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A Mathematical Model of Chagas Disease Transmission

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Abstract. Chagas disease is a parasitic infection caused by protozoan *Trypanosoma cruzi* which is transmitted to human by insects of the subfamily Triatominae, including *Rhodnius prolixus*. This disease is a major problem in several countries of Latin America. A mathematical model of Chagas disease with separate vector reservoir and a neighboring human resident is constructed. The basic reproductive ratio is obtained and stability analysis of the equilibria is shown. We also performed sensitivity populations dynamics of infected humans and infected insects based on migration rate, carrying capacity, and infection rate parameters. Our findings showed that the dynamics of the infected human and insect is mostly affected by carrying capacity insect in the settlement.

INTRODUCTION

Chagas disease was discovered by a Brazilian doctor named Carlos Chagas in 1909. The disease is caused by *Trypanosoma cruzi* parasite which is transmitted to humans through a Triatomine insect. The three major insects of the parasite are *Triatoma infestans, Triatoma dimidiata, and Rhodnius prolixus* [1]. Triatomine insects are blood-sucking insects from mammals including humans. Its habitats that are not far away from humans make these insects easily reach settlements and interact with humans. Triatomine insects generally bite humans at night [9][11]. After biting humans, the triatomine deposits its feces containing the *Trypanosoma cruzi* on the host's skin surface. Then the parasite enters the human body through insect bites or mucous membrane. In the human body, the parasite will divide and attack the existing cells such as the heart and lymph nodes. In chronic conditions this disease can lead to heart failure and swelling of the intestines very seriously. Both of these conditions may lead to death [11].

Chagas disease is a major disease problem in the world, especially Latin America [3]. By 2016, about 6-7 million people worldwide are infected with chagas. More than 30 % of the infected are classified as chronic to the heart and more than 10 % are chronic stages of the digestive and nervous [4]. There are 21 Latin American countries that have problems with the spread of this disease, including: Argentina, Belize, Bolivia, Brazil, Chile, Colombia, Costa Rika, Ecuador, El Salvador, French Guiana, Guatemala, Guyana, Honduras, Mexico, Nicaragua, Panama, Paraguay, Peru, Suriname, Uruguay and Venezuela. Based on DNDi [7], in Colombia, as many as 437,960 people are infected with chagas and 4,800,000 are at risk of infection, with *Rhodnius prolixus* as the main vector of human infection. This condition is caused by the palm trees as a habitat of *Rhodnius prolixus* are abundant and close to the settlement. Transmission of chagas disease to humans requires close interaction between the vector and humans and this generally occurs in the settlements. Therefore, the household infestation is the main factor causing increased chagas disease problems in Colombia [6].

Studying population dynamics to control vector is an effective method of preventing chagas disease [4]. Some researchers have developed a mathematical model for chagas disease. Erazo and cordovez [3] developed a mathematical model of the dynamics of chagas disease by observing the palm-house proximity. Velasco-Hernandez [5] formulated a host-vector model of chagas disease transmission by distinguishing between the acute stage and the chronic stage. Cohen and Gutler [12] developed a mathematical model of household transmission by paying attention to domestic animals. Inaba and Sekine [10] assumed that the infected population is structured by the disease age, the infection rate, and the removed rate depend on the disease age.

In this paper, we developed a new simple mathematical model of chagas disease transmission with separate vector

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reservoir and resident settlements. Different to the researcher mentioned above, we take into account the parameters of migration rate, carrying capacity of vector rhodnius prolixus, and infection rate.

MODEL FORMULATION

In this section we will discuss about the formulation of chagas disease model by taking into account the human population and *Rhodnius prolixus* population. Since there is no recovery in chagas disease [2] then we defined S_h is susceptible humans, E_h is exposed human, and I_h is infected humans. If N_h is the constant of the total human population then $N_h = S_h + E_h + I_h$. In the vector population, we defined M_r is susceptible rhodnius insect in the palm plantation, S_r is susceptible rhodnius insects in the settlement, E_r is exposed insects in the settlement, and I_r is infected rhodnius insects in the settlement.

