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The dynamical behavior of a SEI model with Acute and Chronic Stages and nonlinear incidence rate

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Abstract

According to consequent system of a SEI model, a model with vital dynamical and nonlinear incidence rate of saturated mass action is proposed. By making use of differential equation and characteristic of hepatitis C, we analyze the equilibria of the model with nonlinear incidence rate. When the basic reproduction number $R_0 < 1$, the disease free equilibrium is stable and there are no endemic or two endemic . And we obtain the condition of a unique endemic equilibrium of the system.

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1 Introduction

In this paper, the stability of the equilibrium of a chronic stage on the disease transmission and behavior in an exponentially growing or decaying

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population is the focus of this paper. The framework is brought into the case of hepatitis C, a disease typically characterized by a long chronic stage. As is well known to us, Hepatitis C, formerly referred to as 'non-A, non-B' hepatitis, is an important infection of the liver which was first considered as a separate disease in 1975. In practice, the vast majority of patients with acute hepatitis C develop a chronic infection which is characterized by detection of HCV RNA for a period of at least six months after a newly acquired infection. The most common symptoms of acute hepatitis C are fatigue and jaundice. However, the majority of cases, including those with chronic disease, are asymptomatic. This makes the diagnosis of hepatitis C very difficult and can be explained clearly why the HCV epidemic is often called 'the silent epidemic' [1]. No vaccine is available for hepatitis C. The high mutability of the hepatitis C genome [2] composes its development. There is no evidence that the successful treatment of HCV gives any kind of partial or temporary immunity. Hence the models developed fall within the class of models that treated or recovered individuals move back to the susceptible class.

In fact, the only two works known to the authors are [5]. A model structured by age-since-infection has also been considered in relation to HIV in [6]. Reade et al. discussed an ODE model for infections with acute and chronic Stages with feline calicivirus [3, 4]. In this paper, We suppose that the disease has an exposed period and then the patients enter into the acute and finally they went through the chronic stage. The patients have no immunity after recovering and become susceptible again. We part the population in researched area into four classes: S-susceptible; E-exposed; I-infected with acute hepatitis C; V-infected with chronic hepatitis C. The total number in t time is

$$N(t) = S(t) + I(t) + V(t) + E(t).$$

2 Basic assumptions and the Mathematical model

The basic demographic assumption is:

(i) The birth rate of the population is b ($b > 0$), and the death rate is d ($d > 0$).

The epidemiological assumptions are:

(ii) The disease can not be transmitted during the exposure period.

(iii) Only the acute and chronic stages are differentiated. Patients with either acute or chronic infections are capable of transmitting the disease. Once a person contacts with a susceptible individual he must be infected. β is a coefficient. Total acutely infective rate in this model is

$$\frac{\beta I}{1+\alpha_1 I},$$

where βI measures the infection force of the disease and $\frac{1}{1+\alpha_1 I}$ measures the inhibition effect from the behavioral change of the susceptible individuals. Each chronically infective makes γ contacts per unit times, and then the numbers of contacting susceptible individuals per unit times are respectively $\frac{\beta I}{1+\alpha_1 I}\frac{S}{N}$ and $r\frac{SV}{N}$. Hence, the incidences of the total acutely infective and the total chronically infective are respectively

$$\frac{\beta I}{1+\alpha_1 I}\frac{S}{N} \quad \text{and} \quad \gamma\frac{SV}{N}.$$

(iv) ε ($\varepsilon > 0$) and k ($k > 0$) are respectively the rate of progression to acute stage from the exposed and the rate of progression to chronic stage. α ($\alpha > 0$) is the recovery rate for the chronic state.

(v) The acute stage of infection is short and often asymptomatic and there is no possibility for treatment during this state.

(vi) Since the disease-induced death rate is relatively low, it is ignored.

