Research article

Dynamic behavior of swine influenza transmission during the breed-slaughter process

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Abstract: Global influenza pandemics have brought about various public health crises, such as the 2009 H1N1 swine flu. Actually, most swine influenza infections occur during the breed-slaughter process. However, there is little research about the mathematical model to elaborate on the swine influenza transmission with human-pig interaction. In this paper, a new breed-slaughter model with swine influenza transmission is proposed, and the equilibrium points of the model are calculated subsequently. Meanwhile, we analyze the existence of the equilibrium points by the persistence theory, and discuss their stability by the basic reproduction number. And then, we focus on the invasion process of infected domestic animals into the habitat of humans. Under certain conditions as in Theorem 2, we construct a propagating terrace linking human habitat to animal-human coexistent habitat, then to swine flu natural foci, which is divided by spreading speeds.

1. Introduction

Domestic pigs originated from the Eurasian wild boar (Sus scrofa), which first appeared about 9000 years ago [1]. They are essential for the transmission of swine influenza. Human beings raise domestic pigs, and then slaughter them for pork [2]. Domestic pigs grow in the food and environment provided by human beings, while human beings get the necessary nutrients by eating them. Consequently, in the breeding process, the swine flu virus is transmitted to human beings through domestic pig-human contact [2, 3]. According to this process, a new breed-slaughter model with swine influenza

transmission can be proposed as a model (1.1).

$$
\begin{cases}
\frac{\partial S_1(x,t)}{\partial t} = D_1 \frac{\partial^2 S_1(x,t)}{\partial x^2} + (B_{12}N_2(x,t) - \omega_0 N_1(x,t))N_1(x,t) - s_0 S_1(x,t) \\
\qquad - \beta_{11}I_1(x,t)S_1(x,t) + \gamma_1 I_1(x,t), x \in \mathbb{R}, t > 0, \\
\frac{\partial I_1(x,t)}{\partial t} = D_1 \frac{\partial^2 I_1(x,t)}{\partial x^2} + \beta_{11}I_1(x,t)S_1(x,t) - (s_0 + \gamma_1)I_1(x,t), x \in \mathbb{R}, t > 0, \\
\frac{\partial S_2(x,t)}{\partial t} = D_2 \frac{\partial^2 S_2(x,t)}{\partial x^2} + (b_2 - r_2 \frac{N_2(x,t)}{K_2} + B_{21}N_1(x,t))N_2(x,t) - d_2 S_2(x,t) \\
\qquad - \sum_{j=1}^{2} \beta_{2j}I_j(x,t)S_2(x,t) + \gamma_2 I_2(x,t), x \in \mathbb{R}, t > 0, \\
\frac{\partial I_2(x,t)}{\partial t} = D_2 \frac{\partial^2 I_2(x,t)}{\partial x^2} + \sum_{j=1}^{2} \beta_{2j}I_j(x,t)S_2(x,t) - [e_2 + \gamma_2 + d_2]I_2(x,t), x \in \mathbb{R}, t > 0, \\
N_i(x,t) = S_i(x,t) + I_i(x,t), i = 1, 2, x \in \mathbb{R}, t > 0.
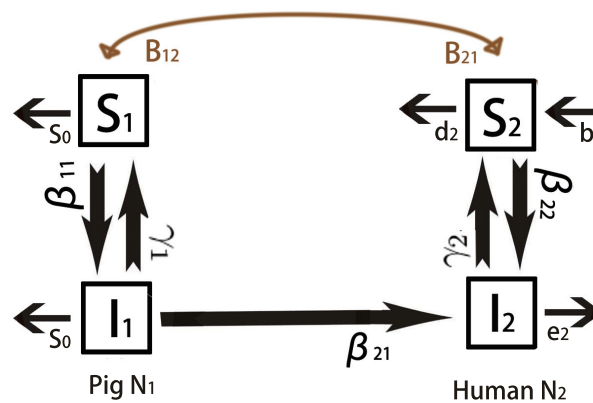\end{cases} \tag{1.1}
$$

Figure 1. Swine flu transmission route from pig to human.

Domestic pig population $N_1(x,t)$ and human population $N_2(x,t)$ are assumed to be divided into 2 epidemiological compartments: susceptibles ($S_i(x,t)$) and infectives ($I_i(x,t)$) at time t and location x, $i = 1, 2$. Susceptibles can become infected by means of intra-species or inter-species transmission and then recover as new susceptibles. The notation B_{12} represents the human breeding parameter for the population growth of domestic pigs, while B_{21} represents the nutrients from eating domestic pigs to increase the birth rate of human beings. The notation s_0 represents the slaughter rate of domestic pigs. It's noteworthy that domestic pigs cannot survive independently without human beings, but human beings can still survive well without the supply of pork [2]. Restrictions on the development of human population mainly come from intra-species competition.