The mathematical model of chagas disease transmission involves two areas: palm plantations and settlements. In this model, it is assumed that there is no vertical transmission on insects or humans and only contact between insects and humans in settlements that can cause infection. Chagas disease infections in humans may occur if infected insects (I_r) make contact with susceptible humans (S_h). Further, insect infections can occur if susceptible insects (S_r) make contact with an infected human (I_h). All parameters used are constant and per day units.

In residential areas, rhodnius prolixus insects generally bite humans at night. We assume at rate a one human can be infected with *Trypanosoma cruzi* parasite and at rate b one insect may be infected with a *Trypanosoma cruzi* parasite. The *Rhodnius prolixus* insect has a birth rate of β and a mortality rate of μ. While humans have a birth rate and death rate of α. The incubation period of chagas disease in humans is $1/\delta$ and the incubation period in insects is $1/\sigma$. Carrying capacity of insects in the settlement is $1/c$. In the plantation area, it is assumed that all the insects are susceptible (M_r). Insects can migrate from palm plantations to settlements at rate ω and insect carrying capacity on plantations is $1/d$. Because it was assumed that no contact between humans and insects could lead to infection in the plantation, the mathematical model in the palm plantation area was a logistic model of *Rhodnius prolixus*. The transmission diagram of chagas disease is presented below.

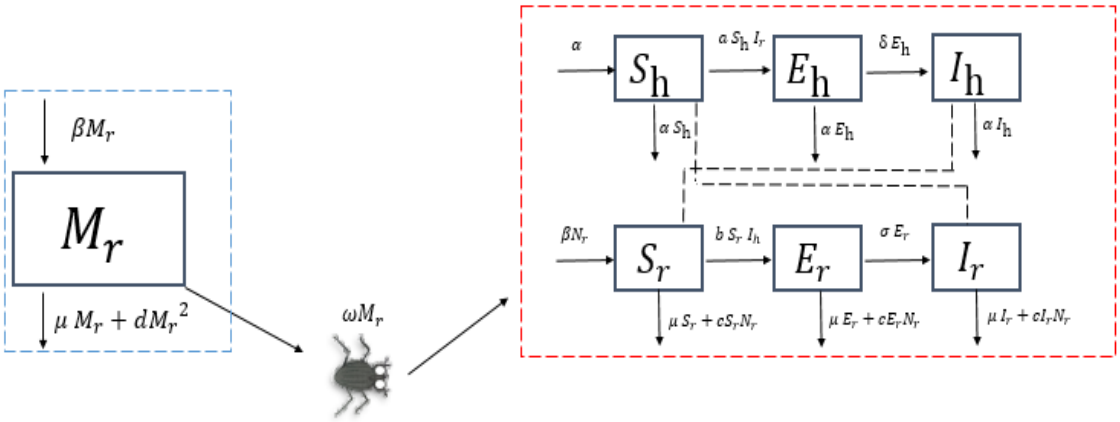


FIGURE 1. Chagas disease transmission diagram with separated vector reservoir and resident settlement. The blue dashed line is palm plantation as vector reservoir and the red dashed line is villages as the resident settlement.

Based on the assumption and the transmission diagram, our normalized mathematical model can be formulated as follows:

$$\frac{dM_r}{dt} = \beta M_r - dM_r^2 - \mu M_r - \omega M_r \tag{1}$$

$$\frac{dS_h}{dt} = \alpha - \alpha S_h - aS_h I_r \tag{2}$$

$$\frac{dE_h}{dt} = aS_h I_r - \alpha E_h - \delta E_h \tag{3}$$

$$\frac{dI_h}{dt} = \delta E_h - \alpha I_h \tag{4}$$

$$\frac{dS_r}{dt} = \beta N_r + \omega M_r - bS_r I_h - \mu S_r - cS_r N_r \tag{5}$$

$$\frac{dE_r}{dt} = bS_r I_h - \mu E_r - \sigma E_r - cE_r N_r \tag{6}$$

$$\frac{dI_r}{dt} = \sigma E_r - \mu I_r - cI_r N_r \tag{7}$$

with region of biological interest $\Omega = \{M_r, S_h, E_h, I_h, S_r, E_r, I_r \in \mathbb{R}^7_+ | \, S_h + E_h + I_h = N_h, \; S_r + E_r + I_r = N_r\}$

