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ON THE GLOBAL STABILITY OF CHOLERA MODEL WITH PREVENTION AND CONTROL

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ABSTRACT

In this study, a system of first order ordinary differential equations is used to analyse the dynamics of cholera disease via a mathematical model extended from Fung (2014) cholera model. The global stability analysis is conducted for the extended model by suitable Lyapunov function and LaSalle's invariance principle. It is shown that the disease free equilibrium (DFE) for the extended model is globally asymptotically stable if $R_0^q < 1$ *and the disease eventually disappears in the population with time while there exists a unique endemic equilibrium that is globally asymptotically stable whenever* $R_0^q > 1$ *for the extended model or* $R_0 > 1$ *for the original model and the disease persists at a positive level though with mild waves (i.e few cases of cholera) in the case of*$R_0^q > 1$. *Numerical simulations for strong, weak, and no prevention and control measures are carried out to verify the analytical results and Maple 18 is used to carry out the computations.*

Keywords: *Model, global stability, equilibrium, simulations.*

1. Introduction

Cholera, a disease of the small intestine, is the most popular of all water-borne infectious diseases. While intensive sanitation and availability of portable water have eliminated cholera in advanced countries of the world, the disease still remains a major threat to Africa and the entire less developed countries. The emergence and re- emergence of cholera in the developing countries has resulted to not only the mortality and morbidity of humans but also increase in the economic predicaments. Despite implementation of various intervention strategies towards the eradication of the disease, the disease continues to occur from time to time in the developing countries.

Performing the global stability analysis of the equilibrium points of cholera models normally becomes a challenging mathematical problem due to the complexity and high dimension of the disease models (Shuai&Driessche, 2013). However, studying the global dynamics of epidemiological models is imperative because the global dynamics is essential in understanding the basic mechanism in disease initiation, spread and persistence, especially for the long term behaviour of the disease and its relationship with initial infection size. Such information will provide adequate guidelines for the public health administrators to design prevention and intervention strategies and to properly scale their efforts (Tian *et al.*, 2010).

Tian *et al.* (2010) extended Codeco's model (2001) by incorporating various control strategies and conducted rigorous stability analysis using the theory of monotone dynamical system. They discovered that with strong control measures, the basic reproduction number will be reduced below unity so that the disease

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free equilibrium is globally asymptotically stable but with weak control, a unique and globally stable endemic equilibrium would occur, though at a lower infection level. They concluded that practical endemism requires a reasonably higher value for the reproduction number which is possible in the absence of intervention.

Apart from monotone dynamical system approach, geometric approach, Kirchoff's matrix tree theorem and Lyapunov function have been employed to study the global dynamics of cholera models and other infectious disease models by a number of researchers most especially to prove the global stability of the endemic equilibrium (Tian& Wang, 2011; Cheng, Wang, & Yang, 2012; Buonomo&Lacitignola, 2010; Buonomo& Vargas-De-Leon, 2013). However, Lyapunov method has become a popular technique to study the global stability of epidemiological models in recent years. The Lyapunov function was applied by Shuai&Driessche (2013) to obtain the sufficient conditions for the global stability of infectious disease models. In what follows, the present study shall establish the global asymptotic stability of the disease free equilibrium of a cholera model using the model of Fung (2014) as a frame by constructing a suitable Lyapunov functions and LaSalle's invariance principle. Vaccination and therapeutic treatment are the prevention and control measures that are used to extend the model of Fung.

2. Methodology

In this section, we present the original Fung model from which the extension and modification are made.

2.1 Model Formulation

The Fung model for cholera transmission is given as

$$\frac{ds}{dt} = -\lambda S + \mu_b N - \mu_d S \tag{1}$$

$$\frac{dI}{dt} = \lambda S - \gamma I - (\mu_c + \mu_d) I \tag{2}$$

$$\frac{dR}{dt} = \gamma I - \mu_d R \tag{3}$$

$$\frac{dB}{dt} = \varepsilon I - \delta \mathrm{B} \tag{4}$$

Where $\lambda = \beta \left[\frac{B}{(B+\aleph)}\right]$, $\mathrm{N} = \mathrm{S} + \mathrm{I} + \mathrm{R}$.

