

# Mathematical Model for the Transmission of *P. Falciparum* and *P. Vivax* Malaria along the Thai-Myanmar Border

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**Abstract**—The most Malaria cases are occur along Thai-Mynmar border. Mathematical model for the transmission of *Plasmodium falciparum* and *Plasmodium vivax* malaria in a mixed population of Thais and migrant Burmese living along the Thai-Myanmar Border is studied. The population is separated into two groups, Thai and Burmese. Each population is divided into susceptible, infected, dormant and recovered subclasses. The loss of immunity by individuals in the infected class causes them to move back into the susceptible class. The person who is infected with *Plasmodium vivax* and is a member of the dormant class can relapse back into the infected class. A standard dynamical method is used to analyze the behaviors of the model. Two stable equilibrium states, a disease-free state and an epidemic state, are found to be possible in each population. A disease-free equilibrium state in the Thai population occurs when there are no infected Burmese entering the community. When infected Burmese enter the Thai community, an epidemic state can occur. It is found that the disease-free state is stable when the threshold number is less than one. The epidemic state is stable when a second threshold number is greater than one. Numerical simulations are used to confirm the results of our model.

**Keywords**—Basic reproduction number, Burmese, local stability, *Plasmodium Vivax* malaria.

## I. INTRODUCTION

MALARIA occurs throughout the tropical and subtropical regions of the world. This disease is a mosquito-borne disease caused by the protozoan parasites of the genus *Plasmodium*. Malaria is due to four species, *P. falciparum*, *P. vivax*, *P. malariae* and *P. ovale*. The two most common malaria infections are caused by the first two: *P. falciparum*, which causes 90% of the malaria in Africa and is the cause of over 2-3 million (mostly child) cases in the world (mainly Africa) [1]; and *P. vivax*, which is the cause of 50% of the malaria outside of Africa. Less than two percent of the infections are due to mixed infection by *P. vivax* and *P. falciparum* together. *P. vivax* and *P. ovale* differ from the other species [2,3,4] in that at the sporozoite stage and after they move to the liver, some of them are transformed into

hypnozoites. Most of these are then transformed into merozoites, which invade the red blood cells where they cause the illness. The remaining hypnozoites lie dormant in the liver for varying lengths of time (up to 3 years). The relapse of malaria occurs when some of these hypnozoites are transformed into schizonts and then into merozoites. They can reinvade the blood stream and cause the illness to recur. Between the relapses of the illness, only small number of the merozoites remains in the blood. *P. vivax* and *P. ovale* seldom cause the death of the human host.

Due to the differences in economic conditions between Thailand and Myanmar, temporary migration of Burmese into Thailand occurs every year. More than 60% of the Burmese in some groups (in Mae Sot and Bo Basi, two provinces in Thailand along the border) are infected with mefloquine-resistant malaria[5]. These economic migrations from neighboring countries into Thailand have caused problems for the malaria control program in Thailand [6]. Especially troubling is multi-drug resistance malaria, the presence of which is now seen in the high transmission areas around the market centers along the migratory routes. The first cases of malaria resistance were found along the Thai-Kampuchean border, another border where the economic conditions on the two sides are again quite different. It is believed that the areas where the parasites have the highest drug resistance are along this latter border. The medical records for malaria in Thailand [7] indicate that most of the malaria infections in Thailand are due to *P. falciparum* and *P. vivax*. The most foreigner cases are Burmese. The data also show that a small number of people are infected with *P. malariae* and a small number have been infected by both *P. falciparum* and *P. vivax*. There is no report of an infection due to *P. ovale*.

To reduce the outbreak of Malaria in Thailand, a new mathematical model should be introduced to anticipate what the response would be to a plan of action when there are two different forms of malaria in co-circulation in a population. It was long assumed that strategies for handling *P. vivax* could be extrapolated from those used against *P. falciparum*. This assumption was challenged at a conference convened by the Multilateral Initiative on Malaria [8]. The transmission of malaria is usually described by the Ross-MacDonald (RM) model [9]. However, the RM model is only suitable for the transmission of *P. falciparum* malaria since it does not address possible relapses of the illness. One of the present authors (IMT) has introduced a simple mathematical model [10] to

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describe the transmission of *P. vivax* malaria. In that model, a dormant class was included in which there are no merozoites in the blood, only dormant hypnozoites in the liver. A person becomes ill when the hypnozoites are re-activated. He does not have to be bitten by an infected mosquito again.

In this study, we formulate a model in which different mathematical models are used to describe the separate transmissions between *P. falciparum* and *P. vivax*. Ethically, there is no place for human experimentation to see what would happen if new therapies were adopted. Mathematical modeling allows one to simulate what could occur. Since we are interested in applying the model to the situation along the Thai-Myanmar border (and to a lesser extent the Thai-Kampuchean border), we have allowed the rates of infections to differ if the infecting malaria is *P. falciparum* (denoted by 'f') or *P. vivax* (denoted by 'v') or if the person is a Thai (denoted by T) or a Burmese (denoted by B). In section 2, we introduce a modification of the model that would make it applicable to the transmission of *P. falciparum* and *P. vivax* between Thai and Burmese. In Section 3, we analyze our model to find the conditions for the local stability of each equilibrium point. Numerical simulations are shown to confirm the local stability of the endemic equilibrium point.

## II. TRANSMISSION MODEL

In 1911, Ross formulated the mathematical model of the epidemiology of malaria (*P. falciparum*) [11] and improved by MacDonald [12]. In the Ross model, an individual in the human population is classified as being in a non-infected or infected state. MacDonald proposed that the human population should instead be divided into three states - non-infected, infected but without any acute clinical signs, infected with acute clinical signs - to reflect the clinical status of the individual better. Others believe that the population should be divided into susceptible, infected but not infectious and infectious.

