Transmission network dynamics of *Plasmodium Vivax* Malaria

P. Pongsumpun, and I.M.Tang

***Abstract*—**One of the top ten killer diseases in the world is Malaria. In each year, there are between 300 to 500 million clinical episodes of malaria and 1.5 to 2.7 million deaths worldwide. The malaria disease is caused by the multiplication of protozoa parasite of the genus Plasmodium. Malaria in humans is due to 4 types of malaria parasites such that Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae and Plasmodium ovale. P.vivax malaria differs from P. falciparum malaria in that a person suffering from P. vivax malaria can experience relapses of the disease. Between the relapses, the malaria parasite will remain dormant in the liver of the patient, leading to the patient being classified as being in the dormant class. In this paper, the dynamical model of P. vivax malaria is formulated to see the network distribution of this disease.

***Keywords*—**Dynamical model, household, *Plasmodium Vivax* Malaria, relapse.

I. Introduction

MALARIA is transmitted by the female anopheles mosquito. The *Plasmodium* genus of protozoa parasites has a life cycle which is split between a vertebrate host and an insect vector. The Plasmodium species, with the exception of *Plasmodium malariae* (which may affect the higher primates) are exclusively parasites of man. The sporozoites from the mosquito salivary gland are injected into the human as the mosquito must infect anticoagulant saliva to ensure an even flowing meal. Once in the human bloodstream, the sporozoites arrive in the liver and penetrate hepatocytes, where they remain for 9-16 days, multiplying within the cells. On release, they return to the blood and penetrate red blood cells in which they produce either merozoites or micro and macrogametocytes, which have no further activity within the human host. Another mosquito arriving to feed on the blood may suck up these gametocytes into its gut, where exflagellation of microgametocytes occurs, and the macrogametocytes are fertilized. The resulting ookinete penetrates the wall of a cell in the midgut, where it develops into an oocyst. Sporogeny within the oocyst produces many sporozoites and, when the oocyst ruptures, the sporozoites migrate to the salivary gland, for injection into another host [1].

Not only are human beings the host (vertebrate) of human *Plasmodium* but also the *Anopheles* mosquitoes are also a host (invertebrate). The life cycle of *Plasmodium vivax* is complex and differs from those of the other malarias. *Plasmodium vivax* malaria is induced into bloodstream by the bite of an infected mosquito in the sporozoite form. The sporozoites travel to the liver and cells divide by asexual reproduction into what is known as merozoite within 7-8 days [2]. The merozoite can then invade the red blood cell and cause the illness. Some sporozoite will however develop into hypnozoite (there is no equivalent state in the other malarias). These hypnozoites will lay dormant in the liver for a long time. When the patient is exhausted, frail or more susceptible some of them will transform themselves into merozoites and produce the illness again. These relapses can occur up to several months or years (average 5 years) after the primary infection. The relapses peter out when there are no more hypnozoite in the liver [2].

The infection can also be transmitted accidentally through blood transfusion when the donating individual has the malaria parasite. This is one of the reasons why people who have been infected with disease can never donate blood. Congenital infection of a newborn from an infected mother also happens, but it is comparatively rare [2].

Natural transmission of malaria depends on the presence of the relationship between the three basic epidemiological factors: the host, the agent, and the environment. The most important environmental factors are temperature and humidity. Malaria parasites stop developing in the mosquitoes when the temperature is below 16 ^{0}C. The best conditions for the development of diseases and the transmission of the infection are when the average temperature is within the range of 20 – 30 ^{0}C, and the average relative humidity is at least 60% [3]. A high relative humidity lengthens the life of the mosquito and it enables them to live long enough to transmit the infection to several persons.

Data of Malaria cases due to the different types of malaria between during 2003 to 2006 in Thailand indicates that the rate of increase of the incidence of *P. vivax* is the highest among the four types. This can be seen in figure 1.

Manuscript received October 24, 2008: Revised version received December 10, 2008.

P. Pongsumpun is with the Department of Mathematics and Computer Science, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Chalongkrung road, Ladkrabang, Bangkok 10520, Thailand. (corresponding author phone: 662-737-3000 ext. 6196; fax: 662-326-4344 ext.284; e-mail: kppuntan@kmitl.ac.th).

I.M. Tang is with the Department of Physics, Faculty of Science, Mahidol University, Rama 6 road, Bangkok 10400, Thailand.

