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# Dynamical Model of Influenza Disease with Vaccination

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***Abstract:-*** Influenza disease is generally found in Thailand. It is a viral infection of the respiratory system, including the nose, throat, and lungs. It can be contacted between people. The influenza transmission model with vaccination is considered in this study. We separated the human population into susceptible, exposed, infectious and recovered human populations. We analyze the dynamical model by using standard dynamical modeling method. The equilibrium states are found. The basic reproduction number is found. The local stability for each equilibrium states are determined. The numerical simulations for our dynamical model are shown.

***Keywords****: Dynamical model, Influenza disease, Vaccination, Standard dynamical method.*

## I. INTRODUCTION

Influenza is a respiratory infectious disease caused by influenza virus. There are three different types of human influenza virues: A, B and C. Influenza A viruses infect various mammals including humans, birds and pigs, whereas influenza B and C viruses mainly infect humans [1]. Influenza A viruses cause seasonal epidemics and occasional pandemics in humans, particularly H1N1 subtype of influenza A is the most important virus, which caused severe pandemics since 1900: the Spanish flu in 1918, the Russian flu pandemic in 1977, and the swine flu pandemic in 2009 [2]. There are also the flu pandemics due to other subtypes of influenza A viruses, the Asian flu in 1957 was global pandemic of influenza A virus subtype H2N2 and the Hongkong flu in 1968 was caused by influenza A subtype H3N2. Human influenza evolves through two types of mechanism of influenza A evolution, antigenic drift and antigenic shift. Antigenic drift describes small and gradual changes in the surface proteins of the virus through random mutational processes. Antigenic shift occurs when the different strains that infect the same cell can reassort genome segments with each other, an animal strain reassorts with a human strain then a novel strain can emerge and becomes adapted to the human to human transmission [3, 4]. Antigenic drift is a major cause of seasonal influenza, annual vaccination is the most effective way to prevent influenza if there is an antigenic match between vaccine strains and circulating strains so the flu vaccines need to be updated annually to match which influenza strains are in circulation [5]. Moreover influenza vaccination also helps to reduce the probability of reassortment [6]. The high risk groups such as pregnant women, young children (excluding young infants), the elderly, people with chronic health conditions and health care workers are recommended to get vaccinated because deaths most commonly occur in high-risk groups [1].

Mathematical modelling is an powerful tool to understand the dynamics of infectious disease influenza, epidemic transmission patterns and effects of prevention the disease through treatment and vaccination. Mathematical models have been created and developed in the presence of up–to–date data. Usman and Siam. [7] extended SIR model by adding T (Treatment) compartment into an influenza epidemic model, T(t) represents the individuals who received the treatment. The Susceptible – Infected – Treatment – Recovered (SITR) model stability is determined by using the Routh – Hurwitz Criterion Method, the primary reproduction number $R_0$ is generated and the dynamics of the model is analyzed by using Next Generation Matrix Method. Numerical simulation results show that the effect of treatment on infected individuals such as medication or vaccination can help to reduce the number of infected individuals. Khalil et al. [8] developed an agent-based model to simulate the spread of pandemic influenza (novel H1N1) in Egypt based on the proposed extension of SIR model states. They propose a stochastic multi-agent model to mimic the daily person-to-person contact of people in a large scale community

affected by a pandemic influenza in Egypt. The proposed model simulates stochastic propagation of pandemic influenza outbreaks, and the impact of the decisions made by the healthcare authorities in population with millions of agents. Alcaraz and León. [9] studied a mathematical model that describes the control measures for influenza A H1N1 epidemics and formulated The SIR epidemic model incorporating vaccination, treatment, quarantine and isolation measures. New compartments, susceptible individuals can be quarantined (QS) and then returned to the pool of susceptible individuals, susceptible individuals can be vaccinated (V) , infected individuals can be treated with antiviral drugs (T) and infected individuals can be isolated (QI) are introduced. They explored qualitatively the control measures of the influenza outbreak using the basic reproduction number of the SIR models and concluded that the SIR model is incorporated vaccination, treatment, quarantine and isolation measures are strategies to reduce the basic reproduction number. Lee et al.[10] Considered the SEIAR model which is an extension of the standard SEIR model by adding A(Asymptomatic) compartment into SEIR model. The proposed model includes seasonal forcing and age structure, and control strategies include vaccination, antiviral treatment, and social distancing. An optimal control problem is formulated by minimizing the incidence of influenza outbreaks while considering intervention costs. The purpose of this study is to minimize the number of infected individuals while considering the cost of each mitigation strategy and suggests some optimal strategies through numerical simulations. S. Mayilvaganan and S. Balamuralitharan [11] considered SEIR numerical model to describe the engendering of Influenza infection among population.

In this study, the formulation of dynamical model for influenza transmission with vaccination are described. The analysis of our dynamical model by standard dynamical model method are shown. The way for reducing the transmission of this disease is introduced.

