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Mathematical Model of Avian Influenza When there is the Traveling of Tourists from the Risk Countries

[1]Jiraporn Lamwong and [2]Puntani Pongsumpun
[1]Thatphanom College, Nakhonphanom University, Phanomphanarak Road,
Thatphanom, 48110 Nakhon Phanom,Thailand
[2]Department of Mathematics, Faculty of Science, King Mongkut's Institute ofTechnology
Ladkrabang, Chalongkrung Road, Ladkrabang, 10520 Bangkok, Thailand

Abstract: Avian influenza is caused by influenza virus type A. First infected case was reported in Hong Kong during a poultry outbreak in 1997. After that, there were the reports of the sporadic outbreak in all regions. In this study, we consider the transmission model of avian influenza when there is the traveling of tourists from the risk countries. We consider the dynamical changes of three population groups: Thai human, Hong Kong human and bird populations. The behaviors of the modified equations are obtained by using a standard dynamical modeling method. This method is used for analyzing the behaviors of solutions. The stability conditions for the disease free and endemic equilibrium states are determined. The threshold parameter is defined by R_0. When $R_0<1$, the disease-free state is locally asymptotically stable. If $R_0>1$, the endemic equilibrium state is locally asymptotically stable. The numerical solutions are shown for supporting the theoretical results.

Key words: Basis reproductive number, disease free steady state, endemic, steady state, stability

INTRODUCTION

Three types of influenza are denoted as type A-C. Avian influenza virus is caused by type A strains of the influenza virus. Avian influenza virus type A with all 16 Haemagglutinin (H1-H16) and all 9 Neuramimidase (N1-N9) influenza A subtypes in the majority of possible combination have been isolated from avian species (Anderson and May, 1992; Liu *et al*., 2015). After the outbreak of the first avian influenza A virus in Hong Kong in 1997 (Liu *et al*., 2015) and in 2004, an epidemic was recognized as the first time in Thai. Avian influenza virus has been infected to human and outbreak in many countries such as Hong Kong, Thai, China, Indonesia and Vietnam . It can be transmitted to human by birds. Human can be infected by direct contact with infectious animals or by touching the phlegm or biological fluid contacts with the feces of infectious animals. Germs can be destroyed by heating at 56°C for 3 h or 60°C for 30 min.

Pongsumpun and Tang (2010) studied infection between the transmission of plasmodium falciparum and plasmodium vivax malaria in mixed population of Thai and migrant Burmese populations living along the Thai-Myanmar show in Fig. 1. They analyzed the model to find the conditions for the local stability of each equilibrium point. Liu *et al*. (2015) used dynamical model for analyzing the avian influenza epidemic models with time delay of virus. They constructed a bird-to-human transmission and proposed a delayed SI-SIR model and take account the incubation periods of avian influenza A virus. Pongsumpun and Lamwong (2016) formulated the mathematical model for describing the transmission of

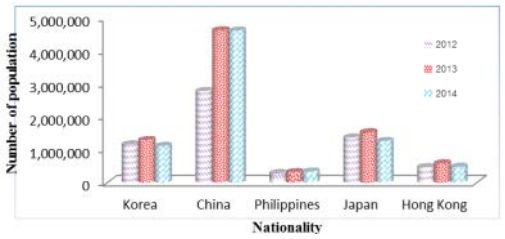

Fig. 1: Number of population who travel in Thai from 2012-2014 (Chong *et al*., 2014)

Corresponding Author: Puntani Pongsumpun, Department of Mathematics, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Chalongkrung Road, Ladkrabang, 10520 Bangkok, Thailand

avian influenza and take into account the age structure of avian influenza patients. We analyzed the model by method of standard dynamical modeling. In this study, we consider the transmission of avian influenza when there is the traveling of tourists from the risk countries. The structure of our model contains bird population (denoted by B) or if the human is Thai (denoted by T) and Hong Kong (denoted by K). We divided the human population into susceptible, infectious and recovered classes (SIR models). Bird population is separated into susceptible and infectious classes (SI model). We analyzed our model by standard dynamical modeling method. The basic reproduction number is found and described in this study.

