Model for the Transmission of Influenza Pandemic Due to a New-Strain of the H1N1 Influenza a Virus with the Risk of Infection in Human

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ABSTRACT

A New-strain of the H1N1 Influenza A Virus is transmitted between the people through coughing and sneezing. The virus spreads when droplets from a cough or sneeze of an infected person are propelled through the air and deposited on the mouth or nose of people nearby. This virus can also be contacted by touching something, contaminated with flu viruses and then touching their eyes. We study the transmission of this disease by constructing the mathematical model. The model is formulated by dividing the human into 5 groups such that **S**usceptible, **E**xposed, **I**nfectious, **Q**uarantine and **R**ecovered classes. The contact between risk and non-risk groups is considered. Analysis of our dynamical model is done by using standard dynamical modeling method. The analytical and numerical results are given.

KEYWORDS: Basic reproductive number, Influenza A virus, model, risk, Routh-Hurwitz, SEIQR model, standard dynamical modeling method,

INTRODUCTION

H1N1 virus transmission is usually found in many countries of the world. The most active areas of pandemic influenza virus transmission currently are in parts of Southeast Asia,West Africa,and in tropical zone of the Americas [1]. Influenza A, influenza B and influenza C are sub three types of Influenza virus. Three types of influenza can cause human flu. Influenza A viruses also infect both pigs and birds, influenza C virus infects pigs but do not infect birds. When influenza virus from different species infects pigs, the virus can be reassortment, a process through two or more influenza viruses can swap genes, produce new and dangerous strains [2]. When reassortment occurs, the emergent virus will have some gene segments from each of the infecting parent viruses and may have different characteristics than either of the parental viruses. It has been determined that the swine flu strain contains genes from five different flu viruses: North American swine influenza, North American avian influenza, human influenza and two swine influenza viruses typically found in Asia and Europe [3]. Over the years, different variations of swine flu viruses have emerged. At this time, there are four main influenza A subtypes that have been isolated in pigs: H1N1, H1N2, H3N2, and H3N1. However, most of the recently isolated influenza virus from pigs is H1N1 virus [4]. The H1N1 influenza virus is "very unstable", meaning it could mix and swap genetic material (reassortment) when exposed to other viruses, whereas a stable (seasonal flu) virus is less likely to take on genetic material. The H1N1 swine flu virus is a human virus spread by people and not by pigs. The only way to get the new swine flu is from another person.The cross–species infections (swine virus to man or human flu virus to pigs) have remained in local areas and have not caused national or worldwide infections in either pigs or humans. The symptoms of H1N1 patients are fever, cough, sore throat, body aches, headache, chills and fatigue, diarrhea and vomiting (may possible) In children, signs of severe disease include apnea, tachypnea, dyspnea, cyanosis, dehydration, altered mental status, and extreme irritability[5],[6]. The virus can transmit when a person touches droplets on surface and then touches their own mouth or nose before washing their hands. After infection it usually takes 1 to 4 days before each person becomes ill. H1N1 cases can start spread flu germs up to a day before symptoms start, and for up to seven days after getting sick [7]. Seasonal influenza occurs every year and the viruses change in each year, but many people have some immunity to the circulating virus that helps limit infections. By contrast, the pandemic swine flu virus was a new virus when it emerged and most people had no or little immunity to it. Therefore, vaccines from human seasonal flu would not provide protection from H1N1swine flu viruses. A study at the CDC published in May 2009 found that children had no preexisting immunity to the new strain but that adults, particularly those over 60, had some degree of immunity. Children showed no cross-reactive antibody reaction to the new strain, adults aged 18 to 64 had 6-9%, and older adults 33%.New vaccines against H1N1 virus are made by growing virus particles in eggs. A serious side effect to vaccines can occur in people who are allergic to eggs; these people should not get flu vaccines. Individuals with active infections or diseases of the nervous system are also not recommended to get flu vaccines. Kids under age 10 years old will need two vaccinations, given apart three weeks [8]. The people who have already been infected with the virus will not receive the vaccine.

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Neil M Ferguson and et al. [9] formulated themodel of influenza transmission to simulate theimpact of neuraminidase inhibitor therapy on infectious rates and transmission of drug-resistant viral strains. D. Klinkenberg, A. Everts-van der Wind and et al. [10] presented a model of CSFV transmission between pig herds which quantifies the effect of control strategies with and without vaccination and estimate the model parameters from data of the 1997/1998 CSFV epidemic in the Netherlands. Fraser et al. [11] constructed the dynamics of influenza A (H1N1) inthe human population, but they did not include cross-species transmission. In 2010, P.Pongsumpun [12] formulated the dynamical model of swine flu transmission of H1N1 but the contact rate between risk and non-risk humans was not considered. In this study, H1N1 virus transmission is studied by constructing the mathematical model considering the chance of getting infected with this disease. The remainder of the paper is organized as follows: In section II, Model equations are given. In section III, Analytical results of our model equations are shown. In section IV, Numerical results are presented to confirm analytical results. Finally, in section IV, Discussion and conclusion are given.

