Effect of Vaccination to the Transmission Model of H1N1 Virus

Rattiya Sungchasit and Puntani Pongsumpun

***Abstract*—A model for the transmission of H1N1 virus in a constant human population is studied. Swine flu is a respiratory disease caused by viruses that infect the respiratory tract of pigs, resulting in nasal secretions, a barking cough, decreased appetite, and listless behavior. Swine flu produces most of the same symptoms in pigs as human flu produces in people. H1N1 influenza epidemic reported severe disease caused by a co-infection of dengue virus and influenza H1N1. Both dengue fever and influenza have a wide range of clinical presentations with many overlapping features, and overlap hinders the differentiation of the two diseases. In this paper, we develop the mathematical model which can describe the transmission of this disease. The standard dynamical modelling method is used for analyzing the model. The simulation outputs for the different set of parameters are given in this paper. The results of this study should introduce the way for reducing the outbreak.**

***Index Terms*—H1N1, SEIR model, transmission model, vaccination.**

I. Introduction

Swine influenza is an infection caused by any one of several types of swine influenza viruses. Swine influenza virus (SIV) or swine-origin influenza virus (S-OIV) is any strain of the influenza family of viruses that is endemic in pigs. As known as H1N1, H1N2, H2N1, H911, H3N1, H3N2 and H2N3 [1], [4], [5], [10]-[12]. Swine flu is a respiratory disease caused by viruses that infect the respiratory tract of pigs, resulting in nasal secretions, a barking cough, decreased appetite, and listless behavior.

Swine flu produces most of the same symptoms in pigs as human flu produces in people. Swine flu can last about one to two weeks in pigs that survive. Swine influenza virus was first isolated from pigs in 1930 in the U.S. and has been recognized by pork producers and veterinarians to cause infections in pigs worldwide [1], [4], [5], [9], [11], [14].

In a number of instances, people have developed the swine flu infection when they are closely associated with pigs, likewise, pig populations have occasionally been infected with the human flu infection. In most instances, the cross-species infections (swine virus to man; human flu virus to pigs) have remained in local areas and have not caused national or worldwide infections in either pigs or humans. Unfortunately, this cross-species situation with influenza viruses has had the potential to change. The eight RNA strands from novel H1N1 flu have one strand derived from human flu strains, two from avian (bird) strains, and five from swine strains.

In the 2009, H1N1 influenza epidemic, countries such as Nicaragua, Puerto Rico, and India reported severe disease caused by a co-infection of dengue virus and influenza H1N1. Both dengue fever and influenza have a wide range of clinical presentations with many overlapping features, and overlap hinders the differentiation of the two diseases.[1], [2], [5]-[8], [12], [15], [16].

In this study, we formulated the dynamic model of H1N1 influenza virus by effect of vaccination to the transmission model and analyzed the parameters in our model. Then, we develop the transmission of dengue fever and influenza by formulating the mathematical models. We used SEIR model for analyzing and finding the method to decrease the outbreak of this disease. We studied the transmission of dengue fever and influenza in Thailand by effect of vaccination [1]-[4], [7], [8], [12], [15].

II. Mathematical Model

In this study, we start with the mathematical model for Swine flu (H1N1) of population. The first assumption is that the human population can be separated into 4 classes in human population and 3 vector population which are succeptibles (S), exposed (E) infectious (I) and recovered (R) for human population. Succeptibles (S), exposed (E) infectious (I) for vector population. Based on the transfer diagram which is shown in Fig. 1, we will show the formulation of the SEIR epidemic model which is in a 4 dimensional system for human population and 3 dimensional system for vector population. [2], [3], [7], [8], [16].

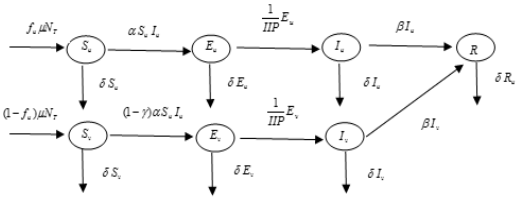

Fig. 1. Dynamical transmission of human and mosquito populations with effect of vaccination.

