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Transmission Dynamics of Hepatitis B Model

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ABSTRACT

Mathematical models are often formulated in order to study the factors that govern infectious disease progression in viral infections. In this paper, we developed an epidemic model that provides knowledge about the transmission of Hepatitis B virus. The model can integrate the birth, death and examine the outcome mathematically. Along the way, we show that how this simple epidemic model assists to lay a theoretical foundation for public health problems.
KEYWORDS: disease, Hepatitis B, transmission, endemic

INTRODUCTION

In literature, it is given that host factors are responsible for determining whether the disease is removed or become chronic [1]. The entrance of Hepatitis B virus in lever through the blood stream causes the occurrence of hepatitis B infection. A large number of new viruses reproduce in the blood stream after entrance the virus into the lever [2]. In case, if the Hepatitis B infection is acute, the immune system of the individual may clear the virus from the body within six months. Commonly the infants between 1 to 6 years of age infected with hepatitis B virus are chronically infected and the disease lasts more than six months [3]. The chronic carriers of hepatitis B virus is a great challenge for health department as they do not develop symptoms even they transmit the virus to other people. To understand the dynamics of viral infections, researchers developed various mathematical models [4-10]. In this paper, we assume a simple SEIR epidemic model of the transmission of Hepatitis B virus and discuss its dynamical behavior.

Model Formulation

We develop an epidemic model for the transmission of hepatitis B virus in which the total human population is divided into four subclasses: the susceptible$S\ \ (t)$, latent $E(t)$, infected $I(t)$ and recovered $R(t)$.

$$N\ \ (t) = S\ \ (t) + E(t) + I(t) + R(t)$$

is the total human population at time t,the proposed model is given by the following system of differential equations.

$$\frac{dS(t)}{dt} = \wedge - \beta_1 S(t)I(t) - \beta_2 S(t)E(t) - \mu S(t)$$

$$\frac{dE(t)}{dt} = \beta_1 S(t)I(t) + \beta_2 S(t)E(t) - \alpha_1 E(t) - \mu E(t)$$

$$\frac{dI(t)}{dt} = \alpha_1 E(t) - \alpha_2 I(t) - \delta I(t) - \mu I(t)$$

$$\frac{dR(t)}{dt} = \alpha_2 I(t) - \mu R(t)$$

with the initial conditions $S(t) \geq 0, E(t) \geq 0, I(t) \geq 0, R(t) \geq 0$.

Here Λ is the rate of recruitment, $\alpha_1$is the effective contact rate between susceptible and exposed classes, α_2 is effective contact rate between susceptible and infected classes, μ is the natural death rate, ε is disease induced death rate, ω is the recovery rate (due to treatment or natural recovery), δ is the natural immunity, γ is the rate of immunity loss.

$$E_0 = \left(\frac{\wedge}{\mu}, 0,0,0\right)$$

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Basic Reproduction Number R_0

This section describes the computation of R_0, which is defined as the number of secondary infections generated by single infections when an infection is introduced into a purely susceptible population. The finding of the reproduction number involves the matrices, F and V, see [11]. It follows from [11] that the matrix F and V can be obtained as:

$$\mathcal{F} = \begin{bmatrix} 0 \\ \beta_1 SI + \beta_2 SE \\ 0 \\ 0 \end{bmatrix} \qquad V = \begin{bmatrix} -\wedge + \mu S \\ \alpha_1 E + \mu E \\ -\alpha_1 E + \alpha_2 I + \delta I + \mu I \\ -\alpha_2 R + \mu R \end{bmatrix}$$

$$F = \begin{bmatrix} \frac{\beta_2 \wedge}{\mu} & \frac{\beta_1 \wedge}{\mu} \\ 0 & 0 \end{bmatrix} \qquad V = \begin{bmatrix} \alpha_1 + \mu & 0 \\ -\alpha_1 \alpha_2 + \delta + \mu & \end{bmatrix}$$

$$V^{-1} = \frac{1}{(\alpha_1 + \mu)(\alpha_2 + \delta + \mu)} \begin{bmatrix} \alpha_2 + \delta + \mu & 0 \\ \alpha_1 \alpha_1 + \mu & \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} \frac{\beta_2 \wedge (\alpha_2 + \delta + \mu) + \beta_1 \wedge \alpha_1}{\mu(\alpha_1 + \mu)(\alpha_2 + \delta + \mu)} & \frac{\beta_2 \wedge (\alpha_2 + \delta + \mu)}{\mu} \\ 0 & 0 \end{bmatrix}$$

The basic reproduction numberR_0 is the spectral radius $\rho(FV^{-1})$, that is

$$R_0 = \frac{\beta_2 \wedge (\alpha_2 + \delta + \mu) + \beta_1 \wedge \alpha_1}{\mu(\alpha_1 + \mu)(\alpha_2 + \delta + \mu)}.$$

Local stability:

The present section describes the local stability of both the cases, disease free and endemic.