MODEL EQUATIONS

In this study, we consider the transmission of H1N1 between two population groups; risk and non-risk groups. Each group is divided into four classes such as susceptible,exposed, infectious, quarantine and recovered classes.We define the variables as follows:

$S_i(t)$ be the number of susceptible human class i^{th} at time t ,

$E_i(t)$ be the number of exposed human class i^{th} at time t ,

$I_i(t)$ be the number of infectious human class i^{th} at time t ,

$Q_i(t)$ be the number of quarantine human class i^{th} at time t ,

$R_i(t)$ be the number of recovered human class i^{th} at time t;

where i = 1 and 2 denote risk and non-risk classes, respectively. The idea of formulating our model is given in fig.1.
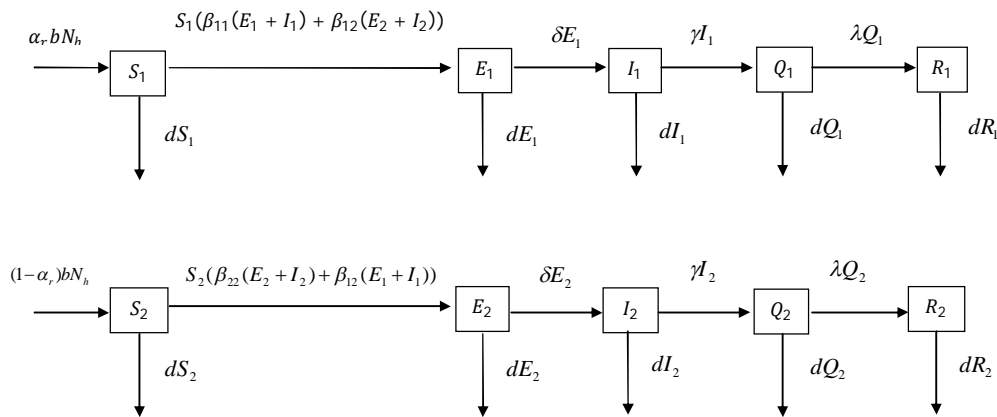

Fig.1 Transmission diagram of H1N1

The dynamical equations are described as follows:
For the risk human class:

$$\frac{d}{dt}S_1(t)=\alpha_r bN_h - S_1(t)(\beta_{11}(E_1(t)+I_1(t))+\beta_{12}(E_2(t)+I_2(t)))-dS_1(t), \qquad (1)$$

$$\frac{d}{dt}E_1(t)=S_1(t)(\beta_{11}(E_1(t)+I_1(t))+\beta_{12}(E_2(t)+I_2(t)))-(\delta+d)E_1(t), \qquad (2)$$

$$\frac{d}{dt}I_1(t)=\delta E_1(t)-(\gamma+d)I_1(t), \qquad (3)$$

$$\frac{d}{dt}Q_1(t)=\gamma I_1(t)-(\lambda+d)Q_1(t), \qquad (4)$$

$$\frac{d}{dt}R_1(t) = \lambda Q_1(t) - dR_1(t) \tag{5}$$

For the non-risk human class:

$$\frac{d}{dt}S_2(t) = (1-\alpha_r)bN_h - S_2(t)(\beta_{22}(E_2(t)+I_2(t)) + \beta_{12}(E_1(t)+I_1(t))) - dS_2(t), \tag{6}$$

$$\frac{d}{dt}E_2(t) = S_2(t)(\beta_{22}(E_2(t)+I_2(t)) + \beta_{12}(E_1(t)+I_1(t))) - (\delta + d)E_2(t), \tag{7}$$

$$\frac{d}{dt}I_2(t) = \delta E_2(t) - (\gamma + d)I_2(t), \tag{8}$$

$$\frac{d}{dt}Q_2(t) = \gamma I_2(t) - (\lambda + d)Q_2(t), \tag{9}$$

$$\frac{d}{dt}R_2(t) = \lambda Q_2(t) - dR_2(t). \tag{10}$$

where the parameters are defined as follows:

b is the birth rate of human populations,

α_r is the risk probability of human populations to be infected with H_1N_1,

β_{11} is the contact rate of H_1N_1 between risk human classes,

β_{12} is the contact rate of H_1N_1 between risk and non-risk human classes,

β_{22} is the contact rate of H_1N_1 between non-risk human classes,

δ is the rate at which exposed human change to be infectious human,

γ is the rate at which infectious human change to be quarantine human,

λ is the rate at which quarantine human change to be recovered human,

N_h is the total human population,

d is the death rate of human population.

We define N_1 is the total risk human class, N_2 is the total non-risk human class and N_h is the total population. Suppose that the total risk group, non-risk group and total population are constant. So rate of change for each group equals to zero. We obtain the relations as follows:

$b = d, N_1 = \alpha_r N_h$ and $N_2 = (1-\alpha_r)N_h$.