In our model, we consider the transmission cycle between humans in the two populations and in the vector populations. Both human populations (Thai and Burmese) are divided into susceptible, infected, dormant and recovered subclasses. The vector population is separated into susceptible and infected subclasses [13]. We let

- $\tilde{S}_T(t)$  is the number of susceptible Thai humans,
- $\tilde{S}_B(t)$  is the number of susceptible Burmese humans,
- $\tilde{I}_T(t)$  is the number of infected Thai humans,
- $\tilde{I}_B(t)$  is the number of infected Burmese humans,
- $\tilde{D}_T(t)$  is the number of dormant Thai humans,
- $\tilde{D}_B(t)$  is the number of dormant Burmese humans,
- $\tilde{R}_T(t)$  is the number of recovered Thai humans,
- $\tilde{R}_B(t)$  is the number of recovered Burmese humans,
- $\tilde{S}_v(t)$  is the number of susceptible vectors,
- $\tilde{I}_v(t)$  is the number of infected vectors,

An infectious human can recover and re-enter the susceptible class. Only the recovered humans who were

infected with *P. vivax* are susceptible to further infections. However, an infected mosquito cannot recover. We define  $\lambda N_T$  as the number of Thais entering the susceptible class through birth and  $r_{5F} \tilde{I}_T(t)$  and  $r_{5V} \tilde{I}_T(t)$  as, respectively, the numbers of infected Thais who were infected with *P. falciparum* or *P. vivax* malaria but have recovered. The rate at which susceptible Thais are lost by becoming infected with *P. falciparum* is  $\gamma'_{hFT} \tilde{I}_v(t) \tilde{S}_T(t)$  and by becoming infected with *P. vivax* is  $\gamma'_{hvT} \tilde{I}_v(t) \tilde{S}_T(t)$ . A susceptible Thai will be infected by the *P. falciparum* (*P. vivax*) parasite if bitten by a mosquito carrying the particular parasite. To take this into account, the infection rates,  $\tilde{I}'_{hFT}$  and  $\tilde{I}'_{hvT}$ , should be proportional to the fraction of the infected mosquitoes with the particular type of parasite. Additional increases in the number of people infected with *P. vivax* malaria occur when the members of the dormant class relapse.

The rate of change of the number of susceptible members is equal to the number entering minus the number leaving. This gives us the following differential equation for the rate of change of the susceptible Thai human population:

$$\begin{aligned} \frac{d}{dt} \tilde{S}_T(t) = & \lambda N_T - \alpha \tilde{r}_{1T} \tilde{I}_T(t) - \mu_h \tilde{S}_T(t) - (\gamma'_{hFT} + \gamma'_{hvT}) \tilde{I}_v(t) \tilde{S}_T(t) \\ & + (r_{1F} + r_{1V}) \tilde{I}_T(t) + r_{3V} \tilde{D}_T(t) + r_{4V} \tilde{R}_T(t) \end{aligned} \quad (1)$$

$$\begin{aligned} \frac{d}{dt} \tilde{I}_T(t) = & (\gamma'_{hFT} + \gamma'_{hvT}) \tilde{I}_v(t) \tilde{S}_T(t) - (r_{1F} + r_{1V}) \tilde{I}_T(t) \\ & - \mu_h \tilde{I}_T(t) - (r_{5F} + r_{5V}) \tilde{I}_T(t) + r_{2V} \tilde{D}_T(t) \end{aligned} \quad (2)$$

$$\frac{d}{dt} \tilde{D}_T(t) = \alpha \tilde{r}_{1T} \tilde{I}_T(t) - (r_{2V} + r_{3V} + \mu_h) \tilde{D}_T(t) \quad (3)$$

$$\frac{d}{dt} \tilde{R}_T(t) = (r_{5F} + r_{5V}) \tilde{I}_T(t) - (r_{4V} + \mu_h) \tilde{R}_T(t) \quad (4)$$

$$\begin{aligned} \frac{d}{dt} \tilde{S}_B(t) = & (1-P)B - \alpha \tilde{r}_{1B} \tilde{I}_B(t) - (\tau + \mu_h) \tilde{S}_B(t) \\ & - (\gamma'_{hFB} + \gamma'_{hvB}) \tilde{I}_v(t) \tilde{S}_B(t) + (r_{1F} + r_{1V}) \tilde{I}_B(t) + r_{3V} \tilde{D}_B(t) + r_{4V} \tilde{R}_B(t) \end{aligned} \quad (5)$$

$$\begin{aligned} \frac{d}{dt} \tilde{I}_B(t) = & PB + (\gamma'_{hFB} + \gamma'_{hvB}) \tilde{I}_v(t) \tilde{S}_B(t) - (r_{1F} + r_{1V}) \tilde{I}_B(t) \\ & - (\tau + \mu_h) \tilde{I}_B(t) - (r_{5F} + r_{5V}) \tilde{I}_B(t) + r_{2V} \tilde{D}_B(t) \end{aligned} \quad (6)$$

$$\frac{d}{dt} \tilde{D}_B(t) = \alpha \tilde{r}_{1B} \tilde{I}_B(t) - (r_{2V} + r_{3V} + \mu_h + \beta) \tilde{D}_B(t) \quad (7)$$

$$\frac{d}{dt} \tilde{R}_B(t) = (r_{5F} + r_{5V}) \tilde{I}_B(t) - (\beta + r_{4V} + \mu_h) \tilde{R}_B(t) \quad (8)$$

where the parameters are defined as follows.  $\mu_h$  is the death rate in the human population,

