International Journal of Applied Mathematics
& Statistical Sciences (IJAMSS)
ISSN 2319-3972
Vol. 2, Issue 3, July 2013, 41-46

International Academy of Science,
Engineering and Technology
Connecting Researchers; Nurturing Innovations

SPR_ SODE MODEL FOR DENGUE FEVER

S. DHEVARAJAN[1], A. IYEMPERUMAL[2], S. P. RAJAGOPALAN[3] & D. KALPANA[4]

[1]Assistant Professor, Dr. MGR Educational and Research Institute University, Chennai, Tamil Nadu, India

[2]Professor, Dr. MGR Educational and Research Institute University, Chennai, Tamil Nadu, India

[3]Professor Emeritus, Dr. MGR Educational and Research Institute University, Chennai, Tamil Nadu, India

[4]Senior Lecturer, Department of Chemistry, PSB Polytechnic College, Chennai, Tamil Nadu, India

ABSTRACT

Millions of people are travelling from country to country every day. The major threat is disease spreading that causes greater health hazards [9]. Dengue fever is one of the emerging threats now a days throughout the world spread by mosquitoes. The mosquito, "Aedes Ageypti" performs the work of a carrier (i.e) the medium for transmitting, for the spread of Dengue fever (DF).

In this paper, Stochastic Ordinary differential equation model (SODE) for DF is proposed for the spread of DF. One can understand the underlying processes and develop effective prevention strategies

KEYWORDS: Dengue Fever, Death, Infection, ODE, Probability, Recovery, Susceptible

INTRODUCTION

Dengue is a reemerging disease mainly in cities throughout the world. This is found in tropical and subtropical region both in urban and semi urban areas. Four distinct but closely related viruses cause this disease [1]. These viruses are transmitted to humans by infective female Aedes Ageypti mosquito[6].

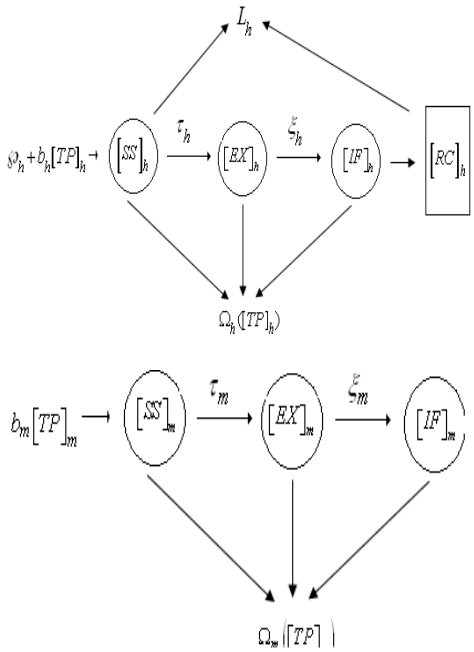
This fever can go up to 39.5 degree to 41.4 degree Celsius. (i.e) 103.1 – 106.52 degree Fahrenheit[3]. It is accompanied by headache and muscle or bone pain. There are also other symptoms like, nausea, vomiting, loss of appetite, pain in eyes, and rashes on skin.

They affect the white blood cells first. Dengue illness is mostly confused with the other viral diseases. This fever may vanish and then reoccur along with skin rashes [8]. There is no drug available for the specific treatment of dengue. This is also called break bone fever. The symptoms of dengue are evident within 2-7 days of infected mosquito bite [1]. There is a need for a mathematical model for dengue in order to protect our society against it.

MODELING THE EPIDEMIOLOGY

There are many mathematical models for various diseases. Consider the model Susceptible(S), Infection (I), Recovery (R) known as SIR by Kermack-McKendrick [10]. SIR is one of the most basic epidemiological models from 1927[4]. This is the most widely used model for the spread of disease. In 1957 Macdonald [4] improved the model to a two dimensional model with one variable representing human as one variable and the other one representing mosquitoes.

The extension of this model was proposed by Dietz, Molineaux and Thomas [2]. But this SIR model is not an apt model for DF, since contact between the infected and susceptible humans is not the only source for new infections. A better dengue model should require tracking of both humans and mosquitoes. Hence, both are included in order to increase the accuracy of the model. The model proposed by Ngwa Shu [5] was considered to develop the model for DF.



Let $\left[SS\right]_h$ represent the number of susceptible humans at any time t. $\left[EX\right]_h$ represents the number of exposed humans at any time t. $\left[IF\right]_h$ represents the number of infectious humans at any time t. $\left[RC\right]_h$ represents the number of recovered humans at any time t. $\left[SS\right]_m$ denotes the number of susceptible mosquitoes at any time t. $\left[EX\right]_m$ denotes the number of exposed mosquitoes at any time t. $\left[IF\right]_m$ denotes the number of infectious mosquitoes at any time t. $\left[TP\right]_h$ denotes the total number of human population at any time t and $\left[TP\right]_m$ denotes the total number of mosquitoes population at any time t.

