} \quad (7)$$

This can be shown to be positively invariant with respect to the system (1 to 4)

Symbols used in the model are listed below:

S	Number of susceptible individuals
I	Number of infected individuals
R	Number of recovered individuals
B	Concentration of toxigenic <i>V. cholerae</i> in contaminated water
N	Total population of humans

b	Per capital birth rate of humans
μ	Per capital natural death rate of humans
a	Rate of exposure to contaminated water
K	Concentration of <i>V. cholerae</i> in water that yields 50% chance of catching cholera
γ	Natural recovery from cholera
τ	Recovery due to treatment
δ	Cholera-induced death rate by I
m	Growth rate of <i>V. cholerae</i> in the aquatic environment
ω	Loss (waning) of immunity by recovered individuals
e	Contribution of each infected person to the population of <i>V. cholerae</i> in the aquatic environment

MODEL ANALYSIS

Analysis of Disease Free Equilibrium State

E_f

At the disease free equilibrium state we have absence of infection. Thus, all the infected classes will be zero and the entire population will comprise of only the susceptible individuals.

Theorem 1: , A disease-free equilibrium state of the model exists at the point

$$E_f = (S^*, I^*, R^*, B^*) = \left(\frac{bN}{\mu}, 0, 0, 0 \right)$$

Proof: at equilibrium state the rate of change of each variable is equal to zero. i.e.

$$\frac{dN}{dt} = \frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = \frac{dB}{dt} = 0 \quad (8)$$

Let

$$(S, I, R, B) = (S^*, I^*, R^*, B^*) \quad (9)$$

At equilibrium state, the equation (1) - (4), (8) and (9) becomes:

$$bN - (a\lambda B^* + \mu)S^* + \omega R^* = 0 \quad (10)$$

$$a\lambda B^* S^* - (\gamma + \mu + \delta)I^* = 0 \quad (11)$$

$$\gamma I^* - (\mu + \omega)R^* = 0 \quad (12)$$

$$mB^* + eI^* = 0 \quad (13)$$

Now, from (13), we have

$$B^* = \frac{eI^*}{m} \quad (14)$$

Substituting (14) in to (11), we obtain

$$a\lambda B^* S^* - (\gamma + \mu + \delta)I^* = 0$$

$$\frac{a\lambda e I^* S^*}{m} - (\gamma + \mu + \delta)I^* = 0 \quad (15)$$

$$\left[\frac{a\lambda e S^*}{m} - (\gamma + \mu + \delta) \right] I^* = 0$$

Thus,

$$I^* = 0$$

or

$$\left[\frac{a\lambda e S^*}{m} - (\gamma + \mu + \delta) \right] = 0 \quad (16)$$

$$\Rightarrow I^* = 0 \quad (17)$$

Equation (14) yields

$$B^* = 0 \quad (18)$$

From equation (10)

$$bN - (a\lambda B^* + \mu)S^* + \omega R^* = 0$$

$$bN = (a\lambda B^* + \mu)S^* + \omega R^*$$

$$S^* = \frac{bN}{a\lambda B^* + \mu + \omega R^*} \quad (19)$$

But

$$B^* = 0$$

Therefore,

$$S^* = \frac{bN}{\mu + \omega R^*} \quad (20)$$

From equation (12)

$$R^* = \frac{\gamma I^*}{\mu + \omega} \quad (21)$$

But

$$I^* = 0$$

Thus,

$$R^* = 0 \quad (22)$$

Equation (9) yields

$$S^* = \frac{bN}{\mu} \quad (23)$$

From (17)

$$\left[\frac{a\lambda e S^*}{m} - (\gamma + \mu + \delta) \right] = 0$$

$$a\lambda e S^* - m(\gamma + \mu + \delta) = 0$$

$$a\lambda eS^* = m(\gamma + \mu + \delta)$$

Therefore,

$$S^* = \frac{m\gamma + \mu + \delta}{a\lambda e} \quad (24)$$

From equation (10)

$$bN - (a\lambda B^* + \mu)S^* + \omega R^* = 0$$

Put (24) into (10), we have

$$bN - \omega R^* = a\lambda \left[\frac{m(\gamma + \mu + \delta)B^*}{a\lambda e} \right] \quad (25)$$

$$(bN - \omega R^*)a\lambda e = a\lambda [m(\gamma + \mu + \delta)]B^* \quad (26)$$

