Global dynamics of the avian-human influenza with horizontal transmission in human population

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Abstract: The family case clusters of highly pathogenic avian influenza A subtype H5N1 in Thailand (2004) and in Sumatra, Indonesia (May 2006) that were due to human-to-human transmission attracted the attention of the responsible agencies. If the H5N1 virus gain the ability of sustained human-to-human transmission a pandemic could result with potentially high mortality. In order to understand the dynamical behavior of the human-to-human transmittable avian influenza, we develop a mathematical model by taking into account the human-to-human transmission of the avian influenza with the exposed compartment in both human and bird population. We show that by using the basic reproduction number the stability of the equilibria in the proposed model can be controlled. The global stability of both the disease-free and the endemic equilibrium is shown by using the Lyapunov function theory. Finally, numerical results are carried out to justify this work.
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Key words: Avian influenza model; Backward bifurcation; Basic reproduction number; Global stability.

1 Introduction

Avian influenza is one of the most dangerous diseases for the wellbeing of animals and humans nowadays. A few years back it was a disease of wild birds and poultry and was of a limited significance [1, 2], but this perspective has changed as the emergence of a strain can infect humans through bird-to-human transmission and can kill about 60 percent of those infected [3]. But its potential to change into an extremely virulent human-to-human transmittable pandemic strain is the real danger for the human health. It requires drastic measure for the control of the spread of avian influenza to reduce such kind of probabilities.

The pathogens of the avian influenza mutates at a very high rate and expands its host range [3]. A large number of wild bird species, species of mammals and species of domestic birds as well as humans have been infected by various strains of avian influenza [4, 5, 6]. It is difficult to control the disease because of the multi-species conglomerate of hosts and because of this difficulty, the researchers directed their efforts to reduce the circulation within the poultry population, as it is the main responsible for the transmission of the disease. In order to control the spread of the disease, only culling was applied in the last decade [3] which caused a significant economic loss by destroying a large number of chickens. Nowadays, to control the spread, multiple control strategies are in attempt like increasing bio security, culling and vaccination of poultry.

A pandemic among humans may cause by the highly pathogenic H5N1 strain, if it acquires a highly efficient human-to-human transmission mechanism, while retaining high pathogenicity. Several reports have so far been made of possible co-infection of humans with an H5N1 strain and a human strain. One of the co-infection reports was of an Indonesian teen in 2008. The other of an Egyptian man, suspected of the co-infection by H5N1 and the pandemic H1N1 strain in 2009 [3]. The reports of such co-infection in humans alarms the threat of future pandemic.

In this work, we combine two nonlinear models, the first one describes the interaction between the susceptible human and the infected human and infected birds populations, and the second one describes the interaction between the susceptible birds and the infected birds populations. We first establish stability results for the proposed model. Analysis of the model reveals that there are two equilibria, the disease-free and the endemic equilibria. Further, it is shown that the model exhibits the phenomenon of backward bifurcation where the locally asymptotically stable disease-free equilibrium co-exists with a locally asymptotically stable endemic equilibrium when the threshold quantity $R_0 < 1$. The local dynamics of the proposed model are completely determined by the basic reproduction

number R_0 . For $R_0 < 1$ the disease-free equilibrium is locally stable while for $R_0 > 1$ the endemic equilibrium is locally stable. By using the Lyapunov function theory, we present the global asymptotic stability. Finally numerical simulations are carried out to support the analytical conclusion and illustrate possible behavioral scenarios of the proposed model.

2 Model frame work

In this section we present a compartmental model that divides the human and birds populations into two different classes. We divide the total human population at time t denoted by $N_h(t)$ into five distinct epidemiological subclasses which are susceptible $X_h(t)$ exposed $E_h(t)$ infected $I_h(t)$ treated $T_h(t)$ and recovered $R_h(t)$ and the birds population $N_b(t)$ into three distinct subclasses which are susceptible $X_b(t)$ exposed $E_b(t)$ and infected $I_b(t)$ The model is represented by the following system of differential equations.