Under the assumptions (i)-(vi), we construct the following model:

$$\begin{cases} \dot{S}(t) = bN - \dfrac{\beta I}{1+\alpha_1 I}\dfrac{S}{N} - \gamma VS - dS + \alpha V, \\ \dot{E}(t) = \dfrac{\beta I}{1+\alpha_1 I}\dfrac{S}{N} + \gamma V\dfrac{S}{N} - dE - \varepsilon E, \\ \dot{I}(t) = \varepsilon E - (d+k)I, \\ \dot{V}(t) = kI - (d+\alpha)V, \\ S(0) = S_0,\ E(0) = E_0,\ I(0) = I_0,\ V(0) = V_0 \end{cases} \tag{2.1}$$

By adding the equations of system (2.1) we obtain

$$\dot{N}(t) = (b-d)N$$

We set $r = b - d$, then $\dot{N}(t) = rN$, hence $N = N_0 e^r t$, terefore r gives the growth rate of the population, if $r > 0$, that is $b > d$, the population exponentially grows, if $r < 0$, that is $b < d$, the population exponentially decreases. The case $r = 0$ or $b = d$ implies that the population is stationary. Setting $N = 1$, then the system (2.1) becomes the following equivalent system:

$$\begin{cases} \dot{S}(t) = b(1-S) - \frac{\beta IS}{1+\alpha_1 I} - \gamma VS + \alpha V, \\ \dot{E}(t) = \frac{\beta IS}{1+\alpha_1 I} + \gamma VS - (b+\varepsilon)E, \\ \dot{I}(t) = \varepsilon E - (b+k)I, \\ \dot{V}(t) = kI - (b+\alpha)V, \\ S(0) = S_0,\ E(0) = E_0,\ I(0) = I_0,\ V(0) = V_0 \end{cases} \tag{2.2}$$

Letting $E = 1 - S - I - V$ substitute E in the third equation of (2.2) and removing the second equation, we obtain

$$\begin{cases} \dot{S}(t) = b(1-S) - \frac{\beta IS}{1+\alpha_1 I} - \gamma VS + \alpha V, \\ \dot{I}(t) = \varepsilon(1 - S - I - V) - (b+k)I, \\ \dot{V}(t) = kI - (b+\alpha)V, \\ S(0) = S_0,\ E(0) = E_0,\ I(0) = I_0,\ V(0) = V_0 \end{cases} \tag{2.3}$$

Setting $\Gamma = \{(S, I, V) \in R^3 \mid \ S > 0,\ I > 0,\ V > 0,\ S + I + V \leq 1\}$, obviously Γ is a invariable set of (2.3).

3 The stability of disease free equilibrium

Let the right hand side of equations (2.3) be zero, one can verify that model (2.3) has one disease free equilibrium at $P_0 = (1, 0, 0)$, The basic reproduction number of system (2.3) R_0 is defined as

$$R_0 = \varepsilon \frac{\beta(b+\alpha) + k\gamma}{(b+\alpha)(\varepsilon+b)(k+b)} = \frac{\beta\varepsilon}{(k+b)(\varepsilon+b)} + \frac{k\epsilon\gamma}{(b+\alpha)(\varepsilon+b)(k+b)}.$$

The first term $\dfrac{\beta\varepsilon}{(k+b)(\varepsilon+b)}$ can be interpreted as the contribution to the reproduction number due to secondary infections generated by an infective with acute hepatitis C. Naturally , it increases of effective contact rate of

chronic individual, γ. The reproduction number R_0 has a more complicated response to variations of the rate of progression to chronic stage, k. Because

$$\frac{dR_0}{dk} = \varepsilon \frac{b(\gamma - \beta) - \beta\alpha}{(b+\alpha)(\varepsilon+b)(k+b)^2},$$

it increases, when $b(\gamma - \beta) - \beta\alpha > 0$, and decreases when the opposite inequality is valid. In particular, when $b(\gamma - \beta) - \beta\alpha = 0$, R_0 can not change as k varies. However, the probability of transmitting the disease from an individual with acute infection is larger than that from an individual with chronic infection, that is, $\beta > \gamma$. Therefore, we expect that for realistic values of the parameters R_0 will decrease as the rate progression to chronic stage increases.

Theorem 3.1. *When $R_0 < 1$, the disease free equilibrium P_0 is locally stable.*

Proof. The matrix of system (2.3) at P_0 is

$$\begin{bmatrix} -b & -\beta & -\gamma+\alpha \\ -\varepsilon & -\varepsilon-k-b & -\varepsilon \\ 0 & k & -\alpha-b \end{bmatrix}.$$

Therefore its characteristic equation at P_0 is

$$\lambda^3 + A\lambda^2 + B\lambda + C = 0, \tag{3.1}$$

where $A = \alpha + \varepsilon + 3b + k$, $B = (b+\alpha)(\varepsilon + k + 2b) + (k+b)(\varepsilon+b) - \beta\varepsilon$, $C = (b+\alpha)(k+b)(\varepsilon+b) - \varepsilon[\beta(\alpha+b) + k\gamma]$. When $R_0 < 1$, $A > 0$, $C > 0$, it follows that form $C > 0$ and $(\alpha+b)(k+b)(\varepsilon+b) - \beta\varepsilon(\alpha+b) > 0$. That is $(k+b)(\varepsilon+b) - \beta\varepsilon > 0$, therefore $B > 0$.

