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Predator–prey model with disease infection in both populations

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A predator–prey model with disease infection in both populations is proposed to account for the possibility of a contagious disease crossing species barrier from prey to predator. We obtain several threshold parameters from local analysis of various equilibria of the proposed system as well as coupled conditions on these threshold parameters which determine the stability of these equilibria. One of the coupled conditions, in the form of an ecological threshold number for the predator–prey ecosystem, always determines the coexistence of predators and prey. The other condition, in the form of a disease basic reproduction number, dictates whether the disease will become endemic in the ecosystem. Under one combination of these coupled conditions, a highly infectious disease could drive the predators to extinction when predators and prey would have coexisted without the disease. For another combination of the conditions, the predation of the more vulnerable infected prey could cause the disease to be eradicated in the ecosystem, in some case even approaching a disease-free periodic solution, when the disease would have otherwise remained endemic in the prey population in the absence of predation. This indicates that the presence of disease in both predators and prey could either promote or impair coexistence, and its precise impact needs to be explored specifically in each particular situation. By considering disease infection in both populations, our model also yields more complex dynamics, allowing for the possibility of bistability and periodic oscillation, in either disease-free or endemic states, in the ecosystem for which the conditions are obtained analytically and with the help of numerical simulations.

Keywords: species barrier; predator–prey coexistence; ecological threshold parameter; disease basic reproduction number; positive equilibrium; periodic oscillation.

1. Introduction

Infectious diseases have been known to be an important regulating factor for human and animal population sizes. In particular, for predator–prey ecosystems, infectious diseases coupled with predator–prey interaction to produce a complex combined effect as regulators of predator and prey sizes. In many ecological studies of predator–prey systems with disease, it is reported that the predators take a disproportionately high number of parasite-infected prey (e.g. Van Dobben, 1952; Vaughn & Coble, 1975; Temple, 1987). Some studies have even shown that parasite could change the external features or behaviour of the prey so that infected prey are more vulnerable to predation (see, e.g. Mech, 1970; Holmes & Bethel, 1972; Schaller, 1972; Krebs, 1978; Dobson, 1988; Peterson & Page, 1988; Moore,

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2002). For a concise and lucid discussion on this subject, the readers are referred to Hethcote *et al.* (2004).

Previous modelling studies of predator–prey system with infected prey include, among others, Anderson & May (1986), Hadeler & Freedman (1989), Venturino (1994, 1995), Chattopadhyay & Arino (1999), Han *et al.* (2001) and Hethcote *et al.* (2004). In particular, Hethcote *et al.* (2004) proposed a predator–prey model with logistic growth in prey to include a susceptible-infective-susceptible (SIS) infection with standard incidence in prey population with the infected prey being more vulnerable to predation. They discovered several interesting cases where the disease infection in prey could promote coexistence. For example, under certain parameter values, the greater vulnerability of the infected prey allows the predator population to persist when it would otherwise become extinct. Moreover, there is a case where predation on the more vulnerable prey can cause the disease to die out when it would remain endemic without the predators.

Most of these previous studies focussed mainly on parasite infection and in prey only, although some studies did consider infection of predator through eating prey (e.g. Anderson & May, 1986; Hadeler & Freedman, 1989; Venturino, 1994) or spread of disease in the predators (Venturino, 2002). Venturino (2001) also studied the dynamics of two competing species when one of them is subject to a disease, but the disease cannot cross the species barrier. However, the recent outbreaks of severe acute respiratory syndrome (SARS) and animal-to-human transmission of avian influenza (H5N1) demonstrated the possibility of infectious disease caused by a microorganism crossing the species barrier between different species by enlarging its host range (Klempner & Shapiro, 2004), including that of between prey and predator populations. Klempner & Shapiro (2004) made further distinction between what they termed as ‘small step to man’ and ‘giant leap to mankind’. The former describes a minor alteration in the microorganism’s host range resulting in intermittent human infections without human-to-human transmission as in the 1997 H5N1 avian influenza outbreak that occurred in Hong Kong that results in six fatal cases including young infants (Meslin *et al.*, 2001), while the latter describes the dreaded scenario of pandemic spread of the disease among humans (e.g. the feared human-to-human transmissible mutation of H5N1 leading to a global avian influenza pandemic). The recent SARS coronavirus presents a ‘middle ground’ of the two extremes crossing from animals to human host with limited (or inefficient) human-to-human transmission. The potential threat of an influenza pandemic also led to recent interest in scientific research to understand how and why some pathogens become capable of crossing host species barriers (Kuiken *et al.*, 2006).

Hadeler & Freedman (1989) had previously studied a predator–prey model with parasite infection where the disease is allowed to cross the species barrier. Moreover, assuming that the predators could get infected by eating prey and the prey could obtain the disease from parasites spread into the environment by predators, they obtained a threshold condition above which an endemic equilibrium or an endemic periodic solution could arise in the case where there is coexistence of the predator with the uninfected prey. Furthermore, they also showed that in the case where the predator cannot survive only on the prey in a disease-free environment, the parasitization could lead to persistence of the predator since the predators could only survive on the prey if some of the prey were more easily captured due to being diseased, provided a certain threshold for disease transmission is surpassed.

In this present work, our aim is to study the scenario where a small step is taken from prey to predator, to paraphrase Klempner & Shapiro (2004), where the predators can be infected upon contact with or being in the close vicinity of an infected prey during the process of predation, but the predators cannot infect each other. To further explore this hypothetical scenario of disease spreading among predators during the process of predation, we introduce a predator–prey model with logistic growth, SI mass action disease incidence in prey and infection of predators from infected prey. The predation is modelled

by Holling type-II functional response with saturation of the infected predators. A similar idea was also exploited in Venturino (2006) on disease in interacting species models.

The paper is organized in the following manner. The proposed 'small-step' model is given in Section 2. In Section 3, we briefly discuss the disease-free model, including a case where a unique globally orbitally stable limit cycle exists. Analysis of the full model will be given in Section 4. Section 5 is devoted to discussion on two disease basic reproduction numbers and three ecological threshold parameters which we had obtained analytically and on how these threshold parameters combined to give biologically meaningful conditions for the various ecologically plausible scenarios. Finally in Section 6, we provide numerical simulations to discuss some biologically interesting cases our model is able to exhibit.

2. The model

Let $S(t)$, $I(t)$, $P_1(t)$ and $P_2(t)$ be the total sizes of susceptible prey population, infected prey population, susceptible predator population and infected predator population, respectively, where t is the time variable. We list the key assumptions of our model as follows:

(A1) The susceptible prey follows logistic growth. Infected prey does not reproduce, but uses resources and so contributes to self-regulation in the predator–prey dynamics.

(A2) The disease is not transmitted horizontally or vertically in predators. The infected prey do not recover or become immune.

(A3) The incidence of prey is given by simple mass action law.

(A4) The predator functional response obeys the Holling type-II curve.

(A5) Growth rate of predators P_1 is proportional to their predation of healthy prey.

(A6) The infection of predators occurs during the process of predation, i.e. either during capturing, handling, consumption or by simply being in close vicinity of an infected prey, and hence is proportional to the predation of infected prey.

(A7) 'No recovery or immunity for infected predators'.

(A8) There is no reward for a predator to handle or catch an infected prey, other than getting infected.

(A9) The infected prey is more likely to be caught than the healthy ones, and the infected predators are more likely to die than the healthy ones.

For our model, the infected predators P_2 do not reproduce. Moreover, they arise only from the susceptible predator class P_1 through infection while in the process of predation that occurs at a rate λ_2 proportional to the rate of predation of susceptible predators on infected prey. Thus, infected predators could conceivably arise even if that subpopulation class P_2 was initially zero as it is bound to occur when a disease initially crosses the species barrier. The form of incidence of infection of predators is the same as the form of the functional response describing the predation rate since the infection is transmitted only by contact with infected prey during the process of predation.

Under the above assumptions, we have the following model equations, with the model flow diagram given in Fig. 1:

$$S' = rS\left(1 - \frac{S+I}{K}\right) - \lambda_1 IS - \frac{\alpha_1 S}{1+a_1 S}(P_1 + P_2),$$

$$I' = \lambda_1 IS - \frac{\alpha_2 I}{1+a_2 I}(P_1 + P_2) - \mu I,$$

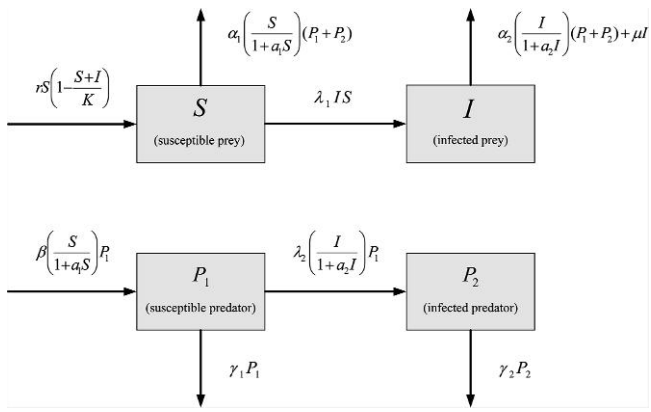

FIG. 1. The flow diagram of the model.

$$P_1' = \frac{\beta S}{1+a_1 S} P_1 - \gamma_1 P_1 - \frac{\lambda_2 I}{1+a_2 I} P_1,$$
$$P_2' = \frac{\lambda_2 I}{1+a_2 I} P_1 - \gamma_2 P_2. \tag{2.1}$$

Here,' ' stands for $\frac{\mathrm{d}}{\mathrm{d}t}$, and the model parameters are given as follows: r denotes the growth rate of the prey, K denotes the carrying capacity, μ denotes the death rate of I, $\lambda_1 IS$ is the incidence of infection of prey and $\lambda_2\left(\frac{I}{1+a_2 I}\right)P_1$ is the incidence of infection of predators, respectively. Moreover, a_1 and a_2 are the respective half saturation rates of S and I, γ_1 and γ_2 are the respective death rates of P_1 and P_2, α_1 and α_2 are the respective search rates of the susceptible and infective prey and 'β/α_1 is the conversion coefficient of P_1'. For the sake of simplicity, we have not included a term for natural death of susceptible prey in the first equation since the death rate of S can be easily incorporated in the growth rate r of S, with an appropriate adjustment for the definition of carrying capacity K. Note that all model parameters are positive. Moreover, to be consistent with the biological assumption (A9), we know $\alpha_1 \leqslant \alpha_2$ since the infected prey is more likely to be caught than the healthy ones and $\gamma_1 \leqslant \gamma_2$ since the infected predators are more likely to die than the healthy ones.

