Available online at http://scik.org
J. Math. Comput. Sci. 5 (2015), No. 3, 394-411
ISSN: 1927-5307

MATHEMATICAL MODELLING OF HCV INFECTIOLOGY IN A COMMUNITY WITH INFLOW OF INFECTED IMMIGRANTS

NETERINDWA AINEA[1,*], ESTOMIH S. MASSAWE[1], OLUWOLE DANIEL MAKINDE[2] AND LUCY NAMKINGA[3]

[1]Mathematics Department, University of Dar es Salaam, P. O. Box 35062, Dar es Salaam, Tanzania

[2]Faculty of Military Science, Stellenbosch University, Private Bag X2, Saldanha 7395, South Africa

[3]Department of Molecular Biology and Biotechnology,University of Dar es Salaam, P. O. Box 35179, Dar es Salaam, Tanzania

Copyright © 2015 Ainea, Massawe, Makinde and Namkinga. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Abstract. This paper examines the HCV infectiology in a community with inflow of infected immigrants. A nonlinear mathematical model for the problem is proposed and analysed qualitatively using the stability theory of the differential equations. The results show that the disease free equilibrium is locally stable at threshold parameter less than unity and unstable at threshold parameter greater than unity. The disease free produced stable equilibrium for the threshold parameter less than unity ($R_0 < 1$), while the backward bifurcation for endemic equilibrium is unstable and the forward bifurcation for endemic equilibrium at $R_0 > 1$ is stable. A recovered individual loses immunity and become immediately susceptible again. However the disease becomes more endemic due to the presence of infected immigrants in the community. Numerical simulation of the model is implemented to investigate the sensitivity of certain key parameters on the HCV infectiology in a community with inflow of infected immigrants.

Keywords: HCV disease, infected immigrants, stability, sensitivity index, Lyapunov method, basic reproductive number.

2010 AMS Subject Classification: 92B05.

1. Introduction

Mathematical modelling of the spread of infectious diseases continues to provide important insights into diseases behaviour and control. Over the years it has also become an important tool

*Corresponding author

Received February 5, 2015

in understanding the dynamics of diseases and in decision making processes regarding intervention programs for controlling diseases in many countries [13]. An estimated 170 million people worldwide (3% of the world's population) are now thought to be HCV chronic carriers [18]. [10] made an analysis on the immigration status, race and language barriers on chronic hepatitis virus infection management and treatment outcomes. [5] conducted a study on disease progression of acute HCV. [1] found that chronic HCV is a progressive condition that accounts for at least one quarter of all cases of chronic liver diseases. [19] made an analysis on the effects of a HCV educational intervention or a motivational intervention on alcohol use and sexual risk behaviours among injection drug users. [7] discovered that chronic HCV complications are increasing, especially among people older than 60 years. [3] investigated the dynamic behaviour of an SEI (Susceptible- Exposed- Infective) model with acute and chronic stages. However, in all the above studies, none of them incorporated the infectiology and inflow of infected immigrants to the population. In this paper, it is intended to examine the HCV infectiology in a community with inflow of infected immigrants.

2. Model Formulation

The model sub-divides the total human population at time t, denoted by $N(t)$, into sub-populations of susceptible individuals $(S(t))$, exposed individuals (infected but not infectious) $(E(t))$, individuals with acute infection (initially infected) $(A(t))$, chronic infected individuals (infectious individuals) $(C(t))$ and recovered individuals $(R(t))$. Total population at time t is given by

$$N(t)=S(t)+E(t)+A(t)+C(t)+R(t). \tag{1}$$

The interaction between the classes will be assumed as follows: Exposed (E), acute infected (A) and chronic infected (C) immigrants enter into the population with the rates π_1, π_2, π_3, respectively. Susceptible individuals contacts with acute and chronic infected individuals at rates $\beta_i (i=1,2)$ respectively. Infected individuals move to the exposed group at a rate $\frac{(\beta_1 A+\beta_2 C)}{N}$. The exposed individuals develop to acute infected group at a rate θ while acute infective develop to chronic group at a rate k_1 and exposed individuals move to chronic class at the rate k_1. The infectious individuals recovered at a rate ρ, and recovered individual loses immunity

and become immediately susceptible again at a rate σ. Acute and chronic infected individuals undergo death due to the disease at the rate a and d respectively.

It is assumed that the rate of contact of susceptibles with chronic individuals is much less than acute infectives $(\beta_2 \le \beta_1)$ because on chronic stage people become aware of their infection and may choose to use control measures and change their behaviour and thus may contribute little in spreading the infection.

Taking into account the above considerations, we have the following schematic flow diagram:

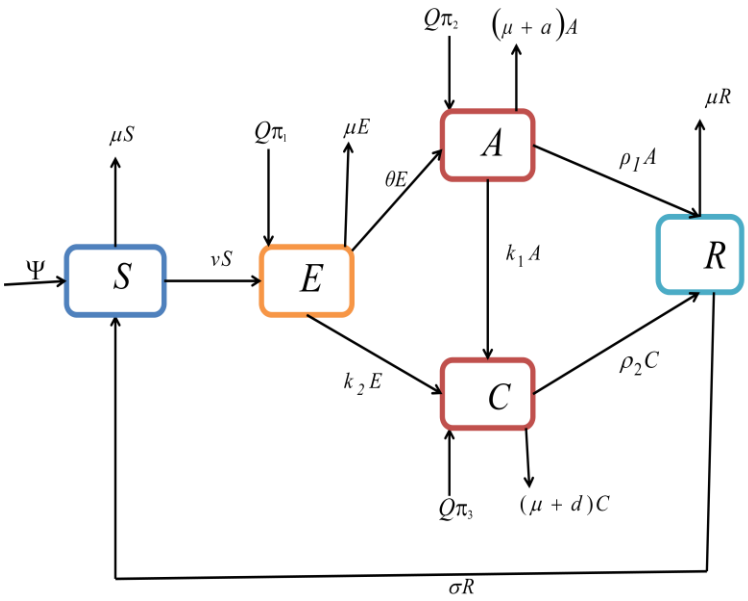

Figure 1. Model Flow Chart

Thus, from the above flow chart and with the force of infection

$$\upsilon = \frac{(\beta_1 A + \beta_2 C)}{N}$$ where $N = S + E + A + C + R$ is the total population size.

