



A Deterministic Mathematical Model for Cholera Transmission Dynamics

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Abstract

Cholera is a global threat to public health and remains major problem in large regions of the globe. It's the key indicator of lack of social development that is currently reported in over 70 countries. African countries reported 3,221,050 suspected cholera cases to the World Health Organization representing 46% of all cases reported globally (WHO, 2015a). Within Africa, half of all cases reported between 1970 and 2015 were notified from only seven countries: Somalia, Nigeria, Congo, South Africa, Angola, Tanzania, and Mozambique. A deterministic mathematical model for Susceptible, Infective, Recovered and Susceptible (SIRS) was formulated. The disease free and endemic equilibrium points were determine and their local stabilities were investigated. The disease free equilibrium for the cholera model system is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. Finally, the numerical simulation are presented to support the results.

Keywords: *Deterministic Model; Reproduction number; Vibrio Cholera; Equilibrium; Epidemics.*

1.0 INTRODUCTION

Cholera are found in Sanskrit back to the 5th century BC, and the disease has existed on the Indian subcontinent for centuries. In 1817, cholera spread beyond the Indian subcontinent, and six worldwide cholera pandemics occurred between 1817 and 1923 (Harris *et al*, 2012). Between 1849 and 1854, London physician John Snow proposed that cholera was a communicable disease and that stool contained infectious material. He suggested that this infectious material could contaminate drinking water supplies, resulting in transmission of cholera. During the 19th century, cholera spread across the

world from its original reservoir in the Ganges delta in India. Six subsequent pandemics killed millions of people across all continents (WHO, 2015a). The disease is now in its seventh pandemic, which began in 1961 in Indonesia and has spread through Asia, Africa (in 1971), and more recently Latin America (in 1991).

Cholera is an infection of the small intestine caused by the gram-negative bacterium, *Vibrio cholera*. Untreated individuals suffer severely from diarrhea and vomiting. It can cause a rapid dehydration and electrolyte imbalance, and can lead to death (Pascual *et al*, 2002). As a water/food-borne disease, cholera is typically infected through pathogen ingestion, such as

drinking sewage-contaminated water, or eating food prepared by an individual with soiled hands (BMC, 2016). Many mathematical models were proposed to investigate the complex epidemic and endemic behavior of cholera, which involve multiple transmission pathways. These involve both direct human to human and indirect environment to human modes leading to combined human – environment epidemiological models (Tian and Wang, 2011). It was estimated that every year, there are roughly 1.4 to 4.3 million cases, and 28,000 to 142000 deaths every year worldwide due to cholera (WHO, 2015b). The infection has short incubation period of 2 hours to 5 days. The disease is virulent and it can kill both children and adult within hours if untreated (CDC, 2014).

Cholera is an easily treatable disease. About 80% of people can be treated successfully through prompt administration of oral rehydration salts (WHO/UNICEF ORS standard sachet) (Britannica, 2016). Very severely dehydrated patients require the administration of intravenous fluids. These patients require appropriate antibiotics to diminish the duration of diarrhea, reduce the volume of rehydration fluids needed. And shorten the duration of v. cholera excretion (Zhou and Cui, 2011). Mass administration of antibiotics is not recommended, as it has no effect on the spread of cholera and contributes to increasing antimicrobial resistance (WHO, 2016a). This paper is motivated by the work of Mukandavire *et al* (2011) and Mukandavire *et al* (2013) where they formulate a deterministic mathematical model to estimate the role of reproduction number for the cholera outbreaks in Zimbabwe (2008) and in Haiti (2010). We incorporate some parameters into their model to study the behavior of the equilibrium state and the role of the basic reproduction number on the local stability of the modified model.

2.0 FORMULATION OF THE CHOLERA MODEL

The Cholera Model has two populations namely, the human population and Vibrios/ Pathogen population. The total human population at time t , denoted by $N(t)$, is sub-divided into three disjoint classes of Susceptible, $S(t)$;

Infectious, $I(t)$; and Removed, $R(t)$ humans.

