

# A modelling study of controlling cholera with logistic growth

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## ABSTRACT

A great significance of mathematical modelling in spreading cholera and its control has been observed in past several decades. A modelling study is conducted to study the effect of cholera bacterium growth along with its control. Analysis and simulation of mathematical model has been presented. These results clearly imply that the disease can be control in a region by applying biological control agents.

## Introduction

The spread of different types of infections are still a challenge faced by the world even [1]. The devastating outbreak of these illnesses makes a larger segment of population at the maximum risk for their survival. Thus high investment at the economic level is a necessary step to be taken to reduce the damage to the human health. These infectious diseases must be controlled in a very short time so that the life expectancy of individuals may improve across the globe [2]. The poor sanitary infrastructure and hygienic environment have given chance for the spread of water borne infections in an environment. These infections also easily spread via immediate contact between the susceptible and the infected ones. Let's take an example of deadly disease like cholera caused by *V. Cholerae* survived easily in aquatic bodies [3]. Still, it is taking millions of lives across the globe. Cholera infection easily spread through consuming the dirty water or food in which cholera bacteria are found.

Dehydration and electrolytic imbalance cause death to the infected individual. Proper treatment is requisite to save a human life [4].

This infection is continuously spreading like Southern Asia occurrence of outbreak twice a year. Disease wave travel across many countries and millions of people are still suffering from the disease. Seven pandemics of cholera have occurred across the globe since 1817. The origin of these pandemics has been found the origin in Asia. 7<sup>th</sup> pandemics started from Indonesia and wave travels across the world from Asia [4].

Haiti experienced biggest outbreak of cholera in 2010, because the of the earthquake devastated sanitary environment completely [5]. Getting safe water there was very difficult due to which people was keep their self away from health [5]. W. H. O. marked in 2010 less amount of clean water available in 2010 [5]. This shows proper sanitation and hygiene

environment are the building block on which human health is secure.

Here, simplification of the bio-cycle of bacteria-phage interaction dynamics is presented using two types of interactions; spread of the cholera disease and Bacteriophage injection in the bacteria.

### Model formulation:

The cholera dynamics with biological control is governed by the following system of non-linear differential equations

$$\frac{dS}{dt} = A - \frac{\beta SB}{k+B} + vI - dS,$$

$$\frac{dI}{dt} = \frac{\beta SB}{k+B} - (v + \alpha + d)I,$$

$$\frac{dB}{dt} = \eta I + rB \left(1 - \frac{B}{L}\right) - \frac{\phi BV}{m+B},$$

$$\frac{dV}{dt} = \frac{\phi BV}{m+B} - \delta V. \quad (1)$$

where the model system (1) is analyzed with the following initial conditions

$$S(0) > 0, I(0) \geq 0, B(0) \geq 0, V(0) \geq 0.$$

In the model system (1), the parameter, A is the rate at which the humans enter the susceptible class either through birth or immigration. A susceptible human becomes infected with cholera through ingestion of water contaminated by susceptible bacteria at a rate,  $\beta$  and infected bacteria at a rate,  $\beta h$ . Infected humans may die at rate,  $\alpha$  and recover from the infection at a rate,  $v$  and they will again move to the susceptible class due to temporary immunity [7,8,9].

Now, we discuss the mechanism that how cholera spreads in the human population. We begin by describing the force of infection in the first equation of the model system (1), which is the per capita rate of infection experienced by susceptible humans due to susceptible and infected bacteria.

We have also assumed that in absence of human shedding and the viruses, the bacteria grow logistically with intrinsic growth rate coefficient,  $r$  and the carrying capacity,  $L$  [10,11].

**Equilibrium analysis:**

The model system (1) has three non-negative equilibria, which are as follows:

- (i) Disease and phage free equilibrium  $E_0 (A/d, 0, 0, 0)$  is always feasible,
- (ii) Endemic equilibrium  $E_1 (S_1, I_1, B_1, 0)$  is feasible always,
- (iii) The coexistence equilibrium  $E^* (S^*, I^*, B^*, V^*)$  is feasible always.