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Rattiya Sungchasit is with Faculty of Science and Technology, Phuket Rajabhat University Muang District, Phuket, 83000, Thailand (e-mail: tan_sungchasit@hotmail.com, rattiya.s@pkru.ac.th).

Puntani Pongsumpun is with Faculty of Science, King Mongkut's Institute of Technology Ladkrabang,Chalongkrung road, Ladkrabang, Bangkok 10520, Thailand (e-mail: kppuntan@kmitl.ac.th).

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The variables and parameters of our model can be described in the following table.

TABLE I: THE VARIABLES AND PARAMETERS OF OUR MODEL

Variables /Parameters	Definitions
S_u	Number of unvaccinated susceptible human to the transmission of H1N1 virus
E_u	Number of unvaccinated exposed human to the transmission of H1N1 virus
I_u	Number of unvaccinated infectious human to the transmission of H1N1 virus
R	Number of recovered human
S_v	Number of vaccinated susceptible vector to the transmission of H1N1 virus
E_v	Number of vaccinated exposed vector to the transmission of H1N1 virus
I_v	Number of vaccinated infectious vector to the transmission of H1N1 virus
μ	Birth rate of human
N_T	Total number of human
N_v	Total number the vector population
f_u	Fraction of newborn unvaccinated
δ	Death rate of human
α	Transmission rate of H1N1 virus
IIP	Number of Incubation for virus
β	Recovery rate of H1N1 virus
γ	Efficiency of vaccine

From Fig. 1, mathematical model for Swine flu (H1N1) can be described in the following linear system of ordinary differential equations.

From Table I, we considered the dynamics of Swine flu (H1N1) model at the disease free and endemic states. The values for the parameters used in this study.

$$\left.\begin{aligned}
\frac{dS_u}{dt} &= f_u\mu N_T - \alpha S_u I_u - \delta S_u \\
\frac{dE_u}{dt} &= \alpha S_u I_u - \frac{1}{IIP}E_u - \delta E_u \\
\frac{dI_u}{dt} &= \frac{1}{IIP}E_u - \beta I_u - \delta E_u \\
\frac{dR}{dt} &= \beta I_u + \beta I_v - \delta R \\
\frac{dS_v}{dt} &= (1-f_u)\mu N_T - (1-\gamma)\alpha S_u I_u - \delta S_v \\
\frac{dE_v}{dt} &= (1-\gamma)\alpha S_u I_u - \frac{1}{IIP}E_v - \delta E_v \\
\frac{dI_v}{dt} &= \frac{1}{IIP}E_v - \beta I_v - \delta I_v
\end{aligned}\right\} \quad (1)$$

The total human population, N_T is $S_u + E_u + I_u + R$ [12, 13, 14]. The equations for the human compartment are the following equation (1) and The total population of vector population, $N_v = S_v + E_v + I_v$. We assume that there are the constant total number of human populations and of vector populations. Therefore rate of change for total human and vector populations are equivalent to zero. Thus, the birth rate of human and death rate are equivalent.

$$\left.\begin{aligned}
S_u' = \frac{S_u}{N_T},\ E_u' = \frac{I_u}{N_T},\ I_u' = \frac{I_u}{N_T},\ R' = \frac{R}{N_T} \\
S_v' = \frac{S_v}{N_v},\ E_v' = \frac{E_v}{N_v},\ I_v' = \frac{I_v}{N_v}
\end{aligned}\right\} \quad (2)$$

Then, we have the reduced equations as follows:

$$\left.\begin{aligned}
\frac{dS_u'}{dt} &= f_u\mu - \alpha S_u' I_u' - \delta S_u' \\
\frac{dE_u'}{dt} &= \alpha S_u' I_u' - \frac{1}{IIP}E_u' - \delta E_u' \\
\frac{dI_u'}{dt} &= \frac{1}{IIP}E_u' - \beta I_u' - \delta E_u' \\
\frac{dE_v'}{dt} &= (1-\gamma)\alpha S_u' N_T I_u' N_T - \frac{1}{IIP}E_v' - \delta E_v' \\
\frac{dI_v'}{dt} &= \frac{1}{IIP}E_v' - \beta I_v' - \delta I_v'
\end{aligned}\right\} \quad (3)$$

where $R' = 1 - S_u' - E_u' - I_u'$.