Hence $\left[TP\right]_h = \left[SS\right]_h + \left[EX\right]_h + \left[IF\right]_h + \left[RC\right]_h$ and $\left[TP\right]_m = \left[SS\right]_m + \left[EX\right]_m + \left[IF\right]_m$

Let the per capita density dependent death and emigration rate for human be $\Omega_h\left(\left[TP\right]_h\right)$. This is equal to the sum of density independent part of the death (and emigration) rate for human $\left[DID\right]_h$ and the product of density dependent part of the death (and emigration) rate for human $\left[DDD\right]_h$ and the total human population at any time 't' $\left[TP\right]_h$.

Hence $\Omega_h\left(\left[TP\right]_h\right) = \left[DID\right]_h + \left[DDD\right]_h\left[TP\right]_h$

The dimension for $\left[DID\right]_h$ and $\left[DID\right]_m$ is $Time^{-1}$. The dimension for $\left[DDD\right]_h$ is $Humans^{-1}\, x\, Time^{-1}$ and for $[DDD]_m$ is $Mosquito^{-1}\, x\, Time^{-1}$

Let the immigration rate for human be $\wp_h$. The dimension for $\wp_h$ becomes $Humans\, x\, Time^{-1}$.

Let per capita density dependent death rate for mosquitoes be $\Omega_m\left(\left[TP\right]_m\right)$. This is equal to the sum of density independent part of the death rate for mosquitoes $\left[DID\right]_m$ and the product of density dependent part of the death rate for

mosquitoes $\left[DDD\right]_m$ and $\left[TP\right]_m$ the total mosquitoes population at any time 't'.

Hence $\Omega_m\left(\left[TP\right]_m\right) = \left[DID\right]_m + \left[DDD\right]_m\left[TP\right]_m$

The probability that the mosquito is infectious is the number of infectious mosquitoes divided by the total number of mosquito population.

Hence we have, $\frac{I_m}{\left[TP\right]_m}$. Let $\frac{I_m}{\left[TP\right]_m} = \beta_m$.

Let Φ_m be the number of times one mosquito would want to bite a human per unit of time, provided the human is freely available. The dimension for Φ_m is $Time^{-1}$.

Let Φ_h be the maximum number of mosquito bites a human can have per unit of time. The dimension for Φ_h is $Time^{-1}$.

Let $\left[MB\right]_h$ and $\left[MB\right]_m$ represent the number of mosquito bites a human can have per unit of time't' and the number of times a mosquito bites humans per unit of time 't' respectively. Hence one can easily interpret that

$$\left[MB\right]_h\left(\left[TP\right]_h,\left[TP\right]_m\right) = \frac{\Phi_m\left[TP\right]_m\Phi_h}{\Phi_m\left[TP\right]_m + \Phi_h\left[TP\right]_h} \text{ and}$$

$\left[MB\right]_m\left(\left[TP\right]_h,\left[TP\right]_m\right) = \frac{\Phi_m\left[TP\right]_h\Phi_h}{\Phi_m\left[TP\right]_m + \Phi_h\left[TP\right]_h}$. The dimensions for $\left[MB\right]_h$ and $\left[MB\right]_m$ is $Time^{-1}$.

The infection rate of human is the product of the number of mosquito bites a human can have per unit of time 't' and the probability of transmission of the viral from mosquito to human P_{mh} . P_{hm} is dimensionless.

Therefore, $\tau_h = \left[MB\right]_h\left(\left[TP\right]_h,\left[TP\right]_m\right)P_{mh}\beta_m$.

In the similar way, one can obtain the infection rate for mosquitoes. Let this be τ_m .

Let $\left[RC\right]_h$ denote at any time t, the number of recovered humans. τ_m is the product of the number of times a mosquito bites humans $\left[MB\right]_m$ and the summation of the force of infection from the infectious human to the recovered human $\left[P_{hm}.\beta_h + \overline{P_{hm}}.\frac{\left[RC\right]_h}{\left[TP\right]_h}\right]$. , where P_{hm} be the probability of transmission of infection from an infectious human to a susceptible mosquito given that there is a contact between two occurs and $\overline{P_{hm}}$ gives the complementary probability of P_{hm} . $\overline{P_{hm}}$ dimensionless, Since, P_{hm} is dimensionless..

Hence $\tau_m = \left[MB\right]_m\left(\left[TP\right]_h,\left[TP\right]_m\right).\left[P_{hm}.\beta_h + \overline{P_{hm}}.\frac{\left[RC\right]_h}{\left[TP\right]_h}\right]$ Let ξ_h be the rate at which the exposed humans move

to the infectious state. Then ultimately, the average duration of the latent period for humans is given by $\frac{1}{\xi_h}$. The dimension of ξ_h is $Time^{-1}$.