## II. DYNAMICAL EQUATIONS

We formulate the dynamical model of influenza disease. The people are separated into 2 classes such as the people with vaccination and the people without vaccination. The population are separated into susceptible, exposed, infectious and recovered. The diagram of this disease is shown in this figure.

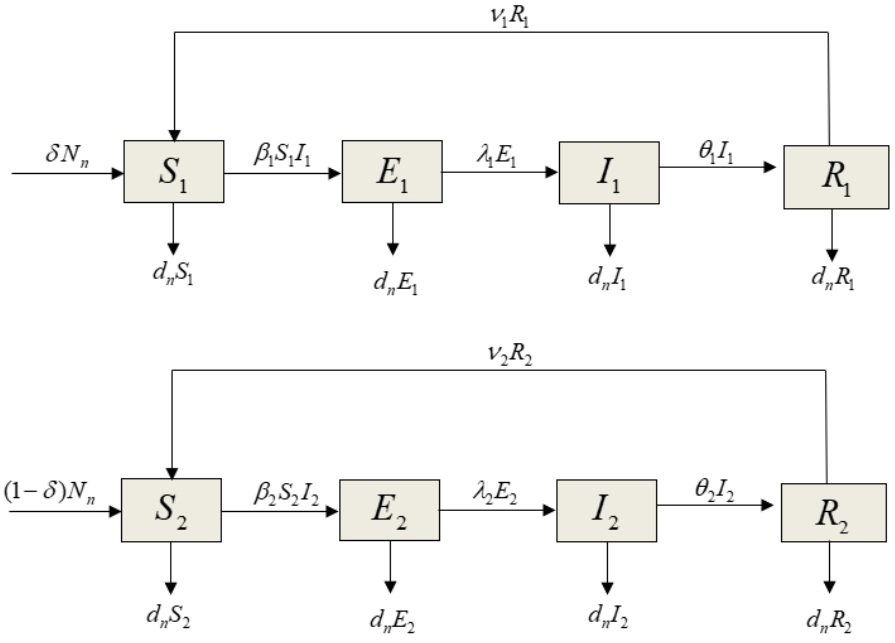



**Figure 1 Diagram of our equations.**

The dynamical model can be described as follows:

$$\frac{dS_1}{dt} = \delta N_h - \beta_1 S_1 I_1 - d_h S_1 + \nu_1 R_1, \quad (1)$$

$$\frac{dE_1}{dt} = \beta_1 S_1 I_1 - (\lambda_1 + d_h) E_1, \quad (2)$$

$$\frac{dI_1}{dt} = \lambda_1 E_1 - (\theta_1 + d_h) I_1, \quad (3)$$

$$\frac{dR_1}{dt} = \theta_1 I_1 - (\nu_1 + d_h) R_1, \quad (4)$$

$$\frac{dS_2}{dt} = (1-\delta) N_h - \beta_2 S_2 I_2 - d_h S_2 + \nu_2 R_2, \quad (5)$$

$$\frac{dE_2}{dt} = \beta_2 S_2 I_2 - (\lambda_2 + d_h) E_2, \quad (6)$$

$$\frac{dI_2}{dt} = \lambda_2 E_2 - (\theta_2 + d_h) I_2, \quad (7)$$

$$\frac{dR_2}{dt} = \theta_2 I_2 - (\nu_2 + d_h) R_2, \quad (8)$$

where

$N_h = N_{h1} + N_{h2}$;

The variables and parameters in our equations are defined as follows:

$N_h$ is the total human population,

$N_{h1}$ is the total human population with vaccination,

$N_{h2}$ is the total human population without vaccination,

$S_1$ is the number of susceptible human population with vaccination,

$E_1$ is the number of exposed human population with vaccination,

$I_1$ is the number of infectious human population with vaccination,

$R_1$ is the number of recovered human population with vaccination,

$S_2$ is the number of susceptible human population without vaccination,

$E_2$ is the number of exposed human population without vaccination,

$I_2$ is the number of infectious human population without vaccination,

$R_2$ is the number of recovered human population without vaccination,

$\delta$ is the rate of vaccination,

$\beta_1$ is the transmission rate of influenza in the human population with vaccination,

$\beta_2$ is the transmission rate of influenza in the human population without vaccination,

$d_h$ is the natural death rate of human population,

$\lambda_1$ is the incubation rate of influenza virus in the human population with vaccination,

$\lambda_2$ is the incubation rate of influenza virus in the human population without vaccination,

$\theta_1$ is the recovery rate of human population with vaccination,

$\theta_2$ is the recovery rate of human population without vaccination,

$\nu_1$ is the rate of change from recovered population to susceptible population with vaccination,

$\nu_2$ is the rate of change from recovered population to susceptible population without vaccination.

## III. ANALYTICAL SOLUTIONS

The equilibrium states are found from setting the difference rate of each human population equal to zero. Thus, we have two equilibrium states.

