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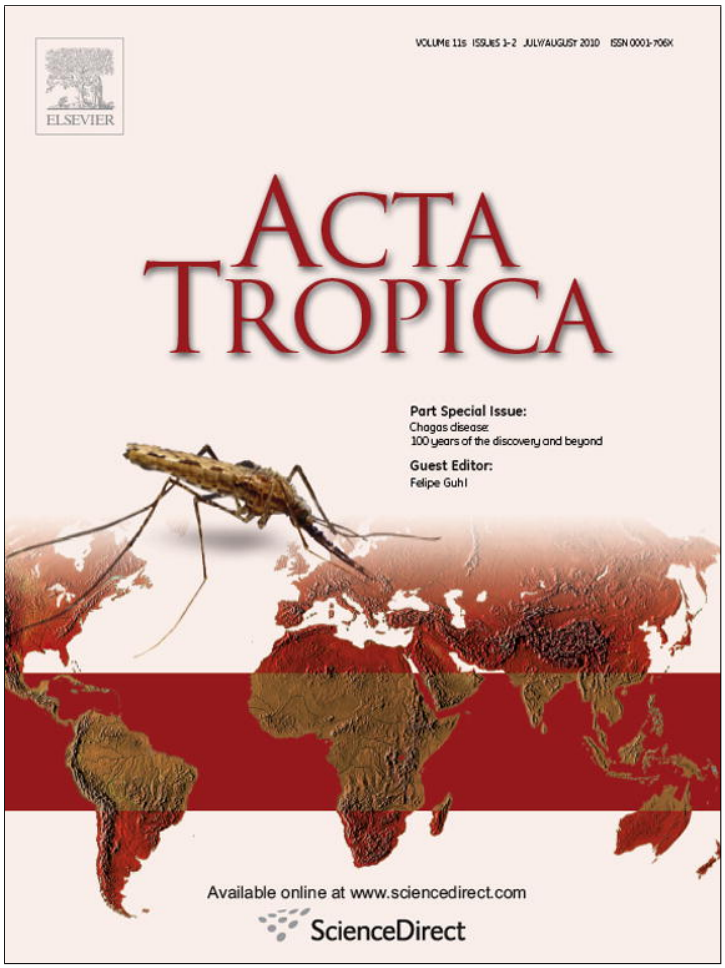

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Mathematical modelling and control of Schistosomiasis in Hubei Province, China☆

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ABSTRACT

Hubei Province, along with four other provinces in the central and eastern China where schistosomiasis is endemic (Anhui, Hunan, Jiangsu, and Jiangxi), is located in the lake and marshland regions along the Yangtze River. High population density, large numbers of farm cattle, and huge areas of snail habitat are the main characteristics that maintain the persistence of the disease and the transmission of the parasite *Schistosoma japonicum* in these regions. Based on the schistosomiasis infection data from Hubei province, we propose a mathematical model for the human–cattle–snail transmission of schistosomiasis. The model is a system consisting of six ordinary differential equations that describe susceptible and infected human, cattle and snail subpopulations. After analyzing the existence of the disease-free equilibrium of the model, we determine the basic reproduction number and use the model to simulate the schistosomiasis infection data from Hubei Province. By carrying out sensitivity analyses of the basic reproduction number on various parameters, we find that the transmission of *S. japonicum* between cattle and snails plays a more important role than that between humans and snails in the endemicity of schistosomiasis in these regions. This strongly suggests that, to control and eventually eradicate schistosomiasis in the lake and marshland regions in China, a more comprehensive approach needs to include environmental factors in order to break the cattle–snail transmission cycle.

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1. Introduction

Over the past 60 years, China has made tremendous progress in treating and controlling schistosomiasis, a parasitic disease caused by *Schistosoma japonicum*. By 1995, schistosomiasis transmission had been interrupted successively in five of the twelve formerly endemic provinces and the number of human infections had been reduced more than 90% (Zhou et al., 2004, 2005). However, schistosomiasis is still one of the most serious parasitic diseases in mainland China and remains endemic in seven provinces. Among them five (Anhui, Hubei, Hunan, Jiangsu, Jiangxi) are in the lake and marshland regions with vast areas of *Oncomelania hupensis* habitat and two (Sichuan, Yunan) are in the mountainous regions with diverse ecologies and slow economic growth (Zhou et al., 2005; Utzinger et al., 2005). According to the third nationwide cluster sample survey conducted in 2004, it was estimated that 726,112 (95% confidence interval 714,497–737,728) individuals were infected with *S. japonicum* in China in 2004 (Zhou et al., 2004).