3. The disease-free case

We first consider the disease-free case. That is, we consider system (2.1) with $I = P_2 = 0$ which is given as follows:

$$S' = rS\left(1-\frac{S}{K}\right) - \alpha_1\left(\frac{S}{1+a_1 S}\right)P_1,$$
$$P_1' = \beta\left(\frac{S}{1+a_1 S}\right)P_1 - \gamma_1 P_1. \tag{3.1}$$

Analytical results for this system are described below, with the proofs given in the appendix. The first equation is well known (e.g. May, 1973, p. 190). Considered together with the second equation, system (3.1) has at most three equilibria. We first consider the local stability of each equilibrium. The Jacobian

matrix of (3.1) is given by

$$A_{(S,P_1)} = \begin{bmatrix} \frac{\partial f_1}{\partial S}(S, P_1) & \frac{\partial f_1}{\partial P_1}(S, P_1) \\ \frac{\partial f_2}{\partial S}(S, P_1) & \frac{\partial f_2}{\partial P_1}(S, P_1) \end{bmatrix} = \begin{bmatrix} \left(1 - \frac{2S}{K}\right)r - \frac{\alpha_1 P_1}{(1+a_1 S)^2} & -\frac{\alpha_1 S}{1+a_1 S} \\ \frac{\beta P_1}{(1+a_1 S)^2} & \frac{\beta S}{1+a_1 S} - \gamma_1 \end{bmatrix}.$$

The equilibria of the system are discussed below.

(1) Trivial equilibrium: $E_0 = (0, 0)$.
Since the eigenvalues of the Jacobian at E_0, r and $-\gamma$, are both positive, 'E_0 is a saddle point with stable manifold given by $\{(0, P_1)\colon P_1 \geqslant 0\}$'.

(2) Boundary equilibrium: $E_{\mathrm{B}} = (K, 0)$.
It is easy to show that if we let $R_1 = \frac{\beta K}{\gamma_1(1+a_1 K)}$, then E_{B} is locally asymptotically stable if and only if $R_1 < 1$. We have the following global result regarding the stability of the boundary equilibrium E_{B}.

LEMMA 3.1

(i) If $R_1 < 1$, then E_{B} is globally asymptotically stable for (3.1).
(ii) If $R_1 > 1$, then E_{B} is unstable for (3.1) and the positive equilibrium E^* exists.
(iii) If $R_1 = 1$, E_{B} is globally asymptotically stable for (3.1).

(3) Interior equilibrium: $E^* = (S^*, P_1^*)$, with $(S^*, P_1^*) = \left(\frac{\gamma_1}{\beta - a_1\gamma_1}, \frac{r}{\alpha_1}\left(1 - \frac{S^*}{K}\right)(1 + a_1 S^*)\right)$.
We have the following stability result when $R_1 > 1$.

LEMMA 3.2

(i) If $1 < R_1 < 1 + \frac{\beta}{a_1\gamma_1(1+a_1 K)}$, then E^* is locally asymptotically stable for (3.1).
(ii) If $R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1 K)}$, then E^* is unstable for (3.1).
(iii) If $R_1 = 1 + \frac{\beta}{a_1\gamma_1(1+a_1 K)}$, then E^* may be either a centre or a spiral point for (3.1).

We now give two theorems pertaining to the global stability of the positive interior equilibrium E^*.

THEOREM 3.3 If $1 < R_1 \leqslant 1 + \frac{\beta}{a_1\gamma_1(1+a_1 K)}$, then E^* is globally asymptotically stable for (3.1).

THEOREM 3.4 If $R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1 K)}$, then E^* is unstable for (3.1) and the system (3.1) has a unique limit cycle which is globally orbitally stable.

In particular, the case where an orbitally stable limit cycle exists in SP_1-plane will be important in the later discussion of the full model. We summarize our results in Table 1. Note that E_0 is unstable for all cases and hence omitted from Table 1.

4. The model with disease

We now proceed to consider the full 4D model in system (2.1), which has as many as five equilibria, depending on the parameter values. We can divide these five equilibria into three types: trivial, boundary and positive interior equilibria. First, we consider the local stability of the trivial equilibrium and the

TABLE 1 *Asymptotic states for disease-free predator–prey model*

Case	$E_{\mathrm{B}} = (K, 0)$	$E^* = (S^*, P_1^*)$
$R_1 \leqslant 1$	GAS	—
$1 < R_1 \leqslant 1 + \beta/a_1\gamma_1(1 + a_1K)$	unstable	GAS
$R_1 > 1 + \beta/a_1\gamma_1(1 + a_1K)$	unstable	unstable (♯)

Note: 'GAS' denotes that equilibrium is globally asymptotically stable; '—' denotes that equilibrium does not exist and '(♯)' denotes that there is a unique limit cycle that is globally orbitally stable.

boundary equilibria. Note that all equilibria in the 4D system are boldfaced to distinguish them from the equilibria of 2D disease-free model. The Jacobian matrix of (2.1) is given by

$$A_{(S,I,P_1,P_2)} = \begin{bmatrix} r\left(1 - \frac{2S+I}{K}\right) - \lambda_1 I - \frac{\alpha_1(P_1+P_2)}{(1+a_1S)^2} & -\left(\frac{r}{K} + \lambda_1\right)S & -\frac{\alpha_1 S}{1+a_1S} & -\frac{\alpha_1 S}{1+a_1S} \\ \lambda_1 I & \lambda_1 S - \frac{\alpha_2(P_1+P_2)}{(1+a_2I)^2} - \mu & -\frac{\alpha_2 I}{1+a_2I} & -\frac{\alpha_2 I}{1+a_2I} \\ \frac{\beta P_1}{(1+a_1S)^2} & -\frac{\lambda_2 P_1}{(1+a_2I)^2} & \frac{\beta S}{1+a_1S} - \gamma_1 - \frac{\lambda_2 I}{1+a_2I} & 0 \\ 0 & \frac{\lambda_2 P_1}{(1+a_2I)^2} & \frac{\lambda_2 I}{1+a_2I} & -\gamma_2 \end{bmatrix}.$$

We then have the following results on the equilibria of system (2.1):

(1) Trivial equilibrium: $\mathbf{E_0} = (0, 0, 0, 0)$.
It is trivial to show that $\mathbf{E_0} = (0, 0, 0, 0)$ always exists but is unstable for (2.1).

(2) Three boundary equilibria.
Subcase (i) $\mathbf{E}_{\mathrm{B}} = (K, 0, 0, 0)$ is the axial equilibrium on S-axis with healthy prey only, which always exists.

LEMMA 4.1 Let $R_0 = \frac{K\lambda_1}{\mu}$.

(i) If $R_0 < 1$ and $R_1 < 1$, then $\mathbf{E}_{\mathrm{B}}$ is locally asymptotically stable for (2.1).
(ii) If $R_0 > 1$ or $R_1 > 1$, then $\mathbf{E}_{\mathrm{B}}$ is unstable for (2.1).
(iii) In all other situation, we need to investigate further.

Subcase (ii) $\overline{\mathbf{E}}_{\mathrm{B}} = (\overline{S}, \overline{I}, 0, 0)$ is the boundary equilibrium on SI-plane with endemic prey population only.

LEMMA 4.2 Let $R_0 > 1$ and $\overline{R}_1 = \frac{\beta\overline{S}}{\gamma_1(1+a_1\overline{S})}$.

(i) If $\overline{R}_1 < 1 + \frac{\lambda_2\overline{I}}{\gamma_1(1+a_2\overline{I})}$, then $\overline{\mathbf{E}}_{\mathrm{B}}$ is locally asymptotically stable for (2.1).
(ii) If $\overline{R}_1 > 1 + \frac{\lambda_2\overline{I}}{\gamma_1(1+a_2\overline{I})}$, then $\overline{\mathbf{E}}_{\mathrm{B}}$ is unstable for (2.1).
(iii) In all other cases, we need to investigate further.