-The disease-free equilibrium state:

$$(\tfrac{\delta N_h}{d_h}, 0, 0, 0, \tfrac{(1-\delta)N_h}{d_h} 0, 0, 0). \quad (9)$$

-The endemic equilibrium state:

$$(S_1^*, E_1^*, I_1^*, R_1^*, S_2^*, E_2^*, I_2^*, R_2^*)$$

where

$$S_1^* = \frac{(d_h+\lambda_1)(d_h+\theta_1)}{\beta_1\lambda_1}, \tag{10}$$

$$E_1^* = \frac{(d_h+\lambda_1)(d_h+\theta_1)(d_h^2+\beta_1\delta\lambda_1 N_h + d_h\lambda_1\theta_1 + d_h^2(\lambda_1+\theta_1)}{\beta_1 d_h\lambda_1((d_h+\lambda_1)^2+(d_h+2\lambda_1)\theta_1)}, \tag{11}$$

$$I_1^* = \frac{(d_h+\lambda_1)(d_h^2+\beta_1\delta\lambda_1 N_h + d_h\lambda_1\theta_1 + d_h^2(\lambda_1+\theta_1)}{\beta_1 d_h((d_h+\lambda_1)^2+(d_h+2\lambda_1)\theta_1)}, \tag{12}$$

$$R_1^* = \frac{\theta_1(d_h^2+\beta_1\delta\lambda_1 N_h + d_h\lambda_1\theta_1 + d_h^2(\lambda_1+\theta_1)}{\beta_1 d_h((d_h+\lambda_1)^2+(d_h+2\lambda_1)\theta_1)}, \tag{13}$$

$$S_2^* = \frac{(d_h+\lambda_2)(d_h+\theta_2)}{\beta_2\lambda_2}, \tag{14}$$

$$E_2^* = \frac{(d_h+\lambda_2)(d_h+\theta_2)(d_h^2+\beta_2(1-\delta)\lambda_2 N_h + d_h\lambda_2\theta_2 + d_h^2(\lambda_2+\theta_2)}{\beta_2 d_h\lambda_2((d_h+\lambda_2)^2+(d_h+2\lambda_2)\theta_2)}, \tag{15}$$

$$I_2^* = \frac{(d_h+\lambda_2)(d_h^2+\beta_2(1-\delta)\lambda_2 N_h + d_h\lambda_2\theta_2 + d_h^2(\lambda_2+\theta_2)}{\beta_2 d_h((d_h+\lambda_2)^2+(d_h+2\lambda_2)\theta_2)}, \tag{16}$$

$$R_2^* = \frac{\theta_2(d_h^2+\beta_2(1-\delta)\lambda_2 N_h + d_h\lambda_2\theta_2 + d_h^2(\lambda_2+\theta_2)}{\beta_2 d_h((d_h+\lambda_2)^2+(d_h+2\lambda_2)\theta_2)}, \tag{17}$$

We find the local stability of each equilibrium state by standard dynamical modeling method. If all eigenvalues have negative real part, then that equilibrium state will be local stable. The eigenvalues $(\alpha_i)$ are found from solving $\det(J-\alpha_i I)=0,$ where $J$ is the Jacobian matrix and $I$ is the identity matrix and i = 1,2,3,…,8 [10],[11].

-The disease-free equilibrium state:

$(\frac{\delta N_h}{d_h}, 0, 0, 0, \frac{(1-\delta)N_h}{d_h} 0, 0, 0).$ We have eigenvalues which are defined by $\alpha_{1,2} = -d_h, \alpha_3 = -d_h-\lambda_1, \alpha_4 = -d_h-\lambda_2,$ (18)

$$\alpha_{5,6} = \frac{1}{2d_h}\begin{pmatrix} -d_h(2d_h+\lambda_1+\theta_1) \\ \pm\sqrt{d_h(4\beta_1\delta\lambda_1 N_h + d_h(\lambda_1-\theta_1)^2} \end{pmatrix}, \tag{19}$$

$$\alpha_{7,8} = \frac{1}{2d_h}\begin{pmatrix} -d_h(2d_h+\lambda_2+\theta_2) \\ \pm\sqrt{d_h(4\beta_2(1-\delta)\lambda_2 N_h + d_h(\lambda_2-\theta_2)^2} \end{pmatrix}. \tag{20}$$

After our calculation, all of eigenvalues have negative real parts for $R_0 < 1$ where

$$R_0 = \frac{4\beta_1\delta\lambda_1 N_h + d_h(\lambda_1-\theta_1)^2}{d_h(2d_h+\lambda_1+\theta_1)^2} + \frac{4\beta_2(1-\delta)\lambda_2 N_h + d_h(\lambda_2-\theta_2)^2}{d_h(2d_h+\lambda_2+\theta_2)^2}. \tag{21}$$

-The endemic equilibrium state:

The eigenvalues are $\alpha_{1,2} = -d_h$ and the other eigenvalues are solved from

$$((d_h+\alpha+\lambda_1)((d_h+\beta_1 I_1^*+\lambda_1)(d_h+\alpha+\lambda_1)$$
$$-\beta_1\lambda_1 S_1^*)+((d_h+\alpha)(d_h+\beta_1 I_1^*+\lambda_1)$$
$$+2(d_h+\beta_1 I_1^*+\alpha)\lambda_1+\lambda_1^2)\theta_1))$$
$$((d_h+\alpha+\lambda_2)((d_h+\beta_2 I_2^*+\alpha)(d_h+\alpha+\lambda_2)$$
$$-\beta_2\lambda_2 S_2^*)+((d_h+\alpha)(d_h+\beta_2 I_2^*+\alpha)$$
$$+2(d_h+\beta_2 I_2^*+\alpha)\lambda_2+\lambda_2^2)\theta_2)]=0. \quad (22)$$

From computations, we can have all of eigenvalues have negative real parts for $R_0>1,$ where

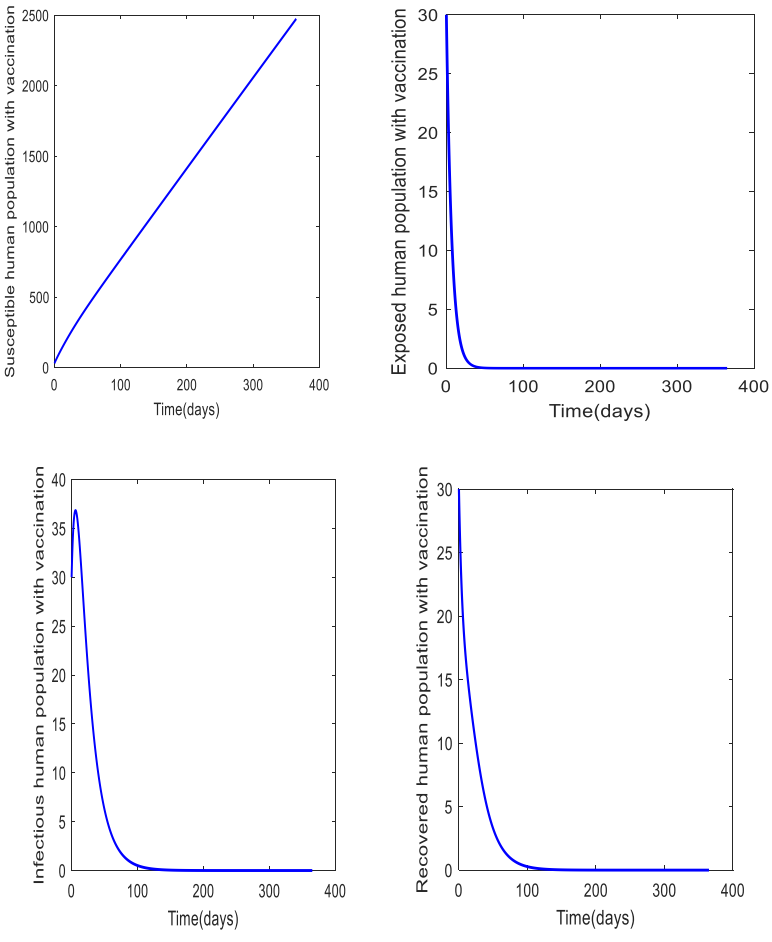
$$R_0=\frac{4\beta_1\delta\lambda_1 N_h+d_h(\lambda_1-\theta_1)^2}{d_h(2d_h+\lambda_1+\theta_1)^2}$$
$$+\frac{4\beta_2(1-\delta)\lambda_2 N_h+d_h(\lambda_2-\theta_2)^2}{d_h(2d_h+\lambda_2+\theta_2)^2}.$$

## IV. NUMERICAL SIMULATIONS

We simulate the numerical solutions by using the real parameters and from references [12-16].

**For the disease free equilibrium state:**

$$\delta=0.65; N_h=10; \beta_1=0.0000000002; \beta_2=0.0000000008;$$
$$d_h=1/(365*70); \lambda_1=\frac{1}{7}; \lambda_2=\frac{1}{7}; \theta_1=\frac{1}{20}; \theta_2=\frac{1}{20}; R_0=0.47.$$



