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Stability analysis of a schistosomiasis model with delays

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Abstract

In this work, a nonlinear deterministic model for schistosomiasis transmission including delays with two general incidence functions is considered. Rigourous mathematical analysis is done. We show that the stability of the disease-free equilibrium and the existence of an endemic equilibrium for the model are stated in terms of key thresholds parameters known as basic reproduction number \mathcal{R}_0 . This study of the dynamic of the model is globally asymptotically stable if $\mathcal{R}_0 \leq 1$, and the unique endemic equilibrium is globally asymptotically stable when $\mathcal{R}_0 > 1$. Some numerical simulations are provided to support the theoretical result with respect to \mathcal{R}_0 in this paper.

Keywords: delays; global stability; mathematical model; Lyapunov function; schistosomiasis; reproduction number

1 Introduction

Schistosomiasis is a serious health problem in developing countries. Indeed, despite the remarkable achievements in schistosomiasis control over the past five decades, there are about 240 million people infected worldwide, and more than 700 million people live in endemic areas [1]. There are two patterns of schistosomiasis. We note the urinary schistosomiasis and the intestinal schistosomiasis. The first one is caused by Schistosoma haematobium, when the second is caused by any of the organisms Schistosoma intercalatum, Schistosoma mansoni, Schistosoma japonicum and Schistosoma mekongi. Mathematical modeling of schistosomiasis transmission can help in the development of the strategies for control. Thus, several mathematical models for this disease have been done (see [2-13]and the references therein). In [11], a discrete delay model for the transmission is studied. The delay appears in the incidence term including masse action SI (S: susceptible, I: infectious). It appears that the incidence function form is determinative in the study of the model system. Then, changing the form of the incidence can potentially change the behaviour of the system. In this paper, a mathematical model is derived with a bounded delay distributed and two general incidence functions term f and g. The model described here considers two population hosts, humans and snails, and is structured as follows: Susceptible (uninfected) and infectious humans and susceptible (uninfected) and infected snails. The paper is organized as follows. In Section 2, we present the mathematical model, and we study the mathematical properties of the model system. In Section 3, we derive some results about the basic reproduction number, the disease-free equilibrium and the endemic equilibrium. Section 4 is devoted to the global stability of the disease-free equilib-



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2 The mathematical model

In this section, we derive a mathematical model for the spread of schistosomiasis. Here, we consider human and snail populations. We assume that all newborns are susceptible, and that the infection does not result in death of human and snail populations. Further, it is assumed that a susceptible host became infected only by contact with water, in which there exist cercariae from infected snails, and a susceptible snail became infected by contact with miracidia coming from parasite eggs released in feces and urine of infected hosts (see Figure 1 below).

We denote by

 H_s the susceptible (uninfected) human population size;

 H_i the infected human population size (infectious humans);

 S_s the susceptible (uninfected) snail population size;

 S_i the infected and shedding snail population size (shedding snail population size).

We also denote by

 Λ_h the recruitment rate of susceptible humans;

 Λ_s the recruitment rate of susceptible snails;

 d_h the *per capita* natural death rate of humans;

*d*_s the *per capita* natural death rate of snails;

 τ_1 the transit time from cercaria in water to schistosomule in a human host;

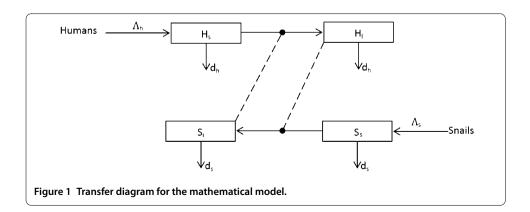
 τ_2 the transit time from parasite eggs to miracidia to infect a snail;

 k_1 and k_2 the Lebesgue integrable functions, which give the relative infectivity of snails and humans (respectively) of different infection ages.

Note that the support of k_1 and k_2 has a positive measure in any open interval having supremum h, so that the interval of integration is not artificially extended by concluding with an interval, for which the integral is automatically zero. On the other hand, we choose in the model two real numbers α and γ , so that $\int_0^h k_1(\tau_1) d\tau_1 = 1$ and $\int_0^h k_2(\tau_2) d\tau_2 = 1$.

As general as possible, the incidence functions f and g must satisfy technical conditions. Thus, we assume that

- H1 f and g are non-negative C^1 functions on the non-negative quadrant,
- H2 for all $(H_S, H_i, S_s, S_i) \in \mathbf{R}^4_+$, $f(H_s, 0) = f(0, S_i) = 0$ and $g(S_s, 0) = g(0, H_i) = 0$.



Remark 2.1 f and g are two incidence functions, which explain the contact between two species. Therefore, f and g are non-negative. Note also that when there is no one infected in the human and snail populations, then the incidence functions are equal to zero. The incidence functions are also equal to zero, when there is no one susceptible in the human and snail populations.

Let us denote by f_1 and f_2 the partial derivatives of f with respect to the first and to the second variable and g_1 and g_2 those of g with respect to the first and to the second variable. For mathematical simplicity, we shall make now a simplification that will allow us to carry out an analysis, namely we assume that the disease-induced death rate is neglected. Using the notations $H_{\tau_2}^i = H_i(t - \tau_2)$ and $S_{\tau_1}^i = S_i(t - \tau_1)$, the model equations are given as follows

$$\frac{dH_s}{dt} = \Lambda_h - d_h H_s - \alpha \int_0^h k_1(\tau_1) f(H_s, S_{\tau_1}^i) d\tau_1,$$

$$\frac{dH_i}{dt} = \alpha \int_0^h k_1(\tau_1) f(H_s, S_{\tau_1}^i) d\tau_1 - d_h H_i,$$

$$\frac{dS_s}{dt} = \Lambda_s - d_s S_s - \gamma \int_0^h k_2(\tau_2) g(S_s, H_{\tau_2}^i) d\tau_2,$$

$$\frac{dS_i}{dt} = \gamma \int_0^h k_2(\tau_2) g(S_s, H_{\tau_2}^i) d\tau_2 - d_s S_i.$$
(2.1)

We assume that system (2.1) holds with given initial conditions

$$(H_s(0), S_s(0)) \in \mathbf{R}^2_+$$
 and $(H_i(\theta), S_i(\theta)) = (v_1(\theta), v_2(\theta))$ for $\theta \in [-h, 0]$,

where $v_1, v_2 \in C([-h, 0], \mathbb{R}^+)$. We also define the sup norm on $C([-h, 0], \mathbb{R}^+)$ as $||v_i|| = \sup_{\theta \in [-h, 0]} v_i(\theta)$, i = 1, 2. Standard theory of functional differential equations (see [14]) can be used to show that solutions of system (2.1) exist and are differentiable for all t > 0.

