Disease Dynamics in Variable Populations: The Chagas' Disease case

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Abstract: Several models of Chagas' disease (American trypanosomiasis) are presented. The models explicitly include the interaction vector-host(s). With them, the long term behavior of the disease is determined. The models include several of the main epidemiological compartments and mechanisms important for the transmission of the disease: The human host population is assumed to be variable and the role of alternative reservoirs of the disease in the existence of endemic states is assessed. There are three important transmission modes in Chagas' disease: congenital transmission, blood transfusion transmission and transmission by vector biting. The relative importance of each on the existence and stability of endemic and disease-free state is evaluated through the definition and use of threshold parameters. In general, the population dynamics of the disease indicates the existence of a locally asymptotically stable endemic equilibrium point.

Key words: Chagas' disease – Multiple reservoirs – Vector transmitted diseases – *Trypanosoma cruzi* – Endemic states – Mathematical model.

1 Introduction

Chagas' disease or American trypanosomiasis is a vector transmitted disease prevalent in large areas of tropical America. It is only second to malaria in the continent with respect to the number of people infected and at risk of contracting it (World Health Organization, 1989; Moncayo, 1986). Chagas' disease is characterized by three main stages. The acute stage appears following the invasion of the protozoan *Trypanosoma cruzi* which parasites the blood of the infected person. This acute stage has a duration of at most one month (Texeira, 1979) and individuals infected may or may not show symptoms of the disease. In this stage small children are the population group with the highest mortality (Texeira, 1979). If the individual does not die during this phase, it enters the so called chronic stage which has variable duration but in average lasts from 10 to 20 years (Molineux and Ashford, 1983; Moncayo, 1986). After this period

of time and for reasons still not well known the disease can follow three different paths: Individuals may develop so called megasyndromes (Moncayo, 1979; Molineux and Ashford, 1983) which are characterized by hyperthrophy of parts of the digestive tract mainly oesophagus and intestines (Molineux and Ashford, 1983). Other individuals may present cardiac problems (myocarditis) which is the terminal form with highest mortality in the group of 20 to 50 years of age. Finally, individuals may remain asymptomatic for the rest of their lives even when parasites can be found in their blood. Individuals in this group may live an otherwise ordinary life although there is growing evidence that some die of 'sudden death' associated with heart failure produced by the parasite (Texeira, 1979; Brener, 1983, Molineux and Ashford, 1983).

The disease is transmitted by hematophagous arthropod (Homoptera: Reduvidae) vectors. Contrary to what happens in malaria and other diseases transmitted by blood-sucking insects, the infective forms of the protozoan are not 'injected' to the individual during feeding. The infection occurs by contamination of the wound produced by the vector bite (Molineux and Ashford, 1983). Vectors associated with transmission of Chagas' disease have a very marked tendency to defecate several times while feeding (Molineux and Ashford, 1983). The infective form of the parasite resides in the feces and penetrates the skin when the bitten person scratches himself to calm the strong hitching produced by the bite.

There are other forms of transmission of *T. cruzi* independent of the vector. The most important of these is blood transfusion transmission. Prevalence levels in blood donors in some Latin American countries can reach levels beyond 20% (Schenone et al 1978; Sagua et al, 1982; Pinto Dias and Brener, 1984). Thus, one would expect unless careful screening of the blood supply is implemented, horizontal transmission risk to be significant. The second form of transmission independent of the vector is congenital or vertical transmission but its epidemiological significance is still not well established (Bittencourt, 1984; Bittencourt et al, 1985).

Infection by *Trypanosoma cruzi* was prevalent in wild animal communities prior to the settlement of humans in the regions of Latin America that are now endemic (Coimbra, 1988). Chagas' disease was then a zoonosis which spread into the human population with the settlement of agricultural communities in those regions (Coimbra, 1988). The type of human dwellings adopted by successful agricultural communities were well suited for invasion by insect vectors. This hypothesis is supported by the fact that to present day nomadic Indians living within jungle regions close to towns and settlements with a high prevalence of the disease, are practically free of it even when other animal species are infected in the same habitat. Moreover, the number of vector species found in their houses is almost zero (Coimbra, 1988) which explains the absence of Chagas in these individuals.

This indicates that housing style and cultural practices are main factors that determine the prevalence and incidence rates of the disease (Zeledón and Rabi-

novich, 1981; Pinto Dias, 1983) in a given community. Coupled with it there is another factor that plays an important role in disease transmission and it has to do with the *domestic* habits of the main vector species responsible for transmission. *Triatoma infestans* for example, is almost exclusively a domiciliated vector that can hardly be found outside human houses. Other species though are not such specialists (Zeledón and Rabinovich, 1981) and can alternate their diet between humans and other (domestic and wild) animals.

This shows that the study of the behavior of the vector and how it relates to its several hosts is important in understanding the mechanisms by which Chagas' disease is transmitted and maintained in a population. In particular, wild and domestic animal reservoirs of *T. cruzi* always exist and vectors with non-domestic habits have the potential to maintain the Chagas' disease cycle even in animal communities living away from human settlements.

Chagas' disease, as many other infectious diseases of the tropics do, thrives in regions with weak economies and populations with high annual growth rates (the so-called 'Third World' countries). This paper presents simple models for the spread of Chagas' disease in such a population. The combined effects of vector and blood transfusion transmission are explored and the consequences of population growth on the dynamics of the disease are assessed. Also models of the interaction of vectors with wild and domestic animal reservoirs are analyzed.

2 A simple model for Chagas' disease

Previous published modeling efforts on Chagas' disease have been scarce. One by Rabinovich and Rossell (1975) explored, through computer simulations, the vector population dynamics and was concerned mainly with the assessment of vector control strategies. One more recent model (Busenberg and Vargas, 1988) explored the spread of the disease in a growing population where the proportion of infected vectors that could transmit the disease to human hosts remained constant. This last model is a S-I-S model that incorporates a proportional mixing assumption for the transmission of Chagas' disease by blood transfusion. Based on previous results obtained by Busenberg and van den Driessche (1990) they showed the existence of three different threshold parameters that control the growth of the *proportion* of infected hosts, the *number* of infected hosts and the growth of the total population.

The model presented here is based on the one analyzed by Busenberg and Vargas (1988). It has similar structure but introduces the effect of variable vector population size into the system. In particular the model does not distinguish infective individuals in the acute and chronic stages. Only one infective compartment is considered. We treat here the case where the vector population tracks the host density in time. Denote by S and I the numbers of susceptible and infective hosts, respectively. The model equations are ('$\prime$' denotes $\frac{d}{dt}$):

$$
\begin{aligned}
S'(t) &= (b - r - \alpha v)S + (\tilde{b}p + c)I - h\frac{SI}{S+I}, \\
I'(t) &= (\tilde{b}q - \tilde{r} - c)I + \alpha v S + h\frac{SI}{S+I}, \\
v'(t) &= \beta(1-v)\frac{I}{S+I} - \delta v.
\end{aligned} \tag{1}
$$

The parameters b, $\tilde{b}$, r, $\tilde{r}$, c, q denote, respectively, the birth rates, removal rates of susceptibles and infectives, the cure rate of infectives and the probability of vertical transmission. Also $p = 1 - q$.