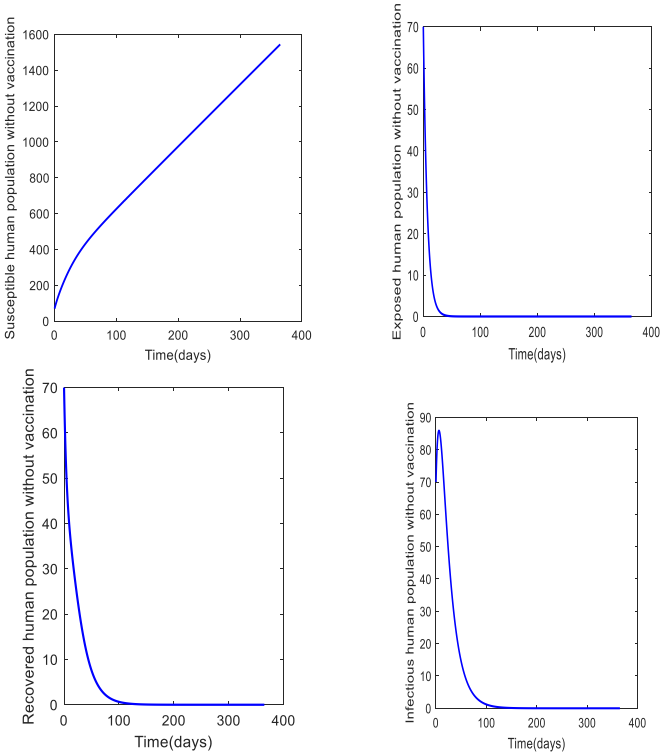
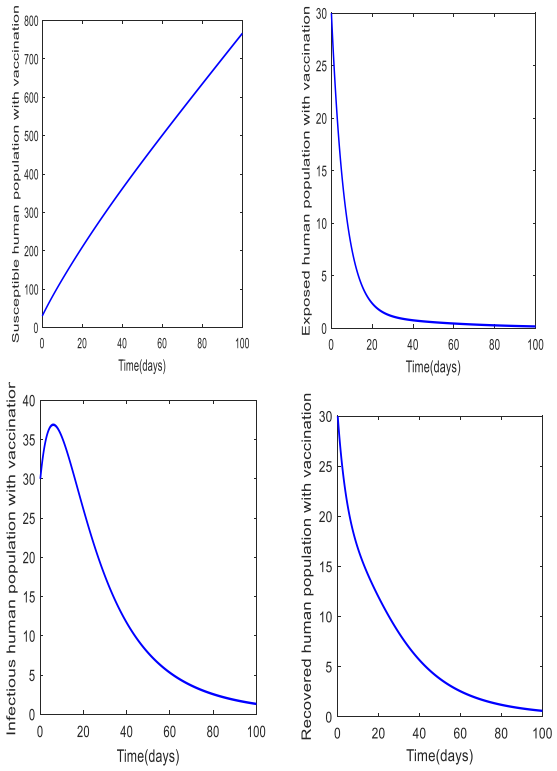



**Figure 2 Time series of each population for the disease free equilibrium state.**

**For the endemic equilibrium state:**

$\delta = 0.65; N_h = 10; \beta_1 = 0.00002; \beta_2 = 0.00008;$

$d_h = 1/(365*70); \lambda_1 = \frac{1}{7}; \lambda_2 = \frac{1}{7}; \theta_1 = \frac{1}{20}; \theta_2 = \frac{1}{20}; R_0 = 161.$