The delay is inspired by the life history of the schistosomiasis. Indeed, it is possible that some hosts or intermediate hosts (snails) die due to natural death during the incubation period, respectively (see [11]).

Theorem 2.2 The positive orthant

 $\{(H_s, H_i, S_s, S_i) \in \mathbf{R}^4 : H_s \ge 0, H_i \ge 0, S_s \ge 0, S_i \ge 0\}$

is positively invariant for system (2.1).

To prove Theorem 2.2, we need the following result.

Theorem 2.3 [15] Let $L : \mathbb{R}^n \longrightarrow \mathbb{R}$ be a differentiable function, and let $a \in \mathbb{R}$. Let X(x) be the vector field, and let G be the closed set $G = \{x \in \mathbb{R}^n : L(x) \le a\}$ such that $\nabla L(x) \ne 0$ for all $x \in L^{-1}(a) = \{x \in \mathbb{R}^n : L(x) = a\}$. If $\langle X(x) | \nabla L(x) \rangle \le 0$ for all $x \in L^{-1}(a)$, then the set G is positively invariant.

Proof of Theorem 2.2 Let

$$x = (H_s, H_i, S_s, S_i). \tag{2.2}$$

We will prove that $\{H_s \ge 0\}$ is positively invariant. Then let

$$L(x)=-H_s.$$

L is differentiable, and $\nabla L(x) = (-1, 0, 0, 0,) \neq 0$ for all $x \in L(x)^{-1}(0) = \{x \in \mathbb{R}^4 / L(x) = 0\}$. The vector field on $\{H_s = 0\}$ is

$$X(x) = \begin{pmatrix} \Lambda_{h} \\ -d_{h}H_{i} \\ \Lambda_{s} - d_{s}S_{s} - \gamma \int_{0}^{h} k_{2}(\tau_{2})g(S_{s}, H_{\tau_{2}}^{i}) d\tau_{2} \\ \gamma \int_{0}^{h} k_{2}(\tau_{2})g(S_{s}, H_{\tau_{2}}^{i}) d\tau_{2} - d_{s}S_{i} \end{pmatrix}.$$
(2.3)

Then $\langle X(x) | \nabla L(x) \rangle = -\Lambda_h < 0$. This proves that $\{H_s \ge 0\}$ is positively invariant. Similarly, we prove that $\{H_i \ge 0\}$, $\{S_s \ge 0\}$, $\{S_i \ge 0\}$ are positively invariant. Then $\{(H_s, H_i, S_s, S_i) \in \mathbb{R}^4 : H_s \ge 0, H_i \ge 0, S_s \ge 0, S_i \ge 0\}$ is positively invariant for system (2.1).

Therefore, the model is mathematically well posed and epidemiologically reasonable since all the variables remain non-negatives for all t > 0.

Theorem 2.4 Assume that $H(t) = H_s(t) + H_i(t)$ and $S(t) = S_s(t) + S_i(t)$.

There exists $\epsilon \ge 0$ *such as all feasible solutions of model system* (2.1) *enter the set*

$$\Gamma_{\epsilon} = \begin{cases} (H_s, H_i) \in \mathbf{R}_+^2 : H \le \frac{\Lambda_h}{d_h} + \frac{\epsilon}{d_h}, \\ (S_s, S_i) \in \mathbf{R}_+^2 : S \le \frac{\Lambda_s}{d_s} + \frac{\epsilon}{d_s}. \end{cases}$$

Proof Let $\epsilon \ge 0$. Adding the first two equations of (2.1), we get

$$\frac{dH}{dt} = \Lambda_h - d_h H$$

$$\leq \Lambda_h + \epsilon - d_h H. \tag{2.4}$$

According to [16], it follows that

$$H(t) \le \frac{\Lambda_h}{d_h} + \frac{\epsilon}{d_h} + \left(H(0) - \frac{\Lambda_h}{d_h} - \frac{\epsilon}{d_h}\right) e^{-d_h t},$$
(2.5)

where $H(0) = H_s(0) + H_i(0)$. Thus, as $t \to \infty$, $H(t) \le \frac{\Lambda_h}{d_h} + \frac{\epsilon}{d_h}$. Similarly, we prove that $S(t) \le \frac{\Lambda_s}{d_s} + \frac{\epsilon}{d_s}$.

3 Basic reproduction number, disease-free equilibrium and endemic equilibrium

The disease-free equilibrium is given by

$$\mathcal{E}_0 = \left(H_s^0, H_i^0, S_s^0, S_i^0\right) = \left(\frac{\Lambda_h}{d_h}, 0, \frac{\Lambda_s}{d_s}, 0\right). \tag{3.1}$$

Proposition 3.1 The basic reproduction number for model system (2.1) is defined by

$$\mathcal{R}_0 = \sqrt{\frac{\alpha \gamma f_2(H_s^0, 0)g_2(S_s^0, 0)}{d_s d_h}}.$$

$$\dot{y} = \psi(y), \tag{3.2}$$

where

$$y = (y_1, y_2, y_3, y_4)^T = (H_s, H_i, S_s, S_i)^T.$$
(3.3)

Now, making the assessment in each compartment j

$$\dot{y}_j = \mathcal{F}_j(y) + \mathcal{V}_j^+(y) - \mathcal{V}_j^-(y), \tag{3.4}$$

where

 $\mathcal{F}_{j}(y)$ denote the rate of appearance of new infections in each class *j*,

 $\mathcal{V}_{i}^{+}(y)$ denote the rate of transfer into each class *j* by all other means,

 $\mathcal{V}_{j}^{-}(y)$ denote the rate of transfer out of each class *j*.

