Analysis of Vertical Transmission Dynamics of Infectious Hepatitis B Virus: Mathematical Model Involving Vaccination and Treatment

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Abstract: **Hepatitis B has been a major global health menace for it's a potentially life-threatening liver disease. Around two billion persons are living with this infectious disease across the world. It's transmitted by infected individual to uninfected person either vertically (transmission before or during birth by carrier mother to the baby) or horizontally—transmission when the bodily fluid of an infected person comes into contact with the hepatitis B virus-free person. This can happen through the sharing of non-sterilized injection syringes, tattooing objects and through sexual intercourse. This particular project studied a mathematical model that combined both vaccination and treatment as a means to controlling the hepatitis B virus (HBV). In our mathematical model, equations are derived from the flow chart representing the HBV transmission dynamics. We determined the disease-free equilibrium (DFE) state, the endemic equilibrium (EE) state and the basic reproduction number R_0. The stability of these points are determined and the results show that the disease-free equilibrium is both locally and globally asymptotically stable i.e $R_0 < 1$. The stability analysis of endemic equilibrium point also reveals that the point is locally and globally asymptotically stable, i.e $R_0 > 1$. The basic reproduction number R_0 is computed using the next generation matrix method. The systems of ordinary differential equations (ODEs), which are non-linear are solved by numerical simulation. This was achieved by use of Runge-kutta method of order four with the help of MATLAB software and techniques. These results show that either of the method, treatment or vaccination, administered is effective in alleviating the spread of HBV disease, however, when both control strategies are combined, the disease is quickly controlled and ultimately brought to eradication.**

Keywords**: Mathematical model, Hepatitis B Virus (HBV), Treatment, Reproduction number, stable, unstable, Disease-free Equilibrium and Endemic Equilibrium**

I. INTRODUCTION

1.1 Background Information

Hepatitis B Virus (HBV) is a hepadnavirus with circular genome composed of partially double-stranded DNA and replicates through intermediate form by reverse transcription, Lacamini (2004). Hepatitis B therefore, is a liver infection caused by HBV and always finally evolves to liver cirrhosis and hepatocarcinom, Klysik (2001). This disease has two routes through which it is transmitted' One is a vertical transmission from an infected mother to the child during birth. This is a mode of infection in which 95 percent of the cases becomes chronic. The second infection route is through horizontal transmission between adults mainly through sexual contact, sharing bloodied needles and injection equipment, Liang (2009) and Rehermann & Nascimeni (2014). In this case, it is known that more than 90 percent of infection becomes acute. The first record of hepatitis B was made in 1885 and the discovery of its associated virus was later made by Bruch Bloomberg in 1986 at the National Health Institute in the USA. Since then, it has remained a major health pandemic. Towards the end end of 1980²s in an attempt to address this menace, WHO designed and initiated a very crucial Demonstration Project, in HBV history, on a large scale controlled clinical trial to vaccinate 80,000 newborns in high incident area of Qidong of Jiansu Province in China, Zuckerman et al, (1983). The Project ended seven years later and it was found that hepatitis B virus vaccination provided 75% protective efficiency against HBV infection. The organization therefore, recommended that hepatitis B vaccination should be included in all the national immunization programs and systems in all the countries of the world.

In Western Europe, and America, the prevalence of Hepatitis B remains very significantly small below 1 percent, while in both South East Asia and Sub-Saharan Africa, it is so high with about 5 percent to 10 percent of the population chronically infected with the disease, World Health Organization [WHO] (2016). The basic control measures of HBV are vaccination, treatment, educating the masses, screening of the blood and all blood products, Centre for Prevention and Control of Diseases [CDC](2005). According to Kenya Medical Research Institute [KEMRI](2004), there is an alarming increase of HBV cases in Kenya. It puts the prevalence rate of HBV at about 10 percent in pregnant women and more than 30 percent among the liver-diseased patients attending clinics. KEMRI further stated that the regions with high prevalence of HBV in Kenya are West Pokot County, Turkana County, Garissa County and Wajir County. The ostensible causes of HBV in the regions are cultural practices such as tattooing and circumcision in which they do not use sterilized implements and because the areas

are dry and people may not be able to get proper nutrition that ensures stronger immunity.

1.2 Statement of the Problem

Owing to the life-threatening nature of hepatitis B virus, global community has attempted to understand its dynamics and mathematics language has become one of the finest ways to comprehend the phenomenon. As such, mathematical modelers have modeled HBV epidemiology and their recommendations have become extremely useful to the public health policy makers in trying to control the disease. Despite all of this work, the existence of HBV still indicates a slow pace of control. Therefore, a lot of work is required to be done in this area. Our work focuses on analyzing Hepatitis B. Virus by using Mathematical model to assess the impacts of vaccinating and treating HBV patients in Turkana County, Kenya's one of the regions, in which prevalence of HBV is so high. In our model we assumed that babies born to carrier mothers are vertically infected as usual but automatically become carriers without incubating in the epidemiological class of latent stage. Besides vaccination, we factored in and focused on the role of treatment to supplement the vaccination control strategy. In this study, we investigated the impact of treatment in the carrier stage. This is because relapse and resistance may occur after treating the patients at the acute stage.

1.3 Justification of the Study

We do acknowledge that much work has been done in attempting to understand the HBV properties and to control its transmission as attested to by an inexhaustible list of models currently in publications. However, to effectively control or even eradicate the infectious hepatitis B virus, vaccination alone, as a path taken by several modelers, is not enough unless it's coupled with treatment since the already infected people cannot be helped by vaccination alone. This gap of knowledge is what our study attempts to close by forming and analyzing the HBV mathematical model. The research is also affordable and time-friendly, making it a worthwhile research undertaking.

1.4 Aim and Objectives

1.4.1 General Objective

The main objective of our study is to establish a mathematical model for Hepatitis B Virus and make an investigative analysis with a view to eradicating or fully control the spread of HBV using vaccination and treatment as the control strategy in a given population.

1.4.2 Specific Objectives

The particular or specific objectives of this study are:

i) Formulation of a mathematical model flowchart
ii) To derive the model equations
iii) To find the reproduction number
iv) Analyze the stability of the model at both the disease-free equilibrium and endemic equilibrium points.
v) Use numerical simulation to investigate the impact of combining vaccination and treatment in controlling HBV pandemic

1.5 Significance of the Study

Since HBV is proving to be life-threatening disease and we are looking for the possible best solutions, the work will help us in understanding the dynamics and control of hepatitis B Virus (HBV) through the effects of vaccination and treatment. It will enable the public health policy makers, by applying the recommendations of the study, to be able to make predictions about HBV and hence accurate policies and control.

The model will enable us to apply the mathematical knowledge, to our real-life situation which in this case is the control of HBV. Because it closes the existing gap of knowledge, just like any other research work, its tentative or possible weaknesses that will have eluded our intellect by the end of the study will excite further research from the interested modeling researchers and hence the advancement of knowledge in this particular field.

II. LITERATURE REVIEW

The World Health Organization [WHO] (2017) reported that more than 0.25 billion people are living with hepatitis B virus infection, most of which resulted in several deaths. According to the WHO reports in 2021, there were more than 820,000 HBV-related deaths in 2019 with 1.5 million infections each year. The infection is spread when the bodily fluid of an infected individual comes into contact with someone who is not yet infected, Sirlert et al, (2014). Hepatitis B virus causes chronic liver disease and chronic infections and puts people at a higher risk of death from cirrhosis of the liver and liver cancer. Hepatitis B infection acquired in adulthood leads to chronic Hepatitis in less than 5 percent of the cases while many of the infant-related infections develop into chronic infection, Hyams (1995) and this is the basis for strengthening and prioritizing infant and childhood vaccination, WHO (2013). The Hepatitis B virus nfant vaccination series (three doses of HBV vaccination) which provides infants with long term protection from HBV infection Peto T.J. (2014), was introduced in immunization programs in all but 12 countries, by 2017, WHO (2016). Elimination of Hepatitis B Virus from liver tissue remains an elusive goal. Chronic HBV results mainly from maternal-neonatal vertical infection, Rehermann (2013). Direct study of the initial HBV-immune dynamics in patients is simply difficult hence, the attention is given to animals and Mathematical modelling, Murray and Goyal, 2015; Congelosi et al, 2017. Mathematical models have therefore, been used to study HBV quite extensively, Ciupe et at, 2007; Fetahi Chenar et al, 2018. Such models have revealed various protection levels, virus clearance rate and half-life of infected cells. The use of mathematical modeling has improved our understanding of contracting factors and how we should control it. Modeling has ranged from simple

model, Anderson 2008; Halfmann et al, 2008, to more complex models involving the contribution of controls such as vaccine, Pang and Zou (2010) and the analysis of impact of immigration, Khan et al, 2013. Hepatitis B infection was one of the two greatest attributes proportion of cancer deaths by risk factor in China, S. Islami et al, 2017. The risk of developing a carrier is dependent on age of infection and the transmission has different routes for adults and children, L. Zou et al, (2017). It is known that sexual transmission is an important route of HBV spread in adults, L. Zou et al, (2015). Looking at all the available literature on this particular disease, research has intensively been geared towards vaccination to control the disease. However, it must be implemented along with treatment if HBV is going to be effectively controlled or eliminated altogether. Our study therefore, introduced treatment to back up vaccination as a means to control HBV. The gap stems from Zou et al (2010) paper who proposed a mathematical model to investigate the transmission dynamics and prevalence of HBV in China where they implemented vaccination alone. Our case study is confined to Turkana County, Kenya where the prevalence is high.