Therefore,

$$N(t) = S(t) + I(t) + R(t) \quad (1)$$

And the pathogen population at a time t , denoted by $P(t)$.

The population of susceptible individuals are generated by the recruitment of individuals (assumed to be susceptible) into the population (at a rate of, b). The susceptible human gain infection by consuming water with vibrios bacteria, Z_1 and through human to human contact, Z_2 . Where

$$Z_1 = \frac{eps}{k+p}, \quad Z_2 = \beta SI \quad (2)$$

And by the loss of infection – acquired immunity among recovered individuals (at a rate, σ). Population decreased by infection through contact capable of leading to infection. Similarly, the population is further decreased by natural death (at a rate, μ). Thus, the rate of change of the susceptible population with time t is given by

$$\frac{dS(t)}{dt} = b + \sigma R - \frac{ePS}{k+P} - \beta SI - \mu S \quad (3)$$

Infective individual's population are generated following the cholera infection of susceptible individuals (at the rate, Z_1 and Z_2). The population of infectious individuals is decreased due to recovery from infection after treatment (at a rate, γ) and natural death (at a rate, μ) and infective may die as a result of cholera infection (at a rate, ψ). The infective population is further decreased due to infected human contribution to the contaminated source (at a rate, τ). Thus,

$$\frac{dI(t)}{dt} = \frac{ePS}{k+P} + \beta SI - (\mu + \gamma + \psi + \tau)I \quad (4)$$

The population of removed individuals is generated following the removal of individuals from cholera infection compartment (at a rate, γ). The population is decreased through the loss of infection – acquired immunity (at a rate, σ) and by natural death (at a rate, μ). We assumes that infection does not confer permanent immunity against re-infection.

$$\frac{dR(t)}{dt} = \gamma I - (\mu + \sigma)R \quad (5)$$

The population of pathogen or vibrios is generated (at a rate, ε) and the growth of the bacteria is enhanced by the infected individuals with the bacteria (at a rate, τ). It assumes that pathogen (vibrios) has a constant natural death α within the aquatic environment. Thus,

$$\frac{dP(t)}{dt} = \varepsilon P + \tau I - \alpha P \quad (6)$$

Hence, putting the above assumptions and derivations leads to the following system of non-linear differential equations:

$$\left. \begin{aligned} \frac{dS(t)}{dt} &= b + \sigma R - \frac{ePS}{k+P} - \beta SI - \mu S \\ \frac{dI(t)}{dt} &= \frac{ePS}{k+P} + \beta SI - (\mu + \sigma + \psi + \tau)I \\ \frac{dR(t)}{dt} &= \gamma I - (\mu + \sigma)R \\ \frac{dP(t)}{dt} &= \varepsilon P + \tau I - \alpha P \end{aligned} \right\} (7)$$

2.1 Basic Properties of the Model

2.1.1 Invariant Region

Since the model is dealing with human being, we assumes that all the parameters and variables of the model are positive for all $t \geq 0$. Hence, total human population $N(t)$ at any time t can be determined. Thus, equation (1) becomes

$$\frac{dN(t)}{dt} = b - \mu N - \psi \quad (8)$$

Thus, in the absence of cholera, we assumes there is no death from cholera disease i.e. $\psi = 0$, then

$$\frac{dN(t)}{dt} \leq b - \mu N \quad (9)$$

and

$$\frac{dN}{dt} < 0 \quad \text{if} \quad N > \frac{b}{\mu} \quad (10)$$

by applying Birkoff and Rotas theorem on differential inequality as apply by (Solomon, 2011) and using a standard comparison theorem as apply (Melesse and Gumel, 2010), we obtained

$$N(t) \leq \frac{b}{\mu} + \left[N(0) - \frac{b}{\mu} \right] e^{-\mu t} \quad (11)$$

As $t \rightarrow \infty$ in equation (11), the population $N(t)$ approaches

$$0 \leq N(t) \leq \frac{b}{\mu} \quad (12)$$

Hence, the set Ω is positively-invariant.