$$\begin{aligned}
\frac{dX_h(t)}{dt} &= \Lambda - \mu_h X_h(t) - (\alpha_1 I_h(t) - \alpha_2 I_b(t)) X_h(t) + \grave{o}_h R_h(t),\\
\frac{dE_h(t)}{dt} &= \alpha_1 X_h(t) I_h(t) + \alpha_2 X_h(t) I_b(t) - (\mu_h + \phi_h) E_h(t),\\
\frac{dI_h(t)}{dt} &= \phi_h E_h(t) - (\rho_h + \beta_h + \mu_h) I_h(t),\\
\frac{dT_h(t)}{dt} &= \rho_h I_h(t) - (\gamma_h + \mu_h) T_h(t),\\
\frac{dR_h(t)}{dt} &= \gamma_h T_h(t) - (\mu_h + \grave{o}_h) R_h(t),\\
\frac{dX_b(t)}{dt} &= \pi - \mu_b X_b - \alpha_3 X_b(t) I_b(t),\\
\frac{dE_b(t)}{dt} &= \alpha_3 X_b(t) I_b(t) - (\mu_b + \phi_b) E_b(t),\\
\frac{dI_b(t)}{dt} &= \phi_b E_b(t) - (\beta_b + \mu_b) I_b(t),
\end{aligned} \tag{1}$$

with the initial conditions

$$\begin{cases} X_h(0) \geq 0,\ E_h(0) \geq 0,\ I_h(0) \geq 0,\ T_h(0) \geq 0, \\ R_h(0) \geq 0,\ X_b(0) \geq 0,\ E_b(0) \geq 0,\ I_b(0) \geq 0. \end{cases} \tag{2}$$

The complete descriptions are given in the following Table 1 and the transmission dynamics are given in Figure 1.

Table 1.

Parameters	Description
Λ	Recruitment rate of human population
α_1	Effective contact rate between the susceptible human and infected human
α_2	Effective contact rate between the susceptible human and infected birds
ε_h	The rate of immunity loss
φ_h	Progression rate of human from exposed class to infected class
ρ_h	The treatment rate of human
μ_h	The natural death rate of human class
β_h	Disease induced death rate in humans
Π	Recruitment rate of birds population
γ_h	Recovery due to treatment
β_b	Disease induced death rate in birds
α_3	Effective contact rate between susceptible birds and the infected birds
φ_b	Progression rate of birds from exposed class to infected class
μ_b	The natural death rate of birds

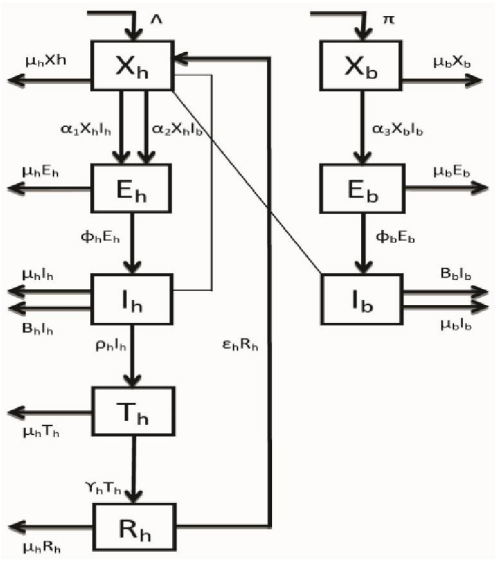

Figure 1: The flow chart represents the transmission dynamics of the avian-human influenza with horizontal transmission.

The total human population dynamics is given by

$$\frac{dN_h(t)}{dt} = \Lambda - \mu_h N_h(t) - \beta_h I_h(t). \tag{3}$$

By the given initial conditions $N_h(0) \geq 0$, so the total population $N_h(t)$ remains positive and bounded for all finite time t > 0. The total dynamics for the birds population is

$$\frac{dN_b(t)}{dt} = \pi - \mu_b N_b(t) - \beta_b I_b(t). \qquad (4)$$

From equation (3) and (4), we have

$$\begin{cases} \dfrac{dN_h(t)}{dt} \leq \Lambda - \mu_h N_h(t), \\ \dfrac{dN_b(t)}{dt} \leq \pi - \mu_b N_b(t). \end{cases} \qquad (5)$$

