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Global Stability of HBV Epidemic Model

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Abstract

In this paper, we present an hepatitis B model with multiple transmission ways of the acute counsel, uncounseland carrier infection classes and derive the basic reproduction number, which indicates that hepatitis B isendemic. Existence of Disease Free and Endemic Equilibrium State are carried-out. The disease free and endemic equilibria are shown to be globally asymptotically stable. In addition, we obtained the numerical simulation to verify the model predictions. The results suggest that the endemic nature of the model was stable. However, if the control measure put in place can be maximize, then the model can be use to predict the effectiveness of the prophylactic vaccination program in sustaining the population from the spread of the disease

Keywords: Hepatitis B, basic reproduction number, endemic, stability, equilibrium

1.0 Introduction

Hepatitis is an inflammation of the liver caused by viruses, bacterial infections, or continuous exposureto alcohol, drugs, or toxic chemicals, such as those found in aerosol sprays and paint thinners (Ganem, D., Prince, A. M. 2004). Inflammation is the painful, red swelling that result when tissues of the body become injured or infected. Inflammation can cause organs to not work properly. Hepatitis can also result from an autoimmune disorder, in which the body mistakenly sends disease-fighting cells to attack its own healthytissue, in this case the liver (Barker et al., 1996). The liver is located in the upper right hand side of the abdomen, mostly behind the rib cage. The liver of an adult normally weighs close to three pounds (Chang,June 2007). No matter what its cause, hepatitis reduces the liver‘s ability to perform life-preserving functions, including filtering harmful infectious agents from the blood, storing blood sugar and converting it to usable energy forms, and producing many proteins necessary for life (Edmund et al., 1993).

Hepatitis B is a potentially life-threatening liver infection caused by the hepatitis B virus (HBV), Edmundet al. (1993). It is a major global health problem and the most serious type of viral hepatitis. Originally knownas ”serum hepatitis”, the disease has caused epidemics in parts of Asia and Africa, and it is endemic in China(Williams, 2006). About a third of the world population has been infected at one point in their lives, including350 million who are chronic carriers which causes 620,000 deaths worldwide each year (WHO, 2004). If an infected individual body is able to fight off the hepatitis B infection, any symptoms that you had should go away over a periodof weeks to months, this is termed acute hepatitis B. some people’s bodies are not able to completely get ridof the hepatitis B infection. This is called chronic hepatitis B.

2.0 Mathematical Model Formulation

We propose a mathematical model to understand the transmission dynamics and prevalence of HBV. The modelis constructed based on the characteristics of HBV transmission and the model of Lan Zou et al. (2010).Therefore, we divide the host population into seven epidemiological groups: the proportion susceptible to infectionS; those latently infected E; uneducated acute infections I_u ;educated acute infections I_e ; carriers C; recoveredR; and Vaccinated V.

We assume that the population of newborn carriers born to carriers is less than the sum of the death of carriersand the population moving from carrier to immune state. In this case we have $\mu\omega\nu < \mu_0 + \mu_1 + \gamma_2$. Otherwise,carriers would keep

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increasing rapidly as long as there is infection; i.e., $\frac{dC}{dt} > 0$ for $C \neq 0$ or $I \neq 0$ *and* $t \geq 0$:

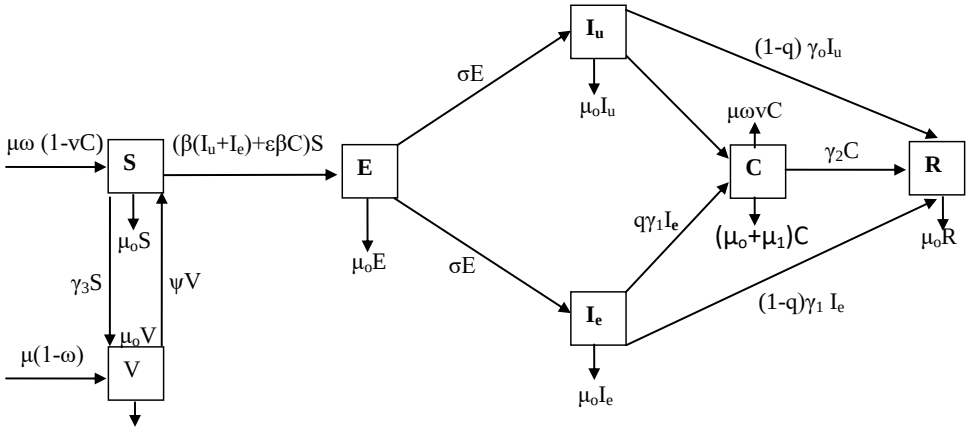

Fig: 2.1: Flow diagram of HBV transmission
The model is given by seven ordinary differential equations:

$$\frac{dS}{dt} = \mu\omega(1-\nu C) + \psi V - \left[\mu_0 + \beta\left(I_u + I_e\right) + \varepsilon\beta C + \gamma_3\right] S \tag{2.1}$$

$$\frac{dE}{dt} = \left[\beta\left(I_u + I_e\right) + \varepsilon\beta C\right] S - \left(\mu_0 + 2\sigma\right) E \tag{2.2}$$

$$\frac{dI_u}{dt} = \sigma E - \left(\mu_0 + \gamma_0\right) I_u \tag{2.3}$$

$$\frac{dI_e}{dt} = \sigma E - \left(\mu_0 + \gamma_1\right) I_e \tag{2.4}$$

$$\frac{dC}{dt} = \mu\omega\nu C + q\left(\gamma_0 I_u + \gamma_1 I_e\right) - \left(\mu_0 + \mu_1 + \gamma_2\right) C \tag{2.5}$$

$$\frac{dR}{dt} = \gamma_2 C + \left(1-q\right)\left(\gamma_0 I_u + \gamma_1 I_e\right) - \mu_0 R \tag{2.6}$$

$$\frac{dV}{dt} = \mu\left(1-\omega\right) + \gamma_3 S - \left(\mu_0 + \psi\right) V \tag{2.7}$$

The total population N(t) can be obtained from the model;

$$N\left(t\right) = S\left(t\right) + E\left(t\right) + I_u\left(t\right) + I_e\left(t\right) + C\left(t\right) + R\left(t\right) + V\left(t\right) \tag{2.8}$$

$$\frac{dN}{dt} = \mu - N\mu_0 - \mu_1 C \tag{2.9}$$

Here, it is important to note that in the absence of the disease $N(t) \to \frac{\mu}{\mu_0}$. Moreover, under the dynamics described by the above systems of equations, the region.

$$\Omega = \{ x = (S, E, I_u, I_e, C, V, N) \in \Re_+^7 \mid S \geq 0, E \geq 0, I_u \geq 0, I_e \geq 0, C \geq 0, V \leq N \leq \frac{\mu}{\mu_0} \},$$

is positively invariant. Hence the system is both mathematically and epidemiologically well-posed. Therefore, for initial starting point $x \in \Re_+^7$, the trajectory lies in Ω. Thus we restrict our analysis to the region Ω. (where the model make biological sense).

2.1 Parameters are Defined Below

μ = birth rate

μ_0 = Natural mortality rate

μ_1 = HBV related mortality rate

ω = proportion of birth without successful vaccination

β = Transmission coefficient or effective contact rate

ε = Reduced transmission rate

σ = Rate of movement from latent to acute

γ_0 = Rate of movement from uncounsel acute to carrier

γ_1 = Rate of movement from counsel acute to carrier

γ_2 = Rate of movement from carrier to immune

γ_3 = vaccination rate

q = Average probability an individual fail to clear an acute infection and develops to carrier state

ψ = Rate of waning vaccine-induced immunity

v = Proportion of prenatally infected (carrier mothers)

3.0 Model Analysis

We determine the effective basic reproduction number; the existence of equilibrium points; and obtaining the conditions for stability of the equilibria points.

3.1 Basic Reproduction Number

The basic reproductive number R_0 is considered as the threshold quantity that determines when an infectioncan invade and persist in a new population. If $R_0 < 1$, then the infection in the population dies out, while if$R_0 > 1$, then there is a unique positive epidemic equilibrium. According to Anderson & May (1991), R_0 isthe average number of secondary infections produced when one infected individual is introduced into a hostpopulation where everyone is susceptible

Using the approach of Diekmann, et al. (1999), the product of the matrix $F V^{-1}$ is called the next generationmatrix for the model and we shall set the reproduction number R_0 as equal to the spectral radius $\rho F V^{-1}$ i.e.