$$\Omega = \left\{ S(t), I(t), R(t) \in R_3^+ : N(t) \leq \frac{b}{\mu} \right\} \quad (13)$$

All initial solutions in Ω remains in Ω for all $t > 0$

Similarly, substituting $I = N_h$ in equation (6) for vibrios population, then

$$\frac{dN_p(t)}{dt} = (\varepsilon - \alpha)N_p + \tau N_h \quad (14)$$

Thus,

$$N_p(t) \leq \frac{\tau b}{\mu(\alpha - \varepsilon)} \quad (15)$$

And

$$N_p(t) \leq \frac{\tau b}{\mu(\alpha - \varepsilon)} + \left(N_p(t) - \frac{\tau b}{\mu(\alpha - \varepsilon)} \right) e^{-(\alpha - \varepsilon)t} \quad (16)$$

As $t \rightarrow \infty$

$$N_p(t) \rightarrow \frac{\tau b}{\mu(\alpha - \varepsilon)}, \quad \text{where} \quad \varepsilon < \alpha \quad (17)$$

Hence, the feasible solution set of the pathogen population enters the region

$$\Omega_p = P(t) \in R^+ \quad (18)$$

Therefore, the feasible set for model system equation (7) is

$$\Omega = \left\{ S(t), I(t), R(t), P(t) \in R_4^+ : S, I, R, P \geq 0; N_h(t) \leq \frac{b}{\mu}; N_p(t) \leq \frac{\tau b}{\mu(\alpha - \varepsilon)} \right\} \quad (19)$$

Hence, the system is epidemiologically meaningful and mathematically well posed in the domain.

2.1.2 Positivity of the Solutions

Lemma: Let initial data be

$$\left\{ (S(0), I(0), R(0), P(0) \geq 0) \in \Omega \right\}$$

Then, the solution set is given by

$$\left\{ (S(t), I(t), R(t), P(t)) \right\} \text{ of the model}$$

system is positive for all $t > 0$.

Proof:

From equation (3) we get

$$\frac{dS}{dt} \geq -\mu S \tag{19}$$

$$\int \frac{dS}{S} \geq -\int \mu dt \tag{20}$$

$$\ln S(t) \geq -\mu t + c \tag{21}$$

$$S(t) \geq S(0)e^{-\mu t} \geq 0 \tag{22}$$

Similarly,

$$\left. \begin{aligned} I(t) &\geq I(0)e^{-(\mu+\gamma+\psi+\tau)t} \\ R(t) &\geq R(0)e^{-(\mu+\sigma)t} \end{aligned} \right\} \tag{23}$$

It can be shown that

$$\left\{ (S(t), I(t), R(t), P(t)) \right\} \geq 0 \quad \text{for all } t > 0. \text{ Hence, the Proof.}$$

3.0 EQUILIBRIUM STATES AND STABILITIES

3.1.1 Disease Free Equilibrium (DFE), E_0 .

The disease free equilibrium points are obtained by setting the right hand of equation (7) equal to zero. Thus, model equation (7) has a DFE given by:

$$E_0 = (S, I, R, P) = \left(\frac{b}{\mu}, 0, 0, 0 \right) \tag{24}$$

3.1.2 Existence of Endemic Equilibrium Point, E_1 .

An equilibrium where at least one of the infected components of the model equation (7) is non-zero. Let

$$E_1 = (S^*, I^*, R^*, P^*) \neq 0 \tag{25}$$

Therefore the endemic equilibrium point, E_1 are:

