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MODELLING THE EPIDEMIOLOGY OF DENGUE WITH LOSS OF IMMUNITY

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ABSTRACT

In the paper, we consider models of SIR – SI dengue epidemic. The model considers the effect of loss (partial) of immunity on different state variables. Therefore the effect of loss of immunity or the immunity parameter (γ_1) plays a very important rule in dengue epidemic model and gives the possibility of occurrence of the dengue diseases. The characteristic roots of the model at disease -free equilibrium (DFE) point are the real and opposite sign, which indicate that no occurrence of dengue virus infection since there are no infected human or infected mosquito population. At DFE point, every human in the population is healthy and not infected with the virus. The characteristic roots at endemic equilibrium point are all negative (real part) and complex; indicate that the focus of dengue fever would be stable. The estimated value of the basic reproduction number is 2.73 with a range (2.14, 3.02). The source for the data is NVBDCP.

KEYWORDS: *Dengue, Endemic, Immunity, Basic Reproduction Number, and Stability*

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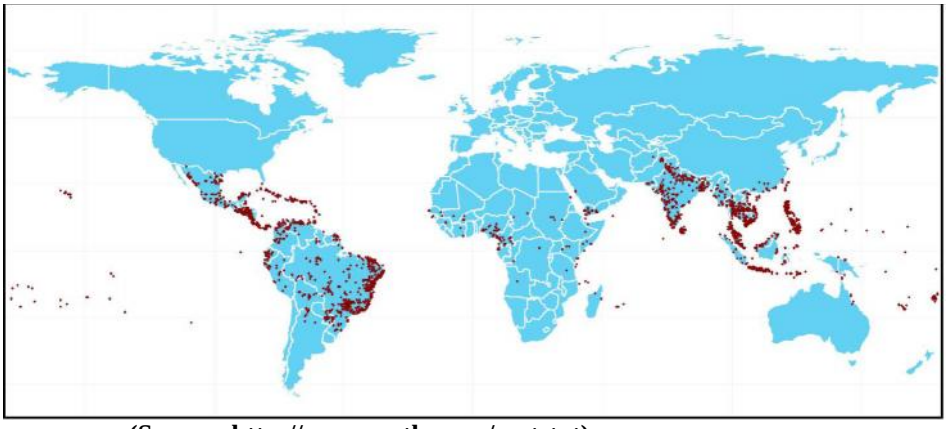
1. INTRODUCTION

1.1 Global Scenario of Dengue

Dengue virus infections are a serious cause of morbidity and mortality in most tropical and subtropical areas of the world especially in Southeast and South Asia, Central and South America, and the Caribbean. Dengue is the most rapidly spreading vector-borne viral disease in the world (Figure 1). Unlike other vector-borne diseases, it is transmitted from infected human to a female *Aedes Aegypti* mosquito by a bite and is the main vector for dengue. The World Health Organization (WHO) in 1998 has listed dengue as the tenth leading cause of death among all infectious diseases. Severe dengue (also known as dengue hemorrhagic fever) is found in tropical and sub-tropical locations in most Asian and Latin American countries. An estimated 500,000 people with severe dengue require hospitalization each year, a large proportion of these are children. About 2.5% of those affected die (Kurane and Takasaki, 2001). The incidence of dengue has grown dramatically around the world in recent decades. The actual numbers of dengue cases are un reported and many cases are misclassified. One recent estimate indicates 390 million dengue infections per year (95% credible interval 284–528 million), of which 96 million (67–136 million) manifest clinically (with any severity of disease) (Bhatt et al., 2015). Another study, of the prevalence of dengue, estimates that 3.9 billion people, in 128 countries, are at risk of infection with dengue viruses (Brady, et al., 2012).

Member States in 3 WHO regions regularly report the annual number of cases. The number of cases reported increased from 2.2 million in 2010 to 3.2 million in 2015. The disease is now endemic in more than 100 countries in the WHO regions of Africa, the Americas, the Eastern Mediterranean, South-East Asia, and the Western Pacific. In 2015, 2.35 million cases of dengue were reported in the Americas alone, of which 10,200 cases were diagnosed as severe dengue causing 1,181 deaths (WHO, 2016). In 2013, cases have occurred in Florida (United States of America) and Yunnan province of China. Dengue also continues to affect several South American countries, notably Costa Rica, Honduras, and Mexico. In Asia, Singapore has reported an increase in cases after a lapse of several years and outbreaks have also been reported in Laos. In 2014, trends indicate increases in the number of cases in the People's Republic of China, the Cook Islands, Fiji, Malaysia, and Vanuatu, with Dengue Type 3 (DEN 3) affecting the Pacific Island countries after a lapse of over 10 years. Dengue was also reported in Japan after a lapse of over 70 years. The year 2015 was characterized by large dengue outbreaks worldwide, with the Philippines are reporting more than 169, 000 cases and Malaysia is exceeding 111, 000 suspected cases, giving about 59.5% and 16% increase respectively as compared to the previous year. Brazil alone reported over 1.5 million cases in 2015, approximately 3 times higher than in 2014. Also in 2015, India (Delhi alone), recorded its worst outbreak since 2006 with over 15,000 cases. (WHO, 2016)