We normalize our model equations by letting

$s_j = S_j / N_j, e_j = E_j / N_j, i_j = I_j / N_j, q_j = Q_j / N_j, r_j = R_j / Nj \quad j = 1,2$. The reduced equations become

$$\frac{d}{dt}s_1(t) = \alpha_r b(1 + \frac{N_2}{N_1}) - (d + \beta_{11}(e_1 + i_1)N_1 + \beta_{12}(e_2 + i_2)N_2)s_1, \tag{11}$$

$$\frac{d}{dt}e_1(t) = (\beta_{11}(e_1 + i_1)N_1 + \beta_{12}(e_2 + i_2)N_2)s_1 - (d + \delta)e_1, \tag{12}$$

$$\frac{d}{dt}i_1(t) = \delta e_1 - (d + \gamma)i_1, \tag{13}$$

$$\frac{d}{dt}q_1(t) = \gamma i_1 - (d + \lambda)q_1, \tag{14}$$

$$\frac{d}{dt}s_2(t) = b(1-\alpha_r) + (1-\alpha_r)b\frac{N_1}{N_2} - (d + \beta_{12}(e_1 + i_1)N_1 + \beta_{22}(e_2 + i_2)N_2)s_2, \tag{15}$$

$$\frac{d}{dt}e_2(t) = \beta_{12}(e_1 + i_1)N_1 s_2 + \beta_{22}(e_2 + i_2)N_2 s_2 - (d + \delta)e_2, \tag{16}$$

$$\frac{d}{dt}i_2(t) = \delta e_2 - (d + \gamma)i_2, \tag{17}$$

$$\frac{d}{dt}q_2(t)=\gamma i_2-(d+\lambda)q_2, \tag{18}$$

with the conditions :

$$s_i+e_i+i_i+q_i+r_j=1; j=1,2. \tag{19}$$

ANALYTICAL RESULTS

We use standard dynamical modeling method for analysis our model. To find steady states of our equations, we set the dynamical change of each population class equivalent to zero; ie.

$$\frac{d}{dt}s_i(t)=\frac{d}{dt}e_i(t)=\frac{d}{dt}i_i(t)=\frac{d}{dt}q_i(t)=0, j=1,2.$$

The steady states are given as follows:

i) Disease free steady state: $M_1=(1,0,0,0,1,0,0,0)$ (20)

ii) Disease endemic state: $M_2=(s_1^*,e_1^*,i_1^*,q_1^*,s_2^*,e_2^*,i_2^*,q_2^*)$ (21)

where $s_j^*=\dfrac{b-(b+\delta)e_j^*}{b},e_j^*=\dfrac{(b+\gamma)}{\delta}i_j^*,q_j^*=\dfrac{\gamma}{b+\lambda}i_j^* ; j=1,2$ (22)

and $i_j^* ; j=1,2$ are found by solving equations

$$2(d\delta+(d+\delta)(d+\gamma)i_1^*+(d+\delta+\gamma)(-b\delta+(d+\delta)(d+\gamma)i_1^*)(\alpha_r\beta_1i_1^*+\beta_{12}i_2^*-\alpha_r\beta_{12}i_2^*)N_h)=0 \text{ and} \tag{23}$$

$$2(d\delta+(d+\delta)(d+\gamma)i_2^*+(d+\delta+\gamma)(-b\delta+(d+\delta)(d+\gamma)i_2^*)(\alpha_r\beta_{12}i_1^*+\beta_{22}i_2^*-\alpha_r\beta_{22}i_2^*)N_h)=0 \tag{24}$$

The locally asymptotical stable of each steady state is determined by the sign of eigenvalues for each steady state. If all eigenvalues have negative real parts, then that steady state is local stability [13]. The eigenvalues are obtainedby solving the following characteristic equation

$$\det(J_{Mj}-\lambda I_8)=0; j=1,2. \tag{25}$$

where I_8 is the identity matrix dimension 8 x 8 and J_{M_i} is the *Jacobian* matrix of the steady state $M_i; j=1,2$.

For the disease free steadystate $M_1=(1,0,0,0,1,0,0,0)$, the *Jacobian* matrix is given by

$$J_{M1=}\begin{pmatrix} j_{11} & j_{12} & j_{13} & j_{14} & j_{15} & j_{16} & j_{17} & j_{18} \\ j_{21} & j_{22} & j_{23} & j_{24} & j_{25} & j_{26} & j_{27} & j_{28} \\ j_{31} & j_{32} & j_{33} & j_{34} & j_{35} & j_{36} & j_{37} & j_{38} \\ j_{41} & j_{42} & j_{43} & j_{44} & j_{45} & j_{46} & j_{47} & j_{48} \\ j_{51} & j_{52} & j_{53} & j_{54} & j_{55} & j_{56} & j_{57} & j_{58} \\ j_{61} & j_{62} & j_{63} & j_{64} & j_{65} & j_{66} & j_{67} & j_{68} \\ j_{71} & j_{72} & j_{73} & j_{74} & j_{75} & j_{76} & j_{77} & j_{78} \\ j_{81} & j_{82} & j_{83} & j_{84} & j_{85} & j_{86} & j_{87} & j_{88} \end{pmatrix}$$

where

$j_{11}=-d, j_{12}=j_{13}=-\alpha_r\beta_{11}N_h, j_{14}=j_{15}=0, j_{16}=j_{17}=(-1+\alpha_r)\beta_{12}N_h, j_{18}=0,$