Then $\lim_{t\to\infty} SupN_h(t) \leq \dfrac{\Lambda}{\mu_h}$,

$\lim_{t\to\infty} SupN_b(t) \leq \dfrac{\pi}{\mu_b}$. Hence the feasible region for the system (1) is given by

$$\Omega = \{(X_h(t), E_h(t), I_h(t), T_h(t), R_h(t), X_b(t), E_b(t), I_b(t)) \in R_+^8, V_1 \leq \frac{\Lambda}{\mu_h}, V_2 \leq \frac{\pi}{\mu_b}\}.$$

3. Disease-free equilibrium

In order to find the dynamical features of the proposed model (1), we set the right hand side of all equations in the system (1) equal to zero. By the direct calculations we get the disease-free equilibrium point $E_1 = (X_h, 0, 0, 0, 0, X_b, 0, 0)$, where $X_h^o = \dfrac{\Lambda}{\mu_h}$ and $X_b^o = \dfrac{\pi}{\mu_b}$. The dynamics of the disease is described by the threshold quantity

$$R_0 = \frac{\pi\alpha_3\phi_b}{\mu_b(\mu_b+\phi_b)(\mu_b+\beta_b)}.$$

The threshold quantity R_0, is known as the basic reproduction number of the disease and it shows the expected number of new infections produced by a single infective when introduced into a susceptible population. The disease dies out if $R_0 < 1$, as it shows that on average each infected individual infects fewer than one individual. The disease will spread if $R_0 < 1$, as it shows that on average each infected individual infects more than one individual.

Theorem 3.1 For $R_0 < 1$, the disease-free equilibrium poin E_1 of the system (1) is locally asymptotically stable if and only if $M_1M_2 > \alpha_1\phi_h X_h^o$.

Proof. By linearizing the system (1) at the equilibrium point $E_1 = (X_h^o, 0, 0, 0, 0, X_b^o, 0, 0)$, We obtain the characteristic equation

$$[\lambda+\mu_h][\lambda+M_1][\lambda+M_1M_2-\alpha_1\phi_h X_h^o][\lambda+\mu_b]\times$$
$$[\lambda+M_5(M_1M_2-\alpha_1\phi_h X_h^o)][\lambda+M_5M_6(M_1M_2-\alpha_1\phi_h X_h^o)]$$
$$\times[\lambda+M_3][\lambda+(M_3M_4+\phi_b\alpha_3 X_b^o)]=0,$$

where

$$M_1 = \mu_h + \phi_h,$$
$$M_2 = \rho_h + \beta_h + \mu_h,$$
$$M_3 = \mu_b + \phi_b,$$
$$M_4 = \beta_b + \mu_b,$$
$$M_5 = \gamma_h + \mu_h,$$
$$M_6 = \mu_h + \text{ò}_h.$$

The eight eigenvalues corresponding to the above characteristic equation are

$$\lambda_1 = -\mu_h < 0, \quad \lambda_2 = -M_1 < 0,$$
$$\lambda_3 = -M_1M_2 + \alpha_1\phi_h X_h^o,$$
$$\lambda_4 = M_5(-M_1M_2 + \alpha_1\phi_h X_h^o),$$
$$\lambda_5 = M_5M_6(-M_1M_2 + \alpha_1\phi_h X_h^o),$$
$$\lambda_6 = -\mu_b < 0, \quad \lambda_7 = -M_3 < 0,$$
$$\lambda_8 = -M_3M_4 + \phi_b\alpha_3 X_b^o = -M_3M_4[1-R_0].$$

We see that all the eigenvalues will have negative real parts only if $M_1M_2 > \alpha_1\phi_h X_h^o$ and $R_0 < 1$. Hence the disease-free equilibrium E_1 is locally asymptotically stable if $M_1M_2 > \alpha_1\phi_h X_h^o$ and $R_0 < 1$.