Since the risk of contracting hepatitis B is essentially related to sexual exposure and/ or other fluid contacts between carriers and uninfected individuals, treating carriers becomes so important. This backs up the immune system which usually mounts high response to fight HBV but sometimes fail due to viral resistance. We have divided the host population into five epidemiological classes in proportions: susceptible class S(t), acutely infected class I(t), chronic carrier class C(t), vaccinated class V(t) and recovered class R(t) where parameter t is the time variable.

III. THE HEPATITIS B VIRUS MODEL

3.1 Mathematical Formation Description of the Model

We formulate a mathematical model in which the total human population is compartmentalized into the following: susceptible individuals S(t), acutely infected persons I(t), chronic carriers C(t), vaccinated individuals V(t) and recovered patients R(t). $\mu\omega(1-\nu c)$ is the rate of recruitment of population into susceptible group. β is the transmission coefficient from susceptible group to acutely infected class while ε is a reduced transmission rate relative to acute infection by chronic carriers. μ_0, μ and μ_1 are the birth rate recruited into susceptible class, natural death rate which occurs in all the five classes and the Hepatitis B Virus -related death rate respectively in the model system. ω is the proportion of birth without vaccination while $(1-\omega)$ is the vaccinated proportion. ν is the proportion of birth vertically infected i.e those children infected during birth. γ_3 is the rate of vaccination while ψ is the rate of waning back to susceptibility when vaccination does not clear the disease. γ_1 is the rate of moving from acute stage to other compartments while q is an average probability an individual fails to clear acute infection but develops carrier stage. $q\gamma_1$ is the rate of moving from acute stage to carrier. Chronic carriers are treated at the rate of α and these treated individuals move from chronic carriers to immunity at the rate of γ_2. $(1-q)\gamma_1$ is the rate of recovery from acute infection.

Table 3.1: Variables and parameters of the model

Description of variable	Symbol
Susceptible population	S(t)
Acutely Infected Members of the Population	I(t)
Individuals who are chronic carriers	C(t)
Vaccinated Individuals of the population	V(t)
Recovered individuals	R(t)
Rate at which children are born into the population	μ
Natural death portion	μ_0
Hepatitis B Virus -related death rate	μ_1
Percentage of birth that is not vaccinated	ω
Percentage of birth vaccinated	ω (1-)
Percentage of birth that has vertical infection	ν
Rate of waning back to susceptibility by vaccinated individuals	ψ
Coefficient of transmission to any class	β
Rate of transition from acute stage to other compartments	γ_1
Probability of failure of individual to clear acute infection stage but instead develops carrier stage	γ_1 q
Rate of transitioning from acute infection to chronic carrier	q
Rate of transitioning from acute infection to recovered class	γ_1 (1-q)
Rate of moving from chronic carrier to immunity	
Vaccination rate of susceptible individuals	γ_3
Reduced transmission rate by acute infection relative to carriers	ε
Rate at which chronic carriers are treated	α

3.1.1 Model Assumptions

The following assumptions are made regarding the model:

i) The members of the population are the same (homogeneous population)
ii) Recruitment of individuals into the population is only through birth
iii) Exiting out of the population is through both natural death and Hepatitis B Virus-related death only
iv) Individuals who received vaccination may not necessarily achieve permanent immunity
v) Infants born to carrier mothers proceed to chronic carrier stage immediately
vi) Treated carriers recover

3.1.2 Flow chart Describing the Model and its associated Equations

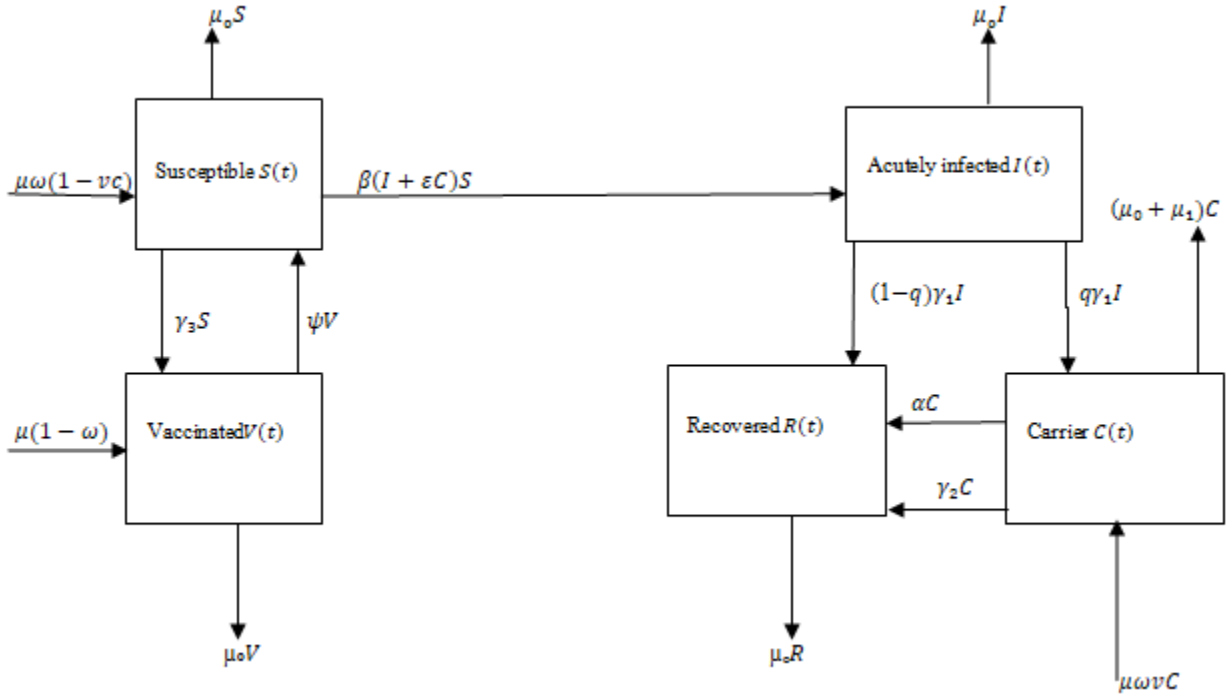

Figure 3.1: Flow chart

The following are the equations we can possibly draw from the flow chart above

$$\frac{dS}{dt} = \mu\omega(1-\nu C) + \psi V - (\mu_0 + \gamma_3 + \beta I + \varepsilon\beta C)S$$
$$\frac{dV}{dt} = \mu(1-\omega) - (\mu_0 + \psi)V + \gamma_3 S$$
$$\frac{dI}{dt} = (\beta I + \varepsilon\beta C)S - (\mu_0 + \gamma_1)I$$
$$\frac{dC}{dt} = q\gamma_1 I + \mu\omega\nu C - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C$$
$$\frac{dR}{dt} = (1-q)\gamma_1 I + (\alpha + \gamma_2)C - \mu_0 R \qquad (3.1)$$

Since R appears only in the last equation, it's sufficient that we discuss only the first four equations which are independent of R.

$$\frac{dS}{dt} = \mu\omega(1-\nu C) + \psi V - (\mu_0 + \gamma_3 + \beta I + \varepsilon\beta C)S$$
$$\frac{dV}{dt} = \mu(1-\omega) - (\mu_0 + \psi)V + \gamma_3 S$$
$$\frac{dI}{dt} = (\beta I + \varepsilon\beta C)S - (\mu_0 + \gamma_1)I$$
$$\frac{dC}{dt} = q\gamma_1 I + \mu\omega\nu C - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C \qquad (3.2)$$

3.2 Analysis of the Model

In this section, we discuss the positivity, boundedness, existence and uniqueness of the solutions. We also discuss the equilibrium points (Disease-free Equilibrium and Endemic equilibrium) and the basic reproduction number.

