ABSTRACT

We study a new model for co-infection of malaria and HIV/AIDS. It is a simplified version of the mathematical model proposed by Chiyaka et al in [9] for malaria transmission, where the HIV transmission dynamics is included. Numerical simulations of the model show that increasing the rate at which susceptible humans are infected with HIV translates in an increase of infectious with malaria and with HIV/AIDS humans, of infectious humans with HIV, and of infectious mosquitoes. Additionally, decreasing the susceptibility to acquire AIDS of the HIV infected individually-dually-infected with malaria, comparatively to those infected with HIV only, results in a decrease of the infectious with malaria and HIV/AIDS, and of infectious with only HIV humans, and of infectious mosquitoes. These results suggest that the proposed model is mathematically and epidemiologically well-posed.

KEY WORDS

Mathematical models, malaria, HIV/AIDS, co-infection, epidemiology.

1 Introduction

The interaction between malaria and HIV/AIDS is a two-way communication process, that turns into a huge global public health and economical problem. Regions with limited resources, such as the sub-Saharan Africa, are most affected by morbidity and mortality caused by the co-infection of both diseases [10, 5, 28, 16]. The World Health Organization (WHO) reported that malaria alone, or in combination with other diseases, kills approximately 1.1 to 2.7 million people all over the world, being 2400 million at high risk of infection. The sub-Saharan Africa is the most affected region with one million deaths estimated annually [29].

Implementing selective and sustainable preventive measures, to halt the deterioration of malaria infection, is extremely important. Measures like insecticide-treated materials, such as mosquitoes nets, indoor residual spraying with (DDT) insecticides, and the insect repellent creams, are among those already implemented with a fair success rate. Other measures such as attractive sugar bait methods may be also effective [3]. Chemoprophylaxis is used as a preventive measure in malaria-endemic regions, specially in pregnant women. It helps to decrease the incidence of low birth weight and severe maternal anaemia [2]. Game-toxicical drugs may be important in preventing malaria. An enormous effort has been made, in the context of developing an effective vaccine, over the last few decades [25]. Nevertheless, nowadays, the control of this disease depends heavily on personal protection and chemotherapy [8, 9].

HIV is the human immunodeficiency virus. Infection by the HIV virus causes the immunological system destruction. Prevention of HIV infection is based, mostly, on correctly using a condom during sexual intercourse, disposable needles and syringes.

HIV and malaria co-infection is a major health problem. Malaria severity can be increased by HIV infection [5]. The low CD4+ T cells count in HIV-infected non immune adults, eases their infection with severe malaria [10]. Co-infection of malaria and HIV, in regions where HIV prevalence is high, is believed to have accelerated malaria geographic expansion [1]. On the other hand, malaria, and also tuberculosis, and bacterial infections, are leading causes of HIV-related morbidity in sub-Saharan Africa [19]. The HIV-1 viral load is higher in patients with malaria than in controls [18, 20]. Moreover, in some patients viral load is reduced with antimalarial therapy [18].

The impact of co-infection of malaria and HIV in risk groups, such as children and pregnant women, has also been studied. In children, HIV infection was associated with severe malaria and the aggravation of neurodevelopmental impairments [15, 24]. Nevertheless, other factors, such as malnutrition or micronutrient deficiencies, may also explain the severity of symptoms. Other diseases, such as pneumonia and measles have also been found to be aggravated by HIV infection [21]. In pregnant women, HIV infection aggravates the typical malaria risk pattern, being more extreme, with higher intensity of parasitaemia (placental and peripheral infection and parasite density), and more frequent [27].

In the co-infection of malaria and HIV/AIDS, there are still some issues that need to be clarified. Namely, mother-to-child transmission of HIV, the effects of co-infection on post-neonatal infant morbidity and mortality,
and the influence of malaria on the clinical course of HIV infection [6]. In the later, overlap of symptoms of the two diseases increases the difficulties in defining AIDS stage and in diagnosing patients at risk of co-infection. Evaluation of HIV-infected patients, with a broad spectrum of symptoms, in endemic malaria regions, should take into account malaria infection [5]. Additionally, opportunistic infection prophylaxis type and timing may be region specific [19].

In this paper, we present a mathematical model for co-infection of malaria and HIV/AIDS. It adds, to a simplified version of the model proposed in [9] for malaria transmission, the dynamics of HIV/AIDS transmission. Our goal is to simulate the effects of co-infection of malaria and HIV/AIDS infection on a population of susceptible individuals, where personal protection strategies and vaccination against malaria are implemented. This is an update to the model proposed in Pinto et al [26].