(Source: http://www.math.su.se/matstat)

Figure 1: Global Distribution of Dengue/Dhf

1.2 Scenario of Dengue in India

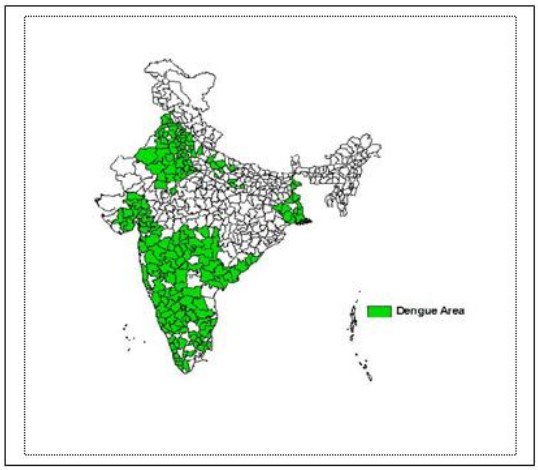
The scenario of dengue outbreaks in India has been recently reviewed. The data on the website of National Vector Borne Diseases Control (NVBDC) program show that dengue has been endemic in 16 states, Andhra Pradesh, Goa, Gujarat, Haryana, Karnataka, Kerala, Madhya Pradesh, Maharashtra, Punjab, Rajasthan, Tamil Nadu, Uttar Pradesh, West Bengal, Chandigarh, Delhi, and Puducherry (Table 1). During 2010–2012, dengue spread to the remaining states. Figure 2 shows that the distribution of dengue cases among the states of India by 2015 (see also Figure 3). Although the number of dengue cases has shown a steady rise for some states with every passing year, the mortality has reduced. Compared with the rest of South-East Asia, the number of dengue shock syndrome (DSS) cases in India remains low (Cecilia, 2014). Yang, et al., (2009a and 2009b) discussed the temperature effect on the *Aedes Aegypti* mosquito. Although dengue has been notifiable in India since 1996, the disease's impact has been underestimated because of insufficient information on incidence and cost of dengue illness. Between 2006 and 2012 the NVBDC program reported an annual average of 20,474 dengue cases and 132 deaths caused by dengue. Regional comparisons suggest that these official numbers reflect only a small fraction of the full impact of the disease (Shepard et al., 2014).

Feng, et al., (1997) constructed a model to study both the epidemiological trends of the disease and conditions that permit coexistence in competing strains. Table 2, gives dengue outbreaks in India (Delhi was frequently affected part).

Table 1: Distribution of Dengue Cases in India for Some Selected States during 2010-15

Affected States	2010	2011	2012	2013	2014	2015
Andhra Pradesh	776	1209	2299	910	1262	3159
Assam	237	0	1058	4526	85	1076
Bihar	510	21	872	1246	297	1771
Goa	242	26	39	198	168	293
Gujarat	2568	1693	3067	6272	2320	5590
Haryana	866	267	768	1784	214	9921
Karnataka	2285	405	3924	6408	3358	5077
Kerala	2597	1304	4172	7938	2575	4075
Madhya Pradesh	175	50	239	1255	2131	2108
Maharashtra	1489	1138	2931	5610	8573	4936
Orissa	29	1816	2255	7132	6433	2450
Punjab	4012	3921	770	4117	472	14128
Rajasthan	1823	1072	1295	4413	1243	4043
Tamil Nadu	2051	2501	12826	6122	2804	4535
Uttar Pradesh	960	155	342	1414	200	2892
Uttrakhand	178	454	110	54	106	1655
West Bengal	805	510	6456	5920	3934	8516
Chandigarh	221	73	351	107	13	966
Delhi	6259	1131	2093	5574	995	15867
Puduchery	96	463	3506	2215	1322	771
India	28179	18209	49373	73215	38505	93829

Source: NVBDCP, June 2016



(**Source :http://www.nvbdcp.gov.in**)