3.2.1 Positivity of the Solutions

We give the proof that for all $t \in [0, t_0]$, $S(t), V(t), I(t), C(t)$ will be positive in $\Re_+^4$. Since it's already known that all the parameters used in the model system are entirely positive, we will place a lower bound on each of the equations of the system (3.2), such that

$$\frac{dS}{dt} = \mu\omega(1-\nu C) + \psi V - (\mu_0 + \gamma_3 + \beta I + \varepsilon\beta C)S \geq -(\mu_0 + \gamma_3 + \beta I)S$$
$$\frac{dV}{dt} = \mu(1-\omega) - (\mu_0 + \psi)V + \gamma_3 S \geq -(\mu_0 + \psi)V$$
$$\frac{dI}{dt} = (\beta I + \varepsilon\beta C)S - (\mu_0 + \gamma_1)I \geq -(\mu_0 + \gamma_1)I$$
$$\frac{dC}{dt} = q\gamma_1 I + \mu\omega\nu C - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C \geq -(\mu_0 + \mu_1 + \gamma_2 + \alpha)C$$

By the method of separation of variables, we obtain the following solutions;

$$S(t) \geq S(0)e^{-\left[(\mu_0+\gamma_3)t + \beta\int I(t)dt + \varepsilon\beta\int C(t)dt\right]}$$

As $t \to \infty$, we have

$$S(t) \geq 0, \forall t \geq 0$$

In view of the second equation and using the method of separation of variables, we have

$$V(t) \geq V(0)e^{-(\mu_0+\psi)t}$$

As $t \to \infty$, we have;

$$V(t) \geq 0 \ \forall t \geq 0$$

The third equation gives us;

$$I(t) \geq I(0)e^{-(\mu_0+\gamma_1)t}$$

As $t \to \infty$, we have

$$I(t) \geq 0 \ \forall t \geq 0$$

Finally, we solve for C(t)

$$C(t) \geq C(0)e^{-(\mu_0+\mu_1+\gamma_1+\alpha)t}$$

As $t \to \infty$, we get $C(t) \geq 0, \forall t \geq 0$

Hence for all $t \in (0, t_0), S(t), V(t), I(t)$ and $C(t)$ will be positive in $\Re_+^4$.

3.2.2 Boundedness of the solutions

Lemma 1

: There exists an $S_M, V_M, I_M, C_M > 0$ such that $S(t), V(t), I(t), C(t), \limsup_{t\to\infty}(S(t)) \leq S_M$

$$\limsup_{t\to\infty}(V(t)) \leq V_M, \ \limsup_{t\to\infty}(I(t)) \leq I_M,$$
$$\limsup_{t\to\infty}(C(t)) \leq C_M, \ \forall t \in [0, t_0]$$

Proof

We must proof that for all $t \in (0, t_0), S(t), V(t), I(t)$ and $C(t)$ will be bounded. We know that all the constants used in the system are positive, thus

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dC}{dt} = \mu\omega - (\mu_0 + \gamma_3)S(t) - (\mu_0 + \gamma_1)I(t) - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C(t)$$
$$\frac{d(S+I+C)}{dt} \leq \mu\omega - \min\{\mu_0 + \gamma_3, \mu_0 + \gamma_1, \mu_0 + \mu_1 + \gamma_2 + \alpha\}(S+I+C)(t)$$
$$(S+I+C)(t) \leq \frac{\mu\omega}{\min(\mu_0 + \gamma_3, \mu_0 + \gamma_2, \mu_0 + \mu_1 + \gamma_2 + \alpha)} + k_0 e^{-\min(\mu_0+\gamma_3, \mu_0+\gamma_1, \mu_0+\mu_1+\gamma_2+\alpha)t}$$

Taking the limSup of both sides,

$$\limsup_{t\to\infty}(S+I+C)(t) \leq \limsup_{t\to\infty}\left(\frac{\mu\omega}{\min(\mu_0 + \gamma_3, \mu_0 + \gamma_1, \mu_0 + \mu_1 + \gamma_2 + \alpha)} + k_0 e^{-\min(\mu_0+\gamma_3, \mu_0+\gamma_1, \mu_0+\mu_1+\gamma_2+\alpha)t}\right)$$
$$= \frac{\mu\omega}{\min(\mu_0 + \gamma_3, \mu_0 + \gamma_1, \mu_0 + \mu_1 + \gamma_2 + \alpha)}$$

So, choose

$$S_M = I_M = C_M = \frac{\mu\omega}{\min(\mu_0 + \gamma_3, \mu_0 + \gamma_1, \mu_0 + \mu_1 + \gamma_2 + \alpha)}$$

Thus (S+I+C)(t) is bounded, so S(t), I(t) and C(t) are all bounded since $(S(t), I(t), C(t)) \leq (S+I+C)(t)$

So, $S(t) \leq S_M$, $I(t) \leq I_M$. and $C(t) \leq C_M \ \forall t \in [0, t_0]$.

Again, since the constants used are positive, we can place an upper bound on $\frac{dV}{dt}$ so,

$$\frac{dV}{dt} = \mu(1-\omega) + \gamma_3 S - (\mu_0 + \omega) \leq \mu(1-\omega) + \gamma_3 S$$

Therefore, we choose;

$$V_M = S_M$$
$$V(t) \leq S_M$$

Since S(t) is bounded for all $t \in [0, t_0]$, we know that V(t) is bounded for all $t \in [0, t_0]$.

3.2.3 Existence and Uniqueness of the Solutions

Lemma 2: *Let* $t_0 > 0$. *In the model, if the initial conditions satisfy* $S(t) > 0, V(t) > 0, I(t) > 0, C(t) > 0$ *then* $\forall t \in \Re, S(t), V(t), I(t)$ and $C(t)$ will exist in $\Re_+^4$

Proof

$$x=\begin{bmatrix} S(t) \\ V(t) \\ I(t) \\ C(t) \end{bmatrix} \text{ and } f(t)=\begin{bmatrix} \mu\omega(1-\nu C)+\psi V-(\mu_0+\gamma_3+\beta I+\varepsilon\beta C)S \\ \mu(1-\omega)+\gamma_3 S-(\mu_0+\psi)V \\ (\beta I+\varepsilon\beta C)S-(\mu_0+\gamma_1)I \\ q\gamma_1 I+\mu\omega\nu C-(\mu_0+\mu_1+\gamma_2+\alpha)C \end{bmatrix}$$

We note that f is continuously differentiable on $\Re^4$ and thus f is locally Lipschitz in $\Re^4$

Theorem 1*: Fundamental Existence and Uniqueness Theorem. Suppose the function* $f:\Re^n \to \Re^n$ *is continuously differentiable, then x(t) is a solution of the differential equation* $\frac{dx}{dt}=f(x)$ on an interval Γ.

If x(t) is differentiable on Γ and if

$\forall t \in \Gamma$, x(t) is in $\Re^4$ and $\frac{dx}{dt}=f(x(t))$ and given $x_0 \in \Re^n$, x(t) is a solution of initial-valued problem.

$$\frac{dx}{dt}=f(x)$$
$$x(t_0)=x_0$$

By the well-known existence and uniqueness theorem we have just stated above without proof, as well as the proved lemmas of positivity and boundedness of the solutions, we can conclude that there exist unique, positive and bounded solutions to the system (3.2) of the ordinary differential equations.

3.2.4 The Disease-free Equilibrium (DFE) point

The point referred to as a disease-free equilibrium of a system is a point that is free of disease or in which there is no infection within the population under study. At a disease-free equilibrium situation, we equate the equations of the system (3.2) to zero, thus;

$$\mu\omega(1-\nu C)+\psi V-(\mu_0+\gamma_3+\beta I+\varepsilon\beta C)S=0$$
$$\mu(1-\omega)-(\mu_0+\psi)V+\gamma_3 S=0$$
$$(\beta I+\varepsilon\beta C)S-(\mu_0+\gamma_1)I=0$$
$$q\gamma_1 I+\mu\omega\nu C-(\mu_0+\mu_1+\gamma_2+\alpha)C=0 \qquad (3.3)$$

Now,

$$\mu\omega(1-\nu C)+\psi V-(\mu_0+\gamma_3+\beta I+\varepsilon\beta C)S=0$$

Since there is no infection, the terms containing I and C vanish so that we have

$$\mu\omega+\psi V-(\mu_0+\gamma_3)S=0.....(i)$$

Also, the second equation becomes

$$\mu-\mu\omega+\gamma_3 S-(\mu_0+\psi)V=0.....(ii)$$

Making V the subject of the formula, we obtain

$$V=\frac{\mu-\mu\omega+\gamma_3 S}{\mu_0+\psi}$$

Substituting expression of V into (i), we obtain

$$\mu\omega+\psi\left(\frac{\mu-\mu\omega+\gamma_3 S}{\mu+\psi}\right)-(\mu_0+\gamma_3)S=0$$

