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ORIGINAL ARTICLE

Stability analysis of an influenza virus model with disease resistance

Nguyen Huu Khanh*

College of Natural Sciences, CanTho University, Viet Nam

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Abstract We study a new model describing the transmission of influenza virus with disease resistance in human. Mathematical analysis shows that dynamics of the spread is determined by the basic reproduction number R_0. If $R_0 \leq 1$, the disease free equilibrium is globally asymptotically stable, and if $R_0 > 1$, the endemic equilibrium is globally asymptotically stable under some conditions. The change of stability of equilibria is explained by transcritical bifurcation. Lyapunov functional method and geometric approach are used for proving the global stability of equilibria. A numerical investigation is carried out to confirm the analytical results. Some effective strategies for eliminating virus are suggested.

2010 Mathematics subject classification: 34D23; 37B25; 92D30

1. Introduction

Influenza, also called the flu, is a disease caused by a virus that affects mainly the nose, throat, bronchi and, occasionally, lungs. The virus can spread from person to person through air by coughs, sneezes or from infected surfaces, and by the direct contact to infected persons. There are three types of influenza virus, namely, A, B, and C. Among these, influenza A viruses are more severe than others for human populations. Mathematical models have provided a useful tool to understand disease dynamics and give out preventive strategies [1,2].

In 2003, Neil and coworkers [3] constructed a mathematical model of influenza transmission simulating the effect of neuraminidase inhibitor therapy on infection rates and transmission of drug-resistant viral strains. They concentrate on numerical investigation without considering the stability of the model. Fraser et al. [4] studied the transmission model of influenza A (H1N1) in the human population, but they did not include cross-species transmission. Coburn [5] presented a complex model for transmission of three species (birds, pigs and human). In [1], Pongsumpun considered the model for the transmission of Swine flu, a new strain of type A influenza virus, with different probability of the patients who have symptomatic and asymptomatic infections. Recently, Zhou and Guo [2] ana-

* Tel.: +84 908791280.
E-mail address: nhkhanh@ctu.edu.vn
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lyzed an influenza model with vaccination. However, many articles did not concern with disease resistance in human.

The stability of epidemic models has been studied in many papers [6–8]. Many authors paid attention to local stability of equilibria. Recently, the study of epidemic models mainly concerns global asymptotic stability. The most successful approaches to the problem are the direct Lyapunov method [9–13] and the geometric method [14,15].

In this paper, we consider a new SEIR model depicting the transmission of influenza virus with disease resistance in human. In the model, a person in exposed group or infected group can come back to susceptible group without treatment. This describes realistic modeling of treatment. The model is given by a system of four differential equations depending on parameters. By using the method of next generation matrix [16], we found a threshold R_0 called basic reproduction number. In general, when $R_0 \leq 1$, the disease dies out and when $R_0 > 1$, the disease persists in the population. If we suppose that the endemic equilibrium also exists for $R_0 < 1$, although it is not true, then the bifurcation occurring in the model can be explained as a transcritical bifurcation. Several various methods are used to determine the stability of equilibria. We concentrate our study on the globally stable stability of equilibria. This is obtained by Lyapunov functional approach and geometric approach. A numerical investigation is carried out by Mathematica software and AUTO software package confirming theoretical results.

The paper is organized as follows. In the next section, we introduce the structure of the transmission model, equilibria and basic reproduction number. Section 3 deals with the local stability of equilibria. In Section 4, we prove the global stability of equilibria by Lyapunov functional approach and geometric approach. Some numerical simulations are given in Section 5. Finally, Section 6 summarizes this work.

2. The model and its basic properties

2.1. The structure of the model

We consider the transmission of influenza virus among the people. The total population, size $N(t)$, is divided into four distinct epidemiological subclasses of individuals which are susceptible, exposed, infectious and recovered, with sizes denoted by $\overline{S}(t), \overline{E}(t), \overline{I}(t), \overline{R}(t)$, respectively. In exposed group, there are people who have been in contact with an infected individual but uninfected. Besides, infectious group has people infected but become exposed without treatment. We assume that the environment is homogeneous and natural death rates have common rate μ.

