Int. J. Adv. Appl. Math. and Mech. 6(3) (2019) 51 – 61 (ISSN: 2347-2529)

Journal homepage: www.ijaamm.com

IJAAMM

International Journal of Advances in Applied Mathematics and Mechanics

Modeling approach to assess the transmission dynamics of Hepatitis B infection in Africa

Research Article

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Received 26 January 2019; accepted (in revised version) 23 February 2019

Abstract: Hepatitis B virus infection remains a major public health concern in many developing countries in the world. In this paper, we formulate and analyse a simple deterministic model to assess the dynamics and control of the disease using ordinary differential equations. To analyse the effect of the initial transmission of the disease we compute the basic reproduction number $\mathscr{R}_0$ and perform stability analysis. The results show that both the disease-free equilibrium and the endemic equilibrium are globally stable with respect to the value of $\mathscr{R}_0$. Results also show that $\mathscr{R}_0$ is highly affected by the vertical transmission and the recovery rate of the chronic carriers after screening and treatment. Therefore, effective mechanisms which will reduce vertical transmission are needed as well as effective screening of individuals, so that those who will be found infected get treated. Further results from numerical analysis show that when the disease is introduced in the population it is persistent and therefore effective control mechanisms are required.

MSC: 00A71 • 93A30 • 93D05 • 93D20 • 97M10

Keywords: Hepatitis B • Hepatitis B virus • basic reproduction number • Metzler matrix • Lozinskii measure

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1. Introduction

Hepatitis B infection is a serious liver disease caused by hepatitis B virus (HBV) [1]. HBV is a member of the family *hepadnavirus* [2]. To date, there is no effective treatment for acute or chronic HBV. Immunization with HB vaccine is the most important preventative measure [1, 3].

HBV is primarily transmitted to human when blood, semen, or other body fluid from an infected person enters the body of someone who is not infected [1, 3]. People can become infected with the virus from: sex with an infected person; birth (perinatal transmission); sharing needles, syringes, or drug preparation equipment; and carelessness in handling an infected person during outbreaks. HBV is not spread through food or water, sharing eating utensils, breastfeeding, hugging, kissing, hand holding, coughing, or sneezing [1, 3].

HBV infection can be acute or chronic. According to WHO [1] and CDC [3], acute hepatitis B is a short-term illness that occurs within the first 6 months after someone is exposed to HBV. An acute infection can range in severity from a mild illness with few or no symptoms to a serious condition requiring hospitalization. Adults, are able to clear the virus without treatment. Those who clear the virus become immune and cannot get infected with the HBV again. Acute infection can, but does not always, lead to chronic infection.

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Chronic hepatitis B is a lifelong infection with the HBV. The possibility that a person develops a chronic infection depends on the age at which some one become infected. Up to 90% of infants with HBV will develop chronic infection, while about 5% of adults will develop chronic infection. About two-thirds of people with chronic infection are chronic careers [4]. Chronic hepatitis B can cause serious health problems, including liver damage, cirrhosis, liver cancer, and even death [5].

HBV infection is of major global health concern because it has caused several epidemics in Africa and Asia [6]. Over time, mathematical models have been used to describe the transmission dynamics of several infectious diseases as well as the possible control mechanisms available for the disease. Modeling the dynamics of infectious disease is useful for it can help to understand the dynamics of the disease and its associated control measures in a very simple way.

Different mathematical models for HBV infection have been developed to study the dynamics of HBV infection. The first time model is that of Anderson and May [7] who deterministically illustrated the effects of carriers on the transmission of HBV. Following that, Anderson [8] and Williams [9] developed mathematical models which included heterogeneous mixing with respect to age and sexual activity. Other models which related HBV infection and age include that of Edmunds [10], Medley [11], and Zhao [12]. A fraction-order model of HBV was developed and analysed by Zhou and Sun [13]. On other hand, Wang [14], and Xu and Ma [15] developed models of HBV with diffusion and delays. Models with control measures have also been developed including those of [4, 16–18], and [19].

While HBV infection is of global concern, little is known in many people in Africa especially its modes of transmission and dynamics, and possible ways to prevent or control the disease. There are several reasons to why HBV still prevail in Africa. Some of these reasons include: lack of information about the virus transmission (including the role of mother to child transmission); the disease burden is not well known; and insufficient treatment and vaccine. Assessing the dynamics of HBV infection will help to give an insight on the dynamics of the disease and help bring awareness to people and have a better understanding of the disease prevention and control, as well as the risks associated with the disease, and enable heath personnel to better plan for health care. Mathematical models which uses a set of mathematical equations derived from a theoretical framework have been widely used to explain the dynamics of infectious diseases in Africa as in Mpeshe [20].

Therefore, in this article we develop a mathematical model using modeling approach that will help assess the dynamics of HBV infection by looking at the basic reproduction number which is the initial transmission of the disease, determine the existence and stability of equilibrium points, and analyse the impact of certain parameters of interest.