S, I, R and B are the state variables denoting susceptible, infectious, recovered and pathogen population respectively at time t, N is the total human population and $\lambda, \mu_b, \mu_d, \gamma, \mu_c, \beta, \aleph, \varepsilon$ *and* δ are parameters representing force of infection, birth rate, death rate unrelated to the disease, recovery rate unrelated to the treatment, death rate due to the disease, contact rate between susceptible individuals and contaminated water, pathogen concentration that yields 50% chance of catching cholera, rate at which infectious individuals contributes to the growth of pathogen and natural death rate of the pathogen respectively.

Fung built the model on the assumptions that cholera confers permanent immunity and that; cholera can only be contracted through the ingestion of contaminated water. These are not realistic assumptions. cholera does not confer permanent immunity upon recovery. An individual who had been

recovered from cholera can still be reinfected if he comes in contact with the infection agents. Besides, the mode of transmission of cholera is not only through the contact with contaminated water but also through the contact with infectious individuals. Above all, the model does not involves control measures.

2.2 The Extension and Modification of the Model

The present study is aimed at improving on the model of Fung. We modify the model to incorporate vaccination and therapeutic treatment as prevention and control measures to cholera outbreak. The possibility of re-infection after recovery and the tendency of disease transmission from person-to-person are also considered. Vaccination is introduced to the susceptible population at a rate v_1 (t), so that v_1 (t) S (t) individuals per time are removed from the susceptible category and added to the recovered population. In the same manner, therapeutic treatment and vaccination are applied to the infected people at a rate ρ (t), and v_2(t) respectively so that ρ (t)I(t) and v_2(t)I(t) individuals per time are removed from the infected class and added to the recovered class. Therapeutic treatment is in the form of administration of antibiotics or rehydration salts. When all these parameters are incorporated, we come about the below model

$$\begin{aligned}
\frac{ds}{dt} &= \pi - \mu S - \varphi S - v_1 S + \sigma R \\
\frac{dI}{dt} &= \varphi s - (\mu + \mu_c + v_2 + \rho + \gamma)\mathrm{I} \\
\frac{dR}{dt} &= \gamma I - \mu R + v_2 I + v_1 S + \rho I - \sigma R \\
\frac{dB}{dt} &= \varepsilon I - \delta B
\end{aligned} \tag{5}$$

$$\varphi = \left[\frac{\beta_1 B}{B + \aleph} + \beta_2 I \right] \tag{6}$$

v_1 and v_2 are vaccination rates before and during the outbreak respectively while β_1 and β_2 are contact rates with contaminated water and cholera patients' wastes respectively. μ *and* μ_c are death rates unrelated to cholera and due to cholera respectively. $\sigma$is the rate of losing immunity while ρ is the treatment rate. φ stands for the force of infection, π is the recruitment rate and the interpretation for the state variables and other parameters remain as defined for Fung model in section 2.1

3.0 Equilibrium Analysis

3.1 Existence of the Disease Free Equilibrium State

The disease free equilibrium (DFE) for model (5) is given by

$$\mathrm{E}_0 = \left(\frac{\pi}{\mu + v_1}, 0, 0, 0 \right). \tag{7}$$

In the absence of disease, the population size converges to the disease-free steady state $\frac{\pi}{\mu + v_1}$. Therefore, equation (5) shall be studied in the following feasible region

$$\Omega = \left\{(S, I, R, B) \epsilon R_+^4 \quad : S \geq 0, I \geq 0, B \geq 0, R \geq 0, S + I + R + B \leq \frac{\pi}{\mu + v_1}\right\} \tag{8}$$

