



A model for influenza with vaccination and awareness



Isa Abdullahi Baba*, Evren Hincal

Department of Mathematics, Near East University TRNC, Turkey

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ABSTRACT

In this paper we consider three strains of influenza (I_1 , I_2 , and I_3) where we have vaccine for strain 1 (V_1) only, and population has enough awareness of strain 2. There is neither vaccine nor awareness for strain 3. Our main aim is to mathematically analyze the effect of the vaccine for strain 1 and awareness of strain 2 on the dynamics of strain 3. It is also in our aim to study the coexistence of these three strains. Six equilibrium points were obtained and their global stability using Lyapunov functions was shown to depend on the magnitude of a threshold quantity, called basic reproduction ratio. It was shown that the coexistence of strain 1 and strain 2 is not possible and the coexistence of the three strains was shown numerically. It can be observed from the numerical simulations that, although vaccine curtail the spread of strain 1, awareness curtail the spread of strain 2, but they both have negative effect on strain 3. This tells the relevant authorities whenever there is influenza epidemic to investigate thoroughly the possibilities of the existence of multiple strains, so as to provide vaccines and enough awareness on all the strains present.

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1. Introduction

Influenza is termed as a serious cytopathogenic, infectious, drastic respiratory disease that is caused by influenza virus [1]. The virus is categorized into three main types; A, B, and C. This categorization is based on the differences that exist between matrix protein (M) and nucleoprotein (NP) [2].

Type A can infect both humans, pigs, whales, birds and especially wild animals. It is the most acute of all the types. It is further subdivided into based on hemagglutinin (HA) and neuraminidase (NA) proteins found on the surface of the virus. There are sixteen subtypes of hemagglutinin (H1–H16) and nine subtypes of neuraminidase (N1–N9). Subtypes of influenza virus are named based on their combination of HA and NA. For example H1N1 virus means, Influenza A that has an HA1 protein and NA1 protein. In humans three of these combinations are most common; H1N1, H1N2, and H3N2. Type B can also infect humans and birds, and can cause epidemics. The last type (C) affects only humans and it can hardly be differentiated from common cold as it causes no epidemics [3].

SIR model was used as a basis for influenza models. Many extensions of the SIR model for influenza includes incorporating seasonality [4,5], as a spatial–temporal model [6], to show the effect

of air travel on its pandemic [1,7], and to show the importance of air travel on geographic spread [8,9].

Mathematical models also provided insight into severity of past influenza epidemics [10,11]. Some models were used to investigate the three most devastating historical pandemics of influenza in the 20th century; Spanish flu (H1N1) 1918 – 1919, Asian flu (H2N2) 1957–1958, and Hong–Kong flu (H3N2) 1968 [12–14]. It was shown using mathematical modeling the effect that interventions may have had in curtailing the H1N1 pandemics of 1918–1919 [12]. The behavioral effects such as quarantine, imposing travel sanctions on the infected individuals, closing schools were also modeled [15–17]. The effectiveness of biomedical interventions such as vaccines, therapeutic treatment, and prophylactic treatment were also shown using mathematical models [18–20].

Many models were also used to assess the problem of anti-viral resistance [21], to compare the relative effectiveness of prophylaxis versus treatment strategies [19,22,23], to assess reappearance factors [24], and to identify the optimal strategy for allocating vaccines [20]. Some models went ahead to evaluate the effectiveness of combining behavioral and biomedical interventions [25]. Varvadas et al. investigated the effect of human behavior towards determining vaccine coverage [26]. These studies illustrate how models can be used in identifying the strength of the interventions that are compulsory in controlling an epidemic or pandemic, but the goals of the control strategy may not necessarily be attained.

Also many diseases such as Tuberculosis, Influenza, Dengue fever, and some other sexually transmitted diseases are caused by more than one strain of pathogen. The dynamics analysis of the

* Corresponding author.

E-mail address: isa.baba@neu.edu.tr (I.A. Baba).

Table 1
Description of variables and parameters of model (2.1).

Parameter	Description
Λ	Recruitment rate
$\frac{1}{\mu}$	Average life expectancy of the population
β_1	Infection rate of strain 1
β_2	Infection rate of strain 2
β_3	Infection rate of strain 3
$\frac{1}{\gamma_1}$	Average infection period of strain 1
$\frac{1}{\gamma_2}$	Average infection period of strain 2
$\frac{1}{\gamma_3}$	Average infection period of strain 3
α	Parameter that measures the psychological or inhibitory effect of the population $\alpha \in [0, 1]$
r_1	Rate of vaccination with strain 1
v_1	Infection induced death rate of strain 1
k	Transmission coefficient of vaccinated individuals V1 to strain 3

pathogen–host interactions with multiple strains has been considered by many researchers [5–7]. It was also shown that, any strain with the largest basic reproduction ratio will automatically outperform the other strains, thereby eliminating them [9]. Mechanisms like co-infection, super - infection, mutation, exponential growth of the host population, and vaccination promote coexistence among the strains [10–14,27–30]. Since new strains are still evolving, there is need for more studies on the coexistence of multiple strains.

In this paper we consider three strains of influenza ($I_1, I_2,$ and I_3) where we have vaccine for strain1 (V_1) only, and population has enough awareness of strain 2. There is neither vaccine nor awareness for strain 3. Our main aim is to mathematically analyze the effect of the vaccine for strain 1 and awareness of strain 2 on the dynamics of strain 3. It is also in our aim to study the coexistence of these three strains.