With a population of more than 60 millions, Hubei Province is located in central China, extending across two major river systems: the Yangtze and Hanjiang. It adjoins Henan on the north, Anhui on the east, Jiangxi on the southeast, Hunan on the south, Chongqing Municipality on the west, and Shaanxi on the northwest. Hubei has a subtropical monsoon climate and covers an area of 185,900 km^2, with 55.5% mountains, 24.5% hills and hillocks, and 20% plain and lake areas. With such climatic and geographic conditions, schistosomiasis has been endemic in Hubei for more than 2000 years. Among the seven schistosomiasis endemic provinces, Hubei was estimated to have a prevalence rate of 3.8%, only second to the neighbor province Hunan in the south of the Dongding lake (where the prevalence rate was 4.2%) (Zhou et al., 2004). Underlying causes include the unusually severe floods in the Yangtze River in 1998 (Zhou et al., 2005) and the construction of the Three Gorges Reservoir (Zheng et al., 2002). Also, as an agricultural province Hubei has a very large number of cattle, which are major reservoirs of *S. japonicum* and are responsible for the persistent schistosomiasis transmission in humans in the lake and marshland regions along the Yangtze River (Chen and Feng, 1999).

Following the pioneering work of Macdonald (1965) on modeling schistosomiasis, various mathematical models have been developed to study the transmission dynamics of schistosomiasis; we refer to Allen and Victory (2003); Barbour (1978); Cohen (1977); Feng et al. (2005); Liang et al. (2002, 2007); May (1977);

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Nåsell and Hirsch (1973); Williams et al. (2002); Woolhouse (1991, 1992, 1996), and the references cited therein. In particular, Liang et al. (2002) proposed a multi-group model for *S. japonicum* transmission dynamics and control in Sichuan Province, China. Williams et al. (2002) extended Barbour's model (Barbour, 1978) to study human–bovine transmission of schistosomiasis in Jiangxi Province, China.

The mathematical model for schistosomiasis infection developed by Allen and Victory (2003) involves the human host, an intermediate snail host, a competitor snail species, and an additional mammalian host, each classified into susceptible and infected subpopulations. Their model consists of eight differential equations. Both deterministic and stochastic versions were considered. In the lake and marshland regions along the Yangtze River, including Anhui, Hubei, Hunan, Jiangsu, and Jiangxi, there are large number of farm cattle and huge areas of snail habitat, and human population density is also very high. In this paper, taking these specific characteristics into consideration and based on Allen and Victory's model, we propose a mathematical model for the human–cattle–snail transmission of schistosomiasis. The model is a system described by six ordinary differential equations counting for susceptible and infected human, cattle and snail subpopulations. After analyzing the existence of the disease-free equilibrium of the model, we shall determine the basic reproduction number and use the model to simulate the schistosomiasis infection data from Hubei Province. By carrying out sensitivity analysis of the basic reproduction number on various parameters, we shall discuss the control of schistosomiasis infection in Hubei Province and other lake and marshland regions in China.

The paper is organized as follows. In Section 2 we present the model, determine the basic reproduction number, and analyze the the existence and stability of the disease-free equilibrium. In Section 3 we use the model to simulate the schistosomiasis infection data from Hubei Province and perform sensitivity analysis of the basic reproduction number on various model parameters. A brief discussion is given in Section 4.

2. Mathematical model and analysis

Human and cattle are regarded as definite hosts and the snail is considered as the intermediate host. We classify each of them into two subclasses: susceptible and infected. Let $S_H(t)$ and $I_H(t)$ denote the densities of susceptible and infected human populations, $S_C(t)$ and $I_C(t)$ denote the densities of susceptible and infected cattle populations, and $S_S(t)$ and $I_S(t)$ denote the densities of susceptible and infected snail populations at time t, respectively.

When parasite eggs are released into the environment from infected humans, they hatch on contact with fresh water to release the free-swimming miracidium. Miracidia then infect fresh-water snails and transform into primary sporocysts. Germ cells within the primary sporocyst divide to produce secondary sporocysts, which in turn divide to produce cercariae. Susceptible humans are infected when the cercaria released from infected snails penetrate the skin and transform into a migrating schistosomulum stage. The transmission of the parasite *S. japonicum* between cattle and snails is the same. The transmission between human and cattle is indirect via snail (Fig. 1).

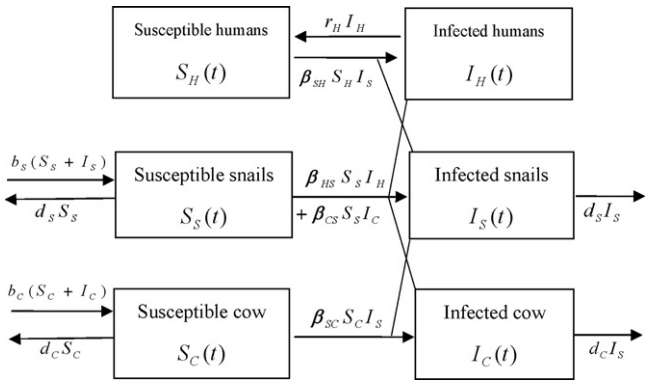

Fig. 1. Flowchart of schistosomiasis transmission between humans, cattle and snails.