**Feasibility of the equilibrium  $E_0, E_1$  and  $E^*$**  Here, we discuss the feasibility of the equilibria  $E_0, E_1$  and  $E^*$ . Firstly, we discuss the feasibility of the equilibrium  $E_0$  and  $E_1$  by solving the following system of algebraic equations

$$A - \frac{\beta SB}{k+B} + vI - dS = 0, \tag{2}$$

$$\frac{\beta SB}{k+B} - (v + \alpha + d)I = 0, \tag{3}$$

$$\eta I + rB \left(1 - \frac{B}{L}\right) - \frac{\phi BV}{m+B} = 0, \tag{4}$$

$$\frac{\phi BV}{m+B} - \delta V = 0. \tag{5}$$

Adding equations (2) and (3), we get

$$A - (\alpha + d)I - dS = 0, \tag{6}$$

Here, we assume  $V = 0$  from equation (5), we may obtain the components of the disease and phage free equilibrium,  $E_0$  i.e., the total human population  $A/d$  susceptible. Next, we find the components of the  $E_1$ . Using  $V = 0$  in (4) we get

$$I_1 = -\frac{1}{\eta} r B_1 \left(1 - \frac{B_1}{L}\right)$$

Thus, existence of one positive solution of  $I_1$  is guaranteed. This shows that the endemic equilibrium  $E_1$  is feasible always.

**Numerical simulation and Bifurcation phenomena**

In this section, we have observed the long-time dynamics of the humans, bacteria and virus populations. We will illustrate some of the important theoretical results through numerical simulation, obtained in this paper. We integrate the model system (1) by using Matlab built-in function ode45,

which is used for fourth-order Runge-Kutta method. The findings of the numerical simulations have been displayed graphically.

In the last one decade, there are very few mathematical models focused on the biological control to cholera disease. In all those studies, how the Bacteriophage infection spread in the bacteria population and its impact in controlling cholera outbreaks. It is assumed that in the early stage of Bacteriophage infection, the bacteria are capable of transmitting the infection to humans. Therefore, we consider the two categories of the bacteria and assume that the susceptible and infected bacteria both will contribute in making the healthy sick with cholera.

To the best of author's knowledge, the work originated on Bacteriophage infection in the marine environment has been proposed by [12]. The infection starts when virus attach to the bacteria cell wall [13,14]. Process begins and various viruses attack but the one virus succeed in inserting the gene material DNA or RNA in the cell. Most studies conducted and observed through experiment that the adsorption rate of bacteriophage is difficult to estimate. Therefore, in this study for the numerical illustration, we have taken the value of the parameter,  $\phi$  in range,  $0 - 0.0012$ , as estimated by [16]. Prey-predator theory measure the conversion rate of bacteria into the viruses. An infected bacterium produces many viruses, which may range from 1 to 400 [17,18]. But we have considered here 200.

For the above set of parameter values, the conditions of existence and stability of coexistence equilibrium,  $E^*$  are satisfied. The components of coexistence equilibrium,  $E^*$  are obtained as

$$S^* = 15736, I^* = 52, B^* = 1036, V^* = 5.40 \times 10^7.$$

The eigenvalues of Jacobian matrix corresponding to the equilibrium,  $E^*$  are obtained as  $-3.3116, -0.2780, -0.00002 + 0.0700i, -0.00001 + 0.0700i, -0.00005$ , which are either negative or with negative real part. Thus, by Routh-Hurwitz criterion, the coexistence equilibrium,  $E^*$  is locally asymptotically stable.

In the process of bacteriophage infection, we consider that the infected bacteria, It may contribute in spread of cholera epidemic in the region. Thus, the parameter,  $h$  may play very important role in increasing the number of infected humans. We have shown the variation of infected humans w. r. to different values in the Fig. 1. From this figure, one can clearly observe that as the value of the parameter,  $h$  increases, the value of infected humans will also increase. In the bacteria-phage dynamics, the growth of the virus population is strictly governed by two factors; one is the death rate of the lysis of the infected bacteria and virus replication factor. In this regard, Fig. 2 shows the effect on the number of infected humans,  $I^*$ . It is evident from this Figure that the number of infected humans will decrease as the value increases. This shows that the bacteria which leave the class of infected bacteria in lysis process, they will increase the virus population. Thus, the infected humans will decrease due to conversion of bacteria

into viruses. Fig. 3 shows the impact of conversion efficiency from bacteria to the viruses during phage attack.

