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EFFECT OF AGE STRUCTURE AND TOURISTS FOR THE ENDEMIC REGION ON THE TRANSMISSION OF DENGUE DISEASE

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ABSTRACT

Dengue disease is a febrile viral disease that can be found in the tropical regions of the world. This disease is transmitted to human by the bites of infected *Aedes Aegypti* mosquitoes. It has increased in both incidence and distribution over the past 40 years. In each year, it is estimated that there are 20 million cases of dengue infection, around 24,000 deaths due to this disease. The data of dengue patients in Thailand indicates that the age structure of the population plays a role in the transmission of this disease. The effects of age structure and tourists on the transmission of dengue virus are the focus of this study. The effects are determined through a mathematical formulation of the transmission cycle.

KEYWORDS: dengue disease, age structure, tourist, stability

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1. INTRODUCTION

The most important arboviral disease that can be found in the tropical regions of the world is dengue disease. In recent years, this disease has become a major international public health concern due to air travel into endemic regions. The disease is a flu-like illness that affects infants, young children and adults but rarely causes death. Dengue hemorrhagic fever (DHF), however, is a potentially lethal complication and is today a leading cause of childhood death in several Asian countries. The clinical characteristics of dengue fever vary according to the age of the patient. Infants and young children may have an illness with rash. Older children and adults may have an illness with high fever, severe headache, pain behind the eyes, muscle and joint pains, and rash. DHF characterized by high fever, hemorrhaging usually with enlargement of the liver and in the most severe cases, circulatory failure [1]. The illness begins with a sudden rise in temperature accompanied by facial flushing and other general symptoms of dengue fever. The fever usually continues for 2-7 days. It can be as high as 40-41° C, and may be accompanied by febrile convulsions. *Aedes Aegypti* is the primary vector of this disease. There are four types of dengue virus, DEN-1, DEN-2, DEN-3 and DEN4. Infection by any single type of dengue virus apparently produces permanent immunity to it, but only temporary cross immunity to the others. The retrospective data of Thailand [2] as shown in figure 1 indicates that most illnesses due to this disease occur in children less than 15 years old.

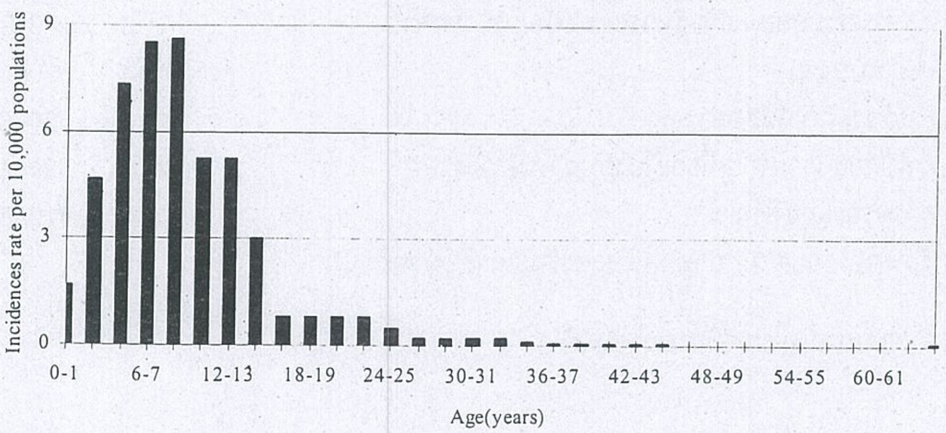

Figure 1. Age distribution of the 1998 epidemic in Mukdahan Province, Thailand[2].

2. EFFECT OF AGE STRUCTURE ON THE TRANSMISSION OF DENGUE VIRUS

2.1 MATHEMATICAL MODEL

Looking at figure 1, we see that while most infections occur in children less than 15 years old, some do occur in adult. This means that there is probability that the dengue virus will survive in the adult human after it is transmitted from the mosquito but the probability will be less than that in children. In our model, we have assumed that there is only one type of virus and that the disease-related death rate is negligible.

Let $S_J(t)$ denotes the susceptible juvenile human proportion,
$I_J(t)$ denotes the infectious juvenile human proportion,
$R_J(t)$ denotes the recovered juvenile human proportion,
$S_A(t)$ denotes the susceptible adult human proportion,
$I_A(t)$ denotes the infectious adult human proportion,
$R_A(t)$ denotes the recovered adult human proportion,
$S_v(t)$ denotes the susceptible vector proportion.
$I_v(t)$ denotes the infectious vector proportion.