3.1 Endemic equilibria and backward bifurcation

In order to find the endemic equilibria of the proposed model (1), we need to take the following steps:

Let $E_2 = (X_h^*, E_h^*, I_h^*, T_h^*, R_h^*, X_b^*, E_b^*, I_b^*)$ represents any arbitrary endemic equilibrium of the model (1). By solving the equations of the system (1) at steady state, we get

$$X_h^* = \frac{\Lambda\phi_h M_5 M_6 + \grave{o}_h\phi_h\gamma_h\rho_h I_h^* - M_1M_2M_5M_6I_h^*}{\mu_h\phi_h M_5M_6},$$

$$E_h^* = \frac{M_2 I_h^*}{\phi_h}, \quad T_h^* = \frac{\rho_h I_h^*}{M_5},$$

$$R_h^* = \frac{\gamma_h\rho_h I_h^*}{M_5M_6}, \quad X_b^* = \frac{M_3M_4}{\alpha_3\phi_b},$$

$$E_b^* = \frac{\mu_h M_1M_2M_4M_5M_6I_h^*}{\alpha_2\phi_b[\Lambda\phi_h M_5M_6 + \grave{o}_h\phi_h\gamma_h\rho_h I_h^* - M_1M_2M_5M_6I_h^*]} - \frac{\alpha_1M_4}{\alpha_2\phi_b},$$

$$I_b^* = \frac{\mu_h M_1M_2M_5M_6I_h^*}{\alpha_2[\Lambda\phi_h M_5M_6 + \grave{o}_h\phi_h\gamma_h\rho_h I_h^* - M_1M_2M_5M_6I_h^*]} - \frac{\alpha_1 I_h^*}{\alpha_2}.$$

If $I_h^* \neq 0$, then by putting values in the system (1) at steady state, we obtain after some calculations the following equation:

$$f(I_h) = aI_h^2 + bI_h + c = 0, \qquad (6)$$

Where

$$a = \alpha_1\alpha_3M_3M_4[M_1M_2M_5M_6 - \gamma_h\rho_h\grave{o}_h\phi_h],$$

$$b = [M_1M_2M_5M_6 - \gamma_h\rho_h\grave{o}_h\phi_h][\pi\alpha_2\alpha_3\phi_b - \alpha_2\mu_bM_3M_4] - \alpha_3M_3M_4M_5M_6[\alpha_1\Lambda\phi_h + \mu_hM_1M_2],$$

$$c = \Lambda\alpha_2\phi_h\mu_bM_3M_4M_5M_6[1-R_o].$$

The coefficient a is always positive as $M_1M_2M_5M_6 > \gamma_h\rho_h\grave{o}_h\phi_h$ and c is positive if R_0 is less than unity and is negative if R_0 is greater than unity. Since $a > 0$, so the positive solution depends on b and c. For R_0 >1 the above equation gives us two roots, one is positive and the other is negative. By substituting R_0 =1, the equation has nonzero solution $I_h = \frac{-b}{a}$, which is positive in case if and only if $b < 0$. For $b > 0$ there is a positive solution for R_0 =1 It means that equilibria depends upon R_0 and there exists an open interval which has two positive roots

$$I_{h1} = \frac{-b-\sqrt{b^2-4ac}}{2a}, \quad I_{h2} = \frac{-b+\sqrt{b^2-4ac}}{2a}.$$

If $c > 0$ and either $b^2 < 4ac$ or $b \geq 0$, the above equation has no positive solution, and thus there are no endemic equilibria. For different range of these parameters the following results are established.

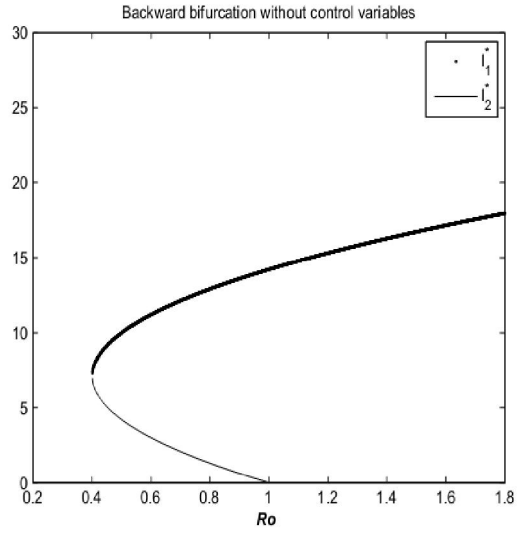

Figure 2. I_1^*, I_2^* versus R_0 shows a backward bifurcation with endemic equilibria when $R_0 < 1$.