Expansion gives

$$\mu\omega(\mu_0+\psi)+\psi(\mu-\mu\omega+\gamma_3 S)-(\mu_0+\psi)(\mu_0+\gamma_3)S=0$$
$$\mu\omega\mu_0+\mu\omega\psi+\psi\mu-\psi\mu\omega+\psi\gamma_3 S-(\mu_0\mu_0+\mu_0\gamma_3+\psi\mu_0+\gamma_3)S=0$$

$$\mu\omega\mu_0+\psi\mu-\mu_0\mu_0 S-\mu_0\gamma_0 S-\psi\mu_0 S=0$$
$$\mu\omega\mu_0+\psi\mu-(\mu_0\mu_0+\mu_0\gamma_3+\psi\mu_0)S=0$$
$$\mu\omega\mu_0+\psi\mu=(\mu_0\mu_0+\mu_0\gamma_3+\mu_0\psi)S$$
$$S=\frac{\mu\omega\mu_0+\psi\mu}{\mu_0\mu_0+\mu_0\gamma_3+\psi\mu_0}$$
$$S^0=\frac{\mu(\mu_0\omega+\psi)}{\mu(\mu_0+\gamma_3+\psi)}$$

We also need to find the expression of V^0

Using equation (ii)

$$\gamma_3 S=(\mu_0+\psi)V-\mu+\mu\omega$$
$$S=\frac{(\mu_0+\omega)V-\mu+\mu\omega}{\gamma_3}$$

Substitute this expression into equation (i)

$$\mu\omega+\psi V-(\mu_0+\gamma_3)\left(\frac{(\mu_0+\psi)V-\mu+\mu\omega}{\gamma_3}\right)=0$$
$$\mu\omega\gamma_3+\psi V\gamma_3-(\mu_0+\gamma_3)(\mu_0 V+\psi V-\mu+\mu\omega)=0$$
$$\mu\omega\gamma_3+\psi V\gamma_3-(\mu_0\mu_0 V+\mu_0\psi V-\mu_0\mu+\mu_0\mu\omega+\gamma_3\mu_0 V+\gamma_3\psi V-\gamma_3\mu+\gamma_3\mu\omega)=0$$

Opening the bracket, we have;

$$-\mu_0\mu_0 V-\mu_0\psi V+\mu_0\mu-\mu_0\mu\omega-\gamma_3\mu_0 V+\gamma_3\mu=0$$
$$-\left(\mu_0\mu_0+\mu_0\psi+\gamma_3\mu_0\right)V+\mu_0\mu-\mu_0\mu\omega+\gamma_3\mu=0$$
$$V=\frac{\mu_0\mu-\mu_0\mu\omega+\gamma_3\mu}{\mu_0\mu_0+\mu_0\psi+\mu_0\gamma_0}$$
$$V^0=\frac{\mu\left(\mu_0-\mu_0\omega+\gamma_3\right)}{\mu_0\left(\mu_0+\psi+\gamma_0\right)}$$

The disease-free equilibrium point is thus given by

$$E^0\left(\frac{\mu\left(\mu_0\omega+\psi\right)}{\mu_0\left(\mu_0+\gamma_3\right)},\frac{\mu\left(\mu_0+\gamma_3-\mu_0\omega\right)}{\mu_0\left(\mu_0+\psi+\gamma_3\right)},0,0\right)$$

$$I^0=C^0=0$$

Threshold for Disease Spread

When dealing with an infectious disease, the major concern is always its ability to attack the completely susceptible population. It's therefore, imperative to get the threshold parameter whose value usually dictates whether the disease will continue to spread or die out. This parameter is referred to as the basic reproduction number $\left(R_0\right)$. This quantity gives the average number of secondary infections generated when one infected individual is introduced into a fully susceptible population. If $R_0<1,$ on average an infected individual produces less than one new infected individual in the course of the infectious period and hence the disease dies out of the population. But if $R_0>1,$ infected individual produces, on average, more than one new infected individual and thus the spread of the disease is possible.

3.2.5 Calculating the Basic Reproduction Number $\left(R_0\right)$

We use the next generation matrix method stipulated by Van den Driessche Watmough (2002) to calculate $R_0.$ The basic reproduction number formula is given by $\rho\left(F_0V_0^{-1}\right).$ F_0 is the Jacobian of f_i at E^0 and f_i is the rate of appearance of new infection in the compartments i while V_0 is the Jacobian of v_i at $E^0.$ v_i represents rate at which are individuals are transferred into and out of the compartment $i.$ The population infected with the disease is represented by the two equations below.

$$\left(\beta I+\varepsilon\beta C\right)S-\left(\mu_0+\gamma_1\right)I=0$$
$$q\gamma_1+\mu\omega\nu C-\left(\mu_0+\mu_1+\gamma_2+\alpha\right)C=0$$

Taking $x=\left(I,C\right)$

$$\frac{dx}{dt}=f_i-v_i$$
$$\begin{bmatrix}\beta IS+\varepsilon\beta CS\\0\end{bmatrix}-\begin{bmatrix}\left(\mu_0+\gamma_1\right)I\\-q\gamma_1+\left(\mu_0+\mu_1+\gamma_2+\alpha\right)C-\mu\omega\nu\end{bmatrix}$$

where,

$$f_i=\begin{bmatrix}\beta IS+\varepsilon\beta CS\\0\end{bmatrix}\text{ and }v_i=\begin{bmatrix}\left(\mu_0+\gamma_1\right)I\\-q\gamma_1 I-\mu\omega\nu C+\left(\mu_0+\mu_1+\gamma_2+\alpha\right)C\end{bmatrix}$$

$$F_0=\text{Jacobian of }f_i\text{ at }E^0=\begin{bmatrix}\beta S^0&\varepsilon\beta S^0\\0&0\end{bmatrix}$$

$$V_0=\text{Jacobian of }v_i\text{ at }E^0=\begin{bmatrix}\left(\mu_0+\gamma_1\right)&0\\-q\gamma_1&\left(\mu_0+\mu_1+\gamma_2+\alpha-\mu\omega\nu\right)\end{bmatrix}$$

$$V_0^{-1}=\begin{bmatrix}\dfrac{\mu_0+\mu_1+\gamma_2+\alpha-\mu\omega\nu}{\mu_0+\gamma_1}&0\\\dfrac{q\gamma_1}{\left(\mu_0+\mu_0+\gamma_2+\alpha-\mu\omega\nu\right)\left(\mu_0+\gamma_1\right)}&\dfrac{\mu_0+\gamma_1}{\mu_0+\mu_1+\gamma_2+\alpha-\mu\omega\nu}\end{bmatrix}$$

Multiplying the two matrices gives

$$F_0V_0^{-1}=\begin{bmatrix}\dfrac{\left(\mu_0+\mu_1+\gamma_2+\alpha-\mu\omega\nu\right)\left(\beta S^0\right)}{\mu_0+\gamma_1}+\dfrac{q\gamma_1\varepsilon\beta S^0}{\left(\mu_0+\mu_1+\gamma_2+\alpha\right)\left(\mu_0+\gamma_1\right)}&\dfrac{\varepsilon\beta S^0\left(\mu_0+\gamma_1\right)}{\mu_0+\mu_0+\gamma_2+\alpha-\mu\omega\nu}\\0&0\end{bmatrix}$$

The basic reproduction number R_0 is given by the spectral radius of the matrix, $F_0V_0^{-1}$ that is, its highest absolute value of eigenvalue.

$$R_0=\rho\left(F_0V_0^{-1}\right)$$

The eigenvalues of the above matrix are;

$$\lambda_1=0,\lambda_2=\frac{\beta\mu\left(\mu_0+\mu_1+\gamma_2+\alpha-\mu\omega\nu\right)\left(\psi+\mu_0+\omega\right)}{\mu_0\left(\mu_0+\gamma_1\right)\left(\mu_0+\gamma_3+\psi\right)}+\frac{\varepsilon\beta\mu\left(\psi+\mu_0+\omega\right)\left(\mu_0+\gamma_1\right)}{\mu_0\left(\mu_0+\gamma_3+\psi\right)\left(\mu_0+\mu_1+\gamma_2+\alpha-\mu\omega\nu\right)}$$

Clearly, the basic reproduction number becomes

$$R_0=\frac{\beta\mu\left(\mu_0+\mu_1+\gamma_2+\alpha-\mu\omega\nu\right)\left(\psi+\mu_0+\omega\right)}{\mu_0\left(\mu_0+\gamma_1\right)\left(\mu_0+\gamma_3+\psi\right)}+\frac{\varepsilon\beta\mu\left(\psi+\mu_0+\omega\right)\left(\mu_0+\gamma_1\right)}{\mu_0\left(\mu_0+\gamma_3+\psi\right)\left(\mu_0+\mu_1+\gamma_2+\alpha-\mu\omega\nu\right)}$$

3.2.6 Endemic Equilibrium (EE) Point.

It is a point at which disease persists within the population under study. For the disease to remain in the population, the vaccinated class, the susceptible class, the infected class and the chronic carriers' class must not be zero. In other words, $E^*\left(S^*, V^*, I^*.C^*\right) \neq 0$.