Let $V_j(y) = V_j^+(y) - V_j^-(y)$, and let $Y_1 = (H_s, S_s)$ be the healthy population and $Y_2 = (H_l, H_i, S_l, S_i)$ the infected population,

$$\mathcal{F}(Y_1, Y_2) = \begin{pmatrix} \alpha f(H_s, S_i) \\ \gamma g(S_s, H_i) \end{pmatrix} \quad \text{and} \quad \mathcal{V}(Y_1, Y_2) = \begin{pmatrix} -d_h H_i \\ -d_s S_i \end{pmatrix}.$$
(3.5)

Then,

$$D_{Y_2}\mathcal{F}(Y_1, Y_2) = F(Y_1, Y_2) = \begin{pmatrix} 0 & \alpha f_2(H_s, S_i) \\ \gamma g_2(S_s, H_i) & 0 \end{pmatrix}$$
(3.6)

and

$$D_{Y_2}\mathcal{V}(Y_1, Y_2) = V(Y_1, Y_2) = \begin{pmatrix} -d_h & 0\\ 0 & -d_s \end{pmatrix}.$$
(3.7)

On $(Y_1, 0)$, we get

$$F(Y_1, 0) = \begin{pmatrix} 0 & \alpha f_2(H_s^0, 0) \\ \gamma g_2(S_s^0, 0) & 0 \end{pmatrix}$$
(3.8)

and

$$V(Y_1, 0) = \begin{pmatrix} -d_h & 0\\ 0 & -d_s \end{pmatrix}.$$
 (3.9)

Thus, we obtain

$$-FV^{-1}(Y_1,0) = \begin{pmatrix} 0 & \frac{\alpha f_2(H_s^0,0)}{d_s} \\ \frac{\gamma g_2(S_s^0,0)}{d_h} & 0 \end{pmatrix}.$$
(3.10)

According to [17], we conclude the proof.

The basic reproduction number \mathcal{R}_0 represents the average number of new case generated by a single infected individual in a completely susceptible population (see [18]).

Theorem 3.2 If $\mathcal{R}_0 < 1$, then \mathcal{E}_0 is locally asymptotically stable.

Proof Suppose that $\mathcal{R}_0 < 1$. Since H2 holds then, $f_1(H_s^0, 0) = 0$ and $g_1(S_s^0, 0) = 0$ for all H_s and S_s . It follows that the linearization of system (2.1) at \mathcal{E}_0 is

$$\frac{dh_s}{dt} = -d_h h_s - \alpha \int_0^h k_1(\tau_1) f_2(H_s^0, 0) s_i(t - \tau_1) d\tau_1,$$

$$\frac{dh_i}{dt} = \alpha \int_0^h k_1(\tau_1) f_2(H_s^0, 0) s_i(t - \tau_1) d\tau_1 - d_h h_i,$$

$$\frac{ds_s}{dt} = -d_s s_s - \gamma \int_0^h k_2(\tau_2) g_2(S_s^0, 0) h_i(t - \tau_2) d\tau_2,$$

$$\frac{ds_i}{dt} = \gamma \int_0^h k_2(\tau_2) g_2(S_s^0, 0) h_i(t - \tau_2) d\tau_2 - d_s s_i.$$
(3.11)

Now, we replace $(h_s(t), h_i(t), s_s(t), s_i(t))$ by $e^{\lambda t}(h_s^0, h_i^0, s_s^0, s_i^0)$ into (3.11) to get

$$\begin{aligned} h_{s}^{0}\lambda e^{\lambda t} &= -d_{h}h_{s}^{0}e^{\lambda t} - \alpha \int_{0}^{h}k_{1}(\tau_{1})f_{2}(H_{s}^{0},0)s_{i}^{0}e^{\lambda(t-\tau_{1})} d\tau_{1}, \\ h_{i}^{0}\lambda e^{\lambda t} &= \alpha \int_{0}^{h}k_{1}(\tau_{1})f_{2}(H_{s}^{0},0)s_{i}^{0}e^{\lambda(t-\tau_{1})} - d_{h}h_{i}^{0}e^{\lambda t}, \\ s_{s}^{0}\lambda e^{\lambda t} &= -d_{s}s_{s}^{0}e^{\lambda t} - \gamma \int_{0}^{h}k_{2}(\tau_{2})g_{2}(S_{s}^{0},0)h_{i}^{0}e^{\lambda(t-\tau_{2})} d\tau_{2}, \\ s_{i}^{0}\lambda e^{\lambda t} &= \gamma \int_{0}^{h}k_{2}(\tau_{2})g_{2}(S_{s}^{0},0)h_{i}^{0}e^{\lambda(t-\tau_{2})} d\tau_{2} - d_{s}s_{i}^{0}e^{\lambda t}. \end{aligned}$$
(3.12)

After that, we rearrange before cancelling $e^{\lambda t}$ from each term, and we obtain

$$\begin{pmatrix} -(\lambda + d_h) & 0 & 0 & -\alpha \mathcal{A}(\lambda) \\ 0 & -(\lambda + d_h) & 0 & \alpha \mathcal{A}(\lambda) \\ 0 & -\gamma \mathcal{B}(\lambda) & -(\lambda + d_s) & 0 \\ 0 & \gamma \mathcal{B}(\lambda) & 0 & -(\lambda + d_s) \end{pmatrix} \begin{pmatrix} h_s^0 \\ h_i^0 \\ s_s^0 \\ s_i^0 \end{pmatrix} = 0,$$
(3.13)

where

$$\mathcal{A}(\lambda) = \int_{0}^{h} k_{1}(\tau_{1}) f_{2}(H_{s}^{0}, 0) e^{-\lambda \tau_{1}} d\tau_{1},$$

$$\mathcal{B}(\lambda) = \int_{0}^{h} k_{2}(\tau_{2}) g_{2}(S_{s}^{0}, 0) e^{-\lambda \tau_{2}} d\tau_{2}.$$
(3.14)

Denote by

$$M_{0} = \begin{pmatrix} -(\lambda + d_{h}) & 0 & 0 & -\alpha \mathcal{A}(\lambda) \\ 0 & -(\lambda + d_{h}) & 0 & \alpha \mathcal{A}(\lambda) \\ 0 & -\gamma \mathcal{B}(\lambda) & -(\lambda + d_{s}) & 0 \\ 0 & \gamma \mathcal{B}(\lambda) & 0 & -(\lambda + d_{s}) \end{pmatrix},$$
(3.15)

then there exist non-zero solutions if and only if $det(M_0) = 0$. It follows that the characteristic equation is given by

$$(\lambda + d_h)(\lambda + d_s) \bigg[(\lambda + d_h)(\lambda + d_s) - \alpha \gamma \int_0^h k_1(\tau_1) f_2(H_s^0, 0) e^{-\lambda \tau_1} d\tau_1 \\ \times \int_0^h k_2(\tau_2) g_2(S_s^0, 0) e^{-\lambda \tau_2} d\tau_2 \bigg] = 0.$$
(3.16)

Now, we will show that all solutions λ of this equation have a negative real part. By contradiction, suppose that λ has non-negative real part. With this in mind, we have $\lambda + d_h \neq 0$ and $\lambda + d_s \neq 0$. Also

$$\begin{aligned} \left| \alpha \gamma \int_0^h k_1(\tau_1) f_2(H^0_s, 0) e^{-\lambda \tau_1} d\tau_1 \times \int_0^h k_2(\tau_2) g_2(S^0_s, 0) e^{-\lambda \tau_2} d\tau_2 \right| &\leq \alpha \gamma f_2(H^0_s, 0) g_2(S^0_s, 0) \\ &= \mathcal{R}_0^2 d_h d_s \\ &< d_h d_s \\ &\leq \left| (\lambda + d_h) (\lambda + d_s) \right|. \end{aligned}$$

This implies that λ cannot be a solution of the characteristic equation. Hence, all eigenvalues have negative real part, and then \mathcal{E}_0 is locally asymptotically stable.