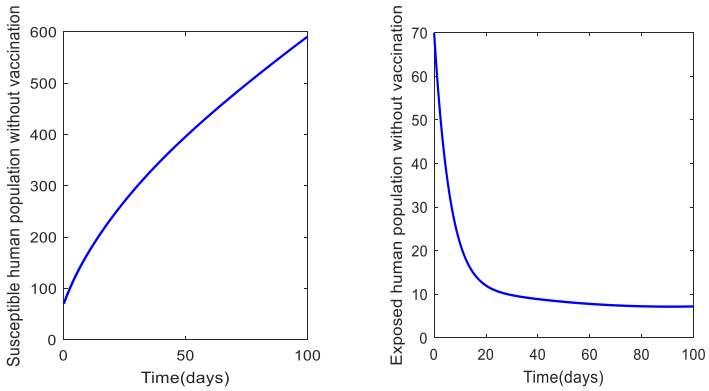



**Figure 3 Time series of each population for the endemic equilibrium state.**

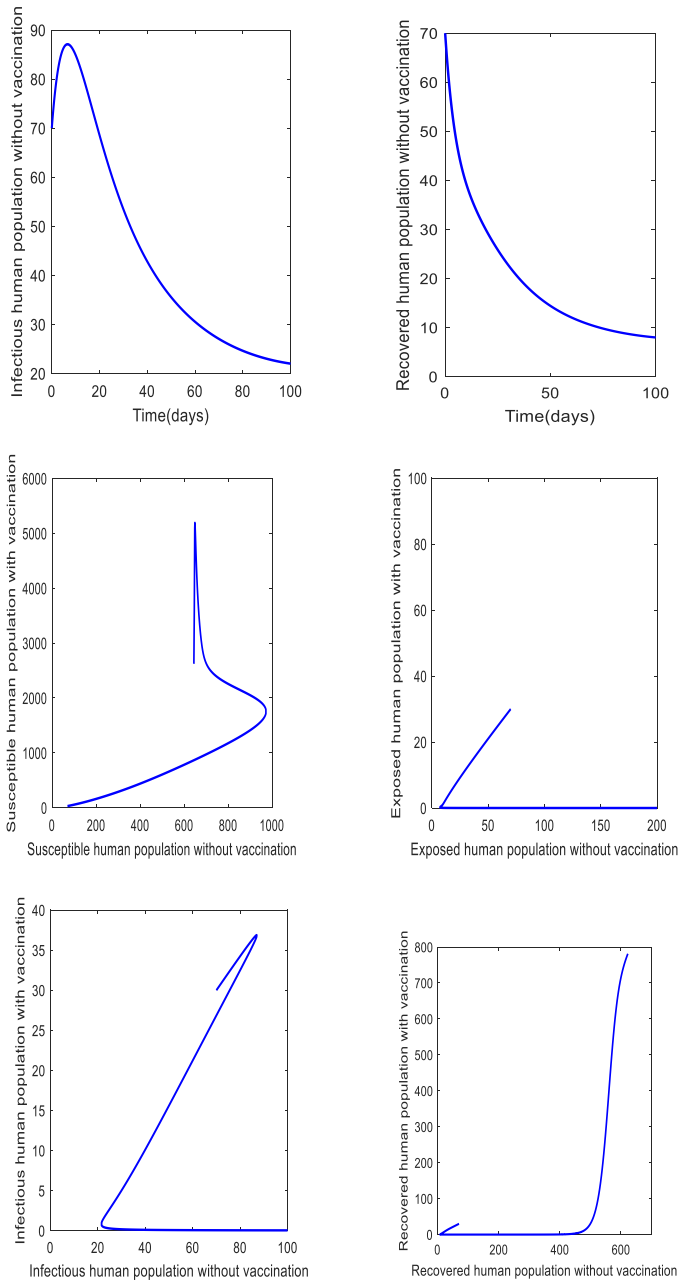
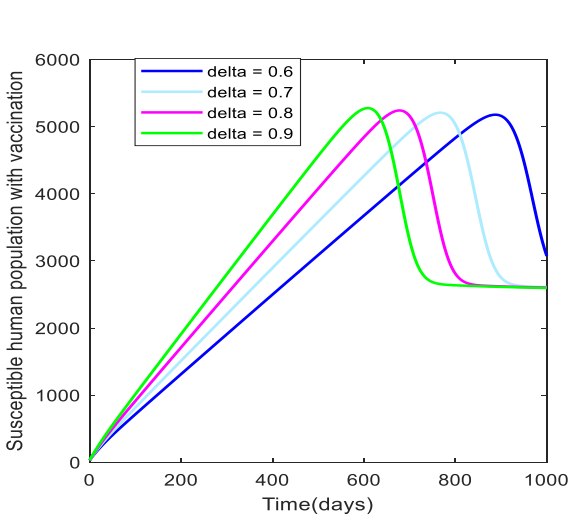
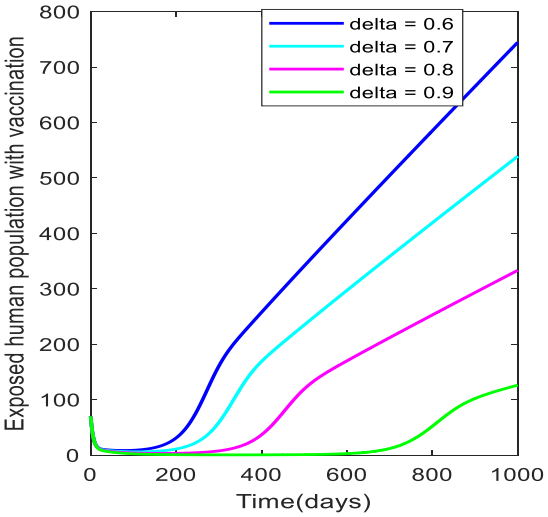
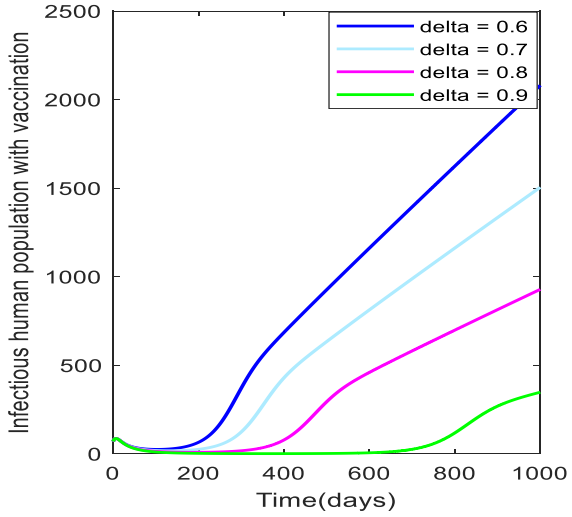