Thus

$$B^* = \frac{(bN - \omega R^*)a\lambda e}{a\lambda m(\gamma + \mu + \delta)} \quad (27)$$

From equation (13)

$$mB^* + eI^* = 0$$

$$\left[m \frac{(bN - \omega R^*)a\lambda e}{a\lambda m(\gamma + \mu + \delta)} \right] + eI^* \quad (28)$$

$$m(bN - \omega R^*)a\lambda e + eI^*(a\lambda m(\gamma + \mu + \delta)) \quad (29)$$

Hence

$$I^* = \frac{(bN - \omega R^*)}{\gamma + \mu + \delta} \quad (30)$$

From equation (12)

$$R^* = \frac{\gamma I^*}{\mu + \omega}$$

Substitute (30) into (12)

We obtain

$$R^* = \frac{\gamma(bN - \omega R^*)}{(\gamma + \mu + \delta)(\mu + \omega)} \quad (31)$$

Thus, a disease-free equilibrium of the model exists at:

$$E_f = (S^*, I^*, R^*, B^*) = \left(\frac{bN}{\mu}, 0, 0, 0 \right) \quad (32)$$

Basic Reproduction Number, R_0

Consideration of stability of a disease-free equilibrium gives certain conditions under which disease will die out or stay in the population called the basic reproduction number, R_0 .

If $R_0 < 1$, then on average, an infected individual produces less than one newly infected individual over the course of its infection period. In this case, the infection may die out in the long run. Conversely, if $R_0 > 1$, each infected individual produces, on average more than one new infection, the infection will be able to spread in a population. A large value of R_0 may indicate the possibility of a major epidemic. A better widely accepted and used method in finding R_0 that reflect its biological meaning is the next generation operator approach described by Diekmann and Heesterbeek (2000) and subsequently analysed by Driessche and Watmough (2002). Using this approach we obtain the basic reproduction number, R_0 of the system (1) to (4) which is the spectral radius (ρ) of the next generation matrix, K . i.e.

$$R_0 = \rho K,$$

where $K = FV^{-1}$

Now,

$$F = \begin{pmatrix} 0 & \beta S^* \\ 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} K_1 & 0 \\ -e & K_3 \end{pmatrix} \quad (33)$$

Where

$$\beta = a\lambda$$

$$k_1 = \gamma + \mu + \delta$$

$$k_2 = \mu + \omega \quad (34)$$

$$k_3 = m$$

Thus,

$$R_0 = \frac{a\lambda b e N}{\mu(\gamma + \mu + \delta)m} \quad (35)$$

Local Stability of Disease Free Equilibrium, E_f

In the absence of infection, the model has a steady state, E_f called the disease-free

equilibrium, where $E_f = \left(\frac{bN}{\mu}, 0, 0, 0 \right)$. To

establish the stability of this equilibrium, the Jacobian of (10) to (13) is computed and evaluated at E_f . The local stability of E_f is

then determined based on the signs of the eigenvalues of this Jacobian. The equilibrium E_f is locally stable if the real parts of these eigenvalues are all negative.

At the steady states of the model, the Jacobian matrix is given by

$$J(E_f) = \begin{pmatrix} -\beta B^* - \mu & 0 & \omega & -\beta S^* \\ \beta B^* & -K_1 & 0 & \beta S^* \\ 0 & \gamma & -K_2 & 0 \\ 0 & e & 0 & -K_3 \end{pmatrix} \quad (37)$$

Evaluating the Jacobian in Eq. (37) at E_f gives

$$J(E_f) = \begin{pmatrix} -\mu & 0 & \omega & -\beta \frac{bN}{\mu} \\ 0 & -K_1 & 0 & \beta \frac{bN}{\mu} \\ 0 & \gamma & -K_2 & 0 \\ 0 & e & 0 & -K_3 \end{pmatrix} \quad (38)$$

Thus, the eigenvalues are

$$\lambda_1 = -\mu < 0, \lambda_2 = -k_1 < 0, \lambda_3 = -k_2 < 0, \lambda_4 = -k_3$$

Simplifying, we have

$$R_0 = \frac{a\lambda b e N}{\mu(\gamma + \mu + \delta)m} < 1$$

Thus, < 0 if $R_0 = 1$ implying all the eigenvalues have negative real parts, we therefore, established the following result.