The model will be governed by the following system of equations:

$$\frac{dS}{dt} = \Psi - \upsilon S + \sigma R - \mu S$$

$$\frac{dE}{dt} = Q\pi_1 - \upsilon S - (\theta + k_2 + \mu)E$$

$$\frac{dA}{dt} = Q\pi_2 + \theta E - (k_1 + \rho_1 + a + \mu)A \tag{2}$$

$$\frac{dC}{dt} = Q\pi_3 + k_2 E + k_1 A - (\rho_2 + d + \mu)C$$

$$\frac{dR}{dt} = \rho_1 A + \rho_2 C - (\sigma + \mu)R$$

Where

$\Psi = Q(1-\pi_1-\pi_2-\pi_3)$ with initial conditions $S(0)=S_0$, $E(0)=E_0$ $A(0)=A_0$, $C(0)=C_0$, $R(0)=R_0$ and $N(0)=N_0$.

$\beta_i (i=1,2)$ are the effective contact rate of individuals with acute and chronic hepatitis C respectively,

$\pi_i (i=1,2,3)$ are the rates at which exposed , acute and Chronic infected immigrants enter into the population respectively,

Q is the recruitment rate,

θ is the rate of progression to acute infected class from exposed class,

$k_i (i=1,2)$ are the rates at which acute and exposed infective develop chronic respectively,

$\rho_i (i=1,2)$ are the rates at which acute and chronic individuals recovered respectively,

σ is the rate at which infectious humans after recovery become immediately susceptible again.

a is the death rate of acute infected group due to the disease,

d is the death rate of chronic infected group due to the disease,

μ is the natural death rate.

3. Model Analysis

For the HCV transmission model (2) to be epidemiological meaningful, it is important to prove that all solutions with non- negative initial data will remain non-negative for all time. The system in equation (2) will be qualitatively analyzed so as to find the conditions for existence and stability of a disease free equilibrium points.

3.1. Invariant Region

Since the model system of equation (2) is HCV model dealing with human population, it is assumed that all state variables and parameters of the model are positive at $t \geq 0$. The model will be analysed in suitable feasible region where all state variables are positive.

Theorem 1: *The solutions of the system (2) are feasible for all* $t > 0$ *if they enter the invariant region* Ω.

Proof :

Let $\Omega = (S,E,A,C,R) \in R^5_+$ be solution of the system (2) with non-negative initial conditions. From equation (2), in the absence of the disease $d = 0$, $a = 0$, system (2) becomes,

$$\dot{N} \leq Q - \mu N$$

$$\Rightarrow \dot{N} + \mu N \leq Q .$$

The integrating factor is (IF) = $e^{\int \mu dt} = e^{\mu t}$.

Then

$$e^{\mu t} N + \mu N e^{\mu t} \leq Q e^{\mu t}$$

$$\Rightarrow \frac{d}{dt}\left(N e^{\mu t} \right) \leq Q e^{\mu t}$$

Integrating on both sides gives

$$N e^{\mu t} \leq \frac{Q}{\mu} e^{\mu t} + c .$$

where c is a constant of integration. Therefore

$$N \leq \frac{Q}{\mu} + c e^{-\mu t} .$$

Using the initial conditions that when $t = 0, N(0) = N_0$, then

$$N_0 - \frac{Q}{\mu} \leq c$$

$$N \leq \frac{Q}{\mu} + \left(N_0 - \frac{Q}{\mu} \right) e^{-\mu t} . \qquad (3)$$

As $t \to \infty$ in (3), the population size, $N \to \frac{Q}{\mu}$, which implies that $0 \le N \le \frac{Q}{\mu}$. Thus, the feasible solutions set if (1) enter and remain in the region

$$\left\{ \Omega = (S,\, E,\, A,\, C,\, R) \in R^5{}_+ \,\middle|\, S > 0,\, E \ge 0,\, A \ge 0,\, C \ge 0,\, R \ge 0,\, N \le \frac{Q}{\mu} \right\}$$

In this case, whenever $N > \frac{Q}{\mu}$, then $\dot{N} < 0$ which means the population decreases asymptotically to the carrying capacity and whenever $N \le \frac{Q}{\mu}$, every solution with initial condition in Ω remains in that region for $t > 0$, so the model is well posed in Ω. Thus, the region is positively invariant (i.e. solutions remain positive for all times, t). Therefore, the basic model is well posed epidemiologically and mathematically. Hence, it is sufficient to study the dynamics of the basic model in Ω.

3.2. Positivity of solutions

Lemma1: *Let the initial data be* $\{S(0),\, E(0),\, A(0),\, C(0),\, R(0) \ge 0\} \in R^5{}_+$

Then, the solution set $\{S(t),\, E(t),\, A(t),\, C(t),\, R(t)\}$ *of the system* (2) *is positive for all* $t > 0$

Proof :

Using the first equation of the model system (2),

$$\frac{dS}{dt} = Q(1 - \pi_1 - \pi_2 - \pi_3) - \nu S + \sigma R - \mu S$$

$$\frac{dS}{dt} + (\upsilon + \mu) S = Q(1 - \pi_1 - \pi_2 - \pi_3) + \sigma R$$

The Integration factor is $B(t) = e^{\int_0^t (\upsilon(s) + \mu)\, ds}$, multiplying both sides by the integration factor and integrating leads to

$$\frac{d}{dt}\left(SB(t)\right) = B(t)\left[Q(1 - \pi_1 - \pi_2 - \pi_3) + \sigma R\right]$$

$$\Rightarrow B(t) = e^{-\int_0^t (\upsilon(s) + \mu) ds} \left[\int_0^t \left(Q(1 - \pi_1 - \pi_2 - \pi_3) + \sigma R \right) B(s)\, ds + C \right] \ge 0 \qquad (4)$$