Figure 2: Distribution of Dengue/Dhf India

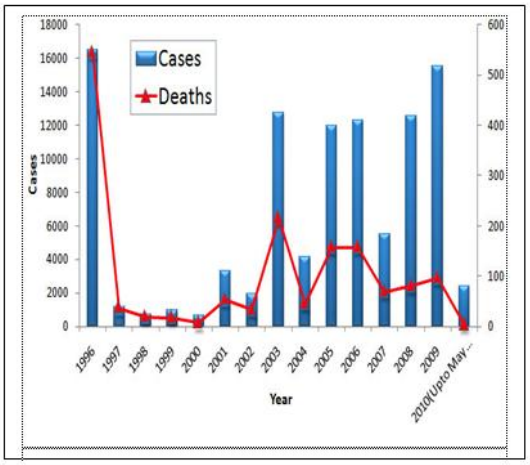


Figure 3: Situation of Dengue from 1996-2010

Due to the lack of effective drugs and vaccines, dengue is considered as a public health problem that carries a huge financial burden on the governments also. Therefore, due to the lack of effective programs to control the disease, a wide range of dengue models was developed to describe and characterize the dynamics of its transmission (Isea and Puerta, 2014; Rodrigues et al., 2011; Side and Noorani, 2013; Nuraini, et al., 2007 and Nishiura, 2006).All these authors were made the effort of proving a better understanding of the nature and dynamics of Dengue disease transmission.

Chowell, et al., (2007) estimated the reproduction number from spatial epidemic data at the level of municipalities using two different approaches, (i) using a standard dengue epidemic model and assuming pure exponential initial epidemic growth and (ii) fitting a more realistic epidemic model for the initial phase of the dengue epidemic curve.

Various aspects of dengue infections in the context of India e.g., occurrence, clinical profile, viral isolations, serological surveys, pathogenicity, and vector ecology have been discussed by Pandya (1982). Modeling of epidemiological diseases is an important tool for understanding disease behavior and prosing effective strategies in fighting against disease spread. Esteva and Vargas (1998) discussed a model for the transmission of dengue fever in a constant human population and variable vector population. The control measures of the vector population are discussed in terms of the threshold condition, which governs the existence and stability of the endemic equilibrium.

In the present paper, we consider the development of dengue epidemic model with loss of immunity because the recovery from infection by one virus provides lifelong immunity against that virus, but confers only partial and transient protection against subsequent infection by the other three viruses. There are 4 closely related serotypes of the virus that cause dengue and the lifelong immunity developed after infection. With the four closely related viruses that can cause the disease, there is a need for a vaccine that would immunize against all four types of dengue to be effective.

2. DEVELOPMENT OF MODEL

The dengue epidemic model identifies two populations, a human (host) population (N_h) and a mosquito (vector) population (N_v). The human population has three state variables; the people who may get infected with dengue virus (Susceptible, S_h), people who are infected with dengue (infected, I_h) and people who have recovered from the disease (removed, R_h). The vector (mosquito) population (N_v) is divided into two compartments; mosquitoes that are potentially may get infected with dengue virus (Susceptible, S_v) and mosquitoes that are infected with dengue virus (infected, I_v).

Table 2: Epidemiological Studies where Dengue Virus was Identified

Year	Region where Study was Conducted	Type of Dengue Virus Detected
1964	Vellore, Tamil Nadu	DV-2
1966	Vellore, Tamil Nadu	DV-3
1968	Vellore, Tamil Nadu	DV- 1,2,3 & 4
1968	Kanpur, Uttar Pradesh	DV-4
1969	Kanpur, Uttar Pradesh	DV-4 and DV-2
1970	Hardoi, Uttar Pradesh	DV-2
1983	Kolkata, West Bengal	DV-3
1985	Jalore town, South-West Rajasthan	DV-3
1988	Delhi	DV-2
1990	Calcutta, West Bengal	DV-3
1988	Rural and urban areas of Gujarat	DV-2
1993	Mangalore, Karnataka	DV-2
1996	Ludhiana, Punjab	DV- 1,2,3 & 4
1996	Lucknow	DV-2
1996	Delhi	DV-2
1997	Delhi	DV-1
1996	Delhi	DV-2 (Genotype IV)
1997	Delhi	DV-1
1996	Rural areas of Haryana	DV-2
2001	Dharmapuri district, Tamil Nadu	DV-2
2001	Gwalior, Madhya Pradesh	DV-2
2001	Chennai, Tamil Nadu	DV-3
2003	Northern India (Delhi & Gwalior)	DV-3

Table 2: Contd.,		
2005	Kolkata, West Bengal	DV-3
2003	Kanyakumari district, Tamil Nadu	DV-3
2003-04	Delhi	DV-3 (subtype III)
2003-05	Delhi	2003 - DV - 1,2,3 & 4 2005 - D - 3
2006	Delhi	DV-3
2006	Delhi	DV-1 & 3
2001-07	North India (Delhi and Gwalior region)	DV-1 (Genotype III)
2006	Delhi	DV-1,3 & 4
2008	Delhi region	DV-1,2 & 3
1956-2005	Entire country	DV-2
2002-06	Delhi	DV-1, 2, 3 & 4
2003	Delhi	DV-3 (Genotype III)
2008	Ernakulam, Kerala	DV-2 & 3
2007	Rural areas of Madurai, Tamil Nadu	DV-3 (Genotype III)
2007	Andhra Pradesh	DV-1 & 4 (Genotype I)
2003-08	Different parts of the country	DV-3 (Genotype III)
2007-09	Delhi	DV 1, 2, 3 & 4
2009-10	Pune, Maharashtra	DV-4 (Genotype I)