**Conclusion and Results**

To see the qualitative behaviour of the dynamics of the model system (1), we have analyzed the proposed model by using the stability theory of differential equations and dynamical system. Possibly, the proposed model has three non-negative equilibrium whose feasibility conditions have been discussed in detail. One can observe that in the absence of bacteria and the viruses, no infected human exists in the region under consideration, therefore the total human population becomes susceptible, i.e., the disease and phage free equilibrium,  $E_0$  is

obtained. The viruses are absent in the second equilibrium, i.e., endemic equilibrium,  $E_1$  is obtained. The bacteria population which exists in the aquatic reservoirs, are assumed to be susceptible, i.e., the human will contract the infection through ingestion of water in which *V. cholerae* is present. Finally, we have got the coexistence equilibrium,  $E^*$ , which confirms the survival of all the populations.

Thus, we conclude from the modelling and analysis perspective that the density of bacteria population can be decreased using the Bacteriophage viruses in the aquatic reservoirs, thus disease can be controlled in the region.

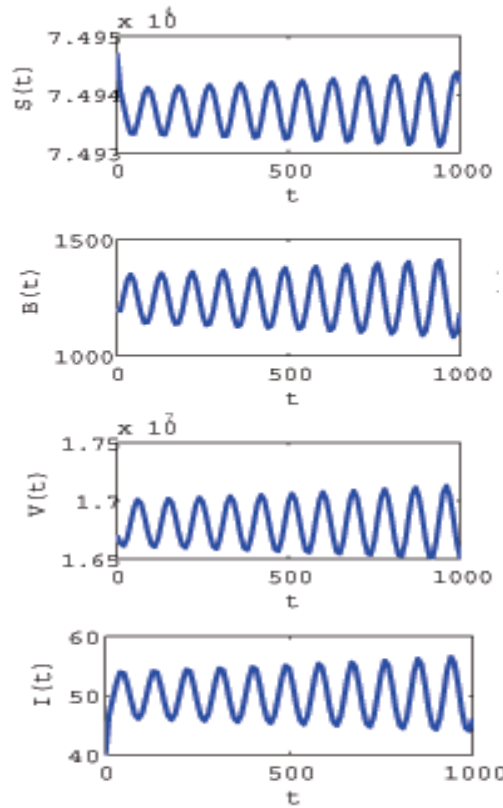


Fig: 1

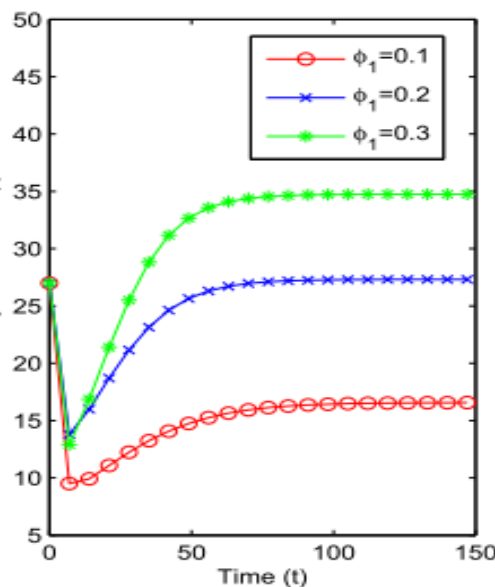


Fig: 2

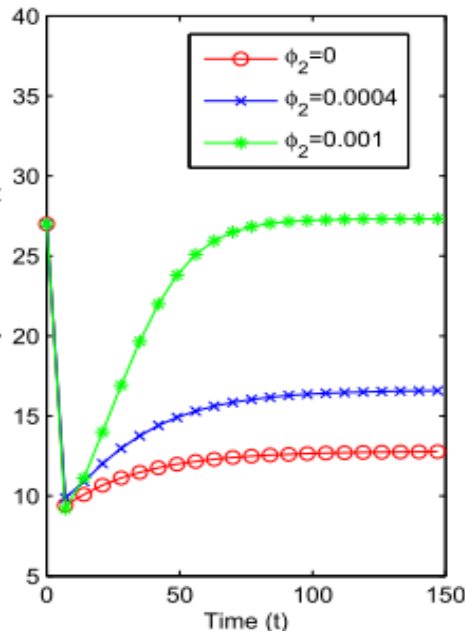


Fig: 3

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