Equations for $E(t), A(t), C(t)$ and $R(t)$ can be similarly be obtained. Thus $S(t), E(t), A(t), C(t)$ and $R(t)$ are positive $\forall t \geq 0$

3.3. The Disease Free Equilibrium Point (DFE)

In absence of the disease, this implies that $(\pi_1 = \pi_2 = \pi_3 = 0, E = 0,\ A = 0,\ C = 0,\ R = 0)$. Therefore the above system reduces to

$$Q - \mu S = 0$$

Solving, we get

$$S_0 = \frac{Q}{\mu}$$

Hence,

$$\Delta_0 = (S_0, E_0, A_0, C_0, R_0) = \left(\frac{Q}{\mu}, 0, 0, 0, 0\right) \tag{5}$$

This represents the state in which there is no infection and is known as the disease-free equilibrium point.

3.4. Local Stability of Disease Free Equilibrium (DFE)

The basic reproduction number, R_0 is calculated by using the next generation operator approach [17]. It is given by

$$R_0 = \frac{\beta_1 \theta}{(\theta + k_2 + \mu_E)(k_1 + \rho_1 + a + \mu_A)} + \frac{\beta_2(\theta k_1 + k_1 k_2 + k_2 \rho_1 + k_2 a + k_2 \mu_A)}{(\theta + k_2 + \mu_E)(k_1 + \rho_1 + a + \mu_A)(\rho_2 + d + \mu_C)} \tag{6}$$

Local stability of disease free equilibrium Δ_0, can be determined by the variational matrix $\mathbf{M}_0$ of the model system (2) corresponding to Δ_0. The Jacobian matrix is computed by differentiating each equation in the system (2) with respect to the state variables S, E, A, C and R. The system is re-defined as;

$$H = Q(1 - \pi_1 - \pi_2 - \pi_3) - vS + \sigma R - \mu S$$

$$G = Q\pi_1 + vS - (\theta + k_2 + \mu)E$$

$$K = Q\pi_2 + \theta E - (k_1 + \rho_1 + a + \mu)A$$

$$Y = Q\pi_3 + k_2 E + k_1 A - (\rho_2 + d + \mu)C$$

$$P = \rho_1 A + \rho_2 C - (\sigma + \mu)R$$

It follows that

$$\mathbf{M}_0 = \begin{pmatrix} \frac{\partial H(\epsilon_0)}{\partial S} & \frac{\partial H(\epsilon_0)}{\partial E} & \frac{\partial H(\epsilon_0)}{\partial A} & \frac{\partial H(\epsilon_0)}{\partial C} & \frac{\partial H(\epsilon_0)}{\partial R} \\ \frac{\partial G(\epsilon_0)}{\partial S} & \frac{\partial G(\epsilon_0)}{\partial E} & \frac{\partial G(\epsilon_0)}{\partial A} & \frac{\partial G(\epsilon_0)}{\partial C} & \frac{\partial G(\epsilon_0)}{\partial R} \\ \frac{\partial K(\epsilon_0)}{\partial S} & \frac{\partial K(\epsilon_0)}{\partial E} & \frac{\partial K(\epsilon_0)}{\partial A} & \frac{\partial K(\epsilon_0)}{\partial C} & \frac{\partial K(\epsilon_0)}{\partial R} \\ \frac{\partial Y(\epsilon_0)}{\partial S} & \frac{\partial Y(\epsilon_0)}{\partial E} & \frac{\partial Y(\epsilon_0)}{\partial A} & \frac{\partial Y(\epsilon_0)}{\partial C} & \frac{\partial Y(\epsilon_0)}{\partial R} \\ \frac{\partial P(\epsilon_0)}{\partial S} & \frac{\partial P(\epsilon_0)}{\partial E} & \frac{\partial P(\epsilon_0)}{\partial A} & \frac{\partial P(\epsilon_0)}{\partial C} & \frac{\partial P(\epsilon_0)}{\partial R} \end{pmatrix} \tag{7}$$

Hence the variational matrix of the model system (2) at steady states is given by

$$\mathbf{M}_0 = \begin{bmatrix} -\mu & 0 & -\beta_1 & -\beta_2 & 0 \\ 0 & -(\theta+k_2+\mu) & \beta_1 & \beta_2 & 0 \\ 0 & \theta & -(k_1+\rho_1+a+\mu) & 0 & 0 \\ 0 & k_2 & k_1 & -(\rho_2+d+\mu) & 0 \\ 0 & 0 & (\rho_1+a) & \rho_2 & -(\delta+\mu) \end{bmatrix} \tag{8}$$

The local stability analysis of the matrix (8) of the system (2) can be done by the trace/determinant method. Where by matrix $(\mathbf{M_0})$ is locally asymptotically stable if and only if the trace of matrix $(\mathbf{M_0})$ is strictly negative and its determinant is strictly positive. Whose trace and determinant are given by

$$\text{Trace}(\mathbf{M_0}) = -\mu - (\theta + k_2 + \mu) - (k_1 + \rho_1 + a + \mu) - (\rho_2 + d + \mu) - (\delta + \mu) < 0 \tag{9}$$

and

$$\det(\mathbf{M_0}) = r_1 r_2 r_3 r_4 - \theta\beta_1 r_3 r_4 - \theta k_1 \beta_2 r_4 - k_2 r_2 \beta_2 r_4 \tag{10}$$

where $r_1 = \theta + k_2 + \mu$, $r_2 = k_1 + \rho_1 + a + \mu$, $r_3 = \rho_2 + d + \mu$, $r_4 = \sigma + \mu$.