Source: Gupta, et al., (2012)

Therefore the model is SIR – SI dengue epidemic model. The transfer diagram of the model is as follows

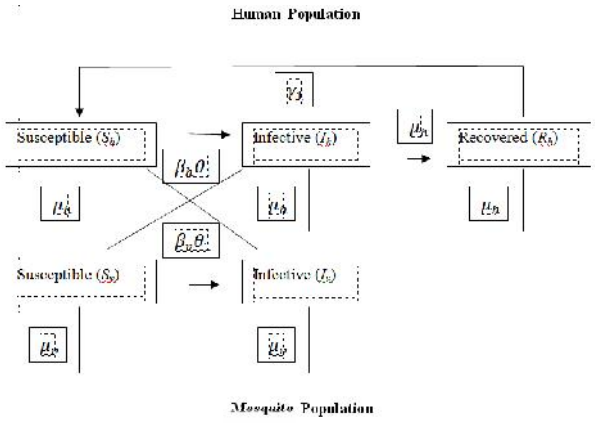


Figure 4: Transfer Diagram of the Different State Variables of Dengue Epidemic

Where β_h the is transmission probability from I_v (per bite), β_v the transmission probability from I_h (per bite), θ_1 the proportion of infected individuals who are infectious, $1/\mu_h$ the average lifespan of humans (in days), $1/\mu_v$ the average lifespan of adult mosquitoes (in days), γ_h the rate of recovery of infected individual and γ_1 the rate at which recovered individuals lose their immunity.

The system of differential equations for the host population is

$$\frac{dS_h}{dt} = \mu_h N_h - \frac{\beta_h \theta_1 I_v S_h}{N_h} - \mu_h S_h + \gamma_1 R_h$$

$$\frac{dI_h}{dt} = \frac{\beta_h \theta_1 I_v S_h}{N_h} - (\mu_h + \gamma_h) I_h \qquad (1)$$

$$\frac{dR_h}{dt} = \gamma_h I_h - (\mu_h + \gamma_1) I_h$$

And the system of differential equations for the vector population is

$$\frac{dS_v}{dt} = \mu_v N_v - \frac{\beta_v \theta_1 I_h S_v}{N_v} - \mu_v S_v$$

$$\frac{dI_v}{dt} = \frac{\beta_v \theta_1 I_h S_v}{N_v} - \mu_v I_v \quad (2)$$

With initial conditions, $S_h + I_h + R_h = N_h \Rightarrow R_h = N_h - S_h - I_h$ and

$S_v + I_v = \frac{A}{\mu_v} \Rightarrow S_v = N_v - I_v = \frac{A}{\mu_v} - I_v$ also

$$\Gamma = \left\{(S_h, I_h, R_h S_v, I_v) \in R_+^5 : (S_h + I_h + R_h \leq N_h,\ S_v + I_v \leq \frac{A}{\mu_v}\right\} \quad (3)$$

Using (3), the system of differential equations for host and vector populations can be rewritten as

$$\frac{dS_h}{dt} = \mu_h N_h - \frac{\beta_h \theta_1 I_v S_h}{N_h} - \mu_h S_h + ¥_1 R_h$$

$$\frac{dI_h}{dt} = \frac{\beta_h \theta_1 I_v S_h}{N_h} - (\mu_h + ¥_h) I_h$$

$$\frac{dR_h}{dt} = ¥_h I_h - (\mu_h + ¥_1) I_h \quad (4)$$

$$\frac{dI_v}{dt} = \frac{\beta_v \theta_1 I_h S_v}{N_v} - \mu_v I_v$$

Some assumptions in this model are (i) the total human population (N_h) is constant, (ii) there is no immigration of infected individuals into the human population, (iii) the population is homogeneous, which means that every individual of a compartment is homogenously mixed with the other individuals, (iv) the coefficient of transmission of the disease is fixed and does not vary seasonally, (v) both human and mosquitoes are assumed to be born susceptible; there is no natural protection and (vi) for the mosquito there is no resistant phase, due to its short lifetime.