Theorem 2: the disease- free equilibrium, E_f of the model is locally asymptotically stable (LAS) if $R_0 < 1$.

The epidemiological implication of the theorem is that cholera can be eliminated (control) from the population when $R_0 < 1$, if the initial size of the sub-populations of the model are in the basin of attraction of the DFE.

Global Stability of Disease Free Equilibrium, E_f

In order to ensure that cholera is independent of the initial size of the sub-populations of the model (1) to (4), it is necessary to show that the DFE is globally- asymptotically stable (GAS). One common approach in studying the global asymptotic stability of the DFE is to construct an appropriate Lyapunov function (Li et al., 1999, Fall et al., 2007, Huo et al., 2010, Garba and Gumel, 2010). However, we

shall apply the result introduced by Castillo-Chavez et al. (2002).

Theorem 3: The disease- free equilibrium E_f of (1) to (4) is globally asymptotically stable (GAS) in Ω if $R_0 < 1$.

Proof: To establish the global stability of the disease free equilibrium, the two conditions (H1) and (H2) as in Castillo-Chavez et al. (2002) must be satisfied for $R_C < 1$. We rewrite the model (1) to (4) in the form:

$$\frac{dX_1}{dt} = F(X_1, X_2) \quad (39)$$

$$\frac{dX_2}{dt} = G(X_1, X_2); G(X_1, 0) = 0$$

Where,

$X_1 = (S^*, R^*)$ and $X_2 = (I^*, B^*)$, with the components of $X_1 \in R^2$ denoting the uninfected population and the components of $X_2 \in R^2$ denoting the infected population.

The disease-free equilibrium is now denoted as

$$E_f = (X_1^*, 0), X_1^* = \left(\frac{bN}{\mu}, 0 \right)$$

Now, for the first condition, that is globally asymptotically stability of X_1^* , we have

$$\frac{dX_1}{dt} = F(X_1, 0) = \begin{bmatrix} bN + \omega R^* - \mu S^* \\ -\gamma R^* \end{bmatrix}$$

a linear differential equation.

Solving, we have

$$S^*(t) = \frac{bN + \omega R^*}{\mu} - \frac{bN + \omega R^*}{\mu} e^{-\mu t} + S^*(0) e^{-\mu t}$$

$$\frac{dS^*}{dt} = bN + \omega R^* - \mu S^*$$

$$\frac{dR^*}{dt} = -\gamma R^*$$

and

$$R^*(t) = R^*(0) e^{-\gamma t}$$

Now, clearly we have:

$S^*(t) + R^*(t) \rightarrow N$ as $t \rightarrow \infty$, regardless of the value of $S^*(0)$ and $R^*(0)$.

Thus $X_1^* = \left(\frac{bN}{\mu}, 0 \right)$ is globally asymptotically stable.

Next, for the second condition, that is

$\hat{G}(X_1, X_2) = AX_2 - G(X_1, X_2)$, we have

$$A = \begin{bmatrix} -K_1 & \beta S^* \\ e & -K_3 \end{bmatrix}$$

This is clearly an M-matrix (the off-diagonal elements of A are non-negative).

$$G(X_1, X_2) = \begin{bmatrix} \beta B^* S^* - (\gamma + \delta + \mu) I^* \\ e I^* - m B^* \end{bmatrix}$$

then,

$$\hat{G}(X_1, X_2) = AX_2 - G(X_1, X_2) = \begin{bmatrix} -K_1 & \beta S^* \\ e & -K_3 \end{bmatrix} \begin{bmatrix} I^* \\ B^* \end{bmatrix} - \begin{bmatrix} \beta S^* - K_1 I^* \\ e I^* - K_3 B^* \end{bmatrix}$$

$$= \begin{bmatrix} -K_1 I^* + \beta S^* B^* \\ e I^* - K_3 B^* \end{bmatrix} - \begin{bmatrix} \beta S^* - K_1 I^* \\ e I^* - K_3 B^* \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

i.e.

$$\hat{G}(X_1, X_2) = [0, 0]^T$$

It is thus obvious that $\hat{G}(X_1, X_2) \geq 0$. Hence, the proof is complete

Conclusion

In this paper, we have developed and analyze a new mathematical model which incorporates SIRS model couple with vibrio cholera (B), vital (births and deaths) dynamics and disease induced death rate. Basic reproduction number R_0 was obtained.