3.2 Existence of Endemic Equilibrium State

Asterisk is used to denote the endemic state of the state variables and the following equations are obtained for the endemic equilibrium

$$\pi - \mu S^* - \frac{\beta_{1B^*}}{B^* + \aleph} S^* - \beta_2 I^* S^* - v_1 S^* + \sigma R^* = \tag{9}$$

$$\frac{\beta_{1B^*}}{B^* + \aleph} S^* + \beta_2 I^* S^* - (\mu + \mu_c + v_2 + \rho + \gamma)\mathrm{I}^* = 0 \tag{10}$$

$$\gamma \mathrm{I}^* - \mu R^* + v_2 \mathrm{I}^* + v_1 S^* + \rho \mathrm{I}^* - \sigma R^* = 0 \tag{11}$$

$$\varepsilon I^* - \delta B^* = 0 \tag{12}$$

Our intention is to solve for I and the algebraic manipulation of eqns (9) – (12) yields

$$I^*\left[\beta_2 \varepsilon \mathrm{I}^{*^2}\{\sigma \mathrm{d} - \mathrm{eb}\} + \mathrm{I}^*\{\mathrm{e}\pi\beta_2\varepsilon + \beta_2\aleph\delta(\sigma d - eb) + \beta_1\varepsilon(\sigma d - eb) - \varepsilon b(ae - \sigma v_1)\} + \{\mathrm{e}\pi\beta_1\varepsilon + e\pi\beta_2\aleph\delta - \aleph\delta b(ae - \sigma v_1)\}\right] = 0 \tag{13}$$

where a =($\mu + v_1$), b = ($\mu + \mu_c + v_2 + \rho + \gamma$), d = ($v_2 + \rho + \gamma$) and e = ($\mu + \sigma$).

Equation (13) has two solutions: $I^* = 0$ which corresponds to the disease-free equilibrium and,

$$\{\sigma \mathrm{d} - \mathrm{eb}\}\beta_2\varepsilon \mathrm{I}^{*^2} + \{\mathrm{e}\pi\beta_2\varepsilon + \beta_2\aleph\delta(\sigma d - eb) + \beta_1\varepsilon(\sigma d - eb) - \varepsilon b(ae - \sigma v_1)\}I^* + \{\mathrm{e}\pi\beta_1\varepsilon + e\pi\beta_2\aleph\delta - \aleph\delta b(ae - \sigma v_1)\} = 0 \tag{14}$$

For simplicity, equation (14) can be written as

$$A_1 \mathrm{I}^{*^2} + \mathrm{A}_2 I^* + \mathrm{A}_3 = 0 \tag{15}$$

Equation (15) is a quadratic equation in I^*

If $A_1 < 0$ and$\mathrm{A}_3 > 0$ in (15) then $I_1^* I_2^* = \frac{\mathrm{A}_3}{A_1} < 0$ and one of I_1^* or I_2^* is necessarily positive. Hence, there exists a unique positive solution for I^* in equation (15).
By using the next generation matrix approach due to van den Driessche and Watmough (2002), the basic reproduction number for the extended model is obtained as

$$R_0{}^q = \frac{\pi\varepsilon\beta_1 + \pi\aleph\delta\beta_2}{\aleph\delta(\mu + v_1)(\mu + \mu_c + v_2 + \rho + \gamma)} \tag{16}$$

The superscript q is used to emphasize the model with controls. Compared to the basic reproduction number for the original no-control model (Fung's model) which is given as

$$R_0 = \frac{\mu_b \beta N}{\aleph \mu_d(\gamma + \mu_c + \mu_d)} \tag{17}$$

4.0 Stability Analysis

4.1 Global Stability of Disease Free Equilibrium (DFE)

The following theorem shall be used to investigate the global asymptotic stability of the disease free equilibrium of the model equation (5)

Theorem 1: (Shuai& van den Driessche, 2013)

If $R_0{}^q < 1$, then the disease free equilibrium E_0 of model (5) is globally asymptotically stable in Ω.

