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Two-strain epidemic model with two vaccinations

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ABSTRACT

In this paper, we studied an epidemic model consisting of two strains with vaccine for each strain. The model consist of four equilibrium points; disease free equilibrium, endemic with respect to strain 1, endemic with respect to strain 2, and endemic with respect to both strains.

The global stability analysis of the equilibrium points was carried out through the use of Lyapunov functions. Two basic reproduction ratios R_1 and R_2 are found, and we have shown that, if both are less than one, the disease dies out, if one of the ratios is less than one, epidemic occurs with respect to the other. It was also shown that, any strain with highest basic reproduction ratio will automatically outperform the other strain, thereby eliminating it. Condition for the existence of endemic equilibria was also given.

Numerical simulations were carried out to support the analytic results and to show the effect of vaccine for strain 1 against strain 2 and the vaccine for strain 2 against strain 1. It is found that the population for infectives to strain 2 increases when vaccine for strain 1 is absent and vice versa.

1. Introduction

Influenza virus are segmented, negative- sense, enveloped RNA viruses [1]. In most cases it is confused with the common cold, but influenza is much more severe disease. It is of three types; A, B and C. Influenza A has antigenic variability which allows it to escape neutralization from anti- bodies [2]. Influenza B internal proteins also exhibits antigenic variability property, but less than that of A. This property is not common in Influenza C, hence Influenza A is more serious than B, and then C [3].

In the 20th century, three influenza pandemics appeared and tens of millions of people died. One of the flu which is known as a Spanish flue effected more than 50 million people. Moreover in 1957–1958 two million people died, and in 1968 one million people died from the disease [4]. Only in 2009 H1N1 virus pandemic was estimated to have caused more than 200,000 deaths during the first 12 months of its circulation [5].

There are many methods of preventing the spread of infectious disease, one of them is vaccination. Vaccination is the administration of agent-specific, but relatively harmless, antigenic components that in vaccinated individuals can induce protective immunity against the corresponding infectious agent [6].

Many researches exist in literature on mathematical models of Influenza virus. Some of them concentrate on the dynamics of the disease [7–9], vaccine and immunization [10–16]. Since influenza virus are of many forms, some researches are on multiple strain influenza virus [17–22]. Rahman and Zou [23] constructed a model on the dynamics of two strain Influenza virus with a single vaccine.

In this paper, we consider two strain influenza model with two vaccination in which strain 2 is the mutation of strain 1. A mutation is the sudden change in the genetic makeup that occurs either due to mistakes when DNA is copied or as a result of environmental factors. Here strain 2 was assumed to be as a result of changes in the proteins that made up strain 1. Proper vaccine administration is a critical component of a successful influenza control program. It is a key part of ensuring that vaccination is as safe and effective as possible. Unfortunately, it is easy to make vaccine administration error. Although some improperly administered vaccines may be valid, sometimes such errors open the possibility of patients being unprotected against the disease. In this paper we want to study the effects of administering vaccine for strain 1 (V1) against strain 2, and administering vaccine for strain 2 (V2) against strain 1.

The paper is organized as follows: In Section 2 we formulate the two strain influenza model with vaccination compartments with respect to strain 1 and strain 2. In Section 3, we determined all possible equilibria, basic reproduction ratios and we determine the global stabilities for the equilibrium points. In Section 4, Numerical Simulations are given to support the analytic results. Lastly, in Section 5, conclusions and discussions are given.

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Table 1
Variables and parameters.

Parameter	Description
Λ	Recruitment of individuals
$\frac{1}{\mu}$	Average time of life expectancy
r_1	Rate of vaccination with strain 1
r_2	Rate of vaccination with strain 2
k_1	Transmission coefficient of vaccinated individuals V_1 to strain 2
k_2	Transmission coefficient of vaccinated individuals V_2 to strain 1
β_1	Transmission coefficient of susceptible individuals to strain 2
β_2	Transmission coefficient of susceptible individuals to strain 1
$\frac{1}{\gamma_1}$	Average infection period of strain 1
$\frac{1}{\gamma_2}$	Average infection period of strain 2
ν_1	Infection induced death rate of strain 1
ν_2	Infection induced death rate of strain 2

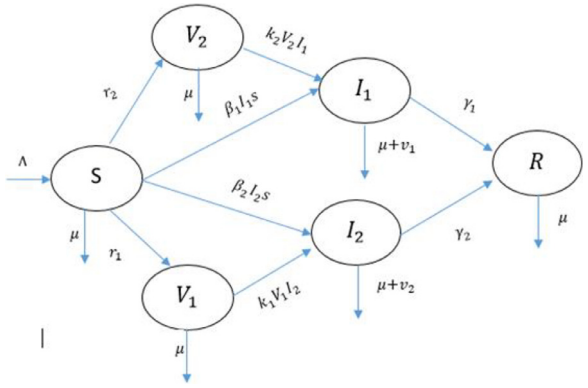

Fig. 1. Transfer diagram of model (1).

2. The model

2.1. Structure of the model

The population N(t) is divided into six compartments by modifying the model of [14]. The compartments are S, V_1, V_2, I_1, I_2 and R, which denotes the sizes of susceptible, immunized with the vaccination for strain 1, immunized with the vaccination for strain 2, infected with strain 1, infected with strain 2 and recovered compartments respectively.