MATERIALS AND METHODS

Transmission model: The total population of Thai human, Hong Kong human and bird are denoted by N_T, N_K and N_B. The Thai population is divided into three population groups: Susceptible (S_T) Infected (I_T) and Recovered (R_T) Thai populations. The number of susceptible Thai human is increased by new-borne human whereas their reduction through natural death and infection. The number of infected Thai population is increased by the infection of susceptible Thai population but they diminish by recovery from the disease, natural death and disease death. Number of recovered Thai population is increased by recovery of infected person and reduced through natural death. The total Thai population is represented by $N_T = S_T + I_T + R_T$. The Hong Kong population is divided into three groups: susceptible (S_K) infected (I_K) and recovered (R_K) classes. The number of susceptible Hong Kong human is increased by Hong Kong move into Thai and decreased due to the infection of susceptible human, natural death and they move out Thai. The number of infected Hong Kong human is increased by infection of susceptible Hong Kong population but they diminished by recovery of infected Hong Kong population, natural death, death due to the disease and Hong Kong move out the country. The number of recovered Hong Kong human is increased by recovery of infected Hong Kong human, reduced by natural death and Hong Kong move out the country. The total Hong Kong population is given by $N_K = S_K + I_K + R_K$ The bird population is divided into two population: susceptible and infected bird population. The number of susceptible bird population is increased by new-born of bird and decreased by natural death. The number of infected bird is increased by infection of susceptible bird and diminished by natural death and death due to the disease. A schematic representation of model is shown in Fig. 2 and Table 1. We use SIR model for human population and SI model for bird population. The variables of our model are defined as follows:

- S_T (t) be the number of susceptible Thai population at time t

Table 1: Definitions of parameters in our model

Parameters	Definitions
C	Birth rate of Thai human population
β_t	Rate at which susceptible Thai human changes to become an infected Thai human
γ_t	Rate at which infected Thai human changes to become recovered Thai human
μ_T	Natural death rate of Thai human
α_t	Death rate due to avian influenza of Thai human
N_t	Total Thai human population
p	Fraction of infectious Hong Kong human when they enter Thailand
K	Contact rate of avian influenza
β_k	Rate at which susceptible Hong Kong human changes to become an infected Hong Kong human
γ_k	Rate at which infected Hong Kong human changes to become recovered Hong Kong human
μ_k	Natural death rate of Hong Kong human
α_2	Death rate due to avian of Hong Kong human
d	Rate at which Hong Kong move out the country
N_k	Total Hong Kong population
B	Birth rate of bird
β_B	Rate at which susceptible bird human changes to become an infected bird human
μ_B	Natural death rate of bird human
α_3	Death rate due to avian of bird human
N_B	Total bird population

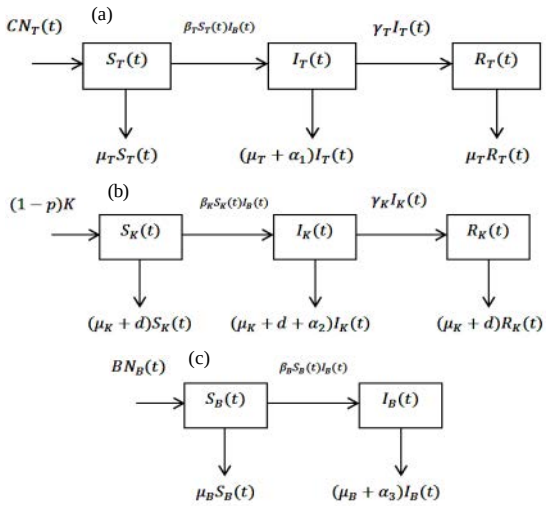

Fig. 2: Flow chart of the dynamics in the model: a) for the Thai human population, b) for the Hong Kong human population and c) for the bird population Thai population

- I_T (t) be the number of infected Thai population at time t
- R_T (t) be the number of recovered Thai population at time t
- S_K (t) be the number of susceptible Hong Kong population at time t
- I_K (t) be the number of infected Hong Kon population at time t
- R_K (t) be the number of recovered Hong Kong population at time t
- S_B (t) be the number of susceptible bird population at time t
- I_B (t) be the number of infected bird population at time t

$$\frac{dS_T(t)}{dt} = CN_T(t) - \beta_T S_T(t) I_B(t) - \mu_T S_T(t) \quad (1)$$

$$\frac{dI_T(t)}{dt} = \beta_T S_T(t) I_B(t) - (\mu_T + \gamma_T + \alpha_1) I_T(t) \quad (2)$$

$$\frac{dR_T(t)}{dt} = \gamma_T I_T(t) - \mu_T R_T(t) \quad (3)$$

Hong Kong population:

$$\frac{dS_K(t)}{dt} = (1-p)K - \beta_K S_K(t) I_B(t) - (\mu_K + d) S_K(t) \quad (4)$$

$$\frac{dI_K(t)}{dt} = \beta_K S_K(t) I_B(t) - (\mu_K + d + \alpha_2 + \gamma_K) I_K(t) \quad (5)$$

$$\frac{dR_K(t)}{dt} = \gamma_K I_K(t) - (\mu_K + d) R_K(t) \quad (6)$$

Bird population:

$$\frac{dS_B(t)}{dt} = BN_B(t) - \beta_B S_B(t) I_B(t) - \mu_B S_B(t) \quad (7)$$

$$\frac{dI_B(t)}{dt} = \beta_B S_B(t) I_B(t) - (\mu_B + a_3) I_B(t) \quad (8)$$

Where:

$$N_T(t) = S_T(t) + I_T(t) + R_T(t) \quad (9)$$

$$N_K(t) = S_K(t) + I_K(t) + R_K(t) \quad (10)$$

And:

$$N_B(t) = S_B(t) + I_B(t) \quad (11)$$

Analytical solutions

Equilibrium points: The standard dynamical method is used for analysis our model. Steady states of our equations are found by setting Eq. 1-11 zero, then we obtain the steady states. The disease free steady state:

$$E_0 = \left(\frac{CN_T}{\mu_T}, 0, 0, \frac{(1-P)K}{d+\mu_K}, 0, 0, \frac{BN_B}{\mu_B}, 0\right)$$

The endemic steady state:

$$E_1 = (S_T^*, I_T^*, R_T^*, S_K^*, I_K^*, R_K^*, S_B^*, I_B^*)$$

$$S_T^* = \frac{CN_T}{\beta_T I_B^* + \mu_T} \quad (12)$$

$$I_T^* = \frac{CN_T \beta T I_B^*}{(\beta_T I_B^* + \mu_T)(\alpha_1 + \gamma_1 + \mu_T)} \quad (13)$$

$$R_T^* = \frac{CN_T \beta_T \gamma_1 I_B^*}{\mu_T (\beta_T I_B^* + \mu_T)(\alpha_1 + \gamma_1 + \mu_T)} \quad (14)$$

$$S_K^* = \frac{(1-P)K}{d + \beta_K I_B^* + \mu_K} \quad (15)$$

$$I_K^* = -\frac{\beta_K K^2 (-1+P) I_B^*}{(d + \beta_K I_B^* + \mu_K)(d + 2 + \gamma_2 + \mu_K)} \quad (16)$$

$$R_K^* = -\frac{\gamma_2 \beta_K k^2 (-1+P) I_B^*}{(d+\mu_K)(d + \beta_K I_B^* + \mu_K)(d + a_2 + \gamma_2 + \mu_K)} \quad (17)$$

$$S_B^* = \frac{BN_B}{\beta_B I_B^* + \mu_B} \quad (18)$$

$$I_B^* = -\frac{\mu_B}{\beta_B} + \frac{BN_B}{\alpha_3 + \mu_B} \quad (19)$$

Local asymptotical stability: The local stability of each equilibrium point is determined by sign of all eigenvalues. The eigenvalues λ are solutions of the characteristic equation.

Disease free state: The Jacobian matrix at E_0 is shown as in Eq. 20:

$$J_{E_0}=\begin{bmatrix} -\mu_T & 0 & 0 & 0 & 0 & 0 & 0 & -(\frac{cN_T}{\mu_T})\beta_T \\ 0 & -(\alpha_1+\gamma_1+\mu_T) & 0 & 0 & 0 & 0 & 0 & (\frac{cN_T}{\mu_T})\beta_T \\ 0 & \gamma_1 & -\mu_T & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -(d+\mu_K) & 0 & 0 & 0 & -(\frac{(1-P)K}{d+\mu_K})\beta_K \\ 0 & 0 & 0 & 0 & -(d+\alpha_2+\gamma_2+\mu_K) & 0 & 0 & (\frac{(1-P)K}{d+\mu_K})\beta_K \\ 0 & 0 & 0 & 0 & \gamma_2 & -(d+\mu_K) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\mu_B & -(\frac{BN_B}{\mu_B})\beta_B \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\alpha_3+(\frac{BN_B}{\mu_B})\beta_B-\mu_B \end{bmatrix}$$