The paper is organized as follows. The model is described in Section 2. Simulation results are presented in Section 3. In Section 4, we state the main conclusions from this work and list future research work.

2 The model for malaria and HIV/AIDS co-infection

The proposed model adds, to a simplified version of the model proposed in [9] for malaria transmission, the dynamics of HIV/AIDS transmission. Our goal is to simulate the effects of co-infection of malaria and HIV/AIDS infection on a population of susceptible individuals, where personal protection strategies and vaccination against malaria are implemented. This is an update to the model proposed in Pinto et al [26].

2.1 Description of the model

We consider two populations: human and mosquitoes. The human population is divided in ten classes, and mosquitoes’ population consists of three classes.

We denote by $N_h(t)$ the total number of individuals in the human population. It is given by $N_h(t) = S_h(t) + V_h(t) + E_h(t) + I_h(t) + Y_h(t) + I_{m_{hiv}}(t) + I_{m_{mhiv}}(t)$, where $\{S_h(t), V_h(t), E_h(t), I_h(t), Y_h(t), I_{hiv}(t), I_{mhiv}(t)\}$ represent, respectively, the numbers of {Susceptibles, Vaccinated, Exposed, Infectious with malaria only, Infectious with HIV only, Infectious with both malaria and HIV} humans.

The total number of individuals in the mosquitoes population, $N_v(t)$, is given by $N_v(t) = S_v(t) + E_v(t) + I_v(t)$, where $\{S_v(t), E_v(t), I_v(t)\}$ denote, respectively, the numbers of {Susceptibles, Exposed, Infectious} mosquitoes.

Figure 1 shows the natural progression of the disease. The rate at which new individuals enter the human population by immigration or by birth is $\Lambda_h$. Susceptible humans acquire malaria infection at a rate $f_h(t)$, given by:

$$f_h(t) = \beta_h c (1 - b z) \frac{I_m(t)}{N_h(t)}$$

(1)

where $\beta_h$ is the probability that a susceptible human is infected after being bitten by an infectious mosquito and $c$ is the rate of female mosquitoes’ bites. Infected susceptible humans move to the exposed class $E_h(t)$. Individual protection is modeled by $(1 - \zeta)$, where $0 < \zeta \leq 1$ measures the efficacy of adopted strategies for individual protection, and $0 < b \leq 1$ is the proportion of individuals in the community that use this protection strategy. Protection of successfully vaccinated humans may be only partial, and therefore they may develop disease at a rate $f_h(t)(1 - \gamma)$, where $0 \leq \gamma \leq 1$ is the efficacy of the vaccine pre-erythrocytic. Eventually, immunity induced by vaccination decreases to zero, and thus vaccinated individuals move to the susceptible class at a rate $\sigma$. Infectious humans may recover at a rate $r_h$ and become susceptibles, or even die from infection at a rate $\alpha_h$. Analogous behavior is described for infectious vaccinated humans, $Y_h$. They recover at a rate $\theta_h r_h$, or die from disease at a rate $(1 - \theta_h) \alpha_h$. Effects of the erythrocytic vaccine in increasing recovery and in reducing mortality due to disease are modeled by parameters $\theta_1 \geq 1$ and $0 < \theta_2 \leq 1$, respectively. Vaccinated humans $V_h$ individuals do not recover.

Parameter $\beta_{h_{hiv}}$ represents the probability of a susceptible human to be infected with the HIV/AIDS virus. Infectious humans with both malaria and HIV/AIDS, $I_{m_{hiv}}$, recover from malaria at a rate $\phi_2$ and enter the class $I_{hiv}$, or they may die from malaria infection at a rate $\phi_{h1}$, and from AIDS at a rate $\alpha_{h2}$. Infectious with only malaria humans, $I_h(t)$, are infected with the HIV/AIDS virus and enter the $I_{m_{hiv}}$ class at a rate $\epsilon_2 \beta_{h_{hiv}}$, where $\epsilon_2$ defines HIV infected individuals dually-infected with malaria that progress to AIDS at a faster rate, compared to those infected with HIV only. The infectious humans with only HIV/AIDS, $I_{hiv}$, are those that recover from malaria infection by individuals dually-infected with HIV/AIDS and malaria at a rate $\phi_2$, and those susceptible individuals that are infected with the HIV virus at a rate $\beta_{h_{hiv}}$. Individuals in this class acquire malaria infection and enter the class $I_{m_{hiv}}$ at a rate $\nu f_h(t)$, where $\nu > 1$ accounts for the assumed increase in susceptibility to malaria infection as a result of HIV infection. Infectious HIV humans may also die from infection with HIV at a rate $\alpha_{h2}$ or from natural death at a rate $\mu_h$. The class of treated humans, considered in the model proposed in [9], was ignored. Treatment of malaria is not considered in this model. We also do not distinguish between individuals infected with HIV and presenting AIDS symptoms from individuals infected with HIV and with no AIDS symptoms.