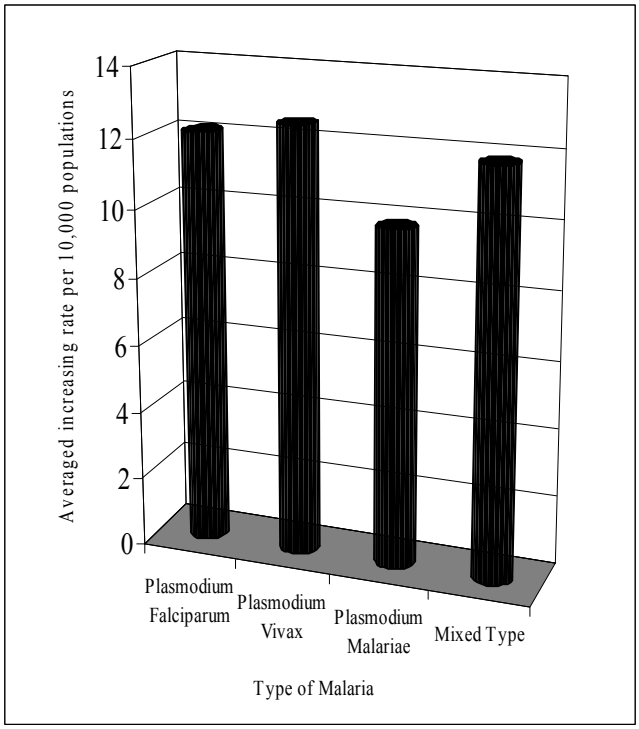

Fig.1. The average increasing rate per 10,000 populations of Malaria in Thailand during 2003-2006[4].

The transmission of malaria is usually described by the Ross-MacDonald (RM) model [2]. This model is only suitable for the transmission of the *P. falciparum* malaria since it does not contain a role of possible relapses of the illness.

In the present state of concern for medical safety, there is no place for human experimentation to see what would happen if new therapies were adopted. Mathematical modeling allows one to simulate what would occur. In this study, the dynamics transmission of *P. vivax* between houses and villages are considered. We introduce in Section 2, the mathematical model which would make it applicable to the transmission of *P. vivax* malaria in the villages and district levels. In Section 3, we simulate the consequences of changing the number of villages, number of houses in each village, contact rates and relapse rates. We discuss in Section 4, the implication of the insights obtained from the simulations. Part of the urgency for doing research on P. *vivax* malaria is due to the fact that P. *vivax* malaria is becoming an emerging public health problem. It is estimated that about 50% of the malaria cases outside of Africa and 10% in Africa are due to P. *vivax* and that the percentages are soaring.

II. TRANSMISSION MODEL

In 1911, Ross [5] formulated the mathematical model of the epidemiology of malaria (*P. falciparum*) and improved on by MacDonald [3]. In the Ross model, an individual in the human population is separated as being in a non-infected or infected state. This gives rise to what is known as a SIS (susceptible-infected-susceptible) model. It has been suggested [2] that the human population should instead be divided into three states; non-infected, infected but without any acute clinical signs, infected with acute clinical sign, to better reflect the clinical status of the individual. Others believe that the population should be divided into susceptible, infected but not infectious and infected and infectious. In this study, we construct the dynamical model of P.Vivax malaria between villages and houses to see the network distribution of this disease.

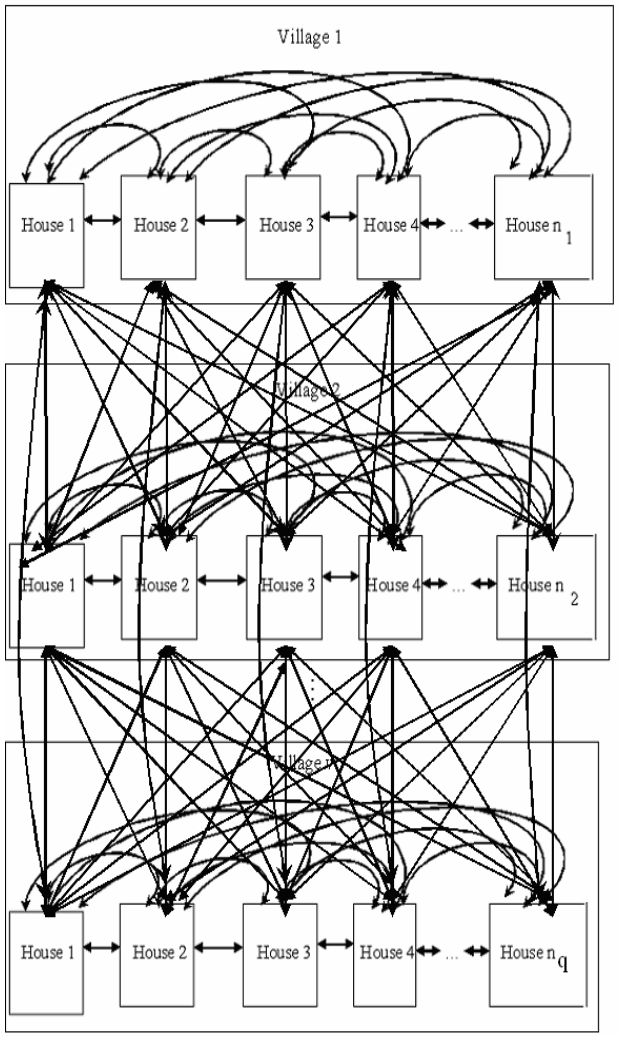

Fig. 2. The diagram shows the movement of the population between villages.

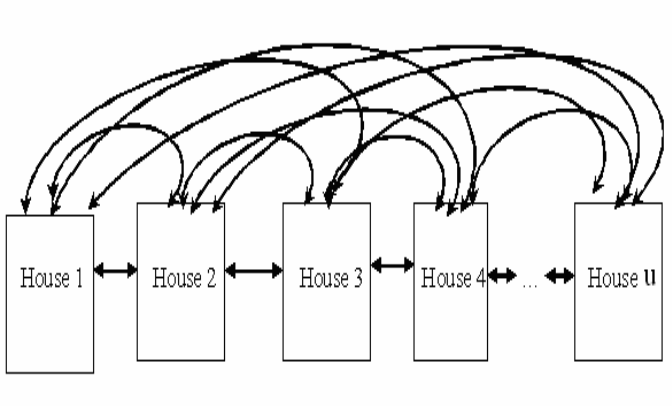

Fig. 3. The diagram shows the movement of the population between houses.