Now, we will study the behaviour of system (2.1) when $\mathcal{R}_0 > 1$.

Theorem 3.3 If $\mathcal{R}_0 > 1$, then there exists an endemic equilibrium.

Proof Let $\mathcal{E}_* = (H_s^*, H_i^*, S_s^*, S_i^*)$. Setting the right-hand side of system (2.1) equal to zero, we know that \mathcal{E}_* is a positive equilibrium if and only if

$$\begin{cases} \Lambda_h - d_h H_s^* - \alpha f(H_s^*, S_i^*) = 0, \\ \alpha f(H_s^*, S_i^*) - d_h H_i^* = 0, \\ \Lambda_s - d_s S_s^* - \gamma g(S_s^*, H_i^*) = 0, \\ \gamma g(S_s^*, H_i^*) - d_s S_i^* = 0. \end{cases}$$
(3.17)

Combining the two first equations and the two last equations of (3.17) gives

$$H_s^* = \frac{\Lambda_h - d_h H_i^*}{d_h} \quad \text{and} \quad S_s^* = \frac{\Lambda_s - d_s S_i^*}{d_s}.$$
(3.18)

Let

$$\phi_1(H_i^*, S_i^*) = \alpha f\left(\frac{\Lambda_h - d_h H_i^*}{d_h}, S_i^*\right) - d_h H_i^*$$
(3.19)

and

$$\phi_2(H_i^*, S_i^*) = \gamma g\left(\frac{\Lambda_s - d_s S_i^*}{d_s}, H_i^*\right) - d_s S_i^*.$$
(3.20)

Now, we define the continuous function ϕ by

$$\phi(H_i^*, S_i^*) = (\phi_1(H_i^*, S_i^*), \phi_2(H_i^*, S_i^*)).$$
(3.21)

Hence, it follows that any solution of equation $\phi = 0$ in the set $(0, \frac{\Lambda_h}{d_h}) \times (0, \frac{\Lambda_s}{d_s})$ corresponds to an equilibrium, with $H_s^*, H_i^*, S_s^*, S_i^* > 0$, that is an equilibrium. Since H2 holds, then $\phi(0,0) = 0$ and $\phi(\frac{\Lambda_h}{d_h}, \frac{\Lambda_s}{d_s}) \leq 0$. Then the sufficient condition for equation $\phi = 0$ to have a solution in $(0, \frac{\Lambda_h}{d_h}) \times (0, \frac{\Lambda_s}{d_s})$ is that ϕ increasing at 0. This implies that an endemic equilibrium exists if

$$\nabla \phi(0,0) > 0, \tag{3.22}$$

where

$$\nabla \phi(0,0) = \left(\nabla \phi_1(0,0), \nabla \phi_2(0,0)\right)$$
$$= \left(-\alpha f_1(H_s^0,0) - d_h + \alpha f_2(H_s^0,0), -\gamma g_1(S_s^0,0) - d_s + \gamma g_2(S_s^0,0)\right).$$
(3.23)

Note that $f_1(H_s^0, 0) = g_1(S_s^0, 0) = 0$. Then, inequality (3.22) becomes

$$\begin{cases} \alpha f_2(H_s^0, 0) > d_h & \text{and} \\ \gamma g_2(S_s^0, 0) > d_s. \end{cases}$$
(3.24)

Hence,

$$\alpha \gamma f_2(H_s^0, 0) g_2(S_s^0, 0) > d_h d_s, \tag{3.25}$$

equivalently, we have

$$\frac{\alpha \gamma f_2(H_s^0, 0)g_2(S_s^0, 0)}{d_h d_s} > 1.$$
(3.26)

Thus, $\mathcal{R}_0 > 1$.

4 Global stability of the disease-free equilibrium

In this section, we study the global behaviour of the disease-free equilibrium. For that, we assume that

H3 for all $(H_S, H_i, S_s, S_i) \in \mathbf{R}^4_+$, $f(H_s, S_i) \le f_2(H_s^0, 0)S_i$ and $g(S_s, H_i) \le g_2(S_s^0, 0)H_i$, H4 $1 \le \alpha f_2(H_s^0, 0)$ and $1 \le \gamma g_2(S_s^0, 0)$.

We have the following result.

Theorem 4.1 Let $\delta = \max(d_s, d_h)$. Assume that H3 and H4 hold, and $\delta \leq 1$, then the disease-free equilibrium is globally asymptotically stable if $\mathcal{R}_0 \leq 1$.

Proof We consider the Lyapunov function

$$V = d_s H_i + d_h S_i. \tag{4.1}$$

Differentiating V with respect to time, we obtain

$$\frac{dV}{dt} = \alpha d_s \int_0^h k_1(\tau_1) f(H_s, S^i_{\tau_1}) d\tau_1
+ \gamma d_h \int_0^h k_2(\tau_2) g(S_s, H^i_{\tau_2}) d\tau_2 - d_s d_h(S_i + H_i).$$
(4.2)

Since H3 holds and $\delta \leq 1$, we get

$$\frac{dV}{dt} \leq \alpha f_2 \big(H_s^0, 0 \big) S_i + \gamma g_2 \big(S_s^0, 0 \big) H_i - d_s d_h (S_i + H_i).$$

$$\tag{4.3}$$

Adding and subtracting the quantity $\alpha \gamma f_2(H_s^0, 0)g_2(S_s^0, 0)(S_i + H_i)$, we have

$$\frac{dV}{dt} \leq \alpha \gamma f_2(H_s^0, 0) g_2(S_s^0, 0) (S_i + H_i) - \alpha \gamma f_2(H_s^0, 0) g_2(S_s^0, 0) (S_i + H_i)
+ \alpha f_2(H_s^0, 0) S_i + \gamma g_2(S_s^0, 0) H_i - d_s d_h (S_i + H_i)
\leq \alpha \gamma f_2(H_s^0, 0) g_2(S_s^0, 0) (S_i + H_i) + \alpha f_2(H_s^0, 0) S_i (1 - \gamma g_2(S_s^0, 0))
+ \gamma g_2(S_s^0, 0) H_i (1 - \alpha f_2(H_s^0, 0)) - d_s d_h (S_i + H_i).$$
(4.4)