The transmission can be described by the following set of differential equations;

$$
\begin{aligned}
\frac{dS_J}{dt} &= (\mu_h + \delta)(1 - S_J) - \frac{\beta_J b}{N_T + c} S_J I_v (A/\mu_v), \\
\frac{dI_J}{dt} &= \frac{\beta_J b}{N_T + c} S_J I_v (A/\mu_v) - (\mu_h + \delta + r) I_J, \\
\frac{dS_A}{dt} &= \mu_h S_J - \varepsilon \frac{\beta_J b}{N_T + c} S_A I_v (A/\mu_v) - \mu_h S_A, \\
\frac{dI_A}{dt} &= \mu_h I_J + \varepsilon \frac{\beta_J b}{N_T + c} S_A I_v (A/\mu_v) - (\mu_h + r) I_A, \\
\frac{dI_v}{dt} &= \frac{\beta_v b}{N_T + c} (1 - I_v)(I_J N_J + I_A N_A) - \mu_v I_v,
\end{aligned}
\tag{1}
$$

with $S_J + I_J + R_J = 1$, $S_A + I_A + R_A = 1$ and $S_v + I_v = 1$

where

μ_h is the average constant birth and death rate of the human population,

N_T is the total number of the human population,

N_J is the total number of the juvenile human population,

N_A is the total number of the adult human population,

r is the constant rate at which an infected human recovers,

A is the constant recruitment rate of mosquitoes,

μ_v is the average constant death rate of mosquitoes,

b is the average number of biting per mosquito per day,

δ is the constant rate at which juveniles pass into adulthood,

c is the number of other hosts available as blood sources,

β_J is the probability that the dengue virus will survive in the juvenile human after it is transmitted from the mosquito,

$\varepsilon\beta_J$ is the probability that the dengue virus will survive in the adult human after it is transmitted from the mosquito,

β_v is the probability that the dengue virus will survive in the mosquito after it is transmitted from the human.

2.2 ANALYTICAL AND NUMERICAL RESULTS

The equilibrium points are found by setting the right hand side of (1) equal to zero. The disease free and endemic disease equilibrium points can thus be obtained. Here, we consider only the endemic disease equilibrium point, $E = (S_J^*, I_J^*, S_A^*, I_A^*, I_v^*)$ where

$$S_J^* = \frac{\beta_1}{\beta_1 + R_1 M_1 I_v^*},$$

$$I_J^* = \frac{R_1 I_v^*}{\beta_1 + R_1 M_1 I_v^*},$$

$$S_A^* = \frac{\beta_1 \beta_2}{(\beta_1 + R_1 M_1 I_v^*)(\beta_2 + \varepsilon R_2 M_2 I_v^*)},$$

$$I_A^* = \frac{R_1 I_v^*}{M_2(\beta_1 + R_1 M_1 I_v^*)} + \varepsilon R_2 \frac{\beta_1 I_v^*}{(\beta_1 + R_1 M_1 I_v^*)(\beta_2 + \varepsilon R_2 M_2 I_v^*)}$$

and $$I_v^* = \frac{-a_1 + \sqrt{a_1^2 - 4a_2 a_0}}{2a_2}$$

where

$$a_2 = \varepsilon M_2(\beta_2 + (\beta_1 + M_1)M_2)\mu_v R_1 R_2,$$

$$a_1 = \beta_2^2 \mu_v R_1 + \beta_1 \varepsilon M_2^2 \mu_v (1 - R_1) R_2 + \beta_2 M_2 \mu_v R_1 \left((1 - \varepsilon R_2) + \frac{r}{\delta + \mu_h} \right) + \beta_1 \beta_2 M_2 \mu_v (R_1 + \varepsilon R_2),$$

$$a_0 = -\beta_2 \mu_v (\beta_2 R_1 + \beta_1 M_2(-1 + R_1 + \varepsilon R_2)),$$

$$\beta_1 = \frac{b\beta_v N_J}{\mu_v(N_T + c)}, \quad M_1 = \frac{\mu_h + \delta + r}{\mu_h + \delta}, \quad R_1 = \frac{b^2\beta_v\beta_J N_J (A/\mu_v)}{\mu_v (N_T + c)^2 (\mu_h + \delta + r)}$$

$$\beta_2 = \frac{b\beta_v N_A}{\mu_v(N_T + c)}, \quad M_2 = \frac{\mu_h + r}{\mu_h}, \quad R_2 = \frac{b^2\beta_v\beta_J N_A (A/\mu_v)}{\mu_v (N_T + c)^2 (\mu_h + r)} \quad \text{and } R_1 + \varepsilon R_2 > 1.$$