Theorem 3.2 The system (1) has

(i) a unique endemic equilibrium in Ω if $c < 0 \Leftrightarrow R_o > 1$;

(ii) a unique endemic equilibrium in Ω if b<0 and $c = 0$ or b^2 - 4ac = 0;

(iii) two endemic equilibria in Ω if $c > 0$, b<0 and b^2 - 4ac > 0

(iv) no endemic equilibria otherwise.

In the above theorem case (iii) indicates the possibility of backward bifurcation in the model (1) when $R_0 < 1$

. To find the backward bifurcation, we set the discriminant b^2 - 4ac to be zero and solved for the critical value of R_0, denoted by R_c is given by

$$R_c = 1 - \frac{b^2}{4a[\Lambda\alpha_2\phi_h\mu_bM_3M_4M_5M_6]}.$$

Hence, $R_c < R_0$ is equivalent to $b^2 - 4ac > 0$ and therefore the backward bifurcation would occur for values of R_0 such that $R_c < R_0 < 1$. We can illustrate it by simulating the proposed model (1) with the following set of parameter values: $\Lambda = 2$,

π =18, $\alpha_1 = 0.001$, $\alpha_2 = 0.019$, $\alpha_3 = 0.35$, $\grave{o}_h = 0.01$, $\phi_h = 0.03$, $\rho_h = 0.05$, $\mu_h = 0.085$, $\mu_b = 0.455$, $\beta_h = 0.018$, $\beta_b = 0.6$, $\phi_b = 0.2$, and $\gamma_h = 0.01$. The phenomenon of backward bifurcation is confirmed by Figure 2 as it clearly shows that for $R_0 < 1$ there exist two locally asymptotically stable equilibria.

Theorem 3.3 The model (1) has a backward bifurcation at $R_0 = 1$ if and only if b<0.

Proof: Let us consider for sufficiency the graph of $y = g(I) = aI^2 + bI + c.$ Since $c = 0$ for $R_0 = 1$ thus g(0)=0 , hence the graph passes through the origin. Further g(I)=0 has a positive root $I = \frac{-b}{a}$ if b<0. On increasing the value of c from zero to some positive value, g(I) being a continuous function of c guarantees that there will be some open interval $(0, \grave{o})$ containing c, on which g(I) has two positive real roots. Thus we have shown that for $R_0 < 1$ there exist two endemic equilibria. The necessity is obvious as $b \geq 0,$ the equation (6) has no positive real roots when $R_0 < 1$.

Theorem 3.4 When $R_0 > 1,$ the unique endemic equilibrium state E_2 is locally asymptotically stable for $M_5 M_6 Q_5 < -\gamma_h \rho_h \phi_h \grave{o}_h Q_2.$

Proof: By linearizing the system (1) at $E_2 = (X_h^*, E_h^*, I_h^*, T_h^*, R_h^*, X_b^*, E_b^*, I_b^*)$, we have the characteristic equation

$$[\lambda - Q_1][\lambda - M_1 Q_1][\lambda - Q_5][\lambda - M_5 Q_5] \times$$
$$[\lambda - M_3 Q_6][\lambda - (M_5 M_6 Q_5 + \gamma_h \rho_h \phi_h \grave{o}_h Q_2)] \times$$
$$[\lambda - Q_6][\lambda - (M_3 M_4 Q_6 + \phi_b Q_7] = 0,$$

where

$$Q_1 = -\mu_h - \alpha_1 I_h^* - \alpha_2 I_b^*,$$
$$Q_2 = \alpha_1 I_h^* + \alpha_2 I_b^*,$$
$$Q_3 = \mu_h \alpha_1 X_h^*,$$
$$Q_4 = \mu_h \alpha_2 X_h^*,$$
$$Q_5 = M_1 M_2 Q_1 + \phi_h Q_3,$$
$$Q_6 = -\mu_b - \alpha_3 I_b^*,$$
$$Q_7 = -\alpha_3 X_b^* Q_6 - \alpha_3^2 I_b^* X_b^*.$$

There are eight eigenvalues corresponding to the above equation. All the eigenvalues will be negative only if $Q_5 = M_1 M_2 Q_1 + \phi_h Q_3 < 0$ and $M_5 M_6 Q_5 < -\gamma_h \rho_h \phi_h \grave{o}_h Q_2$.