Vertical transmission has been reported for Chagas' disease since the very first time the disease was described (Chagas, 1909) but its relative importance with regard to its epidemiology is still under debate (Bittencourt, 1984, World Health Organization, 1989). Nevertheless, we know, form several South American studies (e.g. Castillo et al, 1984; Iglesias et al, 1985) that around one percent of newborn infants from seropositive chagasic mothers are seropositive for Chagas' disease. Of course, being seropositive for Chagas does not imply necessarily that alive parasites where transmitted through the placenta to the offspring. Some isolated documented cases show that newborns infected since birth have a life expectancy of 6 months (Bittencourt, 1984). Thus Chagas' disease affects the reproductive success of the infected individuals by reducing the birth rate. This effect is incorporated into the model to try to evaluate from a theoretical point of view its epidemiological relevance.

On the other hand we are assuming that the rate of transmission through blood transfusion is proportional to $\frac{I}{S+I}$, the proportion of infective individuals that donate blood. Obviously this is an oversimplification since one would expect the blood donation probability of an individual to be age dependent among other things and that only a fraction of the infected asymptomatic individuals participate in blood donation. However since we are interested in assessing the qualitative behavior of the disease this hypothesis gives a reasonable first approximation to the actual situation.

Other aspect of the above model that deserves some discussion is the vector-host contact rate. In the model this rate is given by $\alpha v(t)$ where $v(t)$ is the infected proportion of vectors at time t. According to the classical results derived from the Ross-MacDonald model (Aron and May, 1982), α has to be of the following form

$$\alpha = a \cdot b \cdot m,$$

where a is the average number of bites per unit time, b is the proportion of infected bites that result in host infection, and m is the ratio of vector numbers to host numbers. Thus, in the case of a growing host population interacting with a vector whose total population density remains constant, as is the case in model (1) above, m should be a decreasing function of the total host population. In this model we are assuming, however, α constant. This would constitute a rough approximation to a situation where population growth is associated with

crowding which thus, enhances the effectiveness of vectors in transmitting the disease. This effect is reflected in a constant effective biting rate α (bites that effectively produce infection in the host per unit time).

In the vector equation β is the effective contact rate between infective hosts and susceptible vectors (contacts per unit time that effectively transmit the infection to vectors), and δ is the death rate of vectors. Recall that for this last equation we are assuming constant total population. This makes it possible to view $v(t)$ as the proportion of infective vectors at time t.

The simplest possible situation in this model arises when the total population is constant and it is analyzed next.

Define the total host population as $P = S + I$ and obtain from (1)

$$P'(t) = (b - r)S + (\tilde{b} - \tilde{r})I.$$

Thus $P'(t) = 0$ for all t if and only if, either

$$S(t) = \left(\frac{\tilde{r} - \tilde{b}}{b - r}\right)I(t)$$

or

$$b - r = \tilde{b} - \tilde{r} = 0.$$

The last identity implies P constant with $\tilde{\alpha} = 0$. This case is treated later in Section 3.

From the first identity we obtain

$$P = \left(1 + \frac{\tilde{r} - \tilde{b}}{b - r}\right)I$$

rendering I constant since P is constant. Also $y = I/P$ is constant. Consequently $\frac{dy}{dt} = 0$ and, thus, we have either (y^*, v^*) or $(0, 0)$ for all time, where y^* and v^* denote the non-zero endemic equilibrium points. To investigate the feasibility of the endemic equilibrium point we consider the equation for $\frac{dy}{dt}$, namely,

$$y'(t) = \left[\tilde{b}q - \tilde{r} - c + \alpha\frac{\tilde{r} - \tilde{b}}{b - r}v + \frac{yh(\tilde{r} - \tilde{b})}{\tilde{\alpha}}\right]y, \tag{2}$$

where

$$\tilde{\alpha} = b - \tilde{b} - r + \tilde{r}$$

is positive since we assume that ill individuals have lower growth rate.

The constant solution y^* of (2) is feasible if $\frac{\tilde{r} - \tilde{b}}{b - r} \geq 0$, and $b \neq r$. From equations (2) and the third equation in (1) we can obtain the equilibrium point of the system

$$v = \left[\frac{b-r}{\alpha(\tilde{r}-\tilde{b})}\right]\left[\tilde{r}+c-\tilde{b}q-\frac{yh(\tilde{r}-\tilde{b})}{\tilde{\alpha}}\right],$$

and

$$y = \frac{\delta v}{\beta(1-v)}.$$

There are two equilibria, the disease free equilibrium and a unique endemic equilibrium point that is feasible if

$$y^* = \frac{\tilde{\alpha}(\tilde{r}+c-\tilde{b}q)}{h(\tilde{r}-\tilde{b})} > 0. \tag{3}$$

If we assume that the susceptible subpopulation has positive growth rate $b-r$, then necessarily $\tilde{r}-\tilde{b}>0$. Consequently from (3) we see that $y^*>0$ if and only if $\tilde{r}-\tilde{b}>\tilde{b}q$ that is, if the total removal rate of the infectives is greater that their recruitment rate.

What this condition says is that, in a constant population, an endemic equilibrium may exist only if infected individuals either die of the disease or are cured faster than they are born. Otherwise, if these individuals remain for long periods of time in the infective compartment, it is impossible for the total population to remain constant.

As a first step towards the analysis of the variable population case, we now want to compute the basic reproductive number, R_0, of the infection defined (Diekmann et al., 1990 p. 365) as the expected number of secondary cases produced, in a completely susceptible population, by a typical infected individual during its entire period of infectiousness. To find R_0 fix S and rewrite the last two equations in (1) as

$$I(t) = e^{-(\tilde{r}+c)t}I(0) + \int_0^t e^{-(\tilde{r}+c)(t-\sigma)}[\tilde{b}qI(\sigma) + \alpha v(\sigma)S + h\frac{SI(\sigma)}{S+I(\sigma)}]d\sigma,$$

$$v(t) = e^{-\delta t}v(0) + \int_0^t e^{-\delta(t-\sigma)}[\beta(1-v(\sigma))\frac{I}{S+I(\sigma)}]d\sigma.$$

The *next-generation operator* (Diekman et al, 1990) defined by the above system is given by

$$\begin{pmatrix} \frac{\tilde{b}q+h}{\tilde{r}+c} & \frac{\alpha S}{\tilde{r}+c} \\ \frac{\beta}{S\delta} & 0 \end{pmatrix}.$$

Thus, R_0 is given by the dominant eigenvalue of this matrix, namely

$$R_0 = \frac{1}{2}\left[\frac{\tilde{b}q+h}{\tilde{r}+c} + \sqrt{\left(\frac{\tilde{b}q+h}{\tilde{r}+c}\right)^2 + 4\frac{\alpha\beta}{\delta(\tilde{r}+c)}}\right].$$

With this parameter defined, the usual threshold condition holds (Diekmann et al, 1990):

$R_0 > 1 \Leftrightarrow$ *the parasite will increase in the population when initially rare.*

Notice that the matrix depends on S but R_0 does not. However the corresponding eigenvector does depend on S, and it will be affected if S grows or decreases. The analysis of this case of variable population is treated in section 3.