Proof

The variable S does not appear in the first term of susceptible compartment. Dropping this term, equation (5) reduces to

$$\begin{aligned} S^1 &= -\mu S - \varphi S - v_1 S + \sigma R \\ I^1 &= \varphi S - (\mu + \mu_c + \mathrm{v}_2 + \rho + \gamma)\mathrm{I} \\ \mathrm{R}^1 &= \gamma I - \mu R + v_2 I + v_1 S + \rho I - \sigma R \\ B^1 &= \varepsilon I - \delta B \end{aligned} \tag{18}$$

Define a linearLyapunov- LaSalle function M as

$$\mathrm{M(S, I, R, B)} = a_1 S + a_2\ \mathrm{I} + \ a_3 R + a_4 B \tag{19}$$

Where$a_1 > 0,\ a_2\ > 0,\ a_3 > 0\ and\ a_4 > 0.$

Hence, the derivative of M w.r.t. t in equation (19) is

$$\frac{dM}{dt} = a_1 S^{|} + a_2\ I^{|} + \ a_3 R^{|} + a_4 B^{|} \tag{20}$$

The aim is to show that $\frac{dM}{dt} < 0$ in Ω to establish that $R_0{}^q < 1$

Substituting equation (18) into equation (20) and collecting terms in terms of each variable then,

$$\begin{aligned} \frac{dM}{dt} \quad &= -\ (a_1\mu + a_1\varphi + \ a_1 v_1 - \ a_2\varphi - \ a_3 v_1)S \\ &\quad - [a_2\ (\mu + \mu_c + v_2 + \rho + \gamma) - \ \{a_3(\gamma + v_2 + \rho) + a_4\varepsilon\}]I \\ &\quad - a_4\delta(B) - (a_3\mu + a_3\sigma - \ a_1\sigma)R \end{aligned} \tag{21}$$

Express $(\mu + \mu_c + v_2 + \rho + \gamma), (\gamma + v_2 + \rho), v_1$ and $(\mu + v_1)$ in terms of the reproduction number in equation (16) and put the result in equation (21) then

$$\begin{aligned} \frac{dM}{dt} = &- \left\{a_1\left[\frac{1}{R_0{}^q}\left(\frac{\pi\varepsilon\beta_1 + \pi\aleph\delta\beta_2}{\aleph\delta(\mu+\mu_c+v_2+\rho+\gamma)}\right) + \varphi\right] - a_2\varphi - a_3\left(\frac{\pi\varepsilon\beta_1 + \pi\aleph\delta\beta_2}{(\mu+\mu_c+v_2+\rho+\gamma)\aleph\delta R_0{}^q} - \mu\right)\right\}S \\ &- \left[a_2\ \frac{1}{R_0{}^q}\left(\frac{\pi\varepsilon\beta_1 + \pi\aleph\delta\beta_2}{\aleph\delta(\mu+v_1)}\right) - \left\{a_3\left[\frac{1}{R_0{}^q}\left(\frac{\pi\varepsilon\beta_1 + \pi\aleph\delta\beta_2}{\aleph\delta(\mu+v_1)}\right) - (\mu + \mu_c)\right] + a_4\varepsilon\right\}\right]I \\ &- a_4\delta(B) \end{aligned}$$

$$-\{a_3(\mu+\sigma)-a_1\sigma\}R \tag{22}$$

Since equation (5) monitors human population then all the parameters as well as variables are non- negative and the coefficient of each state variable is considered negative in equation (22) i.e.

$$-\left\{a_1\left[\frac{1}{{R_0}^q}\left(\frac{\pi\varepsilon\beta_1+\pi\aleph\delta\beta_2}{\aleph\delta(\mu+\mu_c+v_2+\rho+\gamma)}\right)+\varphi\right]-a_2\varphi-a_3\left(\frac{\pi\varepsilon\beta_1+\pi\aleph\delta\beta_2}{(\mu+\mu_c+v_2+\rho+\gamma)\aleph\delta{R_0}^q}-\mu\right)\right\}<0 \tag{23}$$

$$-a_4\delta<0 \tag{24}$$

$$-\{a_3(\mu+\sigma)-a_1\sigma\}<0 \tag{25}$$

$$-\left[a_2\ \frac{1}{{R_0}^q}\left(\frac{\pi\varepsilon\beta_1+\pi\aleph\delta\beta_2}{\aleph\delta(\mu+v_1)}\right)-\left\{a_3\left[\frac{1}{{R_0}^q}\left(\frac{\pi\varepsilon\beta_1+\pi\aleph\delta\beta_2}{\aleph\delta(\mu+v_1)}\right)-(\mu+\mu_c)\right]+a_4\varepsilon\right\}\right]<0 \tag{26}$$

