EXISTENCE AND UNIQUENESS ANALYSIS OF TRANSMISSION MODEL OF *Schistosomiasis*

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Abstract: The concept of basic reproduction number (R_N) occupies a fundamental place in epidemic theory. The value of R_N determines the proportion of the population that becomes infected over a course of epidemic. This study investigated *Schistosomiasis* transmission model and tested for the existence and uniqueness of solution using Lipschitz condition to ascertain the efficacy of the model. Findings showed that the stability of disease free equilibrium and the existence of an endemic equilibrium for the model are given in terms of key thresholds parameters known as the reproduction number R_N. The dynamics of the model diseases free equilibrium is globally asymptotically stable if $R_N < 1$ and the unique endemic equilibrium is globally asymptotically stable if $R_N > 1$. Some numerical simulations were also performed to illustrate our main results.

Keywords: *Schistosomiasis*, epidemic, basic reproduction number, mathematical model, threshold

Introduction

Schistosomiasis, also known as bilharzias classified as a Neglected Tropical Disease (NTD) is a dangerous health problem in developing countries. Despite remarkable achievements in *Schoistosomiasis* control over the past five decades, about 240 million people are estimated to be infected worldwide and more than 700 million people live in endemic areas (WHO, 2012; Guiro *et al*., 2017). *Schistosomiasis* is a parasitic disease caused by flatworms of the schistoma. *Schistosomiasis* are digenetic trematodes that spend their adult life in humans and previous stage in aquatic snails (Jordan and Webbe, 1993). Flatworms infect humans by penetrating the skin when exposed to contaminated fresh water (for example, lakes, ponds, dams, rivers) inhabited by fresh water snails carrying the parasite.

There are two forms of *Schistosomiasis*, the urinary *Schistosomiasis* and intestinal *Schistosomiasis.* The *Schistosomiasis* is caused by *Schistosoma haematobium* while the intestinal*Schistosomiasis*caused by any of the organism's *Schistosomain tercalatum, Schistosoma mansoni, Schistosomiasis japonicum* and *Schistosoma mekongi* (Guiro *et al*., 2017). The parasites *Schistosomes* have to undergo through an intermediate host (snails in most cases) to complete their life cycle from eggs tomiracidia, cercaria and finally to adult worm. The prevalence of *Schistosomiasis* is high in tropical and sub-tropical regions, especially in poor rural regions without access to safe drinking water and adequate sanitation.

Mathematical modelling of *Schistosomiasis* transmission is one of the most important tools to assess strategies for control against various infectious diseases (Castillo-Chavez and Thieme, 1994). Consequently, Mathematical modelling of *Schistosomiasis* transmission have been developed by many authors (Macdonald 1968; Jordan *et al*., 1993; Guiro *et al*., 2017; Diaby, 2015). Macdonald (1968) was the first to use simple Mathematics models to study the transmission dynamics of *Schistosomiasis.* Edward (2010) developed a Mathematical modelling within host parasite dynamics of *Schistosomiasis.* In Diaby (2015), stability analysis of *Schistosomiasis* transmission model with control strategies was studied. The model incorporate several realistic features such as density-dependent birth rate of snails and reduced fecundity in snail hosts. Also, the analysis of thedeterministic model was made with respect to the stability of the disease free-equilibrium and the endemic equilibrium. However, it appears that the existence and uniqueness of solutions of the disease free-equilibrium and the endemic equilibrium was not investigated to the best of our knowledge. In this paper, we extend the model developed by Diaby (2015) and analyse the existence and uniqueness of solution of the model using Lipschitz condition to ascertain the efficiency of the model. Threshold analysis of R_N is also investigated and some numerical simulation are reported to buttress the theoretical results with respect to R_N.

The mathematical model

The model is developed to show the interactions between a complex life cycle of parasite *Schistosoma* and its host (human and snails). The parasite populations are modelled explicitly through the miracidia and cercaria denoted by W_m and W_c respectively. The total snails' population at time t is given by $N_s(t)$ and these comprises of the susceptible snail $(S_s(t))$ and infectious snails $(I_s(t))$, thus $N_s(t) = S_s(t) + I_s(t)$. Similarly, the total human population is denoted by $N_h(t)$ also, comprises of the susceptible human $(S_h(t))$ and infected human $(I_h(t))$ and $N_h(t) = S_h(t) + I_h(t)$.