When we substitute E^*, we obtain system (3.4) below.

$$\begin{aligned}
&\mu\omega(1-\nu C^*) + \psi V^* - (\mu_0 + \gamma_3 + \beta I^* + \varepsilon\beta C^*)S^* = 0\\
&\mu(1-\omega) - (\mu_0 + \psi)V^* + \gamma_3 S^* = 0\\
&(\beta I^* + \varepsilon\beta C^*)S^* - (\mu_0 + \gamma_1)I^* = 0\\
&q\gamma_1 I^* + \left[\mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha)\right]C^* = 0
\end{aligned} \tag{3.4}$$

Without the loss of generality, we can as well omit the asterisk $\left[^*\right]$ in our calculations but replace it later.

$$\mu(1-\omega) - (\mu_0 + \psi)V + \gamma_3 S = 0$$

$$V = \frac{\mu(1-\omega)\gamma_3 S}{\mu_0 + \psi} \ldots\ldots\ldots\ldots (iii)$$

Adding the third equation of system (3.2) to the first equation i.e

$$\mu\omega(1-\nu C) + \psi V - (\mu_0 + \gamma_3 + \beta I + \varepsilon\beta C)S = 0$$

$$+$$

$$(\beta I + \varepsilon\beta C)S - (\mu_0 + \gamma_1)I = 0$$

$$\mu\omega(1-\nu C) + \psi V - (\mu_0 + \gamma_3)S - (\mu_0 + \gamma_1)I = 0 \ldots\ldots\ldots (iv)$$

But we know V in terms of S, therefore,

$$\mu\omega(1-\nu C) + \frac{\psi\{\mu(1-\omega) + \gamma_3 S\}}{\mu_0 + \psi} - (\mu_0 + \gamma_3)S - (\mu_0 + \gamma_1)I = 0$$

$$I = \frac{(\mu_0 + \psi)\mu\omega(1-\nu C) + \psi\{\mu(1-\omega) + \gamma_3 S\} - (\mu_0 + \psi)(\mu_0 + \gamma_3)S}{(\mu_0 + \psi)(\mu_0 + \gamma_1)}$$

Simplifying terms containing S i.e,

$$\psi\{(\mu - \mu\omega) + \gamma_3 S\} - (\mu_0 + \psi)(\mu_0 + \gamma_3)S$$

$$\psi\mu - \psi\mu\omega + \psi\gamma_3 S - \mu_0\mu_0 S - \mu_0\gamma_3 S - \psi\mu_0 S - \psi\gamma_3 S$$

$$\psi\mu - \psi\mu\omega - (\mu_0\mu_0 + \mu_0\gamma_3 + \psi\mu_0)S$$

Substituting back we have;

$$I = \frac{(\mu_0 + \psi)\mu\omega(1-\nu C) + \psi\mu - \psi\mu\omega - (\mu_0\mu_P + \mu_0\gamma_3 + \psi\mu_0)S}{(\mu_0 + \psi)(\mu + \gamma_1)} \ldots\ldots\ldots (v)$$

Add second equation of (3.2) to (iv), i.e

$$\mu\omega(1-\nu C) + \psi V - (\mu + \gamma_3)S - (\mu + \gamma_1)I = 0$$

$$+$$

$$\mu(1-\omega) - (\mu_0 + \psi)V + \gamma_3 S = 0$$

Hence

$$\mu\omega(1-\nu C) + \mu(1-\omega) - \mu_0 V - \mu_0 S - (\mu_0 + \gamma_1)I = 0 \ldots\ldots\ldots\ldots\ldots (vi)$$

$$\mu\omega(1-\nu C) + \mu(1-\omega) - \frac{\mu_0\{\mu(1-\omega) + \gamma_3 S\}}{\mu_0 + \psi} - \mu_0 S - (\mu_0 + \gamma_1)I = 0$$

$$(\mu_0 + \psi)\mu\omega(1-\nu C) + (\mu_0 + \psi)\mu(1-\omega) - \mu_0\{\mu(1-\omega) + \gamma_3 S\} - (\mu_0 + \psi)\mu_0 S - (\mu_0 + \psi)(\mu_0 + \gamma_1)I = 0$$

Substituting the expression of I which is equation (v), we obtain

$$(\mu_0 + \psi)\mu\omega(1-\nu C) - (\mu_0 + \psi)\mu(1-\omega) - \mu_0\mu + \mu_0\mu\omega - \mu_0\gamma_3 S - \mu_0(\mu + \psi)S - (\mu_0 + \psi)\mu\omega(1-\nu C)$$
$$-\psi\mu + \psi\mu\omega + (\mu_0\mu_0 + \mu_0\gamma_3 + \psi\mu_0)S = 0$$

Rearranging, we get;

$$\{(\mu_0\mu_0 + \mu_0\mu_0\gamma_3\psi) - \mu_0\gamma_3 - \mu_0(\mu_0 + \psi)\}S = (\mu_0 + \psi)(1-\omega)\mu + \mu_0\mu - \mu_0\mu\omega + \mu\psi - \psi\mu\omega$$

Hence

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

From (iii), we have

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

Therefore,

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

We need to find I^*

Adding the first and fourth equations of (3.2)

$$\mu\omega - \mu\omega\nu C + \psi V - (\mu_0 + \gamma_3 + \beta I + \varepsilon\beta C)S = 0$$

+

$$q\gamma_1 I + \mu\omega\nu C - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C = 0$$

$$\mu\omega + \psi V + q\gamma_1 I - (\mu_0 + \gamma_3 + \beta I + \varepsilon\beta C)S - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C = 0 \text{.....(vii)}$$

Adding (vii) to the third equation of (3.2), we obtain;

$$\mu\omega + \psi V^* + q\gamma_1 I - (\mu_0 + \gamma_3)S^* - (\mu_0 + \gamma_1)I - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C = 0 \text{.....(viii)}$$

From the fourth equation of the system (3.2), we have;

$$C = \frac{q\gamma_1 I}{\mu_0 + \mu_1 + \gamma_2 + \alpha - \mu\omega\nu}$$

Substituting expression of C into (viii) and simplifying, we obtain;

$$I^* = \frac{\{(\mu_0 + \gamma_3)S^* - \mu\omega - \psi V^*\}\{\mu_0 + \mu_1 + \gamma_2 + \alpha - \mu\nu\psi\}}{\{q\gamma_1 - (\mu_0 + \gamma_1)\}\{\mu_0 + \mu_1 + \gamma_2 + \alpha - \mu\omega\nu\} - \{\mu_0 + \mu_1 + \gamma_2 + \alpha - \mu\nu\omega\}}$$

Having known I, our C becomes

$$C^* = \frac{q\gamma_1 I^*}{\mu_0 + \mu_1 + \gamma_2 + \alpha - \mu\omega\nu}$$

$$E^*(S,^* \mathrm{V},^* \mathrm{I},^* \mathrm{C}^*) \neq 0$$

3.3 Stability of the Disease-Free Equilibrium point.

In this section, we discuss the local and global stability of the disease-free equilibrium.

3.3.1 Local Stability of the Disease-Free Equilibrium point.

We would want to find the local stability of the disease-free equilibrium point of the system of ODEs. Local stability is calculated at this point using the Jacobian of the model at E^0. It is achieved using the sign of the real parts of the eigenvalues of the corresponding Jacobian matrix.