Using hypothesis H4, we obtain

$$\frac{dV}{dt} \leq \alpha \gamma f_2 (H_s^0, 0) g_2 (S_s^0, 0) (S_i + H_i) - d_s d_h (S_i + H_i)
\leq d_s d_h (S_i + H_i) \left(\frac{\alpha \gamma f_2 (H_s^0, 0) g_2 (S_s^0, 0)}{d_s d_h} - 1 \right)
\leq d_s d_h (S_i + H_i) (\mathcal{R}_0^2 - 1).$$
(4.5)

For $\mathcal{R}_0 \leq 1$, we get

$$\frac{dV}{dt} \le 0,\tag{4.6}$$

with equality only if $S_i = 0$ and $H_i = 0$. According to LaSalle's extension to Lyapunov's method [19], the limit set of each solution is contained in the largest invariant set, for which $S_i = 0$ and $H_i = 0$, which is the singleton $\{\mathcal{E}_0\}$. This means that the disease-free equilibrium \mathcal{E}_0 is globally asymptotically stable on Γ_{ϵ} .

5 Global stability of the endemic equilibrium

In this section, we assume that f and g satisfies the conditions

- H5 for all $(H_s, H_i, S_s, S_i) \in \mathbf{R}^4_+$, $1 \le \frac{f(H_s, S^i_{\tau_1})}{f(H_s, S^i_t)} \le \frac{S_i}{S^i_i}$ and $1 \le \frac{g(S_s, H^i_{\tau_2})}{g(S_s, H^*_i)} \le \frac{H_i}{H^i_i}$,
- H6 for all $H_s, S_s > 0$, $sign(f(H_s, S_i^*) f(H_s^*, S_i^*)) = sign(H_s H_s^*)$ and $sign(g(S_s, H_i^*) g(S_s^*, H_i^*)) = sign(S_s S_s^*)$.

Theorem 5.1 Assume that H5 and H6 hold, then if $\mathcal{R}_0 > 1$ the endemic equilibrium \mathcal{E}_* is globally asymptotically stable.

Proof Consider system (2.1) at \mathcal{E}_* , we get

$$\Lambda_{h} = d_{h}H_{s} + \alpha \int_{0}^{h} k_{1}(\tau_{1})f(H_{s}^{*}, S_{i}^{*}) d\tau_{1},$$

$$\Lambda_{s} = d_{s}S_{s} + \gamma \int_{0}^{h} k_{2}(\tau_{2})g(S_{s}^{*}, H_{i}^{*}) d\tau_{2},$$

$$d_{h}H_{i}^{*} = \alpha \int_{0}^{h} k_{1}(\tau_{1})f(H_{s}^{*}, S_{i}^{*}) d\tau_{1},$$

$$d_{s}S_{i}^{*} = \gamma \int_{0}^{h} k_{2}(\tau_{2})g(S_{s}^{*}, H_{i}^{*}) d\tau_{2}.$$
(5.1)

Let

$$\mu(y) = y - 1 - \ln y. \tag{5.2}$$

We can see that the function $\mu \ge 0$ for all y > 0, and it has the strict global minimum $\mu(1) = 0$. Now, define the functions

$$\begin{aligned} U_{hs} &= H_s(t) - H_s^* - \int_{H_s^*}^{H_s(t)} \frac{f(H_s^*, S_i^*)}{f(\xi_1, S_i^*)} d\xi_1, \\ U_{hi} &= H_i^* \mu\left(\frac{H_i(t)}{H_i^*}\right), \\ U_{ss} &= S_s(t) - S_s^* - \int_{S_s^*}^{S_s(t)} \frac{g(S_s^*, H_i^*)}{g(\xi_2, H_i^*)} d\xi_2, \\ U_{si} &= S_i^* \mu\left(\frac{S_i(t)}{S_i^*}\right). \end{aligned}$$
(5.3)

Note that $U_{hs} \ge 0$, $U_{hi} \ge 0$, $U_{ss} \ge 0$ and $U_{si} \ge 0$ with equality only if $H_s = H_s^*$, $H_i = H_i^*$, $S_s = S_s^*$ and $S_i = S_i^*$. Now, we consider the Lyapunov function

$$U(t) = g(S_s^*, H_i^*) U_h(t) + f(H_s^*, S_i^*) U_s(t),$$
(5.4)

where $U_h = U_{hs} + U_{hi}$ and $U_s = U_{ss} + U_{si}$. To evaluate $\frac{dU}{dt}$, we will calculate separately the different derivatives $\frac{dU_{hs}}{dt}$, $\frac{dU_{hi}}{dt}$, $\frac{dU_{si}}{dt}$ and $\frac{dU_{si}}{dt}$,

$$\frac{d\mathcal{U}_{hs}}{dt} = \left(1 - \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)}\right) \frac{dH_s}{dt} \\
= \left(1 - \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)}\right) \left(\Lambda_h - d_h H_s - \alpha \int_0^h k_1(\tau_1) f\left(H_s, S_{\tau_1}^i\right) d\tau_1\right).$$
(5.5)

Then we use the first equation of (5.1) to get

$$\begin{aligned} \frac{d\mathcal{U}_{hs}}{dt} &= \left(1 - \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)}\right) \left(d_h (H_s^* - H_s) + \alpha \int_0^h k_1(\tau_1) (f(H_s^*, S_i^*) - f(H_s, S_{\tau_1}^i)) d\tau_1\right) \\ &= -d_h (H_s^* - H_s) \left(1 - \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)}\right) + \alpha \int_0^h k_1(\tau_1) f(H_s^*, S_i^*) \left(1 - \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)}\right) \end{aligned}$$

$$\times \left(1 - \frac{f(H_s, S_{\tau_1}^i)}{f(H_s^*, S_i^*)}\right) d\tau_1$$

$$= -d_h (H_s^* - H_s) \left(1 - \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)}\right) + \alpha \int_0^h k_1(\tau_1) f(H_s^*, S_i^*) \left(\frac{f(H_s, S_{\tau_1}^i)}{f(H_s, S_i^*)} - \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)}\right) - \frac{f(H_s, S_i^*)}{f(H_s, S_i^*)}$$

$$- \frac{f(H_s, S_{\tau_1}^i)}{f(H_s^*, S_i^*)} + 1 \right) d\tau_1.$$
(5.6)