∴equations (23) – (26) establish that $\frac{dM}{dt}<0$ in Ω. Moreover, $\frac{dM}{dt}=0$ iff S= 0, I= 0, B= 0 and R= 0. Hence, the maximum invariant set in $\left\{(S,I,R,B):\frac{dM}{dt}=0\right\}$ is the singleton $\{E_0\}$. By LaSalle's invariance principle as in Bowong *et al*. (2011), E_0 is globally asymptotically stable in the invariant region Ω where E_0 is the disease free equilibrium of the model.

5.0 Result and Analysis

To validate the analytical results obtained in section 4, numerical simulations are provided. The graphical presentations in figures 1 - 3 show the scenario between susceptible, infective and time under the disease free and the endemic equilibria respectively. The graphs represent the results of the simulations and all computations are accomplished by Maple 18 software. Values are assumed for the parameters and state variables of the models to conduct the simulation and the results are presented graphically. The results demonstrate the effects of strong control, weak control and no control on the population of susceptible and infectious individuals over a period of time (30 days). The results obtained are based on the values assumed for the state variables and parameters. We expect fluctuation in these results if the values are varied.

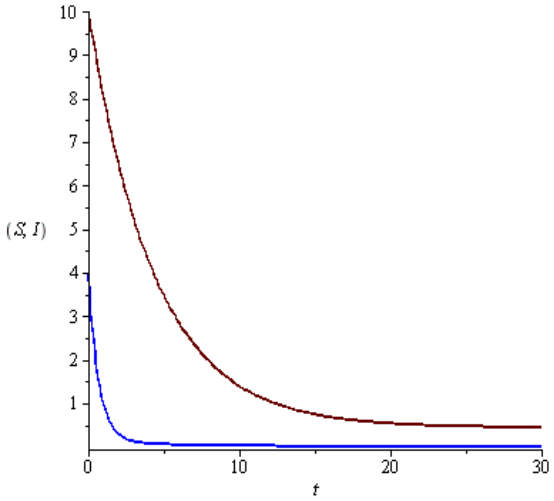

Figure1: Graph of (S, I) against time under strong control. Parameter Values are S=10, I=4, Π=0.1, μ=0.01, $V_1 = 0.2$, $V_2 = 0.4$, $\mu_c = 0.001$, ρ = 0.6, γ= 0.5, ψ= 0.02

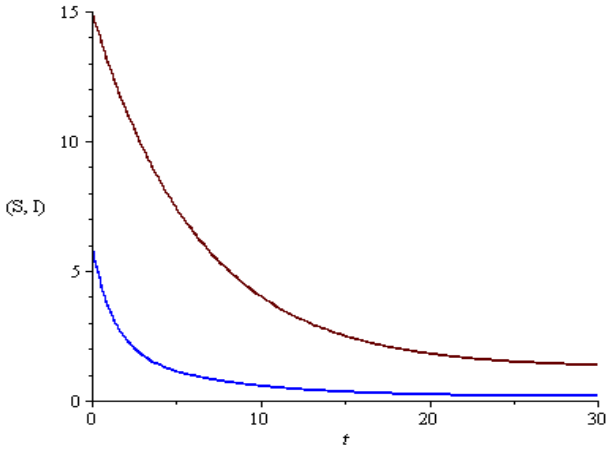

Figure 2: Graph of (S, I) against time under weak control. Parameter Values are S=15, I=6, Π=0.2, μ=0.01, $V_1 = 0.05$, $V_2 = 0.1$, $\mu_c = 0.015$, ρ = 0.2, γ= 0.5, ψ = 0.1

Figure 1 depicts a situation when there is strong control. With the assumed values stated under figure 1 together with π=0.1, ε= 0.01, β_1=0.03, β_2=0.02, א=0.04 and δ=0.5, the reproduction number in equation (16) is simulated to be 0.011 i.e$R_0{}^q = 0.011 < 1$. The disease free equilibrium is globally asymptotically stable under this condition. Figure 1 shows that over the time span of 30 days when $R_0{}^q < 1$, the number of susceptible (S) and infective (I) decreases significantly as the days of infection increase and the disease eventually disappears with time. Figure 1 is obtained from equation (5).