Theorem 2*: The disease-free equilibrium of the system of ODEs is locally asymptotically stable if the reproduction number* $R_0 < 1$ *and unstable if* $R_0 > 1$

Proof

Taking the equations of the system (3.2),

$$J = \begin{bmatrix} -(\mu_0 + \gamma_1 + \beta I + \varepsilon\beta C) & \psi & -\beta S^0 & -(\mu\omega\nu + \varepsilon\beta S^0) \\ \gamma_3 & -(\mu_0 + \psi) & 0 & 0 \\ (\beta I + \varepsilon\beta C) & 0 & \beta S^0 - (\mu_0 + \gamma_1) & \varepsilon\beta S^0 \\ 0 & 0 & q\gamma_1 & \mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha) \end{bmatrix}$$

$$J(E^0) = \begin{bmatrix} -(\mu_0 + \gamma_1) & \psi & -\left(\frac{\beta\mu(\psi + \mu_0 + \omega)}{\mu_0(\mu_0 + \gamma_3 + \psi)}\right) & -\left(\mu\omega\nu + \frac{\varepsilon\beta\mu(\psi + \mu_0 + \omega)}{\mu_0(\mu_0 + \gamma_3 + \psi)}\right) \\ \gamma_3 & -(\mu_0 + \psi) & 0 & 0 \\ 0 & 0 & \beta\mu\frac{(\psi + \mu_0 + \omega)}{\mu_0(\mu_0 + \gamma_3 + \psi)} - (\mu_0 + \gamma_1) & \varepsilon\beta\mu\frac{(\psi + \mu_0 + \omega)}{\mu_0(\mu_0 + \gamma_3 + \psi)} \\ 0 & 0 & q\gamma_1 & \mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha) \end{bmatrix}$$

Or simply

$$\begin{bmatrix} -(\mu_0 + \gamma_1) & \psi & -\beta S^0 & -(\mu\omega\nu + \varepsilon\beta S^0) \\ \gamma_3 & -(\mu_0 + \psi) & 0 & 0 \\ 0 & 0 & \beta S^0 - (\mu_0 + \gamma_1) & \varepsilon\beta S^0 \\ 0 & 0 & q\gamma_1 & \mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha) \end{bmatrix}$$

At a particular time when vaccination becomes effective such that the rate of waning back becomes zero i.e $\psi = 0,$ we have

$$J(E^0) = \begin{bmatrix} -(\mu_0 + \gamma_1) & 0 & -\beta S^0 & -(\mu\omega\nu + \varepsilon\beta S^0) \\ \gamma_3 & -\mu_0 & 0 & 0 \\ 0 & 0 & \beta S^0 - (\mu_0 + \gamma_1) & \varepsilon\beta S^0 \\ 0 & 0 & q\gamma_1 & \mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha) \end{bmatrix}$$

By inspection, it's seen from the matrix above that $\lambda_1 = -\mu_0, \lambda_2 = -(\mu_0 + \gamma_1)$ are the eigenvalues and the other two remaining eigenvalues can be obtained from 2×2 matrix thus,

$$\begin{vmatrix} \beta S^0 - \lambda & \varepsilon\beta S^0 \\ q\gamma_1 & [\mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha)] - \lambda \end{vmatrix} = 0$$

$$\lambda^2 + \left[(\mu_0 + \mu_1 + \gamma_2 + \alpha) - \mu\omega\nu - \beta S^0\right]\lambda - \beta S^0\left[(\mu_0 + \mu_1 + \gamma_2 + \alpha) + \varepsilon q\gamma_1 - \mu\omega\nu\right] = 0$$

$$\text{let } a_1 = \left[(\mu_0 + \mu_1 + \gamma_2 + \alpha) - \mu\omega\nu - \beta S^0\right], a_0 = -\beta S^0\left[(\mu_0 + \mu_1 + \gamma_2 + \alpha) + \varepsilon q\gamma_1 - \mu\omega\nu\right]$$

Such that $\lambda^2 + a_1\lambda + a_0 = 0$

Using Routh-Hurwitz criterion, the disease-free equilibrium point E^0 is locally asymptotically stable if

$a_1 > 0$ and $a_1 a_0 > 0.$

this implies that $a_0 > 0$ i.e

$$a_0 = -\beta S^0\left[(\mu_0 + \mu_1 + \gamma_2 + \alpha) + \varepsilon q\gamma_1 - \mu\omega\nu\right] > 0$$
$$\Rightarrow \left[(\mu_0 + \mu_1 + \gamma_2 + \alpha) + \varepsilon q\gamma_1 - \mu\omega\nu\right] < 0$$
$$\Rightarrow \mu_0 + \mu_1 + \gamma_2 + \alpha + \varepsilon q\gamma_1 < \mu\omega\nu$$

Dividing both sides by $\mu\omega\nu$, we obtain

$$\frac{\mu_0 + \mu_1 + \gamma_2 + \alpha + \varepsilon q\gamma}{\mu\omega\nu} < 1$$

Thus, the proof that $R_0 < 1$ implying the disease-free equilibrium point is asymptotically stable.

3.3.2 Global Stability of the Disease-Free equilibrium Point

Using Castillo-Chavez et al approach (2002), system (3.2) can be expressed as;

$$\frac{dX_1}{dt} = F(X_1, X_2)$$

$$\frac{dX_2}{dt} = G(X_1, X_2), G(X_1, 0) = 0$$

Where $X_1 \in \Re^2 = (S^0, V^0)$, the number of non-infected individuals whereas $X_2 \in \Re^2 = (I, C)$, the infected compartments.

The conditions below are for global stability of disease-free equilibrium point:

1. $\frac{dX_1}{dt} = F(X, 0), X^0$ is asymptotically stable
2. $G(X_1, X_2) = AX_2 - G(X_1, X_2), G(X_1, X_2) \geq 0$ for $(X_1, X_2) \in \Omega$

Where A is the M-matrix for its off-diagonal elements are positive in the area Γ in which model equations make epidemiological sense. If the above two conditions are satisfied by our model system, then the theorem stated below is true

Theorem 3: *Provided that* $R_0 < 1$ *and the conditions 1 and 2 are satisfied, the diseases-free equilibrium point* $E^0 = (X^0, 0)$ *of the system (3.2) is globally asymptotically stable.*

Proof

The DFE is now denoted as:

$$E^0(X_1^*, 0)$$

Where $X_1^* = (N^0, 0)$

Now, the first condition that is globally asymptotically stable (GAS) is

$$\frac{dX_1}{dt} = F(X_1, 0) = \begin{pmatrix} \mu\omega(1-\nu C) + \psi V - (\mu_0 + \mu_1 + \gamma_3 + \beta I + \varepsilon\beta C) \\ \mu(1-\omega) - (\mu_0 + \psi)V + \gamma_3 \end{pmatrix}$$

A linear differential equation solving gives

$$S^0(t) = \frac{\mu\omega + \psi V^0}{k_1} - \frac{\mu\omega + \psi V^0}{k_1} e^{-k_1 t} + S^0(0) e^{-k_1 t}$$

and

$$V^0(t) = \frac{\mu(1-\omega) + \gamma_3 S^0}{k_2} - \frac{\mu(1-\omega) + \gamma_3 S^0}{k_2} e^{-k_2 t} + V^0(0) e^{-k_2 t}$$

Clearly, from the above solutions, we have

$S^0(t) + V^0(t) \to N^0(t)$ as t $\to \infty$ regardless of the values of $S^0(t)$ and $V^0(t)$ thus

$X_1^* = (N^0, 0)$, is globally asymptotically stable

Next, we prove that the second condition is true, that is

$$G(X_1, X_2) = AX_2 - G(X_1, X_2) \text{ where } X_2 = (I^0, C^0)$$

$$G(X_1, X_2) = \begin{bmatrix} (\beta I + \varepsilon\beta C)S - (\mu_0 + \gamma_1)I \\ q\gamma_1 I + \mu\omega\nu C - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C \end{bmatrix}$$

$$A = \begin{bmatrix} \beta S^0 - (\mu_0 + \gamma_1) & \varepsilon\beta S^0 \\ q\gamma_1 & \mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha) \end{bmatrix}$$

$$G(X_1, X_2) = \begin{bmatrix} (\beta I^0 + \varepsilon\beta C^0)S^0 - (\mu_0 + \gamma_1)I^0 \\ q\gamma_1 + \mu\omega\nu C^0 - (\mu_0 + \mu_1 + \gamma_2 + \alpha)C^0 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

$$AX_2 = \begin{bmatrix} \beta S^0 - (\mu_0 + \gamma_1) & \varepsilon\beta S^0 \\ q\gamma_1 & \mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha) \end{bmatrix} \begin{bmatrix} I^0 \\ C^0 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

$$G(X_1, X_2) = \begin{bmatrix} \beta S^0 - (\mu_0 + \gamma_1) & \varepsilon\beta S^0 \\ q\gamma_1 & \mu\omega\nu - (\mu_0 + \mu_1 + \gamma_2 + \alpha) \end{bmatrix} \begin{bmatrix} I^0 \\ C^0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

$$G(X_1, X_2) = \begin{bmatrix} 0 \\ 0 \end{bmatrix}^T, G(0,0) = 0$$

Hence the proof is complete and the disease-free equilibrium is asymptotically stable.