$$\left. \begin{aligned} S^* &= \frac{b(\mu+\sigma+\psi+\tau)(\mu+\sigma)}{(Z_1+Z_2+\mu)(\mu+\sigma+\psi+\tau)(\mu+\sigma)-(Z_1+Z_2)\sigma\gamma} \\ I^* &= \frac{b(Z_1+Z_2)(\mu+\sigma+\psi+\tau)(\mu+\sigma)}{(\mu+\sigma+\psi+\tau)[(Z_1+Z_2+\mu)(\mu+\sigma+\psi+\tau)(\mu+\sigma)-(Z_1+Z_2)\sigma\gamma]} \\ R^* &= \frac{b\gamma(Z_1+Z_2)(\mu+\sigma)}{(\mu+\sigma)[(Z_1+Z_2+\mu)(\mu+\sigma+\psi+\tau)(\mu+\sigma)-(Z_1+Z_2)\sigma\gamma]} \\ P^* &= \frac{b\tau(Z_1+Z_2)(\mu+\sigma)}{(\alpha-\varepsilon)[(Z_1+Z_2+\mu)(\mu+\sigma+\psi+\tau)(\mu+\sigma)-(Z_1+Z_2)\sigma\gamma]} \end{aligned} \right\} \tag{26}$$

Therefore, there is an existence of endemic equilibrium point, E_1 .

3.1.3 Basic Reproduction Number, R_0 .

The stability of cholera disease free, E_0 is studied using next generation operator approach as described by Van den Driessche and Watmough (2002).

Let

(i) $F_i(x)$ be the rate of appearance of new infection in compartment i .

(ii) $V_i^+(x)$ be the transfer of individuals into compartments i by all other means.

(iii) $V_i^-(x)$ be the rate of transfer of individuals out of compartment i .

(iv) E_0 be the disease-free equilibrium point.

According to Diekmann and Heesterbeek (1990), we call FV^{-1} the next generation

Matrix for the model and set the reproduction number,

$$R_0 = \rho(FV^{-1}) \tag{27}$$

Where,

$$F = \left[\frac{\partial F_i(\varepsilon_0)}{\partial x_j} \right] \quad \text{and} \quad V = \left[\frac{\partial V_i(\varepsilon_0)}{\partial x_j} \right] \tag{28}$$

$\rho(A)$ Denotes the spectral radius of a Matrix A

(i.e. FV^{-1}). F and V are $m \times m$ matrices, where m is the number of infected classes.

$$F_i = \begin{bmatrix} \frac{ePS}{k+P} + \beta SI \\ 0 \end{bmatrix} \quad \text{and} \quad V_i = \begin{bmatrix} (\mu+\gamma+\psi+\tau)I \\ \tau I - (\alpha+\varepsilon)P \end{bmatrix} \tag{29}$$

Then,

$$F_i = \begin{bmatrix} \frac{ePS}{k+P} + \beta SI & 0 \\ 0 & 0 \end{bmatrix} \quad \text{and} \quad V_i = \begin{bmatrix} (\mu+\gamma+\psi+\tau)I & 0 \\ -\tau I & (\alpha-\varepsilon)P \end{bmatrix} \tag{30}$$

This give

$$F = \begin{bmatrix} \beta S & \frac{eS}{k} \\ 0 & 0 \end{bmatrix} \quad \text{and} \quad V = \begin{bmatrix} (\mu+\gamma+\psi+\tau) & 0 \\ -\tau & \alpha-\varepsilon \end{bmatrix} \tag{31}$$

Therefore,

$$FV^{-1} = \begin{bmatrix} \frac{\beta b}{\mu} & \frac{eb}{k\mu} \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{(\mu+\gamma+\psi+\tau)} & 0 \\ \frac{-\tau}{(\mu+\gamma+\psi+\tau)(\alpha-\varepsilon)} & \frac{1}{\alpha-\varepsilon} \end{bmatrix} \tag{32}$$

But,

$$FV^{-1} = R_0 \tag{33}$$

Hence, the basic reproduction number is given by

$$R_0 = \frac{\beta b k (\alpha - \varepsilon) + b e \tau}{k \mu (\mu + \gamma + \psi + \tau) (\alpha - \varepsilon)} \tag{34}$$

Thus, the threshold quantity R_0 is the effective reproduction number of the cholera model for equation (7) in the environment. It measures the average number of new infections generated by a single infected individuals in a completely susceptible population.

However, the parameters that affect the reproduction number, R_0 in (34) are α and ε . Obviously, decreasing the α and ε causes a sharp decrease in R_0 , reducing the cholera epidemics in a population.