Suppose that there are q villages, L persons and u houses in each village. The persons move to any houses in this village by random process. This process is done by random the 1st person to the L^{th} person (with uniformly distribution) go to each house everyday. Each day, one person can go only one time in one house of this village. The probability for each person to visit each house is equal. There is no person come from the outside of this village. The persons who stay in any house at the beginning time will come back to their houses at the ending time. We assume that at the first day, there is only one infected human in one house and there is no infected human for the other houses in the village.

In our model for the transmission of *P. vivax* in the local level (village), we divide the host (human) population into susceptible, infected, dormant and recovered classes. The last category, the recovered are susceptible to further infections and so they reenter into the susceptible class. The vector population is separated into susceptible and infected classes.

The variables in our model are defined as follows:
$Sh_{t,i}$ is the number of susceptible persons in house i^{th} after visited at day t ,
$Ih_{t,i}$ is the number of infected persons in house i^{th} after visited at day t,
$Dh_{t,i}$ is the number of dormant persons in house i^{th} after visited at day t,
$Rh_{t,i}$ is the number of recovered persons in house i^{th} after visited at day t,
$Sv_{t,i}$ is the number of susceptible mosquitoes in house i^{th} after visited at day t,
$Iv_{t,i}$ is the number of infected mosquitoes in house i^{th} after visited at day t,
L is the total number of persons,
q is the number of villages,
u is the total number of house,
g is the ending time.

The dynamics of human and vector populations are given by

$$\begin{aligned}
\Delta Sh_{t,i} &= -\gamma\, Iv_{t,i}\, Sh_{t,i} + s_3\, Dh_{t,i} + (1-\alpha)\, s_1\, Ih_{t,i} + s_4\, Rh_{t,i} \\
\Delta Ih_{t,i} &= \gamma\, Iv_{t,i}\, Sh_{t,i} - s_1 Ih_{t,i} + s_2 Dh_{t,i} - s_5\, Ih_{t,i} \\
\Delta Dh_{t,i} &= \alpha\, s_1\, Ih_{t,i} - (s_2 + s_3)\, Dh_{t,i} \\
\Delta Rh_{t,i} &= s_5\, Ih_{t,i} - s_4\, Rh_{t,i} \\
\Delta Sv_{t,i} &= Y_{t,i} - \beta\, Sv_{t,i}\, Ih_{t,i} - \mu_v\, Sv_{t,i} \\
\Delta Iv_{t,i} &= \beta\, Sv_{t,i}\, Ih_{t,i} - \mu_v\, Iv_{t,i}
\end{aligned} \qquad (1)$$

$Y_{t,i} = \mu_v(Sv_{t,i}+Iv_{t,i})$ = Basic recruitment number of the mosquitoes in house i^{th} at day t,
β is the transmission rate of dengue virus from infectious person to susceptible vector,
μ_v is the death rate of the mosquitoes,
α is the percentage of infected human in whom some hypnozoites remain dormant in the liver,
$(1-\alpha)$ is the percentage of infected humans who recover and become susceptible again,
s_1 is the rate at which a person leaves the infected class by recovering or by entering into the dormant class,
s_2 is the rate at which the dormant human relapses back to the infected human,
s_3 is the recovery rate of the dormant human,
s_4 is the rate at which the recovered human relapses back to the susceptible human, and
s_5 is the rate at which the infected human recovers,
γ is the rate at which the *P. vivax* parasite is transmitted from the mosquito to the human and is given by [6-9]

$$\gamma = b\frac{\beta_h}{N_T + m} \qquad (2)$$

where b is the specie-dependent biting rate of the mosquitoes; m is the population of other animals that the mosquitoes can feed on; N_T is the total human populations and β_h is the probability the parasite passed on by the mosquito will continue to thrive in the human. β is the rate at which the mosquitoes become infected with the Plasmodium *vivax* parasite once the mosquito has bitten an infected human. β is defined by [6-9]

$$\beta = b\frac{\beta_v}{N_T + m}$$

where β_v is the probability the parasite passed to the mosquito by biting human.

III. NUMERICAL SOLUTIONS

The simulations of the model are calculated to see the time distributions of this disease. The time distributions of infected and dormant humans for the different situations are shown in the following figures.