- $\alpha$  is the percentage of infected humans in whom some hypnozoites remain dormant in the liver,
- $r_{1F}$  is the rate at which a person infected with *P. falciparum* leaves the infected class,
- $r_{1V}$  is the rate at which a person infected with *P. vivax* leaves the infected class,
- $r_{2V}$  is the rate at which the dormant human relapses back to the human infected by *P. vivax*,
- $r_{3V}$  is the recovery rate of the dormant human due to *P. vivax*,
- $r_{4V}$  is the rate at which the human recovered after *P. vivax* infection relapses back to the susceptible human,
- $r_{5F}$  is the rate at which the human infected by *P. falciparum* recovers,
- $r_{5V}$  is the rate at which the human infected by *P. vivax* recovers,
- $\tau$  is the rate at which Burmese move out the country,
- $P$  is the percentage of Burmese who are infectious when they enter the community,
- $B$  is the constant recruitment rate of Burmese.

We assume that *P. falciparum* and *P. vivax* infections are non-lethal, so the death rates will be the same for all human classes and we will have  $N_T = \tilde{S}_T + \tilde{I}_T + \tilde{D}_T + \tilde{R}_T$  and  $N_B = \tilde{S}_B + \tilde{I}_B + \tilde{D}_B + \tilde{R}_B$ .

The dynamics of the mosquito populations are given by

$$\frac{d}{dt} \tilde{S}_V(t) = A - \mu_V \tilde{S}_V(t) - ((\gamma'_{v_{TF}} + \gamma'_{v_{TV}}) \tilde{I}_T(t) + (\gamma'_{v_{BF}} + \gamma'_{v_{BV}}) \tilde{I}_B(t)) \tilde{S}_V(t) \tag{9}$$

$$\frac{d}{dt} \tilde{I}_V(t) = ((\gamma'_{v_{TF}} + \gamma'_{v_{TV}}) \tilde{I}_T(t) + (\gamma'_{v_{BF}} + \gamma'_{v_{BV}}) \tilde{I}_B(t)) \tilde{S}_V(t) - \mu_V \tilde{I}_V(t) \tag{10}$$

At equilibrium, the total number of female mosquitoes will be  $A/\mu_V$ .  $A$  is the rate at which the mosquitoes are recruited and  $\mu_V$  is the death rate of the mosquitoes.  $\gamma'_{v_{TF}}, \gamma'_{v_{TV}}, \gamma'_{v_{BF}}$  and  $\gamma'_{v_{BV}}$  are the rates at which the mosquitoes become infected with the parasites (*P. falciparum* (F) and *P. vivax* (V)) once the mosquito has bitten an infected human (Thai (T) and Burmese (B)).

We also assume  $N_V = \tilde{S}_V + \tilde{I}_V$ . The working equations of the model are obtained by dividing (1), (2), (3) and (4) by  $N_T$ , (5), (6), (7) and (8) by  $N_B$  and (9) and (10) by  $A/\mu_V$ . This would give us ten equations expressed in terms of the renormalized variables:

$$S_T = \frac{\tilde{S}_T}{N_T}, I_T = \frac{\tilde{I}_T}{N_T}, D_T = \frac{\tilde{D}_T}{N_T}, R_T = \frac{\tilde{R}_T}{N_T},$$

$$S_B = \frac{\tilde{S}_B}{(B/(\tau + \mu_h))}, I_B = \frac{\tilde{I}_B}{(B/(\tau + \mu_h))}, D_B = \frac{\tilde{D}_B}{(B/(\tau + \mu_h))},$$

$$R_B = \frac{\tilde{R}_B}{(B/(\tau + \mu_h))}, S_V = \frac{\tilde{S}_V}{(A/\mu_V)}, I_V = \frac{\tilde{I}_V}{(A/\mu_V)}$$

where  $N_B = \frac{B}{\tau + \mu_h}, N_V = \frac{A}{\mu_V}$ .

Conditions  $S_T + I_T + D_T + R_T = 1, S_B + I_B + D_B + R_B = 1$  and  $S_V + I_V = 1$ , lead to only seven of these being independent. We choose the seven independent equations to be

$$\frac{d}{dt} S_T(t) = \mu_h(1 - S_T(t)) - \alpha r_{1V} I_T(t) - (\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_V(t) S_T(t) + (r_{1F} + r_{1V}) I_T(t) + r_{3V} D_T(t) + r_{4V} (1 - (S_T(t) + I_T(t) + D_T(t))) \tag{11}$$

$$\frac{d}{dt} I_T(t) = (\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_V(t) S_T(t) - (r_{1F} + r_{1V}) I_T(t) - \mu_h I_T(t) - (r_{5F} + r_{5V}) I_T(t) + r_{2V} D_T(t) \tag{12}$$

$$\frac{d}{dt} D_T(t) = \alpha r_{1V} I_T(t) - (r_{2V} + r_{3V} + \mu_h) D_T(t) \tag{13}$$

$$\frac{d}{dt} S_B(t) = (1 - P)(\tau + \mu_h) - \alpha r_{1V} I_B(t) - (\tau + \mu_h) S_B(t) - (\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_V(t) S_B(t) + (r_{1F} + r_{1V}) I_B(t) + r_{3V} D_B(t) + r_{4V} (1 - (S_B(t) + I_B(t) + D_B(t))) \tag{14}$$