ANALYSIS

Basic Reproduction Number

Basic reproduction number (R_0) indicates how many secondary infections when an infected individual/person enter to a virgin population during infection period. It is an important parameter that growth indicator a disease in a population. In this subsection, we derive the formulation (R_0) of this model by using Next Generation Matrix (*NGM*) [13]. In this method, we consider only groups of exposed and infected both human and insect, i.e E_h, I_h, E_r and I_r. Then, we have matrix F and matrix V representing transmission matrix and transition matrix, respectively, that evaluated at E_0. *NGM* is formulated as FV^{-1} and its spectral radius is called R_0. Hence, We have

$$NGM = \begin{bmatrix} 0 & 0 & 0 & \frac{a}{cN_r+\mu} \\ \frac{\delta}{\alpha+\delta} & 0 & 0 & 0 \\ 0 & \frac{b\left(\beta dN_r+\beta\omega-\mu\omega-\omega^2\right)}{d(cN_r+\mu)\alpha} & 0 & 0 \\ 0 & 0 & \frac{\sigma}{cN_r+\mu+\sigma} & 0 \end{bmatrix} \tag{8}$$

Spectral radius of the NGM is

$$R_0 = \sqrt[4]{\frac{ab\delta\sigma\left(\beta dN_r + \beta\omega - \mu\omega - \omega^2\right)}{d\alpha\left(cN_r+\mu\right)^2\left(cN_r+\mu+\sigma\right)\left(\alpha+\delta\right)}} \tag{9}$$

In the next section, we use threshold parameter $R = R_0^4$ in discussing equilibrium points and their stability.

Equilibrium Points and Their Stability

This model has two equilibrium are follows

$$E_0 = \left\{\frac{\beta-\mu-\omega}{d}, 1, \frac{\beta dN_r + \beta\omega - \mu\omega - \omega^2}{d\left(cN_r+\mu\right)}, 0, 0, 0, 0, 0\right\} \quad \text{and} \quad E_1 = \left\{M_r^*, S_h^*, E_h^*, I_h^*, S_r^*, E_r^*, I_r^*\right\}$$

where

$$S_h^* = \frac{\alpha\phi\left(\phi+\sigma\right)\left(\phi\left(\alpha+\delta\right)+b\delta\right)}{b\delta\left(\alpha\phi\left(\phi+\sigma\right)+a\sigma\left(\beta N_r+\omega M_r^*\right)\right)}$$

$$S_r^* = \frac{\left(\alpha+\delta\right)\left(\alpha\phi\left(\phi+\sigma\right)+a\sigma\left(\beta N_r+\omega M_r^*\right)\right)}{a\sigma\left(\phi(\alpha+\delta)+b\delta\right)}$$

$$E_h^* = \frac{\alpha^2\phi^2\left(\phi+\sigma\right)\left(R-1\right)}{b\delta\alpha\phi\left(\phi+\sigma\right)+b\delta a\sigma\left(\beta N_r+\omega M_r^*\right)}$$

$$
\begin{aligned}
E_r^* &= \frac{\alpha\,\phi^2\,(\alpha+\delta)\,(R-1)}{(\alpha\,\phi+b\delta+\delta\,\phi)\,a\sigma} \\
I_h^* &= \frac{\alpha\,\phi^2\ (\phi+\sigma)\,(R-1)}{b\alpha\,\phi\ (\phi+\sigma)+ab\sigma\ \left(\beta\,N_r+\omega\,M_r^*\right)} \\
I_r^* &= \frac{\phi\,N_h\alpha\ (\alpha+\delta)\,(R-1)}{(\alpha\,\phi+\delta\ (\phi+b))\,a}
\end{aligned}
$$

and

$$
M_r^* = \frac{\beta-\mu-\omega}{d}, \quad \phi = cN_r+\mu
$$

Since infection population in E_0 is zero, so it is known as disease free point. While E_1 is known as endemic point where exist if $R > 1$. Now, we discuss stability of E_0 point in the following theorem