$R_0 = \rho F V^{-1}$

$$F=\begin{pmatrix}0 & \beta S & \beta S & \varepsilon\beta S\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0\end{pmatrix} \tag{3.1.2}$$

$$V=\begin{pmatrix}\mu_0+2\sigma & 0 & 0 & 0\\ -\sigma & \mu_0+\gamma_0 & 0 & 0\\ -\sigma & 0 & \mu_0+\gamma_1 & 0\\ 0 & -q\gamma_0 & -q\gamma_1 & -\mu\omega\nu+\mu_0+\mu_1+\gamma_2\end{pmatrix} \tag{3.1.3}$$

$$R_0=\frac{\beta\sigma\mu\left(\mu_0\omega+\psi\right)\left(\left(q\varepsilon\gamma_1+k_3\right)k_1+k_2\left(q\varepsilon\gamma_0+k_3\right)\right)}{\mu_0\left(\mu_0+\gamma_3+\psi\right)k_0k_1k_2k_3}$$

$$R_0=\frac{\beta\sigma\mu\left(\mu_0\omega+\psi\right)\left(\left(q\varepsilon\gamma_1-\mu\omega\nu+\mu_0+\mu_1+\gamma_2\right)\left(\mu_0+\gamma_0\right)+\left(\mu_0+\gamma_1\right)\left(q\varepsilon\gamma_0-\mu\omega\nu+\mu_0+\mu_1+\gamma_2\right)\right)}{\mu_0\left(\mu_0+\gamma_3+\psi\right)\left(\mu_0+2\sigma\right)\left(\mu_0+\gamma_0\right)\left(\mu_0+\gamma_1\right)\left(-\mu\omega\nu+\mu_0+\mu_1+\gamma_2\right)} \tag{3.1.4}$$

3.2 Existence of Disease Free Equilibrium State

The disease free equilibrium state of the above model is calculated by setting I = 0 (all infected class will bezero) and the entire population will comprise of Susceptible and Vaccinated class, thus the result gives;

$$S_0=\frac{\mu\left(\mu_0\omega+\psi\right)}{\mu_0\left(\mu_0+\gamma_3+\psi\right)},\qquad V_0=\frac{\mu\left(\mu_0+\gamma_3-\mu_0\omega\right)}{\mu_0\left(\mu_0+\gamma_3+\psi\right)} \tag{3.2.1}$$

implies

$$\left(S_0, E_0, I_{u0}, I_{e0}, C_0, R_0, V_0 = \frac{\mu\left(\mu_0\omega+\psi\right)}{\mu_0\left(\mu_0+\gamma_3+\psi\right)},\ 0,\ 0,\ 0,\ 0,\ 0,\ \frac{\mu\left(\mu_0+\gamma_3-\mu_0\omega\right)}{\mu_0\left(\mu_0+\gamma_3+\psi\right)}\right) \tag{3.2.2}$$

3.3 Existence of Endemic Equilibrium State

For the endemic equilibrium, there is an existence of infection, hence $I_u\neq 0,\ I_e\neq 0,\ C\neq 0$. The systems of equation should satisfy the following conditions:

$(S^*>0,\ E^*>0,\ I_u^*>0,\ I_e^*>0,\ C^*>0,\ R^*>0,\ V^*>0)$

The endemic equilibrium state is the state in which there is persistence of the disease in the population. Thusthe model is calculated

$$S^*=\frac{\left(\mu_0+\gamma_1\right)\left(\mu_0+\gamma_0\right)\left(\mu_0+2\sigma\right)\left(-\mu\omega\nu+\mu_0+\mu_1+\gamma_2\right)}{\beta\sigma\left[\left(2\mu_0+\gamma_0+\gamma_1\right)\left(-\mu\omega\nu+\mu_0+\mu_1+\gamma_2\right)+\varepsilon q\left[\mu_0\left(\mu_0+\gamma_0+\gamma_1\right)+2\gamma_0\gamma_1\right]\right]} \tag{3.3.1}$$

$$E^*=\frac{\left(\mu_0+\gamma_0\right)I_u^*}{\sigma} \tag{3.3.2}$$

$$I_u^*=\frac{\left(\mu_0+\gamma_1\right)I_e^*}{\left(\mu_0+\gamma_0\right)} \tag{3.3.3}$$