2. The HBV Model

2.1. Model Formulation

The model considers only human populations with natural and disease-dependent death rate for human. Due to vertical transmission in human, a recruitment of infected humans is included to the infected compartment. The population consists of susceptible humans (S), acutely infected humans (I_a), chronic carriers (I_c), and recovered humans (R). Table 1 shows the model parameters and their description as they have been used in this work.

Table 1. Parameters and their description

Parameter	Description
b	birth rate in human
μ	natural death rate of human
μ_0	disease induced death rate of human
β	transmission rate of chronic HBV
γ	transmission rate of acute HBV
α	recovery rate of acute HBV
θ	recovery rate of chronic carrier HBV
ω	failure rate to clear acute HBV
p	probability for newly infected individual to be a carrier
q	vertical transmission rate in human

The mode of transmission of HBV in human is shown by Figure 1. Several assumptions have been made in formulating this model including: $bq < \mu + \mu_0 + \theta$ so that carriers would not increase rapidly; $\beta > \gamma$ because many infected individuals are likely to be unaware of their condition and hence continue with their regular behaviour; acute may become chronic carriers if they fail to clear the infection, and that a chronic carrier mother may give birth to a chronic carrier child; and screening and treatment may help some chronic carriers to recover.

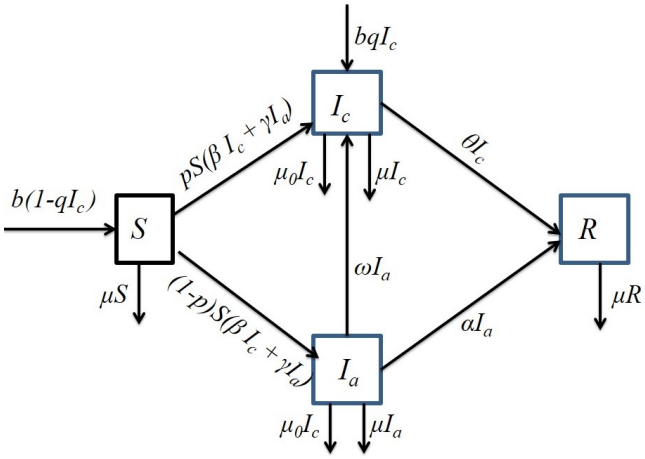

Fig. 1. Flow diagram for the HPB model

Using the parameters in Table 1 and Figure 1, an SIR model is derived using first order nonlinear ordinary differential equations as follows:

$$\frac{dS}{dt} = b(1-qI_c) - \mu S - S(\beta I_c + \gamma I_a), \tag{1a}$$

$$\frac{dI_a}{dt} = (1-p)S(\beta I_c + \gamma I_a) - (\mu + \mu_0 + \omega + \alpha)I_a, \tag{1b}$$

$$\frac{dI_c}{dt} = bqI_c + pS(\beta I_c + \gamma I_a) + \omega I_a - (\mu + \mu_0 + \theta)I_c, \tag{1c}$$

$$\frac{dR}{dt} = \theta I_c + \alpha I_a - \mu R. \tag{1d}$$

2.2. Feasibility of the Model Solution

In this section, we investigate the feasibility of the model solution to determine whether the model is well-posed epidemiologically and mathematically. From (1) we find that

$$\frac{dN}{dt} = b - \mu N - \mu_0(I_a + I_c) \le b - \mu N. \tag{2}$$

Integrating the inequality both side we find that

$$N(t) \le \frac{b}{\mu}(1 - e^{-\mu t}) + N_0(t)e^{-\mu t}. \tag{3}$$

As $t \to \infty$, $e^{-\mu t} \to 0$ and hence

$$N(t) \le \frac{b}{\mu}. \tag{4}$$

Since R does not appear in other equations, then the equation for R can be omitted from the analysis for its value can be obtained when the values for S, I_a, and I_c are known. The remaining system becomes

$$\frac{dS}{dt} = b(1-qI_c) - \mu S - S(\beta I_c + \gamma I_a), \tag{5a}$$

$$\frac{dI_a}{dt} = (1-p)S(\beta I_c + \gamma I_a) - (\mu + \mu_0 + \omega + \alpha)I_a, \tag{5b}$$

$$\frac{dI_c}{dt} = bqI_c + pS(\beta I_c + \gamma I_a) + \omega I_a - (\mu + \mu_0 + \theta)I_c. \tag{5c}$$

Thus, the model solution is feasible and positively invariant in the region

$$\Omega = \{(S, I_a, I_c) \ge 0 \in \mathbb{R}^3_+ : S + I_a + I_c \le \frac{b}{\mu}.\} \tag{6}$$

The existence of the feasibility solution of the model which is positively invariant in $\mathbb{R}^3_+$ implies that the model system is well-posed epidemiologically and mathematically. The well-posedness of the model allows us to continue with other mathematical treatment of the model.