For humans, the notation $r_2 = b_2 - d_2$ is the intrinsic growth rate of humans, where b_2 and d_2 represents the natural natality rate and mortality rate, respectively. K_2 is the environmental carrying capacity of human population without domestic pig supply. e_2 is the additional mortality rate of humans caused by swine flu. For domestic pigs, ω_0 represents the intraspecific competition. During the spread of swine flu, the parameters β_{ij} represent the per capita incidence rate from species j to species i, where

$i, j = 1, 2$. γ_i denote the recovery rate for domestic animals and humans, $i = 1, 2$. D_1 and D_2 are the diffusion coefficients for domestic animals and humans. It is noteworthy that all parameters mentioned above is positive.

The main purpose of this paper is to propose a new breed-slaughter model with swine influenza transmission, and study the dynamic behavior of it. And then, we focus on the invasion process of infected domestic animals into the habitat of humans. Under certain conditions as in Theorem 2, we construct a propagating terrace linking human habitat to animal-human coexistent habitat, then to swine flu natural foci, which is divided by spreading speeds. Firstly, we calculate the equilibrium points of the model without spatial heterogeneity as a model (1.2) and analyze the existence of them by the persistence theory. Secondly, we discuss their stability by the basic reproduction number. Thirdly, we use these equilibrium points to construct a propagating terrace linking them by spreading speeds.

$$\begin{cases} \frac{dS_1(t)}{dt} = (B_{12}N_2(t) - \omega_0 N_1(t))N_1(t) - s_0 S_1(t) - \beta_{11}I_1(t)S_1(t) + \gamma_1 I_1(t), \\ \frac{dI_1(t)}{dt} = \beta_{11}I_1(t)S_1(t) - (s_0 + \gamma_1)I_1(t), \\ \frac{dS_2(t)}{dt} = (b_2 - r_2\frac{N_2(t)}{K_2} + B_{21}N_1(t))N_2(t) - d_2 S_2(t) - \sum_{j=1}^{2}\beta_{2j}I_j(t)S_2(t) + \gamma_2 I_2(t), \\ \frac{dI_2(t)}{dt} = \sum_{j=1}^{2}\beta_{2j}I_j(t)S_2(t) - [e_2 + \gamma_2 + d_2]I_2(t), \\ N_i(t) = S_i(t) + I_i(t), i = 1, 2. \end{cases} \quad (1.2)$$

In model (1.2), domestic pig population $N_1(t)$ and human population $N_2(t)$ are assumed to be divided into 2 epidemiological compartments: susceptibles ($S_i(t)$) and infectives ($I_i(t)$) at time t, $i = 1, 2$. Other parameters are the same with model (1.1).

2. Breed-slaughter system

At first, we focus on the breed-slaughter system without swine flu transmission and spatial heterogeneity.

If $I_1(0) = I_2(0) = 0$, $N_1(0) > 0$ and $N_2(0) > 0$, model (1.2) turns to a new breed-slaughter system without swine influenza transmission as model (2.1).

$$\begin{cases} \frac{dN_1(t)}{dt} = (B_{12}N_2(t) - \omega_0 N_1(t))N_1(t) - s_0 N_1(t), \\ \frac{dN_2(t)}{dt} = r_2(1 - \frac{N_2(t)}{K_2})N_2(t) + B_{21}N_1(t)N_2(t), \\ N_1(0) > 0, N_2(0) > 0, \end{cases} \quad (2.1)$$

Similar to the competition system in [4], breed-slaughter system also has abundant dynamic results. For the positive equilibrium point

$$E^* = (N_1^*, N_2^*) = (\frac{r_2(s_0 - B_{12}K_2)}{B_{12}B_{21}K_2 - \omega_0 r_2}, \frac{K_2(s_0 B_{21} - \omega_0 r_2)}{B_{12}B_{21}K_2 - \omega_0 r_2})$$

of model (2.1), we have three cases:

(a). If $B_{12}B_{21} < \frac{\omega_0 r_2}{K_2}$ and $s_0 < \min\{\frac{\omega_0 r_2}{B_{21}}, B_{12}K_2\}$, the positive equilibrium point E^* of model (2.1) is stable (Figure 2(a)).

(b). If $B_{12}B_{21} > \frac{\omega_0 r_2}{K_2}$ and $s_0 > \max\{\frac{\omega_0 r_2}{B_{21}}, B_{12}K_2\}$, the positive equilibrium point E^* of model (2.1) is unstable (Figure 2(b)).