Theorem 1: If $R_o < 1$ and $\alpha_1 + \alpha_2 + \delta + 2\mu > \frac{\beta_2 \wedge}{\mu}$, then the DFE, E_o of the model (1) is stable locally asymptotically, otherwise unstable.

Proof: At E_0 the following Jacobian matrix is presented:

$$J(E_0) = \begin{bmatrix} -\mu & -\frac{\beta_2 \wedge}{\mu} & -\frac{\beta_1 \wedge}{\mu} & 0 \\ 0 & \frac{\beta_2 \wedge}{\mu} - (\alpha_1 + \mu) & \frac{\beta_1 \wedge}{\mu} & 0 \\ 0 & \alpha_1 & -(\alpha_2 + \delta + \mu) & 0 \\ 0 & 0 & \alpha_2 & -\mu \end{bmatrix},$$

we need to show that all the eigen values of $J(E_0)$ are negative. The first and fourth columns of $J(E_0)$ contain only diagonal elements which form negative eigen values$-\mu$, the other two eigen values can be obtained from the matrix $J_1(E_0)$ which is

$$J_1(E_0) = \begin{bmatrix} \frac{\beta_2 \wedge}{\mu} - (\alpha_1 + \mu) & \frac{\beta_1 \wedge}{\mu} \\ \alpha_1 & -(\alpha_2 + \delta + \mu) \end{bmatrix}$$

The eigen values of $J_1(E_0)$ are the roots of characteristic equation$|J_1(E_0) - \lambda I| = 0$ which gives

$$\left(\frac{\beta_2 \wedge}{\mu} - (\alpha_1 + \mu) - \lambda\right)(-\alpha_2 + \delta + \mu) - \lambda) - \frac{\alpha_1 \beta_1 \wedge}{\mu} = 0$$

$$\Rightarrow \lambda^2 + \left((\alpha_2 + \delta + \mu) - \left(\frac{\beta_2 \wedge}{\mu} - (\alpha_1 + \mu)\right)\right)\lambda - \left(\frac{\beta_2 \wedge (\alpha_2 + \delta + \mu) + \alpha_1 \beta_1 \wedge}{\mu(\alpha_2 + \delta + \mu)(\alpha_1 + \mu)} - 1\right) = 0$$

$$\Rightarrow \lambda^2 + \left((\alpha_2 + \delta + \mu) - \left(\frac{\beta_2 \wedge}{\mu} - (\alpha_1 + \mu)\right)\right)\lambda - (R_0 - 1) = 0$$

$$\Rightarrow A_2\lambda^2 + A_1\lambda + A_0 = 0$$

Where $A_2 = 1, \quad A_1 = \alpha_1 + \alpha_2 + \delta + 2\mu - \frac{\beta_2 \wedge}{\mu}, \quad A_0 = 1 - R_0.$

By Routh-Hurwitz criterion we know that if a polynomial is of second degree and all their coefficients are positive then obviously the polynomial will give negative roots. We see that in the above polynomial $A_2 = 1, A_1$ will be positive only when $\alpha_1 + \alpha_2 + \delta + 2\mu > \frac{\beta_2 \wedge}{\mu}$and A_0 will be positive if $R_0 < 1$. Thus for these two conditions all the roots of the polynomial will be negative. Hence the disease free equilibrium is stable if $R_0 < 1$ and $\alpha_1 + \alpha_2 + \delta + 2\mu > \frac{\beta_2 \wedge}{\mu}$.