The equilibrium points are found by setting the right hand side of equation (3) equal to zero. By doing this, equilibrium points are obtained as follows.

A. The disease free equilibrium is the equilibriums point without infection. $E_0 = (\frac{f_u\mu}{\delta}, 0,0,0,0)$

B. The endemic equilibriums is the equilibrium point with infection.

$$E_1 = (S_u'', E_u'', I_u'', E_v'', I_v'')$$

$$S_u'' = \frac{(\beta+\delta)(1+IIP\,\delta)}{\alpha},$$

$$E_u'' = \frac{IIP\,\delta(\beta+\delta)}{\alpha} - \frac{f_u\,IIP\,\mu}{1+IIP\,\delta},$$

$$I_u'' = \frac{\delta}{\alpha} - \frac{f_u\ \mu}{(\beta+\delta)(1+IIP\,\delta)},$$

$$E_v'' = \frac{IIP\,N_T{}^2(-1+\gamma)(\delta(\beta+\delta)(1+IIP\,\delta) - f_u\,\alpha\,\mu}{\alpha + IIP\,\alpha\,\delta},$$

and

$$I_v'' = N_T{}^2(-1+\gamma)\,(\frac{\delta}{\alpha} - \frac{f_u\,\alpha\,\mu}{(\beta+\delta)(1+IIP\,\delta)}) \quad (4)$$

The local stability of each equilibrium point is

determined by considering the sings of real parts of all eigenvalues. The eigenvalues (ψ) are the solutions of the characteristic equation.

$|J-\psi I|=0$ where J is the Jacobian matrix at the equilibrium point. I is the identity matrix dimension 5X5. If the real parts of all eigenvalues (ψ) are negative then that equilibrium state is locally stable [7,8,9,11,12,13].

i) The disease free state $E_0=(\frac{f_u\mu}{\delta},0,0,0,0)$, the characteristic equation is given by

$$\begin{vmatrix} (-\delta)-\psi & 0 & -(\alpha^*(\frac{f_u\mu}{\delta})) & 0 & 0 \\ 0 & (-(\frac{1}{IIP})-\delta)-\psi & (\alpha^*(\frac{f_u\mu}{\delta})) & 0 & 0 \\ 0 & (\frac{1}{IIP}) & (-(\beta)-(\delta))-\psi & 0 & 0 \\ 0 & 0 & -N_T^2(\frac{f_u\mu}{\delta})\alpha(-1+\gamma) & (-(\frac{1}{IIP})-\delta)-\psi & 0 \\ 0 & 0 & 0 & (\frac{1}{IIP}) & (-(\beta)-(\delta))-\psi \end{vmatrix}=0 \quad (5)$$

We have characteristic equation:

$$\frac{1}{IIP}(\delta+\psi)(\beta+\delta+\psi)(1+IIP\delta+IIP\psi)$$
$$(IIP\delta\ (\beta+\delta+\psi)\ (1+IIP\delta+IIP\psi)-f_u IIp\alpha\mu)=0$$