Theorem 1 *The equilibrium point of E_0 is locally asymptotically stable if $R < 1$, and the point is unstable saddle $R > 1$*

Proof The system (1)-(7) has jacobian matrix at E_0 as follows

$$
J(E_0) = \begin{bmatrix}
-\beta+\mu+\omega & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & -\alpha & 0 & 0 & 0 & 0 & -a \\
0 & 0 & -\alpha-\delta & 0 & 0 & 0 & a \\
0 & 0 & \delta & -\alpha & 0 & 0 & 0 \\
\omega & 0 & 0 & -\frac{b\left(\beta N_r+\omega M_r^*\right)}{\phi} & -\phi & 0 & 0 \\
0 & 0 & 0 & \frac{b\left(\beta N_r+\omega M_r^*\right)}{\phi} & 0 & -M_r^*+\sigma & 0 \\
0 & 0 & 0 & 0 & 0 & \sigma & -\phi
\end{bmatrix} \tag{10}
$$

Stability of the E_0 depend on the roots of one of the factors of characteristic equation of the matrix

$$
\lambda^4 + A_3\lambda^3 + A_2\lambda^2 + A_1\lambda + A_0 = 0
$$

where

$$
\begin{aligned}
A_3 &= (2\,\phi+2\,\alpha+\delta+\sigma) \\
A_2 &= \left(\alpha^2+\delta\,\alpha+4\,\alpha\,\phi+2\,\alpha\,\sigma+2\,\delta\,\phi+\delta\,\sigma+\phi^2+\sigma\,\phi\right) \\
A_1 &= (2\,\alpha+\delta)\,\phi^2+\left(2\,\alpha^2+2\,\alpha\,\delta+2\,\alpha\,\sigma+\delta\,\sigma\right)\phi+\alpha\,\sigma\ (\alpha+\delta) \\
A_0 &= \alpha\,\phi\,(\phi+\sigma)\,(\alpha+\delta)\,(1-R)
\end{aligned}
$$

If $0 < R < 1$ and all parameter values are positive, after some algebraic computation, we obtain

$$
\begin{aligned}
A_1A_2A_3 - A_1^2 - A_3^2A_0 &> A_1A_2A_3 - A_1^2 - \frac{A_3^2A_0}{1-R} \\
&= (2\,\phi+\sigma)\,(\alpha+\phi)\,(\alpha+\phi+\sigma)\,(2\,\alpha+\delta)\,(\alpha+\delta+\phi)\,(\alpha+\delta+\phi+\sigma) \\
&> 0
\end{aligned}
$$

According to Routh-Hurwitz criteria, all roots of the equation are negative. Thus the E_0 point is locally asymptotically stable. The following theorem discuss the stability of the E_1 point

Theorem 2 *The equilibrium point of E_1 is locally asymptotically stable if $R > 1$, and the point is not exist if $R < 1$*

Proof Jacobian matrix at E_2 is

$$\begin{bmatrix} -2\,dM_r^* + \beta - \mu - \omega & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -aI_r^* - \alpha & 0 & 0 & 0 & 0 & -aS_h^* \\ 0 & aI_r^* & -\alpha - \delta & 0 & 0 & 0 & aS_h^* \\ 0 & 0 & \delta & -\alpha & 0 & 0 & 0 \\ \omega & 0 & 0 & -bS_r^* & -bI_h^* - cN_r - \mu & 0 & 0 \\ 0 & 0 & 0 & bS_r^* & bI_h^* & -cN_r - \mu - \sigma & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma & -cN_r - \mu \end{bmatrix} \tag{11}$$