2.3. Equilibrium Points

To determine the disease-free equilibrium and the endemic equilibrium, we set the left-hand side of (5) equal to zero. Setting $I_a = I_c = 0$, we find that the disease free equilibrium for the model is

$$E_0 = (\frac{b}{\mu}, 0, 0), \tag{7}$$

and the endemic equilibrium is $E^* = (S^*, I_a^*, I_c^*)$ where,

$$S^* = \frac{(-bq+\mu+\mu_0+\theta)(\mu+\mu_0+\omega+\alpha)}{\gamma(1-p)(-bq+\mu+\mu_0+\theta)+(1-p)\omega\beta+p\beta(\mu+\mu_0+\alpha)}, \tag{8a}$$

$$I_a^* = \frac{(1-p)S^*\beta I_c^*}{(\mu+\mu_0+\omega+\alpha)-(1-p)\gamma S^*}, \tag{8b}$$

$$I_c^* = \frac{b-S^*(\mu+\gamma I_a^*)}{bq+\beta S^*} \tag{8c}$$

2.4. The Basic Reproduction Number

Basic reproduction number $\mathscr{R}_0$ is a very important measure of the initial transmission of any infectious disease. It is also useful in the establishment of the stability conditions of the equilibrium points. For E^* to exist in the feasible region Ω, the condition $0 < S^* < \frac{b}{\mu}$, or equivalently, $\frac{b}{\mu}\frac{1}{S^*} \geq 1$ is sufficiently necessary. Thus, define the basic reproduction number $\mathscr{R}_0$ by

$$\mathscr{R}_0 = \frac{b}{\mu}\frac{1}{S^*}, \tag{9}$$

then

$$\mathscr{R}_0 = \frac{b}{\mu}\frac{\gamma(1-p)(-bq+\mu+\mu_0+\theta)+(1-p)\omega\beta+p\beta(\mu+\mu_0+\alpha)}{(-bq+\mu+\mu_0+\theta)(\mu+\mu_0+\omega+\alpha)}, \tag{10}$$

3. Stability Analysis

3.1. Stability of the Disease-Free Equilibrium

Theorem 3.1.
The disease-free equilibrium of the HBV model (5) is locally asymptotically stable if $\mathscr{R}_0 < 1$ and unstable if $\mathscr{R}_0 > 1$.

Proof. We show that the Jacobian matrix $J(E_0)$ of the HBV model (5) at $E_0 = (\frac{b}{\mu}, 0, 0)$ has negative eigenvalues. Further computations show that he Jacobian matrix of the HPBV model (5) at E_0 is

$$J(E_0) = \begin{bmatrix} -\mu & -\gamma\frac{b}{\mu} & -bq-\beta\frac{b}{\mu} \\ 0 & (1-p)\gamma\frac{b}{\mu}-(\mu+\mu_0+\omega+\alpha) & (1-p)\beta\frac{b}{\mu} \\ 0 & \omega+p\gamma\frac{b}{\mu} & p\beta\frac{b}{\mu}+bq-(\mu+\mu_0+\theta) \end{bmatrix} \tag{11}$$

From the Jacobian matrix $J(E_0)$ we find that one of the eigenvalue is $\lambda_1 = -\mu$. The remaining eigenvalues are the eigenvalues of the reduced 2×2 matrix

$$J^*(E_0) = \begin{bmatrix} (1-p)\gamma\frac{b}{\mu}-(\mu+\mu_0+\omega+\alpha) & (1-p)\beta\frac{b}{\mu} \\ \omega+p\gamma\frac{b}{\mu} & p\beta\frac{b}{\mu}+bq-(\mu+\mu_0+\theta) \end{bmatrix}. \tag{12}$$

To show that the remaining eigenvalues are negative we need to show that the reduced Jacobian matrix $J^*(E_0)$ satisfy the Ruth-Hurwitz condition, that is, $tr(J^*(E_0)) < 0$ and $det(J^*(E_0)) > 0$. Further computations show that

$$\begin{aligned} tr(J^*(E_0)) &= (1-p)\gamma\frac{b}{\mu}-(\mu+\mu_0+\omega+\alpha)+p\beta\frac{b}{\mu}+bq-(\mu+\mu_0+\theta) \\ &= (\mu+\mu_0+\omega+\alpha)\left[\frac{(1-p)\gamma\frac{b}{\mu}}{\mu+\mu_0+\omega+\alpha}-1\right]+(-bq+\mu+\mu_0+\theta)\left[\frac{p\beta\frac{b}{\mu}}{-bq+\mu+\mu_0+\theta}-1\right]. \end{aligned} \tag{13}$$

Since $\mathscr{R}_0 < 1$ and from our assumption $bq < \mu+\mu_0+\theta$, then

$$\frac{(1-p)\gamma\frac{b}{\mu}}{\mu+\mu_0+\omega+\alpha} < 1 \text{ and } \frac{p\beta\frac{b}{\mu}}{-bq+\mu+\mu_0+\theta} < 1.$$

