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Mathematical model for asymptomatic and symptomatic infections of dengue disease

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Abstract: - The difference for the transmission of dengue disease to asymptomatic and symptomatic infectious human is used to formulate the mathematical model of dengue disease. The human population is separated into susceptible, asymptomatic infectious, symptomatic infectious and recovered classes. The transmission probabilities of dengue virus from the mosquito class to the susceptible human class are different to become asymptomatic or symptomatic infective classes. The standard dynamical analysis method is used to analyze the model. Two equilibrium states are found and the conditions for stability of theses two equilibrium states are established. The numerical results are used to confirm these results. The control of this disease is discussed in the term of the threshold condition.

Key-Words: - mathematical model, SEIR model, dengue disease, threshold number, equilibrium states, asymptomatic and symptomatic infections

1 Introduction

The most important mosquito-transmitted viral disease which occurs in the tropical regions is dengue disease. It is estimated that there are over one hundred million dengue cases worldwide each year. The general symptoms of dengue incidences are high fever, severe headache, backache, joint pains, eye pain, vomiting and rash. Dengue fever (DF), Dengue hemorrhagic fever (DHF) and Dengue shock syndrome (DSS) are three forms of this disease. DF is characterized by the rapid development of a fever that may last from five to seven days with intense headache, joint and muscle pain and a rash. The rash develops on the feet or legs three to four days after the beginning of the fever. The hemorrhagic form of dengue fever, DHF is more severe and associated with loss of appetite, vomiting, high fever, headache and abdominal pain. Shock and circulatory failure may occur, DSS. Untreated hemorrhagic dengue results in death in up to 50 percent of cases. DEN-1, DEN-2, DEN-3 and DEN-4 are four serotypes of dengue virus. Infection with one of the four serotypes of dengue virus usually produces immunity to that serotype but does not provide protection against the other serotypes. This disease is transmitted from one person to another person through the bite of infected *Aedes aegypti* mosquitoes. After each person is infected dengue virus from the mosquito then that person may be symptomatic or asymptomatic infection. The mosquito becomes infected with dengue virus when it bites a person who has dengue or DHF and after about a week can transmit the virus while biting a healthy person [1].

2 Mathematical model

To study the transmission of dengue disease, the human population is divided into four classes, susceptible, asymptomatic infectious, symptomatic infectious and recovered human populations. For the vector population, we divide into two classes, susceptible and infectious vector populations. Susceptible human is the human who both not immune and not infected. Asymptomatic and symptomatic infectious human are the human who are transmitted dengue virus from the infectious vector population and can transmit dengue virus to the susceptible vector. Asymptomatic infectious human is the patient who shows no symptoms but symptomatic infectious human is the patient who shows symptoms of dengue disease. Recovered human is the infected human after the viremia stage until after they recover from dengue virus infection. The vector population is separated into only two classes because it never recovers from infection [2]. Let

$\bar{S}(t)$ is the number of susceptible person at time t,

$\bar{E}(t)$ is the number of asymptomatic infectious person at time t,

$\bar{I}(t)$ is the number of symptomatic infectious person at time t,

$\bar{R}(t)$ is the number of recovered person at time t,

$\bar{S}_v(t)$ is the number of susceptible vector population at time t,

$\bar{I}_v(t)$ is the number of infectious vector population at time t.

In our SEIR model, the dynamics of each component of the human population is given by

$$\frac{d}{dt}\bar{S} = \rho N_t - \frac{b(\beta_{ha}+\beta_{hs})}{N_t}\bar{S}\bar{I}_v - \mu_h\bar{S} \quad (1)$$

$$\frac{d}{dt}\bar{E} = \frac{b\beta_{ha}}{N_t}\bar{S}\bar{I}_v - (\mu_h + r)\bar{E}, \quad (2)$$

$$\frac{d}{dt}\bar{I} = \frac{b\beta_{hs}}{N_t}\bar{S}\bar{I}_v - (\mu_h + r)\bar{I}, \quad (3)$$