$j_{21}=0, j_{22}=-d-\delta+\alpha_r\beta_{11}N_h, j_{23}=\alpha_r\beta_{11}N_h, j_{24}=j_{25}=0, j_{26}=j_{27}=(1-\alpha_r)\beta_{12}N_h, j_{28}=0,$

$j_{31}=0, j_{32}=\delta, j_{33}=-d-\gamma, j_{34}=j_{35}=j_{36}=j_{37}=j_{38}=0,$

$j_{41}=j_{42}=0, j_{43}=\gamma, j_{44}=-d-\lambda, j_{45}=j_{46}=j_{47}=j_{48}=0,$

$j_{51}=0, j_{52}=-\alpha_r\beta_{12}N_h, j_{53}=-\alpha_r\beta_{12}N_h, j_{54}=0, j_{55}=-d, j_{56}=(-1+\alpha_r)\beta_{22}N_h, j_{57}=(-1+\alpha_r)\beta_{22}N_h, j_{58}=0,$

$j_{61}=0, j_{62}=j_{63}=\alpha_r\beta_{12}N_h, j_{64}=j_{65}=0, j_{66}=-d-\delta+(1-\alpha_r)\beta_{22}N_h, j_{67}=(1-\alpha_r)\beta_{22}N_h, j_{68}=0,$

$j_{71}=j_{72}=j_{73}=j_{74}=j_{75}=0, j_{76}=\delta, j_{77}=-d-\gamma, j_{78}=0,$

$j_{81}=j_{82}=j_{83}=j_{84}=j_{85}=j_{86}=0, j_{87}=\gamma, j_{88}=-d-\lambda$

The characteristic equation is defined by

$$(d + \eta)^2 (d + \lambda + \eta)^2 (\eta^4 + A_3 \eta^3 + A_2 \eta^2 + A_1 \eta + A_0)$$

where

$$A_3 = 4d + 2(\delta + \gamma)\text{-}(\alpha_r (\beta_{11}\text{-}\beta_{22}) + \beta_{22})N_h ,$$

$$A_2 = 6d(d + \delta + \delta^2 + \gamma) + \gamma(4\delta + \gamma)\text{-}(\alpha_r (\beta_{11}\text{-}\beta_{22}) + \beta_{22})(3d + 2(\delta + \gamma))N_h + (\text{-}1 + \alpha_r)\alpha_r ,$$

$$A_1 = 2(d + \delta)(d + \gamma)(2d + \delta + \gamma)\text{-}(\alpha_r (\beta_{11}\text{-}\beta_{22}) + \beta_{22})(3d^2 + \delta^2 + 3\delta\gamma + \gamma^2 + 4d(\delta + \gamma))N_h$$
$$+ 2(\text{-}1 + \alpha_r)\alpha_r (\beta_{12}^2\text{-}\beta_{11}\beta_{22})(d + \delta + \gamma)N_h^2 ,$$

$$A_0 = (d + \delta)^2 (d + \gamma)^2 \text{-}(\alpha_r (\beta_{11}\text{-}\beta_{22}) + \beta_{22})(d + \delta)(d + \gamma)(d + \delta + \gamma)N_h$$
$$+ (\text{-}1 + \alpha_r)\alpha_r (\beta_{12}^2\text{-}\beta_{11}\beta_{22})(d + \delta + \gamma)^2 N_h^2 ,$$

Routh Hurwitz criteria can ensure eigenvalues with negative real parts [13]. If the characteristic equation satisfy Routh Hurwitz criteria, we can say that the steady state is local stability. Thus, this disease free state will be

local stability when $\overline{V}_0 < 1$; where $\overline{V}_0 = \dfrac{(\alpha_r \beta_{11} + \beta_{22}(1\text{-}\alpha_r)N_h)}{2b(2b + \delta + \gamma)}$. (26)

On similarly method, we found that the disease endemic state will be local stability when $\overline{V}_0 > 1$;