The following assumptions are made:

(i) There is a constant per capital rate of exposure between host and sensitive parasite
(ii) Individuals are born uninfected
(iii) population has a constant size
(iv) There exist natural death in both the snails and human population
(v) There exist the induce death in both the snails and human population
(vi) All parameters are non-negative

$$\frac{dS_s}{dt} = b_s(S_s + \rho I_s)(1 - c(S_s + I_s) - (d_{sE} + \theta_s)S_s - \beta_s S_s W_m$$
$$\frac{dIs}{dt} = \beta_s S_s W_m - (d_{sE} + \theta_s + \alpha)I_s$$
$$\frac{dWm}{dt} = kI_h - \delta(S_s + I_s)W_m - d_m W_m \quad (1.1)$$
$$\frac{dWc}{dt} = \gamma I_s - (d_{cE} + \theta_c)W_c$$
$$\frac{dSh}{dt} = \Lambda - \beta_h W_c S_h - d_h S_h + \eta I_h$$
$$\frac{dIh}{dt} = \beta_h W_c S_h - (d_h + \pi l + \eta)I_h$$

Where b_s – Birth rate of snails, ρ – Fecundity, c – Competitive intensity

d_s – Death rate of snails, θ_s – Elimination rates of snails, β_S – Rate at which snails are infected

α – Rate of parasite virulence, k – Birth rate of miracidia, δ – Death rate of the miracidia due the infection, d_m – Natural death rate of the miracidia, λ – Birth rate of cercariae, d_{cE} – Death rate of cercariae, θ_c – Elimination of cercariae, β_h – Rate at which human is infected, d_h – Natural death η – Recovery rate of human, μ – Induced death and Λ – Human recruitment (Mouhamadou, 2015) for more details).

Basic properties of models

(1) Positivity of solutions of the model: We consider the positivity of solutions of the system of equation (1.1) and show that all the state variables remain non-negative and the solutions of the system with positive initial conditions remain positive for all $t > 0$.

Theorem 1

Let the initial condition of the system (1.1) be;

$\left\{(ds_{s^{(0)}}, dI_{s^{(0)}}, dw_{m^{(0)}}, dw_{c^{(0)}}, ds_{h^{(0)}}, dI_{h^{(0)}}) > 0\right\}$,

then the solution set

$\left\{(s_s(t), I_s(t), w_m(t), w_c(t), s_h(t), I_h(t))\right\}$ of the system (1.1) is positive for all $t > 0$.

$$\frac{dI_S}{dt} = \beta_s S_s W_m - (d_{sE} + \theta_S + \alpha)I_S$$
$$\frac{dI_s}{dt} \geq -(d_{sE} + \theta_S + \alpha)I_S$$

Assuming $I_S > 0$

$$\int \frac{dI_S}{I_s} \geq \int -(d_{sE} + \theta_S + \alpha)dt$$
$$\ln I_S + c \geq -(d_{sE} + \theta_S + \alpha)t$$
$$I_S + e^c \geq e^{-(d_{sE} + \theta_s + \alpha)t}$$
$$I_s(t) \geq I_s(0)e^{-(d_{sE} + \theta_s + \alpha)t} \geq 0$$

Similar test was carried out for all other equations for $t > 0$. We also use the Lipschitz condition to verify the existence and uniqueness of solutions.

Theorem 2 (Derrick et al., 1976)

Let D denote the region

$|t - t_0| \leq a, \|x - x_0\| \leq 1, x = (x_1, x_2, ..., x_n)$,

$x_0 = (x_{1,0}, x_{2,0}, ..., x_{n,0})$.