3.4 Stability of the endemic Equilibrium

3.4.1 Local Stability of the Endemic Equilibrium

Theorem 4**:** *The Endemic Equilibrium point* $\left(E^*\right)$ *of the system (3.2) is locally asymptotically stable if* $R_0 > 1$

Proof

The Jacobian matrix at the endemic equilibrium is;

$$J\left(E^*\right)=\begin{bmatrix} -\left(\mu_0+\gamma_3+\beta I^*+\varepsilon\beta C^*\right) & \psi & -\beta S^* & -\left(\mu\omega\nu+\varepsilon\beta S^*\right) \\ \gamma_3 & -\left(\mu_0+\psi\right) & 0 & 0 \\ \beta I^*+\varepsilon\beta C^* & 0 & -\left(\mu_0+\gamma_1\right) & \varepsilon\beta S^* \\ 0 & 0 & q\gamma_1 & \mu\omega\nu-\left(\mu_0+\mu_1+\gamma_2+\alpha\right) \end{bmatrix}$$

With effective vaccination, $\psi = 0$

$$\begin{bmatrix} -\left(\mu_0+\gamma_3+\beta I^*+\varepsilon\beta C^*\right) & 0 & \beta S^* & -\left(\mu\omega\nu+\varepsilon\beta C^*\right) \\ \gamma_3 & -\mu_0 & 0 & 0 \\ \beta I^*+\varepsilon\beta C^* & 0 & -\left(\mu_0+\gamma_1\right) & \varepsilon\beta S^* \\ 0 & 0 & q\gamma_1 & \mu\omega\nu-\left(\mu_0+\mu_1+\lambda_2+\alpha\right) \end{bmatrix}$$

By inspection, $\lambda_1 = -\mu_0$ and the rest of eigenvalues can be determined by reducing by reducing $J\left(E^*\right)$ to

$$J_1\left(E^*\right)=\begin{bmatrix} -\left(\mu_0+\gamma_3+\beta I^*+\varepsilon\beta C^*\right) & \beta S^* & -\left(\mu\omega\nu+\varepsilon\beta S^*\right) \\ \beta I^*+\varepsilon\beta C^* & -\left(\mu_0+\gamma_1\right) & \varepsilon\beta S^* \\ 0 & q\gamma_1 & \mu\omega\nu-\left(\mu_0+\mu_1+\gamma_2+\alpha\right) \end{bmatrix}$$

By the use of Routh-Hurwitz criterion regarding the necessary and sufficient conditions as it's well detailed in Enagi et al, the characteristic polynomial has all roots with negative real parts if

$$Tr\left(J_1\left(E^*\right)\right)<0 \text{ and } \mathrm{Det}\left(\mathrm{J}_1\left(E^*\right)\right)>0 \text{ when } R_0>1$$

Now, from our matrix $J_1\left(E^*\right)$ and since all the parameters used are positive,

$$Tr\left(J_1\left(E^*\right)\right)<0 \text{ and } \mathrm{Det}\left(\mathrm{J}_1\left(E^*\right)\right)>0 \text{ iff } \left|\mu\omega\nu\right|<\left|\left(\mu_0+\mu_1+\gamma_2+\alpha\right)\right|$$

Given that $\left|\mu\omega\nu\right|<\left|\left(\mu_0+\mu_1+\gamma_2+\alpha\right)\right|$

$$Tr\left(J_1\left(E^*\right)\right)=-\left(\mu_0+\gamma_3+\beta I^*+\varepsilon\beta C^*+\left(\mu_0+\mu_1+\gamma_2+\alpha\right)-\mu\omega\nu\right)$$

The determinant will be given by;

$$Det\left(J_1(E^*)\right)=-\left\{\beta I^*+\varepsilon\beta C^*\right\}\begin{bmatrix}\left(\mu_0+\gamma_3\right)\left(\mu_0+\gamma_1\right)\left(\mu\omega\nu-\left(\mu_9+\mu_1+\gamma_2+\alpha\right)\right)-\left(\mu_0+\gamma_3\right)\left(\mu\omega\nu+\alpha\beta S^*\right)q\gamma_1 \\ +\beta S^*\left(\mu\omega\nu-\left(\mu_0+\mu_1+\gamma_2+\alpha\right)\right)+q\gamma_1\left(\mu\omega\nu+\varepsilon\beta C^*\right)\end{bmatrix}$$

That is

$$\left|\left(\mu_0+\gamma_3\right)\left(\mu_0+\gamma_1\right)\left(\mu\omega\nu-\left(\mu_0+\mu_1+\gamma_2+\alpha\right)\right)-\left(\mu_0+\gamma_3\right)\left(\mu\omega\nu+\varepsilon\beta S^*\right)q\gamma_1+\beta S^*\left(\mu\omega\nu-\left(\mu_0+\mu_1+\gamma_2+\alpha\right)\right)\right|$$
$$>\left|q\gamma_1\left(\mu\omega\nu+\varepsilon\beta C^*\right)\right|$$

Now, $Tr\left(J_1(E^*)\right)<0, \text{ and } \mathrm{Det}\left(\mathrm{J}_1(E^*)\right)>0 \text{ if } R_0>1,$ meaning all the eigenvalues of $J_1\left(E^*\right)$ have real parts with negative sign if $R_0 > 1.$

Therefore, $J\left(E^*\right)$ is locally asymptotically stable provided $R_0 > 1.$

3.4.2 Global Stability of the Endemic Equilibrium Point

Theorem 5: *The Endemic Equilibrium Point* E^* *of the system (3.2) is globally asymptotically stable if* $R_0 > 1.$

Proof

To give the proof of global stability of E^*, we need to use the approach of LaSalle (1976) to construct the appropriate Lyapunov function as shown.

$$U(S,V,I,C)=\left(S-S^*\ln\frac{S}{S^*}\right)+\left(V-V^*\ln\frac{V}{V^*}\right)+\left(I-I^*\ln\frac{I}{I^*}\right)+\left(C-C^*\ln\frac{C}{C^*}\right)$$

Differentiating U, we obtain;

$$\frac{dU}{dt}=\left(1-\frac{S^*}{S}\right)\frac{dS}{dt}+\left(1-\frac{V^*}{V}\right)\frac{dV}{dt}+\left(1-\frac{I^*}{I}\right)\frac{dI}{dt}+\left(1-\frac{C^*}{C}\right)\frac{dC}{dt}$$

Substituting $\frac{dS}{dt}, \frac{dV}{dt}, \frac{dI}{dt}, \text{and } \frac{dC}{dt}$ from system (3.2), we have;

$$\frac{dU}{dt}=\left(1-\frac{S^*}{S}\right)\left[\mu\omega(1-\nu C)+\psi V-\left(\mu_0+\gamma_3+\beta I+\varepsilon\beta C\right)S\right]+\left(1-\frac{V^*}{V}\right)\left[\mu(1-\omega)-\left(\mu_0+\psi\right)V+\gamma_3 S\right]$$
$$+\left(1-\frac{I^*}{I}\right)\left[\left(\beta I+\varepsilon\beta C\right)S-\left(\mu_0+\gamma_3\right)I\right]+\left(1-\frac{C^*}{C}\right)\left[q\gamma_1 I+\mu\omega\nu C-\left(\mu_0+\mu_1+\gamma_2+\alpha\right)C\right]$$

From system (3.4), we have;

$$\mu\omega=\mu\omega\nu C^*-\psi V^*+\left(\mu_0+\mu_1+\beta I^*+\varepsilon\beta C^*\right)S^*$$

$$\left(\mu+\psi\right)=\frac{\mu(1-\omega)+\gamma_3 S^*}{V^*}$$

$$\left(\mu_0+\gamma_1\right)=\frac{\left(\beta I^*+\varepsilon\beta C^*\right)S^*}{I^*}$$

$$\left(\mu_0+\mu_1+\gamma_2+\alpha\right)=\frac{q\gamma_1 I^*}{C^*} \qquad (3.5)$$

$$\frac{dU}{dt}=\left(1-\frac{S^*}{S}\right)\left[\left(\mu\omega vC^*-\psi V^*+\left(\mu_0+\gamma_1+\beta I^*+\varepsilon\beta C^*\right)S^*\right)\left(\mu\omega vC^*\right)-\psi V^*+\left(\mu_0+\mu_1+\beta I^*+\varepsilon\beta C^*\right)S^*\right]$$
$$+\left(1-\frac{V^*}{V}\right)\left[\left(\mu-\mu\omega\right)-\frac{\left(\left(\mu-\mu\omega\right)+\gamma_3 S^*\right)}{V^*}V+\gamma_3 S^*\right]+\left(1-\frac{I^*}{I}\right)\left[\left(\beta I^*+\varepsilon\beta C^*\right)S^*-\frac{\left(\beta I^*+\varepsilon\beta C^*\right)}{I^*}I^*\right]$$
$$+\left(1-\frac{C^*}{C}\right)\left[q\gamma_1+\frac{q\gamma_1 I^*}{C^*}C\right]\le 0$$

Setting

$S=S^*$, $V=V^*$, $I=I^*$ and $C=C^*$, we obtain $\frac{dU}{dt}=0$

Therefore, $\frac{dU}{dt}=0$ holds. By LaSalle invariant principle, (LaSalle 1976), as $t\to\infty$, every solution to the system (3.2) approaches endemic equilibrium hence the point is globally asymptotically stable.