Hence $\det(\mathbf{M_0}) > 0$ if $\theta\beta_1 r_3 r_4 + \theta k_1 \beta_2 r_4 + k_2 r_2 \beta_2 r_4 < r_1 r_2 r_3 r_4$

That is equivalent to

$$\frac{(\theta\beta_1 r_3 r_4 + \theta k_1 \beta_2 r_4 + k_2 r_2 \beta_2 r_4)}{r_1 r_2 r_3 r_4} < 1$$

since $\frac{(\theta\beta_1 r_3 r_4 + \theta k_1 \beta_2 r_4 + k_2 r_2 \beta_2 r_4)}{r_1 r_2 r_3 r_4} = R_0$

Thus, $\mathbf{M_0}$ is locally asymptotically stable if and only if $R_0 < 1$. These results are summarized with the following theorem.

Theorem 2: *The disease free equilibrium of the model system (2) is locally asymptotically stable if* $R_0 < 1$ *and unstable If* $R_0 > 1$.

3.5. Existence of Endemic Equilibrium Point Δ^*

The endemic equilibrium of the model system (2) is given by $\Delta^*\left(S^*, E^*, A^*, C^*, R^*\right)$

It is obtained by setting the right hand side of each equation of the model system (2) equal to zero which exists for $\Re_0 < 1$. S^*, E^*, A^*, C^*, and R^* satisfy the following relations:

$$\begin{aligned} S^* &= \frac{r_8 + (r_9 + r_{10}R_0)A^*}{(r_{11} + r_{12}R_0)A^* + r_{13}} \\ E^* &= \frac{(k_1 + \rho_1 + a + \mu)A^* - Q\pi_2}{\theta} \\ C^* &= (R_0 r_1 - r_2)A^* + r_3 \\ R^* &= r_4 + R_0 r_5 - r_6)A^* + r_7 \end{aligned} \tag{11}$$

where,

$$r_1 = \frac{(\theta + k_2 + \mu)(k_1 + \rho_1 + a + \mu)}{\beta_2 \theta}, \quad r_2 = \frac{\beta_1}{\beta_2}, \quad r_3 = \frac{\theta Q\pi_3 - k_2 Q\pi_3}{(\rho_2 + d + \mu)\theta}, \quad r_4 = \frac{\rho_1}{\sigma + \mu},$$

$$r_5 = \frac{\rho_2 r_1}{\sigma + \mu}, \quad r_6 = \frac{\rho_2 r_2}{\sigma + \mu}, \quad r_7 = \frac{r_3}{\sigma + \mu}, \quad r_8 = N(Q - Q\pi_1 - Q\pi_2 - Q\pi_3 + \delta r_7),$$

$$r_9 = \delta r_4 N - \delta r_6 N, \; r_{10} = \delta r_5 N, \; r_{11} = \beta_1 - \beta_2 r_2, \; r_{12} = \beta_2 r_1, \quad r_{13} = \beta_2 r_3 + \mu N$$

$$r_{14} = (\theta + k_2 + \mu)(k_1 + \rho_1 + a + \mu)N, \; r_{15} = Q\pi_2(\theta + k_2 + \mu), \; r_{16} = Q\pi_2(\theta + k_2 + \mu)r_{13}N,$$

$$r_{17} = r_{14} r_{13}$$

and A^* is the solution of the quadratic polynomial

$$f\left(A^*\right) = G\left(A^*\right)^2 + H\left(A^*\right) + K = 0 \tag{12}$$

where

$$G = -(r_{14}r_{11} + r_{12}r_{14}R_0) + \theta\left[\beta_1(r_9 + R_0 r_{10}) + (R_0\beta_2 r_1 - \beta_2 r_2)(r_9 + R_0 r_{10})\right]$$

$$H = r_{11}r_{15}N + r_{12}r_{15}NR_0 - r_{17} + Q\pi_1\theta N(r_{11} + r_{12}R_0) + \left[\beta_1 r_8 + r_8(R_0\beta_2 r_1 - \beta_2 r_2) + \beta_2 r_3(r_9 + R_0 r_{10})\right]\theta$$

$$K = \beta_2 r_3 r_8 \theta + Q\pi_1 N r_{13} + r_{16}$$

Thus, the following results from the quadratic equation (12).

Theorem 3*:*

(a) If $H > 0$, *then the model* (2) *has forward bifurcation at* $R_0 = 1$.

(b) If $H < 0$, *then the model* (2) *undergoes backward bifurcation at* $R_0 = 1$.

Since the model parameters are non-negative, it is clear that $G > 0$. However it is important to note that H is positive only if $R_0 > 1$ and

$$r_{11} r_{15} N + r_{12} r_{15} N R_0 + \beta_2 r_3 (r_9 + R_0 r_{10}) + Q\pi_1 \theta N (r_{11} + r_{12} R_0) \theta + [\beta_1 r_8 + r_8 (R_0 \beta_2 r_1)] \theta > r_8 \beta_2 r_2 \theta + r_{17}$$

and K is positive only if $\beta_2 r_3 r_8 \theta + Q\pi_1 N r_{13} + r_{16} > 0$.

3.6. Local Stability of the Endemic Equilibrium Point Δ^*

The local asymptotic stability of endemic equilibrium point will be analysed by using the Centre Manifold Theory according to [4]. The existence and stability of endemic equilibrium is determined through the investigation of the possibility of existence of the backward or forward bifurcation. This is demonstrated graphically in Fig. 2 (the figure shows a backward bifurcation).