We obtained the characteristic equation,

$$\psi^5+A_1\psi^4+A_2\psi^3+A_3\psi^2+A_4\psi+A_5=0$$

$$A_1=\frac{2IIP^2\delta+2IIP^3\beta\delta+5IIP^3\delta^2}{IIP^3\delta}$$

$$A_2=\frac{1}{IIP^3\delta}(IIP\delta+4IIP^2\beta\delta+IIP^3\beta^2\delta^2+8IIP^2\delta^2$$
$$+8IIP^3\beta\delta^2+10IIP^3\delta^3-f_u IIP^2\alpha\mu)$$

$$A_3=\frac{1}{IIP^3\delta}(2IIP\beta\delta+2IIP^2\beta^2\delta+3IIP\delta^2+$$
$$12IIP^2\beta\delta^2+3IIP^3\beta^2\delta^2+12IIP^2\delta^3+$$
$$12IIP^3\beta\delta^2+10IIP^3\delta^4-f_u IIP\alpha\mu-$$
$$f_u IIP^2\alpha\mu\beta-3f_u IIP^2\alpha\mu\beta)$$

$$A_4=\frac{1}{IIP^3\delta}(2IIP\beta^2\delta+4IIP\beta\delta^2+4IIP^2\beta^2\delta^3\delta^2+$$
$$3IIP\delta^3+12IIP^2\beta\delta^3+3IIP^3\beta^2\delta^3+8IIP^2\delta^4+$$
$$8IIP^3\beta\delta^4+5IIP^3\delta^5-f_u IIP\alpha\mu\beta-2f_u IIP\alpha\mu\delta-$$
$$2f_u IIP^2\alpha\mu\beta\delta\quad f_u IIP\alpha\mu-3f_u IIP^2\alpha\mu\delta^2)$$

$$A_5=[(\beta+\delta)(1+IIP\delta)(\delta(\beta+\delta)$$
$$(1+IIP\delta)-f_u\alpha\mu]/IIP^2 \quad (6)$$

We check the stability of endemic equilibrium state by using the Routh-Hurwitz conditions (6), the results are given in Fig. 3.

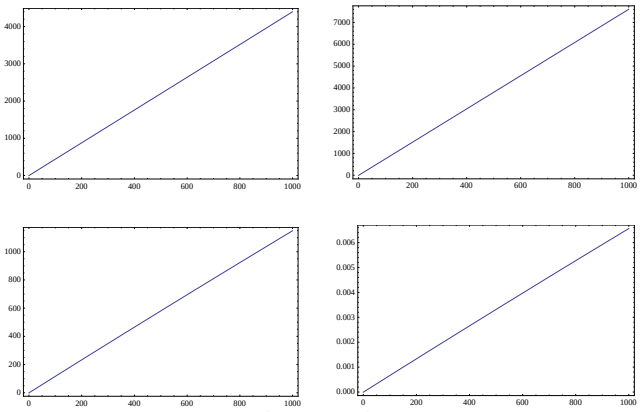


Fig. 2. The parameter spaces for disease free state equilibrium state which satisfies the Routh-Hurwitz conditions with the value of parameters: respectively, for with $\psi^5+A_1\psi^4+A_2\psi^3+A_3\psi^2+A_4\psi+A_5=0$

ii) The endemic state $E_1=(S_u'',E_u'',I_u'',E_v'',I_v'')$, the characteristic equation is given by

$$\begin{vmatrix} (-(\alpha^*I_u)-(\delta))-\psi & 0 & -(\alpha^*S_u) & 0 & 0 \\ (\alpha^*I_u) & (-(\frac{1}{IIP})-\delta)-\psi & (\alpha^*S_u) & 0 & 0 \\ 0 & (\frac{1}{IIP}) & (-(\beta)-(\delta))-\psi & 0 & 0 \\ I_u N_T^2\alpha(-1+\gamma) & 0 & -N_T^2 S_u\alpha(-1+\gamma) & (-(\frac{1}{IIP})-\delta)-\psi & 0 \\ 0 & 0 & 0 & (\frac{1}{IIP}) & (-(\beta)-(\delta))-\psi \end{vmatrix}=0 \quad (7)$$

We have characteristic equation:

$$\frac{1}{IIP}(\beta+\delta+\psi)(\_1-IIP\delta-IIP\psi)$$
$$(IIP S_u\alpha\psi+IIP S_u\alpha\psi-IIP(\beta+\delta+\psi) = 0$$
$$(I_u\alpha+\delta+IIP I_u\alpha\delta+IIP\delta^2+\psi+IIPI_u\alpha\psi$$
$$+2IIP\delta\psi+IIP\psi^2$$