The model is a system of six ordinary differential equations:

$$\begin{aligned}
\frac{dS_H}{dt} &= -\beta_{SH}S_H(t)I_S(t) + r_H I_H(t),\\
\frac{dI_H}{dt} &= \beta_{SH}S_H(t)I_S(t) - r_H I_H(t),\\
\frac{dS_C}{dt} &= b_C(S_C(t)+I_C(t)) - \beta_{SC}S_C(t)I_S(t) + r_C I_C(t) - d_C S_C(t) - k_C S_C(t)(S_C(t)+I_C(t)),\\
\frac{dI_C}{dt} &= \beta_{SC}S_C(t)I_S(t) - r_C I_C(t) - d_C I_C(t) - k_C I_C(t)(S_C(t)+I_C(t)),\\
\frac{dS_S}{dt} &= b_S(S_S(t)+I_S(t)) - \beta_{HS}S_S(t)I_H(t) - \beta_{CS}S_S(t)I_C(t) - d_S S_S(t) - k_S S_S(t)(S_S(t)+I_S(t)),\\
\frac{dI_S}{dt} &= \beta_{HS}S_S(t)I_H(t) + \beta_{CS}S_S(t)I_C(t) - d_S I_S(t) - k_S I_S(t)(S_S(t)+I_S(t)).
\end{aligned} \tag{2.1}$$

The parameters are described as follows:

- β_{SH} – transmission rate from infected snails to humans;
- r_H – recovery rate of infected humans;
- b_C – natural birth rate of cattle;
- β_{SC} – transmission rate from infected snails to cattle;
- d_C – death rate of infected cattle;
- $(b_C - d_C)/k_C$ – carrying capacity of cattle;
- r_C – recovery rate of infected cattle;
- b_S – natural birth rate of snails;
- β_{HS} – transmission rate from infected humans to snails;
- β_{CS} – transmission rate from infected cattle to snails;
- d_S – death rate of infected snails;
- $(b_S - d_S)/k_S$ – carrying capacity of snails.

Notice that from the first and second equations in model (2.1) we have

$$\frac{d(S_H + I_H)}{dt} = 0.$$

Thus, the human population remains constant, and we denote it by N_H. We choose the initial population $S_H(0) = S_0 > 0$ as the population size of the region, $I_H(0) = I_0 \geq 0$. Thus, $S_0 + I_0 = N_H$.

From the third and fourth equations in model (2.1) we have

$$\frac{d(S_C(t)+I_C(t))}{dt} = (b_C - d_C)(S_C(t)+I_C(t))\left[1 - \frac{S_C(t)+I_C(t)}{(b_C - d_C)/k_C}\right],$$

which means that the total cattle population satisfies the logistic equation with intrinsic growth rate $b_C - d_C$ and carrying capacity $(b_C - d_C)/k_C$. Similarly, the total snail population also satisfies the logistic equation with intrinsic growth rate $b_S - d_S$ and

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carrying capacity $(b_S - d_S)/k_S$. Without loss of generality, we make the following assumption:

Assumption. We assume that (i) human, cattle and snail populations are all positive, i.e., $N_H > 0$, $S_C + I_C > 0$ and $S_S + I_S > 0$. (ii) The birth rate is greater than the death rate for both cattle and snails, i.e., $b_C - d_C > 0$ and $b_S - d_S > 0$.

Therefore, we do not consider those boundary equilibria with either $N_H = 0$, $S_C + I_C = 0$, or $S_S + I_S = 0$, when we discuss the disease-free equilibria. The system (2.1) always has a disease-free equilibrium $E_0 = (S_H^0, I_H^0, S_C^0, I_C^0, S_S^0, I_S^0)$, where

$$S_H^0 = N_H, S_C^0 = \frac{b_C - d_C}{k_C}, S_S^0 = \frac{b_S - d_S}{k_S}, I_H^0 = I_C^0 = I_S^0 = 0.$$

The basic reproduction number is defined as the expected number of secondary infections produced by an index case. Following the recipe of van den Driessche and Watmough (2002) or Diekmann et al. (1990), we obtain the basic reproduction number as follows

$$R_0 = \sqrt{\frac{b_S - d_S}{b_S k_S}\left(\frac{\beta_{SH} N_H \beta_{HS}}{r_H} + \frac{\beta_{SC}\beta_{CS}(b_C - d_C)}{k_C(b_C + r_C)}\right)}, \tag{2.2}$$

which is composed of two parts: the influence of infectious humans and infectious cattle.

To discuss the endemic equilibria, we consider the equations

$$\beta_{SH} S_H I_S - r_H I_H = 0, \tag{2.3}$$

$$b_C(S_C + I_C) - \beta_{SC} S_C I_S - d_C S_C - k_C S_C(S_C + I_C) + r_C I_C = 0, \tag{2.4}$$

$$\beta_{SC} S_C I_S - d_C I_C - k_C I_C(S_C + I_C) - r_C I_C = 0, \tag{2.5}$$

$$b_S(S_S + I_S) - \beta_{HS} S_S I_H - \beta_{CS} S_S I_C - d_S S_S - k_S S_S(S_S + I_S) = 0, \tag{2.6}$$

$$\beta_{HS} S_S I_H + \beta_{CS} S_S I_C - d_S I_S - k_S I_S(S_S + I_S) = 0. \tag{2.7}$$

Note that $S_H(t) + I_H(t) = N_H$. Then (2.3) implies that

$$I_H = \frac{\beta_{SH} I_S N_H}{\beta_{SH} I_S + r_H}, \quad S_H = \frac{r_H N_H}{\beta_{SH} I_S + r_H}.$$