Therefore,

$$\frac{(1-p)\gamma\frac{b}{\mu}}{\mu+\mu_0+\omega+\alpha}-1<0 \text{ and } \frac{p\beta\frac{b}{\mu}}{-bq+\mu+\mu_0+\theta}-1<0.$$

Hence $tr(J^*(E_0))<0$. Also,

$$\begin{aligned} det(J^*(E_0)) &= (1-p)\gamma\frac{b}{\mu}(bq-(\mu+\mu_0+\theta))-(\mu+\mu_0+\omega+\alpha)(bq-(\mu+\mu_0+\theta)) \\ &\quad -(\mu+\mu_0+\omega+\alpha)p\beta\frac{b}{\mu}-(1-p)\omega\beta\frac{b}{\mu} \\ &= (\mu+\mu_0+\omega+\alpha)(-bq+\mu+\mu_0+\theta)(1-\mathscr{R}_0). \end{aligned} \tag{14}$$

Hence, $det(J^*(E_0))>0$ if and only if $\mathscr{R}_0<1$. This completes the proof. □

Theorem 3.2.
The disease-free equilibrium is of the HBV model (5) is globally asymptotically stable if $\mathscr{R}_0<1$ and unstable if $\mathscr{R}_0>1$.

Proof. To analyse the global stability of the disease free equilibrium we apply the Castillo-Chavez [21] approach. We write the HBV model (5) in the form

$$\begin{cases} \frac{dX_s}{dt}=A(X_s-X_{DFE,s})+A_1X_i, \\ \frac{dX_i}{dt}=A_2X_i \end{cases} \tag{15}$$

where X_s is the vector representing the non-transmitting class, and X_i is the vector representing the transmitting class. The disease-free equilibrium is globally asymptotically stable if A has negative real eigenvalues and A_2 is a Metzler matrix. From the HBV model (5) we have $X_s=S$ and $X_i=(I_a,I_c)^T$. Further analysis gives

$$A=(-\mu),$$

$$A_1=(-\gamma S,-bq-\beta S),$$

and

$$A_2=\begin{bmatrix} (1-p)\gamma S-(\mu+\mu_0+\omega+\alpha) & (1-p)\beta S \\ \omega+p\gamma S & p\beta S+bq-(\mu+\mu_0+\theta) \end{bmatrix}. \tag{16}$$

It can be easily seen that A has negative real eigenvalue, and that the matrix A_2 is a Metzler matrix because all the off-diagonal elements are positive. Hence, the disease-free equilibrium E_0 is globally asymptotically stable. □

3.2. Stability of the Endemic Equilibrium

The local stability of the disease free equilibrium imply a local stability of the endemic equilibrium. Therefore, we need only to establish the global stability of the endemic equilibrium. There are mainly two approaches for establishing the global stability of endemic equilibrium: the Lyapunov function approach as in Korobeinikov [22, 23], and the geometrical approach as in Li and Muldowney [24]. In this study, we adapt the Li and Muldowney's geometrical approach. The approach can be seen in many papers including Khan [25]. A brief description of the approach is here summerised.

Let $\Omega\subset\mathbb{R}^n$ be an open subset and $f:\Omega\to\mathbb{R}^n$ be a map such that each solution $x(t)$ to the differential equation

$$x'=f(x) \tag{17}$$

is uniquely determined by its initial value $x(0)=x_0$. An equilibrium point $\overline{x}\subset\Omega$ of (17) is said to be globally stable in Ω if it is stable in Ω and all trajectories in Ω converge to $\overline{x}$.

Theorem 3.3 (Li and Muldowney, 1998).
Assume that

(H1) Ω is simply connected;

(H2) there is a compact absorbing set $K\subset\Omega$;

(H3) $\overline{x}$ is the only equilibrium of (17) in Ω.

Then $\overline{x}$ is globally stable in Ω if there exists a function $P(x)$ and a Lozinskii measure μ such that $\overline{q_2} < 0$, where

$$\overline{q_2} = \limsup_{t\to\infty} \sup_{x_0\in K} \frac{1}{t}\int_0^t \mu(B(x(s,x_0)))ds,$$

and

$$B = P_f P^{-1} + PJ^{[2]}P^{-1}$$

with $J^{[2]}$ the second additive compound matrix of the Jacobian of f at x.

Proof. Let $x \rightarrowtail P(x)$ be an $\binom{n}{2} \times \binom{n}{2}$ matrix-valued function that is differentiable in Ω. Assume that $P^{-1}(x)$ exists and is continuous for $x \in K$. Then, the matrix P_f is obtained by replacing each entry p_{ij} in P by its directional derivative in the direction of f, $(p_{ij})_f$. We therefore need to construct a 3×3 matrix-valued function P according to (5), and choose a suitable vector norm $|.|$ in $\mathbb{R}^3 \cong \mathbb{R}^{\binom{3}{2}}$ such that the corresponding Lozinskii measure μ and $\overline{q_2}$ satisfies $\overline{q_2} < 0$.