The model is given by a system of ordinary differential equations:

$$\begin{aligned}
\frac{d\overline{S}}{dt} &= \Lambda - \gamma \overline{S}(t)\frac{\overline{E}(t)+\overline{I}(t)}{N(t)} + c\overline{E}(t) + b\overline{I}(t) \\
&\quad + \alpha \overline{R}(t) - \mu \overline{S}(t) \\
\frac{d\overline{E}}{dt} &= \gamma \overline{S}(t)\frac{\overline{E}(t)+\overline{I}(t)}{N(t)} - (c+\varepsilon+\mu)\overline{E}(t) \\
\frac{d\overline{I}}{dt} &= \varepsilon \overline{E}(t) - (\beta+b+\mu)\overline{I}(t) \\
\frac{d\overline{R}}{dt} &= \beta \overline{I}(t) - (\alpha+\mu)\overline{R}(t),
\end{aligned} \tag{1}$$

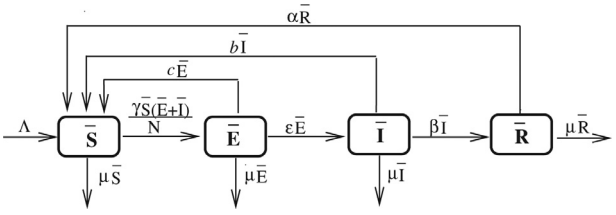

Figure 1 Transfer diagram of the model (1).

where Λ is a constant recruitment of susceptible human, γ is the contact rate of virus transmission, c is the rate at which the exposed human become to be susceptible human without treatment, b is the rate at which the infectious human become to be the susceptible human without treatment, $\varepsilon = 1/\mathrm{IIP}$ where IIP is the intrinsic incubation period of virus, α is the rate at which the recovered human become to be the susceptible human again, β is the rate at which the infectious human become to be the recovered human, and μ is the natural death rate of the human population. Fig. 1 shows the transfer diagram of the model (1).

We assume that the total size of population $N(t)$ is constant, that is $N(t) = N$. Then $\overline{S}(t) + \overline{E}(t) + \overline{I}(t) + \overline{R}(t) = N$.

Let $S(t) = \frac{\overline{S}(t)}{N}$, $E(t) = \frac{\overline{E}(t)}{N}$, $I(t) = \frac{\overline{I}(t)}{N}$, $R(t) = \frac{\overline{R}(t)}{N}$. We obtain the reduced system

$$\begin{aligned}
\frac{dS}{dt} &= \mu - \gamma S(t)(E(t)+I(t)) + cE(t) + bI(t) \\
&\quad + \alpha R(t) - \mu S(t) \\
\frac{dE}{dt} &= \gamma S(t)(E(t)+I(t)) - (c+\varepsilon+\mu)E(t) \\
\frac{dI}{dt} &= \varepsilon E(t) - (\beta+b+\mu)I(t) \\
\frac{dR}{dt} &= \beta I(t) - (\alpha+\mu)R(t),
\end{aligned} \tag{2}$$

with the condition $S(t) + E(t) + I(t) + R(t) = 1$.

It follows from the system (2) that $(S+E+I+R)' = \Lambda - \mu(S+E+I+R) = \Lambda - \mu$. Then $\limsup_{t\to\infty}(S+E+I+R) \leq \frac{\Lambda}{\mu}$. Therefore, the feasible region for system (2) is $\Omega = \{(S,E,I,R) : S > 0, E \geq 0, I \geq 0, R \geq 0, S+E+I+R \leq \frac{\Lambda}{\mu}\}$.

It is easy to verify that the region Ω is positively invariant with respect to system (2).

2.2. Equilibria

To find equilibria, we set the right-hand side of the system (2) equals zero. Then we get two equilibria in the coordinate (S,E,I,R):

(i) Disease free equilibrium $P_0(1,0,0,0)$. It is seen that the equilibrium P_0 always exists.

(ii) Disease endemic equilibrium $P_1(S^*,E^*,I^*,R^*)$ with positive components:

$$S^* = \frac{1}{R_0},$$

$$E^* = \frac{(\alpha+\mu)(\beta+b+\mu)G_1}{G_2},$$

$$I^* = \frac{\varepsilon(\alpha+\mu)G_1}{G_2},$$