Nonlinear Analysis: Real World Applications 13 (2012) 1379–1390

Contents lists available at SciVerse ScienceDirect

Nonlinear Analysis: Real World Applications

journal homepage: www.elsevier.com/locate/nonrwa

Does co-infection with malaria boost persistence of trypanosomiasis?

B. Nannyonga, J.Y.T. Mugisha *, L.S. Luboobi

Department of Mathematics, Makerere University, P.O. Box 7062 Kampala, Uganda

ARTICLE INFO

Article history:
Received 14 April 2010
Accepted 2 November 2011

Keywords:
Malaria
Trypanosomiasis
Co-infection
Invasibility
Co-existence

ABSTRACT

A mathematical model for the interaction of malaria and trypanosomiasis is developed to determine whether the endemicity of malaria increases persistence of trypanosomiasis. In this study, we have allowed protection against both diseases by incorporating parameters ϕ_t and ϕ_m in the model. Results indicate that protection against trypanosomiasis reduces prevalence of the disease. In this case, the tsetse fly will have to bite more for the disease to prevail, that is, $\frac{d}{N}\uparrow$. However, presence of malaria increases the persistence of trypanosomiasis in the population. The reduction in trypanosomiasis prevalence as the malaria basic reproduction number is increased indicates a reduced number of contacts with the tsetse fly when the individual has malaria.

1. Introduction

Human African Trypanosomiasis (sleeping sickness) is a vector-borne disease caused by protozoan parasites. It is a major health threat to rural poor several African countries and kills over 60,000 people every year [1]. Trypanosomiasis is endemic in 36 countries in Sub-Saharan Africa but its epidemiological status is poorly understood [2]. The parasites responsible for causing Trypanosomiasis belong to a group of closely related trypanosomes in the *Trypanosoma brucei* species complex, which enter the blood stream via the bite of blood feeding tsetse flies *Glossina species*. The disease exists in chronic form, caused by *Trypanosoma brucei gambiense* and acute form caused by *Trypanosoma brucei rhodesiense* [3]. The tsetse fly can acquire these parasites by feeding on infected animals or infected human individuals. The fly remains infective for life which makes human/fly contact a crucial component of the disease. With increasing parasite drug-resistance, and mosquito insecticide-resistance, malaria has been making a comeback in many parts of the world. The burden of malaria is not favored by the increasing number of malaria co-infections with many other killer diseases such as trypanosomiasis. Co-infections with malaria often lead to complications and severe cases for parasitic diseases and these co-infections have long been recognized as major contributors to anemia in endemic countries, where severe anemia accounts for up to one half of the malaria-attributable deaths in children younger than 5 years of age [4].

Trypanosomiasis, like malaria is a vector-borne protozoal disease which disproportionately affects the poor giving rise to immense human suffering. Malaria exerts its effect directly on human health, while trypanosomiasis causes damage largely through its effect on the health and productivity of the livestock on which so many poor people depend [5]. Both diseases are poorly understood combined with complex life cycles characterized by multiple stages in both the spreading vectors and human host with incubation periods ranging from weeks to months [6]. After the incubation period, the clinical symptoms are similar such as intermittent fever that correlates with high or low levels of parasitemia, headache, sleep disturbance, palsies, eventually invading the central nervous system with months to years of chronic infection. In acute infections, both diseases lead to coma and are usually fatal. Trypanosomiasis parasites are very hard to treat especially when the parasites have reached the central nervous system [7]. This renders a co-infection of trypanosomiasis with malaria so severe that the chances of treatment may be minimal to none.

* Corresponding author.
E-mail address: jytmugisha@math.mak.ac.ug (J.Y.T. Mugisha).

1468-1218/$ – see front matter © 2011 Elsevier Ltd. All rights reserved.
doi:10.1016/j.nonrwa.2011.11.002