From (2.4) and (2.5), we obtain that

$$I_C = \frac{\beta_{SC}(b_C - d_C) I_S}{k_C(\beta_{SC} I_S + b_C + r_C)}, \quad S_C = \frac{(b_C + r_C)(b_C - d_C)}{k_C(\beta_{SC} I_S + b_C + r_C)}.$$

From (2.7), we see that $I_S > 0$ implies that the coefficient of S_S is greater than 0, i.e., $\beta_{HS} I_H + \beta_{CS} I_C - k_S I_S > 0$, because all parameters are greater than 0. Therefore,

$$S_S = \frac{d_S I_S + k_S I_S^2}{\beta_{HS} I_H + \beta_{CS} I_C - k_S I_S}.$$

Substituting I_H, S_H, I_C, S_C and S_S into (2.6), we see that (2.6) is equivalent to

$$C_2 I_S^2 + C_1 I_S + C_0 = 0, \tag{2.8}$$

where

$$\begin{aligned}
C_2 &= \beta_{SH}\beta_{SC}k_S[k_C N_H \beta_{HS} + k_C b_S + \beta_{CS}(b_C - d_C)],\\
C_1 &= \beta_{SC}[b_S k_S k_C r_H - \beta_{SH}\beta_{HS} N_H k_C(b_S - d_S)] + \beta_{SH}\beta_{HS} N_H k_S k_C(b_C + r_C) + \beta_{CS}\beta_{SC} r_H(b_C - d_C) + \beta_{SH}[b_S k_S k_C(b_C + r_C) - \beta_{SC}\beta_{CS}(b_S - d_S)(b_C - d_C)],\\
C_0 &= b_S k_S k_C r_H(r_C + b_C) - (b_S - d_S)[\beta_{HS}\beta_{SH} N_H k_C(b_C + r_C) + \beta_{CS}\beta_{SC} r_H(b_C - d_C)].
\end{aligned}$$

Clearly, $C_2 > 0$. Eq. (2.8) has one positive root and one negative root if $C_0 < 0$, which is equivalent to $R_0 > 1$. On the other hand, $R_0 \le 1$ implies that $b_S k_S \beta_{SC} - \beta_{SH}\beta_{HS} N_H(b_S - d_S) > 0$, and $b_S k_S k_C(b_C + r_C) - \beta_{SC}\beta_{CS}(b_S - d_S)(b_C - d_C) > 0$, which implies that $C_1 > 0$. Hence, Eq. (2.8) has only negative roots if $R_0 \le 1$. Finally, system (2.1) has an endemic equilibrium if and only if $R_0 > 1$.

Since the total population of human is constant, we substitute $S_H = N_H - I_H$ into (2.1) and obtain the following equations:

$$\begin{aligned}
\frac{dI_H}{dt} &= \beta_{SH}(N_H - I_H(t))I_S(t) - r_H I_H(t),\\
\frac{dS_C}{dt} &= b_C(S_C(t) + I_C(t)) - \beta_{SC} S_C(t) I_S(t) - d_C S_C(t) - k_C S_C(t)(S_C(t) + I_C(t)),\\
\frac{dI_C}{dt} &= \beta_{SC} S_C(t) I_S(t) - d_C I_C(t) - k_C I_C(t)(S_C(t) + I_C(t)),\\
\frac{dS_S}{dt} &= b_S(S_S(t) + I_S(t)) - \beta_{HS} S_S(t) I_H(t) - \beta_{CS} S_S(t) I_C(t) - d_S S_S(t) - k_S S_S(t)(S_S(t) + I_S(t)),\\
\frac{dI_S}{dt} &= \beta_{HS} S_S(t) I_H(t) + \beta_{CS} S_S(t) I_C(t) - d_S I_S(t) - k_S I_S(t)(S_S(t) + I_S(t)).
\end{aligned} \tag{2.9}$$

The characteristic equation of the disease free equilibrium $E_0 = (0, S_C^0, 0, S_S^0, 0)$ is

$$\lambda^5 + \Lambda_{04}\lambda^4 + \Lambda_{03}\lambda^3 + \Lambda_{02}\lambda^2 + \Lambda_{01}\lambda + \Lambda_{00} = 0,$$

where

$$\Lambda_{04} = r_H - d_C + r_C - d_S + 2(b_C + b_S),$$

$$\begin{aligned}
\Lambda_{03} &= (b_C - d_C)(b_C + r_C) + b_S(b_S - d_S) + (2b_S - d_S)(2b_C - d_C\\
&\quad + r_H + r_C) + r_H(2b_C - d_C + r_C) - (b_S - d_S)\\
&\quad \times \left(\frac{\beta_{HS}\beta_{SH} N_H}{k_S} + \frac{\beta_{CS}\beta_{SC}(b_C - d_C)}{k_S k_C}\right)
\end{aligned}$$