For the moment we discuss R_0. Notice that if there is no vectorial transmission ($\alpha\beta = 0$), the disease may spread to an endemic level only because of the action of horizontal and vertical transmission. In this case we have

$$R_0 = \frac{\tilde{b}q + h}{\tilde{r} + c}.$$

If, on the other hand, q and h are zero (i.e., the disease is transmitted only by host-vector contact), we have

$$R_0 = \sqrt{\frac{\alpha\beta}{\delta(\tilde{r} + c)}}.$$

3 Assuming the total host population not in equilibrium.

We deal now with the case of a variable human population. As was mentioned in the introduction, Chagas' disease prevails in a region characterized by high demographic growth rates. Thus we do not impose any condition on $P'(t)$ and define

$$x = \frac{S}{P}, \qquad y = \frac{I}{P}$$

as the proportion of susceptibles and infectives in the population respectively. Thus we obtain a new transformed system of equations

$$\begin{aligned} x' &= -\alpha v x + (c + \tilde{b}p)y - (h - \tilde{\alpha})xy, \\ y' &= -(c + \tilde{b}q)y + \alpha v x + (h - \tilde{\alpha})xy, \end{aligned}$$

We can reduce the above to a single equation for y using $x + y = 1$ to obtain

$$\begin{aligned} y' &= \alpha v - (\alpha v + c + \tilde{b}p - h + \tilde{\alpha})y - (h - \tilde{\alpha})y^2, \\ v' &= \beta(1 - v)y - \delta v. \end{aligned} \tag{4}$$

Recall that exponential solutions to (1) correspond with equilibria in (4) and that we define an exponential solution of (1) as stable if the corresponding stationary point in (4) is stable (Hadeler, 1989). By looking at (4) we can readily see that we have to consider two cases determined by the relative strength of the horizontal transmission rate h. Notice that $h = \tilde{\alpha}$ cancels out the quadratic nonlinearity in (4). Thus we could say, based on the information provided by this model, that blood transfusion transmission has a more important effect in the overall epidemiology of Chagas' disease than vertical transmission. As we will see, vertical transmission plays a relatively modest role in the determination of the

nature of the endemic equilibrium. Notice also that the condition $h = \tilde{\alpha}$ states that the growth rate and the horizontal transmission rate exactly compensate and thus is qualitatively equivalent to the case where h is negligible and the birth and removal rates of susceptibles and infectives are equal. Moreover, as we will see below, $\tilde{\alpha}$ works as a threshold for h: if $h \leq \tilde{\alpha}$ the disease is mainly driven by the vectorial transmission while if the opposite inequality holds, disease dynamics is controlled by h.

To begin the analysis we consider first the case $\tilde{\alpha} = h$. In this case the equation for y in (4) reduces to

$$y' = \alpha v - (\alpha v + c + \tilde{b}p)y.$$

The unique endemic equilibrium point is given by

$$v^* = \frac{\alpha\beta - \delta(c + \tilde{b}p)}{\alpha\delta + \beta}, \qquad y^* = \frac{\alpha v^*}{\alpha v^* + c + \tilde{b}p}. \tag{5}$$

Thus, the ratio $y = I/P$ reaches asymptotically a fixed value if and only if the following threshold condition holds

$$Q = \frac{\alpha\beta}{\delta(c + \tilde{b}p)} > 1.$$

Note that Q does not depend on h. Thus, when $h = 0$ we have

$$R_0 = \frac{1}{2}\Big(\frac{\tilde{b}q}{\tilde{r} + c} + \sqrt{(\frac{\tilde{b}q}{\tilde{r} + c})^2 + 4\frac{\alpha\beta}{\delta(\tilde{r} + c)}}\Big),$$

and $Q > 1$ does not imply $R_0 > 1$. This means that it is possible for the infective agent (*Trypanosoma cruzi*) not to spread into the susceptible population but, nevertheless, the ratio $y = I/P$ is held constant. This case can only happen if P decreases; that is, if the growth rate of I equals (asymptotically), the growth rate of the infective population.

To determine the stability of (5) we first look at the disease-free equilibrium. Here the Jacobian matrix of the system is

$$\begin{pmatrix} -(c + \tilde{b}p) & \alpha \\ \beta & -\delta \end{pmatrix},$$

with trace and determinant

$$-(c + \tilde{b}p) - \delta, \qquad \delta(c + \tilde{b}p) - \alpha\beta$$

respectively. Thus, if $Q \leq 1$ the disease-free equilibrium is locally stable. By applying Dulac's criterion with $\rho = (vy)^{-1}$ and f the right hand side of (4), we see that there cannot be periodic solutions in $\Omega = \{(y, v) \in \mathbf{R}^2 : 0 \leq v, y \leq 1\}$. If, however, $Q > 1$, then it is unstable. Thus, $Q \leq 1$ implies that the disease-free equilibrium is globally asymptotically stable. When $Q > 1$, this implies global asymptotic stability for (5) since, once more, there are no periodic solutions in Ω by the Poincaré-Bendixon Theorem.

Suppose now $\tilde{\alpha} \neq h$. The threshold parameter for this case is

$$Q = \frac{\alpha\beta}{\delta(c + \tilde{b}p - (h - \tilde{\alpha}))}. \tag{6}$$

Notice that if $h \leq \tilde{\alpha}$, Q is always nonnegative and hence well defined (from the biological point of view). However if $h > \tilde{\alpha}$, for h sufficiently large Q becomes negative and the endemic equilibrium always exists. We look at the Jacobian matrix of the system evaluated at the origin

$$\begin{pmatrix} -(c + \tilde{b}p - h + \tilde{\alpha}) & \alpha \\ \beta & -\delta \end{pmatrix},$$

with trace and determinant

$$-a_1 = -(c + \tilde{b}p - h + \tilde{\alpha}) - \delta \qquad a_2 = \delta(c + \tilde{b}p - h + \tilde{\alpha}) - \alpha\beta$$

respectively. Thus, by the Routh-Hurwitz criteria, if $Q > 1$, $(0,0)$ is unstable.

As for the existence of a feasible equilibrium point (v^*, y^*), we see that it must be a solution to the equations

$$v = \frac{y[c + \tilde{b}p - (h - \tilde{\alpha})(1 - y)]}{\alpha(1 - y)}, \quad v = \frac{\beta y}{\delta + \beta y.} \tag{7}$$

The first expression in (7) vanishes at

$$y_a = 0 \qquad\qquad y_b = 1 - \frac{c + \tilde{b}p}{h - \tilde{\alpha}},$$

and it is monotonically increasing for $y > max\{y_a^*, y_b^*\}$. Moreover the function tends to infinity as $y \to 1$. Assume that $h > \tilde{\alpha}$, i. e., blood transfusion transmission is significant. Define

$$\mathcal{B}_T = \frac{h - \tilde{\alpha}}{c + \tilde{b}p}$$

(which we might call *the transfusion threshold*). We have

Lemma 1 *If $\mathcal{B}_T > 1$ the endemic equilibrium point given by (7) always exists and it is unique.*

Remark: $\mathcal{B}_T$ is well defined (i. e., has an epidemiological interpretation) only if $h > \tilde{\alpha}$. Notice that under the condition of Lemma 1, Q plays the main role in the determination of the *existence* of an endemic state of the disease. This happens when blood transfusion transmission is strong ($\mathcal{B}_T > 1$) (more important than vectorial transmission). However, when $\mathcal{B}_T < 1$, h is still important for the transmission process but it is not strong enough as to overshadow the effect of the vector transmission mechanism. In this case Q determines the existence of an endemic state.

We now collect our results in the following

Theorem 1 *Equations (4) possess the following behavior in* $\Omega = \{(y,v) \in \mathbf{R}^2 : 0 \leq y \leq 1, 0 \leq v \leq 1\}$.