Subcase (iii) $\mathbf{E}^*_{\mathrm{B}} = (S^*, 0, P_1^*, 0)$ is the boundary equilibrium on SP_1-plane with disease-free coexistence of predators and prey. S^* and P_1^* are as defined in Section 3.

LEMMA 4.3 Let $R_0^* = \frac{\lambda_1 S^*}{\alpha_2 P_1^* + \mu}$.

(i) If $R_0^* < 1$ and $1 < R_1 < 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$, then $\mathbf{E}_{\mathrm{B}}^*$ is locally asymptotically stable for (2.1).
(ii) If $R_0^* > 1$ or $R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$, then $\mathbf{E}_{\mathrm{B}}^*$ is unstable for (2.1).
(iii) In all other situations, we need to investigate further.

The proofs of Lemmas 4.1–4.3 are given in the appendix.

(3) Positive interior equilibrium $\widetilde{\mathbf{E}} = (\widetilde{S}, \widetilde{I}, \widetilde{P}_1, \widetilde{P}_2)$ with endemic coexistence.
We have the following result on the existence of $\widetilde{\mathbf{E}}$, also proved in the appendix.

LEMMA 4.4 Let $\widetilde{R}_1 = \frac{\beta\widetilde{S}}{\gamma_1(1+a_1\widetilde{S})}$. If $\widetilde{S}$ satisfies $\overline{S} < \widetilde{S}$ and $\widetilde{S} + \widetilde{I} < K$ and if $1 < \widetilde{R}_1 < 1 + \frac{\lambda_2}{a_2\gamma_1}$, $\widetilde{\mathbf{E}} = (\widetilde{S}, \widetilde{I}, \widetilde{P}_1, \widetilde{P}_2)$ exists and is a positive equilibrium of (2.1) with $\widetilde{I} = \frac{\widetilde{S}(\beta - a_1\gamma_1) - \gamma_1}{\lambda_2(1+a_1\widetilde{S}) - a_2[\widetilde{S}(\beta - a_1\gamma_1) - \gamma_1]}$, $\widetilde{P}_1 = \frac{1}{\alpha_2}(\lambda_1\widetilde{S} - \mu)(1 + a_2\widetilde{I})\big[1 + \frac{\lambda_2}{\gamma_2}\big(\frac{\widetilde{I}}{1+a_2\widetilde{I}}\big)\big]^{-1}$ and $\widetilde{P}_2 = \frac{\lambda_2}{\gamma_2}\big(\frac{\widetilde{I}}{1+a_2\widetilde{I}}\big)\widetilde{P}_1$.

Note that when $(\beta - a_1\gamma_1) - \lambda_2 = 0$, the positive equilibrium is unique, otherwise the uniqueness of $\widetilde{\mathbf{E}}$ is determined by the sign of $b^2 - 4ac$ which is difficult to determine. Moreover, the stability of $\widetilde{E}$, when it exists, is difficult to analyse. We will make use of numerical simulations to discuss the possible cases.

5. Ecological and disease threshold parameters

We first discuss the biological significance of the five threshold parameters obtained, each of which has clear and distinct biological meaning.

(a) $R_1 = \frac{\beta K}{\gamma_1(1+a_1K)}$ determines the local stability of $E_{\mathrm{B}} = (K, 0)$, the axial equilibrium on S-axis, in the disease-free system (3.1). Here, $\frac{\beta K}{1+a_1K}$ is the birth rate of predator at E_{B} and $\frac{1}{\gamma_1}$ is the mean lifespan of a predator. Subsequently, their product gives the mean number of newborn predators by a predator, which can be interpreted as the 'ecological' basic reproduction number of a predator–prey system without disease. We note also that this term, first formulated and explained by Pielou (1969), is the average number of prey converted to predator biomass in a course of the predator's life span (Hethcote *et al.*, 2004).

(b) $R_0 = \frac{K\lambda_1}{\mu}$, together with R_1, determines the local stability of $\mathbf{E}_{\mathrm{B}} = (K, 0, 0, 0)$, the axial equilibrium on S-axis, in the 4D system (2.1). Here, $K\lambda_1$ is the infection rate of a new infective prey appearing in a totally susceptible prey population and $\frac{1}{\mu}$ is the duration of infectivity of an infective prey, the product of which is the disease basic reproduction number of disease in the prey population. $R_1 < 1$ implies that the predators will become extinct, while $R_0 < 1$ implies that the disease will be eradicated in the prey population. Hence, the combination of these two conditions results in $\mathbf{E}_{\mathrm{B}}$ being locally asymptotically stable for system (2.1).

(c) $\overline{R}_1 = \frac{\beta\overline{S}}{\gamma_1(1+a_1\overline{S})}$, together with R_0, determines the local stability of $\overline{\mathbf{E}}_{\mathrm{B}} = (\overline{S}, \overline{I}, 0, 0)$, the boundary equilibrium at which disease persists in the prey population while the predator population becomes extinct. Here, $\frac{\beta\overline{S}}{1+a_1\overline{S}}$ is the growth rate of a newborn predator at $\overline{\mathbf{E}}_{\mathrm{B}}$ and γ_1 is the removal rate of predators without disease, hence $\overline{R}_1$ gives the ecological basic reproduction number of the predator population when disease is endemic in the prey population. Moreover,

$\overline{R}_1 < 1 + \frac{\lambda_2 \overline{I}}{\gamma_1(1+a_2\overline{I})}$ implies that the predators will become extinct in an environment when disease is prevalent in the prey population which, together with $R_0 > 1$ guaranteeing the endemicity of disease in prey, gives the condition for the locally asymptotic stability of $\overline{\mathbf{E}}_{\mathrm{B}}$. Note also that since $f(x) = \frac{\beta x}{1+a_1 x}$ is an increasing function and $\overline{S} < K$, it follows that $\overline{R}_1 < R_1$.

(d) $R_0^* = \frac{\lambda_1 S^*}{\alpha_2 P_1^* + \mu}$, together with R_1, determines the local stability of $\mathbf{E}_{\mathrm{B}}^* = (S^*, 0, P_1^*, 0)$, the boundary equilibrium at which the predator and prey populations coexist with no disease. Here, $\lambda_1 S^*$ is the infection rate of an infective prey at $\mathbf{E}_{\mathrm{B}}^*$ and $\alpha_2 P^* + \mu$ is the removal rate of infective prey at $\mathbf{E}_{\mathrm{B}}^*$, subsequently R_0^* is the disease basic reproduction number of an infected prey when entering a disease-free environment where predators and prey coexist. It follows that R_1 determines the (disease-free) coexistence of predator–prey populations, while $R_0^* < 1$ ensures low level of infection from infected prey to predators, combining the two yields the local asymptotic stability of $\mathbf{E}_{\mathrm{B}}^*$. When $R_0^* > 1$, clearly the disease will become endemic. However, when $R_0^* < 1$, the situation is more complicated. We have shown that if $1 < R_1 < 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$, $\mathbf{E}_{\mathrm{B}}^*$ is asymptotically stable. Moreover, if $R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$, $\mathbf{E}_{\mathrm{B}}^*$ is unstable. Numerical simulations showed that in this case there is a unique periodic solution in SP_1-plane, the disease-free region, which is orbitally stable, although we have no formal proof for this to hold. Note that if $R_1 > 1$, $\mathbf{E}_{\mathrm{B}}^*$ exists and $K > S^*$, which implies that $R_0 > R_0^*$. That is, the condition for endemicity at coexistence ($R_0^* > 1$) is stronger than the endemicity condition for prey population alone ($R_0 > 1$).

(e) $\widetilde{R}_1 = \frac{\beta \widetilde{S}}{\gamma_1(1+a_1\widetilde{S})}$, together with R_0^*, determines the existence of $\widetilde{\mathbf{E}} = (\widetilde{S}, \widetilde{I}, \widetilde{P}_1, \widetilde{P}_2)$, the endemic positive equilibrium at which predators and prey coexist. Here, again $\widetilde{R}_1$ is the ecological basic reproduction number of the predator–prey system at $\widetilde{\mathbf{E}}$ when both populations coexist and with disease being endemic. $1 < \widetilde{R}_1 < 1 + \frac{\lambda_2}{a_2\gamma_1}$ implies the coexistence of predator–prey system near $\widetilde{\mathbf{E}}$, while $R_0^* > 1$ ensures the disease becoming endemic, together of the two yields the local asymptotic stability of $\widetilde{\mathbf{E}}$. Moreover, it is easy to see that $\overline{R}_1 < \widetilde{R}_1 < R_1$. Biologically, the inequality indicates that the persistence condition for prey population at endemic state ($\overline{R}_1 > 1$) is stronger than that of the coexistence at endemic state ($\widetilde{R}_1 > 1$), which in turn is stronger than that of disease-free coexistence ($R_1 > 1$).

Note that case (d) above with the disease-free periodic solution in SP_1-plane is interesting biologically. When $R_0^* < 1$ and $R_0 > 1$, the populations could sustain but without maintaining an endemic steady state ($\widetilde{\mathbf{E}}$ either does not exist or is unstable). That is, if the reproduction level of the prey is high enough $\left(\text{i.e. } R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}\right)$, the infective populations could persist, albeit fluctuating and approaching an orbitally stable limit cycle. Moreover, $R_1 > 1$ by itself no longer guarantees the coexistence of prey and predator when in the presence of disease. More precisely, the basic reproduction number of prey population must be sufficiently larger than 1 to insure persistence of predators. Similarly for (e), where $\widetilde{R}_1 > 1$ does not guarantee the coexistence of prey and predator at the positive (endemic) equilibrium $\widetilde{\mathbf{E}}$, requiring the stronger condition of $\widetilde{R}_1 > 1 + \frac{\lambda_2}{a_2\gamma_1}$.