The characteristic equation of the above Jacobian matrix is:

$$(-\lambda-\mu_B)\left(-a_3-\lambda+\frac{BN_B\beta_B}{\mu_B}-\mu_B\right)(-d-\lambda-\mu_K)^2(-d-a_2-\gamma_2-\lambda-\mu_K)(-\lambda-\mu_T)\left(a_1\lambda+\gamma_1\lambda+\lambda^2+\alpha_1\mu_T+\gamma_1\mu_T+2\mu_T\lambda+{\mu_T}^2\right)=0 \quad (21)$$

Where:

$$\lambda_1=-\mu_B\ ,\lambda_2=-d-\mu_K\ ,\lambda_3=-d-\mu_K\ ,\ \lambda_4=-d-a_2-\gamma_2-\mu_K,\ \lambda_{5,6}=-\mu_T\ ,\ \lambda_7=-a_1-\gamma_1-\mu_T$$

And:

$$\lambda_8=-\alpha_3+\frac{BN_B\beta_B}{\mu_B}-\mu_B$$

From evaluating all eigenvalues, the real parts of all eigenvalues have negative signs when $R_0<1$ where:

$$R_0=\max\left\{\frac{BN_B\beta_B}{\mu_B(\alpha_3+\mu_B)},\frac{\beta_K}{\mu_B\mu_K}\left(d+\frac{BN_B}{\alpha_3+\mu_B}+\mu_K\right),\frac{B\beta_TN_B}{\mu_B(\alpha_3+\mu_B)}+\frac{\mu_T}{\mu_B}\right\}$$

Disease endemic equilibrium: To define the stability of the endemic equilibrium point E_1, we find the eigenvalues of Jacobian matrix at E_1:

$$J_{E_1}=\begin{bmatrix} -\beta_TI_B^*-\mu_T & 0 & 0 & 0 & 0 & 0 & 0 & -\beta_TS_T^* \\ \beta_TI_B^* & -(\alpha_1+\gamma_1+\mu_T) & 0 & 0 & 0 & 0 & 0 & \beta_TS_T^* \\ 0 & \gamma_1 & -\mu_T & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -d-\beta_KI_B^*-\mu_K & 0 & 0 & 0 & -\beta_KS_K^* \\ 0 & 0 & 0 & \beta_KI_B^* & -(d+\alpha_2+\gamma_2+\mu_K) & 0 & 0 & \beta_KS_K^* \\ 0 & 0 & 0 & 0 & \gamma_2 & -(d+\mu_K) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\beta_BI_B^*-\mu_B & -\beta_BS_B^* \\ 0 & 0 & 0 & 0 & 0 & 0 & \beta_BI_B^* & -\alpha_3+\beta_BS_B^*-\mu_B \end{bmatrix}$$

The characteristic equation is given by:

$$\begin{pmatrix} a_3\beta_BI_B^*+a_3\lambda+\beta_BI_B^*\lambda-\beta_BS_B^*\lambda+\lambda^2+a_3\mu_B+ \\ \beta_B\mu_BI_B^*-\beta_B\mu_BS_B^*+2\mu_B\lambda+{\mu_B}^2 \end{pmatrix}(-d-\lambda-\mu_K) \qquad \begin{matrix}(-d-\beta_KI_B^*-\lambda-\mu_K)(-d-\alpha_2-\gamma_2-\lambda-\mu_K)(-\lambda-\mu_T) \\ (-\beta_TI_B^*-\lambda-\mu_T)(-\alpha_1-\gamma_1-\lambda-\mu_T)=0\end{matrix} \quad (23)$$

where, S^*_T, I^*_T, S^*_K, R^*_K, S^*_B and I^*_B are defined in Eq. 12-19. From evaluation, all eigenvalues have negative real parts for $R_0<1$ where:

$$R_0 = \max\left\{\frac{BN_B\beta_B}{\mu_B(a_3+\mu_B)}, \frac{\beta_K}{\mu_B\mu_K}\left(d+\frac{BN_B}{a_3+\mu_B}+\mu_K\right), \frac{B\beta_T N_B}{\mu_B(a_3+\mu_B)}+\frac{\mu_T}{\mu_B}\right\}$$

RESULTS AND DISCUSSION

Numerical solutions: Table 2 shows that:

Stability of disease-free state: The values are B = 0.1, β_B = 0.04, μ_B = 1/100. α_3 = 5 and N_B = 1. We obtain: λ_1 = -4.61, λ_2 = -0.512537, λ_3 = -0.0650365, λ_4 = -0.01, λ_5 = -0.002536533, λ_6 = -0.00253653, λ_7 = -0.0000365297, λ_8 = -0.0000365297 and R_0 = 0.307922.