We obtained the characteristic equation,

$$\psi^5+A_1\psi^4+A_2\psi^3+A_3\psi^2+A_4\psi+A_5=0$$

$$A_1=\frac{2IIP^2+IIP^3 I_u\alpha+2IIP^3\beta+5IIP^3\delta}{IIP^3}$$

$$A_2=\frac{1}{IIP^3}(IIP+2IIP^2 I_u\alpha-IIP^2 S_u\alpha+4IIP^2\beta$$
$$+2IIP^3 I_u\alpha\beta+IIP^3\beta^2+8IIP^2\delta$$
$$+4IIP^3 I_u\alpha\delta+8IIP^3\delta\beta+10IIP^3\delta^2)$$

$$A_3=\frac{1}{IIP^3}(IIPI_u\alpha-IIP S_u\alpha+2IIP\beta+4IIP^2 I_u\beta\alpha$$
$$-IIP^2 S_u\alpha\beta+2IIP^2\beta^2+$$
$$IIP^3\beta^2\alpha I_u+3IIP\delta+6IIP^2 I_u\alpha\delta$$
$$-3IIP^2 S_u\alpha\delta+12IIP\delta\beta+6IIP^3\beta\alpha I_u\delta$$
$$+3IIP^3\beta^2\delta+12IIP^2\delta^2+6IIP^3\alpha I_u\delta^2$$
$$+12IIP^3\beta\delta^2+10IIP^3\delta^3)$$

$$A_4 = \frac{1}{IIP^3}(2\,IIPI_u\alpha\beta - IIP\,S_u\alpha\beta + IIP\beta^2 + 2\,IIP^2 I_u\alpha\beta^2 + 2IIPI_u\alpha\delta - 2IIP\,S_u\alpha\delta + 4IIP\beta\delta + 8IIP^2 I_u\alpha\delta\beta - 2IIP^2 S_u\alpha\beta\delta + 4IIP^2\beta^2\delta + 2\,IIP^3\beta^2\alpha I_u\delta + 3IIP^2\delta^2 + 6\,IIP^2 I_u\alpha\delta^2 - 3\,IIP^2 S_u\alpha\delta^2 + 12IIP^2\beta\delta^2 + 6IIP^3\beta\alpha I_u\delta^2 + 3\,IIP^3\beta^2\delta^2 + 8\,IIP^3\delta^3 + 4\,IIP^3 I_u\alpha\delta^3 + 8\,IIP^3\beta\delta^3 + 5\,IIP^3\delta^4)$$

$$A_5 = \frac{1}{IIP^2}(\beta+\delta)(1+IIP\delta)(I_u\alpha(\beta+\delta)(1+IIP\delta) + \delta(-S_u\alpha + (\beta+\delta)(1+IIP\delta)))$$

when $I_u = \frac{\delta}{\alpha} - \frac{f_u\ \mu}{(\beta+\delta)(1+IIP\delta)}$ and

$$S_u = \frac{(\beta+\delta)(1+IIP\delta)}{\alpha} \quad (8)$$

We check the stability of endemic equilibrium state by using the Routh-Hurwitz conditions (8), the results are given in Fig. 3.