$$\frac{d}{dt} I_B(t) = P(\tau + \mu_h) + (\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_V(t) S_B(t) - (r_{1F} + r_{1V}) I_B(t) - (\tau + \mu_h) I_B(t) - (r_{5F} + r_{5V}) I_B(t) + r_{2V} D_B(t) \tag{15}$$

$$\frac{d}{dt} D_B(t) = \alpha r_{1V} I_B(t) - (r_{2V} + r_{3V} + \mu_h + \tau) D_B(t) \tag{16}$$

and

$$\frac{d}{dt} I_V(t) = ((\gamma_{v_{TF}} + \gamma_{v_{TV}}) I_T(t) + (\gamma_{v_{BF}} + \gamma_{v_{BV}}) I_B(t)) (1 - I_V(t)) - \mu_V I_V(t) \tag{17}$$

where the new transmission rates are

$$\begin{aligned} \gamma_{h_{FT}} &= \gamma'_{h_{FT}} (A / \mu_v), \gamma_{h_{VT}} = \gamma'_{h_{VT}} (A / \mu_v), \\ \gamma_{h_{FB}} &= \gamma'_{h_{FB}} (A / \mu_v), \gamma_{h_{VB}} = \gamma'_{h_{VB}} (A / \mu_v) \\ \gamma_{v_{TF}} &= \gamma'_{v_{TF}} N_T, \gamma_{v_{TV}} = \gamma'_{v_{TV}} N_T, \\ \gamma_{v_{BF}} &= \gamma'_{v_{BF}} \left( \frac{B}{\beta + \mu_h} \right), \gamma_{v_{BV}} = \gamma'_{v_{BF}} \left( \frac{B}{\beta + \mu_h} \right) \end{aligned} \tag{18}$$

The domain of solutions is

$$\begin{aligned} \Omega = \{ & (0 \leq S_T + I_T + D_T + R_T \leq 1, 0 \leq S_B + I_B + D_B + R_B \leq 1, \\ & 0 \leq S_v + I_v \leq 1) \} \end{aligned} \tag{19}$$

At this point, we should mention that (14) and (15) contain an explicit dependence on P, the percentage of Burmese entering Thailand who are infected with the malaria parasite. These are the people who will be responsible for malaria epidemics along the Thai-Myanmar border.

### III. ANALYTICAL RESULTS

To find the equilibrium points, we set the RHSs of (11) to (17) to zero. This yields the equilibrium state

$(S_T^*, I_T^*, D_T^*, S_B^*, I_B^*, D_B^*, I_v^*)$  where

$$S_T^* = \frac{D_T^* r_{3v} + I_T^* (r_{1f} + (1-\alpha)r_{1v} - r_{4v}) + r_{4v} (1 - D_T^*) + \mu_h}{r_{4v} + (\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + \mu_h} \tag{20}$$

$$D_T^* = \frac{\alpha I_T^* r_{1v}}{r_{2v} + r_{3v} + \mu_h} \tag{21}$$

$$S_B^* = \frac{(\tau + \mu_h)(1-P) + D_B^* r_{3v} + I_B^* (r_{1f} + r_{1v} (1-\alpha) - r_{4v}) + r_{4v} (1 - D_B^*)}{(\tau + (\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* + \mu_h + r_{4v})} \tag{22}$$

$$D_B^* = \frac{\alpha I_B^* r_{1v}}{\tau + r_{2v} + r_{3v} + \mu_h}, \tag{23}$$

$$\begin{aligned} I_T^* &= \frac{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* (\mu_h + r_{4v})}{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + r_{4v} + \mu_h} \\ &= \left[ \frac{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* ((1-\alpha)r_{1v} + r_{4v} + r_{1f})}{\mu_h + r_{1f} + r_{1v} - \frac{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* ((1-\alpha)r_{1v} + r_{4v} + r_{1f})}{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + r_{4v} + \mu_h}} + (r_{5f} + r_{5v}) \right. \\ &\quad \left. - \frac{\alpha r_{1v} r_{2v}}{r_{2v} + r_{3v} + \mu_h} - \frac{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* \alpha r_{1v} (r_{3v} + r_{4v})}{((\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + \mu_h + r_{4v})(r_{2v} + r_{3v} + \mu_h)} \right] \end{aligned} \tag{24}$$

$$\begin{aligned} I_B^* &= \frac{(\beta + \mu_h)P + \frac{(\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* ((1-P)(\tau + \mu_h) + r_{4v})}{(\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* + \mu_h + r_{4v} + \tau}}{\left[ \frac{(\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* (r_{1f} + (1-\alpha)r_{1v} - r_{4v})}{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + \mu_h + r_{4v} + \tau} + (r_{5f} + r_{5v}) \right.} \\ &\quad \left. - \frac{\alpha r_{1v} r_{2v}}{\mu_h + (r_{2v} + r_{3v}) + \tau} - \frac{(\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* \alpha r_{1v} (r_{3v} - r_{4v})}{((\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* + \mu_h + r_{4v})(\tau + \mu_h + r_{2v} + r_{3v})} \right] \end{aligned} \tag{25}$$