The characteristic equation is

$$\lambda^5 + d_4\lambda^4 + d_3\lambda^3 + d_2\lambda^2 + d_1\lambda + d_0 = 0$$

where d_0, d_1, d_2, d_3 and d_4 are found by solving

$$\det(J_E - \lambda I_5) = 0, \quad I_5 \text{ is the identity matrix dimension } 5\times 5.$$

The local stability can be determined by applying the Routh-Hurwitz criteria [3].

i) $d_i > 0$ for $i = 0,1,\dots,4$

ii) $d_2 d_3 d_4 > d_2^2 + d_4^2 d_1$,

iii) $(d_1 d_4 - d_0)(d_2 d_3 d_4 - d_2^2 - d_4^2 d_1) > d_0(d_3 d_4 - d_2)^2 - d_4 d_0^2$

Conditions (i) to (iii) are satisfied for $B_A = R_1 + \varepsilon R_2 > 1$.

Therefore the endemic equilibrium point is local asymptotically stable for $B_A > 1$.

$(\because B_A = R_1 + \varepsilon R_2)$, $B_A = \dfrac{b^2\beta_v\beta_J N_J (A/\mu_v)}{\mu_v (N_T + c)^2 (\mu_h + \delta + r)} + \varepsilon \dfrac{b^2\beta_v\beta_J N_A (A/\mu_v)}{\mu_v (N_T + c)^2 (\mu_h + r)}$. Numerical solution for each individual population oscillates to the endemic disease equilibrium point as shown in figure 2.

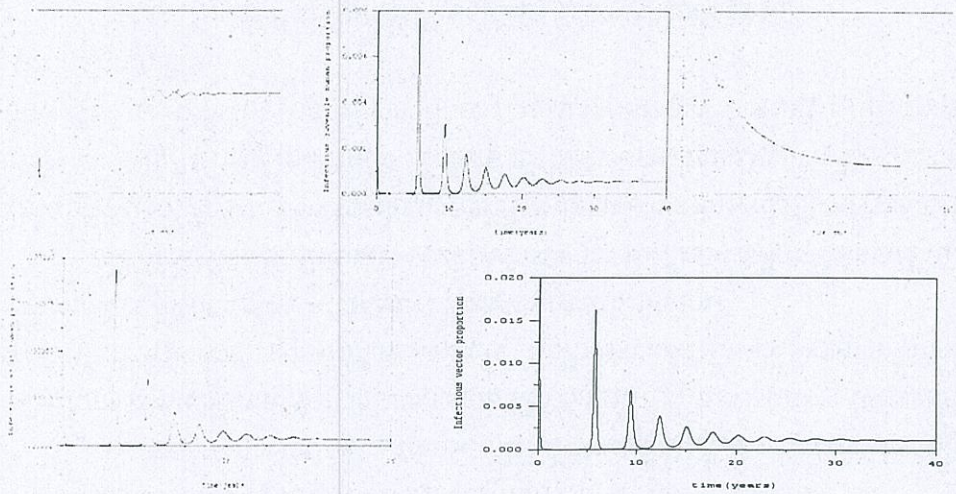

Figure 2. Numerical solution of the system (1) demonstrates the time series of S_J, I_J, S_A, I_A and I_v, respectively for $B_A > 1$ with $\mu_h = 1/(365\times70)$ day^{-1}, $\mu_v = 1/14$ day^{-1}, $b = 1/3$ day^{-1}, $\beta_J = 0.5$, $\beta_v = 0.75$, $r = 1/3$ day^{-1}, $A = 30{,}000$, $c = 0$, $\delta = 1/(365\times 15)$ day^{-1}, $\varepsilon = 0{:}1$, $N_J = 60{,}000$, $N_A = 40{,}000$, $N_T = 100{,}000$, $\beta_1 = 2.1$, $M_1 = 1503.941176$, $R_1 = 4.40707$, $\beta_2 = 1.4$, $M_2 = 8517.67$, $R_2 = 2.93965$ and $B_A = 4.70103$.