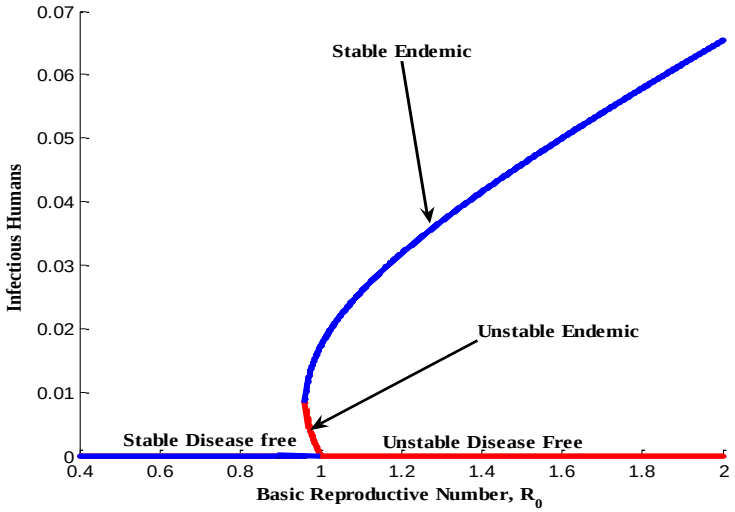

Figure 2: The Backward Bifurcation.

The DFE produced stable equilibrium for the $R_0 < 1$, while the backward bifurcation for Endemic Equilibrium (EE) is unstable and the forward bifurcation for EE at $R_0 > 1$ is stable. The implication of the occurrence of backward bifurcation in the model (2) is that for the disease to be eradicated, it is no longer enough that the basic reproductive number R_0 is less than one. In fact, to achieve eradication, additional efforts and costs are required to bring R_0 bellow a critical value $R_0 < 1$**.**

3.7. Global Stability of the Endemic Equilibrium Point Δ^*

The global stability of the endemic equilibrium Δ^* is analysed using the following constructed Lyapunov function by [3]

Theorem 4: *If* $R_0 > 1$, *the endemic equilibrium* Δ^* *of the model* (2) *is globally asymptotically stable.*

Proof: To establish the global stability of the endemic equilibrium Δ^*, we construct the following Lyapunov function:

$$V\left(S^*,E^*,A^*,C^*,R^*\right)=\left(S-S^*-S^*log\frac{s^*}{s}\right)+\left(E-E^*-E^*log\frac{E^*}{E}\right)$$

$$+\left(A-A^*-A^*log\frac{A^*}{A}\right)+\left(C-C^*-C^*log\frac{C^*}{C}\right)+\left(R-R^*-R^*log\frac{R^*}{R}\right)$$

By direct calculating the derivative of V along the solution of (2) we have;

$$\frac{dV}{dt}=\left(\frac{S-S^*}{S}\right)\frac{dS}{dt}+\left(\frac{E-E^*}{E}\right)\frac{dE}{dt}+\left(\frac{A-A^*}{A}\right)\frac{dA}{dt}+\left(\frac{C-C^*}{C}\right)\frac{dC}{dt}+\left(\frac{R-R^*}{R}\right)\frac{dR}{dt}$$

which gives

$$\frac{dV}{dt}=P\text{-}Q \tag{13}$$

where,

$$P=\left(\frac{\left(S-S^*\right)^2}{S}\right)\left[\left(\frac{(\beta_1 A+\beta_2 C)}{N}\right)-\mu\right]+\sigma R+\frac{S^*}{S}\delta R^*+\left(\frac{(\beta_1 A+\beta_2 C)}{N}\right)S$$

$$+\left(\frac{(\beta_1 A^*+\beta_2 C^*)}{N}\right)S^*+\theta E+\frac{A^*}{A}\theta E^*+k_2E+k_1A+\frac{C^*}{C}k_2E^*+\frac{C^*}{C}k_1A^*+\rho_1A+\rho_{\,2}C$$

$$+\frac{R^*}{R}\left(\rho_{\,1}+a\right)A^*+\frac{R^*}{R}\rho_{\,2}C^*+\mathrm{Q}\left(1-\pi_1-\pi_2-\pi_3\right)+\pi_1Q+\pi_2Q+\pi_3Q$$

$$\mathrm{Q}=\text{-}\delta R^*-\frac{S^*}{S}\delta R-\left(\frac{\left(E-E^*\right)^2}{E}\right)\left[\theta+k_2+\mu\right]\text{-}\left(\frac{(\beta_1 A+\beta_2 C)}{N}\right)S^*-\frac{\mathrm{S}^*}{\mathrm{S}}\mathrm{Q}\left(1-\pi_1-\pi_2-\pi_3\right)$$

$$-\left(\frac{(\beta_1 A^* + \beta_2 C^*)}{N}\right)S - \left(\frac{\left(A - A^*\right)^2}{A}\right)[k_1 + \rho_1 + a + \mu] - \theta E^* - \frac{A^*}{A}\theta E - \frac{A^*}{A}\pi_2 Q - \frac{E^*}{E}\pi_1 Q$$

$$-\frac{C^*}{C}\pi_3 Q - \left(\frac{\left(C - C^*\right)^2}{C}\right)[\rho_2 + d + \mu] - k_2 E - k_1 A^* - \frac{C^*}{C}k_2 E - \frac{C^*}{C}k_1 A$$

$$-\left(\frac{\left(R - R^*\right)^2}{R}\right)[\delta + \mu] - \rho_1 A^* - \rho_2 C^* - \frac{R^*}{R}\rho_1 A - \frac{R^*}{R}\rho_2 C$$

Thus if $P < Q$ then $\frac{dV}{dt} \le 0$; Noting that $\frac{dV}{dt} = 0$ if and only if $S = S^*$; $E = E^*$; $A = A^*$; $C = C^*$; $R = R^*$

Therefore, the largest compact invariant set in $\left\{\left(S^*, E^*, A^*, C^*, R^*\right) \in \Omega : \frac{dV}{dt} = 0\right\}$ is the singleton $\left\{\Delta^*\right\}$ where Δ^* is the endemic equilibrium of the system (2). By LaSalle's invariant principle, it implies that Δ^* is globally asymptotically stable in Ω if $P < Q$.