$$I_e^*=\frac{\left(\mu_0+\gamma_0\right)\left(-\mu\omega\nu+\mu_0+\mu_1+\gamma_2\right)C^*}{q\left[\mu_0\left(\gamma_0+\gamma_1\right)+2\gamma_0\gamma_1\right]} \tag{3.3.4}$$

$$S^*=\frac{q\left[\mu\omega+\psi V^*-\left(\mu_0+\gamma_3\right)S^*\right]\left[\mu_0\left(\mu_0+\gamma_0+\gamma_1\right)+2\gamma_0\gamma_1\right]}{q\left[\mu_0\left(\mu_0+\gamma_0+\gamma_1\right)+2\gamma_0\gamma_1\right]\left(\varepsilon\beta S^*-\mu\omega\nu\right)+\beta S^*\left(2\mu_0+\gamma_0+\gamma_1\right)\left(-\mu\omega\nu+\mu_0+\mu_1+\gamma_2\right)} \tag{3.3.5}$$

$$V^* = \frac{\mu(1-\omega)+\gamma_3 S^*}{(\mu_0+\psi)} \tag{3.3.6}$$

3.4 Global Stability of Disease Free Equilibrium State

Theorem 1: The disease free equilibrium of the model (2.1-2.7) is globally asymptotically stable (GAS) in Ω if $R_0 < 1$.

Proof:

To establish the global stability of the disease free equilibrium, the two conditions of Castillo-Chavex et al.(2002) must be satisfied for $R_0 < 1$. The model is rewritten in the form:

$$\frac{dX_1}{dt} = F(X_1,\ X_2), \quad \frac{dX_2}{dt} = G(X_1,\ X_2); \quad G(X_1,\ 0) = 0 \tag{3.4.1}$$

where $X_1 = (S,\ V)$ *and* $X_2 = (E,\ I_u,\ I_e,\ C)$ also $X_1 \in \Re^2$ is the component denoting the uninfected population and $X_2 \in \Re^4$ is the component denoting the infected population. Since the disease free is

$$\mathrm{E}_f = \left(X_1^*,\ 0\right), \quad X_1^* = \left(S_0 = \frac{\mu(\mu_0\omega+\psi)}{\mu_0(\mu_0+\gamma_3+\psi)}, \qquad V_0 = \frac{\mu(\mu_0+\gamma_3-\mu_0\omega)}{\mu_0(\mu_0+\gamma_3+\psi)} \right)$$

For the **First Condition**, that is globally asymptotically stability of X_1^*, we have

$$\frac{dX_1}{dt} = F(X_1,\ 0) = \begin{pmatrix} \mu\omega+\psi V-(\mu_0+\gamma_3)S \\ \mu(1-\omega)+\gamma_3 S-(\mu_0+\psi)V \end{pmatrix} \tag{3.4.2}$$

as a linear differential equation

Solving the differential equation, we have.

$$S(t) = \frac{(\mu\omega+\psi V)}{(\mu_0+\gamma_3)} - \frac{(\mu\omega+\psi V)}{(\mu_0+\gamma_3)}\exp^{-(\mu_0+\gamma_3)t} + S(0)\exp^{-(\mu_0+\gamma_3)t} \tag{3.4.3}$$

$$V(t) = \frac{(\mu(1-\omega)+\gamma_3 S(t))}{(\mu_0+\psi)} - \frac{(\mu(1-\omega)+\gamma_3 S(0))}{(\mu_0+\psi)}\exp^{-(\mu_0+\psi)t} + V(0)\exp^{-(\mu_0+\psi)t} \tag{3.4.4}$$

Now since $S(t)+V(t)\to 1$ as $t\to\infty$ Thus, $X_1^* = \left(\frac{\mu(\mu_0\omega+\psi)}{\mu_0(\mu_0+\gamma_3+\psi)}, \ \frac{\mu(\mu_0+\gamma_3-\mu_0\omega)}{\mu_0(\mu_0+\gamma_3+\psi)} \right)$ is globally asymptotically stable.