To simplify, we normalize the system of equations (4) by defining new variables

$$p = \frac{S_h}{N_h}, q = \frac{I_h}{N_h}, r = \frac{R_h}{N_h} \text{ and } s = \frac{I_v}{N_v} = \frac{I_v}{A/\mu_v} \quad (5)$$

Therefore, using (5), the system of equations (4) can written as

$$p' = \mu_h(1 - p(t)) - \alpha\, p(t)\, s(t) + \lambda_1\, r(t) \quad (6)$$

$$q' = \alpha\, p(t) s(t) - ¥_1\, q(t) \quad (7)$$

$$r' = \lambda\, q(t) - \beta_2\, r(t) \quad (8)$$

$$s' = \gamma(1 - s(t)) q(t) - \delta s(t) \quad (9)$$

Where after reparameterization, we have

$\beta_1 = \gamma_h + \mu_h, \beta_2 = \gamma_1 + \mu_h, \alpha = \frac{\beta_h \theta_1 A}{\mu_v N_h}, \gamma = \beta_v \theta_1, \delta = \mu_v, \lambda = \gamma_h$ and $\lambda_1 = \gamma_1$

Solving the system of equations (6) – (9) for the state variables p, q, r and s, we get

$$p^* = \frac{\beta_1\beta_2 ¥«_h + (\beta_1\beta_2 - a a_1)\,\delta}{(\beta_1\beta_2 - a a_1) + ¥«_h\beta_1\beta_2}$$

$$q^* = \frac{\alpha\, p^* ¥«_h (1-p^*)}{\beta_1 (¥«_h (1-p^*) + (\beta_1 - \frac{a a_1}{\beta_2})\,\delta)}$$

$$r^* = \frac{a\,\alpha\, p^* ¥«_h (1-p^*)}{\beta_1\beta_2 (¥«_h (1-p^*) + (\beta_1 - \frac{a a_1}{\beta_2})\,\delta)} \qquad (10)$$

$$S^* = \frac{¥«_h (1-p^*)}{¥«_h (1-p^*) + (\beta_1 - \frac{a a_1}{\beta_2})\,\delta_1}$$

The system of equations (6) – (9) yields two equilibrium points, one is disease- free equilibrium (DFE) point P^0 = (1, 0, 0, 0) and the other is endemic equilibrium point P^* = (p^*, q^*, r^*, s^*). Where p^*, q^*, r^* and s^* are defined in (10).

Linearization of a systems of differential equations (6) – (9) on the DFE point (1,0,0,0) yields the following characteristic equation

$$\begin{pmatrix} p^1 \\ q^1 \\ r^1 \\ s^1 \end{pmatrix} = \begin{pmatrix} -\mu_h & 0 & a_1 & -\alpha \\ 0 & -\beta_1 & 0 & \alpha \\ 0 & a & -\beta_2 & 0 \\ 0 & ¥ & 0 & -¢ \end{pmatrix} \begin{pmatrix} p \\ q \\ 0 \\ s \end{pmatrix}$$

Therefore

$$\begin{vmatrix} -\mu_h - a^* & 0 & a_1 & -\alpha \\ 0 & -\beta_1 - a^* & 0 & \alpha \\ 0 & a & -\beta_2 - a^* & 0 \\ 0 & ¥ & 0 & -\delta - a^* \end{vmatrix} = 0 \qquad (11)$$

This is the determinant of jacobian matrix at DFE point, P^0 = (1, 0, 0,0). Solving (11), we get λ^*_1 =- μ_h and another three roots are obtained by solving the Characteristic polynomial equation,

$$\lambda^{*3} + (\beta_1 + \beta_2 + \delta)\lambda^{*2} + (\beta_1\beta_2 + \beta_1\delta + \beta_2\delta + \alpha\gamma)\lambda^{*} + (\beta_1\beta_2\delta + \alpha\beta_2\gamma) = 0 \quad (12)$$

Similarly, linearization of the system of equations (6) – (9) on the endemic equilibrium point, $P^* = (p^*, q^*, r^*, s^*)$ gives the following Jacobian matrix evaluated at P^* using (10)

$$J(P^*) = \begin{pmatrix} -\mu_h - \alpha\frac{S_1}{S_2} & 0 & a_1 & -\alpha\frac{B}{A} \\ \alpha\frac{S_1}{S_2} & -\beta_1 & 0 & \alpha\frac{B}{A} \\ 0 & a & -\beta_2 & 0 \\ 0 & ¥(1 - \frac{S_1}{S_2}) & 0 & -¥\frac{Q_1}{Q_2} - ¢ \end{pmatrix} \quad (13)$$

Where $S_1 = ¥«_h(A - B)$

$$S_2 = ¥«_h(A - B) + A(\beta_1 - \frac{aa_1}{\beta_2})\delta$$

$$Q_1 = \alpha\beta¥«_h(A - B)$$

$$Q_2 = A\beta_1¥«_h(A - B) + A(\beta_1 - \frac{aa_1}{\beta_2})\delta$$

$$A = \beta_1\beta_2(¥«_h + 1) - aa_1$$

$$B = \beta_1\beta_2(¥«_h + \delta) - aa_1\delta$$

3. EFFECT OF LOSS OF IMMUNITY

We consider the effect of loss of immunity on different state variables. Here the recovery of an individual from infection by one virus provides lifelong immunity against that virus, but confers only partial and transient protection against subsequent infection by the other three forms of dengue viruses.