In the following, we will calculate $AB - C.AB - C = (\alpha+\varepsilon+2b)[(\alpha+b)(\varepsilon+k+2b) + (k+b)(\varepsilon+b) - \beta\varepsilon] + (k+b)[(\alpha+b)(k+b) + (k+b)(\varepsilon+b) - \beta\varepsilon] + \varepsilon[\beta(\alpha+b) + k\gamma] > 0$. The last inequality is due to $R_0 < 1$. By Routh-Hurwitz theorem, the roots of the equation (3.1) all have negative real parts. Therefore when $R_0 < 1$, the disease free equilibrium P_0 is locally stable. □

Lemma 3.2. *Assuming $f : [0,\infty) \to R$ is bounded, $k \in L^1(0,\infty)$, then*

$$\lim_{t\to\infty} sup\left| \int_0^t k(\theta) f(t-\theta) d\theta \right| \le |f|^\infty \|k\|_{L^1(0,\infty)},$$

where $|f|^\infty = \lim_{t\to\infty} sup|f(t)|$.

Theorem 3.3. *When $R_0 < 1$, the disease free equilibrium $P_0(1,0,0)$ is globally stable.*

Proof. By Theorem 3.1, it can prove that P_0 is attractive globally for $R_0 < 1$. We note that the global attractive of P_0 is equivalent to that of the disease free equilibrium (1, 0, 0, 0). The second equation of (2.2) yields

$$\dot{E}(t) \leq (\beta I + \gamma V) - (\varepsilon + b)E.$$

Firstly, we solve the comparative equation $\dot{x}(t) = (\beta I + \gamma V) - (\varepsilon + b)x$, which yields

$$E(t) = E_0 e^{-(\varepsilon+b)t} + \int_0^t (\frac{\beta I}{1+\alpha_1 I} + \gamma V) S e^{-(\varepsilon+b)(t-S)} dS.$$

By the comparative principle, we have :

$$\lim_{t\to\infty} supE(t) \leq \lim_{t\to\infty} sup \int_0^t [\frac{\beta I}{1+\alpha_1 I}(t-S) + \gamma V(t-S)] e^{-(\varepsilon+b)(t-S)} dS$$

From the Lemma 3.2, we have

$$\begin{aligned} \lim_{t\to\infty} supE(t) &\leq [\beta \lim_{t\to\infty} supI(t) + \gamma \lim_{t\to\infty} supV(t)] \int_0^\infty e^{-(\varepsilon+b)S} dS \\ &= \frac{\beta}{\varepsilon+b} \lim_{t\to\infty} supI(t) + \frac{\gamma}{\varepsilon+b} \lim_{t\to\infty} supV(t) \end{aligned} \tag{3.2}$$

By the last equation of (2.3), we have

$$V(t) = e^{-(b+\alpha)t} V_0 + k \int_0^t e^{-(b+\alpha)S} I(t-S) dS.$$

Therefore,

$$\begin{aligned} \lim_{t\to\infty} supV(t) &\leq k \lim_{t\to\infty} supI(t) \int_0^\infty e^{-(b+\alpha)S} dS \\ &= \frac{k}{b+\alpha} \lim_{t\to\infty} supI(t). \end{aligned} \tag{3.3}$$

Substituting $\lim_{t\to\infty} supE(t)$ of inequality (3.2) for the right side of the inequality (3.3) yields

$$\lim_{t\to\infty} supE(t) \leq \frac{\beta}{\varepsilon+b} \lim_{t\to\infty} supI(t) + \frac{\gamma k}{(b+\varepsilon)(b+\alpha)} \lim_{t\to\infty} supI(t). \tag{3.4}$$

By the second equation of (2.2), we obtain

$$I(t) = I_0 e^{-(k+b)S} + \varepsilon \int_0^t E(S) e^{-(k+b)(t-S)} dS.$$

Therefore

$$\lim_{t\to\infty} supI(t) \le \frac{\varepsilon}{k+b} \lim_{t\to\infty} supE(t), \tag{3.5}$$