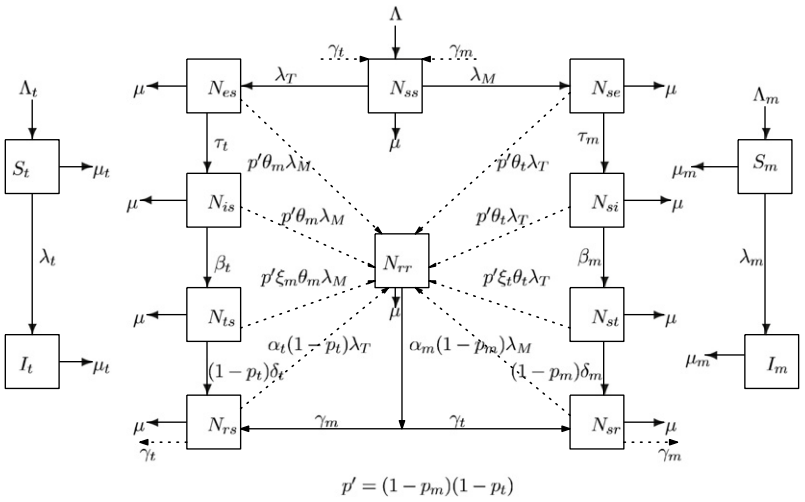

Fig. 2.1. Compartmentalized model for the co-infection.

Recently, multi-pathogen/multi-host mathematical models have been developed to track the dynamics of pathogen interactions over immuno-ecological landscapes. These models stem from the fact that competition between infecting pathogens is fundamental to disease evolution. The role of cross-immunity between two different strains of *leishmania* was studied and found that the basic reproduction number decreased as cross-immunity increased, [8]. It was also concluded that reducing the basic reproduction number to less than unity is not enough to eradicate the disease when there is partial cross-immunity. In most cases, diseases have been shown to die out eventually if the basic reproduction number is less than unity, [9–11]. In some *SIR* models, pulse vaccination and distributed time delay are sufficient for the eradication of the disease, [12]. In *leishmania* however, human treatment would help in controlling the disease, especially if its in synergy with vector control [13], although in some control models, complex dynamics including period-doubling bifurcation, chaos and strange attractors have been shown, [14].

This body of past work makes clear that related and unrelated pathogens can potentially interact through a variety of immunological and ecological mechanisms, many of which share common dynamical outcomes. However, a systematic study of the interaction between malaria and trypanosomiasis is still lacking. In this paper, a mathematical model to study the effects of endemic malaria on the persistence of trypanosomiasis is developed. This model is to determine whether presence of malaria in the population increases persistence of trypanosomiasis. We formulate the model in Section 2. It is analyzed and simulated in Section 3 and the results are discussed and summarized in Section 4.

2. Model formulation

The model is a *SEIR* based on [15–17]. In this framework, an individual is categorized according to their infection status and passes sequentially through the series of susceptible, exposed, infectious and recovered classes. Ecological interactions between the pathogens such as the period of convalescence [18,19], or disease-induced mortality as in [20], are incorporated in addition to immune-mediated interactions such as co-infection [21], cross-immunity [22], or cross-enhancement [23] and immunosuppression. In the model, it is assumed that there is a constant recruitment into the population through births and immigration, and all the new recruits are susceptible to both infections (see Fig. 2.1).

In this setup, an individual becomes infected with malaria or trypanosomiasis after being bitten by an infected mosquito or tsetse fly. Once infected with trypanosomiasis or malaria, the individual becomes exposed but not infectious and has a relatively high probability of contracting malaria or trypanosomiasis simultaneously, governed by the co-infection parameter θ_i, $i = t, m$. After the latent period, the individual becomes infectious and has the same chance of being infected by the other disease. Upon displaying clinical symptoms, the disease is diagnosed and the individual is sent for recovery for an average period of $\frac{1}{\delta_i}$, but may contract the other disease at a modulated rate ξ_i. If $0 \leq \xi_i < 1$, the recovery process represents a reduced contact rate or reduced susceptibility. If $\xi_i > 1$, then the recovery process may represent immunosuppression via increased susceptibility. During the recovery process, the individual may not survive and succumb to the infection.

The chance of survival is represented by $1 - p_i$ where p_i is the per capita infection-induced mortality probabilities of disease i. It is assumed that disease-induced mortality occurs late in infection. Upon recovery from the first infection, the individual is assumed temporarily immune to the infection but remains susceptible to the second infection if not previously exposed to it. The term α_i explores the implications of long-lasting cross immunity if $\alpha_i < 1$ or immunosuppression if $\alpha_i > 1$, for the transmission rate of disease i following infection with disease j. We further assume that due to cross-immunity and cross-enhancement, it is the infectiousness rather than susceptibility that is altered. Therefore, introducing a parameter