We assume that there is equal birth and equal death in the population, and we assume that there is no double infection. The variables and parameters are positive and their meanings are given in Table 1, Fig. 1 also gives the transfer diagram of the model. With these assumptions the model is given by a system of ordinary differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (\beta_1 I_1 + \beta_2 I_2 + \lambda)S \\
\frac{dV_1}{dt} &= r_1 S - (k_1 I_2 + \mu)V_1 \\
\frac{dV_2}{dt} &= r_2 S - (k_2 I_1 + \mu)V_2 \\
\frac{dI_1}{dt} &= (k_2 V_2 + \beta_1 S)I_1 - \alpha_1 I_1 \\
\frac{dI_2}{dt} &= (k_1 V_1 + \beta_2 S)I_2 - \alpha_2 I_2 \\
\frac{dR}{dt} &= \gamma_1 I_1 + \gamma_2 I_2 - \mu R
\end{aligned} \tag{1}$$

where $\lambda = r_1 + r_2 + \mu$, $\alpha_1 = \mu + \nu_1 + \gamma_1$ and $\alpha_2 = \mu + \nu_2 + \gamma_2$, With the condition $S + V_1 + V_2 + I_1 + I_2 + R = N$.

3. Disease dynamics

It follows from the system (1) that

$$\begin{aligned}
0 &\le \frac{dS}{dt} + \frac{dV_1}{dt} + \frac{dV_2}{dt} + \frac{dI_1}{dt} + \frac{dI_2}{dt} + \frac{dR}{dt} \\
&= \Lambda - \mu N - \nu_1 I_1 - \nu_2 I_2 \le \Lambda - \mu N
\end{aligned}$$

Therefore, $\limsup_{t\to\infty}(S + V_1 + V_2 + I_1 + I_2 + R) \le \frac{\Lambda}{\mu}$. Hence the feasible region for system (1) is

$$\Omega = \left\{ (S + V_1 + V_2 + I_1 + I_2 + R) : \; S > 0, V_1 > 0, I_1 > 0, I_2 > 0, \right.$$
$$\left. \times R > 0, \; S + V_1 + V_2 + I_1 + I_2 + R \; \le \frac{\Lambda}{\mu} \right\}.$$

3.1. Equilibria

Setting the equations in (1) equal to zero, and solving simultaneously we get four equilibrium points:

(I) Disease free equilibrium, $E_0 = (\frac{\Lambda}{\lambda}, \frac{r_1\Lambda}{\lambda\mu}, \frac{r_2\Lambda}{\lambda\mu}, 0, 0)$,

Since all the coordinates of E_0 are positive, it is biologically meaningful.

(II) Strain 2 disease free equilibrium (strain 1 infection equilibrium) E_1,

$$\bar{S} = \frac{\Lambda}{\beta_1 I_1^1 + \lambda}, \; \overline{V_1} = \frac{r_1\Lambda}{\mu(\beta_1 I_1 + \lambda)},$$
$$\overline{V_2} = \frac{r_2\Lambda}{(\beta_1 I_1 + \lambda)(\mu + k_2 I_1)}, \quad \overline{I_2} = 0$$

And $\overline{I_1}$ is the root of,

$$AI_1^2 + BI_1 + C = 0 \tag{2}$$

Where $A = \alpha_1\beta_1 k_2$, $B = \alpha_1\beta_1\mu - k_2\beta_1\Lambda + \alpha_1\lambda k_2$, $C = \alpha_1\lambda\mu - k_2 r_2\Lambda - \beta_1\Lambda\mu$.

Since $\bar{S}, \overline{V_1}$ and $\overline{V_2}$ are all positive, to check the biologically meaningfulness of E_1 we need to check the root of Eq. (2),

First, assume that $C \ge 0$

$$\begin{aligned}
&\alpha_1\lambda\mu - k_2 r_2\Lambda - \beta_1\Lambda\mu \ge 0 \\
&\Rightarrow \alpha_1(r_1 + r_2 + \mu)\mu \ge k_2 r_2\Lambda + \beta_1\Lambda\mu \\
&\Rightarrow \alpha_1 \ge \frac{k_2 r_2\Lambda + \beta_1\Lambda\mu}{(r_1 + r_2 + \mu)\mu}
\end{aligned} \tag{3}$$

And when $C \ge 0$, B must be less than zero otherwise (if $B \ge 0$) Eq. (2) has no positive root. But when $B \le 0$,

$$\begin{aligned}
&\alpha_1\beta_1\mu - k_2\beta_1\Lambda + \alpha_1\lambda k_2 \le 0 \\
&\Rightarrow \alpha_1(\beta_1\mu + \lambda k_2) \le k_2\beta_1\Lambda \\
&\Rightarrow \frac{1}{\alpha_1} \ge \frac{\beta_1\mu + (r_1 + r_2 + \mu)k_2}{k_2\beta_1\Lambda}
\end{aligned} \tag{4}$$

From (3) and (4) we get

$$1 \ge \frac{k_2 r_2\Lambda + \beta_1\Lambda\mu}{(r_1 + r_2 + \mu)\mu} \frac{\beta_1\mu + (r_1 + r_2 + \mu)k_2}{k_2\beta_1\Lambda}$$

After some simplification we have

$$0 \ge (k_2 r_2\Lambda + \beta_1\mu\Lambda)\beta_1\mu + (r_1 + r_2 + \mu)k_2^2 r_2\Lambda \tag{5}$$

Which is a contradiction since all coefficients in Eq. (5) are positive. Therefore when $C \ge 0$, B must be greater than zero, it means there is no positive solution of Eq. (2) and so E_1 is meaningless.