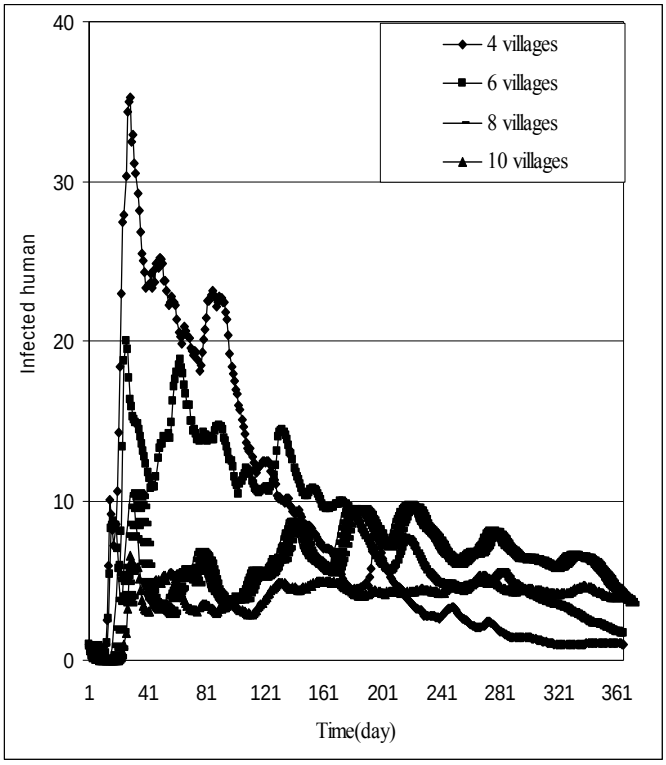

Fig.4 Model outputs display the time distribution of infected human for the different number of villages in each district. The parameters in our model are $s_1 = 1/14$, $s_2 = 1/(365*3)$, $s_3 = 1/(25)$, $s_4 = 1/(365*10)$, $s_5 = 1/3$, $\gamma = 0.55$, $\beta = 0.45$, $\mu_v = 0.04$, L = 1,000, g = 365.

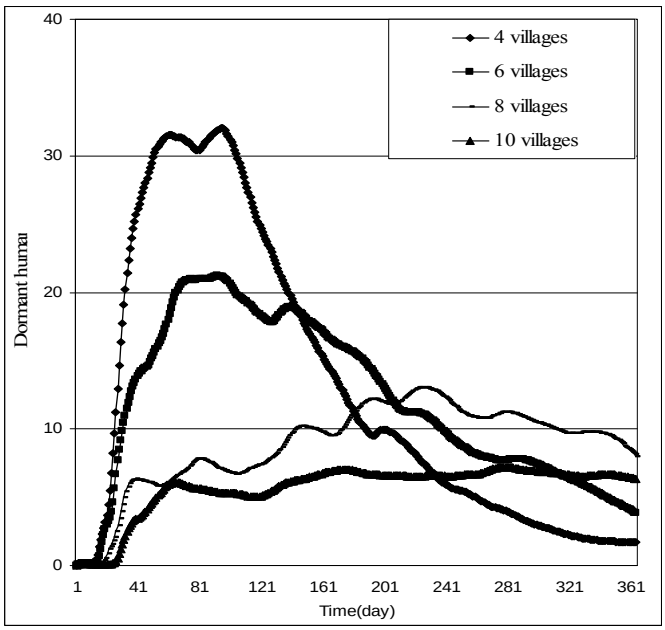

Fig.5**.** Model outputs display the time distribution of dormant human for the different number of villages in each district. The parameters are same as fig. 4.

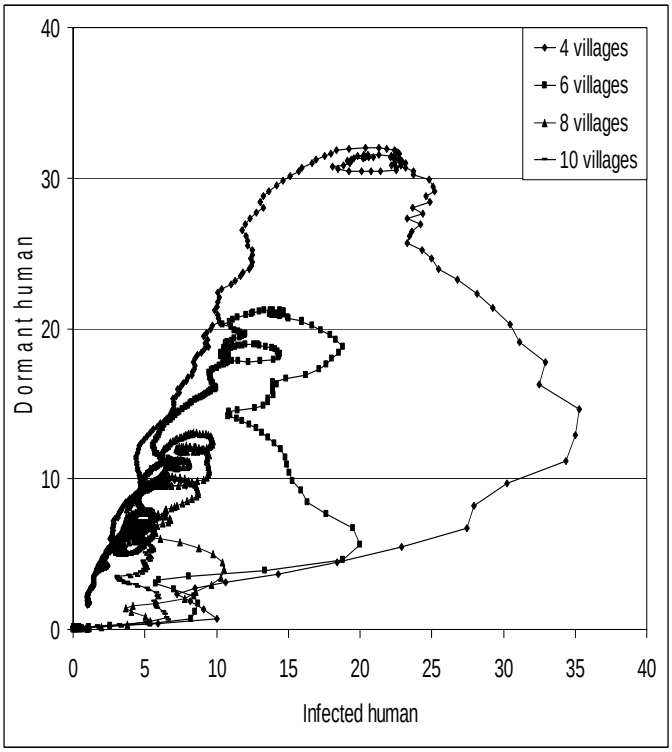

Fig.6**.** Model outputs display the 2D D_h-I_h plane for the different number of villages in each district. The parameters are same as fig. 4.