Let $x = (S, I_a, I_c) \in \Omega$ and $f(x)$ denote the the vector field of (5). The jacobian matrix J along each solution of (5) is

$$J = \begin{bmatrix} -(\mu+\beta I_c+\gamma I_a) & -\gamma S & -bq-\beta S \\ (1-p)(\beta I_c+\gamma I_a) & (1-p)\gamma S-(\mu+\mu_0+\omega+\alpha) & (1-p)\beta S \\ p(\beta I_c+\gamma I_a) & \omega+p\gamma S & p\beta S+bq-(\mu+\mu_0+\theta) \end{bmatrix},$$

and its second additive compound matrix $J^{[2]}$ is

$$J^{[2]} = \begin{bmatrix} a_{11} & (1-p)\beta S & bq+\beta S \\ \omega+p\gamma S & a_{22} & -\gamma S \\ -p(\beta I_c+\gamma I_a) & (1-p)(\beta I_c+\gamma I_a) & a_{33} \end{bmatrix}$$

where

$$\begin{aligned} a_{11} &= -(\mu+\beta I_c+\gamma I_a)+(1-p)\gamma S-(\mu+\mu_0+\omega+\alpha) \\ a_{22} &= -(\mu+\beta I_c+\gamma I_a)+p\beta S+bq-(\mu+\mu_0+\theta) \\ a_{33} &= (1-p)\gamma S-(\mu+\mu_0+\omega+\alpha)+p\beta S+bq-(\mu+\mu_0+\theta) \end{aligned}$$

If we set $P(x) = P(S, I_a, I_c)$ as

$$P = diag\{1, \frac{I_a}{I_c}, \frac{I_a}{I_c}\}$$

then we have

$$P^{-1} = diag\{1, \frac{I_c}{I_a}, \frac{I_c}{I_a}\}$$

and

$$P_f P^{-1} = diag\{0, \frac{I_a'}{I_a}-\frac{I_c'}{I_c}, \frac{I_a'}{I_a}-\frac{I_c'}{I_c}\}.$$

Therefore,

$$B = \begin{bmatrix} b_{11} & (1-p)\beta S\frac{I_c}{I_a} & (bq+\beta S)\frac{I_c}{I_a} \\ (\omega+p\gamma S)\frac{I_a}{I_c} & b_{22} & -\gamma S \\ -p(\beta I_c+\gamma I_a)\frac{I_a}{I_c} & (1-p)(\beta I_c+\gamma I_a) & b_{33} \end{bmatrix}$$

where

$$\begin{aligned} b_{11} &= -(\mu+\beta I_c+\gamma I_a)+(1-p)\gamma S-(\mu+\mu_0+\omega+\alpha) \\ b_{22} &= \frac{I_a'}{I_a}-\frac{I_c'}{I_c}-(\mu+\beta I_c+\gamma I_a)+p\beta S+bq-(\mu+\mu_0+\theta) \\ b_{33} &= \frac{I_a'}{I_a}-\frac{I_c'}{I_c}+(1-p)\gamma S-(\mu+\mu_0+\omega+\alpha)+p\beta S+bq-(\mu+\mu_0+\theta) \end{aligned}$$

The matrix B can be reduced to a block matrix of the form

$$B = \begin{bmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{bmatrix}.$$

with

$$B_{11} = -(\mu + \beta I_c + \gamma I_a) + (1-p)\gamma S - (\mu + \mu_0 + \omega + \alpha)$$
$$B_{12} = \begin{bmatrix} (1-p)\beta S\dfrac{I_c}{I_a} & (bq + \beta S)\dfrac{I_c}{I_a} \end{bmatrix}$$
$$B_{21} = \begin{bmatrix} (\omega + p\gamma S)\dfrac{I_a}{I_c} & -p(\beta I_c + \gamma I_a)\dfrac{I_a}{I_c} \end{bmatrix}^T$$

and

$$B_{22} = \begin{bmatrix} c_{11} & -\gamma S \\ (1-p)(\beta I_c + \gamma I_a) & c_{22} \end{bmatrix}$$

where

$$c_{11} = \frac{I_a'}{I_a} - \frac{I_c'}{I_c} - (\mu + \beta I_c + \gamma I_a) + p\beta S + bq - (\mu + \mu_0 + \theta)$$
$$c_{22} = \frac{I_a'}{I_a} - \frac{I_c'}{I_c} + (1-p)\gamma S - (\mu + \mu_0 + \omega + \alpha) + p\beta S + bq - (\mu + \mu_0 + \theta)$$

Define a vector norm in $\mathbb{R}^n$ by

$$|(u, v, w)| = \max\{|u|, |v| + |w|\}$$

where $(u, v, w) \in \mathbb{R}^n$. The Lozinskii measure, $\mu(B)$ with respect to the norm is defined as

$$\mu(B) \leq max\{g_1, g_2\}$$

where $g_1 = \mu_1(B_{11}) + |B_{12}|$, $g_2 = |B_{21}| + \mu_1(B_{22})$, with $|B_{12}|$ and $|B_{21}|$ the matrix norms with respect to l_1 norm and μ_1 is the Lozinskii measure of the matrix with respect to l_1 norm.