$$\frac{d}{dt}\bar{R} = r(\bar{E}+\bar{I}) - \mu_h\bar{R}, \quad (4)$$

For the vector population categories, we have

$$\frac{d}{dt}\bar{S}_v = C - \frac{b\beta_v}{N_t}\bar{S}_v(\bar{E}+\bar{I}) - \mu_v\bar{S}_v \quad (5)$$

$$\frac{d}{dt}\bar{I}_v = \frac{b\beta_v}{N_t}\bar{S}_v(\bar{E}+\bar{I}) - \mu_v\bar{I}_v \quad (6)$$

where

N_t is the total number of human population,

ρ is the birth rate of the human population,

b is the biting rate of the vector population,

β_{ha} is the transmission probability of dengue virus from vector population to human population and become asymptomatic infectious human population,

β_{hs} is the transmission probability of dengue virus from vector population to human population and become symptomatic infectious human population,

β_v is the transmission probability of dengue virus from human population to vector population,

μ_h is the death rate of the human population,

r is the recover rate of the human population,

C is the constant recruitment rate of the vector population,

μ_v is the death rate of the vector population.

We divide the human class by total human population and the mosquito classes by the total mosquito populations; we get the densities for each class. We also have $S + E + I + R = 1$ and $S_v + I_v = 1$ where the absence of the prime denotes a density. Because of these two constrains, only four equations are needed to define the model, i.e.,

$$\frac{d}{dt}S = \rho - (\theta_{ha} + \theta_{hs})SI_v - \mu_h S, \quad (7)$$

$$\frac{d}{dt}E = \theta_{ha}SI_v - (\mu_h + r)E, \quad (8)$$

$$\frac{d}{dt}I = \theta_{hs}SI_v - (\mu_h + r)I, \quad (9)$$

and

$$\frac{d}{dt}I_v = \theta_v(1 - I_v)(E + I) - \mu_v I_v \quad (10)$$

where

$$\theta_v = b\beta_v \quad (11)$$

and

$\theta_{ha} = b\beta_{ha}q$, $\theta_{hs} = b\beta_{hs}q$ with

$$q = \frac{(C/\mu_v)}{N_T} \quad (12)$$

3 Analysis of the mathematical model

3.1 Analytical results

The equilibrium states are obtained by setting the RHS of equations (7) to (10) to zero. We get two equilibrium states, the disease free state, $B_0' = (1,0,0,0)$ and the endemic equilibrium state, $B_1' = (S^*, E^*, I^*, I_v^*)$

where
$$S^* = \frac{\varphi + N}{\varphi + NH}, \quad (13)$$

$$E^* = \frac{H_a}{H}\frac{(H-1)}{(\varphi + NH)}, \quad (14)$$

$$I^* = \frac{H_s}{H}\frac{(H-1)}{(\varphi + NH)}, \quad (15)$$

$$I_v^* = \frac{\varphi}{H}\frac{(H-1)}{(\varphi + N)} \quad (16)$$

where

$$\varphi = \frac{b\beta_v}{\mu_v}, \qquad N = \frac{\mu_h + r}{\mu_h},$$

$$H_a = \frac{b^2\beta_{ha}\beta_v q}{\mu_v(\mu_h + r)}, \qquad H_s = \frac{b^2\beta_{hs}\beta_v q}{\mu_v(\mu_h + r)}$$

and
$$H = \frac{b^2(\beta_{ha} + \beta_{hs})\beta_v q}{\mu_v(\mu_h + r)} \quad (17)$$

The local stability of an equilibrium state is determined from the Jacobian (gradient) matrix of the RHS of equations (7)-(10) evaluated at the equilibrium state. If all eigenvalues (obtained by diagonalizing the Jacobian matrix) have negative real parts, then the equilibrium state is locally asymptotically stable.

i) For the disease free state, $B_0' = (1,0,0,0)$,

the eigenvalues are

$$\lambda_1 = -\mu_h,$$
$$\lambda_2 = -N\mu_h,$$
$$\lambda_3 = \frac{-(N\mu_h + \mu_v) - \sqrt{(N\mu_h - \mu_v)^2 + 4N\mu_h\mu_v H}}{2},$$
$$\lambda_4 = \frac{-(N\mu_h + \mu_v) + \sqrt{(N\mu_h - \mu_v)^2 + 4N\mu_h\mu_v H}}{2}.$$

It can be easily seen that λ_1, λ_2 and λ_3 have negative real parts. Next, we check the sign for the real part of eigenvalue λ_4.