For the **Second Condition**,

$$\hat{G}(X_1,\ X_2) = AX_2 - G(X_1,\ X_2) \tag{3.4.5}$$

we have

$$AX_2 = \begin{pmatrix} -(\mu_0+2\sigma) & \beta S & \beta S & \varepsilon\beta S \\ \sigma & -(\mu_0+\gamma_0) & 0 & 0 \\ \sigma & 0 & -(\mu_0+\gamma_1) & 0 \\ 0 & q\gamma_0 & q\gamma_1 & (\mu\omega\nu-(\mu_0+\mu_1+\gamma_2)) \end{pmatrix} \begin{pmatrix} E \\ I_u \\ I_e \\ C \end{pmatrix} \tag{3.4.6}$$

$$G(X_1,\ X_2)=\begin{pmatrix}\left[\beta(I_u+I_e)+\varepsilon\beta C\right]S-(\mu_0+2\sigma)E\\ \sigma E-(\mu_0+\gamma_0)I_u\\ \sigma E-(\mu_0+\gamma_1)I_e\\ \mu\omega\nu C+q(\gamma_0 I_u+\gamma_1 I_e)-(\mu_0+\mu_1+\gamma_2)C\end{pmatrix} \tag{3.4.7}$$

$$\hat{G}(X_1,\ X_2)=AX_2-G(X_1,\ X_2)=\begin{pmatrix}0&0&0&0\\0&0&0&0\\0&0&0&0\\0&0&0&0\end{pmatrix} \tag{3.4.8}$$

Its obvious that since $\hat{G}(X_1,\ X_2)\geq 0$ Hence the proof is complete.

3.5 Global Stability of Endemic Equilibrium State

Theorem 2: The endemic equilibrium of the reduced model, given by (2.1-2.7), is globally asymptotically stable (GAS) in Ω, if $R_0> 1$.

Proof Consider the reduced model in constructing the following nonlinear Lyapunov function:

$$\mathrm{F}=S-S^*-S^*\ln\left(\frac{S}{S^*}\right)+E-E^*-E^*\ln\left(\frac{E}{E^*}\right)+\frac{k_0}{\sigma}\left[I_u-{I_u}^*-{I_u}^*\ln\left(\frac{I_u}{{I_u}^*}\right)\right]+\frac{k_1}{q\gamma_0}\left[C-C^*-C^*\ln\left(\frac{C}{C^*}\right)\right] \tag{3.5.1}$$

Lyapunov derivatives gives;

$$\dot{\mathrm{F}}=\dot{S}-\frac{S^*}{S}\dot{S}+\dot{E}-\frac{E^*}{E}\dot{E}+\frac{k_0}{\sigma}\left[\dot{I}_u-\frac{{I_u}^*}{I_u}\dot{I}_u\right]+\frac{k_1}{q\gamma_0}\left[\dot{C}-\frac{C^*}{C}\dot{C}\right] \tag{3.5.2}$$

Substituting the reduced model,

$$\begin{aligned}\dot{\mathrm{F}}=&\mu\omega(1-\nu C)+\psi V-\left[\mu_0+\beta(I_u+I_e)+\varepsilon\beta C+\gamma_3\right]S-\frac{S^*}{S}\begin{bmatrix}\mu\omega(1-\nu C)+\psi V\\-\left[\mu_0+\beta(I_u+I_e)+\varepsilon\beta C+\gamma_3\right]S\end{bmatrix}\\&+\left[\beta(I_u+I_e)+\varepsilon\beta C\right]S-(\mu_0+2\sigma)E-\frac{E^*}{E}\left[(\beta(I_u+I_e)+\varepsilon\beta C)S-(\mu_0+2\sigma)E\right]\\&+\frac{k_0}{\sigma}\begin{bmatrix}\sigma E-(\mu_0+\gamma_0)I_u\\-\frac{{I_u}^*}{I_u}(\sigma E-(\mu_0+\gamma_0)I_u)\end{bmatrix}+\frac{k_1}{q\gamma_0}\begin{bmatrix}\mu\omega\nu C+q(\gamma_0 I_u+\gamma_1 I_e)-(\mu_0+\mu_1+\gamma_2)C\\-\frac{C^*}{C}\left[\mu\omega\nu C+q(\gamma_0 I_u+\gamma_1 I_e)-(\mu_0+\mu_1+\gamma_2)C\right]\end{bmatrix}\end{aligned} \tag{3.5.3}$$

expanding the above and let $f(I_u)=(I_u+I_e)$, we have ;