$$\begin{aligned}
\Lambda_{02} &= +b_S(b_S - d_S)(r_H + r_C) + (b_C - d_C)(r_H(b_C + r_C) - r_C d_S)\\
&\quad + (2b_S - d_S)(r_H(2b_C - d_C + r_C) + b_C(b_C - d_C)) - b_S(2b_C - d_C)(b_S - d_S + r_C)\\
&\quad - \frac{b_s - d_S}{k_S}\left[\beta_{HS}\beta_{SH} N_H(b_S - d_S + 2b_C - d_C + r_C) + \frac{(b_C - d_C)\beta_{CS}\beta_{SC}}{k_C}(r_H + b_C - d_C + b_S - d_S)\right],
\end{aligned}$$

$$\begin{aligned}
\Lambda_{01} &= b_S(b_C - d_C)(b_S - d_S)(b_C + r_C) + (b_C(b_C - d_C)(2b_S - d_S)\\
&\quad + b_S(b_S - d_S)(2b_C - d_C))r_H + ((2b_S - d_S)(b_C - d_C)\\
&\quad + b_S(b_S - d_S))r_H r_C - \frac{\beta_{SH}\beta_{HS} N_H(b_S - d_S)}{k_S}((b_C - d_C)(b_C + r_C)\\
&\quad + (b_S - d_S)(2b_C - d_C + r_C)) + \frac{\beta_{CS}\beta_{SC}(b_C - d_C)(b_S - d_S)}{k_S k_C}\\
&\quad \times (-r_H(b_C - d_C + b_S - d_S) + b_C(b_S - 2d_S) - (b_S - d_S)(2b_C - d_C)),
\end{aligned}$$

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Table 1
Schistosomiasis infection data of Hubei Province.

Year	Examined human population	Confirmed human cases	Examined cattle population	Confirmed cattle cases	Snail area (10,000 m^2)	Evaluated area of infected snail (10,000 m^2)
2005	1,595,316	153,187	423,033	14,816	79,169	22,537.30
2006	1,567,374	172,520	385,649	13,224	78,536	21,607.81
2007	4,260,282	304,359	351,942	9,166	75,469	20,632.25

Table 2
Schistosomiasis infection rate of Hubei Province.

Year	Infection rate of human	Infection rate of cattle	Evaluated infection rate of snails
2005	3.78%	5.63%	28.47%
2006	3.29%	4.06%	27.52%
2007	2.33%	3.35%	27.34%

$$\Lambda_{00} = r_H b_S (b_S - d_S)(b_C + r_C)(b_C - d_C) - \frac{\beta_{SH}\beta_{HS} N_H (b_S - d_S)^2 (b_C - d_C)(b_C + r_C)}{k_S} + \frac{r_H \beta_{CS} (b_S - d_S)^2 (b_C - d_C)(\beta_{SC}(b_C - 3d_C) - 4(b_C - d_C))}{k_C k_S}.$$

It is clear that $\Lambda_{04} > 0$. By Routh–Hurwitz criteria, we have the following result:

Theorem. *If* $\Lambda_{03} > 0, \Lambda_{02} > 0, \Lambda_{01} > 0, \Lambda_{00} > 0, \Lambda_{04}\Lambda_{03}\Lambda_{02} > \Lambda_{02}^2 + \Lambda_{04}^2\Lambda_{01}$ *and* $(\Lambda_{04}\Lambda_{01} - \Lambda_{00})(\Lambda_{04}\Lambda_{03}\Lambda_{02} - \Lambda_{02}^2 - \Lambda_{04}^2\Lambda_{01}) > \Lambda_{00}(\Lambda_{04}\Lambda_{03} - \Lambda_{02})^2 + \Lambda_{04}\Lambda_{00}^2$, *then the disease-free equilibrium* $E_0 = (N_H, 0, S_C^0, 0, S_S^0, 0)$ *is locally asymptotically stable.* □

3. Simulations and sensitivity analysis

In this section, we first use model (2.1) to simulate the reported schistosomiasis infection data from Hubei Province, China (Tables 1 and 2).

In order to simulate, we need to estimate the parameters of the model. Since the duration of infection of humans and cattle is 4 and 1.5 years respectively Williams et al. (2002), we assume the recovery rates of infected humans and cattle are 1/4 and 1/1.5 respectively. We also assume that the average life of cattle is 25 years and the average life of snails is 12 months.

The numerical simulations of the infection rates of humans and cattle using model (2.1) are shown in Fig. 2(a) and (b) respectively. We simulate the data from 2005 to 2007 and predict the infection rates of humans and cattle in 2008 and 2009. Fig. 2(a) and (b) indicate that simulations of our model with reasonable parameters values provide a good match to the schistosomiasis data on infected human and cattle in Hubei Province from 2005 to 2007. With the current control measures and management policies, our model predicts that the infection rates in both human and cattle would decrease after 2007.

Next, we perform some sensitivity analysis of the basic reproduction number R_0 in terms of the model parameters.