Of the five parameters, R_0 and R_0^* are disease basic reproduction numbers which determine the local stability of the two disease-free equilibria $\mathbf{E}_{\mathrm{B}}$ and $\mathbf{E}_{\mathrm{B}}^*$, respectively; while R_1, $\overline{R}_1$ and $\widetilde{R}_1$ are the average numbers of prey converted to predator biomass in a course of the predator's life span. Note that if we define a function $R_1(S) = \frac{\beta S}{\gamma_1(1+a_1S)}$, then it follows that $R_1 = R_1(K)$, $\overline{R}_1 = R_1(\overline{S})$ and $\widetilde{R}_1 = R_1(\widetilde{S})$, which are the respective threshold parameters or ecological basic reproduction numbers for the predator–prey system at E_{B}, $\overline{\mathbf{E}}_{\mathrm{B}}$ and $\widetilde{\mathbf{E}}$ that determine the coexistence of prey and predators at these equilibria.

It is interesting to note that in all cases involving the 4D system (2.1), i.e. cases (b)–(e), coupled conditions are needed for the local stability of the equilibria under consideration. One of the condition always determine the coexistence of the predator–prey system, the other condition dictates whether the disease will be eradicated. This phenomenon of dual threshold parameters has previously been observed in Han *et al.* (2001) and Hethcote *et al.* (2004).

6. Numerical examples and discussions

Due to the difficulty in fully analysing the stability of the equilibria for the full 4D system (2.1), we discuss the possible cases with the aid of the threshold parameters and numerical examples. We first note that, from Section 4, the trivial equilibrium $\mathbf{E_0}$ always exists and is unstable, and hence need not be considered here. The boundary equilibrium $\mathbf{E}_{\mathrm{B}}$ always exists and if it is asymptotically stable (i.e. $R_0 < 1$ and $R_1 < 1$), then $\overline{\mathbf{E}}_{\mathrm{B}}$ and $\mathbf{E}^*_{\mathrm{B}}$ will not exist. Moreover, when $\overline{\mathbf{E}}_{\mathrm{B}}$ or $\mathbf{E}^*_{\mathrm{B}}$ do not exist (i.e. $R_0 \leqslant 1$ or $R_1 \leqslant 1$), there is no positive interior equilibrium. When $\overline{\mathbf{E}}_{\mathrm{B}}$ and $\mathbf{E}^*_{\mathrm{B}}$ exist, $\mathbf{E}_{\mathrm{B}}$ is unstable. Furthermore, if $\overline{\mathbf{E}}_{\mathrm{B}}$ exists with $\overline{R}_1 > 1 + \frac{\lambda_2 \overline{I}}{\gamma_1(1+a_2\overline{I})}$ since $\overline{R}_1 < R_1$, we have that $R_1 > 1$ and $\mathbf{E}^*_{\mathrm{B}}$ exist. On the other hand, if $\mathbf{E}^*_{\mathrm{B}}$ does exist with $R^*_0 \geqslant 1$, we have that $R_0 > 1$ and $\overline{\mathbf{E}}_{\mathrm{B}}$ exist. In Table 2, we list the conditions for nine cases.

We now give 3D figures of simulated examples in SIP_1-space for some of the more interesting cases. For all examples, P_2 is omitted since its value at all equilibria is 0 except at the positive equilibrium

TABLE 2 *Asymptotic states for the full model*

	Case (simulation figure)	$\mathbf{E}_{\mathrm{B}}$	$\overline{\mathbf{E}}_{\mathrm{B}}$	$\mathbf{E}^*_{\mathrm{B}}$	$\widetilde{\mathbf{E}}$
1	$R_0 < 1, R_1 < 1$	AS	—	—	—
2	$R_0 > 1, R_1 \leqslant 1$	unstable	AS	—	—
3	$R_0 \leqslant 1, 1 < R_1 < 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$	unstable	—	AS	—
4	$R^*_0 < R_0 \leqslant 1, R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$ (Fig. 2)	unstable	—	unstable (♯)	—
5	$R_0 > R^*_0 > 1, \overline{R}_1 < 1 + \frac{\lambda_2\overline{I}}{\gamma_1(1+a_2\overline{I})}$, $1 < R_1 < 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$ (Fig. 3)	unstable	AS	unstable	—
6	$1 + \frac{\beta}{a_1\gamma_1(1+a_1K)} > R_1 > \overline{R}_1 > 1 + \frac{\lambda_2\overline{I}}{\gamma_1(1+a_2\overline{I})}$, $R_0 > 1 > R^*_0$ (Fig. 4)	unstable	unstable	AS	—
7	$R_0 > 1 > R^*_0, \overline{R}_1 > 1 + \frac{\lambda_2\overline{I}}{\gamma_1(1+a_2\overline{I})}$, $R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$ (Fig. 5)	unstable	unstable	unstable (♯)	—
8	$R_0 > 1 > R^*_0, \overline{R}_1 < 1 + \frac{\lambda_2\overline{I}}{\gamma_1(1+a_2\overline{I})}$, $1 < R_1 < 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$ (Fig. 6)	unstable	AS	AS	(*)
9	$R_0 > 1 > R^*_0, \overline{R}_1 < 1 + \frac{\lambda_2\overline{I}}{\gamma_1(1+a_2\overline{I})}$, $R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$ (Fig. 7)	unstable	AS	unstable (♯)	(*)

Note: 'AS' denotes that the equilibrium is asymptotically stable; '—' denotes that the equilibrium does not exist; '(♯)' denotes that numerical simulation showed that in this case there is a unique periodic solution in SP_1-plane which is orbitally stable and '(*)'denotes that numerical simulations showed that in this case the unique positive interior equilibrium is unstable.

(cases 7 and 8), where all elements are positive. Case 1 in Table 2 is straightforward with the disease-free boundary equilibrium $\mathbf{E}_{\mathrm{B}}$ (globally) asymptotically stable, and $\overline{\mathbf{E}}_{\mathrm{B}}$, $\mathbf{E}_{\mathrm{B}}^{*}$ and $\widetilde{\mathbf{E}}$ do not exist. Here, the predators become extinct and the prey goes to K, its disease-free carrying capacity, and hence we do not provide the simulation result. Case 2, with the predators becoming extinct and the prey population becoming endemic with population size below its carrying capacity K, and case 3, with all solutions starting in $\mathcal{S}$ going to the disease-free coexistence of predators and prey $\mathbf{E}_{\mathrm{B}}^{*}$, are also straightforward and hence no simulations are given.

For the numerical simulations, for which we used the Phaser 2.1 scientific software for simulating dynamical systems, the following parameters values in Table 2 are the same for all simulations: $r = 2$, $\lambda_2 = 0.1$, $a_1 = 0.01$, $\beta = 0.015$, $\gamma_1 = 1$, $\gamma_2 = 0.5$ and $\alpha_1 = 0.1$. There are three trajectories symbolized by blue, green and grey in these figures and starting at SI-plane, SP_1-plane, IP_1-plane and the interior region $\mathcal{S} = \{(S, I, P_1) \in \mathcal{R}^3 | S > 0, I > 0, P_1 > 0\}$, respectively. We are able to disregard the variable P_1 in our figures because P_1 goes to 0 if the variable I goes to 0, hence we only need to make a distinction when I does not go to 0. Note also that the equilibrium at the origin $\mathbf{E_0}$ always exists but is unstable with a stable region of the I-axis. Moreover, the ranges on the axes were omitted from each figure for the sake of brevity.

For case 4 (see Fig. 2), we let $K = 600$, $\mu = 0.9$, $\lambda_1 = 0.0014$, $a_2 = 0.5$ and $\alpha_2 = 0.5$. $\mathbf{E}_{\mathrm{B}}$ and $\mathbf{E}_{\mathrm{B}}^{*}$ are unstable. $\overline{\mathbf{E}}_{\mathrm{B}}$ and $\widetilde{\mathbf{E}}$ do not exist. The blue trajectory approaches $\mathbf{E}_{\mathrm{B}}$. The green and grey trajectories approach the unique and orbitally stable limit cycle. Similar to case 3, all solutions starting in $\mathcal{S}$ go to disease-free coexistence of predators and prey, but in an oscillatory manner.

For case 5 (see Fig. 3), we let $K = 490$, $\mu = 0.9$, $\lambda_1 = 0.002$, $a_2 = 0.5$ and $\alpha_2 = 0.01$. $\mathbf{E}_{\mathrm{B}}$ and $\mathbf{E}_{\mathrm{B}}^{*}$ are unstable, $\widetilde{\mathbf{E}}$ does not exist and $\overline{\mathbf{E}}_{\mathrm{B}}$ is asymptotically stable. The blue and grey trajectories approach $\overline{\mathbf{E}}_{\mathrm{B}}$. The green trajectory approaches $\mathbf{E}_{\mathrm{B}}^{*}$. Here, unless the trajectory starts from the disease-free region SP_1-plane, the predators become extinct and the prey population goes to endemic steady state. This case indicates the important role which a highly infectious disease ($R_0 > R_0^{*} > 1$) can play in driving the predators to extinction when the predators and prey would have coexisted without the disease ($R_1 > 1$). It is interesting that this seems to be the exact opposite of case 3 in Hethcote *et al.* (2004), where the greater vulnerability of infected prey allows the predators to persist when they would have become extinct without the disease.