Noting the inequality (3.4), we have

$$\begin{aligned} \lim_{t\to\infty} supE(t) &\le [\frac{\beta\varepsilon}{(\varepsilon+b)(k+b)} + \frac{\varepsilon\gamma k}{(\varepsilon+b)(k+b)(b+\alpha)}] \lim_{t\to\infty} supE(t) \\ &= R_0 \lim_{t\to\infty} supE(t) \end{aligned} \tag{3.6}$$

By $R_0 < 1$ and (3.6), we have $\lim_{t\to\infty} supE(t) = 0$, and $\lim_{t\to\infty} supE(t) = 0$. By the inequality (3.5) and (3.3), we have $\lim_{t\to\infty} supI(t) = 0$, $\lim_{t\to\infty} supV(t) = 0$. From $S(t)+E(t)+V(t)+I(t) = 1$, it follows that $\lim_{t\to\infty} supS(t) = 1$. Therefore, when $R_0 < 1$, the disease free equilibrium $P_0(1, 0, 0)$ is globally stable. □

Theorem 3.3 indicates that the epidemic can not be prevalent only if R_0 is smaller than 1. From the above analysis, we know that R_0 will decrease when β and γ decrease or k increases. Numerical simulations confirm that the disease free equilibrium P_0 is asymptotically stable as proved in Theorem 3.3.

4 Existence of the endemic equilibrium

Denote

$$\begin{aligned} A_1 &= \frac{\langle b[(k+b)(\varepsilon+b+\alpha)+\varepsilon\alpha]+\alpha\varepsilon k\rangle(b+\alpha)\alpha_1 + g_1 g_2}{\gamma k \varepsilon \alpha_1}, \\ \hat{R_0} &= \frac{4\gamma k\alpha_1 \varepsilon g_1 g_2 (b+\alpha)}{\langle g_1[(b+\alpha)(b\alpha_1+\beta)+\gamma k]+(b+\alpha)\alpha_1\varepsilon k(\alpha-\gamma)\rangle^2 + 4\gamma k\alpha_1 g_1 g_2 (b+\alpha)}, \end{aligned}$$

where $g_1 = (k+b)(\varepsilon+b+\alpha)+\varepsilon\alpha$, $g_2 = \beta(b+\alpha)+\gamma k$. From the analysis, we can get the result regarding the number of endemic equilibrium.

Theorem 4.1. *For the model (2.3), with A_1 and $\hat{R}_0$ defined as above, we have*

1. *When* $R_0 > 1$, *there is a unique endemic equilibrium* E^*.
2. *When* $R_0 = 1$ *and* $b + \alpha > A_1$, *there is a unique endemic equilibrium* E^*.
3. *When* $R_0 \leq 1$ *and* $b + \alpha \leq A_1$, *there is no endemic equilibria.*
4. *When* $1 > R_0 > \hat{R}_0$ *and* $b + \alpha > A_1$, *there are two endemic equilibria* E^* *and* E_*.
5. *When* $R_0 = \hat{R}_0$ *and* $b + \alpha > A_1$, E^* *and* E_* *coalesce at a unique endemic equilibrium of multiplicity 2.*
6. *When* $R_0 < \hat{R}_0$ *and* $b + \alpha > A_1$, *there is no endemic equilibria.*

Where, when exist, $E^*(S^*, I^*, V^*)$ *and* $E_*(S_*, I_*, V_*)$ *are the corresponding equilibrium, and* $I^* = \dfrac{-b_1 + \sqrt{\triangle}}{2b_0}$, $I_* = \dfrac{-b_1 - \sqrt{\triangle}}{2b_0}$.

Theorem 4.2. *For the model (2.3), with* A_1, β_1^*, β_2^* *defined as above, we have*

1. *When* $\beta > \beta_1^*$, *there is a unique endemic equilibrium* E^*.
2. *When* $\beta = \beta_1^*$ *and* $b + \alpha > A_1$, *there is a unique endemic equilibrium* E^*.
3. *When* $\beta \leq \beta_1^*$ *and* $b + \alpha \leq A_1$, *there is no endemic equilibria.*
4. *When* $\beta_2^* < \beta < \beta_1^*$ *and* $b + \alpha > A_1$, *there are two endemic* E^* *and* E_*.
5. *When* $\beta = \beta_2^*$ *and* $b+\alpha > A_1$, E^* *and* E_* *coalesce at a unique endemic equilibrium of multiplicity 2.*
6. *When* $\beta < \beta_2^*$ *and* $b + \alpha > A_1$, *there is no endemic equilibria.*

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