and  $I_v^*$  being the solutions of

$$\begin{aligned} & \mu_v I_v^* - (1 - I_v^*) ((\gamma_{h_{FT}} + \gamma_{h_{VT}}) (\gamma_{v_{TF}} + \gamma_{v_{TV}}) I_v^* (\mu_h + r_{4v})) / ((\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* \\ & + \mu_h + r_{4v}) (\mu_h + r_{1f} + r_{1v} - \frac{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* (r_{1f} + (1-\alpha)r_{1v} - r_{4v})}{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + \mu_h + r_{4v}} + r_{5f} + r_{5v} \\ & - \frac{\alpha r_{1v} r_{2v}}{\mu_h + r_{2v} + r_{3v}} - \frac{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) \alpha r_{1v} (r_{3v} + r_{4v})}{((\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + \mu_h + r_{4v})(\mu_h + r_{2v} + r_{3v})} \\ & \left. \left( \left( \gamma_{v_{BF}} + \gamma_{v_{BV}} \right) (\tau + \mu_h) P + \frac{(\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* (\tau - \mu_h + (\tau + \mu_h) P - r_{4v})}{\tau + (\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* + \mu_h + r_{4v}} \right) / \right. \\ & \left( \tau + \mu_h + r_{1f} + r_{1v} - \frac{(\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* (r_{1f} + r_{1v} (1-\alpha) - r_{4v})}{\tau + (\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* + \mu_h + r_{4v}} \right. \\ & \left. + r_{5f} + r_{5v} - \frac{\alpha r_{1v} r_{2v}}{\tau + \mu_h + r_{2v} + r_{3v}} - \frac{\alpha (\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* r_{1v} (r_{3v} - r_{4v})}{(\tau + (\gamma_{h_{FB}} + \gamma_{h_{VB}}) I_v^* + \mu_h + r_{4v})(\tau + \mu_h + r_{2v} + r_{3v})} \right) \end{aligned} \tag{26}$$

The solution to (26) will be physically meaningless if it is negative since the normalized infectious mosquito population must be a non-negative real number. So we need to find all possible conditions for  $I_v^*$  to be real and positive. P is in the range [0, 1]. We consider two cases: P = 0 and 0 < P ≤ 1.

For P = 0, (26) becomes

$$\begin{aligned} & I_v^* (\mu_v - (1 - I_v^*) ((\gamma_{h_{FT}} + \gamma_{h_{VT}}) (\gamma_{v_{TF}} + \gamma_{v_{TV}}) (\mu_h + r_{4v})) / ( \\ & ((\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + \mu_h + r_{4v}) \\ & (\mu_h + r_{1f} + r_{1v} - \frac{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* (r_{1f} + (1-\alpha)r_{1v} - r_{4v})}{(\gamma_{h_{FT}} + \gamma_{h_{VT}}) I_v^* + \mu_h + r_{4v}} \\ & + r_{5f} + r_{5v} - \frac{\alpha r_{1v} r_{2v}}{\mu_h + r_{2v} + r_{3v}} \end{aligned}$$

$$\begin{aligned}
 & \left. \left( \frac{(\gamma_{hF_T} + \gamma_{hV_T}) \alpha_{I_v}^* I_v^* (r_{3v} + r_{4v})}{(\gamma_{hF_T} + \gamma_{hV_T}) I_v^* + \mu_h + r_{4v}} \right) \right) \\
 & + \left( \frac{(\gamma_{vBF} + \gamma_{vBF}) (\gamma_{hFB} + \gamma_{hVB}) (\tau - \mu_h - r_{4v})}{\tau + (\gamma_{hFB} + \gamma_{hVB}) I_v^* + \mu_h + r_{4v}} \right) \\
 & \left. \left( \frac{(\tau + \mu_h + r_{1F} + r_{1v})}{(\gamma_{hFB} + \gamma_{hVB}) I_v^* (r_{1F} + r_{1v} (1 - \alpha) - r_{4v})} \right) \right) \\
 & \left. \left( \frac{\alpha_{I_v} r_{2v}}{\tau + \mu_h + r_{2v} + r_{3v}} \right) \right) \\
 & - \left. \left( \frac{\alpha (\gamma_{hFB} + \gamma_{hVB}) I_v^* r_{1v} (r_{3v} - r_{4v})}{(\tau + (\gamma_{hFB} + \gamma_{hVB}) I_v^* + \mu_h + r_{4v}) (\tau + \mu_h + r_{2v} + r_{3v})} \right) \right) \right) \quad (27)
 \end{aligned}$$

One of the solutions of (27) is  $I_v^* = 0$ . The other solutions are the solutions of a quadratic equation. The numerical values of these two solutions will depend on the numerical values of the parameters in the model. These are often unknown. Using standard dynamical analysis (based on the Hopf Bifurcation Theory [14]), we can establish the conditions for the stability of the disease-free state. We find the condition is

$$R_0 < 1 \quad \text{where} \quad R_0 = R_T + R_B \quad (28)$$

with

$$R_T = \frac{(\gamma_{hF_T} + \gamma_{hV_T}) (\gamma_{vTF} + \gamma_{vTV}) (\mu_h + r_{2v} + r_{3v})}{\mu_v (\mu_h^2 + (r_{1F} + r_{5F} + r_{5v}) (r_{2v} + r_{3v}) + r_{1v} (r_{2v} (1 - \alpha) + r_{3v}) + \mu_h (r_{1F} + r_{1v} + r_{2v} + r_{3v} + r_{5F} + r_{5v}))}$$

and

$$R_B = \frac{(\gamma_{hFB} + \gamma_{hVB}) (\gamma_{vBF} + \gamma_{vBV}) (\tau + \mu_h + r_{2v} + r_{3v})}{\mu_v (\tau^2 + \mu_h^2 + (r_{1F} + r_{5F} + r_{5v}) (r_{2v} + r_{3v}) + r_{1v} (r_{2v} (1 - \alpha) + r_{3v}) + (\tau + \mu_h) (r_{1F} + r_{1v} + r_{2v} + r_{3v} + r_{5F} + r_{5v}))} \quad (29)$$

Determining whether the numerical values of the parameters satisfy (28) is not of direct concern to us in this paper. The important thing to remember is that the disease-free state is one of the equilibrium states. This means that in the absence of any infectious Burmese entering Thailand, malaria will not become epidemic in Thailand provided that the values of the parameters lead to the conditions given by (28).