For case 6 (see Fig. 4), we let $K = 490$, $\mu = 0.9$, $\lambda_1 = 0.002$, $a_2 = 0.5$ and $\alpha_2 = 0.5$. $\mathbf{E}_{\mathrm{B}}$ and $\overline{\mathbf{E}}_{\mathrm{B}}$ are unstable, $\mathbf{E}_{\mathrm{B}}^{*}$ is asymptotically stable and $\widetilde{\mathbf{E}}$ does not exist. The blue trajectory approaches $\overline{\mathbf{E}}_{\mathrm{B}}$. The green

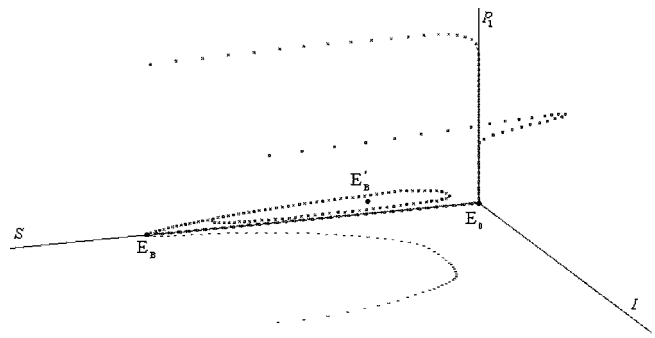

FIG. 2. Simulation for case 4 of Table 2. The dashed (-) trajectory approaches $\mathbf{E}_{\mathrm{B}}$. The crossed (x) and boxed trajectories approach the unique and orbitally stable limit cycle.

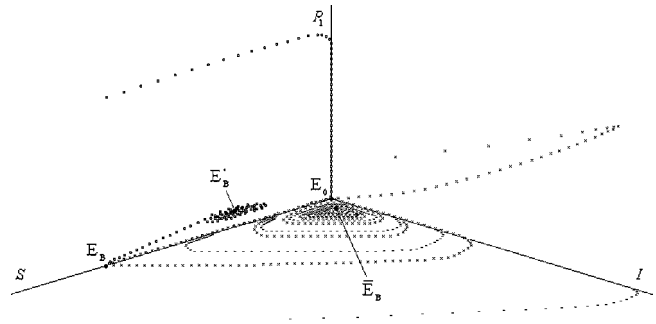

FIG. 3. Simulation for case 5 of Table 2. The dashed (-) and boxed trajectories approach $\overline{\mathbf{E}}_{\mathrm{B}}$. The crossed (x) trajectory approaches $\mathbf{E}_{\mathrm{B}}^{*}$.

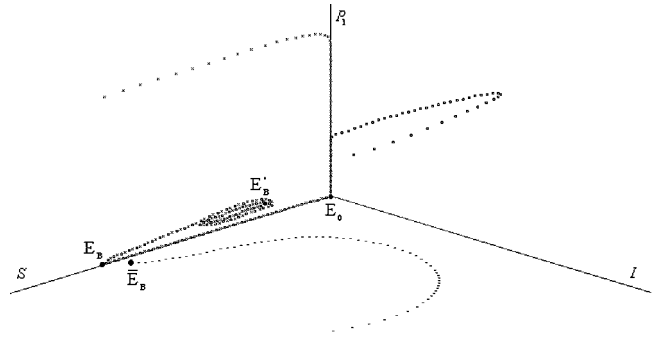

FIG. 4. Simulation for case 6 of Table 2. The dashed (-) trajectory approaches $\overline{\mathbf{E}}_{\mathrm{B}}$. The crossed (x) and boxed trajectories approach $\mathbf{E}_{\mathrm{B}}^{*}$.

and grey trajectories approach $\mathbf{E}_{\mathrm{B}}^{*}$. That is, all solutions starting in $\mathcal{S}$ go to disease-free coexistence of predators and prey. This interesting case is similar to case 5 in Hethcote *et al.* (2004), where the predation of the more vulnerable infected prey causes the disease to be eradicated in the ecosystem ($R_0^{*} < 1$) when it would have remained endemic in prey in the absence of predation ($R_0 > 1$).

For case 7 (see Fig. 5), we let $K = 600$, $\mu = 0.9$, $\lambda_1 = 0.002$, $a_2 = 0.5$ and $\alpha_2 = 0.5$. $\mathbf{E}_{\mathrm{B}}$, $\overline{\mathbf{E}}_{\mathrm{B}}$ and $\mathbf{E}_{\mathrm{B}}^{*}$ are all unstable and $\widetilde{\mathbf{E}}$ does not exist. The blue trajectory approaches $\overline{\mathbf{E}}_{\mathrm{B}}$. The green and grey trajectories approach the unique limit cycle which is orbitally stable. Here again, the predation of the more vulnerable infected prey causes the disease to be eradicated in the ecosystem ($R_0^{*} < 1$), albeit in an oscillatory manner, when it would have remained endemic in prey in the absence of predation ($R_0 > 1$).

For case 8 (see Fig. 6), we let $K = 490$, $\mu = 0.4$, $\lambda_1 = 0.002$, $a_2 = 0.402$ and $\alpha_2 = 0.5$. $\mathbf{E}_{\mathrm{B}}$ is unstable, $\overline{\mathbf{E}}_{\mathrm{B}}$ and $\mathbf{E}_{\mathrm{B}}^{*}$ are asymptotically stable and we have bistability. Note also that there is a unique positive interior equilibrium $\widetilde{\mathbf{E}}$ which is unstable from our simulations. Thus, we have another purple trajectory which starts near the positive interior equilibrium. The blue trajectory approaches $\overline{\mathbf{E}}_{\mathrm{B}}$ and the green, grey and purple trajectories approach $\mathbf{E}_{\mathrm{B}}^{*}$. The bistability means that there is a stable manifold of $\widetilde{\mathbf{E}}$ which separates the regions of stability for $\overline{\mathbf{E}}_{\mathrm{B}}$ and $\mathbf{E}_{\mathrm{B}}^{*}$. Biologically, it indicates that trajectories starting in different regions will approach either the disease-free coexistence or the endemic steady state of prey alone. Note also that this case differs from case 6 only in smaller $\overline{R_1}$, the ecological basic reproduction number for prey population at endemic state.

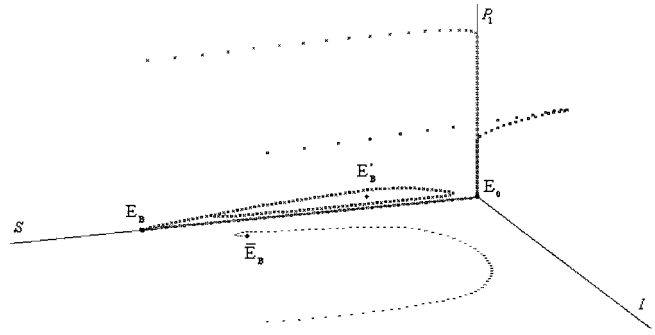

FIG. 5. Simulation for case 7 of Table 2. The dashed (-) trajectory approaches $\overline{\mathbf{E}}_{\mathrm{B}}$. The crossed (x) and boxed trajectories approach the unique limit cycle which is orbitally stable.

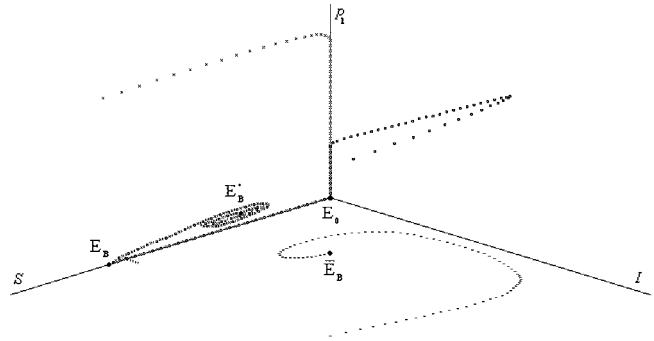

FIG. 6. Simulation for case 8 of Table 2. There is another vertical dashed trajectory that starts near the positive interior equilibrium. The dashed (-) trajectory approaches $\overline{\mathbf{E}}_{\mathrm{B}}$, and the crossed (x), boxed and vertical dashed trajectories approach $\mathbf{E}_{\mathrm{B}}^*$.