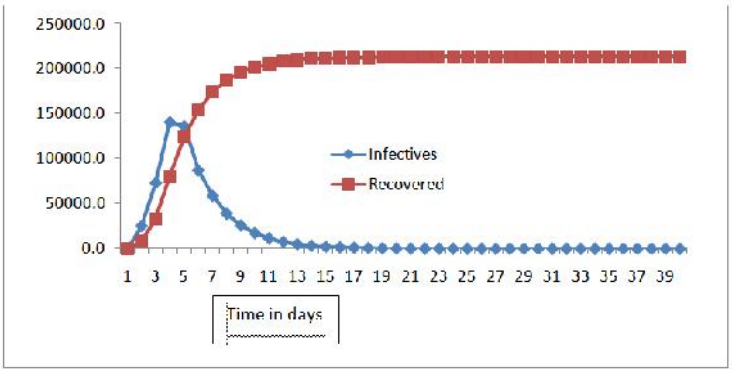


Figure 5: Effect of Recovery Rate on State Variables, when Individuals Confer Permanent Immunity

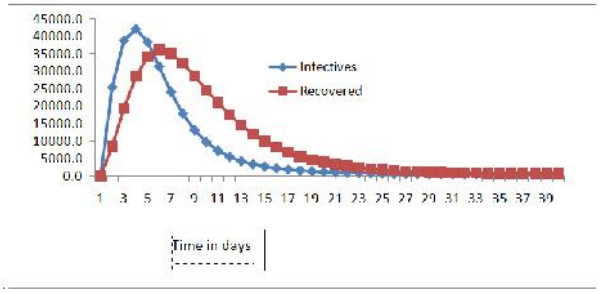


Figure 6: Effect Recovery Rate on the State Variables, When Individuals Lose their Immunity

The parameter values used for this are given in **Table 3**. From **Figure 5**, it is observed that when an individual doesn't lose his/her immunity the maximum number of individuals can be protected and from Figure 6, it is observed that, up to certain time, the recovered individuals increase, once they start losing their immunity, the recovered individuals move to susceptible class thereby recovered individuals get reduced.

4. NUMERICAL ILLUSTRATION OF THE MODEL

The following table gives model parameters, their values and the sources of parameters.

Table 3: Parameter Values and their Sources

Parameter	Value	Source
N_h	480000	Rodrigues, et al., (2011): Chowell, et al., (2007)
θ_1	4.5	Estimated
β_{vh}	0.3	Asmaidi, et al,.(2014): Rodrigues, et al., (2011)
β_{hv}	0.3	Asmaidi, et al,.(2014): Rodrigues, et al., (2011)
μ_h	1/71 x 365	Rodrigues, et al., (2011)
[illegible]	1/3	Asmaidi, et al,.(2014)
[illegible]	¼	Rodrigues, et al., (2011)
μ_v	1/11	Rodrigues, et al., (2011): Chowell, et al., (2007)
N_v	3 N_h	Rodrigues, et al., (2011)

To determine the critical point, the equations (6)-(9) were set equal to zero and using the parameters value, we get

$$0.00004(1-p) - 4.5ps + 0.25\,r = 0$$

$$4.5\,ps - 0.33334\,q = 0 \qquad (14)$$

$$0.33334\,q - 0.25\,r = 0$$

$$0.15(1-s)q - 0.1s = 0$$

The characteristic roots at D F E point, P^0 = (1, 0, 0, 0) are obtained as

λ_1 = -0.00004, λ_2 = -0.25, λ_3 = 0.9663 and λ_4 = 0.7330

Similarly the characteristic roots at the endemic equilibrium point, P^* = (p^*, q^*, r^*, s^*) are obtained as λ_1 = -0.3907, λ_2 =-0.2741 + 0.1721i, λ_3 =-0.2741 +0.1721i and λ_4 = -0.0977.

The characteristic roots at DFE point are a real and opposite sign, which indicate that no occurrence of dengue virus infection since there are no infected human population or infected mosquito population. At DFE point, every human in the population is healthy and not infected with the virus. The characteristic roots at an endemic equilibrium point are all negative (real part) and complex; indicate that the focus of dengue fever would be stable.

5. BASIC REPRODUCTION NUMBER

An important measure of disease transmissibility is the epidemiological concept of the basic reproduction number. It provides an invasion criterion for the initial spread of the virus in a susceptible population. The basic reproduction number, denoted by R_0, is defined as the average number of secondary infections that occurs when one infective is introduced into a completely susceptible population. Using the next generation operator approach (Diekmann and Heesterbeek, 2000), we compute the basic reproductive number R_0 associated with the disease-free equilibrium point. The basic reproduction number of the model (4) is

$$R_0 = \frac{\theta_1^2 \beta_h \beta_v}{\mu_v(\mu_h+\gamma_h)} \tag{15}$$

We observe that R_0, the reproduction number of dengue, depends on the mosquito and human vital parameters, on the fraction between the susceptible mosquito and the total human population size, and also on the product of the transmission coefficients and the square of mosquitoes biting rate, $\theta_1^2\beta_h\beta_v$, emphasizing that a new case of dengue can occur only after two bites from the same mosquito. On the other hand, we also observe that dengue control appears explicitly in the expression of R_0, only on γ_h. The basic reproduction number (R_0) decreases as γ_h increases resulting in a decrease of mosquito susceptible population.