Those humans who are infected only can move to the recovery state. Let the rate of those humans who are moving from the infectious state to the recovered state be θ_h. Then the average duration of the infectious period for human is given by $\frac{1}{\theta_h}$. The dimension of θ_h is $Time^{-1}$.

Let L_h be the rate of the immune period for humans. Then the average duration of the immune period for humans is given by $\frac{1}{L_h}$. The dimension of L_h is $Time^{-1}$.

In order to investigate about the transmission of the disease in an area, one has choose the values of $\left[DID\right]_h$ and $\left[DDD\right]_h$ appropriately and that should stabilize the human population. The same interpretation can be given corresponding to the mosquito parameters $\left[DID\right]_m$ and $\left[DDD\right]_m$ also. Let $\left[BIR\right]_h$ and $\left[BIR\right]_m$ denote per capita birth rate for humans and mosquitoes respectively.

In this paper, up to17 parameters and 9 states are defined. All these parameters and the figure, which is acting as a flow diagram, satisfy the following system of Ordinary differential equations, which become SODE model for DF.

$$\frac{d}{dt}\left[SS_h\right]=\wp_h+b_h\left[\left[TP\right]_h\right]+L_h\left[\left[RC\right]_h\right]-\tau_h(t)\left[SS\right]_h-\Omega_h\left[\left[TP\right]_h\right]\left[SS\right]_h$$

$$\frac{d}{dt}\left[EX_h\right]=\tau_h(t)\left[SS\right]_h-\xi_h\left[EX\right]_h-\Omega_h\left(\left[TP\right]_h\right)\left[EX\right]_h$$

$$\frac{d}{dt}\left[IF_h\right]=\xi_h\left[EX\right]_h-\left[RC\right]_h\left[IF\right]_h-\Omega_h\left(\left[TP\right]_h\right)\left[RC\right]_h$$

$$\frac{d}{dt}\left[RC_h\right]=\theta_h\left[IF\right]_h-L_h\left[RC\right]_h-\Omega_h\left(\left[TP\right]_h\right)\left[IF\right]_h-\eta\left[IF\right]_h$$

$$\frac{d}{dt}\left[SS_m\right]=[BIR]_m\left[TP\right]_m-\tau_m(t)\left[SS\right]_m-\Omega_m\left(\left[TP\right]_m\right)\left[SS\right]_m$$

$$\frac{d}{dt}\left[EX_m\right]=\tau_m(t)\left[SS\right]_m-\xi_m\left[EX\right]_m-\Omega_m\left(\left[TP\right]_m\right)\left[EX\right]_m$$

$$\frac{d}{dt}\left[IF_h\right]=\xi_m\left[EX\right]_m-\Omega_m\left(\left[TP\right]_m\right)\left[IF\right]_m \quad \text{.....(A)}$$

Analysis of SODE Model

Dividing each state population by the total population one can scale the state population. Let us denote each scaled population by small letters. (i.e) $\left[ex\right]_h,\left[if\right]_h,\left[rc\right]_h,\left[ex\right]_m$ and $\left[if\right]_m$ denote at time‘t’, the proportion of exposed human, infected human, recovered human, exposed mosquitoes and infected mosquitoes respectively.

$$\frac{d}{dt}[ex]_h = \frac{\phi_h\phi_m P_{mh}[if]_m}{\phi_m[TP]_m + \phi_h[TP]_h}.[TP]_m.[1-[ex]_h-[if]_h-[re]_h] - \left[\xi_h + [BIR]_h + \frac{\wp_h}{[TP]_h}\right][ex]_h + \eta_h[if]_h[ex]_h$$

$$\frac{d}{dt}[if]_h = \xi_h[ex]_h - \left(\theta_h + [BIR]_h + \frac{\wp_h}{[TP]_h}\right)[if]_h + \eta_h[if]_h^2$$

$$\frac{d}{dt}[rc]_h = \theta_h[if]_h - \left(L_h + [BIR]_h \frac{\wp_h}{[TP]_h}\right)[rc]_h + \eta_h[if]_h[TP]_h$$

$$\frac{d}{dt}[TP]_h = \wp_h + \theta_h[TP]_h - \left([DID]_h + [DDD]_h[TP]_h\right).[TP]_h - \eta_h[if]_h[TP]_h$$

$$\frac{d}{dt}[ex]_m = \frac{\phi_h\phi_m}{\phi_m[TP]_m + \phi_h[TP]_h}.[TP]_h.[P_{mh}[if]_h + P_{mh}[rc]_h].[1-[ex]_h-[if]_h] - [\xi_h + [BIR]_m][ex]_m$$

$$\frac{d}{dt}[if]_h = \xi_m[ex]_m - [BIR]_m[if]_m.$$

$$\frac{d}{dt}[TP]_m = [BIR]_m[TP]_m - \left([DID]_m + [DDD]_m[TP]_m\right)[TP]_m \quad \ldots\ldots(B)$$

It can be shown that DF model (B) has exactly one equilibrium point $x_{nodis} = \left(0,0,0,N_h^*,0,0,N_m^*\right)$, with no disease in the population.