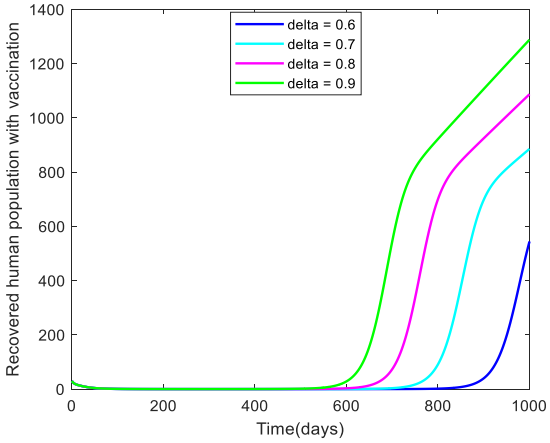

**Figure 4 The dynamical change for each population for the endemic equilibrium state.**

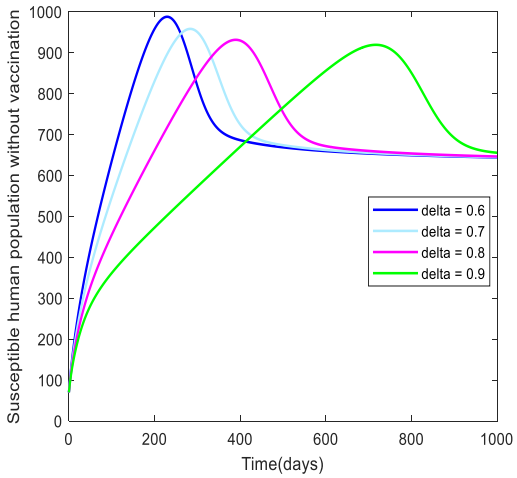
We can see that the solutions oscillate to the disease free equilibrium state (166075,0,0,0,89425,0,0,0) for $R_0 = 0.47$ as shown in figure 2. For $R_0 = 161.$ the solutions oscillate to the endemic equilibrium state (2502.64,33699.49, 96208.95,33663.91,625.66,18294.61, 52229.435, 18275.29) as shown in figure 3 and figure4.