λ_4 has negative real part when

$$\sqrt{(N\mu_h - \mu_v)^2 + 4N\mu_h\mu_v H} < (N\mu_h + \mu_v)$$
$$(N\mu_h - \mu_v)^2 + 4N\mu_h\mu_v H < (N\mu_h + \mu_v)^2$$
$$H < 1.$$

Thus all eigenvalues have negative real part for $H < 1$.

ii) For the endemic equilibrium state, $B_1' = (S^*, E^*, I^*, I_v^*)$, the eigenvalues are found

by solving the characteristic equation.

$$(\lambda + N\mu_h)(\lambda^3 + A_2\lambda^2 + A_1\lambda + A_0) = 0 \quad (18)$$

where

$$A_2 = \frac{(\varphi + N(N+H+\varphi))\mu_h}{N+\varphi} + \frac{H(N+\varphi)\mu_v}{NH+\varphi}$$

$$A_1 = \frac{N(NH+\varphi)\mu_h^2}{N+\varphi} + \frac{(H\varphi + N(H^2+(H-1)\varphi))\mu_h\mu_v}{NH+\varphi}$$

$$A_0 = N(H-1)\mu_h^2\mu_v \quad (19)$$

It can be seen that one eigenvalue has negative real part. The other eigenvalues have negative real part if it satisfies the Routh-Hurwitz criteria [3], that is

$$A_2 > 0, A_1 > 0 \text{ and } A_2A_1 > A_0 \quad (20)$$

It can be demonstrated that the coefficients A_2, A_1 and A_0 satisfy (20) for $H > 1$.

Therefore the endemic equilibrium state would be local asymptotically stable if $H > 1$.

3.2 Numerical results

We are interested in the transmission of diseases, we should only be interested in whether a person is infectious or not and is immune or not, not whether he is sick. Both asymptomatic and symptomatic infectious human can transmit dengue virus. The susceptible class is made up of persons who have no immunity and are not infectious. A person infected with the dengue virus is only infectious during the period of viremia, which lasts around three days. After that, the person remains sick for one or two weeks. Once the person becomes well, he enters into the recovery class with life long immunity to the virus. While the person is infected with the virus, he also has immunity to further infection by a new virus. Accordingly, a recovered person is the same as an infected person after the viremia period. Since the viremia period last three days [4]. the recovery rate should be equal to 1/3 per day and not the inverse of the length of the illness. Most of the other parameters are determined by the real life observations. They are μ_h = 0.0000456 day^{-1}, corresponding to a life expectancy of 60 years; μ_v = 0.071 per day, corresponding to a mosquito mean life of 14 days; b = 0.33, one bite providing enough blood meal for three days; the transmission probabilities (β_{ha}, β_{hs}, β_v) are chosen: β_{ha} = 0.8, β_{hs} = 0.2 and β_v = 0.75. The ratio q can be adjusted to give a desired value of H. We let q equals to 0.2 and 3, we find that H = 0.7 and 10. The equilibrium state would be the disease free equilibrium state (1,0,0,0) and the endemic equilibrium state (0.0966436, 0.00009885, 0.0000247124, 0.000430542), respectively.

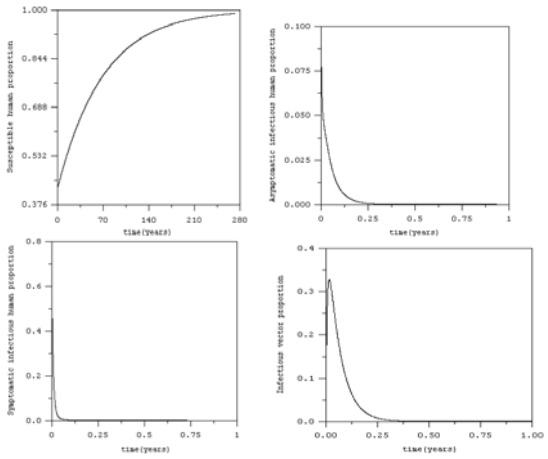

Fig.1. Time series of susceptible human, Asymptomatic infectious, Symptomatic infectious and infectious vector population. The values of the parameter are μ_h = 0.0000456 day^{-1}, μ_v = 0.071 day^{-1}, b = 1/3 day^{-1}, β_{ha} = 0.8, β_{hs} = 0.2, β_v = 0.75, q = 0.2, r = 1/3 day^{-1}, H = 0.7.