1. *If* $\alpha = h$, *there exist a unique endemic equilibrium point that is globally asymptotically stable if* $Q = \dfrac{\alpha\beta}{\delta(c+\tilde{b}p)}$ *is larger than one. The trivial equilibrium is unstable in this case. If, however,* $Q \leq 1$ *then the unique equilibrium point in* Ω *is* $(0,0)$ *and it is globally asymptotically stable.*
2. *If* $h-\tilde{\alpha} > 0$, *and* $\mathcal{B}_T > 1$, *then there exists a unique endemic equilibrium point which is globally asymptotically stable. There is no disease-free state. Also, if* Q *in (6) is greater than one then the endemic equilibrium is globally asymptotically stable and the disease-free equilibrium is unstable. If, on the contrary,* Q *is less than or equal to 1, then* $(0,0)$ *is globally asymptotically stable and unique in* Ω.
3. *If* $h - \tilde{\alpha} < 0$, *and* $Q > 1$ *then the endemic equilibrium is globally asymptotically stable with* $(0,0)$ *unstable. However, if* $Q \leq 1$ *then* $(0,0)$ *globally asymptotically stable and unique.*

Proof. Existence of the endemic equilibrium point under the conditions stated in the Theorem easily follows from (7). To study its stability we compute the Jacobian matrix of the system

$$\begin{pmatrix} -(\alpha v^* + c + \tilde{b}p - h + \tilde{\alpha}) - 2(h-\tilde{\alpha})y^* & \alpha(1-y^*) \\ \beta(1-v^*) & -\beta y^* - \delta \end{pmatrix}.$$

At the origin (except for the case $\mathcal{B}_T > 1$) we obtain

$$\begin{pmatrix} -(c+\tilde{b}p-(h-\tilde{\alpha})) & \alpha \\ \beta & -\delta \end{pmatrix}.$$

If $Q > 1$ the Routh-Hurwitz criteria implies instability. On the other hand if $Q \leq 1$ there is a unique equilibrium point given by the disease-free state which is locally stable. Note that this argument holds both when $h < \tilde{\alpha}$ and when $\mathcal{B}_T < 1$. Now, the stability of the endemic equilibrium is determined in all cases by Q. Indeed, if Q, the Jacobian matrix has negative trace and positive determinant. Defining $\rho(v,y) = (vy)^{-1}$ we see that $\nabla \cdot (\rho f, \rho g)$ is always negative ((f,g) being the right hand side of (4) respectively). Thus by Dulac's criterion no periodic solutions are allowed in Ω and the Poincaré-Bendixon Theorem implies the global asymptotic stability of the endemic state. □

Remark: May and Anderson (1985) explored the form of the basic reproductive number for a directly transmited disease in a growing population. They derived this threshold parameter from a model of an age structured population and concluded that R_0 could be reasonable approximated by the ratio B/A, where B is the reciprocal of the birth rate and A is the mean age of infection. The model analyzed here does not include the effect of age on the dynamics of the disease but still some comparisons are passable. May and Anderson (1985) argued that

even in the case of a growing population, the mean age of infection A can be estimated as

$$A = \frac{1}{\lambda}$$

where λ is the force of infection assumed to be linearly proportional to the proportion of infective individuals. For the model being analyzed here, when there is no vertical nor horizontal transmission, one of the factors of R_0, namely

$$R_h = \sqrt{\frac{\alpha}{c+\tilde{r}}},$$

λ is given by $\sqrt{abm}$. Thus the component of the basic reproductive number that corresponds to the transmission from vector to host has the form computed by May and Anderson (1985) provided α is constant, and $B = \left(\sqrt{(c+\tilde{r})}\right)^{-1}$. As discussed before, α constant roughly corresponds to crowding associated with population growth. When this assumption can not be made, then the parameter m becomes most important for the efficiency of disease transmission and the modeling approach to the disease, and hence the computation of the basic reproductive number, must be refined.

4 Threshold parameters for a growing population

In the previous section we studied how the infective proportions of both vector and host behave through time. We found that there are two thresholds that trigger the existence of endemic steady states. One, $\mathcal{B}_T$, is controlled mainly by the horizontal transmission rate whereas the other Q (expression (6)) depends strongly on the vector infectivity and contact rates. Here we analyze how the actual numbers of infected individuals change as the total population P grows or decreases in size. Some previous studies explore this aspect of disease dynamics (May and Anderson, 1985; Busenberg and van den Driessche, 1990). In particular the work of Busenberg and Vargas (1988) indicates that the number of individuals in the infective compartment and the proportion of infected individuals are related through three parameters controlling the growth of the total population, the existence of a nonzero infected *proportion* of P, and the growth of the infected subpopulation. For the model discussed here, we have found two of them, namely, the basic reproductive number R_0 (derived from the next-generator operator), and the threshold parameter Q which describes the stability of exponential solutions to (1) (through the determination of stability conditions for the proportion $y = I/P$).

Now, rewrite (1) in the following form

$$\begin{aligned} P' &= (b - r - \tilde{\alpha}y^*)P \\ I'(t) &= (\tilde{b}q - \tilde{r} - c + h(1-y^*))I(t) + \alpha v^*(1-y^*)P(t) \end{aligned} \tag{8}$$

by adding the equations defining $S'(t)$ and $I'(t)$, substituting $S = xP$, $I = yP$ and using $x + y = 1$. As in Busenberg and Vargas (1988), we are interested in

knowing whether or not horizontal transmission by itself can maintain the disease in an endemic proportion. In fact, R_0 already provides us with this information by assuming absence of vectorial transmission ($\alpha\beta = 0$). However, we want to reach the same conclusion directly from equation (8) which has the advantage of stressing the role played by blood transfusion transmission.

Suppose that in a very short period of time the infective vectors are removed from the site, e.g., by insecticide spraying. There are two possible responses to the elimination of the vector population which are determined by the relative strength of the horizontal transmission, as we shall see now. Once $v = 0$, we look at the first equation in (4) which becomes

$$y'(t) = -(c + \tilde{b}q - h + \tilde{\alpha})y - (h - \tilde{\alpha})y^2. \tag{9}$$

The equilibrium solutions for this equation are $y^* = 0$ and

$$y^* = 1 - \mathcal{B}_T^{-1}.$$

Thus, if $\mathcal{B}_T > 1$, y^* is positive and an endemic equilibrium exists even in the absence of vectors, as stated in Lemma 1 above. However, if $\mathcal{B}_T < 1$, $y^* \to 0$ and, hence, the new equilibrium state of the system is $(y^*, v^*) = (0,0)$. In this later case, we see that the second equation in (8) becomes

$$I'(t) = (\tilde{b}q - \tilde{r} - c + h)I(t) \tag{10}$$

and the following holds

Proposition 1 *Define the threshold parameter*

$$R_1 = \frac{\tilde{b}q + h}{\tilde{r} + c}.$$

Then, if $\mathcal{B}_T < 1$, the removal of the vectors from the habitat drives the Chagas' disease system to the equilibrium solution $(y^*, v^*) = (0,0)$ with the number of infected individuals in the population increasing or decreasing according to whether $R_1 > 1$ or $R_1 \leq 1$, respectively.

Remark: Note that the basic reproductive ratio R_0 derived from the next-generation operator, can be rewritten as

$$R_0 = \frac{1}{2}\left(R_1 + \sqrt{R_1^2 + 4R_2}\right),$$

where

$$R_2 = \frac{\alpha\beta}{\delta(\tilde{r} + c)}.$$

Notice that if R_2 is exactly one, even a small amount of vertical transmission or blood transfusion will send (slowly) the system to an endemic state. Moreover, it is possible to have $R_0 > 1$ with both ratios R_1 and R_2 less than one.

