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Research Article

Persistence of an SEIR Model with Immigration Dependent on the Prevalence of Infection

Wenjuan Wang, Jingqi Xin, and Fengqin Zhang

Department of Mathematics, Yuncheng University, Yuncheng, Shanxi 044000, China

Correspondence should be addressed to Fengqin Zhang, zhafq@263.net

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We incorporate the immigration of susceptible individuals into an SEIR epidemic model, assuming that the immigration rate decreases as the spread of infection increases. For this model, the basic reproduction number, R_0, is found, which determines that the disease is either extinct or persistent ultimately. The obtained results show that the disease becomes extinct as $R_0 < 1$ and persists in the population as $R_0 > 1$.

1. Introduction

Mathematical models have been used to predict the spread of infectious diseases of humans and animals since the pioneering work of Anderson and May [1]. Many diseases such as tuberculosis and chronic hepatitis have the longer exposed period; thus, in some common researches, a population is divided into four classes: susceptible, exposed, infective, and recovered. In many studies on epidemic models, the goal is to understand the key factors affecting disease transmission [2–5], and this often includes determining a threshold condition for the persistence and extinction of the disease.

Many diseases such as influenza, measles, and sexually transmitted diseases are easily spread between regions (such as countries and cities) due to travel. This population dispersal is an important aspect to consider when studying the spread of a disease [6–8]. We will investigate a disease transmission model with population immigration from other regions to the one considered.

In many models, it is assumed that, in the absence of infection, the growth rate of population is given by $N' = A - \mu N$, where A is thought to be the input rate of population. Here, we consider A as the sum of two parts, A_1 and A_2, where A_1 is the birth rate of the population and A_2 is the immigration rate from other regions. Since the spread of the infection usually affects the immigration to the region, then we will introduce the effect into an SEIR epidemic model and consider this persistence and extinction of the disease in this paper.

2. Model

In this paper, we consider an SEIR epidemic model with immigration:

$$\begin{aligned} S' &= \mu_1 B_1 + \frac{\mu_1 B_2}{1+mI} - \mu_1 S - \beta S I, \\ E' &= \beta S I - (\mu_1 + \varepsilon) E, \\ I' &= \varepsilon E - (\mu_1 + \alpha + \gamma) I, \\ R' &= \gamma I - \mu_1 R. \end{aligned} \tag{2.1}$$

Here, $S = S(t)$, $E = E(t)$, $I = I(t)$, and $R = R(t)$ represent the numbers of susceptible, exposed, infectious, and recovery individuals at time t, respectively. $\mu_1 B_1$ is the input rate; $\mu_1 B_2/(1 + mI)$ is the immigration rate from other regions (such as countries or cities); it depends on the number of infectious individuals in the region considered, where $\mu_1 B_2$ is the immigration rate in the absence of disease and m reflects the effect of infection on immigration from other regions; μ_1 is the percapita natural death rate; β is the transmission coefficient of infection; ε is the transfer rate from the exposed compartment to the infectious one; γ is the percapita recovery rate; α is the percapita disease-induced death rate.

From model (2.1) we have

$$\begin{aligned} (S+E+I+R)' &= \mu_1 B_1 + \frac{\mu_1 B_2}{1+mI} - \mu_1 (S+E+I+R) - \alpha I \\ &\le \mu_1 [(B_1 + B_2) - (S+E+I+R)]. \end{aligned} \tag{2.2}$$

It follows that $\limsup_{t\to\infty}(S+E+I+R) \le B_1 + B_2$, then system (2.1) is bounded.

Since the variable R does not appear explicitly in the first three equations in system (2.1), then we need only to consider the dynamics of a subsystem consisting of the first three equations in system (2.1). For this subsystem, making the following variable transformations:

$$S = \frac{\beta}{(\varepsilon m^2)} \cdot \overline{S}, \qquad E = \frac{\beta}{(\varepsilon m^2)} \cdot \overline{E}, \qquad I = \frac{1}{m} \cdot \overline{I}, \qquad t = \frac{m}{\beta} \cdot \overline{t}, \tag{2.3}$$

and removing the bar in $\overline{S}$, $\overline{E}$, $\overline{I}$, and $\overline{t}$, then we obtain the simplified system

$$\begin{aligned} S' &= \mu A_1 + \frac{\mu A_2}{1+I} - \mu S - S I, \\ E' &= S I - b_1 E, \\ I' &= E - b_2 I, \end{aligned} \tag{2.4}$$

where $\mu = \mu_1 m/\beta$, $A_1 = \varepsilon m^2 B_1/\beta$, $A_2 = \varepsilon m^2 B_2/\beta$, $b_1 = (\mu_1 + \varepsilon) m/\beta$, and $b_2 = (\mu_1 + \alpha + \gamma) m/\beta$.