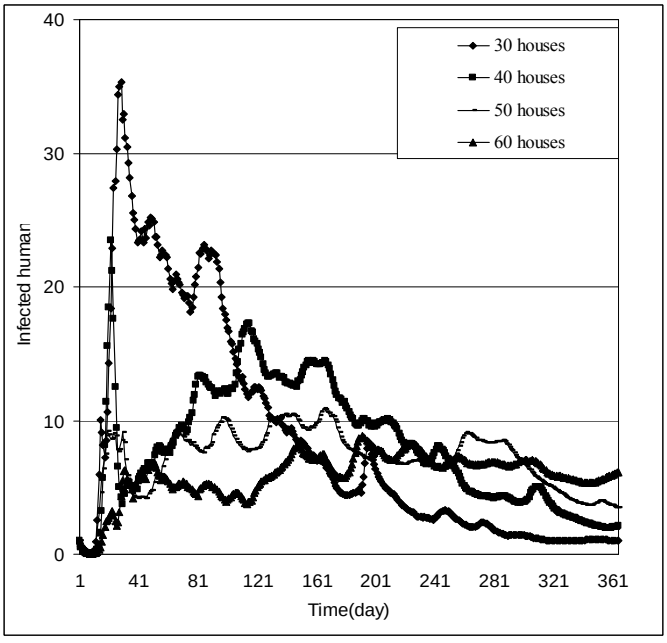

Fig.7. Model outputs display the time distribution of infected human for the different number of house in each village. The parameters in our model are $s_1 = 1/14$, $s_2 = 1/(365*3)$, $s_3 = 1/(25)$, $s_4 = 1/(365*10)$, $s_5 = 1/3$, $\gamma = 0.55$, $\beta = 0.45$, $\mu_v = 0.04$, L = 100, g = 365.

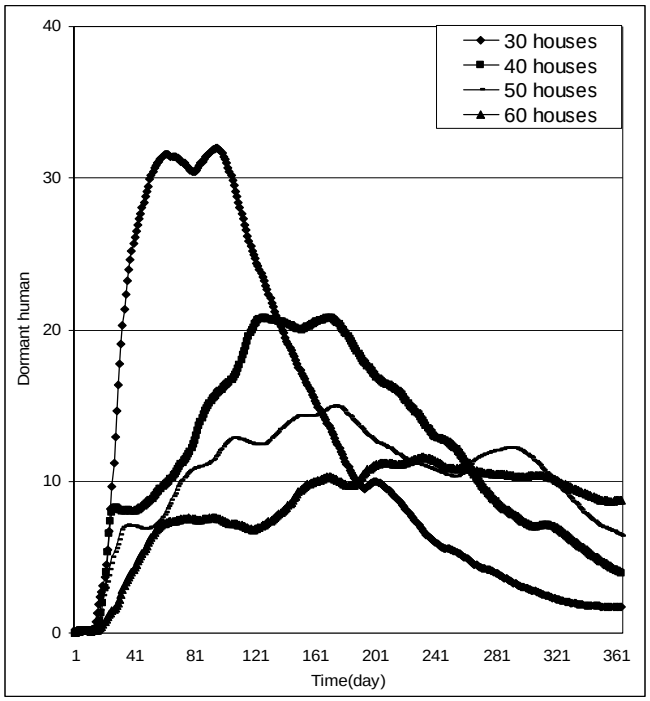

Fig.8. Model outputs display the time distribution of dormant human for the different number of house in each village. The parameters are same as fig. 7.

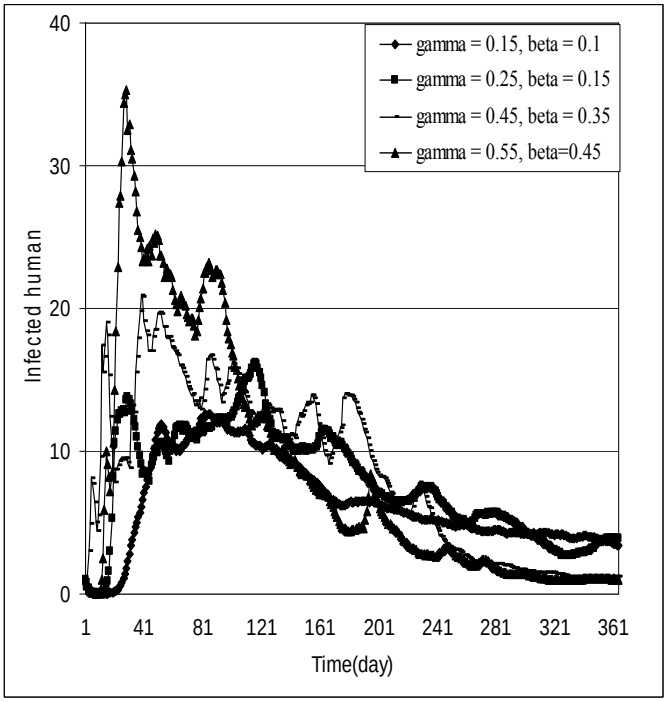

Fig.10. Model outputs display the time distribution of infected human for the different contact rates in each village. There are 30 houses in each village. The parameters are same as fig. 7 except the contact rates.