NUMERICAL RESULTS

The output of our model are simulated for 2 cases. The parameters are given as follows: b = 1/(365*65) corresponds to the life expectancy of 65 years for human, δ = 1/5 corresponds to the 5 days at which the exposed human can change to be infectious human, γ = 1/10 corresponds to the 10 days at which quarantine human change to be recovered human. The other parameters are arbitrary chosen.
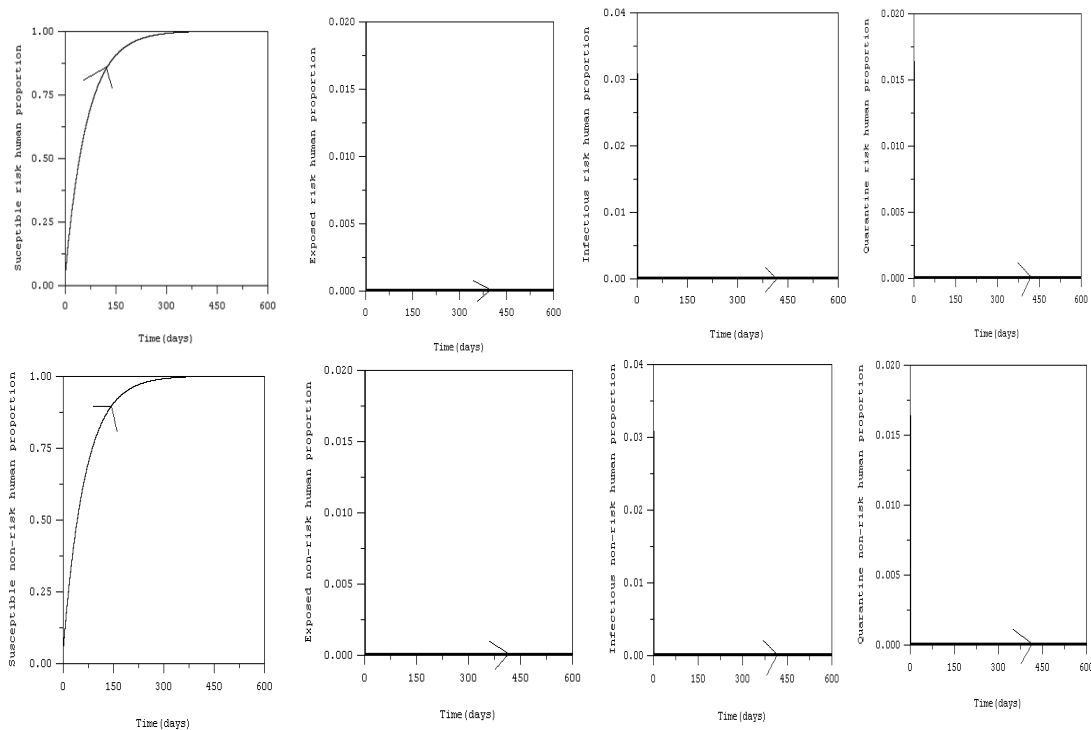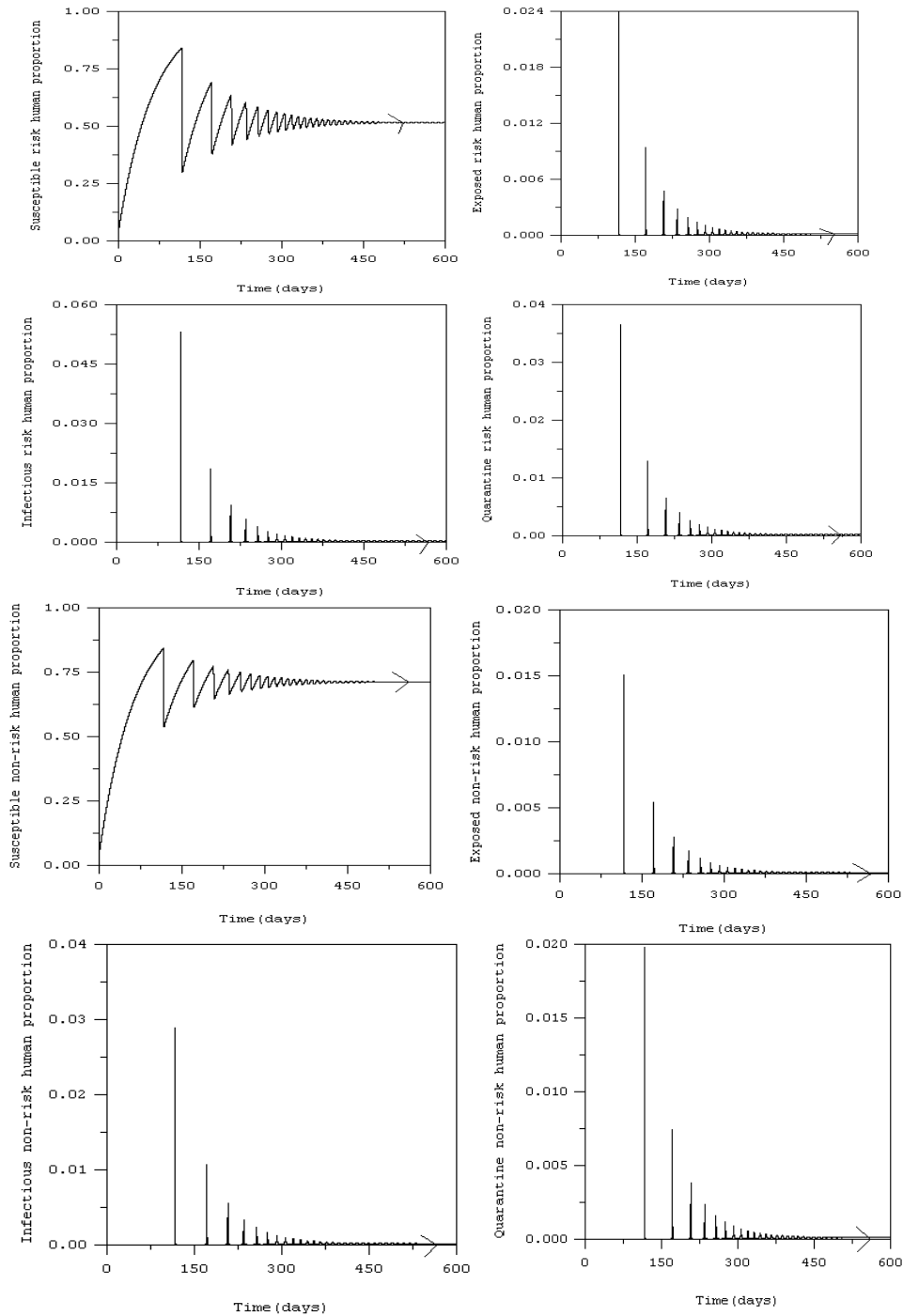
Case1 for $\overline{V}_0 < 1$;