3. EFFECT OF TOURIST ON THE TRANSMISSION OF DENGUE VIRUS

3.1 MATHEMATICAL MODEL

From the reports of increased number of tourists to Thailand who are being infected with the dengue virus. A special report issued by the surveillance net TropNetEurop [4] points out that during 2002, 61.4% of the 68 reported cases (among German or Swiss tourists) had become infected while they were visiting Ko Phangan and Ko Samui, two islands in the Gulf of Thailand. During the previous three years, only 20.4% of the imported dengue cases among this group of tourists originated in Thailand. In a study of Swedish tourists [5], 71% of the imported dengue cases during 1998-99 were infected in Thailand. A similar preponderance was seen among Israel tourists during 1994-1995, i.e., 14/18 confirmed infections originated on the island of Ko-Pangan [6]. The average duration of the tourists in these three studies was three to four weeks. A prospective study of Israeli tourists to tropical countries who stay a long time (at least three months) indicates that the incident rate of dengue infection for these travelers may be as high as 600 per 100,000 travelers [7].

The effects of the tourists on the trransmission can be determined by considering the following mathematical model;

Let $S_h(t)$ denotes the susceptible host human proportion,
$I_h(t)$ denotes the infectious host human proportion,
$R_h(t)$ denotes the recovered host human proportion,
$S_t(t)$ denotes the susceptible tourist proportion,
$I_t(t)$ denotes the infectious tourist proportion,
$R_t(t)$ denotes the recovered tourist proportion,
$S_v(t)$ denotes the susceptible vector proportion.
$I_v(t)$ denotes the infectious vector proportion.

The differential equations can be described by

$$\begin{aligned}
\frac{dS_h}{dt} &= \mu_h(1-S_h) - b\beta_h \frac{(A/\mu_v)}{N_T+c} S_h I_v, \\
\frac{dI_h}{dt} &= b\beta_h \frac{(A/\mu_v)}{N_T+c} S_h I_v - (r+\mu_h)I_h, \\
\frac{dS_t}{dt} &= ((1/\tau)+\mu_h)(1-S_t) - b\beta_h \frac{(A/\mu_v)}{N_T+c} S_t I_v, \\
\frac{dI_t}{dt} &= b\beta_h \frac{(A/\mu_v)}{N_T+c} S_t I_v - ((1/\tau)+r+\mu_h)I_t, \\
\frac{dI_v}{dt} &= \left(b\beta_v \frac{(D/((1/\tau)+\mu_h))}{N_T+c} I_t + b\beta_v \frac{N_h}{N_T+c} I_h \right)(1-I_v) - \mu_v I_v
\end{aligned} \tag{2}$$

with $S_h + I_h + R_h = 1$, $S_t + I_t + R_t = 1$ and $S_v + I_v = 1$,
where
N_h is the total number of the host population,
N_t is the total number of tourists,
N_T is the total number of the human population ($N_T = N_h + N_t$),
β_h is the probability that the dengue virus will survive in the human after it is transmitted from the mosquito,
D is the number of tourists entering into the region ,
$1/\tau$ is the rate at which the tourist leaving the region.

3.2 ANALYTICAL AND NUMERICAL RESULTS

The endemic equilibrium point P is $(S_h^*, I_h^*, S_t^*, I_t^*, I_v^*)$ where

$$S_h^* = \frac{1}{1+\varepsilon_1 I_v^*}, \qquad I_h^* = \frac{\varepsilon_2 I_v^*}{1+\varepsilon_1 I_v^*},$$

$$S_t^* = \frac{1}{1+\varepsilon_3 I_v^*}, \qquad I_t^* = \frac{\varepsilon_4 I_v^*}{1+\varepsilon_3 I_v^*},$$

$$I_v^* = \frac{-e_1+\sqrt{e_1^2-4e_2e_0}}{2e_2}$$

and
$$e_2 = \mu_v\varepsilon_3(B_t+\varepsilon_1)+\delta_{v,t}\varepsilon_1\varepsilon_4,$$
$$e_1 = \mu_v\varepsilon_3(1-B_t)+\mu_v(B_t+\varepsilon_1)+\delta_{v,t}\varepsilon_4(1-\varepsilon_1),$$
$$e_0 = \mu_v(1-B_t)-\delta_{v,t}\varepsilon_4$$

with $\varepsilon_1 = \dfrac{\delta_T}{\mu_h}$, $\varepsilon_2 = \dfrac{\delta_T}{r+\mu_h}$, $\varepsilon_3 = \dfrac{\delta_T}{(1/\tau)+\mu_h}$, $\varepsilon_4 = \dfrac{\delta_T}{(1/\tau)+r+\mu_h}$,

$$\delta_T = \frac{b\beta_h(A/\mu_v)}{N_T+c} \quad \text{and} \quad B_t = \frac{b^2\beta_h\beta_v(A/\mu_v)N_h}{(N_T+c)^2\mu_v(r+\mu_h)} > 1.$$