Theorem 1:

The Disease Free Equilibrium (DFE) point of the model system is Locally Asymptotically Stable (LAS) if $R_0 < 1$ and Unstable if $R_0 > 1$.

Parameter	
b	Recruitment rate of Human population.
e	Exposure rate due to contact with contaminated water.
β	Rate of contracting vibrios between human to human.
τ	Contribution of infected human to the contaminated water.
σ	Progression into susceptible population.
ε	Rate of generating population of Vibrios.
ψ	Death rate due to cholera infection.
α	Death rate of Vibrios.
γ	Removal rate.
μ	Natural Death rate
K	Concentration of Cholera in water.

4.0 NUMERICAL SIMULATION

4.1.1 Description of Variables and Parameters of the Model

Table 1. Description of Variables and Parameters

Variable	Description
$S(t)$	Susceptible individuals
$I(t)$	Infectious individuals
$R(t)$	Removed individuals
$P(t)$	Pathogen population

4.1.2 Parameters and their values used in numerical simulations to support the formulated model.

Table 2. Parameter and Estimated values.

Parameter	Description	Value	Reference
B	Recruitment rate of Human population.	10/ day	Assumed
e	Exposure rate due to Contact with contaminated source.	0.2143/day	Hartley <i>et al</i> (2006)
β	Rate of contracting vibrios from human to human.	0.00011/day	Mukandavire <i>et al</i> (2011).
τ	Rate of contribution of infected human to contaminated source.	10 cells/L per day	Codeco (2001).
σ	Progression rate into susceptible class.	0.2/day	Hartley <i>et al</i> (2006).
ε	Rate of generating population of Vibrios.	0.73/day	Hendrix (1971).
ψ	Death rate due to cholera infection.		

α	Death rate of Vibrios	0.015/day	Hartley <i>et al</i> (2006).
γ	Removal rate.	1.06/day	Codeco (2001).
μ	Natural Death rate	0.15/day	Hendrix (1971).
k	Concentration of V.cholera in water.	5.48×10^{-5} /day	Mukandavire <i>et al</i> (2007).
		10^6 cells/ml	Codeco (2001).

5.0 CONCLUSION AND RECOMMENDATIONS

5.1 Conclusion

This study aim to minimize the cholera infected population and to maximize susceptible and recovered populations. A cholera model was formulated and analyzed. We started with a basic model which comprises of system of four non – linear differential equations. The study investigated the positivity and the invariant region of the formulated model and it was established that the model is epidemiologically and mathematically well posed. In Table 2, the parameter values were used to verify the statement of the theorem 1 above for R_0 . If $R_0 < 1$ it is assumes that each individual produces on average less than one new infected individuals and hence, the disease dies out. If $R_0 > 1$ each individuals produce more than one new infected individuals and thus, the disease persists and it will invade the population.

5.2 Recommendations

The duration of the disease is relatively short. The causative organisms may be found in the nose and throat secretions, the stomach contents, the stool and the urine, (WHO, 2016b). The research make the following recommendation:

1. **Care:** All contaminated material should be cleaned up as soon as possible after use.
2. **Diet:** During first 3 days vomiting is almost constant. Intravenous saline solution is usually given. Diet (boiled Milk, Tea, etc) may be given as soon as it can be retained.
3. **Temperature:** The patient should be placed in a quiet, private room, which should be warm (70^0 F) well ventilated and well screened, and kept out of draughts. If the temperature is below normal external heat should be applied.

4. **Personal Hygiene:** A partial bath may be given. The buttocks area should be kept clean with warm water and soap sponges, rubbed dry, and baby oil applied.
5. **Good oral hygiene should be maintained:** The teeth should be cleaned thoroughly at least twice daily. When vomiting occurs an antiseptic mouthwash should be used.
6. **Hands Cleaning:** Hands should be scrubbed and disinfected thoroughly immediately before meals and before coming in contact with any object that may reach the nose or mouth.
7. **Insects Avoid:** Flies and all other insects should be excluded from the room.

6.0 REFERENCES

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