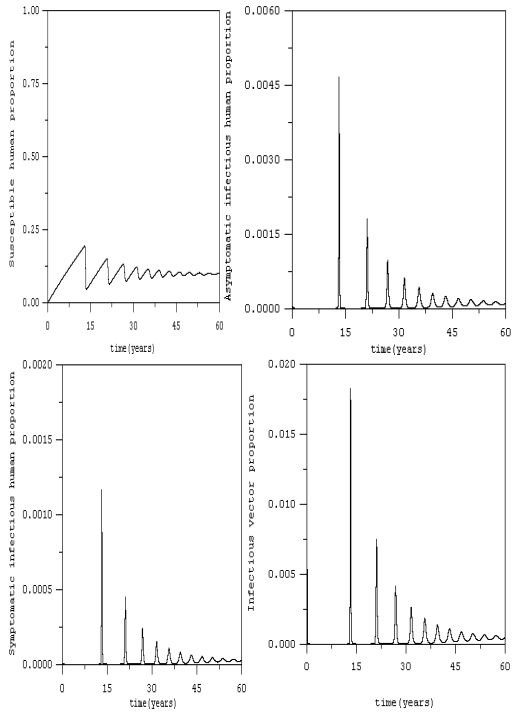

Fig.2. Time series of susceptible human, Asymptomatic infectious, Symptomatic infectious and infectious vector population. The values of the parameter are $\mu_h = 0.0000456$ day^{-1}, $\mu_v = 0.071$ day^{-1}, b = 1/3 day^{-1}, $\beta_{ha} = 0.8$, $\beta_{hs} = 0.2$, $\beta_v = 0.75$, q = 3, r = 1/3 day^{-1}, H = 10.

We show the time development of susceptible human, Asymptomatic infectious, Symptomatic infectious and infectious vector population. The value of H less than 1, the numerical solutions are shown in figure 1. Figure 2 show the numerical solutions for H greater than 1. We will see that the numerical solutions oscillate to the disease free and endemic equilibrium states, respectively.

4 Discussion and conclusion

The mathematical model which we analyze in this study, the human and vector population are assumed that constant size. The quantity $H' = \sqrt{H}$ is the basic reproductive number of the disease where $H = \dfrac{b^2(\beta_{ha} + \beta_{hs})\beta_v(C/\mu_v)}{\mu_v(\mu_h + r)N_t}$, it indicates that average number of secondary patients that one patient can produce if introduced into a susceptible person. For a disease to be capable of invading and establishing itself in a host person, this must be greater than one. If the number is less than one, then every successive generation will diminish in size until its number approaches zero. To determine what this number is, we note that an infectious human will be bitten by $\dfrac{b(C/\mu_v)}{(\mu_h + r)N_t}$ mosquitoes, during the time of human is infectious. A proportion of them will become infectious (the above numbers multiplied by β_V). One of these infectious mosquitoes will in turn bite $\dfrac{b}{\mu_v}$. Multiplying this number by $\beta_a + \beta_s$, we obtain the number of human infected by an infectious mosquito. Multiplying the number of infected human by the number of mosquitoes infected during the lifetime of the infectious human, we obtain the value of H.

The expressions for the basic reproduction number are yielded in the different models. Theses expressions have provided for the control of the various diseases. For example, the expression of the basic reproduction number for the spread of Malaria is given by

$$H = \frac{b^2\beta_h\beta_v q}{\mu_v(\mu_h + r)} \qquad (21)$$

where q is the ratio between the vector population and the human population. Corresponding to the epidemiological data, Molineaux and Gramiccia [5] estimated H to be 80 for the Malaria epidemic in Northern Nigeria. The implication of this (each infective person infects 80 other people) points to possible shortcoming of the model.

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