From the first equation in system (2.4), we have $S' \leq \mu[(A_1 + A_2) - S]$; it implies that $\limsup_{t\to\infty} S(t) \leq A_1 + A_2$; therefore, the set $\Omega = \{(S, E, I) \in R_+^3 : S \leq A_1 + A_2\}$ is positively invariant to system (2.4). Thus, we only consider the dynamical behavior of system (2.4) on the set Ω.

3. The Existence and Local Stability of Equilibria

It is obvious that system (2.4) always has the disease-free equilibrium $E_0(A_1 + A_2, 0, 0)$. Its endemic equilibrium $E^*(S^*, E^*, I^*)$ is determined by the following equations:

$$\begin{aligned} \mu A_1 + \frac{\mu A_2}{1+I} - \mu S - SI &= 0, \\ SI - b_1 E &= 0, \\ E - b_2 I &= 0. \end{aligned} \tag{3.1}$$

From the last two equations in (3.1), we have $S = b_1 b_2$ and $E = b_2 I$ for $I \neq 0$. Substituting $S = b_1 b_2$ into the first equation in (3.1) gives

$$\mu\left(A_1 + \frac{A_2}{1+I}\right) = b_1 b_2(\mu + I), \tag{3.2}$$

then I^* is the positive root of (3.2).

According to the monotonicity of functions at the two sides of (3.2), we know that (3.2) has a unique positive root if $(A_1 + A_2)/(b_1 b_2) > 1$ and no positive roots if $(A_1 + A_2)/(b_1 b_2) \leq 1$. Therefore, with respect to the existence of equilibria of system (2.4), we have the following theorem.

Theorem 3.1. *Denote that $R_0 = (A_1 + A_2)/(b_1 b_2)$. When $R_0 \leq 1$, system* (2.4) *has only the disease-free equilibrium $E_0(A_1 + A_2, 0, 0)$ on the set Ω; when $R_0 > 1$, besides the disease-free equilibrium E_0, system* (2.4) *also has a unique endemic equilibrium $E^*(S^*, E^*, I^*)$, where $S^* = b_1 b_2, E^* = b_2 I^*$, and I^* is determined by* (3.2).

With respect to the local stability of equilibria E_0 and E^* of system (2.4), we have the following theorem.

Theorem 3.2. *The disease-free equilibrium E_0 is locally asymptotically stable as $R_0 < 1$ and unstable as $R_0 > 1$. The endemic equilibrium E^* is locally asymptotically stable as it exists.*

Proof. (i) From the Jacobian matrix of system (2.4) at the disease-free equilibrium E_0, it is easy to know that the disease-free equilibrium E_0 is locally asymptotically stable as $R_0 < 1$ and unstable as $R_0 > 1$.

(ii) For the Jacobian matrix of system (2.4) at the endemic equilibrium E^*, the characteristic equation is given by $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$, where $a_1 = \mu + I^* + b_1 + b_2$, $a_2 = (\mu + I^*)(b_1 + b_2)$, and $a_3 = I^*[\mu A_2/(1+I^*)^2 + b_1b_2]$, then

$$a_1a_2 - a_3 = (\mu + I^* + b_1 + b_2)(\mu + I^*)(b_1 + b_2) - I^*\left[\frac{\mu A_2}{(1+I^*)^2} + b_1b_2\right]. \tag{3.3}$$

Notice that (3.2) can be rewritten as

$$\begin{aligned} (\mu + I)(1+I) &= \frac{\mu[(A_1 + A_2) + A_1 I]}{(b_1b_2)}, \\ \frac{\mu A_2}{(1+I)} &= b_1b_2 I + \mu(b_1b_2 - A_1). \end{aligned} \tag{3.4}$$

Using (3.4) gives

$$\begin{aligned} (1+I^*)(a_1a_2 - a_3) = {} & \left[\frac{\mu A_1(b_1+b_2)}{b_1b_2} - 2b_1b_2\right]I^{*2} + \frac{\mu(A_1+A_2)(b_1+b_2)(\mu+b_1+b_2)}{b_1b_2} \\ & + \left\{\frac{\mu(b_1+b_2)}{b_1b_2}\left[(A_1+A_2) + A_1(\mu+b_1+b_2)\right] - (1+\mu)b_1b_2 + \mu A_1\right\}I^* \\ \triangleq {} & f_1(I^*). \end{aligned} \tag{3.5}$$