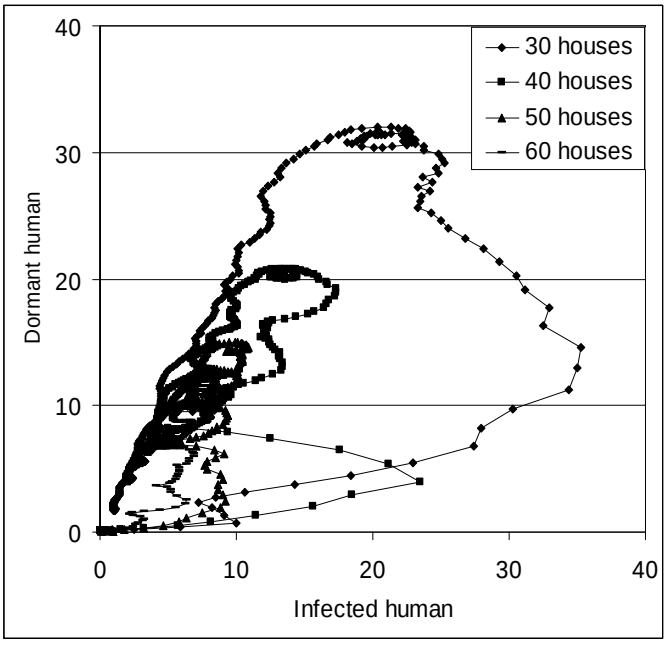

Fig.9**.** Model outputs display the 2D D_h-I_h plane for the different number of houses in each village. The parameters are same as fig. 7.

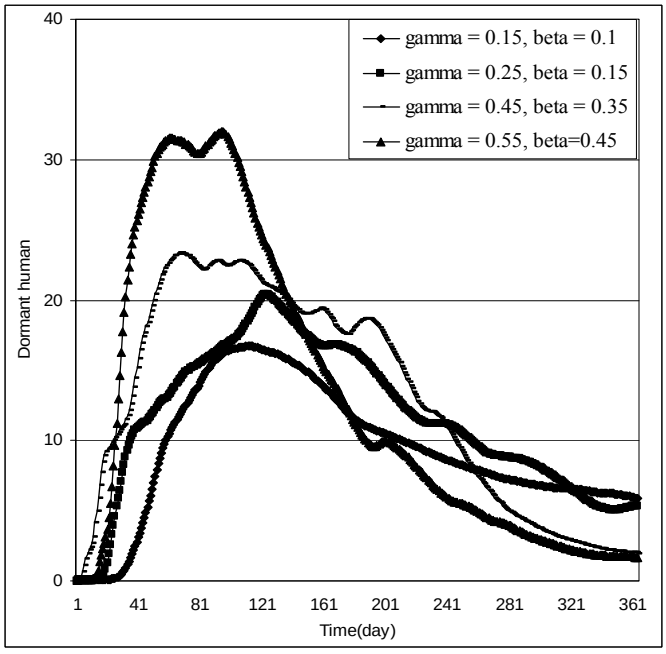

Fig.11. Model outputs display the time distribution of dormant human for the different contact rates in each village. The parameters are same as fig. 10.

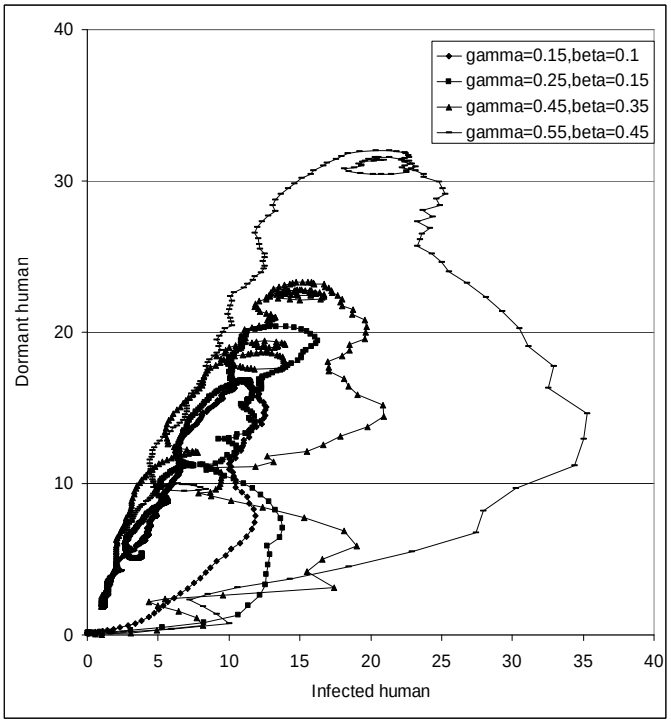

Fig.12. Model outputs display the 2D D_h-I_h plane for the different number of houses in each village. The parameters are same as fig. 10.