From Fig. 3, we can see that the influence of cattle on the basic reproduction number R_0 is greater than humans. In fact, if we fix all the parameters except β_{SH}, β_{SC}, β_{HS} and β_{CS}, the basic reproduction number increases as any of the transmission coefficients increases. However, R_0 increases rapidly as the transmission coefficient from cattle to snails β_{SC} increases as shown in Fig. 3(b), while the change is tiny when the transmission coefficient from humans to snails β_{SH} increases as shown in Fig. 3(a). Similarly, the influence of the transmission coefficient from snails to cattle β_{SC} as in Fig. 3(d), is greater than that from snails to humans β_{SH} as in Fig. 3(c). Thus, controlling the infection between cattle and snails is very important in controlling and eliminating schistosomiasis infection.

Fig. 4 reflects the relation between the basic reproduction number R_0 and death rate of snails d_S and the death rate d_C of cattle. In Fig. 4(a), R_0 decreases as d_C increases. In Fig. 4(b), R_0 decreases as d_S increases. From Fig. 4, we can conclude that decrease the population of either snails or cattle is helpful for controlling the schistosomiasis infection.

Fig. 5 reflects the relation between the basic reproduction number R_0 and recovery rate of humans r_H and recovery rate of cattle r_C. In Fig. 5(a), R_0 decreases as r_H increases. In Fig. 5(b), R_0 decreases as r_C increases. From Fig. 5, we can conclude that increase the curing rate of either infected humans or infected cattle is helpful for controlling the schistosomiasis infection. Comparing Fig. 5(a) and (b) we see that when both r_H and r_C change, R_0 in 5(b) changes greater than in 5(a). This suggests that curing infected cattle is even more important now for controlling the schistosomiasis infection.

4. Discussion

Because of the complex river systems, large numbers of lakes and mountains, and high densities of hosts and snail populations in China, controlling schistosomiasis there is a very difficult and long-

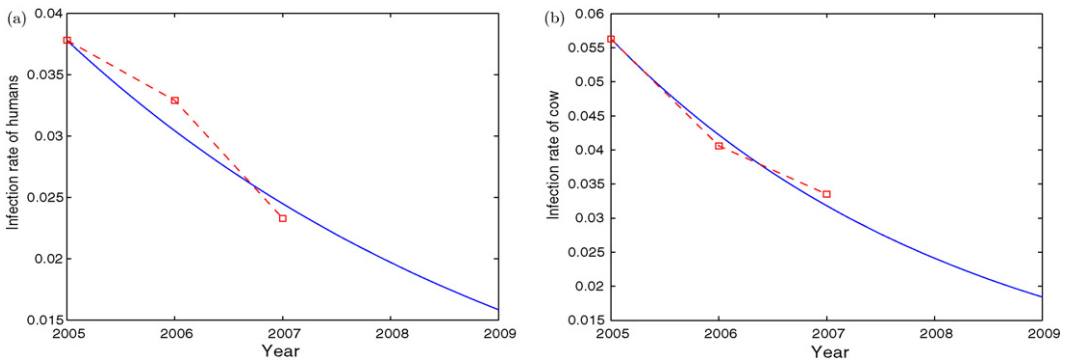

Fig. 2. (a) Simulation of the infection rate of humans over time in Hubei Province. (b) Simulation of the infection rate of cattle over time in Hubei Province. The dashed lines represent the reported infection rates while the solid lines are the simulated infection rates based on the model.

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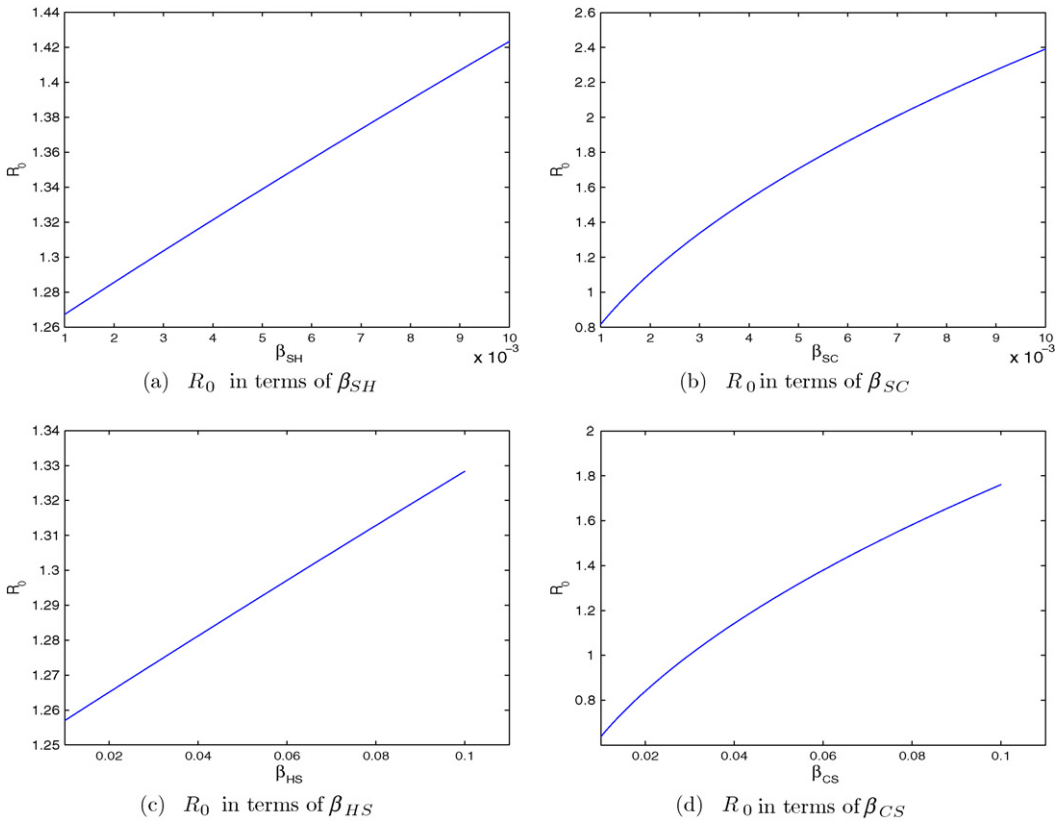