For  $0 < P \leq 1$ , the equilibrium state will not be the disease-free state since the difference between (26) and (27) is the term  $(\gamma_{vBF} + \gamma_{vBV}) (\tau + \mu_h) P$  in (26). If we substitute  $I_v^* = 0$  into (26), all the terms except  $(\gamma_{vBF} + \gamma_{vBV}) (\tau + \mu_h) P$  would vanish, leaving only that term present. Since the term is non zero,  $I_v^* = 0$  can not be a solution to Eqn. (26). For this case, the equilibrium state will

be the epidemic state  $E_1 = (S_T^*, I_T^*, D_T^*, S_B^*, I_B^*, D_B^*, I_v^*)$ . It remains to be determined if this state is stable. Performing an analysis similar to the one used to establish the conditions under which the disease-free state is stable, we find that the epidemic state will be stable if

$$R_E > 1 \quad (30)$$

where  $R_E = \frac{R_{E1}}{R_{E2}}$ ,

with

$$\begin{aligned}
 R_{E1} &= (\tau + (\gamma_{hFB} + \gamma_{hVB}) i_v^* + \mu_h + r_{4v}) \\
 & \quad (\tau + (\gamma_{vBF} + \gamma_{vBV}) i_B^* + (\gamma_{vTF} + \gamma_{vTV}) i_T^* \\
 & \quad + (\gamma_{hFT} + \gamma_{hVT}) i_v^* + \mu_h + \mu_v + r_{1F} + r_{1v} \\
 & \quad + r_{2v} + r_{3v} + r_{4v} + r_{5F} + r_{5v}) \\
 R_{E2} &= (\alpha \alpha_{I_v} r_{2v} + (\gamma_{hFT} + \gamma_{hVT} + \gamma_{hFB} + \gamma_{hVB}) i_v^* \\
 & \quad (r_{1F} + (1 - \alpha) r_{1v} - r_{4v}) + (\gamma_{hFB} + \gamma_{hVB}) \\
 & \quad (\gamma_{vBF} + \gamma_{vBV}) (1 - i_v^*) s_B^* + (\gamma_{hFT} + \gamma_{hVT}) \\
 & \quad (\gamma_{vTF} + \gamma_{vTV}) s_T^* \quad (31)
 \end{aligned}$$

The numerical values of the equilibrium epidemic will again depend on the numerical values of the parameters. Stability analysis of the eigenvalues of dynamical systems will place limits on the values of the parameters that would lead the epidemic state to be stable. Again, what these values are is of no direct concern in this paper. What is known is that the equilibrium state will not be the disease-free state but will instead be the epidemic state. Without infectious Burmese entering the community, there will be no infected population provided the numerical values of the parameters in the model are such that the conditions given by (28) are satisfied.

#### IV. NUMERICAL RESULTS

In this section, we present the results of our numerical simulations for the case of  $P = 0$  in Fig. 1a). The values of the parameters are taken from real life observations. We have set  $\mu_h = 0.0000391$  per day which corresponds to the real life expectancy of 70 years for human, and  $\mu_v = 1/30$ , which corresponds to the life expectancy of 30 days for the Anopheline mosquito. The values  $r_{1F} = 1/20$  per day,  $r_{1v} = 1/14$  per day correspond to the time it takes people who are infected with *P. falciparum* and *P. vivax* to leave the infected class and become susceptible again, i.e., 20 days for *P. falciparum* and 14 days for *P. vivax*. The values  $r_{2v} = 1/365$  per day,  $r_{3v} = 1/(2*365)$  per day correspond to the time it takes people who are infected with *P. vivax* to leave the dormant class, i.e., 1 year to enter the infected class and 2

years to enter the susceptible class. The value  $r_{4v} = 1/(3 \times 365)$  per day corresponds to 3 years for the people who are infected with *P. vivax* to relapse. The values  $r_{5F} = 1/30$  per day,  $r_{5v} = 1/25$  per day correspond to the time it takes people who are infected with *P. falciparum* and *P. vivax* to recover, i.e., 30 days for *P. falciparum* and 25 days for *P. vivax*.  $1/\tau$  is the average time a Burmese stays in Thailand and we take this to be  $\tau = 0.000183$  per day. To have the disease-free state as the stable equilibrium state, we set  $P = 0$ . To have the stable equilibrium state as the epidemic state, we set  $P = 0.6$  [5]. The transmission rates

$\gamma_{h_{FT}}, \gamma_{h_{vT}}, \gamma_{h_{FB}}, \gamma_{h_{vB}}$  are arbitrarily chosen.