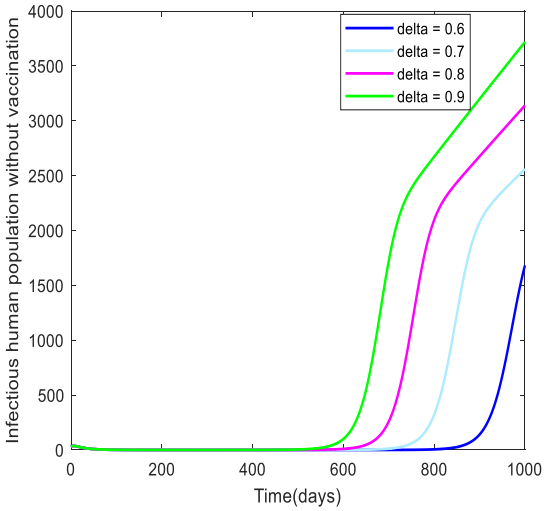


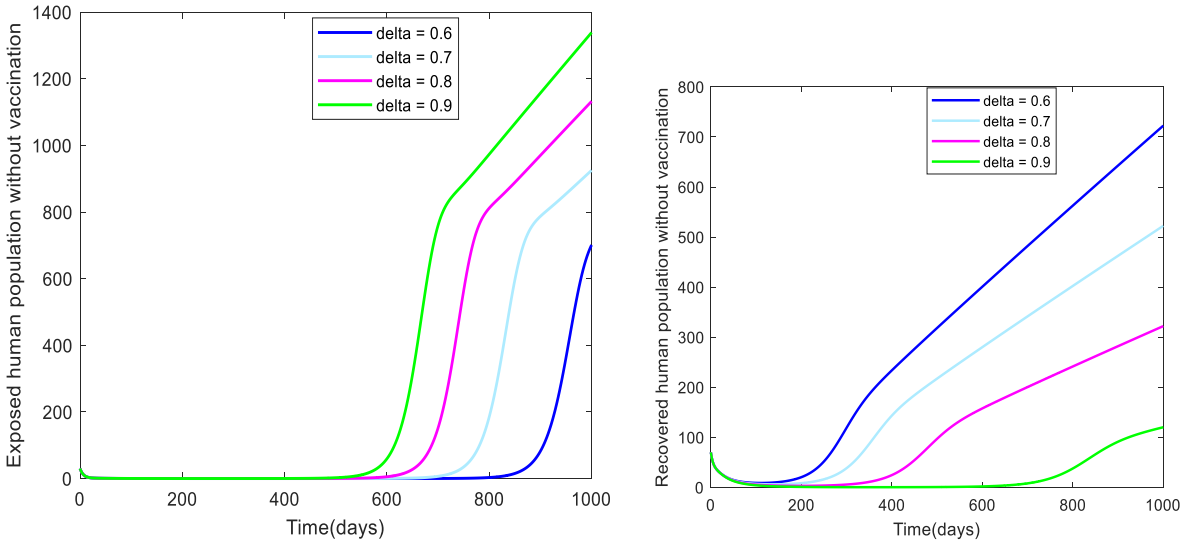



**Figure 4 Time series of each population for the different rate of vaccination.**

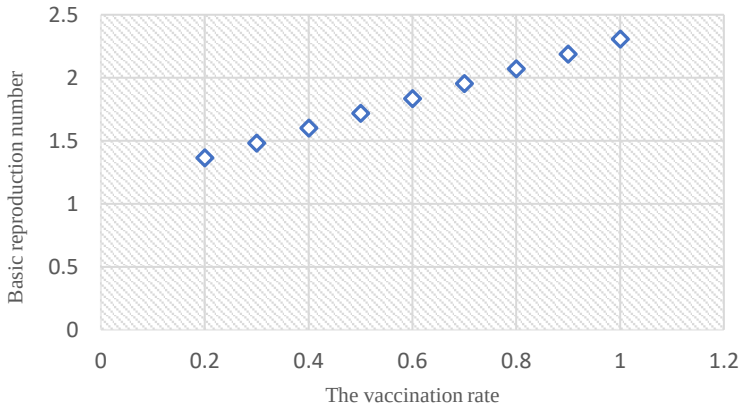
We can see that when the rate of vaccination is increased, the susceptible, exposed and infectious human population with vaccinations are decreased but the recovered human population with vaccinations is increased. But the susceptible, exposed and infectious human population without vaccinations are increased and the recovered human population without vaccinations is decreased when the rate of vaccination is increased.

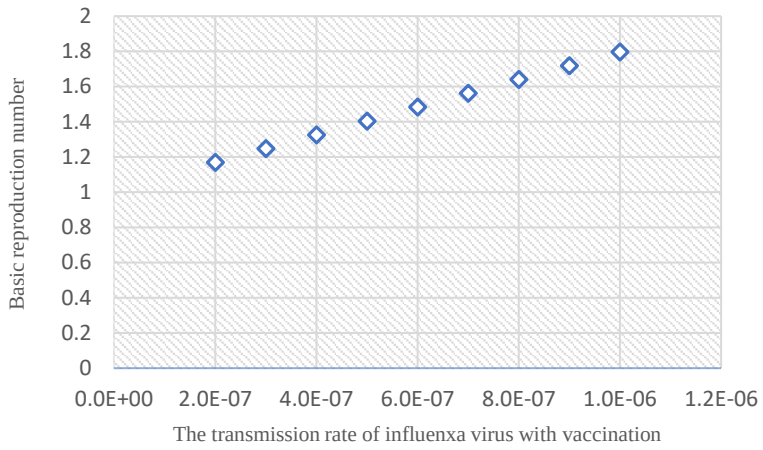
## V. DISCUSSION AND CONCLUSION

The transmission of influenza disease with vaccination are considered by using dynamical model. The condition for local stability is

$$R_0 = \frac{4\beta_1\delta\lambda_1 N_h + d_h(\lambda_1-\theta_1)^2}{d_h(2d_h+\lambda_1+\theta_1)^2} + \frac{4\beta_2(1-\delta)\lambda_2 N_h + d_h(\lambda_2-\theta_2)^2}{d_h(2d_h+\lambda_2+\theta_2)^2}.$$

If $R_0 < 1$, the disease free equilibrium state is local stability. The endemic equilibrium state is local stability for $R_0 > 1$. We can see that the basic reproduction number is increased when the vaccination rate and transmission rates are increased as we see in figure 5.





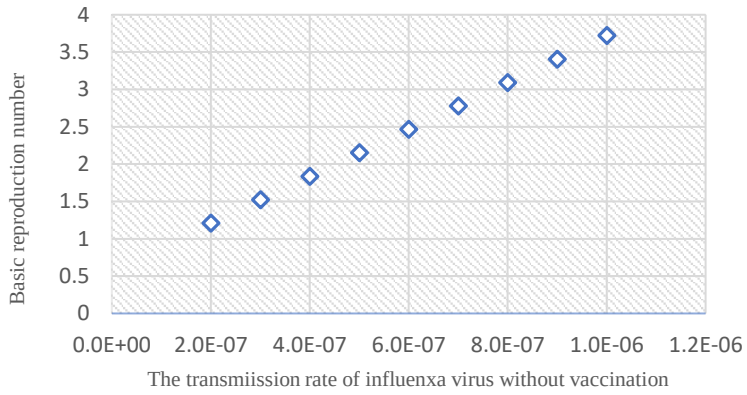




**Figure 5 The basic reproduction rate for the difference rate of vaccination and transmission**

We can see that vaccination rates influence to the transmission rate of influenza virus. If we have vaccination for influenza virus, the transmission of this disease will be introduced. The influenza vaccine contains 3 strains of influenza, divided into 2 strains of type A, H1N1 and H3N2, and 1 strain of type B. The influenza vaccine has changes in the composition of the virus strains that will be contained in every vaccine. Currently, it is recommended that all pregnant women receive the influenza vaccine. It must be an inactivated vaccine. Immunity from the flu will appear after 6-12 months. it's best to get vaccinated every year. This is because the incubation period for influenza is very short. It is necessary to have a sufficiently high immune system when the infection enters the body. Vaccination once a year provides immunity levels.

## ACKNOWLEDGEMENTS

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