4. Numerical Sensitivity Analysis

In determining how best to reduce human mortality and morbidity due to HCV, we calculate the sensitivity indices of the basic reproduction number, R_0 to the parameters in the model using approach of [6]. Sensitivity analysis determines parameters that have a high impact on R_0 and should be targeted by intervention strategies. Sensitivity indices allow us to measure the relative change in a state variable when a parameter changes [6]. The normalized forward sensitivity index of a variable to a parameter is a ratio of the relative change in the variable to the relative change in the parameter. When a variable is a differentiable function of the parameter, the sensitivity index may be alternatively defined using partial derivatives.

Table 1: Numerical values of sensitivity indices of R_0

Parameter Symbol	Sensitivity Index
a	-0.2515
β_2	0.6658
ρ_2	-0.5202
β_1	0.3341
ρ_1	-0.1006
d	-0.1040
k_2	0.0521
θ	-0.0304
k_1	0.0281
μ	-0.07341

Definition 1: The normalised forward sensitivity index of a variable ' p ' that depends differentiable on a parameter ' q ' is defined as:

$$X_q^p = \frac{\partial p}{\partial q} \times \frac{q}{p} \tag{14}$$

Having an explicit formula for R_0 in equation (14), we derive an analytical expression for the sensitivity of R_0 as $X_q^{R_0} = \frac{\partial R_0}{\partial q} \times \frac{q}{R_0}$ to each of parameters involved in R_0. For example the sensitivity indices of R_0 with respect to β_1 and θ are given by

$X_{\beta_1}^{R_0} = \frac{\partial R_0}{\partial \beta_1} \times \frac{\beta_1}{R_0}$ =0.3543534857 and $X_{\theta}^{R_0} = \frac{\partial R_0}{\partial \theta} \times \frac{\theta}{R_0}$ = -0.0264093485. Other indices

$X_{\beta_2}^{R_0}$, $X_{u_1}^{R_0}$, $X_a^{R_0}$, $X_{\rho_2}^{R_0}$, $X_{\rho_1}^{R_0}$, $X_d^{R_0}$, $X_{\mu_A}^{R_0}$, $X_{\mu_E}^{R_0}$, $X_{\mu_c}^{R_0}$, $X_{k_1}^{R_0}$ and $X_{k_2}^{R_0}$,

were obtained following the same method and tabulated as follows:

From Table (1), it shows that when the parameters β_2, β_1, k_2 and k_1 are increased keeping other parameters constant they increase the value of R_0 implying that they increase the endemicity of the disease as they have positive indices. While the parameters a, ρ_2, ρ_1 d, θ

and μ decrease the value of R_0 when they are increased while keeping the other parameters constant, implying that they decrease the endemicity of the disease as they have negative indices. The specific interpretation of each parameter shows that, the most sensitive parameter is the effective contact rate of individuals with chronic disease β_2, followed by recovered rate of chronic individuals due to treatment ρ_2, effective contact rate of individuals with acute β_1, followed by recovery rate naturally from acute a, death rate of chronic infected d, recovered rate of acute individuals due to treatment ρ_1, natural mortality rate μ, rate at which exposed develop chronic k_2, the rate at which acute infective are detected by a screening method from exposed group θ, the rate at which screened develop to chronic k_1, which is the least sensitive parameter.

5. Numerical Simulations

In order to verify the theoretical predictions of the model, the numerical simulations of the model (2) are carried out using the following set of estimated parameter values: $\beta_1 = 0.8$, $\beta_2 = 0.3$, $\theta = 0.5$, $k_1 = 0.5$, $k_2 = 0.34$, $\rho_1 = 0.3$, $\rho_2 = 0.1$, $\rho_3 = 0.05$, $\sigma = 0.13\text{-}0.5$, $a = 0.034$, $d = 0.5$.

Figures. 3-4 show the proportion of exposed population, HCV infective populations (acute and chronic infectives) and recovered group, plotted against the proportion of susceptible population. This shows the dynamic behaviour of the endemic equilibrium of the model (2) using the above parameter values.

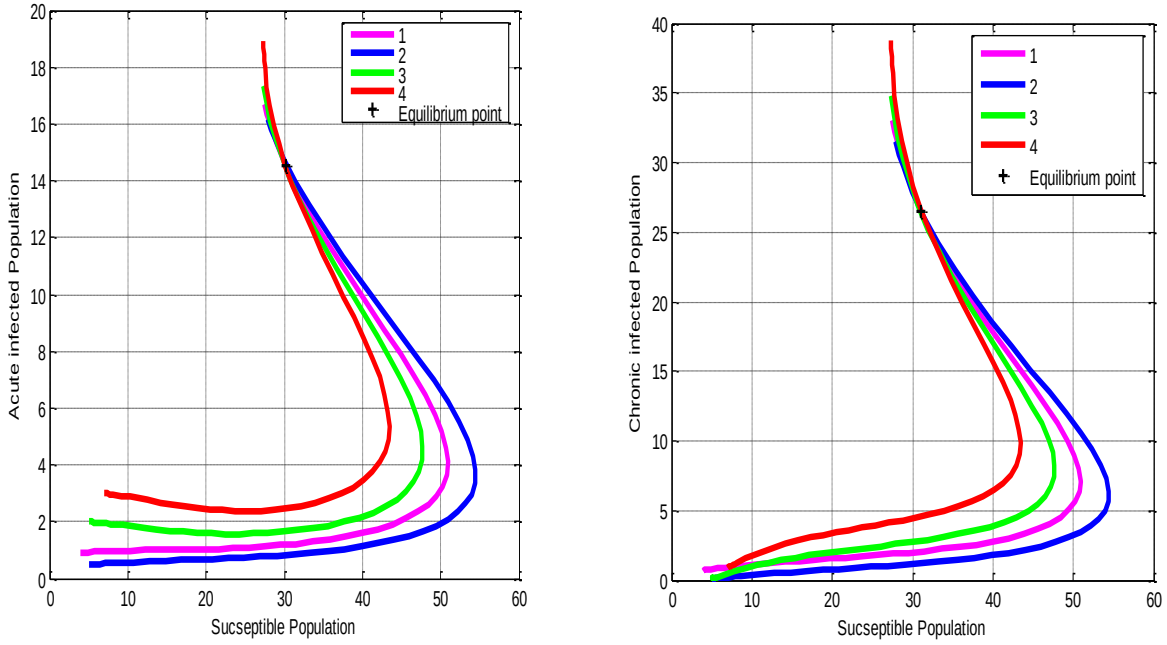

Fig. 3: Phase portrait of the dynamics of susceptibles and the infected population.