After that, we evaluate $\frac{dU_{hi}}{dt}$,

$$\frac{dU_{hi}}{dt} = \left(1 - \frac{H_i^*}{H_i}\right) \frac{dH_i}{dt} = \left(1 - \frac{H_i^*}{H_i}\right) \left(\alpha \int_0^h k_1(\tau_1) f\left(H_s, S_{\tau_1}^i\right) d\tau_1 - d_h H_i\right) \\
= \left(1 - \frac{H_i^*}{H_i}\right) \left(\alpha \int_0^h k_1(\tau_1) f\left(H_s^*, S_i^*\right) \frac{f(H_s, S_{\tau_1}^i)}{f(H_s^*, S_i^*)} d\tau_1 - d_h H_i^* \frac{H_i}{H_i^*}\right).$$
(5.7)

Then, using the third equation of (5.1), we obtain

$$\frac{dU_{hi}}{dt} = \alpha \left(1 - \frac{H_i^*}{H_i}\right) \int_0^h k_1(\tau_1) f\left(H_s^*, S_i^*\right) \left(\frac{f(H_s, S_{\tau_1}^i)}{f(H_s^*, S_i^*)} - \frac{H_i}{H_i^*}\right) d\tau_1
= \alpha \int_0^h k_1(\tau_1) f\left(H_s^*, S_i^*\right) \left(\frac{f(H_s, S_{\tau_1}^i)}{f(H_s^*, S_i^*)} - \frac{H_i}{H_i^*} - \frac{H_i^*}{H_i} \frac{f(H_s, S_{\tau_1}^i)}{f(H_s^*, S_i^*)} + 1\right) d\tau_1.$$
(5.8)

Then, combining (5.6) and (5.8), we get

$$\frac{dU_{h}}{dt} = -d_{h} \left(H_{s}^{*} - H_{s}\right) \left(1 - \frac{f(H_{s}^{*}, S_{i}^{*})}{f(H_{s}, S_{i}^{*})}\right) g\left(S_{s}^{*}, H_{i}^{*}\right)
+ \alpha g\left(S_{s}^{*}, H_{i}^{*}\right) \int_{0}^{h} k_{1}(\tau_{1}) f\left(H_{s}^{*}, S_{i}^{*}\right) A(\tau_{1}) d\tau_{1},$$
(5.9)

where $A(\tau_1) = 2 - \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)} + \frac{f(H_s, S_{\tau_1}^i)}{f(H_s, S_i^*)} - \frac{H_i^* f(H_s, S_{\tau_1}^i)}{H_i} - \frac{H_i}{f(H_s, S_i^*)} - \frac{H_i}{H_i^*}.$ Adding and subtracting the quantity $1 + \ln \frac{f(H_s, S_{\tau_1}^i)}{f(H_s, S_i^*)} + \ln \frac{f(H_s^*, S_i^*)}{f(H_s, S_i^*)} + \ln \frac{H_i}{H_i^*}$, we obtain

$$A(\tau_{1}) = \left(-\frac{f(H_{s}^{*}, S_{i}^{*})}{f(H_{s}, S_{i}^{*})} + 1 + \ln\frac{f(H_{s}^{*}, S_{i}^{*})}{f(H_{s}, S_{i}^{*})}\right) + \left(-\frac{H_{i}^{*}}{H_{i}}\frac{f(H_{s}, S_{\tau_{1}}^{i})}{f(H_{s}, S_{i}^{*})} + 1 + \ln\frac{H_{i}^{*}}{H_{i}}\frac{f(H_{s}, S_{\tau_{1}}^{i})}{f(H_{s}^{*}, S_{i}^{*})}\right) \\ + \left(-\frac{H_{i}}{H_{i}^{*}} + 1 + \ln\frac{H_{i}}{H_{i}^{*}}\right) + \left(\frac{f(H_{s}, S_{\tau_{1}}^{i})}{f(H_{s}, S_{i}^{*})} - 1 - \ln\frac{f(H_{s}, S_{\tau_{1}}^{i})}{f(H_{s}, S_{i}^{*})}\right) \\ = -\mu\left(\frac{f(H_{s}^{*}, S_{i}^{*})}{f(H_{s}, S_{i}^{*})}\right) - \mu\left(\frac{H_{i}^{*}}{H_{i}}\frac{f(H_{s}, S_{\tau_{1}}^{i})}{f(H_{s}^{*}, S_{i}^{*})}\right) - \mu\left(\frac{H_{i}}{H_{i}^{*}}\right) + \mu\left(\frac{f(H_{s}, S_{\tau_{1}}^{i})}{f(H_{s}, S_{i}^{*})}\right).$$
(5.10)

Next, we calculate $\frac{dU_{ss}}{dt}$,

$$\frac{dU_{ss}}{dt} = \left(1 - \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)}\right) \frac{dS_s}{dt} \\
= \left(1 - \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)}\right) \left(\Lambda_s - d_s S_s - \gamma \int_0^h k_2(\tau_2) g(S_s, H_{\tau_2}^i) d\tau_2\right).$$
(5.11)

Then, we use the second equation of (5.1) to get

$$\frac{d\mathcal{U}_{ss}}{dt} = \left(1 - \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)}\right) \left(d_s(S_s^* - S_s) + \gamma \int_0^h k_2(\tau_2) \left(g(S_s^*, H_i^*) - g(S_s, H_{\tau_2}^i)\right) d\tau_2\right) \\
= -d_s(S_s^* - S_s) \left(1 - \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)}\right) + \gamma \int_0^h k_2(\tau_2) g(S_s^*, H_i^*) \left(1 - \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)}\right) \\
\times \left(1 - \frac{g(S_s, H_{\tau_2}^i)}{g(S_s^*, H_i^*)}\right) d\tau_2 \\
= -d_s(S_s^* - S_s) \left(1 - \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)}\right) + \gamma \int_0^h k_2(\tau_2) g(S_s^*, H_i^*) \left(\frac{g(S_s, H_{\tau_2}^i)}{g(S_s, H_i^*)} - \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)}\right) \\
- \frac{g(S_s, H_{\tau_2}^i)}{g(S_s^*, H_i^*)} + 1\right) d\tau_2.$$
(5.12)

Now, we evaluate $\frac{dU_{si}}{dt}$,

$$\frac{dU_{si}}{dt} = \left(1 - \frac{S_i^*}{S_i}\right) \frac{dS_i}{dt}
= \left(1 - \frac{S_i^*}{S_i}\right) \left(\gamma \int_0^h k_2(\tau_2) g(S_s, H_{\tau_2}^i) d\tau_2 - d_s S_i\right)
= \left(1 - \frac{S_i^*}{S_i}\right) \left(\gamma \int_0^h k_2(\tau_2) g(S_s^*, H_i^*) \frac{g(S_s, H_{\tau_2}^i)}{g(S_s^*, H_i^*)} d\tau_2 - d_s S_i^* \frac{S_i}{S_i^*}\right).$$
(5.13)