Since B_{11} is a scalar, its Lozinskii measure with respect to 1-norm is

$$\mu_1(B_{11}) = -(\mu + \beta I_c + \gamma I_a) + (1-p)\gamma S - (\mu + \mu_0 + \omega + \alpha).$$

Also

$$\mu_1(B_{22}) = \frac{I_a'}{I_a} - \frac{I_c'}{I_c} + p\beta S + bq - (\mu + \mu_0 + \theta) + \max\{-(\mu + \beta I_c + \gamma I_a), (1-p)\gamma S - (\mu + \mu_0 + \omega + \alpha)\}$$

and

$$|B_{12}| = \max\{(1-p)\beta S\frac{I_c}{I_a}, (bq + \beta S)\frac{I_c}{I_a}\} = (bq + \beta S)\frac{I_c}{I_a}$$
$$|B_{21}| = \max\{(\omega + p\gamma S)\frac{I_a}{I_c}, -p(\beta I_c + \gamma I_a)\frac{I_a}{I_c}\} = (\omega + p\gamma S)\frac{I_a}{I_c}.$$

Now

$$\begin{aligned} g_1 &= -(\mu + \beta I_c + \gamma I_a) + (1-p)\gamma S - (\mu + \mu_0 + \omega + \alpha) + (bq + \beta S)\frac{I_c}{I_a} \\ &= -(\mu + \beta I_c + \gamma I_a) + (1-p)\gamma S - (\mu + \mu_0 + \omega + \alpha) + bq\frac{I_c}{I_a} + p\beta S\frac{I_c}{I_a} + (1-p)\beta S\frac{I_c}{I_a} \\ &\leq -(\mu + \beta I_c + \gamma I_a) + (1-p)\gamma S - (\mu + \mu_0 + \omega + \alpha) + bqI_c + p\beta SI_c + (1-p)\beta S\frac{I_c}{I_a} \end{aligned}$$

and

$$g_2 = \frac{I_a'}{I_a} - \frac{I_c'}{I_c} + p\beta S + bq - (\mu + \mu_0 + \theta) + \max\{-(\mu + \beta I_c + \gamma I_a), (1-p)\gamma S - (\mu + \mu_0 + \omega + \alpha)\} + (\omega + p\gamma S)\frac{I_a}{I_c}$$

From the equation in (5) we have

$$(1-p)\beta S\frac{I_c}{I_a} = \frac{I_a'}{I_a} - (1-p)\gamma S + (\mu+\mu_0+\omega+\alpha)$$
$$(\omega+p\gamma S)\frac{I_a}{I_c} = \frac{I_c'}{I_c} - p\beta S - bq + (\mu+\mu_0+\theta)$$

Hence

$$\begin{aligned} g_1 &\le -(\mu+\beta I_c+\gamma I_a) + bqI_c + p\beta S I_c + \frac{I_a'}{I_a} \\ &\le \frac{I_a'}{I_a} - \mu - (\beta - bq + p\beta S)I_c - \gamma I_c \\ &\le \frac{I_a'}{I_a} - \mu, \\ g2 &= \frac{I_a'}{I_a} - \min\{(\mu+\beta I_c+\gamma I_a),\ (\mu+\mu_0+\omega+\alpha) - (1-p)\gamma S\} \\ &= \frac{I_a'}{I_a} - \delta \end{aligned}$$

where $\delta = \min\{(\mu+\beta I_c+\gamma I_a),\ (\mu+\mu_0+\omega+\alpha) - (1-p)\gamma S\} > 0$.

Thus,

$$\mu(B) \le \max\{\frac{I_a'}{I_a} - \mu,\ \frac{I_a'}{I_a} - \delta\} = \frac{I_a'}{I_a} - \tau$$

where $\tau = \min\{\mu, \delta\}$.