Stability of the E_0 depend on the roots of one of the factors of characteristic equation of the matrix

$$\lambda^4 + B_3\lambda^3 + B_2\lambda^2 + B_1\lambda + B_0 = 0$$

where

$$\begin{aligned} B_3 &= aI_r^* + bI_h^* + 2\,cN_r + 2\,\alpha + \delta + 2\,\mu + \sigma \\ B_2 &= abI_h^*I_r^* + b\,(\phi + 2\,\alpha + \delta + \sigma)\,I_h^* + a\,(2\,\phi + \alpha + \delta + \sigma)\,I_r^* + \phi\ (\phi + 4\,\alpha + 2\,\delta + \sigma) + \alpha\ (\alpha + \delta) + \sigma\ (2\,\alpha + \delta) \\ B_1 &= ab\,(\phi + \alpha + \delta + \sigma)\,I_h^*I_r^* + b\,(\phi\ (2\,\alpha + \delta) + (\alpha + \sigma)\,(\alpha + \delta) + \alpha\,\sigma)\,I_h^* \\ &\quad + a\,(\phi\ (\phi + 2\,\alpha + 2\,\delta + \sigma) + \sigma\ (\alpha + \delta))\,I_r^* + \phi\,(2\,\alpha\ (\alpha + \delta) + (\phi + \sigma)\,(2\,\alpha + \delta)) + \alpha\,\sigma\ (\alpha + \delta) \\ B_0 &= ab\,(\phi + \sigma)\,(\alpha + \delta)\,I_h^*I_r^* + \alpha\,b\,(\phi + \sigma)\,(\alpha + \delta)\,I_h^* + a\phi\ (\phi + \sigma)\,(\alpha + \delta)\,I_r^* \\ &\quad - \sigma\,abS_h^*S_r^*\delta + \alpha^2\phi^2 + \alpha\,\delta\,\phi^2 + \alpha^2\sigma\,\phi + \alpha\,\delta\,\sigma\,\phi \end{aligned}$$

next we substitute elements of $I_h^*, I_r^*, S_h^*, S_r^*$ in E_1 to B_0, we have

$$B_0 = \frac{\alpha\,\phi^2\,(\alpha + \delta)\,(\phi + \sigma)\,(d\alpha\phi\,(\phi + \sigma) + a\sigma\,d\,(\beta\,N_r + \omega\,M_r^*))\,((\alpha + \delta)\,\phi + \delta\,b)^2\,(\phi + \sigma)\,(\alpha + \delta)\,(R - 1)}{(\alpha\,d\phi^2 + a\beta\,d\sigma\,N_r + \alpha\,d\sigma\phi + a\omega\sigma\,M_r^*)\,(\alpha + \delta)\,\phi\,(\phi + \sigma)\,(\alpha\phi + \delta\mu + b\delta)^2}$$

If $R > 0$, then all coefficients of the equation are positive. After some arrangements, we obtain

$$\begin{aligned} B_1B_2B_3 - B_1^2 - B_3^2B_0 &> B_1B_2B_3 - B_1^2 - B_3^2B_0' \\ &= \left(bI_h^* + \phi + \sigma\right)(\phi + \alpha + \delta + \sigma)\left(bI_h^* + \phi + \alpha + \delta\right)(aI_r + 2\,\alpha + \delta) \\ &\quad (aI_r^* + \phi + \alpha + \sigma)\left(aI_r^* + bI_h^* + \phi + \alpha\right) \\ &> 0 \end{aligned}$$

where $B_0' = B_0 + \delta\sigma\,abS_h^*S_r^*$. According to the Routh Hurwitz criteria, all roots of the equation are negative. Thus the point of E_1 is locally asymptotically stable. Theorem 1 and theorem 2 give us information that the disease will tend become endemic in long time if $R > 1$ and become extinct if $R < 1$.