Our analysis reveals that the disease can be control if the basic reproduction number, R_0 is less than one regardless of the initial population profile. Therefore every effort must be put in place by all concerned to prevent the cholera infection by reducing R_0 strictly less than unity.

Finally, there is need for further research work on the effects of various control strategy such as environmental sanitation, water hygiene and vaccination on the transmission dynamics of cholera disease.

REFERENCES

Codeço, C. (2001). Endemic and epidemic dynamics of cholera: the role of the

aquatic reservoir. *BMC Infectious Diseases*, 1. doi:10.1186/1471-2334-1-1.

Colwell, R. R. and Huq, A. (1994). Environmental reservoir of *Vibrio cholerae*, the causative agent of cholera. *Ann. N.Y. Acad. Sci.*, 740, 44–53.

Castillo-Chavez C., Feng Z. and Huang W., On the computation of R_0 and its role on global stability, in: Castillo-Chavez C., Blower S., Van den Driessche P., Krirschner D. and Yakubu A. A. (2002). Mathematical approaches for emerging and reemerging infectious diseases: An introduction. The IMA volumes in mathematics and its applications. Springer Verlag, New York. 125:229-250.

Diekmann O. and Heesterbeek (2000). Mathematical Epidemiology of Infectious Diseases: Model Building, Analysis and Integration. Wiley, New York.

Fall A., Iggidr A., Sallet G. and Tewa J. J.(2007). Mathematical Modelling of natural Phenomena. 2 (1): Epidemiology pp. 55 – 73.

Garba S. M. and Gumel A. B. (2010), Mathematical Recipe for HIV Elimination in Nigeria. Journal of the Nigeria Mathematical Society, 29:51-112.

Hartley, D. M., Morris Jr., J. G., & Smith, D. L. (2006). Hiperinfectivity: a critical element in the ability of *V. cholerae* to cause epidemics? *PLoS Med.*, 3(1), 63–69.

Huo, HF., Dang SJ., and Li, YN. (2010). Stability of a Two-Strain Tuberculosis Model with General Contact Rate. Abstract and Applied Analysis. ID 293747, 31 pages. Doi: 10.1155/2010/293747.

Hove musekwa et.al (2011). Modelling and analysis of the effects of **malnutrition** in the spread of cholera. *Mathematical and Computer Modelling*, Volume 53, Issues 9–10, May 2011, Pages 1583-1595.

- Kaplan E. and Brandeau M. (1994). *Modelling AIDS and the AIDS Epidemic*. Raven, New York.
- Li M. Y., Graef J. R., Wang L. and Karsai J. (1999), Global Stability for the SEIR model with varying total population size, *Mathematical Biosciences*, 160:191-213
- Ma J. and Ma Z. (2006). Epidemic Threshold Conditions for Seasonally Forced SEIR Models. *Journal of Mathematical Biosciences and Engineering*, 3(1):161 – 172.
- Sanches, R. P., Ferreira, C. P., & Kraenkel, R. A. (2011). The role of immunity and seasonality in cholera epidemic. *Bull. Math. Biol.*, 73, 2916–2931.
- Van de Driessche P. and Watmough J. (2002), Reproduction Numbers and Sub-Threshold Endermic Equilibria for Compartmental Models of Disease Transmission. *Math. Bios.* 180:29 – 48.
- World Health Organization (2013). Media center: cholera. <http://www.who.int/mediacentre/factsheets/fs107/en/>. Accessed: 10 February 2013.
- Zhou, X., & Cui, J. (2010). Modeling and stability analysis for a cholera model with vaccination. *Math. Methods Appl. Sci.*, 34, 1711–1724.