Also note that the growth of the total population is controlled by the threshold parameter

$$R = \frac{b}{r + \tilde{\alpha} y^*}$$

which implies that as the proportion of infected individuals in the population vanishes, the control of the population dynamics is regained by the usual demographic parameter $r_{net} = b - r$, the intrinsic net rate of population growth. So we have

Proposition 2 *P grows or decreases if $R > 1$ or $R \leq 1$ respectively.*

Remark: The results of this section are essentially the same as those obtained in Busenberg and Vargas (1988) for the case of constant vector population. The important aspect to consider here is that, as Busenberg and Vargas (1988) pointed out, the *number* of infective individuals in the population may increase or decrease independently of the trend in the *proportion* of the population which is sick. Thus, in a growing population, two alternative policies can be pursued towards the control of the disease. One is to reduce the number of individuals infected and the other is to reduce the proportion of individuals infected. They are not equivalent though. If one reduces $y = I/P$ it means that, relative to the growth of the total population, the infected population is small. However, *T.cruzi* can still be spreading in the susceptible population even when $y \to 0$ asymptotically (e.g., if horizontal transmission is sufficiently high I grows). On the other hand, if one tries to reduce I then one must try to get $R_0 < 1$, stopping in this way the spread of the parasite in the host population.

5 Models of the human and wild cycles: Chagas' disease in rural environments.

In the introduction we mentioned that *T. cruzi* has multiple alternative reservoirs in wild animal species that inhabit the surroundings of human settlements. These alternative reservoirs can be grossly subdivided into three cycles: the wild, the domestic and the peridomestic cycles. The first of these is composed of animal species that live exclusively outside human settlements like armadillos, bats, etc (Pinto Dias, 1985). The second is comprised of domestic animals like donkeys, cows, chickens, etc (Bertoglia et al, 1984; Burchard et al, 1984; Pinto Dias, 1985). The third cycle is made up of those opportunistic animals that are able to commute between the wild and domestic environments such as opossums, tejones (*Nasua narica*), cats, and dogs.

5.1 Dynamics of Chagas' disease in wild populations.

The model of this section try to evaluate the importance of the wild cycles as it affects only the animal subsystem independent of the direct action or presence of the human population.

We assume that wild animal populations are not regulated by the disease itself but by density dependent factors. To our knowledge, Chagas' disease is unable to regulate animal numbers in the wild. Wild animals are thus reservoirs for *T. cruzi*. In this section we analyze the dynamics of Chagas' disease in these animals without the interaction with human hosts. The model stands as follows

$$\begin{aligned} S'(t) &= ((b-r)S + \tilde{b}pI)g(T) - \alpha v S, \\ I'(t) &= (\tilde{b}q - \tilde{r})g(T)I + \alpha v S, \\ v'(t) &= \beta(1-v)\frac{I}{S+I} - \delta v. \end{aligned} \tag{11}$$

Here S and I are the number of susceptible and infective hosts respectively, $T = S + I$, and v is the proportion of infective vectors; b, r, $\tilde{b}$ and $\tilde{r}$ are the birth and removal rates of susceptibles and infectives respectively, α is the effective contact rate between vectors and susceptible hosts and the other parameters are as in the previous model. We are assuming that $g(T)$ satisfies $g(T) \geq 0$, if $T \neq T^*$, $g(T^*) = 0$ and $g'(T^*) < 0$.

If we define as always

$$x = \frac{S}{T} \qquad y = \frac{I}{T},$$

we obtain, after using the formula $x + y = 1$, the following equivalent system of equations

$$\begin{aligned} y' &= g(T)(\tilde{\alpha}y - \tilde{\alpha}_q)y + \alpha v(1-y) \\ T' &= g(T))[b - r - \tilde{\alpha}y]T, \\ v' &= \beta(1-v)y - \delta v, \end{aligned} \tag{12}$$

where $\tilde{\alpha} = b - r - \tilde{b} + \tilde{r}$ and $\tilde{\alpha}_q = b - r - \tilde{b}q + \tilde{r}$.

Proposition 3 *Suppose $T'(t) = 0$ for all t. (i) If $T = T^*$, hence $g(T^*) = 0$, then $(y^*, v^*) = (1, \frac{\beta}{\delta+\beta})$ is the unique endemic equilibrium point. (ii) If $y^* = \frac{b-r}{\tilde{\alpha}}$ then there is a unique endemic equilibrium point only if the total population T satisfies the condition*

$$g(T)(\tilde{b}q - \tilde{r})(b-r) = \frac{\alpha\beta(\tilde{b}-\tilde{r})}{\delta+\beta};$$

holds. Otherwise the disease-free equilibrium is unique.

Proof. The proof follows directly from substituting the conditions stated in the hypotheses into the equations for v and y. □

To study the stability of the equilibria we linearize our model around them obtaining the Jacobian matrix

$$\begin{pmatrix} g(T)(2\tilde{\alpha}y - \tilde{\alpha}_q) - \alpha v & g'(T)y(\tilde{\alpha}y - \tilde{\alpha}_q) & \alpha(1-y) \\ -g(T)\tilde{\alpha}T & (g(T) + Tg'(T))(b - r - \tilde{\alpha}y) & 0 \\ \beta(1-v) & 0 & -\delta - \beta y \end{pmatrix}.$$

We analyze only the equilibrium point given in case (1) of Proposition (3) since the other occurs under very restrictive conditions and is biologically unfeasible.

Proposition 4 *Suppose that $b > r$ and $\tilde{b} > \tilde{r}$. Then, the equilibrium point given by $g(T^*) = 0$, $v^* = \dfrac{\beta}{\delta + \beta}$, $y^* = 1$ is asymptotically stable.*

Proof. Evaluating the Jacobian matrix at the non-trivial equilibrium we obtain

$$\begin{pmatrix} -\dfrac{\alpha\beta}{\delta+\beta} & -g'(T^*)(1-q)b & 0 \\ 0 & T^*g'(T^*)(\tilde{b} - \tilde{r}) & 0 \\ \frac{\beta\delta}{\delta+\beta} & 0 & -\delta - \beta \end{pmatrix}.$$

The characteristic values are

$$\lambda_1 = T^*g'(T^*)(\tilde{b} - \tilde{r}), \quad \lambda_2 = -\delta - \beta, \quad \lambda_3 = -\frac{\alpha\beta}{\alpha + \beta}.$$

Since $g'(T^*) < 0$, all three of them are real and negative implying the local asymptotic stability of the equilibrium.

The Jacobian matrix at the disease free equilibrium $(0, T^*, 0)$ is

$$\begin{pmatrix} 0 & 0 & \alpha \\ 0 & g'(T)(b-r) & 0 \\ \beta & 0 & -\delta \end{pmatrix}.$$

A simple calculation shows that this equilibrium is unstable. The theorem is proved. □

As a summary of the findings of this section we have the following

1. The total population converges to the equilibrium density T^* provided both the infective and susceptible subpopulations have positive net growth rate, i.e., $b > r$ and $\tilde{b} > \tilde{r}$.
2. Congenital transmission does not affect the equilibrium's stability.
3. The animal population always reaches the equilibrium state $y^* = 1$, that is, eventually all individuals are infected.

As a general conclusion one can say that the wild cycle of Chagas' disease constitutes a very 'strong' reservoir of *T. cruzi* and that it constitutes a major problem when implementing eradication policies in human populations living in rural habitats. Chagas' disease was in fact a epizootia long before humans

invaded habitats where it is now endemic. In the next section we study models of the coupling of both the human and wild cycles of the disease.