On the other hand, (3.2) can become

$$f_2(I) \triangleq b_1b_2I^2 + \left[b_1b_2(1+\mu) - \mu A_1\right]I + \mu[b_1b_2 - (A_1 + A_2)] = 0, \tag{3.6}$$

then

$$f_1(I^*) + 2f_2(I^*) = c_1I^{*2} + c_2I^* + c_3\mu > 0, \tag{3.7}$$

where $c_1 = \mu A_1(b_1+b_2)/(b_1b_2)$, $c_2 = b_1b_2(1+\mu) + \mu[(b_1+b_2)(A_1+A_2+\mu A_1) + A_1(b_1^2 + b_2^2 + b_1b_2)]/(b_1b_2)$, and $c_3 = (A_1+A_2)[\mu(b_1+b_2) + b_1^2 + b_2^2]/(b_1b_2) + 2b_1b_2$. It follows from $f_2(I^*) = 0$ that $f_1(I^*) > 0$, that is, $a_1a_2 - a_3 > 0$. Therefore, it follows from Hurwitz criterion that the endemic equilibrium E^* is locally asymptotically stable. □

4. The Extinction and Persistence of Infection

In this section, we will consider the ultimate state of infection; that is, the disease will be whether extinct or persistent ultimately.

When $R_0 < 1$, define function $V_1 = \rho E + I$, where $\rho \in (1/b_1, b_2/(A_1 + A_2))$, then the derivative of V_1 with respect to t along the solution of (2.4) on the set Ω is given by

$$V_1' = (1 - \rho b_1)E + [\rho(A_1 + A_2) - b_2]I. \tag{4.1}$$

It follows from $\rho \in (1/b_1, b_2/(A_1+A_2))$ that $1-\rho b_1 < 0$ and $\rho(A_1+A_2)-b_2 < 0$, then there exists a positive number σ such that $1 - \rho b_1 < \sigma\rho(R_0 - 1)$ and $\rho(A_1 + A_2) - b_2 < \sigma(R_0 - 1)$. Therefore, from (4.1) we have $V_1' \le \sigma(R_0 - 1)V_1$, then $V_1(t) \le V_1(0)\exp[\sigma(R_0 - 1)t]$, where $V_1(0) = \rho E(0) + I(0)$, therefore, $\lim_{t\to\infty} V_1(t) = 0$ for $R_0 < 1$; that is, $\lim_{t\to\infty} E(t) = \lim_{t\to\infty} I(t) = 0$ as $R_0 < 1$. It implies that the disease will be extinct ultimately when $R_0 < 1$.

In order to discuss the persistence of the disease, we first introduce some definitions and lemmas.

Assume that X is a locally compact metric space with metric d, and let F be a closed subset of X with the boundary ∂F and the interior $\operatorname{int} F$. Let π be a semidynamical system defined on F.

We say that π is persistent if, for all $u \in \operatorname{int} F$, $\liminf_{t\to+\infty} d(\pi(u,t), \partial F) > 0$ and that π is uniformly persistent if there is $\xi > 0$ such that, for all $u \in \operatorname{int} F$, $\liminf_{t\to+\infty} d(\pi(u,t), \partial F) > \xi$.

In [3], Fonda gives a result about persistence in terms of repellers. A subset Σ of F is said to be a uniform repeller if there is an $\eta > 0$ such that, for each $u \in F \setminus \Sigma$, $\liminf_{t\to+\infty} d(\pi(u,t), \Sigma) > \eta$. A semiflow on a closed subset F of a locally compact metric space is uniformly persistent if the boundary of F is repelling in a suitable strong sense [9]. The result by Fonda is as follows.

Lemma 4.1. *Let Σ be a compact subset of X such that $X \setminus \Sigma$ is positively invariant. A necessary and sufficient condition for Σ to be a uniform repeller is that there exists a neighborhood U of Σ and a continuous function $P : X \to R_+$ satisfying*

(1) $P(u) = 0$ *if and only if* $u \in \Sigma$,

(2) *for all* $u \in U \setminus \Sigma$ *there is a* $T_u > 0$ *such that* $P(\pi(u, T_u)) > P(u)$.

For any $u_0 = (S_0, E_0, I_0) \in \Omega$, there is a unique solution $\pi(u_0, t) = (S, E, I)(t; u_0)$ of system (2.4), which is defined in R_+ and satisfies $\pi(u_0, 0) = (S_0, E_0, I_0)$. Since Ω is a positively invariant set of system (2.4), then $\pi(u_0, t) \in \Omega$ for $t \in R_+$ and is a semidynamical system in Ω.

In the following, we will prove that, when $R_0 > 1$, $\Sigma = \{(S, E, I) \in \Sigma : I = 0\}$ is a uniform repeller, which implies that the semidynamic system π is uniformly persistent.