Endemic Equilibrium

To find the endemic equilibrium of the proposed model, we set the left side of (1) equals zero and obtain

$$S^* = \frac{(\alpha_1 + \mu)(\alpha_2 + \delta + \mu)}{\alpha_1\beta_1 + \alpha_1\beta_2(\alpha_2 + \delta + \mu)}, E^* = \frac{(\alpha_2 + \delta + \mu)I^*}{\alpha_1}, R^* = \frac{\alpha_2 I^*}{\mu},$$

$$I^* = \frac{\frac{\wedge - \mu(\alpha_1+\mu)(\alpha_2+\delta+\mu)}{\alpha_1\beta_1+\alpha_1\beta_2(\alpha_2+\delta+\mu)}}{\frac{\beta_1(\alpha_1+\mu)(\alpha_2+\delta+\mu)}{\alpha_1\beta_1+\alpha_1\beta_2(\alpha_2+\delta+\mu)} + \left(\frac{\beta_2(\alpha_1+\mu)(\alpha_2+\delta+\mu)}{\alpha_1\beta_1+\alpha_1\beta_2(\alpha_2+\delta+\mu)}\right)\left(\frac{\alpha_2+\delta+\mu}{\alpha_1}\right)}.$$

In the following Theorem 2, we prove the local stability of endemic case.

Theorem 2: The endemic equilibriaE_1 is locally asymptotically stablefor$R_0 > 1$, $\beta_3 {i_h}^* + \mu_h > (\mu_h + \rho_h)\left(\mu_h + \beta_1 {i_v}^* + \beta_2 {i_h}^*\right)$ and $\mu_v(\mu_h + \rho_h - \beta_2) > M$.

Proof: The Jacobian matrix of (1) evaluated at EE,E_1,is

$$J(E_1) = \begin{bmatrix} -(\beta_1 I^* + \beta_2 E^* + \mu) & -\beta_2 S^* & -\beta_1 S^* & 0 \\ \beta_1 I^* + \beta_2 E^* & \beta_2 S^* - (\alpha_1 + \mu) & \beta_1 S^* & 0 \\ 0 & \alpha_1 & -(\alpha_2 + \delta + \mu) & 0 \\ 0 & 0 & \alpha_2 & -\mu \end{bmatrix}$$

After some row operations, we get

$$J(E_1) = \begin{bmatrix} -G_2H_1 + H_2G_1 & 0 & 0 & 0 \\ -G_1 & -G_2 & 0 & 0 \\ 0 & \alpha_1 & -A_3 & 0 \\ 0 & 0 & \alpha_2 & -\mu \end{bmatrix}$$

Where

$$H_1 = A_1A_3, H_2 = A_3B_1 - \alpha_1B_2, G_1 = A_3B_3, G_2 = A_3A_2 - \alpha_1B_2,$$

$$A_1 = \beta_1 I^* + \beta_2 E^* + \mu, \; A_2 = \beta_2 S^* - (\alpha_1 + \mu), \; A_3 = \alpha_2 + \delta + \mu,$$

$$B_1 = \beta_2 S^*, B_2 = \beta_1 S^*, B_3 = \beta_1 I^* + \beta_2 E^*.$$

The characteristic equation of $J(E_1)$ gives the eigen values as follows

$$\lambda_1 = -\mu, \lambda_2 = -A_3, \lambda_3 = -G_2, \lambda_4 = -G_2H_1 + H_2G_1.$$

We see that the first two eigen values are negative and the last two eigen values are negative if $\beta_2 S^* > (\alpha_1 + \mu)$ and ${A_3}^2A_2A_1 > {A_3}^2B_1B_3$. Hence, the model (1) is stable locally asymptotically if $\beta_2 S^* > (\alpha_1 + \mu)$ and ${A_3}^2A_2A_1 > {A_3}^2B_1B_3$.

Global Dynamics

The proposed section is dedicated to analyze the global stability of the proposed model by using the lyapunov function theory [12]for both the cases. In Theorem 3, the global stability of DFE case is presented.

Theorem 3: In the interior of Γ, the model (1) at the infection free equilibrium$E_0$is stable globally asymptotically.

Proof: We consider the following lyapunov function

$$\mathcal{L}(t) = \frac{1}{\mu}(S + E + I).$$

Taking time derivate of"$\mathcal{L}$", we have

$$\mathcal{L}'(\mathrm{t}) = \frac{1}{\mu}(\wedge - \mu S - \mu E - (\alpha_2 + \delta + \mu)I)$$

$$= \frac{\wedge}{\mu} - S - E - \frac{\alpha_2 + \delta + \mu}{\mu} I$$
$$= (S^0 - S) - E - \frac{\alpha_2 + \delta + \mu}{\mu} I$$
$$< 0$$

Thus the time derivative of Lyapunov function is negative, and $\mathcal{L}'(\mathrm{t}) = 0$ if and only if $S = S^0, \mathrm{E} = \mathrm{I} = 0$. Hence by Lassalle's invariance principal [12], $E_0$is globally asymptotically stable.