After simplification we see that $Q_5 < 0$ only if $R_0 > 1$. Thus all the eigenvalues have negative real parts, which indicates that E_2 is locally asymptotically stable.

4 Global stability analysis

We illustrate the global property of the disease-free and the endemic equilibrium of the system (1) by the following theorems.

Theorem 4.1 The disease-free equilibrium of the system (1) is globally asymptotically stable on Ω.

Proof: We construct the Lyapunov function for the global stability of the system (1) at the disease-free equilibrium E_1 as follows:

$$F(t) = [(X_h(t) - X_h^o) + E_h(t) + I_h(t) + T_h(t) + R_h(t)]^{\frac{3}{2}}$$
$$+ [(X_b(t) - X_b^o) + E_b(t) + I_b(t)]^2.$$

By taking the time derivative, we have

$$F'(t) = \frac{3}{2}[(X_h(t) - X_h^o) + E_h(t) + I_h(t) + T_h(t) + R_h(t)]^{\frac{1}{2}} \times$$
$$[\Lambda - \beta_h I_h(t) - \mu_h N_h(t)] + 2[(X_b - X_b^o) + E_b + I_b]$$
$$\times [\pi - \beta_b I_b - \mu_b N_b],$$

Where

$N_h(t) = X_h(t) + E_h(t) + I_h(t) + T_h(t) + R_h(t),$

$N_b(t) = X_b(t) + E_b(t) + I_b(t)$

(') denotes the derivative with respect to time t.

Using $X_h^o = \frac{\Lambda}{\mu_h}$ and $X_b^o = \frac{\phi}{\mu_b}$, we have

$$F'(t) = \frac{3}{2}[(X_h(t) - X_h^o) + N_h(t) - X_h(t)]^{\frac{1}{2}} \times$$
$$[-\mu_h (X_h(t) - X_h^o) - \beta_h I_h(t) - \mu_h (N_h(t) - X_h(t))]$$
$$+ 2[(X_b(t) - X_b^o) + E_b(t) + I_b(t)] \times$$
$$[-\mu_b (X_b(t) - X_b^o) - \beta_b I_b(t) - \mu_b (N_b(t) - X_b(t))].$$

Thus $F'(t)$ is negative and $F'(t) = 0$ if and only if

$E_h(t) = I_h(t) = T_h(t) = R_h(t) = E_b(t) = I_b(t) = 0$ and

$X_h(t) = X_h^o$, $X_b(t) = X_b^o$. Hence by Lasalle's invariant principle [7], the disease-free equilibrium state E_1 is globally asymptotically stable on Ω.

Theorem 4.2 The endemic equilibrium E_2 of the system (1) is globally asymptotically stable on Ω for $\Lambda = \mu_h N_h^* + \beta_h I_h^*$ and $\pi = \mu_b N_b^* + \beta_b I_b^*$.

Proof: We define the Lyapunov function for the endemic equilibrium as

$$L(t) = [X_h(t) - X_h^*] + [V_h(t) - V_h^*] + [E_h(t) - E_h^*] + T_h(t) + R_h(t) + [X_b(t) - X_b^*] + E_b(t) + I_b(t).$$

By calculating the time dependent derivative of the above function along the solutions of the system (1), we have

$$L'(t) = \Lambda + \pi - \beta_h I_h - \beta_b I_b - \mu_h N_h - \mu_b N_b.$$

Using $\Lambda = \mu_h N_h^* + \beta_h I_h^*$ and $\pi = \mu_b N_b^* + \beta_b I_b^*$, we have

$$L'(t) = -\mu_h (N_h(t) - N_h^*) - \mu_b (N_b(t) - N_b^*) - \beta_h (I_h(t) - I_h^*) - \beta_b (I_b(t) - I_b^*),$$

where $N_h^* = X_h^* + E_h^* + I_h^* + T_h^* + R_h^*$ and $N_b^* = X_b^* + E_b^* + I_b^*$.

Thus $L'(t)$ is negative and $L'(t) = 0$ if and only if $X_h(t) = X_h^*$, $E_h(t) = E_h^*$, $I_h(t) = I_h^*$, $T_h(t) = T_h^*$, $R_h(t) = R_h^*$, $X_b(t) = X_b^*$, $E_b(t) = E_b^*$, $I_b(t) = I_b^*$.