IV. NUMERICAL SIMULATION GRAPHS

We used MATLAB to simulate system (3.2) and investigate the impact of both vaccination and treatment as a control strategy against infectious HBV on chronic carriers and acutely infected individuals.

The values of the parameters used are as shown below.

Table 4.1: Parameter values used in the numerical simulation

Parameter	Value	Reference
μ	0.0367	USAID (2009)
μ_0	0.0166	USAID (2009)
μ_1	0.1	Assumed
ω	0.1	Assumed
v	0.11	Zou et al (2009)
ψ	0.1	Zou et al (2009)
β	0.95	Edmunds et al (1996a)
q	0.885	Zou et al (2009)
γ_1	4. per annum	Zou et al (2009)
γ_2	0.025	Zou et al (2009)
γ_3	0.9	Assumed
ε	0.16	Edmunds et al (1996a)
α	0.9	Assumed value

Results of simulation presented in graphical forms

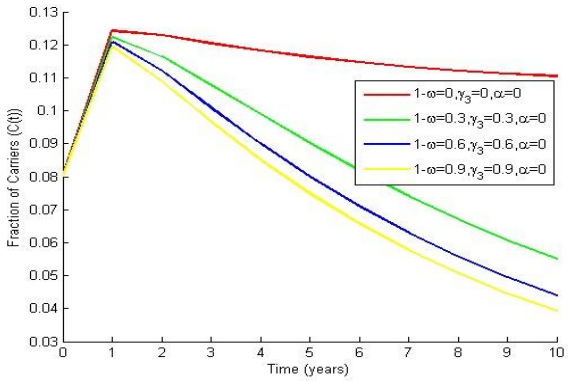

Figure 4.1: Impacts of vaccination on chronic carriers without treatment

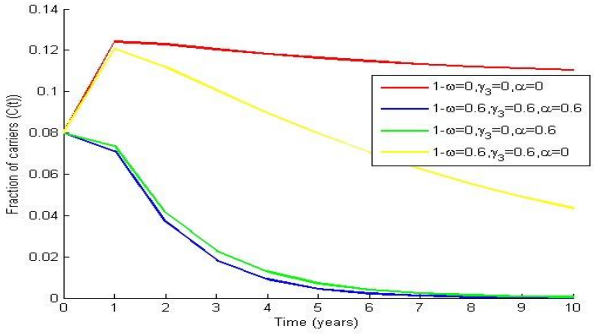

Figure 4.2: Impact of low treatment and vaccination on chronic carriers.

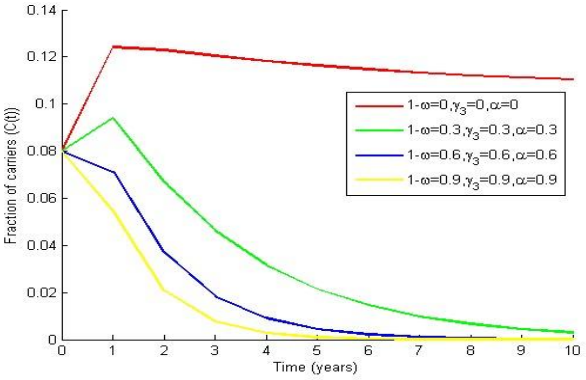

Figure 4.3: Impact of equal rate of vaccination and treatment on chronic carriers

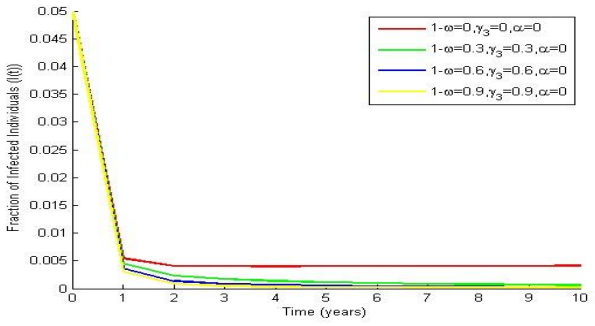

Figure 4.4 Impact of increased treatment on acutely infected individuals

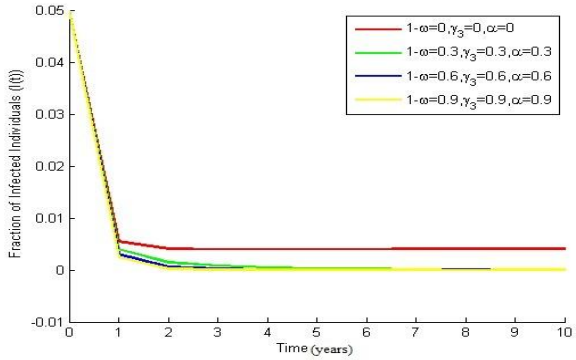

Figure 4.5: Impact of both vaccination and treatment on acutely infected individuals.

V. DISCUSSION

Our study focused on the possibility of eradicating infectious HBV by varying the data values assigned to vaccination and treatment. We take vaccination and treatment as the major control method of Hepatitis B Virus as discussed below.

Figure 1 indicates the existence of infectious Hepatitis B Virus in the carrier population with vaccination intervention but no treatment administered. At the initial point where there is no both vaccination and treatment, $(1-\omega)=0, \gamma_3=0$ and $\alpha=0$, the disease increases to the peak and slightly decreases and then remain almost stable throughout the population. The peak represents the epidemic crisis while the "almost stable state" indicates how the entire population is diseased. However, vaccination at varying rates helps alter the almost stable state of the pandemic and reduces it as shown by green, blue and yellow graphs.

Figure 2 shows that without any intervention strategy, $(1-\omega)=0, \gamma_3=0,$ and $\alpha=0$, the carrier population remains alarmingly high, almost constant. However, when a relatively high vaccination and treatment efforts are made at the same rate, $(1-\omega)=0.6, \gamma_3=0.6,$ and $\alpha=0.6$, the disease prevalence drastically reduces as shown by the blue graph among the carriers. Interestingly, treating carriers tends to be effective than vaccinating them at the same rate as shown by the graphs of $(1-\omega)=0, \gamma_3=0, \alpha=0.6$ compared to that of $(1-\omega)=0.6, \gamma_3=0.6, \alpha=0$

This is because of relapse and resistance of infection to antibodies of the immune system.

Figure 3 shows that when we treat and vaccinate the carriers at the same rate, the disease decreases but eradication is possible when the efforts are increased. This is attested to by the graph of $(1-\omega)=0.9, \gamma_3=0.9,$ and $\alpha=0.9$ in which intervention strategies are very high.

Figure 4 shows infected population proportions in which only vaccination is administered and no treatment. The natural immune system fights the disease up to a relatively stable state. But increasing vaccination helps supplement the immune system in the fight and reduction of the prevalence of disease among acutely infected individuals.

Figure 5 reveals that when we combine administering both treatment and vaccination, the disease is fully eradicated. The graph also indicates that for us to effectively bring full control over the infectious HBV disease, we have to increase the rate of implementing the two strategies.

VI. CONCLUSION

We studied a mathematical model of an infectious Hepatitis B Virus in which both treatment and vaccination are combined in an attempt to eradicate the disease in a completely susceptible population. In our work, we formed the flow chart which represents the disease transmission dynamics. From this flow chart we derived five model equations. The disease-free equilibrium point, the basic reproduction number associated with the system of equations, as well as the endemic equilibrium point and the stability of those two equilibrium points were determined. Using MATLAB, we employed the method of Runge-Kutta of order four to obtain numerical simulation results. According to our analysis, vaccination and treatment can be effective intervention efforts to mitigate the prevalence of infectious HBV. However, combination of both treatment and vaccination eradicates the epidemic, the HBV, hence the two should always be combined and employed as single control strategy.

VII. RECOMMENDATIONS

- The government should periodically carry out mass vaccination of expecting mothers and children.
- Educating the masses about the need to go for regular testing so that chronic carrier cases are detected and treated.
- Educating the nomad communities which are tightly held to unhealthy cultures like FGM and traditional methods of circumcision. This will help in eliminating unnecessary transmission of HBV which is usually contracted as a result of using non-sterilized objects for tattooing and circumcision.
- Further research on impact of waning health conditions on completely susceptible population when the same methods of control are employed

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