An equilibrium point P is biologically meaningful if and only if $P \in \Gamma$, where Γ is defined in (3). The biologically meaningful equilibrium points are said to be disease- free or endemic, depending on I_h and I_v: if there is no disease for both populations of humans and mosquitoes, that is, if $I_h = I_v = 0$, then the equilibrium point is said to be a Disease- Free Equilibrium (DFE), P^0; otherwise, if $I_h \neq 0$ or $I_v \neq 0$, in other words, if $I_h > 0$ *or* $I_v > 0$, then the equilibrium point is called endemic, P^*

If $R_0 < 1$, then the disease cannot invade the population and the infection will die out over a period of time. The amount of time this will take generally depends on how small the basic number is. If $R_0 > 1$, then an invasion is possible and infection can spread through the population. Generally, the larger the value of R_0, the more severe, the epidemic will be. In determining how best to reduce human mortality and morbidity due to dengue, it is necessary to know the relative importance of the different factors responsible for its transmission. **Figure 7** gives the uncertainty of the basic reproduction number related to the parameters in the model.

The basic reproduction number is most often estimated from data in the early epidemic phase, that is, prior to the introduction of initial interventions, including behavioral changes, and at a time when the effects of susceptible depletion are negligible. Using approximation (Favier et al., 2006) to (15), we derive the basic reproduction number with force of infection, Λ, which is obtained assuming the cumulative number of infections follow exponential (that is, cumulative total $\propto e^{\Lambda t}$) as

$$R_0 = \left(1 + \frac{\Lambda}{\mu_v + \gamma_h}\right)\left(1 + \frac{\Lambda}{\mu_v}\right) \tag{16}$$

Equation (16) gives the relation between the basic reproductive number, R_0 and the force of infection, Λ.

Substituting these parameter values (**Table 3**) (no vector control was in course during this epidemic) in equation (16) we obtain the estimated value of R_0 = 2.73 (with minimum and maximum values relative to the human parameter's range of R_0 = 2.14 and 3.02) with an initial growth rate of the epidemic (or the force of infection), 0.099. We have used

dengue cases in India (1996-2015) for estimating R_0. The data we used for estimation is taken from national vector -borne disease control (NVBDC) programme.

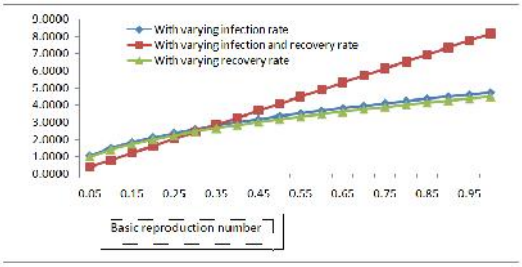


Figure 7: Basic Reproduction Number with Varying Infection and Recovery Rates

Figure 7 indicates that there is no advantage of having with varying recovery rate when infection rate is also varying. We observe that the curves similar when infection is varying, where the constant rate recovery is adopted and having a varying recovery rate when a rate of infection is constant.

6. CONCLUSIONS

The characteristic roots at DFE point are a real and opposite sign, which indicate that no occurrence of dengue virus infection since there are no infected human or mosquito population. At DFE point, every human in the population is healthy and not infected with the virus. Whereas the characteristic roots at an endemic equilibrium point are all negative (real part) and complex with the negative real part, indicates that the focus of dengue fever would be stable.

The model considers the effect of loss (partial) of immunity on different state variables. Because the recovery of an individual from infection by one virus provides lifelong immunity against that virus, but confers only partial and transient protection against subsequent infection by the other three forms of dengue viruses. Therefore the effect of loss of immunity or the immunity parameter (γ_1) plays a very important rule in dengue epidemic model and gives the possibility of occurrence of the dengue diseases. **Table 2** gives occurrence of different forms of dengue in India. For the sensitivity of the parameter, we can observe **Figure 5 and 6**. The estimated value of the basic reproduction number is 2.73 with a range (2.14, 3.02).