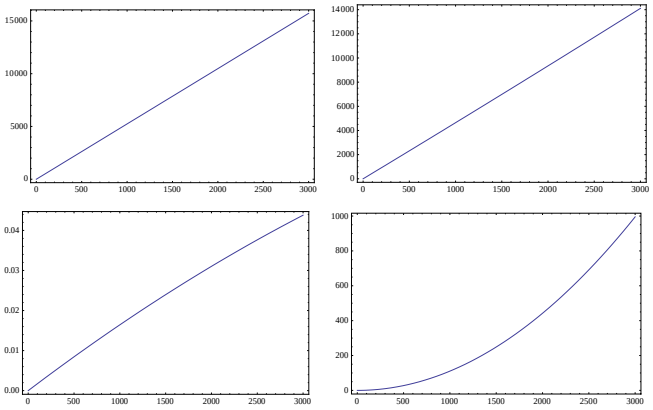


Fig. 3. The parameter spaces for endemic disease equilibrium state which satisfies the Routh-Hurwitz conditions with the value of parameters: respectively, for with $\psi^5 + A_1\psi^4 + A_2\psi^3 + A_3\psi^2 + A_4\psi + A_5 = 0$

We have checked both disease free equilibrium and endemic equilibrium solutions which both cases are local asymptotically stable when $R_0 < 1$ for disease free equilibrium state and $R_0 > 1$ for endemic equilibrium state. The R_0 value is obtained as following [2], [5], [8], [14]-[16]:

$$R_0 = \frac{\gamma\delta^2(1+IIP(\beta+\delta)) + f_u\alpha\mu}{\delta(\beta+\delta)(1+IIP\delta) + f_u\alpha\mu\gamma}$$

III. Results and Discussion

The transmission of H1N1 virus disease in this study is based on the SEIR model. We considered the dynamics of SEIR model at the disease free and endemic states. The values for the parameters used in this study are shown in Table II. The numerical results are shown in Fig. 2 and Fig. 3 below.

TABLE II: Parameters Used in Simulation for SEIR Model

Parameters	Biological meaning	Value
μ	Birth rate of human	$1/(365*74)$ per day
f_u	Fraction of newborn unvaccinated	0.0714 per day
δ	Death rate of human	$1/(365*74)$ per day
α	Transmission rate of H1N1 virus	0.0001 - 0.9 per day
IIP	Number of Incubation for dengue virus	1/((1+3)/2) per day
β	Recovery rate of H1N1 virus	0.2 per day
γ	Efficiency of vaccine	0.01 – 0.9

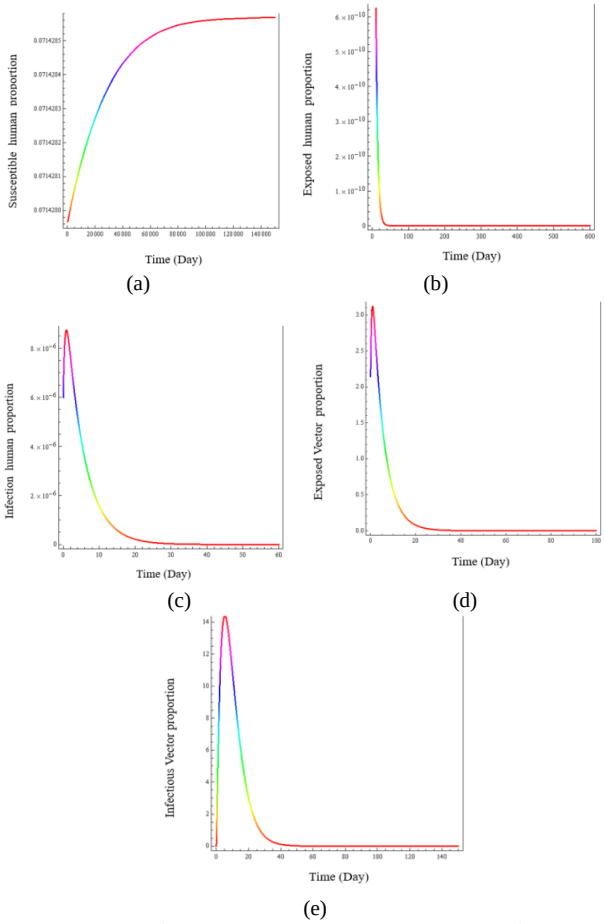


Fig. 4. Time series of susceptible human to the transmission of H1N1 virus (a), exposed human to the transmission of H1N1 virus(b), infectious human to the transmission of H1N1 virus(c), exposed vector to the transmission of H1N1 virus (d) and infectious vector to the transmission of H1N1 virus (e). We can see that the solutions equation approach to the disease free equilibrium state. (0.0714,0,0,0,0) When R0 = 0.00374.