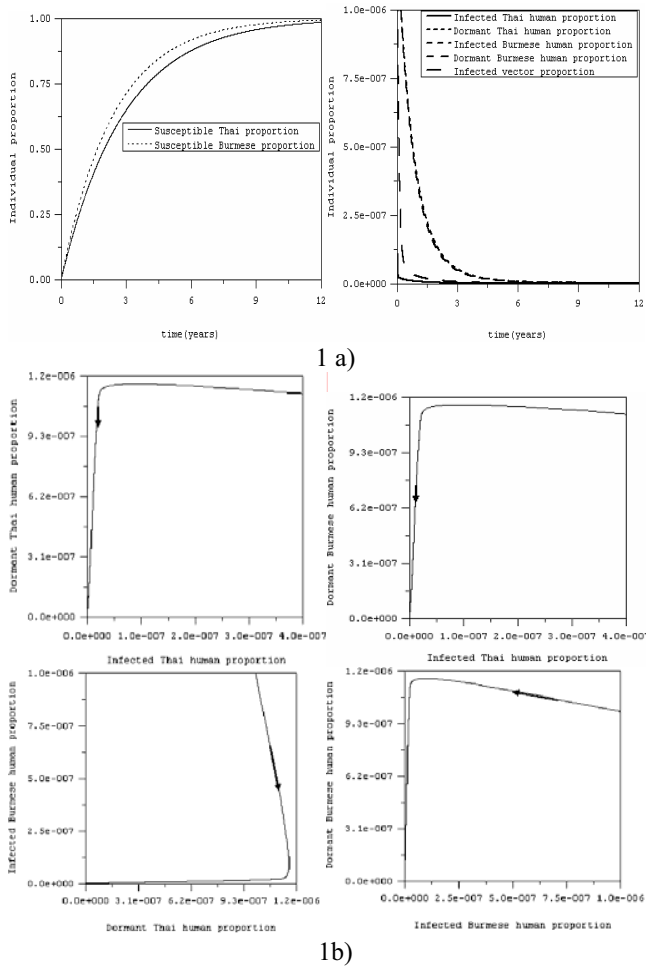


Fig. 1 a) Time series of  $S_T, I_T, D_T, S_B, I_B, D_B$  and  $i_v$ .

The parameters for the transmission rate are as follows:

$$\gamma_{h_{FT}} = 0.025, \gamma_{h_{vT}} = 0.024, \gamma_{h_{FB}} = 0.03, \gamma_{h_{vB}} = 0.019,$$

$$\gamma_{v_{TF}} = 0.03, \gamma_{v_{Tv}} = 0.02, \gamma_{v_{BF}} = 0.035, \gamma_{v_{Bv}} = 0.0225.$$

The other parameters are given in the text, and  $R_0 = 0.9$ .

1b) The solution trajectories of our model. The parameters are similar to fig.1a).

As we see in Fig.1a), the seven populations go to  $(1,0,0,1,0,0,0)$  as  $t \rightarrow \infty$ , meaning that the equilibrium state is the disease-free state. The numerical values of the parameters lead to a threshold number  $R_0 = 0.9$ . The trajectories of the solutions in the 2D:  $D_T - I_T$  plane,  $D_B - I_T$  plane,  $I_B - D_T$  plane and  $D_B - I_B$  plane are shown in Fig. 1b). The arrows in these planes show the directions of the trajectories as  $t \rightarrow \infty$ , which are towards the disease-free state. The numerical simulation is therefore in agreement with the behavior predicted when  $R_0 < 1$ .

We now change the values of the parameters and set  $P = 0.6$ . The values are given in the caption of Fig.2. These values give  $R_E = 98$ . This is the condition for the epidemic state  $E_1 = (S_T^*, I_T^*, D_T^*, S_B^*, I_B^*, D_B^*, I_v^*)$  to be the stable equilibrium state. This is indeed seen in Fig. 2a). The trajectories of the solutions in the 2D:  $D_T - I_T$  plane,  $D_B - I_T$  plane,  $I_B - D_T$  plane and  $D_B - I_B$  plane are shown in Fig. 2b). As  $t \rightarrow \infty$ , the trajectories tend to the limiting values indicated on Fig.2a).

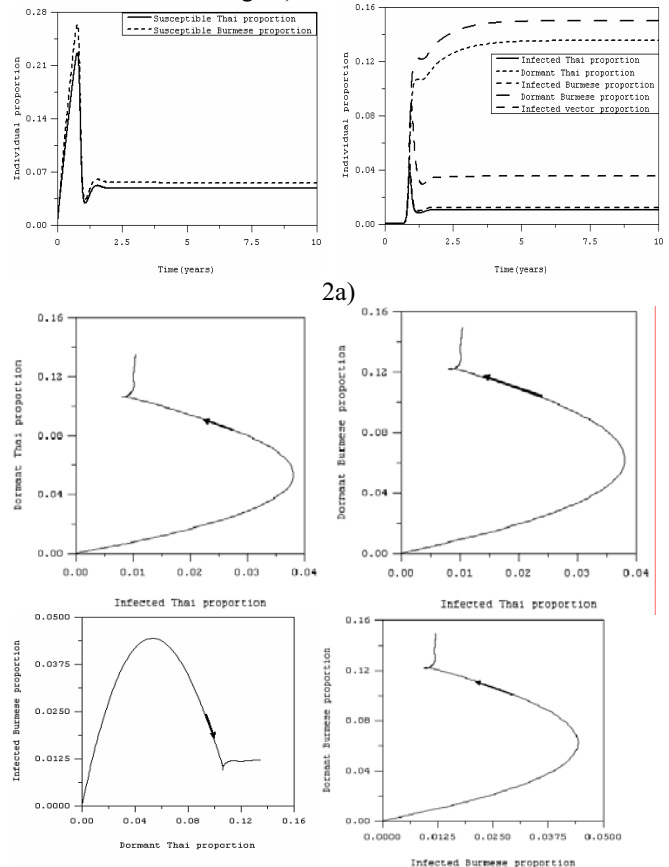


Fig. 2 a) Time series of  $S_T, I_T, D_T, S_B, I_B, D_B$  and  $I_v$ .