Stability of endemic state: we change the values of total bird population from 1change to be 100 total Thai human population from 10 change to be 1000 fraction of infectious Hong Kong human when they enter Thailand from 0 change to be 0.2 and keep the other values of the parameters the same. We obtain: λ_1 = -0.510062, λ_2 = 0.0873619, λ_3 = -0.0873369, λ_4 = -0.0650365, λ_5 = -0.00253653, λ_6 = -0.00253653, λ_7 = -0.0000365297, λ_8 = -0.0000365297 and R_8 = 0.307922. Eigenvalues have to be negative real parts and reproductive number is more than one, the equilibrium point will be the endemic state, E_1 as shown in Fig. 3.

In this study, we constructed the mathematical model of avian influenza when there is the traveling of tourists from the risk countries by case H5N1. The results by using standard dynamical modeling (Leah,1988). The basic reproductive number is denote by R_0 when:

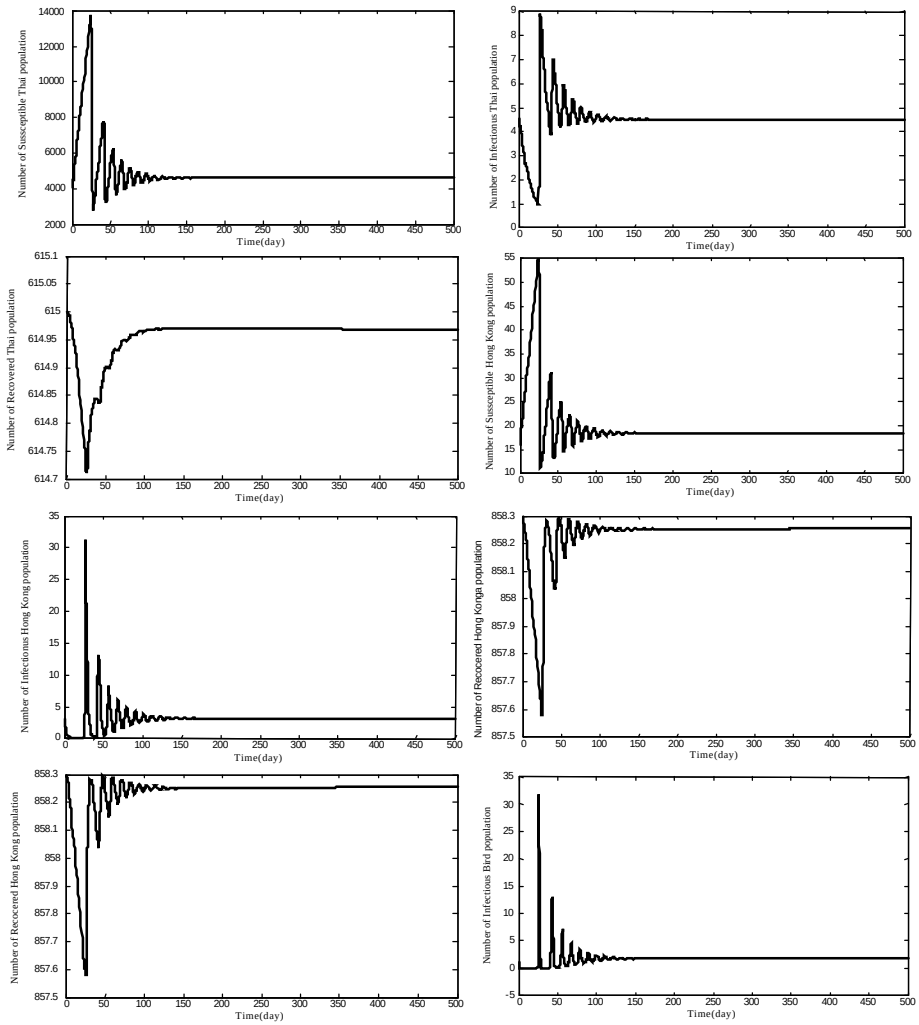

Fig. 3: Time series solutions of susceptible Thai population, infections Thai population, recovered Thai population, susceptible Hong Kong population, infections Hong Kong population, recovered Hong Kong population susceptible bird population and infectious bird population