The characteristic equation is

$$\lambda^5+h_4\lambda^4+h_3\lambda^3+h_2\lambda^2+h_1\lambda+h_0 = 0$$

where h_0, h_1, h_2, h_3 and h_4 are found by solving

$$\det(J_P-\lambda I_5) = 0,$$ I_5 is the identity matrix dimension 5×5.

By using Routh-Hurwitz criteria[3] we found that the endemic equilibrium point is local asymptotically stable for $B_t' > 1$, $B_t' = \dfrac{b^2\beta_h\beta_v(A/\mu_v)N_T}{(N_T+c)^2\mu_v(r+\mu_h)}$. Numerical solution for each individual proportion oscillates to the endemic disease equilibrium point as shown in figure 3.

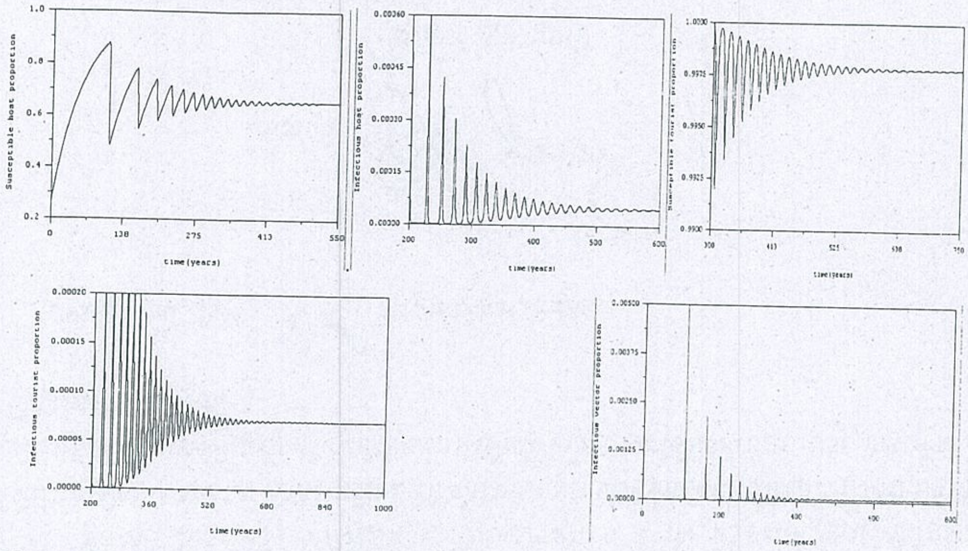

Figure 3. Numerical solution of the system (2) demonstrates the time series of S_h, I_h, S_t, I_t and I_v, respectively for $B_t^{'} > 1$ with $\tau = 90$ days, $\mu_h = 1/(365\times70)$ day^{-1}, $\mu_v = 1/14$ day^{-1}, $b = 1/3$ day^{-1}, $\beta_h = 0.5$, $\beta_v = 0.75$, $m_v = 3.0$, $\varepsilon_1 = 12775$, $\varepsilon_2 = 1.49982$, $\varepsilon_3 = 44.842$, $\varepsilon_4 = 1.45145$, $m_h = 0.3$, $m_t = 0.009$, $r = 1/3$ day^{-1}, $B_t = 1.57482$ and $B_t^{'} = 1.6220$.

4. CONCLUSION

For each model, there is a threshold parameter (B_A and $B_t^{'}$), the basic reproductive number for which the endemic state will prevail if and only if the basic reproduction number exceeds one. The numerical simulations are used to confirm these results. The control of the vector population can be described in the basis of their effects on the basic reproductive number. If an outbreak of dengue disease starts in an endemic region; the basic reproductive number will exceed one. When the insecticide treatment is used during a short time period, the mortality rate of adult vector will increase then the basic reproductive number will decrease temporality to levels below one. The infectious mosquitoes will disappear, but the infectious human will remain. When the larvae develop into adult vectors, they can bite the infectious human. The basic reproductive number will return to a level above one.

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