Then, using the fourth equation of (5.1), we obtain

$$\frac{dU_{si}}{dt} = \gamma \left(1 - \frac{S_i^*}{S_i}\right) \int_0^h k_2(\tau_2) g\left(S_s^*, H_i^*\right) \left(\frac{g(S_s, H_{\tau_2}^i)}{g(S_s^*, H_i^*)} - \frac{S_i}{S_i^*}\right) d\tau_2
= \gamma \int_0^h k_2(\tau_2) g\left(S_s^*, H_i^*\right) \left(\frac{g(S_s, H_{\tau_2}^i)}{g(S_s^*, H_i^*)} - \frac{S_i}{S_i^*} - \frac{S_i^*}{S_i}\frac{g(S_s, H_{\tau_2}^i)}{g(S_s^*, H_i^*)} + 1\right) d\tau_2.$$
(5.14)

Then, combining (5.12) and (5.14), we get

$$\frac{dU_s}{dt} = -d_s \left(S_s^* - S_s\right) \left(1 - \frac{f(S_s^*, S_i^*)}{g(S_s, H_i^*)}\right) f\left(H_s^*, S_i^*\right)
+ \gamma f\left(H_s^*, S_i^*\right) \int_0^h k_2(\tau_2) g\left(S_s^*, H_i^*\right) B(\tau_2) d\tau_2,$$
(5.15)

where $B(\tau_2) = 2 - \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)} + \frac{g(S_s, H_{\tau_1}^i)}{g(S_s, H_i^*)} - \frac{S_i^*}{S_i} \frac{g(S_s, H_{\tau_2}^i)}{g(S_s^*, H_i^*)} - \frac{S_i}{S_i^*}.$ Adding and subtracting the quantity $1 + \ln \frac{g(S_s, H_{\tau_2}^i)}{g(S_s, H_i^*)} + \ln \frac{g(S_s^*, H_i^*)}{g(S_s, H_i^*)} + \ln \frac{S_i}{S_i^*}$, we obtain

$$B(\tau_{2}) = \left(-\frac{g(S_{s}^{*}, H_{i}^{*})}{g(S_{s}, H_{i}^{*})} + 1 + \ln\frac{g(S_{s}^{*}, H_{i}^{*})}{g(S_{s}, H_{i}^{*})}\right) + \left(-\frac{S_{i}^{*}}{S_{i}}\frac{g(S_{s}, H_{\tau_{2}}^{i})}{g(S_{s}^{*}, H_{i}^{*})} + 1 + \ln\frac{S_{i}^{*}}{S_{i}}\frac{g(S_{s}, H_{\tau_{2}}^{i})}{g(S_{s}^{*}, H_{i}^{*})}\right) \\ + \left(-\frac{S_{i}}{S_{i}^{*}} + 1 + \ln\frac{S_{i}}{S_{i}^{*}}\right) + \left(\frac{g(S_{s}, H_{\tau_{2}}^{i})}{g(S_{s}, H_{i}^{*})} - 1 - \ln\frac{g(S_{s}, H_{\tau_{2}}^{i})}{g(S_{s}, H_{i}^{*})}\right) \\ = -\mu\left(\frac{g(S_{s}^{*}, H_{i}^{*})}{g(S_{s}, H_{i}^{*})}\right) - \mu\left(\frac{S_{i}^{*}}{S_{i}}\frac{g(S_{s}, H_{\tau_{2}}^{i})}{g(S_{s}^{*}, H_{i}^{*})}\right) - \mu\left(\frac{S_{i}}{S_{i}^{*}}\right) + \mu\left(\frac{g(S_{s}, H_{\tau_{2}}^{i})}{g(S_{s}, H_{i}^{*})}\right).$$
(5.16)

Since H5 holds, then $\mu(\frac{f(H_s, S_{\tau_1}^i)}{f(H_s, S_i^*)}) \leq \mu(\frac{S_i}{S_i^*})$ and $\mu(\frac{g(S_s, H_{\tau_2}^i)}{g(S_s, H_i^*)}) \leq \mu(\frac{H_i}{H_i^*})$. It follows that

$$\frac{dU}{dt} \leq -d_{h} \left(H_{s}^{*} - H_{s}\right) \left(1 - \frac{f(H_{s}^{*}, S_{i}^{*})}{f(H_{s}, S_{i}^{*})}\right) g\left(S_{s}^{*}, H_{i}^{*}\right) - d_{s}\left(S_{s}^{*} - S_{s}\right) \left(1 - \frac{f(S_{s}^{*}, S_{i}^{*})}{g(S_{s}, H_{i}^{*})}\right) f\left(H_{s}^{*}, S_{i}^{*}\right)
+ \alpha f\left(H_{s}^{*}, S_{i}^{*}\right) g\left(S_{s}^{*}, H_{i}^{*}\right) \int_{0}^{h} k_{1}(\tau_{1}) \left[-\mu\left(\frac{f(H_{s}^{*}, S_{i}^{*})}{f(H_{s}, S_{i}^{*})}\right) - \mu\left(\frac{H_{i}^{*}}{H_{i}} \frac{f(H_{s}, S_{\tau_{1}}^{i})}{f(H_{s}^{*}, S_{i}^{*})}\right)\right] d\tau_{1}
+ \gamma f\left(H_{s}^{*}, S_{i}^{*}\right) g\left(S_{s}^{*}, H_{i}^{*}\right) \int_{0}^{h} k_{2}(\tau_{2})
\times \left[-\mu\left(\frac{g(S_{s}^{*}, H_{i}^{*})}{g(S_{s}, H_{i}^{*})}\right) - \mu\left(\frac{S_{i}^{*}}{S_{i}} \frac{g(S_{s}, H_{i}^{*})}{g(S_{s}^{*}, H_{i}^{*})}\right)\right] d\tau_{2}.$$
(5.17)