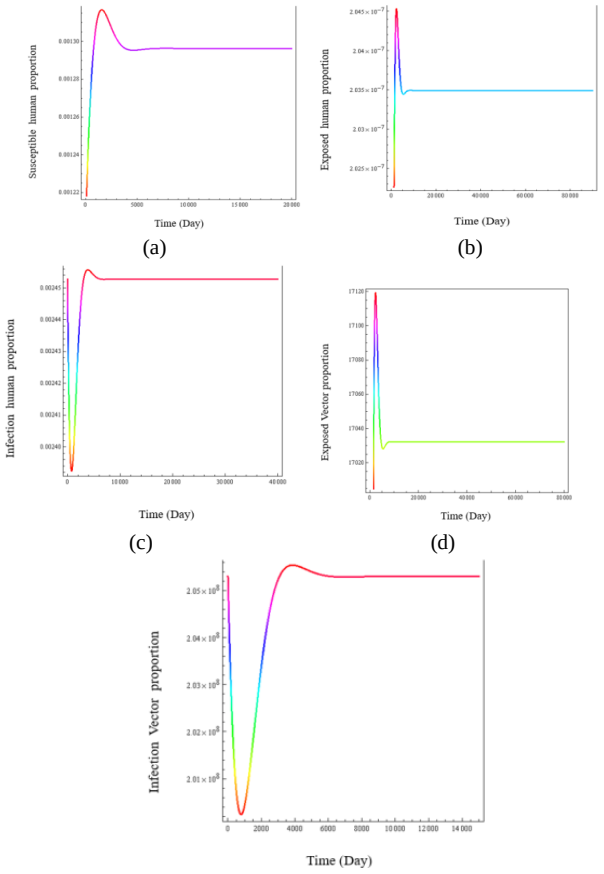
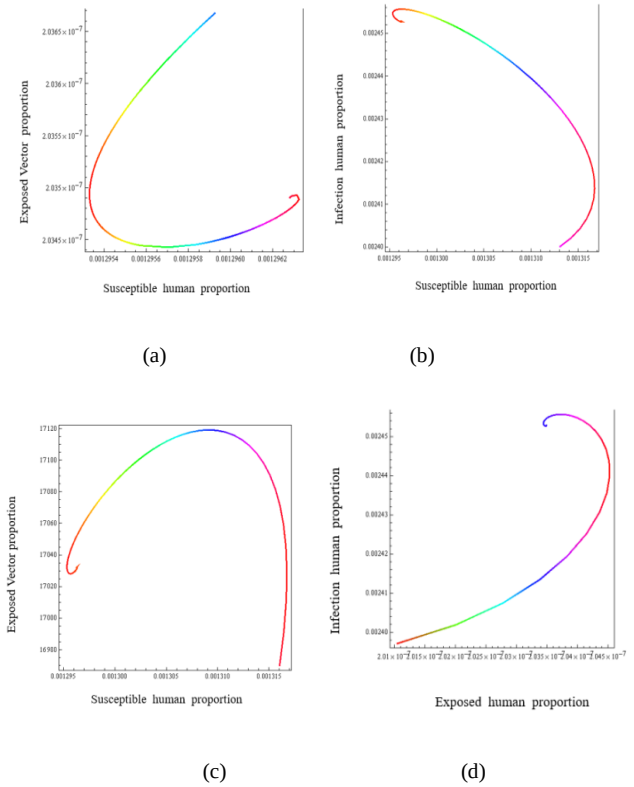


Fig. 5. Time series of susceptible human to the transmission of H1N1 virus(a) , exposed human to the transmission of H1N1 virus(b), infectious human to the transmission of H1N1 virus(c), exposed vector to the transmission of H1N1 virus(d) and infectious vector to the transmission of H1N1 virus (e). We can see that the solutions equation approach to the endemic equilibrium state. (0.0012, 0.0000002043, 0.0024, 17032.2, 0.00000002053) When R0 = 11.29.