NUMERICAL SIMULATIONS

Host-vector model simulation is done by first determining the required parameters. The parameters are determined based on estimates and literature that have been assessed. The description of all parameters and their values are provided in the following table. Based on these parameters, obtained $R_0 = 11.012 > 0$ which means that the endemic point is stable and the disease free point is unstable.

Here we discuss how the effect of parameter changes on the dynamics of the infected vector and the infected host. Three parameters that were examined were the vector migration rate (ω), infection rate (a) and vector carrying capacity in the settlement (c^{-1}). The graphs are presented in Figure 2,3, and 4.

Based on figure 2, there is no significant change in the infected human population. This is because migratory insects are all healthy insects, therefore, can not infect humans directly. Conversely, there is a significant change in

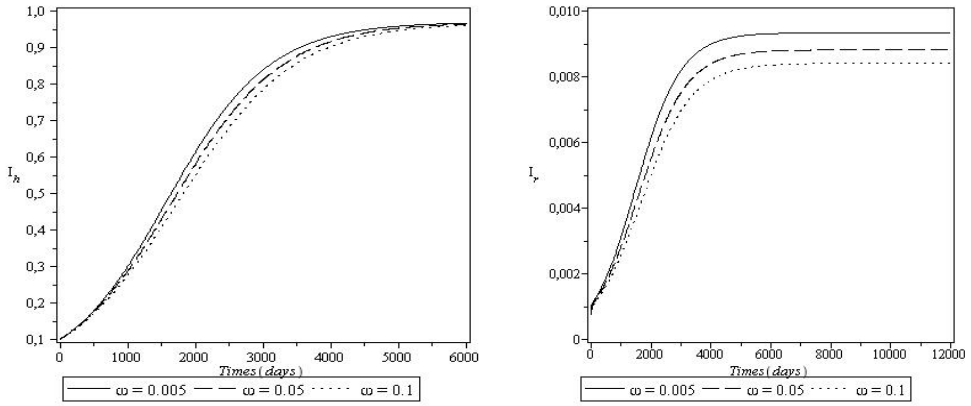
TABLE 1. Parameters Description

Parameters	Description	Value	Unit	References
a	Infection rate between infected vector and susceptible host	0.137	day^{-1}	assumed
b	Infection rate between infected host and susceptible vector	0.096	day^{-1}	assumed
α^{-1}	Host recruitment rate	70×365	day^{-1}	assumed
β	Birth rate of vector	0.8	day^{-1}	assumed
μ	Natural death of vector	0.05	day^{-1}	[3]
δ^{-1}	Human incubation rate	12	day^{-1}	[1]
σ^{-1}	Vector incubation rate	7	day^{-1}	[1]
c^{-1}	Carrying capacity of vector in settlement	3/4	day^{-1}	assumed
d^{-1}	Carrying capacity of vector in palm plantation	5/4	day^{-1}	assumed
ω	Migration rate of vector	0.05	day^{-1}	[3]

the population of infected insects. This is because healthy insects can be directly infected if they deal directly with infected humans. In addition, it can be seen that the increasing migration rate has resulted in an increasing population of infected humans and insects.

Based on figure 3, there is a considerable change in human populations and insect populations. This can happen because the greater of carrying capacity can make the number of insects in the settlement is increased therefore the chance of human or insect to get infected is also increased. On the basis of this, the greater carrying capacity (c^{-1}) will result in the greater number of infected humans and insects.

Based on figure 4, there is an appreciable change in the infected human population. This is because the infection rate (a) is a successful chance of an infected insect to infect a healthy human. Therefore humans get a direct influence on the magnitude of the infection rate. inversely related to it, there is no significant change in the population of infected insects. This is because the magnitude of infection rate (a) does not directly affect the number of infected insects.