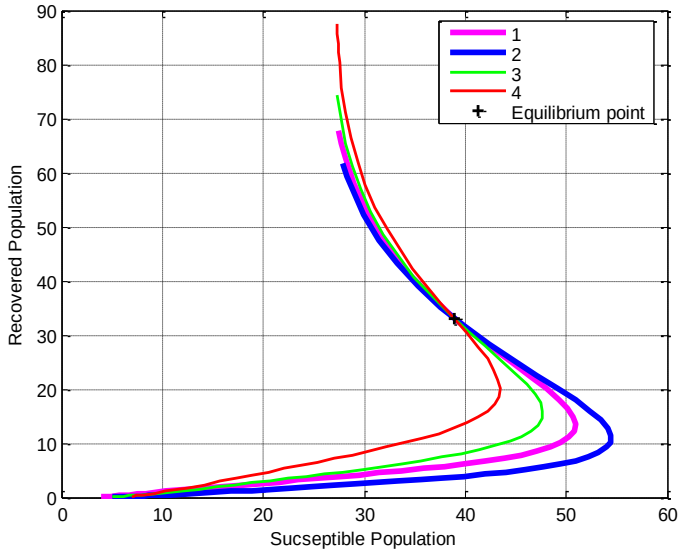

Fig. 4: Phase portrait of the dynamics of susceptibles and recovered population.

The phase portrait in **Figures. 3 and 4** show that for any initial starting point or initial value, the solution curves tend to the endemic equilibrium point Δ^*. Hence, we infer that the system (2) is globally stable about the endemic equilibrium point Δ^* for the set of parameters above**.**

Figures 5 and 6 show the variation of exposed and infected population for different values of infected immigrants

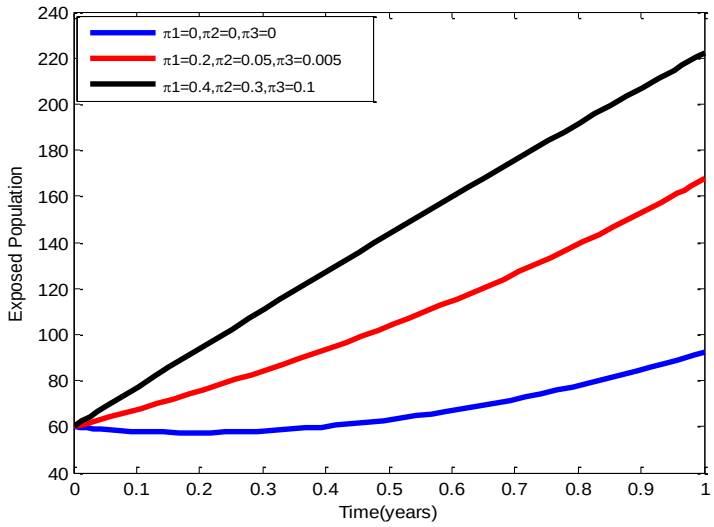

Fig.5: Variation of exposed population for different values of infected immigrants

(a) **(b)**

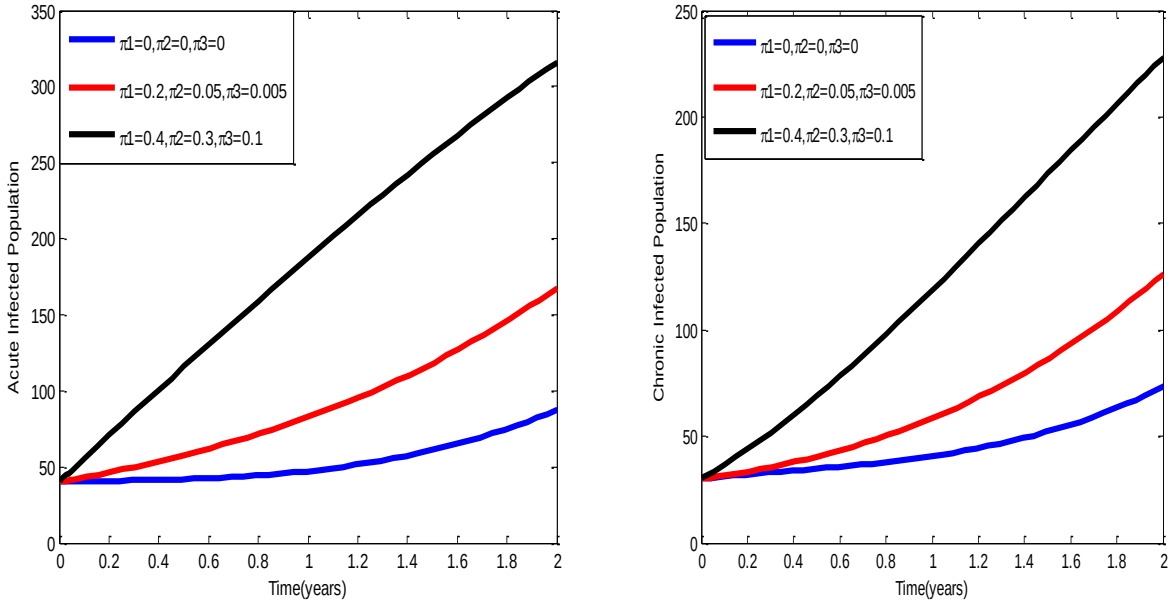

Fig. 6: Variation of infected population for different values of infected immigrants

Figures 5 and 6 show the variation of exposed individuals, acute and chronic infected populations respectively. It is observed that as the infected immigrant increases in the community, the exposed population increases with time (see Fig. 5). The exposed individuals shifted to acute class at the rate θ which results to the increase of the number of acute infective. Then, the exposed and acute infected individuals shifted to chronic population at the rate k_2 and k_1, respectively, leading to the increase of the number of chronic infected population (see Fig. 6).