5.2 The human and wild cycles of Chagas' disease: vector-reservoir-host models.

In this section we analyze two different models for the case where both the wild and the human cycles are coupled. This case constitutes the most common situation in endemic regions in Latin America. Through the models, we evaluate, from a theoretical perspective, the relative importance of modes of transmission, the effect of the population dynamics of reservoirs on the stability properties of equilibria, and identify parameters that are important in the existence, uniqueness and stability properties of endemic and disease-free states. Throughout this section we make the assumption that no vertical transmission occurs in either population and that the birth rates of both susceptible and infective subpopulations are equal.

Infective reservoirs with removal rate independent of population density.

The first model of the coupling of the wild and human cycles assumes that Chagas' disease induces a removal rate independent of the removal rate produced by crowding. In this case the model stands:

$$\begin{aligned}
S_0' &= b_0 T_0 - (r_0 + \alpha_0 v) S_0 + \gamma I_0 - h\frac{S_0 I_0}{T_0};\\
I_0' &= -(\tilde{r}_0 + \gamma) I_0 + \alpha_0 v S_0 + h\frac{S_0 I_0}{T_0};\\
S_1' &= b_1 g(T_1) T_1 - r_1 S_1 - \alpha_1 v S_1;\\
I_1' &= -r_1' I_1 + \alpha_1 v S_1;\\
v' &= a(c_0\frac{I_0}{T_0} + c_1\frac{I_1}{T_1})(1 - v) - \delta v
\end{aligned} \tag{13}$$

where, for $i = 0, 1$ $T_i = S_i + I_i$,. All other symbols have the same meaning as in the previous model. To simplify the analysis assume also that $r_0 = r_{0,}$, $r_1 = r_1'$, but $h > 0$; that is, horizontal transmission rate is not negligible. Fixing S_0 and S_1, the next-generation matrix of (13) in this case is given by

$$\begin{pmatrix}
\frac{h}{\tilde{r}_0 + \gamma} & 0 & \frac{\alpha_0 S_0}{r_0' + \gamma}\\
0 & 0 & \frac{\alpha_1 S_1}{r_1'}\\
\frac{ac_0}{\delta S_0} & \frac{ac_1}{\delta S_1} & 0
\end{pmatrix}.$$

Note that the submatrix

$$\begin{pmatrix} 0 & \frac{\alpha_1 S_1}{r_1'} \\ \frac{ac_1}{\delta S_1} & 0 \end{pmatrix}$$

represents the interaction vector-reservoir and has dominant eigenvalue

$$R_w = \sqrt{\frac{ac_1\alpha}{\delta r_1}}.$$

If there were no reservoirs, the next-generation matrix would describe the interaction human host-vector and, consequently, the dominant eigenvalue would be given by

$$R_0 = \frac{1}{2}\Big[\frac{h}{r_0'+\gamma} + \sqrt{\Big(\frac{h}{r_0'+\gamma}\Big)^2 + 4\frac{\alpha_0 a c_0}{\delta(r_0'+\gamma)}}\Big].$$

which is exactly the same basic reproductive number obtained for model (1) in section 2 (here we are assuming no vertical transmission). Thus, heterogeniety in host type determines the following cases

1. $R_0 > 1$, $R_w > 1$, the disease spreads in both host populations.
2. $R_0 > 1$, $R_w < 1$ or $R_0 < 1$, $R_w > 1$, the population spreads only in one host population (the one with the reproductive number greater than one).
3. $R_0 < 1$, $R_w < 1$, the disease dies out. There is no endemic state.

Again, we see that the basic dominant eigenvalue of the next-generation operator does not depend on either S_0 or S_1. However, the associated eigenvector does. To study the behavior of the system when both host populations are variable through time we proceed as follows:

Changing variables in (13) to $x_i = S_i/T_i$, and $y_i = I_i/T_i$, and using $x_i + y_i = 1$ we obtain the equivalent system

$$\begin{aligned} y_0' &= \alpha_0 v + [h - b_0 - \alpha_0 v - \gamma]y_0 - h y_0^2 \\ y_1' &= \alpha_1 v - (\alpha_1 v + b_1 g(T_1))y_1 \\ T_1' &= (b_1 g(T_1) - r_1)T_1 \\ v' &= a(c_0 y_0 + c_1 y_1)(1-v) - \delta v. \end{aligned} \tag{14}$$

The existence of equilibria depends on the fullfillment of the feasibility condition:

$$\frac{h}{b_0 + \alpha_0 v + \gamma} < 1.$$

From the equation for y_1 we obtain that, at equilibrium,

$$y_1 = \frac{\alpha_1 v}{\alpha_1 v + g(T_1)}. \tag{15}$$

Thus, if there exist a T^* such that $g(T^*) = 0$, then $y_1^* = 1$, and we would have similar equilibrium levels as in the previous model. However, at equilibrium, the equation for T_1 implies that

$$\frac{b_1 g(T_1)}{r_1} = 1 \tag{16}$$

Thus, such T^* does not exist since $\dfrac{b_1 g(T^*)}{r_1} = 0$. From the equations for y_0 and v, one can see that if (15) and (16) hold, there exist a unique non-trivial equilibrium point for (14) besides the trivial equilibrium.

To study the stability properties of the equilibria, we obtain the Jacobian matrix of the system. At the endemic equilibrium it is given by

$$\begin{pmatrix} -(b_0+\gamma+\alpha_0 v^*)+h & 0 & 0 & \alpha_0(1-y_0^*) \\ 0 & -r_1-\alpha_1 v & -b_1 y_1^* g'(T_1^*) & \alpha_1(1-y_1^*) \\ 0 & 0 & b_1 T_1^* g'(T_1^*) & 0 \\ ac_0(1-v^*) & ac_1(1-v^*) & 0 & -\delta - a(c_0 y_0^* + c_1 y_1^*) \end{pmatrix}.$$

Notice that one real negative eigenvalue is given by $\lambda_1 = b_1 T_1^* g'(T^*)$ since $g'(T_1^*) < 0$. The others can be extracted from the submatrix obtained by deleting the third row and third column of the Jacobian matrix. This matrix has negative diagonal elements, and all off-diagonal entries are non-positive. Thus, the system is locally asymptotically stable in a small neighborhood of the endemic equilibrium.

On the other hand, the Jacobian matrix at the disease-free state is given by

$$\begin{pmatrix} -(b_0+\gamma) & 0 & 0 & \alpha_0 \\ 0 & 0 & 0 & \alpha_1 \\ 0 & 0 & b_1 T_1^* g'(T_1^*) & 0 \\ ac_0 & ac_1 & 0 & -\delta \end{pmatrix}.$$

It has one eigenvalue equal to $b_1 T_1^* g'(T_1^*)$ which is real and negative. The others are given by the polynomial

$$\lambda^3 + (b_0+\gamma)\lambda^2 + \big((b_0+\gamma)\delta - (\alpha_0 ac_0 - \alpha_1 ac_1)\big)\lambda + (b_0+\gamma)\alpha_1 ac_1.$$

Applying Descartes' rule of signs to the above and to the polynomial obtained by the change of variable $\tilde{\lambda} = -\lambda$, one sees that there is exactly one negative root if

$$Q^* = \frac{a(\alpha_0 c_0 - \alpha_1 c_1)}{(b_0+\gamma)\delta} > 1.$$

If this condition holds, the Routh-Hurwitz criteria implies that the other two roots do not have negative real part. Hence it is unstable. If on the contrary

$$\frac{a\alpha_1 c_1}{(1-Q^*)\delta(b_0+\gamma+\delta)} < 1 \tag{17}$$

and $Q^* < 1$, the Routh-Hurwitz criterion implies the local asymptotic stability of the disease-free state.