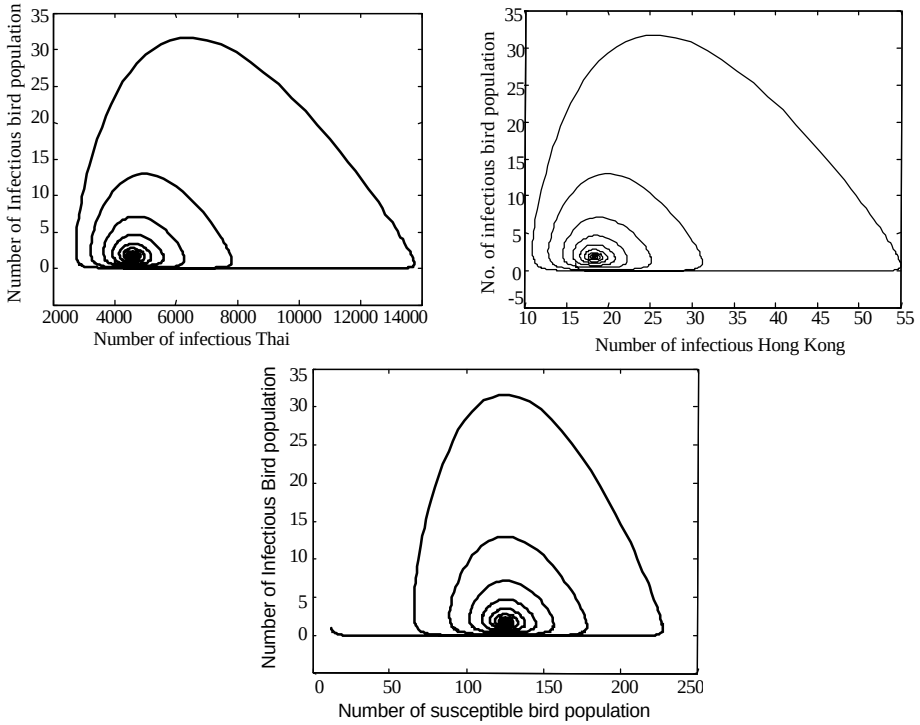

Fig. 4: Plot of the number of infected Thai population and infected bird population, infected Hong Kong population and infected bird population and susceptible bird population and infected bird population

Table 2: Parameters values to endemic state

References	Parameters	Values
Simulated value	C	0.4
Gumel (2009) and Chong *et al.* (2014)	μ_T	1/(75×365)
Iwami *et al.* (2007) and Chong *et al.* (2014)	α_r	0.06
Simulated value	N_r	1000
Simulated value	p	0.2
Simulated value	K	2
Gumel (2009) and Chong *et al.* (2014)	β_k	0.05
Gumel (2009) and Chong *et al.* (2014)	γ_k	0.01
Official statistics Thailand	1/(75×365)	μ_k
Iwami *et al.* (2007)	α_2	0.5
Simulated value	d	0.000025
Simulated value	B	0.1
Iwami *et al.* (2007)	β_B	0.04
Gumel (2009) and Chong *et al.* (2014)	μ_B	1/100
Iwami *et al.* (2007) and Chong *et al.* (2014)	α_3	5
Simulated value	N_B	100

$$R_0 = \max\left\{\frac{BN_B\beta_B}{\mu_B(\alpha_3+\mu_B)}, \frac{\beta_K}{\mu_B\mu_K}\left(d+\frac{BN_B}{\alpha_3+\mu_B}+\mu_K\right), \frac{B\beta_T N_B}{\mu_B(\alpha_3+\mu_B)}+\frac{\mu_T}{\mu_B}\right\} \quad (24)$$

The quantity $R_0^{11}=\sqrt{R_0}$ is the basic reproductive number of the disease. It represents the number of secondary cases that one case can produce if introduced into a susceptible population (Anderson and May, 1992). Figure 3 show time series solutions of susceptible Thai population, infections Thai population, recovered Thai population, susceptible Hong Kong population, infections Hong Kong population, recovered Hong Kong population susceptible bird population and infectious bird population. We can see that the solutions approach to the endemic state show in Fig. 4 E_1(4579, 4.5182, 614.955, 18.3146, 3.134664, 858.261, 125, 1.74601) when R_0>1.

CONCULSION

We analyze the method for controlling the transmission of influenza virus. The results of this study introduce the way for reducing the outbreak time of epidemic.

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