Fig.2 Time series solutions of susceptible, exposed, infectious and quarantine risk and non-risk human classes, respectively. The parameters are $\alpha_r = 0.5$, b =1/(365*65),

$\beta_{11} = 0.000001$, $\beta_{12} = 0.0000008$, $\beta_{22} = 0.0000002$, δ =1/5, γ = 1/10,

$$\lambda = 1/7, N_h = 1,000, \overline{V}_0 = 0.81.$$

Case2 for $\overline{V}_0 > 1$;

Fig.3 Time series solutions of susceptible, exposed, infectious and quarantine risk and non-risk human classes, respectively. The parameters are $\alpha_r = 0.5$, b = 1/(365*65),

$\beta_{11} = 0.0002$, $\beta_{12} = 0.0001$, $\beta_{22} = 0.00002$, $\delta = 1/5$, $\gamma = 1/10$, $\lambda = 1/7, N_h = 1,000, \overline{V}_0 = 400$.

From fig.2 and fig.3, we can see that for $\overline{V}_0 < 1$, the fractions of populations converge to the disease free state $M_1 = (1,0,0,0,1,0,0,0)$. For $\overline{V}_0 > 1$, The fractions of populations oscillate to the endemic state $M_2 = (0.514,0.0001,0.0002,0.00014,0.710,0.00006,0.0001,0.00008)$

DISCUSSION AND CONCLUSION

In this study, we formulate the mathematical model of H1N1 virus and the chance of getting infected with this disease is considered. The threshold condition is defined by

$$\overline{V}_0 = \frac{(\alpha_r \beta_{11} + \beta_{22}(1-\alpha_r)N_h}{2b(2b+\delta+\gamma)}.$$