To interpret the above relations, define the product $\alpha\beta = \alpha_0 c_0 - \alpha_1 c_1$. If c_0 and c_1 were equal, say $c_0 = c_1$, we would have

$$\bar{\alpha\beta} = \bar{\alpha}\bar{\beta} = (\alpha_0 - \alpha_1)ac_1,$$

and then Q^* can be rewritten as

$$Q^* = \frac{\bar{\alpha}}{b_0 + \gamma} \cdot \frac{\bar{\beta}}{\delta}.$$

Thus, $Q_h^* = \dfrac{\bar{\beta}}{\delta}$ would be the factor of the threshold parameter Q^* corresponding to the transmission host-vector. The other factor,

$$Q_v^* = \frac{\bar{\alpha}}{b_0 + \gamma}$$

that correspond to the transmission from vector to host depends on the difference between the effective biting rates α_i, $i = 0, 1$. Thus, in principle, in this multiple host-one vector interaction where the infectivity c_i, $i = 0, 1$, in both directions is assumed equal, the disease-free equilibrium is unstable only if the 'effective biting rate' from vector to host (α_0) is greater than the 'effective biting rate' from host to vector (α_1). On the other hand, the disease-free state is locally asymptotically stable if (17) holds. To interpret this relation we rewrite it in the following form:

$$Q_h^* \cdot \frac{a}{b_0 + \gamma + \delta} > 1 - Q^*.$$

Thus, the product of the biting rates host-vector, vector-host has to be small (less than one), to prevent an endemic state in the propotion of infective hosts. Note that the dynamics and stability of the *exponential solutions* of the host-reservoir-vector system described by model (1), requires of very strong conditions imposed onto the parameters of the equations.

In the case when $c_1 \neq c_0$, $\bar{\alpha\beta} = \alpha_0 c_0 - \alpha_1 c_1$. If we take the hypothesis on which this model is based as correct, then in the regions where Chagas' disease is endemic $\bar{\alpha\beta}$ is large. This could happen in three ways:

1. If α_0 and α_1 are approximately of the same magnitude, then the infectivity of human blood to the vector is greater that the corresponding infectivity of animal blood, or
2. If the infectivities c_i, $i = 0, 1$ are comparable, then the effective biting rate on humans is greater that the effective biting rate on wild reservoirs.
3. Both α_0 and c_0 are greater than α_1 and c_1.

This is in agreement (at least qualitatively) with data that shows high levels of infestation of houses in endemic zones, that could imply a high overall biting rate on humans (Coura, 1988) provided that the infectivities of reservoirs and human hosts are more ore less equal. Nevertheless, the conditions imposed on the parameters of the model for y^* to be stable are very strong. For example, in the case of $R_0 > 1$ and an increasing human population, the existence of a stable exponential solution requires the disease to spread exponentially on the host population at a rate asymptotically equal to that of the host.

Infective reservoirs with density dependent removal rate.

In the first model we assume that crowding reduces the death rate of the infective reservoirs. With the notation used in the last section the model equations are:

$$\begin{aligned} S_0' &= b_0 T_0 - (r_0 + \alpha_0 v) S_0 + \gamma I_0 - h\frac{S_0 I_0}{T_0}; \\ I_0' &= -(\tilde{r}_0 + \gamma) I_0 + \alpha_0 v S_0 + h\frac{S_0 I_0}{T_0}; \\ S_1' &= g(T_1)(b_1 T_1 - r_1 S_1) - \alpha_1 v S_1; \\ I_1' &= -g(T_1) r_1' I_1 + \alpha_1 v S_1; \\ v' &= a(c_0\frac{I_0}{T_0} + c1\frac{I_1}{T_1})(1 - v) - \delta v \end{aligned} \tag{18}$$

where, for $i = 0, 1$

$$T_i = S_i + I_i.$$

The effect of crowding on I_1 is justified as follows. Let $\tilde{r}_1$ be the removal rate of infective animals. Then $\tilde{r}_1 I_1(t)$ is the number of infective individuals of the reservoir population that are removed at time t. However, we assume that, as the number of individuals in the population increases, crowding becomes the driving force that determines the demography of the population. Thus the term $g(T_1) r_1' I_1$ vanishes as $T_1 \to T_1^*$ $(g(T_1^*) = 0)$.

Now, by defining $x_i = \dfrac{S_i}{T_i}$ and $y_i = \dfrac{I_i}{T_i}$, and, after changing variables using the relation $1 = x_i + y_i$, we obtain the following system of differential equations equivalent to (18),

$$\begin{aligned} y_0' &= \alpha_0 v + [h - B_0 - \alpha_0 v - \gamma] y_0 - (h - \tilde{\alpha}) y_0^2 \\ y_1' &= \alpha_1 v - y_1(g(T_1) B_1 - \alpha_1 v) - g(T_1)(r_1 - \tilde{r}_1) y_1^2 \\ T_1' &= g(T_1) T_1 [b_1 - r_1 - (r_1' - r_1) y_1] \\ v' &= a(c_0 y_0 + c_1 y_1)(1 - v) - \delta v. \end{aligned} \tag{19}$$

In (19) we have defined $B_i = b_i - r_i + \tilde{r}_i$ and $\tilde{\alpha} = \tilde{r}_0 - r_0$.

We consider now the case $h = \tilde{\alpha}$ which makes sense only if $\tilde{r}_0 - r_0$ is positive. Here, the unique feasible equilibrium point is given by

$$(y_0^*, y_1^*, T_1^*, v^*) = \Big(\frac{\alpha_0 v^*}{b_0 + \alpha_0 v^* + \gamma}, 1, T_1^*, a\frac{c_0 y_0^* + c_1}{\delta + a(c_0 y_0^* + c_1)}\Big),$$

where T_1^* is determined by requiring $g(T_1^*) = 0$. Notice that the endemic equilibrium always exists.

In analogy to what we discussed in the last section, $h = \tilde{\alpha}$ is a threshold that determines the qualitative changes that the dynamics of the disease has as function of the horizontal transmission rate. If equality holds, the nonlinearity in the non-vectorial transmission rate of the human population disappears. Note that

the interaction between host and reservoir in the model is indirect through the vector population. Also, the equilibrium density of the total reservoir population can be reached in two ways. One is given by T_1^* such that $g(T_1^*) = 0$. The other is when $y_1^* = \dfrac{b_1 - r_1}{\tilde{r}_1 - r_1}$. The former is compatible with an equilibrium proportion of infected reservoir as can be seen from the third equation in (19). The later is not. Thus, when $T_1 = T_1^*$ (when the reservoir population reaches the steady state determined purely by density dependent effects), we have that $y^* = 1$ is the unique nontrivial (both in the mathematical and biological sense) equilibrium solution for the second equation in (19). Now suppose v is very small. Thus we can approximate y_0 in (19) as

$$y_0' = [h - B_0 - \gamma]y_0 - (h - \tilde{\alpha})y_0^2$$

which is a logistic equation with carrying capacity

$$\mathcal{K} = \frac{h - \tilde{\alpha}}{h - B_0 - \gamma}$$

if $h > \tilde{\alpha}$. Thus, when h is above the threshold $\tilde{\alpha}$, system (14) reaches an stable equilibrium solution close to

$$\left(\mathcal{K}, 1, T_1^*, \frac{a(c_0\mathcal{K} + c_1)}{\delta + a(c_0\mathcal{K} + c_1)}\right).$$

On the other hand if $h < \tilde{\alpha}$ we can not longer neglect v to compute the equilibrium solution for y^*. Thus, in what follows, we assume that h is below the threshold but so close that we can approximate this case by taking $h = \tilde{\alpha}$. Note that the way equilibrium solutions are determined agrees with the known fact of Chagas' disease being a zoonosis that exists (and existed before human invasion of endemic habitats), independently of human hosts (Coura, 1988; Coimbra, 1988).