REFERENCES

1. *Asmaidi, Sianturi, P. and Nugrahani, E. H. (2014). A SIR Mathematical Model of Dengue Transmission and Its Simulation, IOSR Journal of Mathematics (IOSR-JM) e-ISSN: 2278-5728, p-ISSN: 2319-765X. Volume 10, Issue 5 Ver. II (Sep-Oct. 2014), PP 56-65 www.iosrjournals.org.*
2. *Bhatt, S., Gething, P.W., Brady, O.J., Messina, J.P., Farlow, A.W., Moyes, C.L., et al. (2015). The global distribution and burden of dengue. Nature, 496:504-507.*
3. *Brady, O.J., Gething, P.W., Bhatt, S., Messina, J.P., Brownstein, J.S., Hoen, A.G. et al. (2012). Refining the global spatial limits of dengue virus transmission by evidence-based consensus. PLoS Negl Trop Dis.;6:e1760. doi:10.1371/journal.pntd.0001760.*
4. *Cecilia, D. (2014). Current status of dengue and chikungunya in India, WHO South-East Asia Journal of Public Health, 3 (1)*

5. *Chowell, G., Diaz-Duenas, P., Miller, J.C., Alcazar-Velazco, A., Hyman, J.M., Fenimore, P.W. and Castillo-Chavez, C. (2007). Estimation of the reproduction number of dengue fever from spatial epidemic data, Mathematical Biosciences, xxx,: xxx–xxx.*

6. *Diekmann, O. and Heesterbeek J. A. P. Mathematical Epidemiology of Infectious Diseases: Model Building, Analysis and Interpretation. Wiley, New York, 2000.*

7. *Esteva, L. and Vargas, C. (1998). Analysis of a dengue disease transmission model, Mathematical Biosciences 150 : 131-151.*

8. *Favier, C., Degallier, N., Rosa-Freitas, M.G., Boulanger, J.P., Costa Lima, J.R., Luitgards-Moura, J.F., Menkes, C.E., Mondet, B., Oliveira, C., Weimann, E.T. and Tsouris, P. (2006). Early determination of the reproduction number for vector-borne diseases: the case of dengue in Brazil, Tropical Medicine and International Health 11:332–340.*

9. *Feng, Z., Jorge, X. and Velasco-Hernandez, (1997). Competitive exclusion in a vector-host model for the dengue fever, J. Math. Biol., 35: 523-544*

10. *Gupta, N., Srivastava, S., Jain, A. and Chaturvedi, U. C. (2012). Dengue in India, Indian J Med Res, 136, September 2012, 373-390.*

11. *http://www.math.su.se/matstat, 2016*

12. *http://www.nvbdcp.gov.in, 2016*

13. *Isea, R. and Puerta, H. (2014). Analysis of an SEIR-SEI four-strain epidemic dengue model with primary and secondary infections. Revista Electrónica Conocimiento Libre y Licenciamiento (CLIC); 7: 3-7.*

14. *Kurane and Takasaki (2001). Dengue fever and dengue haemorrhagic fever: challenges of controlling an enemy still at large, Medical Virolgy, Vol. 11(5), 301-311.*

15. *S. Dhevarajan, A. Iyemperumal, S. P. Rajagopalan & D. Kalpana, SPR_ SODE Model for Dengue Fever, International Journal of Applied Mathematics & Statistical Sciences, Volume 2, Issue 3, June-July 2013, pp. 41-46*

16. *Nishiura, H. (2006). Mathematical and statistical analyses of the spread of dengue, Dengue Bull, 30: 51–67.*

17. *Nuraini, N., Soewono, E. and Sidarto, K.A. (2007). Mathematical Model of Dengue Disease Transmission with Severe DHF Compartment, Bull. Malays. Math. Sci. Soc. (2) 30(2) : 143–157*

18. *Pandya, G. (1982). Prevalence of Dengue Infections in India, Def Sci J, Vol.32, No 4: 359-370*

19. *Rodrigues, H. S., Teresa, M., Monteiro, T., Torres, D. F. M. and Zinober, A. (2011). Dengue disease, basic reproduction number and control, International Journal of Computer Mathematics, 1–13, iFirst.*

20. *Shepard, D. S., Halasa, Y. A., Tyagi, B. K., Vivek Adhish, S., Nandan, D., Karthiga, K. S., Chellaswamy, V., Gaba, M., Arora, N. K. and the INCLEN Study Group (2014). Economic and Disease Burden of Dengue Illness in India, Am. J. Trop. Med. Hyg., 91(6): 1235–1242*

21. *Side, S. and Noorani, S. Md. (2013). A SIR Model for Spread of engue Fever Disease (Simulation for South Sulawesi, Indonesia and Selangor, Malaysia), World Journal of Modelling and Simulation, Vol. 9 (2): 96-105*
22. *Yang, H.M., Macoris, M. L. G., Galvani, K.C., Andrighetti, M. T. M., and Wanderley, D.M.V. (2009a). Assessing the effects of temperature on dengue transmission. Epidemiol. Infect., 137(8): 1179-1187.*
23. *Yang, H.M., Macoris, M. L. G., Galvani, K.C., Andrighetti, M. T. M., and Wanderley, D.M.V. (2009b). Assesing the effects of temperature on the population of Aedes aegypti, the vector of dengue. Epidemiol. Infect. 137: 1188-1202.*
24. *WHO: http://www.who.int/mediacentre/factsheets/fs117/en/ July 2016.*