Hence by Lasalle's invariant principle [7], the endemic equilibrium state E_2 is globally asymptotically stable on Ω.

5 Numerical results and discussion

We solve the proposed model by using Runge-Kutta fourth order scheme. Some of the parameter values in the proposed model based on reality, for example the duration of the infectious period, natural death rate, disease induced death rate, etc. (see Table 2). As a person infected with the avian influenza virus is only infectious for almost seven days, the recovery rate should be equal to 0.143 per day and not the inverse of the length of the illness. The natural death rate of human $\mu_h = 0.0000421$ per day, corresponding to the life expectancy of the human is 70 years. α_1, α_2 are the effective contact rates between S_h and E_h and between S_h and I_b respectively, α_3 is the effective contact rates between S_b and I_b, we choose these parameters arbitrarily as $\alpha_1 = 0.0002$, $\alpha_2 = 0.0025$ and $\alpha_3 = 0.01$. The values used for numerical simulations are given in Table 2, with $\pi = 10$, $\phi_h = 0.14$ and $\phi_b = 0.4$, which are biologically feasible. Figure 3 represents the human population and Figure 4 represents the birds population.

Table 2. Parameter values used for numerical simulations

Notation	Values	Resourse
Λ	2.5/day	[8]
μ_h	0.0000421/day	[9]
μ_b	0.00137/day	[10]
β_h	0.002/day	[11]
β_b	0.1/day	[10]
μ_h^{-1}	70 years	[12]
ε_h	0.00137/day	[13]
ρ_h	0.4	[14]

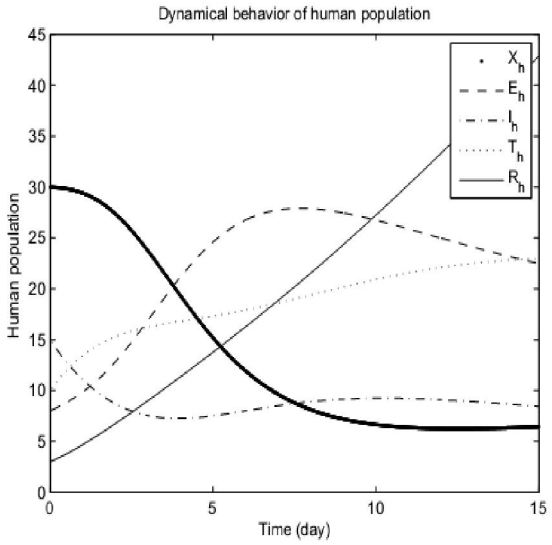

Figure 3. Plot shows human population

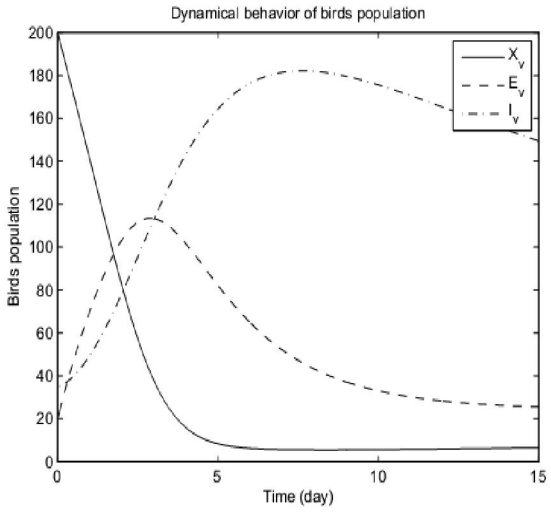

Figure 4. Plot shows bird population

6 Conclusion

In this work, we discussed the compartmental avian influenza model. As in epidemiological models, our model has two steady states, an uninfected steady state and endemically infected steady state. By establishing the stability results we found both the disease-free and the endemic equilibria. We also presented that the proposed model exhibits the phenomenon of backward bifurcation, where for $R_0 < 1,$ the locally asymptotically stable disease-free equilibrium co-exists with a locally asymptotically stable endemic equilibrium. Then to present the global stability of both the disease-free and endemic states, we developed Lyapunov functions. We believe that this new analysis is biologically more plausible than the previous assumptions.

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