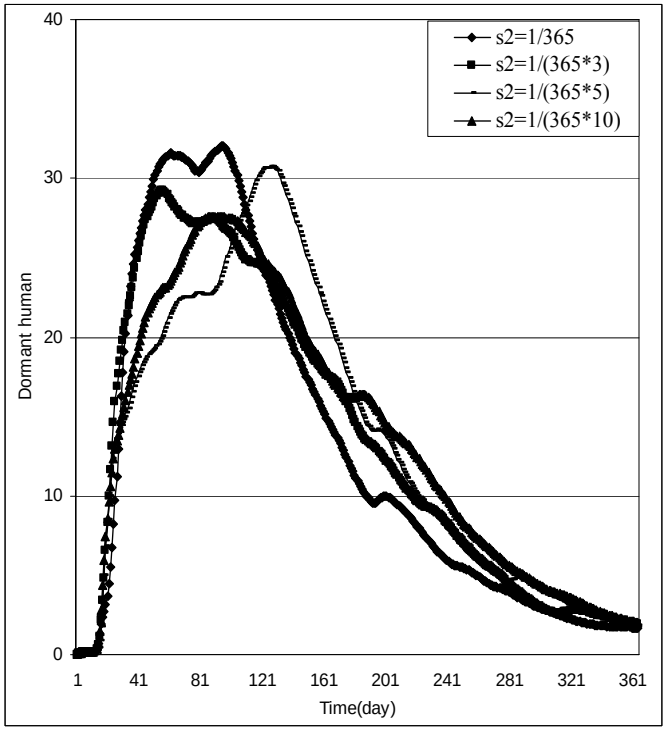

Fig.14. Model outputs display the time distribution of dormant human for the different rate at which the dormant human relapses back to the infected human in each village. The parameters are same as fig. 13.

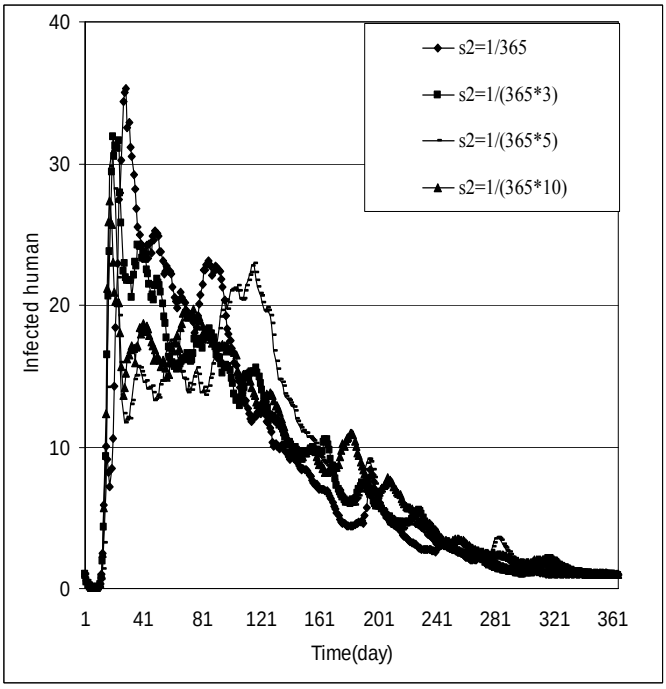

Fig.13. Model outputs display the time distribution of infected human for the different rate at which the dormant human relapses back to the infected human in each village. There are 30 houses in each village. The other parameters are same as fig. 11 except s_2.

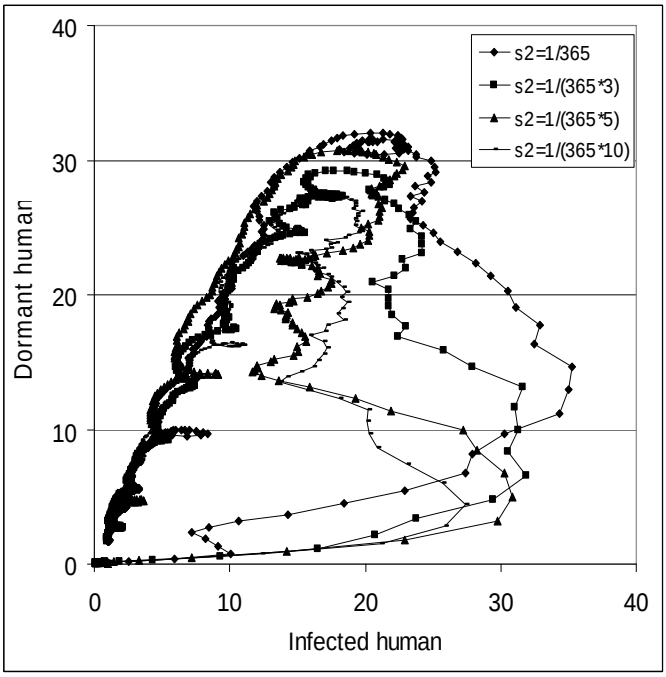

Fig.15. Model outputs display the 2D D_h-I_h plane for the different rate at which the dormant human relapses back to the infected human in each village. The parameters are same as fig. 13.

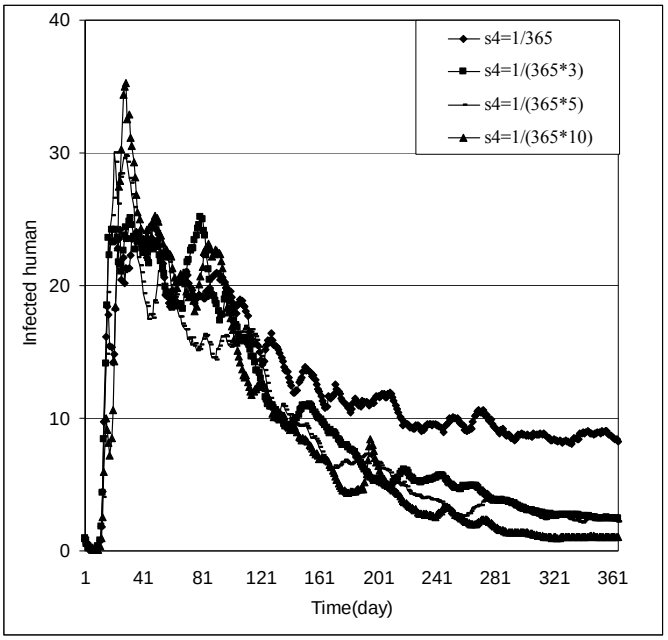

Fig.16. Model outputs display the time distribution of infected human for the different rate at which the recovered human relapses back to the susceptible human in each village. There are 30 houses in each village. The other parameters are same as fig. 10 except s_4.