Suppose that the HBV model (5) is uniformly persistent when $\mathscr{R}_0 > 1$. Then, there exists $c > 0$ and $T > 0$ such that $t > T$ implies that $I_a(t) \ge c$, $I_c(t) \ge c$ and

$$\frac{1}{t}\log I_a(t) < \frac{\tau}{2}$$

for all $(S(0), I_a(0), I_c(0)) \in K$. Thus,

$$\frac{1}{t}\int_0^t \mu(B)dB < \frac{\log I_a(t)}{t} - \tau < -\frac{\tau}{2}$$

for all $(S(0), I_a(0), I_c(0)) \in K$, which implies that $\overline{q_2} < 0$. Hence, the endemic equilibrium E^* is globally asymptotically stable. □

4. Impact of Vertical Transmission, and Screening and Treatment

In this section we look into the impact of the chronic carriers on $\mathscr{R}_0$ which is the initial transmission. Specifically, we look into the impact of the probability for newly infected individuals to be carriers, p, the recovery rate of chronic carriers due to screening and treatment, θ, and the vertical transmission, q, which are directly related to I_c and appears in the expression of $\mathscr{R}_0$. Using partial differentiation we find that

$$\begin{aligned} \frac{\partial \mathscr{R}_0}{\partial p} &= \frac{b}{\mu}\frac{-\gamma(-bq+\mu+\mu_0+\theta)+\beta(\mu+\mu_0+\omega+\alpha)}{(-bq+\mu+\mu_0+\theta)(\mu+\mu_0+\omega+\alpha)} \\ &> 0 \text{ iff } \beta > \frac{\gamma - bq+\mu+\mu_0+\theta}{(\mu+\mu_0+\omega+\alpha)} \end{aligned} \tag{18}$$

That means the increase in $\mathscr{R}_0$ due to change in the probability for individuals to be chronic carrier will depend on the transmission rate β of chronic carrier. The increase in p results an increase in $\mathscr{R}_0$. Similarly,

$$\frac{\partial \mathscr{R}_0}{\partial \theta} = -\frac{1}{(-bq+\mu+\mu_0+\theta)^2}\left[\frac{(1-p)\omega\beta\frac{b}{\mu}}{\mu+\mu_0+\omega+\alpha} + p\beta\frac{b}{\mu}\right] < 0 \tag{19}$$

The equation significantly shows that increase in θ will always reduce $\mathscr{R}_0$. The result provide a clue for control measure of HBV infection, that is, screening and treatment could be a good strategy for controlling HBV infection. Also,

$$\frac{\partial \mathscr{R}_0}{\partial q} = \frac{b}{(-bq+\mu+\mu_0+\theta)^2}\left[\frac{(1-p)\omega\beta\frac{b}{\mu}}{\mu+\mu_0+\omega+\alpha} + p\beta\frac{b}{\mu}\right] > 0 \tag{20}$$

The equation significantly show that increase in q will always increase $\mathscr{R}_0$.

From (19) and (20) we find that

$$\frac{\partial \mathscr{R}_0}{\partial q} = -b\frac{\partial \mathscr{R}_0}{\partial \theta} \tag{21}$$

and hence

$$\mathscr{R}_0 = f\left(q - \frac{\theta}{b}\right) \tag{22}$$

which means that $\mathscr{R}_0$ can be influenced only by the three parameters: θ, q, and b. When b is constant, $\mathscr{R}_0$ is a function of θ and q, that is, increase in the rate of screening and treating decreases $\mathscr{R}_0$ and vice versa, while increase in vertical transmission increases $\mathscr{R}_0$. Figure 2 support the above explanations.

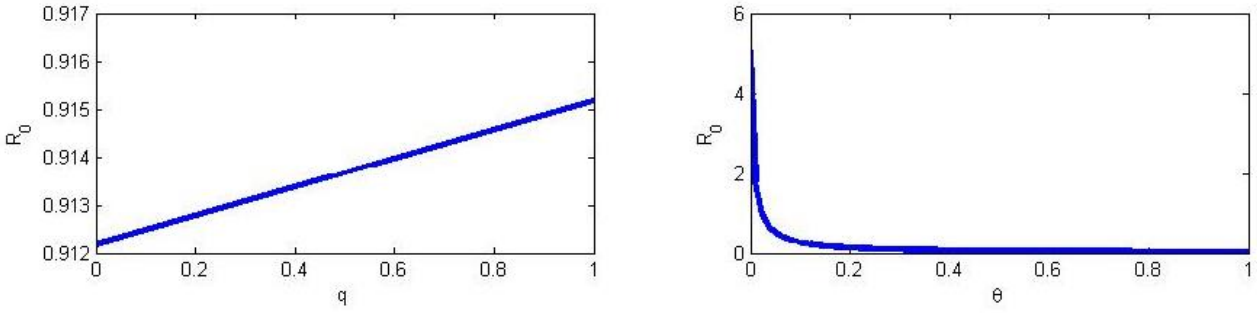

Fig. 2. Graph of $\mathscr{R}_0$ versus vertical transmission q, and screening and treating rate θ

5. Numerical Simulations

In this section, numerical simulation are carried out using parameter values given in Table 2. Numerical simulation help to study the persistence of the disease when introduced in a closed or isolated system. The initial values used in simulations are $S = 1000$, $I_a = 100$, $I_c = 100$, and $R = 0$.