6. Discussions and Conclusions

In this paper, a mathematical model of HCV showing the HCV infectiology in a community with inflow of infected immigrants has been established and analysed. Both qualitative and numerical analysis of the model was performed. The model incorporates the assumption that infected immigrants enter in the community. It was shown that there exists a feasible region where the model is well posed in which a unique disease free equilibrium point exists. The disease free and endemic equilibrium points were obtained and their stabilities investigated. Sensitivity analysis and numerical study of the model has been performed to see the effect of certain key parameters on the spread of the disease. It was observed that the disease become more endemic due to the presence of infected immigrants in the community. As the infected immigrants increase, the exposed, acute and chronic infective individuals also increase in the population. The national health cares to HCV should therefore seek to ensure that all people at risk or that have been at risk in the past, have access to and are supported in the use of HCV education, health care and prevention services, regardless of their social and economic status.

Conflict of Interests

The authors declare that there is no conflict of interests.

REFERENCES

[1] Mehta, R. Pawson, S. Rajan, G. Hazlehurst, G. Dusheiko, R. Miller, Hewitt, Hepatitis C lookback programme: a single hospital experience. Transfusion Medicine, 9(1999):189-93.

[2] A.L. Bowring, N. Luhmann, S. Pont, C. Debaulieu, S. Derozier, T. Asouab, A. Toufik, C. Gemert, P. Dietze and M. Stoove , An urgent need to scale-up injecting drug harmreduction services in Tanzania: Prevalence of

blood-borne viruses among drug users in Temeke District, Dar-es-Salaam, International Journal of Drug Policy, 1(2012): 326-31.

[3] L. Cai and X. Li, A note on global stability of an SEI epidemic model with acute and chronic stages, Applied Mathematics and Computation, 196 (2007) :923-930.

[4] Chavez-Castillo and B. Song, Dynamical Models of Tuberculosis and their Applications, Mathematical Biosciences and Engineering, 2 (2004) **:**361-404 .

[5] C.D. Mazoff, Disease Progression: Acute Hepatitis C, Alan Franciscus, 2008

[6] N. Chitnis, J.M. Hyman and J.M. Cushing, Determining Important Parameters in the Spread of Malaria Through the Sensitivity Analysis of a Mathematical Model, Bulletin of Mathematical Biology, 70 (2008): 1272-1296.

[7] G.L. Davis, M.J. Alter, H. El-Serag, Aging of the Hepatitis C Virus-Infected Persons in the United States: A Multiple Cohort Model of HCV Prevalence and Disease Progression. Gastroenterology, 2 (2010) :513-521.

[8] Diekmann, J.A.P. Heesterbeek. and J.A.P. Metz, On the definition and computation of the basic reproduction ratio $\mathfrak{R}_0$ in the model of infectious disease in heterogeneous populations, Journal. Math, (1990): 265-382.

[9] L.R. Fischer, D.H. Tope, S. Kathleen , R. Conboy, B.D. Hedblom, E. Ronberg, D.K. Shewmake and J.C. Butter, Screening for Hepatitis C virus in a Health Maintenance Organisation, Arch Intern Med, 11 (2000):1665-1673.

[10] Giordano, B. Hutton and C. Cooper, Influence of Immigration status on chronic hepatitis c virus infection management, Ottawa Health Research Institute Methods Centre, (2008): 236.

[11] K. Johns, *Hepatitis C*: Symptoms and treatment, Helium, USA, 2008.

[12] Kenny, Increased liver-related mortality to hepatitis C viremia defined on the20th anniversary of its identification, Health Service Executive, Dublin, Ireland, 2009.

[13] Makinde and K.O. Okosun, Impact of Chemo-therapy on Optimal Control of Malaria Disease with Infected Immigrants, BioSystems, 104(2011) **:**32-41.

[14] Mehta , R. Pawson, S. Rajan, G. Hazlehurst, G. Dusheiko, R. Miller and P. HewittHepatitis C look back programme: a single hospital experience. Transfusion Medicine 3 (1999)**:**189 – 193.

[15] B.D. Smith, R.L. Morgan, G.A. Beckett, Y. Falck-Ytter, D. Holtzman, C. Teo, A. Jewett , D.B. Rein, N. Patel, M. Alter, A. Yartel and J. WardRecommendations for the Identification of Chronic hepatitis C Virus Infection Among Persons Born During,MMWR Recommend, 61 (1945-1965)**:** 1-32.

[16] J.B. Wong, Silent killer, American Journal of Public Health, 90 **(**2000).

[17] P. Van den Driessche, and J. Watmough, Reproduction numbers and Sub- threshold endemic equilibria for compartmental models of disease transmission, Mathematical Bio-sciences, 180 (2002)**:** 29-48.

[18] World Health Organization, Hepatitis C – global prevalence (update), Wkly Epidemiol, 2007.

[19] W.A. Zule, E.C. Costenbader, C.M. Coomes and W,M. Wechsberg, Effects of a hepatitisCvirus educational intervention or a motivational intervention on alcohol use,injection drug use, and sexual risk behaviours among injection drug users. National centre for Biotechnology Information, U. S. National Library of Medicine, Bethesda MD, USA, 2009.