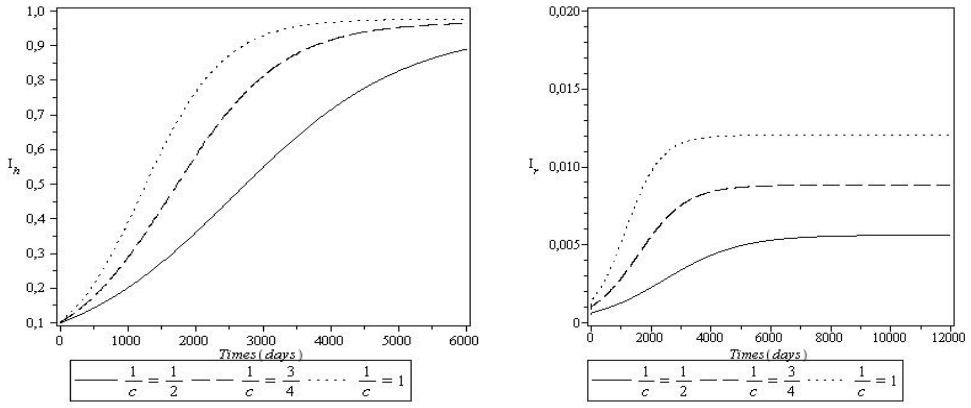


(a) (b)

FIGURE 2. The infected vector and infected host dynamics in relation to varying migration rates (ω) of *Rhodnius prolixus*: a. dynamics of infected human (I_h) b. dynamics of infected *Rhodnius prolixus*(I_r).

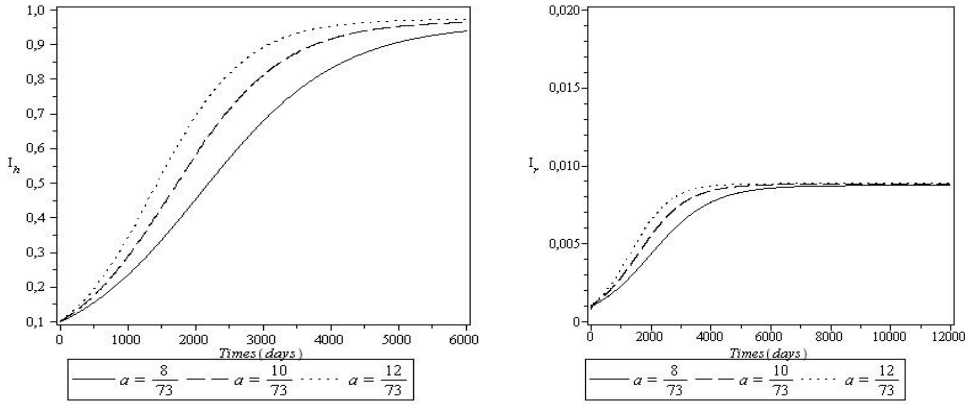
DISCUSSION AND CONCLUSION

The model of chagas disease transmission using the host-vector model is presented in the system (1)-(7). Based on the model, discussed two equilibrium points i.e disease free point and endemic point. By using New Generation Matrix (NGM) obtained basic reproductive ratio (R_0). The result shows that if $R_0 < 1$ then chagas disease will disappear both in host population and vector population. On the other hand, If $R_0 > 1$ then the disease will still exist in population vector and host. Based on the sensitivity analysis we have discussed the dynamics of population vectors and infected



(a) (b)

FIGURE 3. The infected vector and infected host dynamics in relation to the varying carrying capacity of *Rhodnius prolixus* in settlement (c^{-1}) : a. dynamics of infected human (I_h) b. dynamics of infected *Rhodnius prolixus*(I_r).



(a) (b)

FIGURE 4. The infected vector and infected host dynamics in relation to varying infection rates (a): a. dynamics of infected human (I_h) b. dynamics of infected *Rhodnius prolixus*(I_r).

hosts depending on migration rate parameters (ω), infection rate (a), and carrying capacity vectors in the settlement (c^{-1}). We conclude that the dynamics of the infected human and insects is mostly affected by carrying capacity of insect in the settlement.

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