Theorem 4: In the interior of Γ, the model (1) at the endemic equilibrium$E_1$is stable globally asymptotically.
Proof: To show the result, we define the following lyapunov function

$$\mathfrak{Z}(t) = S(t) + E(t) + I(t) + R(t) + \int \delta I^* dt$$

Taking the time derivate of"ג", we have

$$\begin{aligned}\mathfrak{Z}'(t) &= \wedge - \mu S - \mu E - (\delta + \mu) I - \mu R + \delta I^* \\ &= \wedge - \mu(S + E + I + R) - \delta I + \delta I^* \\ &= \wedge - \mu N - \delta(I - I^*) \\ &= -\delta(I - I^*) \\ &< 0\end{aligned}$$

Thus the time derivative of Lyapunov function is negative and $\mathfrak{Z}'(\mathrm{t}) = 0$ for$\mathrm{I}(\mathrm{t}) = \mathrm{I}^*$. Hence by Lassalle's invariance principal [12],E_1 is globally asymptotically stable on Γ.

Numerical results
We find the numerical solution of the proposed model (1) by choosing the base line for the susceptible population S=40, Exposed population E=10, Infected population I=20, Recovered population R=10. The parameters and their values are given as$\wedge = 1, \mu = 0.1,\ \beta_1 = 0.001,\ \beta_2 = 0.0012, \alpha_1 = 0.001,\ \alpha_2 = 0.25\ and\ \delta = 0.4$. Figure 1 shows the behavior of distinct classes of the Hepatitis B model.

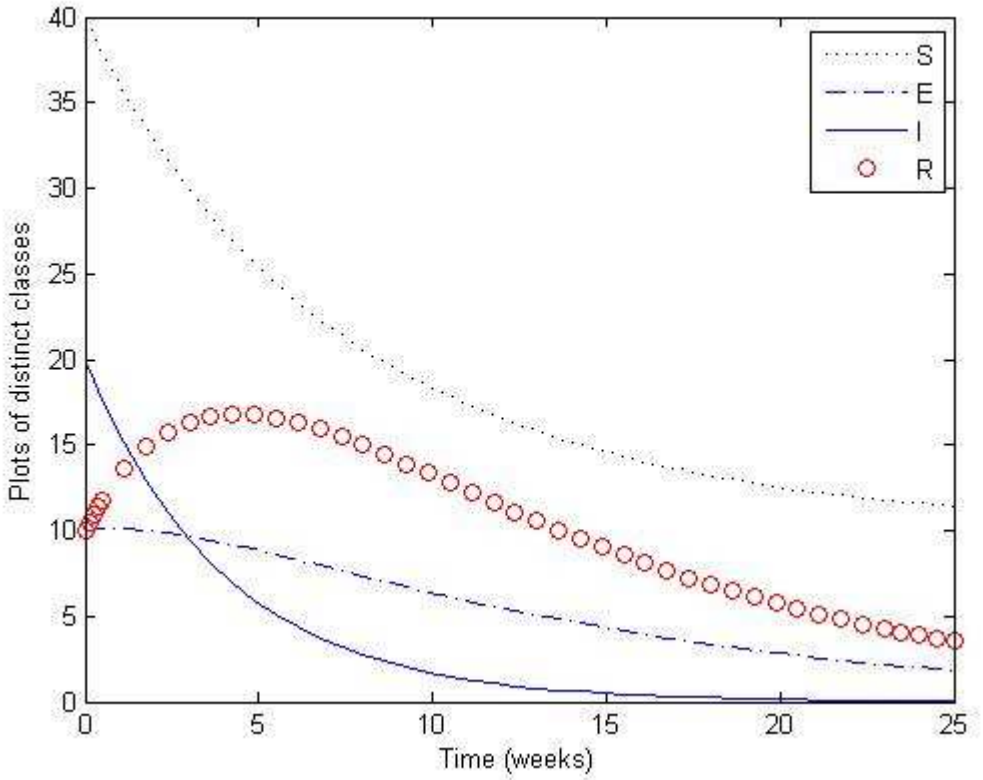

Figure 1: Dynamical behavior of the proposed model.

Conclusion

We considered a simple mathematical model that gives the idea of transmission of Hepatitis B virus. Analysis of our proposed model showed that two equilibria exist; that is, the disease free and endemic. The local dynamics of the proposed model have been discussed and analyzed by the basic reproduction number.

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