By setting, the LHS of (B) equal to zero, $[ex]_h, [if]_h, [rc]_h, [ex]_m, [if]_m$ all equal to zero and solving for $[TP]_h$ and $[TP]_m$ one can get, $[TP]_h^* = \frac{([BIR]_h - [DID]_h) + \sqrt{[[BIR]_h - [DID]_h]^2 - 4[DDD]_h\wp_h}}{[DDD]_h}$ and $[TP]_m^* = \frac{[BIR]_m - [DID]_m}{[DDD]_m}$.

Now, one of the parameters in epidemiological models is the reproductive number R_0. This R_0 can be defined as the number of infections that would result from one infectious individual (Either human or mosquito) over the infectious period, given that all the other individuals are susceptible.

This can be defined as, $R_0 = \sqrt{\Re_{hm}.\Re_{mh}}$, where $\Re_{hm}$ and $\Re_{mh}$ are the number of humans that one mosquito infects throughout its infectious lifetime if all humans are susceptible and the number of mosquitoes that one human infects through the duration of the infectious period, if all mosquitoes are susceptible respectively. This can be written in mathematical notation as,

$$\Re_{hm} = \frac{\xi_m}{\xi_m + [DID]_m + [DDD]_m[TP]_m^*} \frac{\phi_h\phi_m P_{mh}[TP]_h^*}{\phi_m[TP]_m^* + \phi_h[TP]_h^*} P_{mh}\left[[DID]_m + [DDD]_m[TP]_m^*\right]^{-1}$$

$$\Re_{mh} = \frac{\xi_h}{\xi_h + [DID]_h + [DDD]_h[TP]_h^*} \frac{\phi_h\phi_m P_{mh}[TP]_m^*}{\phi_h[TP]_h^* + \phi_m[TP]_m^*} \left(\theta_h + \eta_h + [DID]_h + [DDD]_h[TP]_h^*\right)^{-1}$$
$$\left[P_{mh} + \overline{P_{mh}}.\theta_h\left(\eta_h + [DID]_m + [DDD]_m[TP]_h^*\right)^{-1}\right]$$

It can also be shown that the disease free equilibrium point $x_{nodis} = \left(0,0,0,N_h^*,0,0,N_m^*\right)$, is locally asymptotically stable, if $R_0 < 1$ and unstable if $R_0 > 1$

CONCLUSIONS

In this paper, it is proposed to present a mathematical model for DF. The step by step construction of the model is illustrated. The model is analyzed by finding equilibrium point and reproductive ratio. The accuracy of this model can be improved by introducing more variables.

REFERENCES

1. Chen LH, Wilson ME "Dengue and chikungunya infections in travelers". Curr. Opin. Infect. Dis. **23** (5): 438–44.
2. Dietz.K , L. Molineaux, and A. Thomas. A malaria model tested in the african savannah. Bulletin World Health Organ, 50:347{357, 1990.
3. Gubler.DJ. Dengue and Dengue hemorrhagic fever, clinical morphology reviews, 11, 480-496. 1998.
4. G. MacDonald. The Epidemiology and Control of Malaria. Oxford University Press, London, 1957.
5. A. Ngwa and W.S Shu. A mathematical model for endemic malaria with variable human and mosquito populations. Math. Comput. Modelling, 32:747-763, 2000.
6. Reiter P. et al. (2003). Texas Lifestyle Limits Transmission of Dengue Virus. Emerging Infectious Diseases, 9:86-89.
7. Scott TW, et al. (2000) Longitudinal studies of Aedes aegypti (Diptera: Culicidae) in Thailand and Puerto Rico: Blood feeding frequency. J Med Entomol 37:89–101.
8. WHO (2012). Dengue and severe dengue - Fact sheet N°117, November 2012. http:// www. who. int/mediacentre/factsheets/fs117/en/# (Accessed 2013-03-20).
9. W.O.Kermack and A.G.Kendric. A contribution to the mathematical theory of epidemics. Proceedings of the Royal society of London series A, containing papers of mathematical and physical character, 115:700 – 721, 1927.
10. Wolff K, Johnson RA (eds.) (2009). "Viral infections of skin and mu cosa". Fitzpatrick's color atlas and synopsis of clinical dermatology (6th ed.). New York: McGraw-Hill Medical. pp. 810–2. ISBN 978-0-07-159975-7