The parameters for the transmission rate are as follows:

$$\gamma_{h_{FT}} = 0.51, \gamma_{h_{vT}} = 0.48, \gamma_{h_{FB}} = 0.6, \gamma_{h_{vB}} = 0.4,$$

$$\gamma_{v_{TF}} = 0.03, \gamma_{v_{Tv}} = 0.02, \gamma_{v_{BF}} = 0.035, \gamma_{v_{Bv}} = 0.0225.$$

The other parameters are given in the text, and  $R_E = 98$ .

2b) The solution trajectories of our model. The parameters are similar to fig.2a).

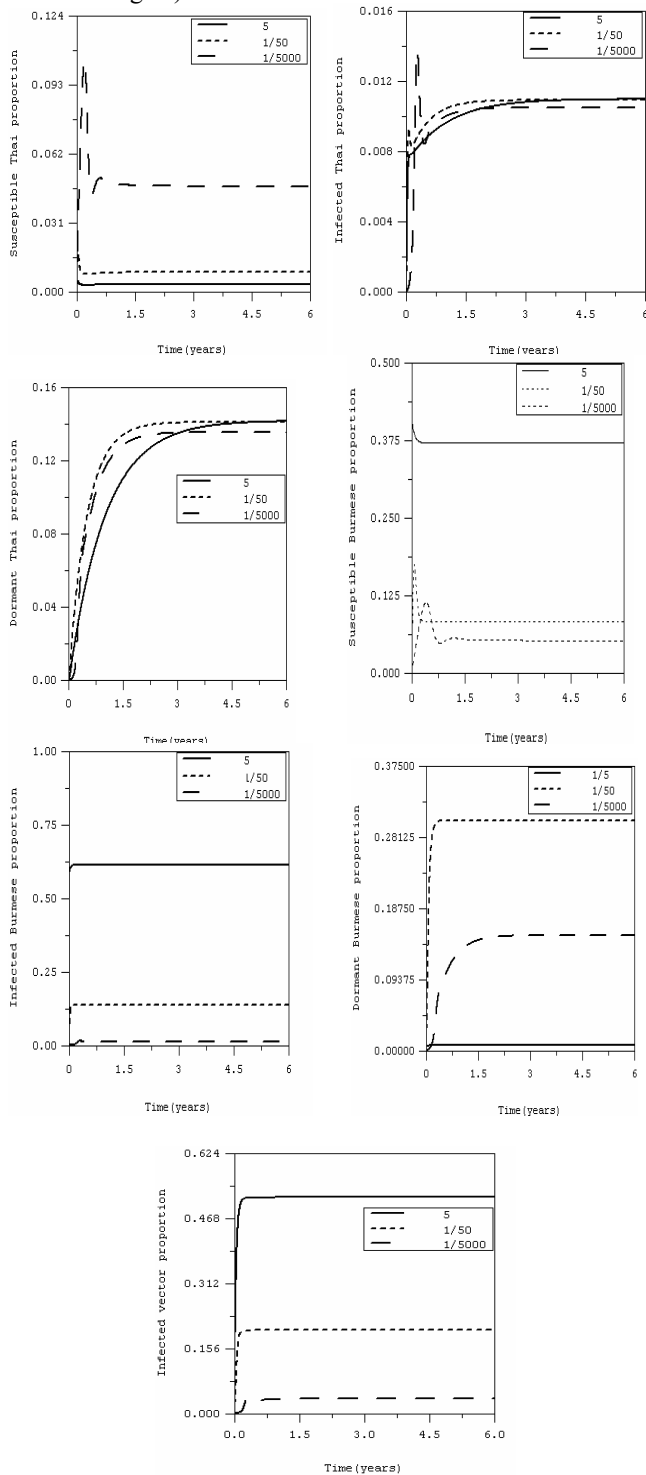


Fig. 3. Time series of  $I_T, I_B$  and  $I_V$  for the different values of  $\tau$ . The values of the other parameters are similar to fig. 2.

In Fig. 3, we plot the time evolution of the three infected population ( $I_T(t)$ ,  $I_B(t)$  and  $I_V(t)$ ) for different values of  $\beta$ , the reciprocal of the time the Burmese stay in Thailand

before they return to Myanmar. The time evolutions of the three populations shown in Fig. 2a) are those when the Burmese stay a long time. The present behaviors are for the case when the Burmese stay 1/5 day, 50 days and 5000 days. Fig. 3 shows that a higher number of Thais will be infected if the Burmese stay in Thailand for shorter periods. If the Burmese stay for longer periods, the number of Thais who are infectious at a given time will be lower. The reason for this is that, initially, the Burmese have a higher incidence rate of active malaria infection. They would be able to pass the illness to the Thais at the beginning. If they stay longer, they would develop the same incidence rate as the Thais and are less likely to pass on the malaria.

### V. DISCUSSION

In this study, we have analyzed a mathematical model of malaria that could describe the situation along the Thai-Myanmar border. Along this border there are two major types of malaria in circulation, *P. falciparum* and *P. vivax*. There is a migration of Burmese into Thailand. We find that there are two equilibrium states, a disease-free state and an epidemic state. We establish the threshold conditions needed for each of the equilibrium states to exist. The numerical results confirm our analytical results (see Fig. 1 and 2). When  $R_0$  is less than one, the normalized individual populations tend to the disease-free state. The normalized individual population tends to the epidemic state when  $R_E$  is greater than one.

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