Table 2. Parameters and their description

Parameter	Description	Range value
b	birth rate in human	0.0001
μ	natural death rate of human	0.00045
μ_0	disease induced death rate of human	0.001
β	transmission rate of chronic HPB	0.0025
γ	transmission rate of acute HPB	0.00015
α	recovery rate of acute HPB	0.075
θ	recovery rate of chronic carrier HPB	0.025
ω	failure rate to clear acute HPB	0.05
p	probability for newly infected individual to be a carrier	0.05
q	vertical transmission rate in human	0.001

Figure 3 show the graph of the variation of each compartment in HBV model with respect to time over a period of 100 days. The simulation results indicate the existence of both disease-free equilibrium and endemic equilibrium of the HBV transmission dynamics. From the graph, the disease-free equilibrium and endemic equilibrium are stable whenever they exist.

6. Discussion

In this paper, we used a modeling approach to investigate the dynamics and control of HBV infection. To study the effect of initial transmission of the disease we computed the basic reproduction number $\mathscr{R}_0$ of the model

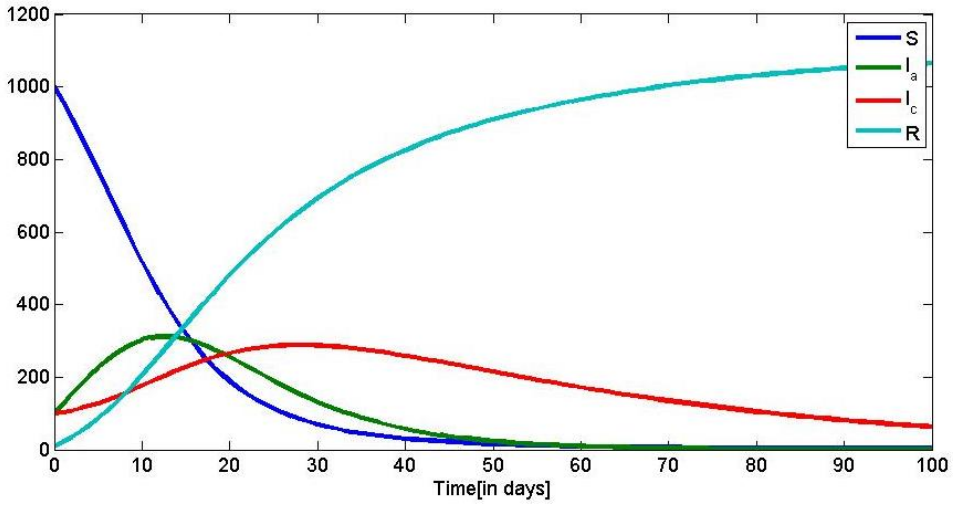

Fig. 3. Graphs for each compartment in HPBV model

used it to analyse the stability of the disease equilibrium points, as well as the relative effect of changes of some parameter values to $\mathscr{R}_0$. Analysis os the equilibrium points indicate that the disease-free equilibrium of the model is globally asymptotically stable when $\mathscr{R}_0 < 1$ and unstable otherwise. This means that when there is an outbreak it is possible to control the disease provided that $\mathscr{R}_0 < 1$. We also found that the disease endemic equilibrium is globally asymptotically stable when $\mathscr{R}_0 > 1$.

The impact of number of births, b, the vertical transmission, q, the recovery rate of chronic carriers, θ, and the probability of an individual to be chronic carrier, p, to $\mathscr{R}_0$ were also examined using calculus. It was observed that the increase in $\mathscr{R}_0$ due to changes in the probability for individual to be chronic carrier will depend largely on the transmission rate, β, of the chronic carriers. However, increase in recovery rate, θ, of chronic carriers due to screening and treatment will reduce $\mathscr{R}_0$, and increase in vertical transmission rate, q, will also increase $\mathscr{R}_0$. These findings agree with the intuitive expectations of the effect of these parameters over $\mathscr{R}_0$.

To analyse the variation of subpopulation in the model with respect to time we performed numerical simulations. The results of numerical simulation are shown in Figure 3. From the graph we see that whenever there is an outbreak, the disease is likely to persist in the first two months and there after it will start to slow down. Therefore, increasing the recovery rate while reducing the infection from vertical transmission will at this stage will help to control the disease.

7. Conclusion

As already highlighted earlier, HBV infection will remain a potential threat to many countries in the world because of its nature of infection where a person may become a chronic carrier. Results have shown that when the number of births is constant, the $\mathscr{R}_0$ is highly affected by the vertical transmission rate and the recovery rate of chronic carriers due to screening and treatment. Therefore, it is important to look into mechanisms which will reduce vertical transmission and at the same time increase recovery rate of carriers in order to reduce $\mathscr{R}_0$. Effective educational campaign about the disease will help to bring awareness to people on safe motherhood and attending clinics for screening and hence treatment where applicable.

Acknowledgments

The authors would like to thank all the people who contributed in the completion of this article.

Conflict of Interest

The authors declares no conflict of interest regarding the publication of this manuscript.

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