Obviously, $I(t) > 0$ for $t > 0$ if $I(0) > 0$, then $\Omega \setminus \Sigma$ is invariant to (2.4). Again the set Σ is a compact subset of Ω.

Let $P : \Omega \to R_+$ be defined by $P(S, E, I) = I$, and let $U = \{(S, E, I) \in \Omega : P(S, E, I) < \eta_1\}$, where $\eta_1 > 0$ is small enough so that

$$\frac{\mu}{\mu + 2\beta\eta_1}\left(A_1 + \frac{A_2}{1 + \eta_1}\right) > b_1 b_2. \tag{4.2}$$

Since $R_0 > 1$ is equivalent to $A_1 + A_2 > b_1 b_2$, then there exists a positive number η_1 such small that inequality (4.2) holds.

Assume that there is $\overline{u} \in U$ ($\overline{u} = (\overline{S}, \overline{E}, \overline{I})$) such that for each $t > 0$ we have $P(\pi(\overline{u}, t)) < P(\overline{u}) < \eta_1$, which implies that $I(t; \overline{u}) < \eta_1$ for $t > 0$. From the first equation in system (2.4) we have

$$S' \geq \mu\left(A_1 + \frac{A_2}{1+\eta_1}\right) - (\mu + \eta_1)S, \tag{4.3}$$

then

$$\liminf_{t\to\infty} S(t; \overline{u}) \geq \frac{\mu}{\mu + \eta_1}\left(A_1 + \frac{A_2}{1+\eta_1}\right). \tag{4.4}$$

So there is a sufficiently large number $T > 0$ such that $S(t; \overline{u}) > \mu[A_1 + A_2/(1+\eta_1)]/(\mu + 2\eta_1)$ for $t \geq T$.

Define the auxiliary function $V_2(t) = (1 - \eta_2)E(t) + b_1 I(t)$, where $\eta_2 (0 < \eta_2 < 1)$ is a sufficiently small constant so that $\mu(1-\eta_2)/(\mu + 2\eta_1) \cdot [A_1 + A_2/(1+\eta_1)] > b_1 b_2$. Direct calculation gives the derivative of $V_2(t)$ along with $\pi(\overline{u}, t)$ as follows:

$$V_2' = b_1 \eta_2 E + \left[(1-\eta_2)S - b_1 b_2\right] I. \tag{4.5}$$

Then, for $t \geq T$, we have

$$V_2' \geq b_1 \eta_2 E + \left[\frac{\mu(1-\eta_2)}{\mu + 2\eta_1}\left(A_1 + \frac{A_2}{1+\eta_1}\right) - b_1 b_2\right] I > \sigma V_2, \tag{4.6}$$

where

$$\sigma = \min\left\{\frac{b_1 \eta_2}{1-\eta_2}, \frac{1}{b_1}\left[\frac{\mu(1-\eta_2)}{\mu + 2\eta_1}\left(A_1 + \frac{A_2}{1+\eta_1}\right) - b_1 b_2\right]\right\} > 0, \tag{4.7}$$

therefore, $\lim_{t\to\infty} V_2(t) = +\infty$.

On the other hand, the boundedness of the solution of (2.1) implies that of $V_2(t)$ on the set Ω. It implies that the assumption above is not true. Therefore, the above proof shows that, for each $u \in \Omega \setminus \Sigma$ with u belonging to a suitably small neighborhood of Σ, there is some T_u such that $P(\pi(u, T_u)) > P(u)$. Therefore, it follows from Lemma 4.1 that $\Sigma = \{(S, E, I) \in \Sigma : I = 0\}$ is a uniform repeller when $R_0 > 1$; that is, the infection is uniformly persistent. So we have the following theorem.

Theorem 4.2. *For system* (2.4), *the infection will be extinct when* $R_0 < 1$ *and persistent when* $R_0 > 1$.

5. Conclusion and Discussion

In Sections 3 and 4, for system (2.4) we investigated the qualitative behavior and obtained the threshold R_0 determining the persistence of infection. Corresponding to the original model (2.1), the basic reproduction number is $R_0 = (\beta_1 + \beta_2)\varepsilon / [(\mu_1 + \varepsilon)(\mu_1 + \alpha + \gamma)]$. According to the results in Sections 3 and 4, model (2.1) only has the disease-free equilibrium which is globally stable when $R_0 < 1$; it implies that the disease is extinct ultimately; when $R_0 > 1$, model (2.1) has a unique endemic equilibrium which is locally asymptotically stable and the disease persists in the population. Since the expression of R_0 here is independent of the parameter m, then this shows that this parameter has no effect on the persistence of disease, but it can affect the strength of spread of disease according to Theorem 3.1.

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