Fig. 3. The relationship between basic reproduction number and the infection coefficients.

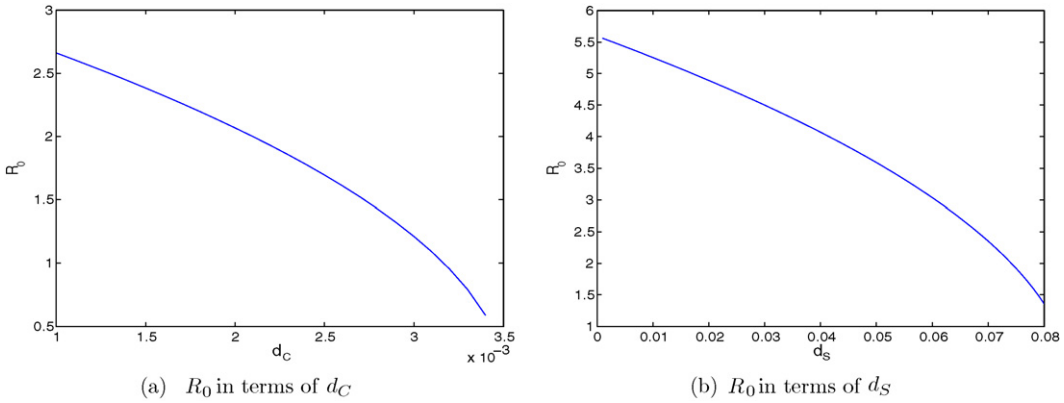

Fig. 4. The relationship between R_0 and d_S, d_C.

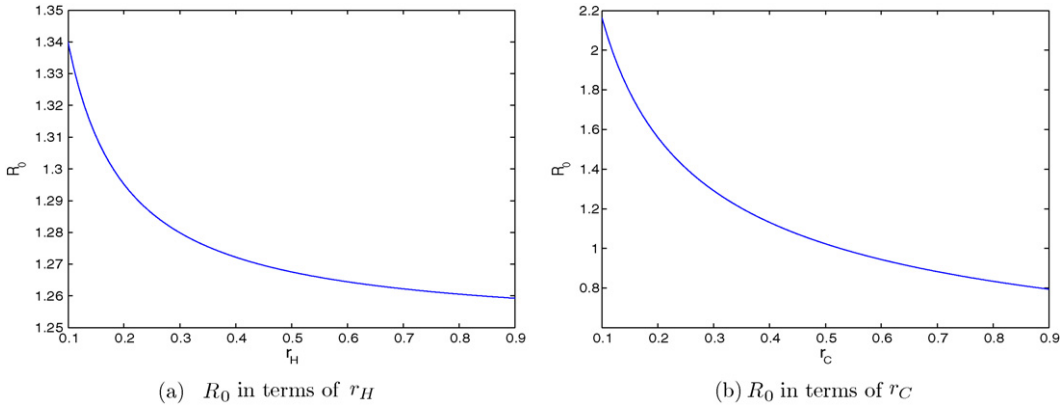

Fig. 5. The relationship between R_0 and r_H, r_C.

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term task. Mathematical modeling of schistosomiasis can help in examining the current control and prevention policies and developing new control strategies.

The classical model for schistosomiasis transmission proposed by Macdonald (1965) was indeed of Ross' type (see Barbour, 1978) which involves the human host and snail populations. Barbour (1996) generalized Macdonald's model to include two hosts: the human host and a mammalian host. Williams et al. (2002) extended Barbour's two-host model to study human–bovine transmission of schistosomiasis in Jiangxi Province, China. Gray et al. (2008) further generalized Barbour's model to include multiple hosts to study the transmission dynamics of *S. japonicum* in the lakes and marshlands in China.

In all of the above mentioned models, only the infected populations were considered explicitly. Recently, Allen and Victory (2003) constructed a mathematical model for schistosomiasis infection involving the human host, a mammalian host, an intermediate snail host, and a competitor snail species. They further classified them into susceptible and infected subpopulations. In this paper, based on Allen and Victory's model and taking the specific characteristics of schistosomiasis infection in Hubei Province, China, into consideration, we proposed a mathematical model for the human–cattle–snail transmission of schistosomiasis. The model is a system of six ordinary differential equations and includes susceptible and infected human, cattle and snail subpopulations. We determined the basic reproduction number and analyzed the existence and stability of the disease-free equilibrium of the model. We also used the model to simulate the schistosomiasis infection data from Hubei Province and carried out sensitivity analysis of the basic reproduction number on various parameters.