$$\begin{aligned}\dot{\mathrm{F}}=&B-(\mu_0+\gamma_3)S-(\beta f(I_u)+\varepsilon\beta C)S-B\frac{S^*}{S}+(\mu_0+\gamma_3)S^*-(\beta f(I_u)+\varepsilon\beta C)S^*\\&+(\beta f(I_u)+\varepsilon\beta C)S-k_0E-(\beta f(I_u)+\varepsilon\beta C)\frac{SE^*}{E}+k_0E^*+k_0E-\frac{k_0k_1I_u}{\sigma}-\frac{k_0EI_u^*}{I_u}\\&+\frac{k_0k_1{I_u}^*}{\sigma}+k_1I_u+\frac{k_1\gamma_1I_e}{\gamma_0}-\frac{k_1k_3C}{q\gamma_0}+\frac{k_1I_uC^*}{C}-\frac{k_1\gamma_1I_eC^*}{\gamma_0C}+\frac{k_1k_3C^*}{q\gamma_0}\end{aligned} \tag{3.5.4}$$

Simplifying and factorizing the common factors,

$$\begin{aligned}\dot{\mathrm{F}}=&\left(B-(\mu_0+\gamma_3)S\right)\left(1-\frac{S^*}{S}\right)+(\beta f(I_u)+\varepsilon\beta C)S^*\left(1-\frac{E^*S}{ES^*}\right)+k_0E\left(\frac{E^*}{E}-1\right)\\&+\left(k_1I_u+\frac{k_1\gamma_1I_e}{\gamma_0}-\frac{k_1k_3C}{q\gamma_0}\right)\left(1-\frac{C^*}{C}\right)+\left(k_0E-\frac{k_0k_1I_u}{\sigma}\right)\left(1-\frac{I_u^*}{I_u}\right)\end{aligned} \tag{3.5.5}$$

Considering the following from the above;

$$\left(1-\frac{S^*}{S}\right)\le 0,\quad \left(1-\frac{E^*S}{ES^*}\right)\le 0,\quad \left(\frac{E^*}{E}-1\right)\le 0,\quad \left(1-\frac{C^*}{C}\right)\le 0,\quad \left(1-\frac{I_u^*}{I_u}\right)\le 0.$$

Since all the model parameters are nonnegative, it follows that $\dot{F} \le 0$ for all $R_0 > 1$ and with $\dot{F} = 0$ if andonly if $S = S^*,\quad E = E^*,\quad I_u = I_u^*,\ and\ C = C^*$ Hence F is a Lyapunov function on Ω.

4.0 Numerical Simulation

We simulated numerically with the aid of Maple software to check and determine the effect and behaviorof the parameters of the model.

Table 4a

Parameters					Model (R_0)	
β	γ_3	γ_2	ω	q	DFE	Remark
1.0	0.05	0.015	1.0	0.885	15.35676149	unstable
0.9	0.15	0.025	0.9	0.885	8.664470025	unstable
0.8	0.25	0.035	0.8	0.885	5.409741319	unstable
0.7	0.35	0.045	0.7	0.885	3.558030986	unstable
0.6	0.45	0.055	0.6	0.885	2.399263298	unstable
0.5	0.55	0.065	0.5	0.885	1.625657877	unstable
0.4	0.65	0.075	0.4	0.885	1.084266791	unstable
0.3	0.75	0.085	0.3	0.885	0.6914963784	stable
0.2	0.85	0.095	0.2	0.885	0.3983200916	stable
0.1	0.95	0.105	0.1	0.885	0.1743709001	stable

4.1 Discussion of Results

The simulations were done using MAPLE 18 software. We derive some parameters from literature for our modelas follows; $\mu = 0.0121$, $\mu_0 = 0.00693$, $\mu_1 = 0.2$ percent, β = from 0.95 to 20.49, $\varepsilon = 0.16$, $\sigma = 6$ per year, $\gamma_0 = 4$ per year, $\gamma_1 = 2$ per year, $\gamma_2 = 0.025$ per year, $\gamma_3 = 0$ - 100 percent, $\omega = 0$ - 100 percent, $q = 0.885$, $\psi = 0.1$, $v = 0.11$. We calculated the basic reproduction number as $R_0 = 2.971185193$.Since R_0 is greater thanunity in some cases, it mean that the rate of infection exceeds the rate of recovery and less than unity if thereverse is true.

Thus, proper immunization of both newborns and susceptible individuals is an efficient intervention. Simulations conducted confirm the findings and suggest possible way to curb the outbreak of the disease epidemic.

5.0 Reference

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