This paper is organized as follows; Section 1 is the introduction. In Section 2, we formulate the model. Section 3 is the study of existence of equilibria and the computation of basic reproduction numbers. Stability analysis of the equilibria follows in Section 4, and finally Section 5 is discussion of the results with numerical simulations to support the analytic results.

2. Formulation of the model

Three strain epidemic model with vaccination consisting of system of six ordinary differential equations is considered. The compartments are $S(t), I_1(t), V_1(t), I_2(t), I_3(t)$ and $R(t)$ which denotes the population of susceptible, infective with respect to strain 1, vaccine of strain 1, infective with respect to strain2, infective with respect to strain 3 and removed individuals at time t , respectively.

We assume that there is a constant recruitment into susceptible class through birth and immigration, 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 the following system of ordinary differential equations:

$$\begin{aligned} \frac{dS}{dt} &= \Lambda - \left(\beta_1 I_1 + \frac{\beta_2 I_2}{1 + \alpha S} + \beta_3 I_3 + \theta_1 \right) S \\ \frac{dV_1}{dt} &= r_1 S - (k I_3 + \mu) V_1 \\ \frac{dI_1}{dt} &= \beta_1 I_1 S - \theta_2 I_1 \\ \frac{dI_2}{dt} &= \frac{\beta_2 I_2 S}{1 + \alpha S} - \theta_3 I_2 \\ \frac{dI_3}{dt} &= (k V_1 + \beta_3 S) I_3 - \theta_4 I_3 \end{aligned}$$

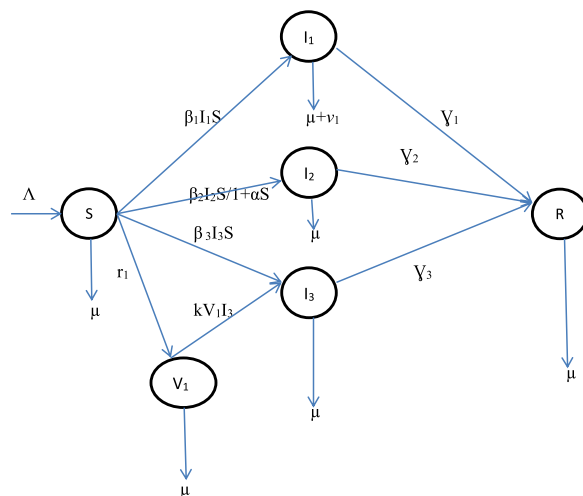


Fig. 1. Transfer diagram of model (1).

$$\frac{dR}{dt} = \gamma_1 I_1 + \gamma_2 I_2 + \gamma_3 I_3 - \mu R \tag{1}$$

where,

$$\theta_1 = \mu + r_1, \quad \theta_2 = \mu + v_1 + \gamma_1, \quad \theta_3 = \mu + \gamma_2, \quad \theta_4 = \mu + \gamma_3,$$

and

$$N = S + V_1 + I_1 + I_2 + I_3 + R$$

3. Equilibria, boundedness, and basic reproduction ratio

3.1. Existence of equilibrium solutions

Setting the system (1) to zero and solving the equations simultaneously we obtain the following equilibrium solutions;

$$E_1 = \left\{ S = \frac{\Lambda}{\theta_1}, \quad V_1 = \frac{\Lambda r_1}{\theta_1 \mu}, \quad I_1 = 0, \quad I_2 = 0, \quad I_3 = 0 \right\}$$

Since all the parameters in this equilibrium are either greater than or equal to zero, the equilibrium solution always exist.

$$E_2 = \left\{ S = \frac{\theta_2}{\beta_1}, \quad V_1 = \frac{\theta_2 r_1}{\beta_1 \mu}, \quad I_1 = \frac{-\Lambda \beta_1 + \theta_1 \theta_2}{\theta_2 \beta_1}, \quad I_2 = 0, \quad I_3 = 0 \right\}$$

This equilibrium solution exists only when $I_1 \geq 0$, that is when $\frac{\Lambda \beta_1}{\theta_1 \theta_2} \geq 1$.

$$E_3 = \left\{ S = \frac{-\theta_3}{-\beta_2 + \alpha \theta_3}, \quad V_1 = \frac{-\theta_3 r_1}{\mu(-\beta_2 + \alpha \theta_3)}, \quad I_1 = 0, \right. \\ \left. I_2 = \frac{-\Lambda \beta_2 + \alpha \Lambda \theta_3 + \theta_1 \theta_3}{\theta_2 \beta_1}, \quad I_3 = 0 \right\}$$

This equilibrium solution exists only when $S > 0, V_1 \geq 0,$ and $I_2 \geq 0$

$$S > 0, \quad \text{if } \frac{\beta_2}{\alpha \theta_3} > 1$$

$$V_1 \geq 0, \quad I_2 \geq 0 \quad \text{if } \frac{\beta_2}{\alpha \theta_3} \geq 1$$

$$E_4 = \left\{ S = \frac{\Lambda}{\beta_3 I_3 + \theta_1}, \quad V_1 = \frac{r_1 \Lambda}{(\beta_3 I_3 + \theta_1)(k I_3 + \mu)}, \quad I_1 = 0, \right. \\ \left. I_2 = 0, \quad I_3 = \frac{1}{2} \frac{\alpha k \beta_3 - \mu \theta_4 \beta_3 - k \theta_1 \theta_4 \pm \sqrt{\Omega_1}}{\theta_4 \beta_3 k} \right\}$$

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