The disease free equilibrium of (19) is

$$(0, 0, T_1^*, 0).$$

The Jacobian matrix at the endemic equilibrium is given by

$$\begin{pmatrix} -(b_0 + \alpha v^* + \gamma) & 0 & 0 & \alpha_0(1 - y_0^*) \\ 0 & -\alpha_1 v^* & -g'(T_1^*)b_1 & \alpha_1(1 - y_1^*) \\ 0 & 0 & (b_1 - r_1')T_1^* g'(T_1^*) & 0 \\ \alpha_0 c_0(1 - v^*) & ac_1(1 - v^*) & 0 & -\delta - a(c_0 y_0^* + c_1 y_1^*) \end{pmatrix} \tag{20}$$

And at the disease-free equilibrium we have

$$\begin{pmatrix} -(b_0 + \gamma) & 0 & 0 & \alpha_0 \\ 0 & 0 & 0 & \alpha_1 \\ 0 & 0 & (b_1 - r_1)T_1^* g'(T_1^*) & 0 \\ ac_0 & ac_1 & 0 & -\delta \end{pmatrix}$$

which is practically the same as the disease-free state for model (19). Consequently the same discusion and conclusion holds and will not be repeated here. To determine the stability properties of each of the above Jacobians we make use of results on monotone systems (Smith, 1988), in particular, well known results on the theory of M-matrices (Berman and Plemmons, 1979). Let A be the Jacobian matrix (20). One can see immediately that two eigenvalues are given by

$$\lambda_1 = (b_1 - r_1')g(T_1^*)T_1^* \qquad \lambda_2 = -\alpha_1 v^*$$

which are real and negative. The remaining eigenvalues may be analyzed by looking at the submatrix

$$\begin{pmatrix} -(b_0 + \alpha v^* + \gamma) & 0 & \alpha_0(1 - y_0^*) \\ 0 & -\alpha_1 v^* & \alpha_1(1 - y_1^*) \\ \alpha_0 c_0(1 - v^*) & ac_1(1 - v^*) & -\delta - a(c_0 y_0^* + c_1 y_1^*) \end{pmatrix}.$$

We know that one eigenvalue of this matrix is $-\alpha_1 v$. However, the submatrix provides us with better information. It has non-positive off-diagonal and negative diagonal entries. This implies (Smith, 1988) local stability for the endemic equilibrium point. Moreover, in a small neighborhood of $(y_0^*, y_1^*, T_1^*, v^*)$, there are no attracting periodic orbits and, hence, local asymptotic stability can be guaranteed.

6 Conclusions

The main difference between the results concerning model (1) of this paper and those in Busenberg and Vargas (1988) resides in the definition and properties of the basic reproductive number R_0 and the threshold parameter Q (6). Here the fact that v is not assumed to be constant produces, when coupled with the process of horizontal transmission, a new threshold parameter, $\mathcal{B}_T$ that measures the strength of the horizontal transmission and controls the existence of a disease-free state. Remember that if $\mathcal{B}_T > 1$, no matter how effective the vector control measures might be, the disease will always be endemic and sutained by blood transfusion transmission. Recall that the above results depend largely on comparing h, the horizontal transmission rate, and $\tilde{\alpha}$ which has been called the *net fitness loss caused by the infection* (Busenberg and Vargas, 1988). To interpret this relation suppose that $S(0)$ is the number of susceptible individuals at the beginning of our observation. For a moment take $\tilde{b} = \tilde{r}$. Then $S(0)e^{-(\tilde{b}-\tilde{r})t} = S(0)e^{-\tilde{\alpha}t}$ is the number of original susceptible individuals still susceptible at time t. On the other hand $S(0)e^{-ht}$ is the expected number of susceptibles remaining at time t if horizontal transmission where the only possible removal mechanism. If h were so large as to make this last number less than that of the former, we have that the existence gf the endemic state is determined by $\mathcal{B}_T$. Now, when $\tilde{b} > \tilde{r}$, then $S(0)e^{-(\tilde{b}-\tilde{r})t} < S(0)e^{-\tilde{\alpha}t}$ which reflects the fact that infective individuals contribute to the recruitment rate of susceptibles thus

enhancing the survival rate. However $h > \tilde{\alpha}$ means that the mean time to infection by blood transfusion of a susceptible individual is still shorter than the life expectancy.

The models for the interaction of vector-host-reservoirs has important implications regarding the endemic equilibrium of the disease. The most important one is that, considered as a system, the vector-host-reservoir interaction does not allow the existence of a unique disease-free state. The endemic equilibrium always exists and the stability properties of the disease-free equilibrium depend on the relative strength of the interactions vector-host and vector-reservoir. As discussed in the text, the disease-free state is ejective if the effective biting rate of vector on humans is greater that the corresponding one on animal reservoirs. This seems to imply that human host are more efficient transmitors of the infection to the insects that bite them, than the wild animals are, at least in the highly endemic regions of Latin America. This conclusion holds for both models, regardless on the assumption made on the action of crowding effects on the animal population. In fact, the robustness of the endemic equilibrium (it always exists and it is locally asymptotically stable) is determined mainly by the population and disease dynamics of the reservoirs. With the first mechanism of density regulation, the endemic state in the animal populations is given by $y_1^* = 1$. In the second, this level is not reached but, nontheless, the qualitative dynamics of the system is practically the same.

In rural communities the main mode of transmission is through vector bites. Moreover, the effective contact rate $\alpha = abm$ is high mainly because a, the number of bites per unit time, is high and because the ratio m is also high. Since, as discussed at the end of Section 3, we have found that in the case of vector transmitted diseases the component of the basic reproductive number that corresponds to the transmission from vector to host has the form B/A, where

$$A = \frac{1}{\alpha},$$

we see that the mean age of infection, roughly given by A, corresponds to children. Notice that in the case where $h > \tilde{\alpha}$ some interesting changes in the form of the basic reproductive number occur. When horizontal transmission is strong ($h > \tilde{\alpha}$), the mean age of infection shifts from childhood (when vectorial transmission is the main infection process characterized high values of $\alpha = abm$) to late adolescence or early adulthood (when these individuals may become recipients of infected blood characterized by small values of $h - \tilde{\alpha}$) as reflected by the parameter $\mathcal{B}_T$. Thus, according to the analogy discussed in Section 3, the higher the contact rate α, would mean the younger the children newly infected. Recall that this age group is also the one with the highest mortality during the acute phase of the disease (Moncayo, 1986). In urban communities, however, the trend may be interpreted as being reversed. In this case blood transfusion transmission would be the main transmission mechanism which is controlled by the parameter $\mathcal{B}_T$. In this case the mean age of infection would be roughly given by

$$A = \frac{1}{h - \tilde{\alpha}}.$$

Thus in an urban population the age group with the higher prevalence of Chagas' disease is not fixed and depends on the strength of the blood transfusion transmission. If $h - \tilde{\alpha}$ is small, the adult population would be the most affected and, as h increases, the mean age of infection through blood transfusion shifts towards the younger age classes.

To conclude, I would like to mention that Chagas' disease is a consequence of poverty. Modes of transmission and the characteristics of its epidemiology are simply the reflection of a sad socioeconomic reality.

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