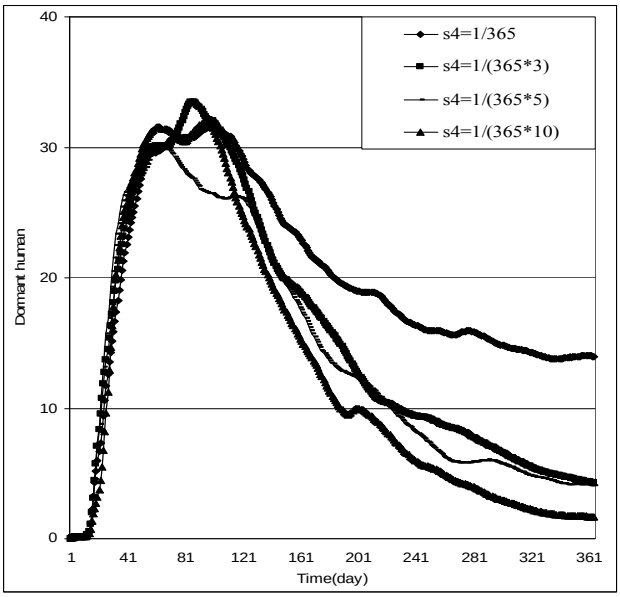

Fig.17. Model outputs display the time distribution of dormant human for the different rate at which the recovered human relapses back to the susceptible human in each village. The other parameters are same as fig. 16.

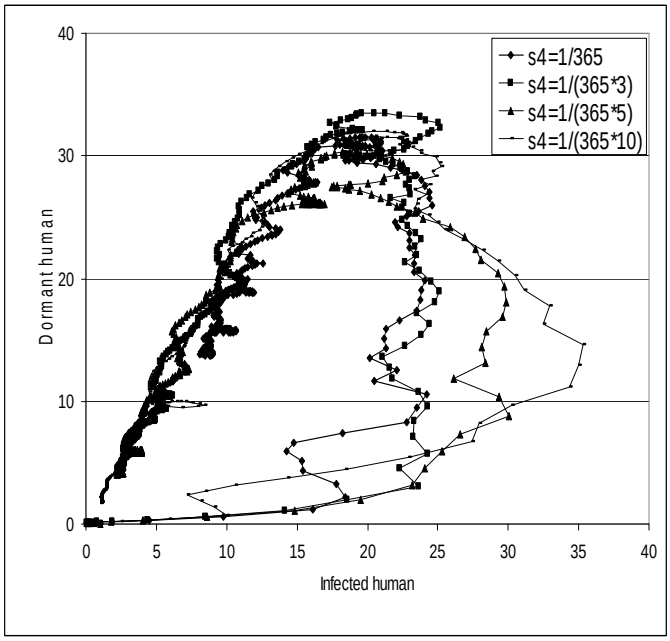

Fig.18. Model outputs display the 2D D_h-I_h plane for the different rate at which the recovered human relapses back to the susceptible human in each village. The parameters are same as fig. 16.

IV. CONCLUSION

In this study, we have compared the results of the simulation when different values of several parameters are used. Figures 4, 5 and 6 show the time distributions of infected human, dormant human and the 2D Dormant-Infected human plane, respective, when the number of villages in each district is difference. Figures 7, 8 and 9 show the time distributions of infected human, dormant human and the 2D Dormant-Infected human plane, respective; when the number of houses in each village is difference. Figures 10, 11 and 12 show the time distributions of infected, dormant human and the 2D Dormant-Infected human plane, respective; when the contact rates in each village are difference. Figures 13, 14 and 15 show the time distributions of infected human, dormant human and the 2D Dormant-Infected human plane, respective, when the rate at which the dormant human relapses back to the infected human in each village is difference. Figures 16, 17 and 18 show the time distributions of infected, dormant human and the 2D Dormant-Infected human plane, respective, when the rate at which the recovered human relapses back to the susceptible human in each village is difference. We will see that the epidemic sizes are higher when the smaller number of villages, the smaller number of households and the higher contact rates. But when the rate at which the dormant human relapses back to the infected human and the rate at which the recovered human relapses back to the susceptible human are higher, the epidemic sizes are smaller. The important parameters will be the role of traveling of people between villages.

ACKNOWLEDGMENT

This work is supported by Commission on Higher Education and the Thailand Research Fund according to contract number MRG5080078. The authors would like to thank Dr.Sopon Iamsirithaworn, Ministry of Public Health, Thailand for supporting the data.

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