And suppose that $f(t, x)$ satisfies the Lipschitz condition

$$\|f(t, x_1) - f(t, x_2)\| \leq k\|x_1 - x_2\|$$

Whenever the pairs (t, x_1) and (t, x_2) belong to D, where k is a positive constant. Then, there is a constant $\delta \geq 0$ such that there exists a unique continuous vector solution $x(t)$ of the system (1.1) in the interval $t - t_0 \leq \delta$. It is important to note that the condition is satisfied by the requirement that, $\frac{\partial f_i}{\partial x_j}$ $i, j = 1, 2, 3...$, be continuous and bounded in D.

Let D denote region $0 \leq \alpha \leq R,$ the equation have a unique solution. We show that $\frac{\partial f_i}{\partial x_j}$ $i, j = 1, 2, 3, 4, 5, 6$ are continuous and bounded.

For f_1

$|\frac{\partial f_1}{\partial s_s}| = |b_s - d_s - cb_s(2s_s - I_s(\rho + 1)) - \beta_s w_m| < \infty$, $|\frac{\partial f_1}{\partial s_s}| = |-cb_s + b_s\rho - cb_s s_s - 2cb_s\rho I_s| < \infty$

$|\frac{\partial f_1}{\partial w_m}| = |-\beta_s s_s| < \infty$, $|\frac{\partial f_1}{\partial w_c}| = 0 < \infty$, $|\frac{\partial f_1}{\partial s_h}| = 0 < \infty$, $|\frac{\partial f_1}{\partial I_h}| = 0 < \infty$

For f_2

$|\frac{\partial f_2}{\partial s_s}| = |\beta_s w_m| < \infty$, $|\frac{\partial f_2}{\partial w_m}| = |\beta_s s_s| < \infty$, $|\frac{\partial f_2}{\partial I_s}| = |-(ds_E + \theta_s + \alpha)| < \infty$, $|\frac{\partial f_2}{\partial w_c}| = 0 < \infty$

$|\frac{\partial f_2}{\partial s_h}| = 0 < \infty$, $|\frac{\partial f_2}{\partial I_h}| = 0 < \infty$

These partial derivatives exist, continuous and are bounded. Similarly, for f_3 to f_6. Hence from the above theorem, the model (1.1) has a unique solution.

The basic reproduction number of the model

The basic reproductive number R_N is defined as the effective number of secondary infections caused by typical infected individual. It is obtained by taking the largest (dominant) of

$$R_N = \left[\frac{\partial f_i(x_0)}{\partial x_j}\right]\left[\frac{\partial v_i(x_0)}{\partial x_j}\right],$$

where f_i is the rate of appearance of new infected in the compartments, v_i is the transfer individuals out of the

compartments by another means , x_0 the disease free equilibrium

$$f_i = \begin{pmatrix} \beta_s s_s w_m \\ \beta_h s_h w_c \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \Rightarrow F \begin{pmatrix} 0 & 0 & \frac{\beta_s (b_s - d_s}{b_s c} & 0 \\ 0 & 0 & 0 & \frac{\beta h \Lambda}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

$$v_i = \begin{pmatrix} (ds+\alpha) I_h \\ -kI_h + \delta(s_s + I_s) w_m + d_m w_m \\ -\mu I_s + d_c w_c \\ -b_s (s_s - \rho I_s)(1 - c(s_s + I_s) + d_s s_s + \beta_s s_s w_m \\ -\Lambda + \beta_h w_c s_h + \mu I_h + \eta I_h \end{pmatrix}$$

$$\Rightarrow V = \begin{pmatrix} \alpha + \delta s & 0 & 0 & 0 \\ 0 & \eta + \mu & 0 & 0 \\ 0 & -k & \frac{\delta(b_s - d_s)}{b_s c} + d_m & 0 \\ -\gamma & 0 & 0 & d_c \end{pmatrix}$$

Taking the spectral radius of the next generation matrix, we have

$$R_N = \rho(Fv^{-1}) = \sqrt{\frac{\beta_s \gamma k \Lambda (b_s - d_s) \beta_h}{d_h d_c (d_s + \alpha)(\eta + \mu + d_h)(b_s (c d_m + \delta) - \delta d_s)}} \quad (1.2)$$