Traditional strategies in controlling schistosomiasis include chemotherapy, health education, livestock chemotherapy, and snail control in risk areas (Sun et al., 2002; Zhao et al., 2005), relying more on treating humans and animals. The sensitivity analysis of the basic reproduction number R_0 on various parameters (Figs. 3 and 4) demonstrated that these are all important measures to control schistosomiasis infection. The most interesting simulations are in Fig. 3(c) and (d) which indicate that transmission between cattle and snails plays a much more important role than the human–snail transmission in sustaining the schistosomiasis infection. This strongly suggests that, to control and eventually eradicate schistosomiasis in China, a more comprehensive approach needs to include environmental factors (Liang et al., 2007) in order to break the cattle–snail transmission cycle. These control measures include more comprehensive surveillance on cattle population, early diagnosis and chemotherapy of cattle, and snail control by means of environment management.

Our model was based on and applied to the schistosomiasis infection data from Hubei Province. As five of the seven schistosomiasis endemic provinces have similar geographic characteristics, being in lake and marshland regions, we believe that our model applies to all these five provinces and the control measures are similar.

There are some limitations in this study. Firstly, host heterogeneities were not included in the model, while different human groups may have different infection rates and different transmission patterns. For example, farmers certainly have higher infection rates than city residents, and school students are more likely to be infected in the summer. Secondly, the data we used were limited. Thirdly, we only did some local sensitivity analysis of the basic reproduction number for some parameters. Future studies should consider host heterogeneities and dispersal in the model. Also, more data need to be collected so that the model parameters can be measured or estimated more accurately. Further, more detailed sensitivity analysis should be performed (see Blower and Dowlatabadi, 1994) in order to design new effective control and prevention strategies. We leave these for future consideration.

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Appendix A. Computation of R_0

Following Diekmann et al. (1990) or van den Driessche and Watmough (2002), we rewrite system (2.1) as the form

$$\dot{x} = \mathcal{F}(x) - \mathcal{V}(x),$$

where

$$\mathcal{F}(x) = (\beta_{SH}S_HI_S, \beta_{SC}S_CI_S, \beta_{HS}S_SI_H + \beta_{CS}S_SI_C, 0, 0, 0)^{\mathrm{T}},$$

$$\mathcal{V}(x) = \begin{pmatrix} r_HI_H \\ d_CI_C + k_CI_C(S_C + I_C) \\ d_SI_S + k_SI_S(S_S + I_S) \\ \beta_{SH}S_HI_S - r_HI_H \\ -b_C(S_C + I_C) + \beta_{SC}S_CI_S + d_CS_C + k_CS_C(S_C + I_C) \\ b_S(S_S + I_S) + \beta_{HS}S_SI_H + \beta_{CS}S_SI_C + d_SS_S + k_SS_S(S_S + I_S) \end{pmatrix},$$

$$x = (I_H, I_C, I_S, S_H, S_C, S_S)^{\mathrm{T}}.$$

Then, we have the derivatives at the disease-free equilibrium E_0

$$D\mathcal{F}(E_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix}, \quad D\mathcal{V}(E_0) = \begin{pmatrix} V & 0 \\ J_3 & J_4 \end{pmatrix},$$

where

$$F = \begin{pmatrix} 0 & 0 & \beta_{SH}N_H \\ 0 & 0 & \dfrac{\beta_{SC}(b_C - d_C)}{k_C} \\ \dfrac{\beta_{HS}(b_S - d_S)}{k_S} & \dfrac{\beta_{CS}(b_S - d_S)}{k_S} & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} r_H & 0 & 0 \\ 0 & b_C + r_C & 0 \\ 0 & 0 & b_S + r_S \end{pmatrix}.$$

Thus, the next generation matrix for system (2.1) is given by

$$FV^{-1} = \begin{pmatrix} 0 & 0 & \dfrac{\beta_{SH}N_H}{b_S} \\ 0 & 0 & \dfrac{\beta_{SC}(b_C - d_C)}{k_Cb_S} \\ \dfrac{\beta_{HS}(b_S - d_S)}{k_Sr_H} & \dfrac{\beta_{CS}(b_S - d_S)}{k_S(b_C + r_C)} & 0 \end{pmatrix},$$

which has three eigenvalues 0, $\pm\sqrt{(b_S - d_S/b_Sk_S)((\beta_{SH}\beta_{HS}N_H/r_H) + (\beta_{SC}\beta_{CS}(b_C - d_C)/k_C(b_C + r_C)))}$. Therefore, the basic reproduction number for system (2.1) is

$$R_0 = \sqrt{\frac{b_S - d_S}{b_Sk_S}\left(\frac{\beta_{SH}N_H\beta_{HS}}{r_H} + \frac{\beta_{SC}\beta_{CS}(b_C - d_C)}{k_C(b_C + r_C)}\right)}.$$

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