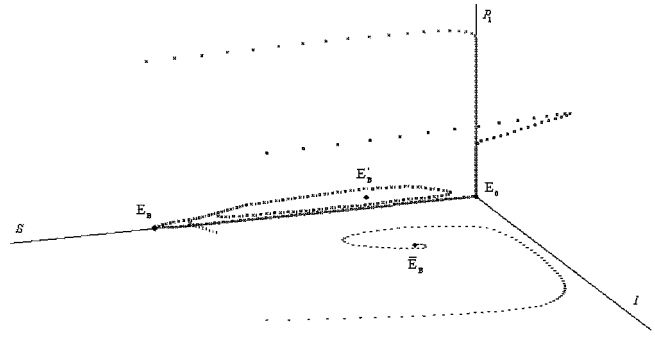

FIG. 7. Simulation for case 9 of Table 2. The vertical dashed trajectory starts near the positive interior equilibrium. The dashed (-) trajectory approaches $\overline{\mathbf{E}}_{\mathrm{B}}$. The crossed (x), boxed and vertical dashed trajectories approach the limit cycle.

For case 9 (see Fig. 7), we let $K = 600$, $\mu = 0.4$, $\lambda_1 = 0.002$, $a_2 = 0.402$ and $\alpha_2 = 0.5$. $\mathbf{E}_{\mathrm{B}}$ and $\mathbf{E}_{\mathrm{B}}^*$ are unstable and $\overline{\mathbf{E}}_{\mathrm{B}}$ is asymptotically stable. The system has a unique positive interior equilibrium $\widetilde{\mathbf{E}}$ which is again unstable from the simulations we made. Moreover, there is a unique limit cycle in SP_1-plane which is orbitally stable. Again, we have a purple trajectory which starts near the positive interior equilibrium. The blue trajectory approaches $\overline{\mathbf{E}}_{\mathrm{B}}$. The green, grey and purple trajectories approach the orbitally stable limit cycle. Interestingly, this is the only case we could find where, asymptotically, the predators and prey coexist in endemic state, albeit in an oscillatory manner.

Comparing to the model of Hethcote *et al.* (2004) with disease in prey only, the absence of the case where the vulnerability of infected prey allows the predators to persist when they would not have survived otherwise without the disease clearly exhibits the importance of a disease which could also infect the predators that leads to changes in the basic dynamics of the system. On the contrary, the present model includes the possibility (case 5) of a highly infectious disease ($R_0 > R_0^* > 1$) driving the predators to extinction when the predators and prey would have coexisted without the disease ($R_1 > 1$), which further highlights the possibly damaging role played by a disease that infects both predators and prey. On the other hand, under a different range of parameters (as demonstrated by cases 6 and 7), the predation of more vulnerable infected prey could cause the disease to be eradicated in the ecosystem ($R_0^* < 1$), albeit perhaps in an oscillatory manner, when it would have remained endemic in prey in the absence of predation ($R_0 > 1$). Hence, the presence of disease in both predators and prey could be either promote or impair coexistence, and needs to be explored further in each particular relevant situation.

Our model with disease in both predator and prey populations provides complex dynamics, allowing for the possibility of bistability and periodic oscillation in the ecosystem. The existence of an interior equilibrium with predators and prey coexisting and both endemic is also interesting biologically, although we are not able to fully analyse it, and hence is an appealing open problem for future studies. Moreover, the analysis on interior equilibrium in Section 4 indicates that, under a complicated set of conditions, it is possible theoretically for multiple interior equilibria to exist. However, we have not been able to find a numerical example for this case.

The parameters relating to P_2, namely λ_2 and γ_2, does not appear in any of the threshold parameters we obtained in Section 5. However, λ_2 does appear in the range of values for $\bar{R}_1$ in cases 5–9. For example, by comparing cases 7 (Fig. 5) and 9 (Fig. 7), we note that λ_2 plays a role in determining whether trajectories starting in the SI-plane approach $\bar{E}_B$ (as in Fig. 7) or the limit cycle. Hence, P_2 plays only a minor and indirect role in the spread of disease when compared to the other subpopulations mainly due to the assumption that the infected predators are unable to infect other members of the population.

A problem of modelling interest is when one assumes that once the predators are infected, they can infect other predators—a current issue of interest considering the speculation regarding the potential threat of H5N1 mutating to human-to-human transmissible strain. There has been some documentation of the possible human-to-human infection of H5N1 (Ungchusak *et al.*, 2005). Mathematically, it would further complicate the dynamics by adding at least one more boundary equilibrium, $\hat{E_{\mathrm{B}}} = (\hat{S}, 0, \hat{P}_1, \hat{P}_2)$, where disease-free prey coexists with endemic predator population yielding a corresponding additional disease basic reproduction number for this scenario. For our present study, we have not included either infection between predators or even infection by a third migratory population (e.g. wild migratory waterfowl).

Furthermore, we had assumed no vertical transmission. However, a recent report on pathology of SARS indicates that there is some evidence of viral replication in the circulating mononuclear cells of the fetus, which supports the possibility of vertical transmission for SARS (Ng & To, 2007). In order

to account for this remote possibility of vertical transmission of disease in either predators or prey, however, major modification in our model would be required to include the growth in infected prey (I) due to birth as well as the growth in infected predators (P_2) due to predation of (susceptible and sick) prey by infected predators, and hence is not pursued in this work.

Another related issue is that of disease control to eliminate disease in either prey or predator population. For control of avian influenza epidemic in birds, vaccination has been suggested as an option for the prevention of bird infections (Lee & Suarez, 2005) and is being used by some countries like China on a historically massive scale in an attempt to prevent a potentially massive influenza pandemic (Cyranoski, 2005). However, the present difficulty in implementation, risks and delays involved in a massive bird vaccination program made it considerably less efficient and effective as an option for prevention (Normile, 2004). It has even been suggested that a possible source of the continuing H5N1 pandemic threat may be that the pathogenicity of H5N1 viruses is masked by bad agricultural vaccines (Webster *et al.*, 2006). Vaccination and culling had both been modelled in recent years for the control of foot-and-mouth disease (FMD) epidemics (e.g. Woolhouse *et al.*, 1996; Woolhouse, 2003; Chowell *et al.*, 2006; Hutber *et al.*, 2006). Culling has traditionally been used in the prevention of animal disease outbreaks, sometimes in combination with other measures and mixed success (Courtenay *et al.*, 2002). Many of the above-mentioned studies on impact of control measures for FMD include culling as a major component, which has been found to be especially effective and remains to be the method of choice for disease control of FMD. Interestingly, Hadeler & Freedman (1989) showed, under their modelling assumptions, culling the predator to lead to extinction of both predator and prey populations, perhaps indicating the complexity involved in modelling control measures in a predator–prey system.

These features could conceivably be added to the model in subsequent studies, given the possibility that these events may indeed occur in the future. However, we note that modelling transmission of H5N1, which might include both animal-to-human and possibly human-to-human infections, essentially amounts to modelling a 'giant leap to mankind' (as described by Klempner & Shapiro, 2004) which can be very difficult to quantify. Moreover, this interaction between humans and birds might not be best represented as a predator–prey interaction with Holling type-II functional response, which would require substantial modification in our model that is beyond the scope of this study.

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Appendix

Proof of Lemma 3.1. For (i), if $R_1 < 1$, then E_B is asymptotically stable for (3.1). Moreover, since E_B is the unique asymptotically stable equilibrium of (3.1) and on the boundary of the first quadrant which is the feasible region for (3.1), E_B must be globally asymptotically stable for (3.1). Part (ii) of the lemma follows trivially from Jacobian of E_B.

For (iii), we proceed to show that E_B is globally asymptotically stable for (3.1) as follows. First, suppose that $(\phi_1(t), \phi_2(t))$ is a solution of the system (3.1) which starts at a point $\mathbf{x} = (x_1, x_2)$ with $K < x_1 < \infty$, $0 < x_2 < \infty$. Also

$$\frac{d\phi_2}{d\phi_1} = \frac{\left(\dfrac{\phi_1(\beta - a_1\gamma_1) - \gamma_1}{1 + a_1\phi_1}\right)\phi_2}{\dfrac{r\phi_1(K - \phi_1)}{K} - \dfrac{\alpha_1\phi_1\phi_2}{1+a_1\phi_1}} \longrightarrow 0 \quad \text{as } \phi_1 \longrightarrow K.$$

Thus, the solution cannot become infinite between $\mathbf{x}$ and the line L: $S = K$, and must cross L at a point $\mathrm{y} = (K, y_2)$ with $x_2 < y_2 < \infty$. Now, let U be the region bounded by $P_1 = y_2$, $P_1 = 0$, $S = x_1$ and $S > 0$ and the line segment $\overline{xy}$. From the analysis of flow direction on the boundary of U, we can see that U is an invariant set with respect to the system (3.1). Since there is no positive interior equilibrium, the system has no any periodic solutions. Thus for any solution starting in U, its positive limit set is E_B. Furthermore, since the region U is arbitrary, it follows from Brauer & Nohel (1969) (Lemma 5.4, p. 212) that E_B is globally asymptotically stable for (3.1). □