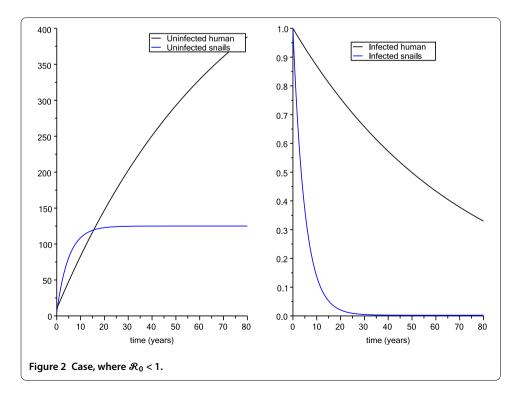
Since H6 holds, it follows that

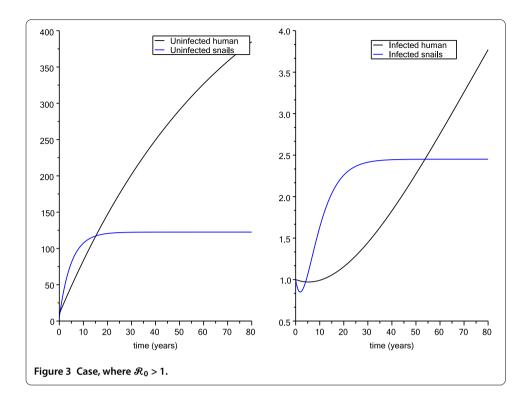
$$\frac{dU}{dt} \le 0 \tag{5.18}$$

for all $(H_s, H_i, S_s, S_i) \in \Gamma_{\epsilon}$ with equality only for $H_s = H_s^*$, $H_i = H_i^*$, $S_s = S_s^*$ and $S_i = S_i^*$. Hence, the endemic equilibrium \mathcal{E}_* is the only positively invariant set of system (2.1) contained in $\{(H_s, H_i, S_s, S_i) \in \mathbb{R}^4_+; H_s = H_s^*, H_i = H_i^*, S_s = S_s^*, S_i = S_i^*\}$. Then it follows that \mathcal{E}_* is globally asymptotically stable on Γ_{ϵ} (see [19]).

6 Numerical simulation

In this section, we derive the computation work that supports our study. In this computation, the functions f and g are chosen as follows: $f(H_s, S_i) = H_s S_i$ and $g(S_s, H_i) = S_s H_i$ (mass action). Two different cases of computational simulations are studied: in the first case (see Figure 2), $\mathcal{R}_0 \leq 1$, while in the second case (see Figure 3), $\mathcal{R}_0 > 1$. The parameters values





used are the following (see [20]): $\Lambda_h = 8$, $\Lambda_s = 25$, $d_h = 0.014$, $d_s = 0.2$. We also use the delays parameters $\tau_1 = \tau_2 = 5$. For the first case, we use $\alpha = 0.00000027$ and $\gamma = 0.000004$, which give $\mathcal{R}_0 < 1$. In the second case, we use $\alpha = 0.00027$ and $\gamma = 0.004$ to get $\mathcal{R}_0 > 1$.

7 Conclusion

In this paper, a deterministic model of transmission of schistosomiasis with two general nonlinear incidence functions including distributed delay is derived. The global behaviour of the model system was studied. We proved that, if $\mathcal{R}_0 \leq 1$ holds, then the disease-free equilibrium is globally asymptotically stable, which implies that the disease fades out from the population. If $\mathcal{R}_0 > 1$, then there exists a unique endemic equilibrium which is globally asymptotically stable, and this implies that the disease will persist in the population. This result suggests that the latent period in infection affects the prevalence of schistosomiasis, and it is an effective strategy on schistosomiasis control to lengthen in prepatent period on infected definitive hosts by drug treatment, for example.

Threshold analysis of the basic reproduction number shows that the use of public health education campaign could have positive, more determinant impact on the control of the schistosomiasis. Overall, an effective education campaign which focuses on drug treatment with reasonable coverage level could be helpful for countries concerned with the disease.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

All authors carried out the paper. All authors read and approved the final manuscript.

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References

- 1. World Health Organization. http://www.who.int/schistosomiasis/en/. Available on May, 2012
- Allen, EJ, Victory, HD: Modelling and simulation of a schistosomiasis infection with biological control. Acta Trop. 87, 251-267 (2003)
- Anderson, RM, May, RM: Prevalence of schistosome infections within molluscan populations: observed patterns and theoretical predictions. Parasitology 79, 63-94 (1979)
- Anderson, RM, May, RM: Helminth infections of humans: mathematical models, population dynamics, and control. Adv. Parasitol. 24, 1-101 (1985)
- 5. Cohen, JE: Mathematical models of schistosomiasis. Annu. Rev. Ecol. Syst. 8, 209-233 (1977)
- Feng, Z, Li, C, Milner, FA: Schistosomiasis models with density dependence and age of infection in snail dynamics. Math. Biosci. 177-178, 271-286 (2002)
- 7. Feng, Z, Li, C, Milner, FA: Schistosomiasis models with two migrating human groups. Math. Comput. Model. **41**(11-12), 1213-1230 (2005)
- 8. Feng, Z, Milner, FA: A new mathematical model of schistosomiasis. In: Mathematical Models in Medical and Health Science (Nashville, TN, 1997). Innov. Appl. Math., pp. 117-128. Vanderbilt Univ. Press, Nashville (1998)
- 9. Macdonald, G: The dynamics of helminth infections, with special reference to schistosomiasis. Trans. R. Soc. Trop. Med. Hyg. 59, 489-506 (1965)
- 10. Nasell, I: A hybrid model of schistosomiasis with snail latency. Theor. Popul. Biol. 10, 47-69 (1976)
- 11. Yang, Y, Xiao, D: A mathematical model with delays for schistosomiasis. Chin. Ann. Math., Ser. B 31(4), 433-446 (2010)
- 12. Woolhouse, MEJ: On the application of mathematical models of schistosome transmission dynamics. I. Natural transmission. Acta Trop. 49, 1241-1270 (1991)
- Woolhouse, MEJ: On the application of mathematical models of schistosome transmission dynamics. II. Control. Acta Trop. 50, 189-204 (1992)
- 14. Hale, JK, Verduyn Lunel, S: Introduction to Functional Differential Equations. Springer, Berlin (1993)
- Bony, JM: Principe du maximum, inégalite de Harnack et unicité du problème de Cauchy pour les opérateurs elliptiques dégénérés. Ann. Inst. Fourier (Grenoble) 19(1), 277-304 (1969)
- 16. Birkhoff, G, Rota, GC: Ordinary Differential Equations. Ginn, Boston (1982)
- 17. Van den Driesche, P, Watmough, J: Reproduction numbers and subthreshold endemic equilibria for the compartmental models of disease transmission. Math. Biosci. **180**, 29-48 (2002)
- 18. Anderson, RM, May, RM: Infectious Disease of Human, pp. 17-19. Oxford University Press, Oxford (1991)
- 19. LaSalle, JP: The Stability of Dynamical Systems. SIAM, Philadelphia (1976)
- Feng, Z, Milner, FA, Eppert, A, Minchella, DJ: Estimation of parameters governing the transmission dynamics of schistosomes. Appl. Math. Lett. 17(10), 1105-1112 (2004)

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