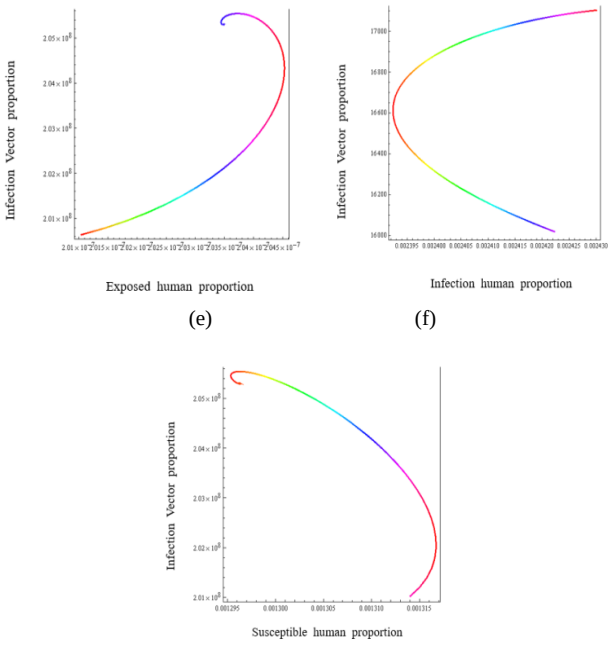


Fig. 6. The trajectories of dengue disease for the solutions equation approach to the endemic equilibrium state onto (Su, Eu) (a), (Su, Iu) (b), (Su, Ev) (c), (Eu, Iu) (d), (Eu, IV) (e), (Iu, Iv) (f), (Su, Iv) (g).

IV. Conclusions

For the purposes of this study, we formulated and analyzed the transmission of a SEIR model by considering the effects of vaccination to the transmission of H1N1 virus. We obtained the basic reproductive number R_0, when $R_0 < 1$, and we found that the trajectory solution as approached to the disease free equilibrium state as shown in Fig. 4. When $R_0 > 1$, the trajectory solution as approached to the endemic equilibrium state as shown in Fig. 5 and Fig. 6. Numerical simulations showed that the effectiveness of the influenza is in fact effective for controlling the spread of SEIR, the results are shown in Table II. The existence of oscillations around the endemic equilibrium E_2 are depend on the eigenvalue with imaginary part different from zero. For the simulation shown in Fig. 5 and fig. 6, the imaginary part of the complex roots is approximately 0.00101765 which can estimate the period of the oscillations by means of the solutions of the linearized system that is obtained as $2\pi/0.00101765 \approx 17.01$ years. This value is the approximation to the period of the solutions [9], [11]-[14]. We can see that the disease can be reduced when the parameters satisfied to the conditions given in the above section.

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R. Sungchasit received her bachelor of education (graduate in mathematics) from Phuket Institute Rajahat, Thailand; the master of business administration (finance and banging) from Sripatum University, Thailand; the master of science program in applied statistics (statistics) from National Institute of Development Administration, Thailand; the doctor of philosophy (applied mathematics) from King Mongkut's Institute of Technology Landkrabang, Thailand. From 2007 till now, she is a lecturer in mathematics in Phuket Rajabhat University, Thailand. Her research interests are mathematical modelling.

P. Pongsumpun received her bachelor of science in mathematics (second class honors) and the doctor of philosophy in mathematics (international programme) from Mahidol University, Thailand. From 2004 to 2012, she was an as assistant professor ofmathematics. From 2012 till date, she is an associate professor of mathematics, the Ph.D. and M.Sc. advisors in King Mongkut's Institute of Technology Ladkrabang, Thailand. Her research interests are mathematical modelling in medical science, differential equations and numerical analysis.