Similarly, using parameter values under figure 2 together withπ=0.2, ε= 0.03, β_1=0.045, β_2=0.035, א=0.06 and δ=0.5 to simulate equation (16) then $R_0{}^q = 3.232 > 1$ and the disease free equilibrium is unstable. This implies that there exists a unique endemic equilibrium that is globally asymptotically stable. Figure 2 is a situation when the control is weak. From figure 2, it is observed that during the period of simulations the number of susceptible S and infectious I descend continuously though at a lower rate than figure 1. This shows that the number of infectious individuals after 5 days is higher in figure 2 than in figure 1. Therefore strong control measures perform better in eradicating cholera disease. Figure 2 is also obtained from equation (5).

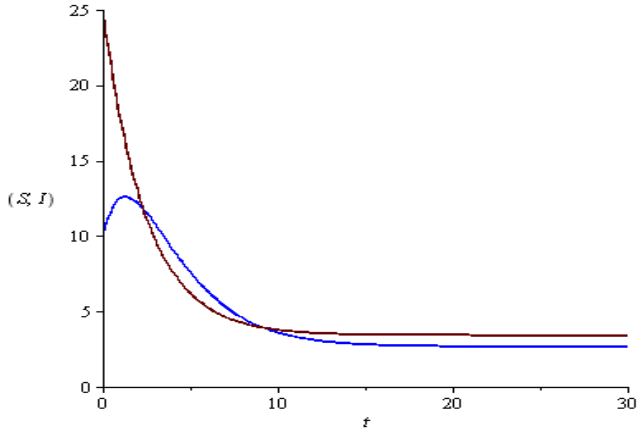

Figure 3: Graph of (S, I) against time under no control. Parameter Values are S=25, I=10, λ=0.4, μ_δ=0.04, μ_c = 0.003, μ_d= 0. 01 , N= 35, γ= 0.5

Moreover, by using parameter values under figure 3 together with β =0.5, א=0.4to simulate equation (17) then, R_0 = 341.131 >1 and the disease free equilibrium is unstable. It is observed from figure 3 that during the period of simulations the number of susceptible S and infectious I falls very slowly as the curves move away from the origin with larger number of infectious population at the end of the simulation which signals a major cholera tragedy in the population. Figure 3 is obtained from equations (1) – (4).

6.0 Conclusion

This work examined the global asymptotic stability of the two equilibrium states of a cholera model with prevention and control strategies. The DFE is globally asymptotically stable if ${R_0}^q$ <1 while the endemic equilibrium is globally asymptotically stable if ${R_0}^q$ >1. Graphical representations of the two cases i.e the DFE and the EE are provided with separate cases of mild endemism and major endemism i.e ${R_0}^q$ >1 and $R_0 > 1$. The graphs are used to illustrate the effect of strong control, weak control and no control on the dynamics of cholera disease with reference to the existence of ${R_0}^q$ <1, ${R_0}^q$ >1 and $R_0 > 1$ .The results obtained in this work strongly suggest that each community especially in less developed countries like Nigeria should be on red alert against the possibility of cholera outbreak. Besides, we find that to prevent and eliminate cholera in the population, there is a need to decrease the transmission rate and increase the treatment rate through adequate prevention and control measures. On that ground, relevant agencies should deem it fit to provide adequate enlightenment and sensitization to the general public on the need for environmental sanitation, personal hygiene and the dangers of land and water pollutants. Besides, provision of drinkable water and immunization are also necessary as all these will work together to reduce the parameters א, $\varepsilon, \beta_1, \mu_c$, and$\beta_2$. Above all, immediate response to cholera outbreak by the Government, health practitioners and the general public are capable of increasing the parameters v_2 and ρ and eventually bring the outbreak under control.

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