In what concerns the mosquitoes population, it is assumed that the susceptible mosquitoes are recruited, at a constant rate $\Lambda_m$. All mosquitoes are subjected to a natural death, which occurs at a rate of $\mu_m$. Susceptibles mosquitoes, $S_m$, are infected by the Anopheles parasite at
a rate \( f_m(t) \), given by:

\[
f_m(t) = \beta_m c(1-bz) \frac{I_m(t) + I_{mhiv}(t) + (1-\epsilon)Y_h(t)}{N_h(t)}
\]

(2)

The transmission dynamics of the mosquitoes population is described as follows. Susceptible mosquitoes are recruited at a constant rate \( \Lambda_m \). Mosquitoes in every class are subjected to a natural death, which occurs at a rate \( \mu_m \). The rate \( f_m(t) \) at which susceptibles mosquitoes, \( S_m \), get infected by the malaria parasite is given by:

\[
f_m(t) = \beta_m c(1-bz) \frac{I_m(t) + I_{mhiv}(t) + (1-\epsilon)Y_h(t)}{N_h(t)} \]

(3)

where \( \beta_m \) is the probability that a mosquito is infected after having bitted a susceptible human, carrying infectious gametophytes. Vaccine efficacy in blocking disease transmission is modeled by parameter \( \epsilon \in [0, 1] \). Susceptible infected mosquitoes move to the exposed class, and become infectious after a time period \( \tau_m \). There is an increase in the mosquitoes mortality rate, due to the presence of the parasite in their body at a rate \( \alpha_m \), which translates in a non recovering [9].

The system of delay differential equations for the proposed model is the following:

3 Numerical simulations

In this section, we present numerical simulations of model (4), for variation of parameters \( \Lambda_{hi} \) and \( \beta_{hiv} \) and \( \epsilon_2 \). The simulations were performed using XPPAUT [14].

For increasing values of \( \epsilon_2 \), the values of \( I_{mhiv}(t) \) (Figure 4), \( I_{hiv}(t) \) (Figure 5), \( Y_h(t) \) and \( I_m(t) \) increase. The values of \( S_h(t) \), \( V_h(t) \), \( I_h(t) \) and \( S_m(t) \) decrease.

The parameter values used in the simulations for model (4) can be found in Table 1 and initial conditions are \( N_h(t) = 450 \), \( S_h(t) = 300 \), \( V_h(t) = 100 \), \( I_h(t) = 5 \), \( I_{mhiv}(t) = 5 \), \( I_{hiv}(t) = 5 \), \( Y_h(t) = 5 \), \( N_m(t) = 480 \), \( S_m(t) = 430 \), \( I_m(t) = 20 \).

4 Conclusion

In this paper we propose a mathematical model for co-infection of malaria and HIV/AIDS. It is obtained by
Adding the HIV/AIDS dynamics to a simplified version of the model, proposed in [9], for malaria transmission. Numerical simulations have been performed for the model. Increasing the rate at which susceptible humans are infected with HIV translates in an increase of infectious with malaria and with HIV/AIDS humans, of infectious humans with HIV, and of infectious mosquitoes. Decreasing the susceptibility to acquire AIDS of the HIV infected individuals dually-infected with malaria, comparatively to those infected with HIV only, results in a decrease of the infectious with malaria and HIV/AIDS, of infectious with only HIV humans, and of infectious mosquitoes. These results suggest that the two proposed models are mathematically

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Table 1. Parameters used in the numerical simulations of model (4).

Figure 3. Number of infectious humans with HIV for variation of the parameter $\beta_{hiv}$ ($\beta_{hiv} = 0.0005$ and $\beta_{hiv} = 0.002$).

Figure 4. Number of infectious humans with malaria and HIV for variation of the parameter $\epsilon_2$ ($\epsilon_2 = 1$ and $\epsilon_2 = 3$).
Figure 5. Number of infectious humans with HIV for variation of the parameter $\epsilon_2$ ($\epsilon_2 = 1$ and $\epsilon_2 = 3$).

and epidemiologically well-posed.

Future work will consider adding the effects of genetics in the immunity against malaria transmission and the effects of seasonality.

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References