The basic reproductive number (V_0) is defined as the geometric mean of $\overline{V}_0$ [14]. It represents the number of secondary cases that one casecan produce if introduced into a susceptible person. We compare the solution behaviors when there is the different basic reproductive numbers as shown in fig.4.
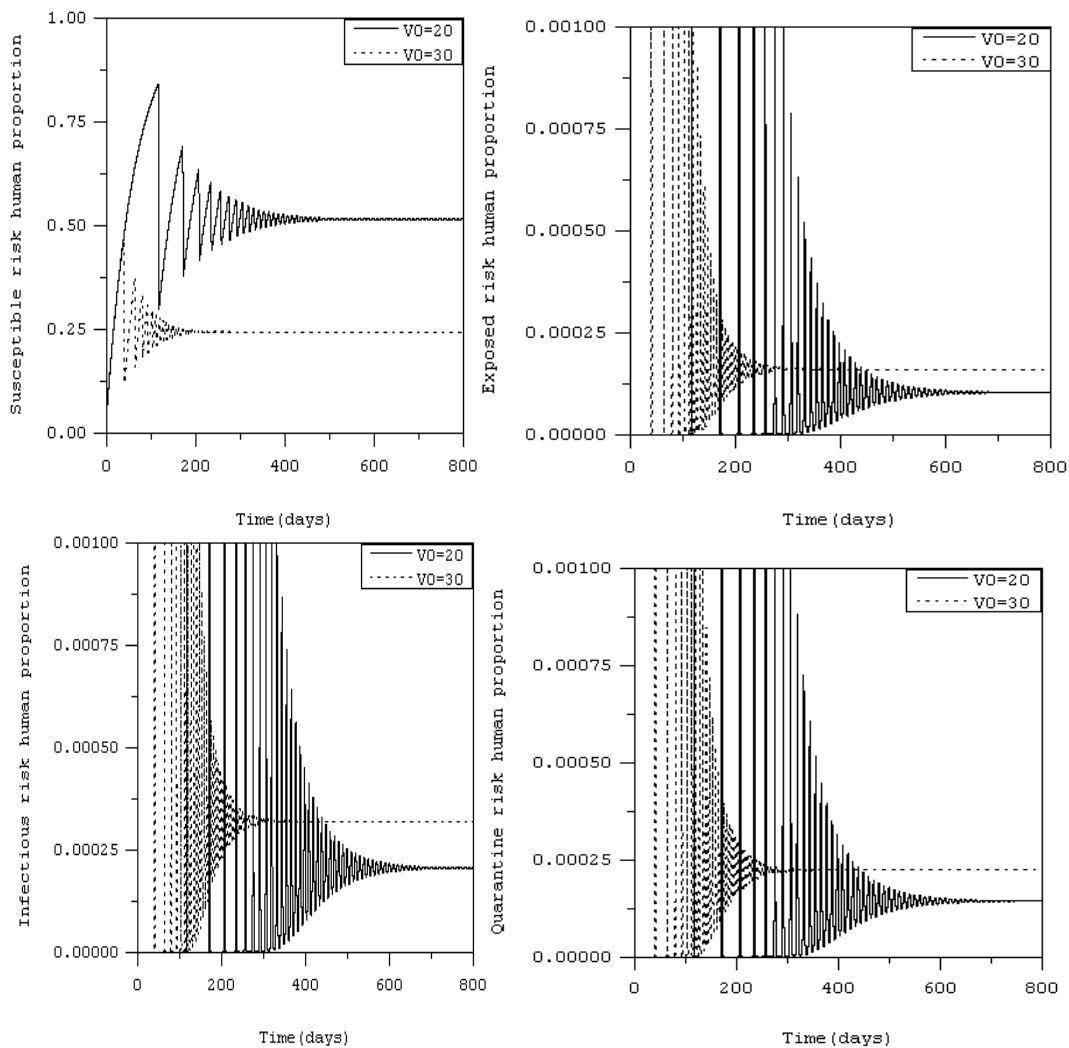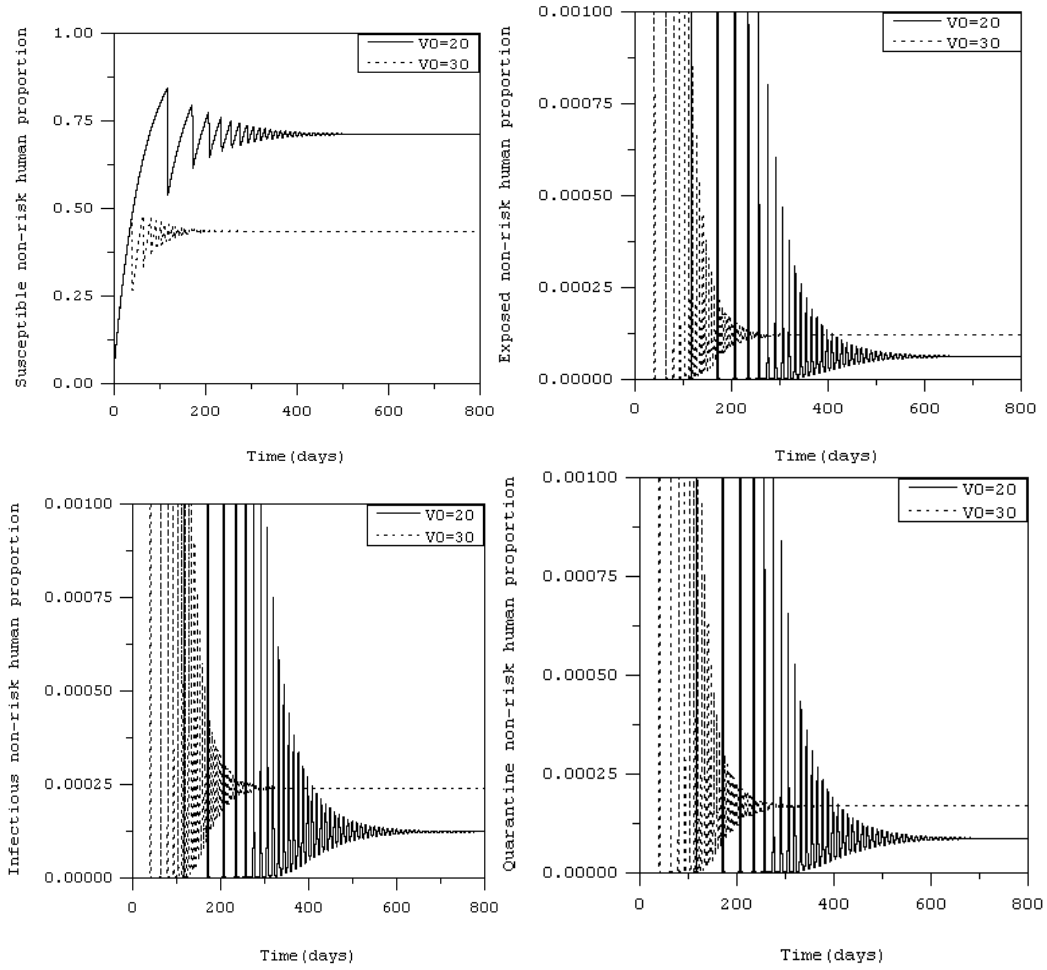
Fig.4 The comparison of solution behaviors when there is the different basic reproductive numbers.
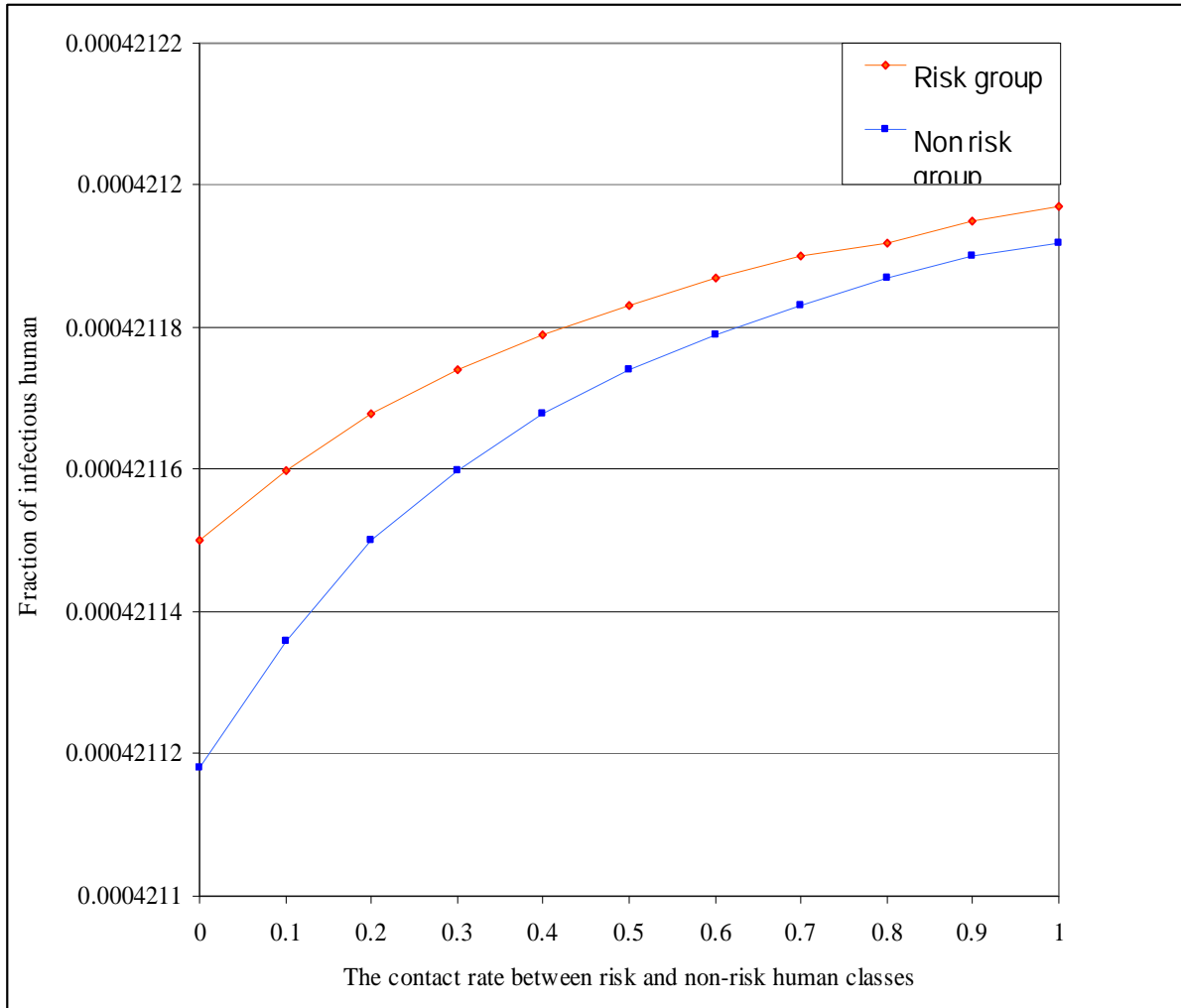
Fig.5 The fraction of infectious human versus the contact rate between risk and non-risk human classes.

From fig.4, we can see that the length of epidemic outburst is shorter and the fraction of populations is higher when the basic reproductive number is bigger. The period of oscillations as they oscillate to the endemic state by means of solutions of the linearized system are calculated, we get 9 days, 5 days for $V_0 = 20$ and $V_0 = 30$, respectively. This means that if the number of secondary infectious cases reproduced from primary cases is higher, then the time for controlling the epidemic outbreak is shorter. From fig.5, we can see that the fraction of infectious risk group is higher than the fraction of infectious non-risk group because the risk group has the higher chance of getting infected. The basic reproductive numbers are used for reducing the transmission of many diseases [15-18].The simulated output of this model should introduce the way for reducing the transmission of this disease.

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