Proof of Lemma 3.2. First, we have $P_1' = 0 \Rightarrow S^* = \frac{\gamma_1}{\beta - a_1\gamma_1}$ provided $\beta - a_1\gamma_1 > 0$, which is satisfied as long as $R_1 \geqslant 0$. Also from $S' = 0$, one obtains $P_1^* = \frac{r}{\alpha_1}\left(1 - \frac{\gamma_1}{K(\beta - a_1\gamma_1)}\right)\left(1 + \frac{a_1\gamma_1}{\beta - a_1\gamma_1}\right)$ provided $0 < S^* = \frac{\gamma_1}{\beta - a_1\gamma_1} < K$. Thus, $(S^*, P_1^*) = \left(\frac{\gamma_1}{\beta - a_1\gamma_1}, \frac{r}{\alpha_1}\left(1 - \frac{\gamma_1}{K(\beta - a_1\gamma_1)}\right)\left(1 + \frac{a_1\gamma_1}{\beta - a_1\gamma_1}\right)\right)$ is the unique positive interior equilibrium of (3.1). Note that E^* exists if and only if $R_1 > 1$. Now, we have the Jacobian at E^*:

$$A_{E^*} = \begin{bmatrix} \dfrac{a_1[K(\beta - a_1\gamma_1) - \gamma_1] - \beta}{K\beta(\beta - a_1\gamma_1)}\gamma_1 r & -\dfrac{\alpha_1\gamma_1}{\beta} \\ \dfrac{K(\beta - a_1\gamma_1) - \gamma_1}{K\alpha_1} r & 0 \end{bmatrix}.$$

Since

$$\det(A_{E^*} - \lambda I_2) = \lambda^2 - \left(\frac{a_1[K(\beta - a_1\gamma_1) - \gamma_1] - \beta}{K\beta(\beta - a_1\gamma_1)}\gamma_1 r\right)\lambda + \left(\frac{K(\beta - a_1\gamma_1) - \gamma_1}{K\beta}\gamma_1 r\right) = 0,$$

if we let $c_1 = -\frac{a_1[K(\beta - a_1\gamma_1) - \gamma_1] - \beta}{K\beta(\beta - a_1\gamma_1)}\gamma_1 r$ and $c_2 = \frac{K(\beta - a_1\gamma_1) - \gamma_1}{K\beta}\gamma_1 r$, it follows that $S^* = \frac{\gamma_1}{\beta - a_1\gamma_1} < K$ implies that $K(\beta - a_1\gamma_1) - \gamma_1 > 0$, and hence $c_2 > 0$. Now, we consider the local stability property of E^* for (3.1) using Routh–Hurwitz criterion and yield $D_1 = c_1$ and $D_2 = c_1c_2$. Since $\beta - a_1\gamma_1 > 0$ and $K(\beta - a_1\gamma_1) - \gamma_1 > 0$, then

$$c_1 > 0 \Leftrightarrow a_1[K(\beta - a_1\gamma_1) - \gamma_1] - \beta < 0 \Leftrightarrow R_1 < 1 + \frac{\beta}{a_1\gamma_1(1 + a_1K)},$$

$$c_1 < 0 \Leftrightarrow a_1[K(\beta - a_1\gamma_1) - \gamma_1] - \beta > 0 \Leftrightarrow R_1 > 1 + \frac{\beta}{a_1\gamma_1(1 + a_1K)},$$

$$c_1 = 0 \Leftrightarrow a_1[K(\beta - a_1\gamma_1) - \gamma_1] - \beta = 0 \Leftrightarrow R_1 = 1 + \frac{\beta}{a_1\gamma_1(1 + a_1K)}.$$

Part (iii) follows from a theorem in Coddington & Levinson (1955, p. 382). □

Proof of Theorem 3.3. The proof basically follows from Lemma 4.4 of Hsu *et al.* (1978). First, let

$$f_1(S, P_1) = rS\left(1 - \frac{S}{K}\right) - \alpha_1\left(\frac{S}{1 + a_1S}\right)P_1,$$

$$f_2(S, P_1) = \beta\left(\frac{S}{1 + a_1S}\right)P_1 - \gamma_1P_1,$$

$$h(S, P_1) = \left(\frac{1 + a_1S}{S}\right)^A P_1^B,$$

where $A, B \in \mathcal{R}$ will be selected below. Now,

$$\frac{\partial(f_1h)}{\partial S} + \frac{\partial(f_2h)}{\partial P_1} = [-\alpha_1 P_1^{B+1} S^A (1 + a_1S)^{-(A+2)}](A + 1) + [rP_1^B S^A (1 + a_1S)^{-(A+1)}]G_{A,C}(S),$$

where $C = \frac{B+1}{r}$ and

$$G_{A,C}(S) = -\left(\frac{2a_1}{K}\right)S^2 + \left[(\beta - a_1\gamma_1)C + \left(a_1 - \frac{A + 2}{K}\right)\right]S + [(A + 1) - C\gamma_1].$$

We look for $A \geqslant -1$ and C such that $G_{A,C}(S) \leqslant 0$ for all S. To do this, we first consider the discriminant $D_A(C)$ of $G_{A,C}(S)$ and the discriminant $D(A)$ of $D_A(C)$ which are given by

$$D_A(C) = (\beta - a_1\gamma_1)^2 C^2 + 2\left[(\beta - a_1\gamma_1)\left(a_1 - \frac{A+2}{K}\right) - \frac{4a_1\gamma_1}{K}\right]C$$

$$+ \left(a_1 - \frac{A+2}{K}\right)^2 + \frac{8a_1(A+1)}{K},$$

$$D(A) = \frac{32a_1}{K^2}\{(\beta - a_1\gamma_1)[\gamma_1 - K(\beta - a_1\gamma_1)]A + \beta[2\gamma_1 - K(\beta - a_1\gamma_1)]\}.$$

Now we take $A = -1$, then

$$D(-1) = -\frac{32a_1\gamma_1}{K^2}\{a_1[K(\beta - a_1\gamma_1) - \gamma_1] - \beta\}.$$

Since $R_1 \leqslant 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$ implies that $D(-1) \geqslant 0$, the polynomial $D_{-1}(C) = 0$ has two real roots C_1 and C_2 with $C_1 \leqslant C_2$. Thus, we can take a C^* with $C_1 \leqslant C^* \leqslant C_2$ such that $D_{-1}(C^*) \leqslant 0$ implies that $G_{-1,C^*}(S) \leqslant 0$. Hence, the expression $\frac{\partial(f_1 h)}{\partial S} + \frac{\partial(f_2 h)}{\partial P_1}$ does not change sign. By Dulac criterion (Hahn, 1967, p. 67), system (3.1) has no periodic orbit in the first quadrant and thus E^* is globally asymptotically stable for (3.1). □

Proof of Theorem 3.4. The uniqueness of a limit cycle for a predator–prey system is proved first by Cheng (1981). The rest of proof follows from Theorem 4.2 in Kuang & Freedman (1988). First, let

$$g(S) = r\left(1 - \frac{S}{K}\right), \quad p(S) = \frac{\alpha_1 S}{1 + a_1 S}, \quad q(S) = \frac{\beta S}{1 + a_1 S}.$$

Then, the assumptions (H1)–(H8) of Theorem 4.2 in Kuang & Freedman (1988) are satisfied. To apply that theorem, we require the following:

$$\frac{\mathrm{d}}{\mathrm{d}S}\left(\frac{Sg'(S) + g(S) - Sg(S)\frac{p'(S)}{p(S)}}{-\gamma_1 + q(S)}\right)$$

$$= \frac{\mathrm{d}}{\mathrm{d}S}\left(\frac{r}{K} \cdot \frac{-2a_1S^2 + (a_1K - 1)S}{(\beta - a_1\gamma_1)S - \gamma_1}\right) \leqslant 0 \quad \text{for } 0 \leqslant S < S^*, \ \ S^* < S \leqslant K$$

$$\Leftrightarrow \frac{\mathrm{d}}{\mathrm{d}S}\left(\frac{2a_1S^2 + (a_1K - 1)S}{S - S^*}\right)$$

$$= \frac{2a_1S^2 - 4a_1S^*S + (a_1K - 1)S^*}{(S - S^*)^2} \geqslant 0 \quad \text{for } 0 \leqslant S < S^*, \ S^* < S \leqslant K$$

$$\Leftrightarrow D(S) = 2a_1S^2 - 4a_1S^*S + (a_1K - 1)S^* \geqslant 0 \quad \text{for } 0 \leqslant S < S^*, \ \ S^* < S \leqslant K.$$

Now, note that $D'(S) = 4a_1(S - S^*)$ implies that $D(S^*)$ is the local minimum of $D(S)$. Also $R_1 > 1 + \frac{\beta}{a_1\gamma_1(1+a_1K)}$ implies that $a_1K - 1 - 2a_1S^* > 0$, hence

$$D(0) = (a_1K - 1)S^* > 0,$$

$$D(S^*) = (a_1K - 1 - 2a_1S^*)S^* > 0.$$

Subsequently, we have $D(S) \geqslant 0$ for $0 \leqslant S < S^*$, $S^* < S \leqslant K$. Under the above assumptions, this implies that the system (3.1) has a unique limit cycle that is globally asymptotically orbitally stable. □

Proof of Lemma 4.1. From

$$A_{\mathbf{E_0}} = \begin{bmatrix} r & -(r + K\lambda_1) & -\frac{\alpha_1 K}{1+a_1K} & -\frac{\alpha_1 K}{1+a_1K} \\ 0 & K\lambda_1 - \mu & 0 & 0 \\ 0 & 0 & \frac{\beta K}{1+a_1K} - \gamma_1 & 0 \\ 0 & 0 & 0 & -\gamma_2 \end{bmatrix},$$

it follows that if we let $R_0 = \frac{K\lambda_1}{\mu}$, the disease basic reproduction number of the prey, we have the stability result for $\mathbf{E}_\mathrm{B}$. □