Threshold analysis of parameters

The impact of some major parameters like β_s, β_h, γ on the transmission dynamics of *Schistosomiasis* plays vital roles for the determination of control measure. This analysis will afford the opportunity of identifying the impact factor of these parameters on the basic reproduction number of the model;

Theorem 4.1: For the reproduction number in (1.2) of the model equations (1.1), the threshold analysis of each parameter has an increasing effect on R_N if $\frac{\partial R_0}{\partial x_i} > 0$ and decreasing effect on R_N if $\frac{\partial R_0}{\partial x_i} < 0$ for each of the parameters x_i (Pelli *et al.*, 2009). The threshold analysis of β_s is

$$R_N = \left(\frac{\beta_s \gamma k \Lambda (b_s - d_s) \beta_h}{d_h d_c (d_s + \alpha)(\eta + \mu + d_h)(b_s (c d_m + \delta) - \delta d_s)} \right)^{\frac{1}{2}}$$

$$\frac{\partial R_N}{\partial \beta_s} = \frac{1}{\frac{1}{2}\sqrt{\frac{k \Lambda \gamma (b_s - d_s) \beta_h}{d_h d_c (d_s + \alpha)(\eta + \mu + d_h)(b_s (c d_m + \delta) - \delta d_s)}}} > 0$$

$$\frac{\partial R_N}{\partial \beta_h} = \frac{1}{\frac{1}{2}\sqrt{\frac{\beta_s \gamma k \Lambda (b_s - d_s)}{d_h d_c (d_s + \alpha)(\eta + \mu + d_h)(b_s (c d_m + \delta) - \delta d_s)}}} > 0$$

$$\frac{\partial R_N}{\partial \gamma} = \frac{1}{\frac{1}{2}\sqrt{\frac{\beta_s k \Lambda (b_s - d_s) \beta_h}{d_h d_c (d_s + \alpha)(\eta + \mu + d_h)(b_s (c d_m + \delta) - \delta d_s)}}} > 0$$

Fundamentally, positivity of an expression confirms a positive effect in the number of secondary infection rate. Hence, increasing in β_s (birth rate of snails), β_h (rate at which humans are infected), γ (birth rate of cercariae), k (birth rate of miracida) increases the value of the basic reproduction number and make the equilibrium rate approaches endemic value. In other to control the disease, the birth rate of snails, cercariae, miracida and the rate at which humans are infected should be control and possibly brought to the barest minimum.

Numerical simulation

To understand the dynamics of the model, our system of equation (1.2) was simulated using the parameter values

$S_s = 1000, I_S = 50000, w_m = 5000, w_c = 9000, S_h = 2000, I_h = 550, \delta = 0.0039, \theta_s = 0$

$c = 0.025, \beta_s = 0.005, \beta_h = 0.406, k = 0.00232, \mu = 100, \theta_c = 0, \eta = 0$. Our simulation showed that the diseases becomes endemic when the basic reproduction number $R_N = 2.2331 > 1.$ Also,

$\theta_c = 10, \theta_s = 0.05, \delta = 0.009, S_s = 10000, I_s = 50000, I_h = 550, w_c = 9000, \Lambda = 8000, \delta = 0.009$

$S_h = 2000, \eta = 0, k = 0.00232, \beta_s = 0.06, \beta_h = 0.0406, d_h = 0.00003, d_m = 2.5,$

The basic reproduction number is $R_N = 0.7219 < 1,$ hence not endemics, the disease will die out with time.

Discussion and Conclusion

In this paper, the dynamics of *Schistosomiasis* has been presented. We have carried out qualitative analysis for the existence and uniqueness of the solution of the model and also solved for the positivity of the solutionof the model. The basic reproduction number of the model was calculated using the next generation matrix method.Threshold analysis of the basic reproduction number to the model parameter was performed to investigate the parameters that possess greater influence on the model. In terms of the basic reproduction number, it was observed that when $R < 1$(less than unity) the diseases will die out with time and $R_N > 1$ (greater than unity), the

disease is at endemic point. Numerical simulation were carried out in order to verify some of the analytical results.

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Conflict of Interest
Authors declare that there is no conflict of interest related to this study.

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