Proof of Lemma 4.2. When $R_0 > 1$, $(\overline{S}, \overline{I}, 0, 0) = \left(\frac{\mu}{\lambda_1}, \frac{r(K\lambda_1-\mu)}{\lambda_1(r+K\lambda_1)}, 0, 0\right)$ exists. It is easy to show that $\overline{S} + \overline{I} < K$ when $R_0 > 1$. We have

$$A_{\overline{\mathbf{E}}_\mathrm{B}} = \begin{bmatrix} -\frac{r\mu}{K\lambda_1} & -\left(\frac{r\mu}{K\lambda_1} + \mu\right) & -\frac{\alpha_1\mu}{\lambda_1+a_1\mu} & -\frac{\alpha_1\mu}{\lambda_1+a_1\mu} \\ \frac{r(K\lambda_1-\mu)}{r+\lambda_1K} & 0 & -\frac{\alpha_2 r(K\lambda_1-\mu)}{\lambda_1(r+K\lambda_1)+a_2r(K\lambda_1-\mu)} & -\frac{\alpha_2 r(K\lambda_1-\mu)}{\lambda_1(r+K\lambda_1)+a_2r(K\lambda_1-\mu)} \\ 0 & 0 & M & 0 \\ 0 & 0 & \frac{\lambda_2 r(K\lambda_1-\mu)}{\lambda_1(r+K\lambda_1)+a_2r(K\lambda_1-\mu)} & -\gamma_2 \end{bmatrix},$$

where $M = \frac{\beta\overline{S}}{1+a_1\overline{S}} - \frac{\lambda_2\overline{I}}{1+a_2\overline{I}} - \gamma_1$. Since $\det(A_{\overline{\mathbf{E}}_\mathrm{B}} - \lambda I_4) = (M - \lambda)(-\gamma_2 - \lambda)\left[\lambda^2 + \left(\frac{r\mu}{K\lambda_1}\right)\lambda + \frac{r(K\lambda_1-\mu)}{(r+\lambda_1K)} \cdot \frac{\alpha\mu}{\lambda_1+a_1\mu}\right] = 0$ and $M < 0$ is equivalent to $\overline{R}_1 < 1 + \frac{\lambda_2\overline{I}}{\gamma_1(1+a_2\overline{I})}$, where $\overline{R}_1 = \frac{\beta\overline{S}}{\gamma_1(1+a_1\overline{S})}$, we have the stability result for $\overline{\mathbf{E}}_\mathrm{B}$. □

Proof of Lemma 4.3. When $R_1 > 1$, $(S^*, 0, P_1^*, 0) = \left(\frac{\gamma_1}{\beta-a_1\gamma_1}, 0, \frac{r}{\alpha_1}\left(1 - \frac{\gamma_1}{K(\beta-a_1\gamma_1)}\right)\left(1 + \frac{a_1\gamma_1}{\beta-a_1\gamma_1}\right), 0\right)$ exists.

$$A_{\mathbf{E}_\mathrm{B}^*} = \begin{bmatrix} \frac{a_1[K(\beta-a_1\gamma_1)-\gamma_1]-\beta}{K\beta(\beta-a_1\gamma_1)}\gamma_1 r & -\left(\frac{r}{K} + \lambda_1\right)\frac{\gamma_1}{\beta-a_1\gamma_1} & -\frac{\alpha_1\gamma_1}{\beta} & -\frac{\alpha_1\gamma_1}{\beta} \\ 0 & N & 0 & 0 \\ \frac{K(\beta-a_1\gamma_1)-\gamma_1}{K\alpha_1}r & -\frac{r\lambda_2}{\alpha_1}\left(1 - \frac{\gamma_1}{K(\beta-a_1\gamma_1)}\right)\left(1 + \frac{a_1\gamma_1}{\beta-a_1\gamma_1}\right)^{-1} & 0 & 0 \\ 0 & \frac{r\lambda_2}{\alpha_1}\left(1 - \frac{\gamma_1}{K(\beta-a_1\gamma_1)}\right)\left(1 + \frac{a_1\gamma_1}{\beta-a_1\gamma_1}\right) & 0 & -\gamma_2 \end{bmatrix},$$

where $N = \lambda_1 S^* - \alpha_2 P_1^* - \mu$. From $\det\big(A_{\mathbf{E}_\mathrm{B}^*} - \lambda I_4\big) = (N-\lambda)(-\gamma_2-\lambda)\cdot\det\big(A_{E_\mathrm{B}^*} - \lambda I_2\big)$ and $R_0^* = \frac{\lambda_1 S^*}{\alpha_2 P_1^* + \mu}$, we have the stability result for $\mathbf{E}_\mathrm{B}^*$. □

Proof of Lemma 4.4. To show the existence of $\widetilde{\mathbf{E}}$, we know

$$P_1' = 0 \Longrightarrow \frac{\beta S}{1+a_1 S} - \gamma_1 - \frac{\lambda_2 I}{1+a_2 I} = 0$$

$$\Longrightarrow \widetilde{I} = \frac{\widetilde{S}(\beta - a_1\gamma_1) - \gamma_1}{\lambda_2(1+a_1\widetilde{S}) - a_2[\widetilde{S}(\beta - a_1\gamma_1) - \gamma_1]},$$

provided that $\widetilde{S}(\beta - a_1\gamma_1) - \gamma_1 > 0$ and $\lambda_2(1+a_1\widetilde{S}) - a_2[\widetilde{S}(\beta - a_1\gamma_1) - \gamma_1] > 0$. Note that $1 < \widetilde{R}_1 < 1 + \frac{\lambda_2}{a_2\gamma_1}$ is equivalent to $\widetilde{S}(\beta - a_1\gamma_1) - \gamma_1 > 0$ and $\lambda_2(1+a_1\widetilde{S}) - a_2[\widetilde{S}(\beta - a_1\gamma_1) - \gamma_1] > 0$. From $P_2' = 0$, obtain $\widetilde{P}_2 = \frac{\lambda_2}{\gamma_2}\big(\frac{\widetilde{I}}{1+a_2\widetilde{I}}\big)\widetilde{P}_1$. Also

$$I' = 0 \Longrightarrow \lambda_1 S - \frac{\alpha_2}{1+a_2 I}(P_1+P_2) - \mu = 0 \Longrightarrow P_1 + P_2 = \frac{1}{\alpha_2}(\lambda_1 S - \mu)(1+a_2 I)$$

$$\Longrightarrow \widetilde{P}_1 = \frac{1}{\alpha_2}(\lambda_1\widetilde{S} - \mu)(1+a_2\widetilde{I})\left[1 + \frac{\lambda_2}{\gamma_2}\left(\frac{\widetilde{I}}{1+a_2\widetilde{I}}\right)\right]^{-1}, \quad \text{if } \widetilde{S} > \frac{\mu}{\lambda_1}.$$

From $S' = 0$, we obtain

$$\frac{r}{K}(K - S - I) - \lambda_1 I - \frac{\alpha_1}{\alpha_2}\cdot\frac{1}{1+a_1 S}(\lambda_1 S - \mu)(1+a_2 I) = 0$$

$$\Longrightarrow a_1\alpha_2 r[(\beta - a_1\gamma_1) - \lambda_2]S^2 + \{K\{a_1\alpha_2 r[\lambda_2 - (\beta - a_1\gamma_1)]$$

$$- \alpha_2\lambda_1(\beta - a_1\gamma_1) - \alpha_1\lambda_1\lambda_2\} - \alpha_2 r[(\beta - a_1\gamma_1) + \lambda_2 + a_2\gamma_1]\}S$$

$$+ \{K\{\alpha_2 r + [\lambda_2 + a_2\gamma_1] + \alpha_2\lambda_1\gamma_1 + \alpha_1\lambda_2\mu\} + \alpha_2\gamma_1 r\} = 0$$

$$\Longrightarrow \widetilde{S} = \begin{cases} \dfrac{-b \pm \sqrt{b^2 - 4ac}}{2a}, & \text{if } (\beta - a_1\gamma_1) - \lambda_2 \neq 0 \text{ and } b^2 - 4ac > 0, \\ \dfrac{K[\alpha_2(\beta r + \lambda_1\gamma_1) + \alpha_1\lambda_2\mu] + \alpha_2\gamma_1 r}{K\lambda_1\lambda_2(\alpha_1+\alpha_2) + \alpha_2 r(2\lambda_1 + a_2\gamma_1)}, & \text{if } (\beta - a_1\gamma_1) - \lambda_2 = 0, \end{cases}$$

where

$$a = a_1\alpha_2 r[(\beta - a_1\gamma_1) - \lambda_2],$$

$$b = \{K\{a_1\alpha_2 r[\lambda_2 - (\beta - a_1\gamma_1)] - \alpha_2\lambda_1(\beta - a_1\gamma_1) - \alpha_1\lambda_1\lambda_2\} - \alpha_2 r[(\beta - a_1\gamma_1) + \lambda_2 + a_2\gamma_1]\},$$

$$c = \{K\{\alpha_2 r + [\lambda_2 + a_2\gamma_1] + \alpha_2\lambda_1\gamma_1 + \alpha_1\lambda_2\mu\} + \alpha_2\gamma_1 r\}.$$

Thus we have the desired result. □