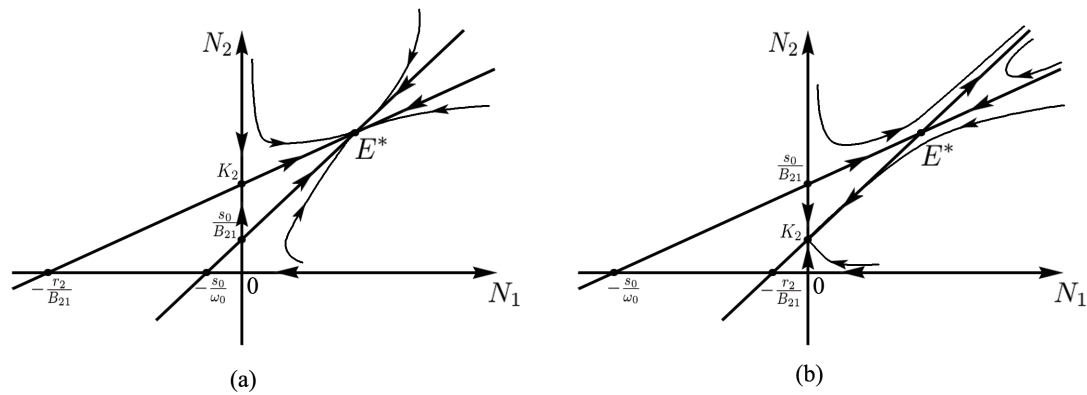(c). Other than the condition as (a) or (b), the positive equilibrium point E^* of model (2.1) does not exist.

Figure 2. Phase diagram of E^*.

3. Breed-slaughter system with swine flu transmission

In order to reflect the effect of interspecific interaction on swine influenza transmission during breeding process as model (1.2), we suppose that $B_{12}B_{21} < \dfrac{\omega_0 r_2}{K_2}$ and $s_0 < \min\left\{\dfrac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$ to guarantee the existence and the stability of the boundary equilibrium point

$$E_3 = (\frac{r_2(s_0 - B_{12}K_2)}{B_{12}B_{21}K_2 - \omega_0 r_2}, 0, \frac{K_2(s_0 B_{21} - \omega_0 r_2)}{B_{12}B_{21}K_2 - \omega_0 r_2}, 0)$$

with $I_1(0) = I_2(0) = 0$ in model (1.2).

After calculation, we summarize that there are at most 6 equilibrium points in $\mathbb{R}_+^4$ of the system (1.2): $E_0 = (0,0,0,0)$, $E_1 = (0,0,K_2,0)$, $E_2 = (0,0,\overline{S}_2,\overline{I}_2)$, $E_3 = (N_1^*,0,N_2^*,0)$, $E_4 = (N_1',0,S_2',I_2')$, $E_5 = (S_1^*,I_1^*,S_2^*,I_2^*)$, where $\overline{S}_2 = \frac{e_2+\gamma_2+d_2}{\beta_{22}}$, $\overline{I}_2 = \frac{\beta_{22}K_2-(e_2+\gamma_2+d_2)}{\beta_{22}}$, $N_1^* = N_1' = \frac{r_2(s_0-B_{12}K_2)}{B_{12}B_{21}K_2-\omega_0 r_2}$, $N_2^* = \frac{K_2(s_0B_{21}-\omega_0 r_2)}{B_{12}B_{21}K_2-\omega_0 r_2}$, $S_2' = \frac{e_2+\gamma_2+d_2}{\beta_{22}}$, $I_2' = \frac{\beta_{22}K_2(1+\frac{s_0B_{21}-B_{12}B_{21}K_2}{B_{12}B_{21}K_2-\omega_0 r_2})-(e_2+\gamma_2+d_2)}{\beta_{22}}$. The exact expression of E_5 is unknown. However, under certain conditions as in Theorem 2, we can obtain its existence by persistence theory [5–7].

If there is no domestic pigs participation, namely $N_1(0) = S_1(0) = I_1(0) = 0$, The persistence and the stability of boundary equilibrium $E_2 = (0,0,\overline{S}_2,\overline{I}_2)$ has been proved in [8]. Similarly, we define $R_0 = \frac{\beta_{22}K_1}{b_2+e_2+\gamma_2}$. And then, we can get the following lemma.

Lemma 1. *If $N_1(0) = S_1(0) = I_1(0) = 0$ and $I_2(0) > 0$, $\{0\} \times \{0\} \times \mathbb{R}_+^2$ is a invariant set of system (1.2). The trivial equilibrium point E_0 in model (1.2) is unstable, and we have following two cases:*

(a) If $R_0 \le 1$, the disease-free equilibrium point E_1 of model (1.2) is stable;

(b) If $R_0 > 1$, model (1.2) has a unique equilibrium point E_2 in the interior of $\{0\} \times \{0\} \times \mathbb{R}_+^2$, which is stable, and E_1 is unstable.

Furthermore, we consider the transmission process of human influenza with domestic pigs participating, but not infected from them. Namely $I_1(0) = 0$, $I_2(0) > 0$ and $N_i(0) > 0$, $i = 1, 2$. The persistence and the stability of boundary equilibrium $E_4 = (N_1',0,S_2',I_2')$ is similar to **Lemma 1**.

Taking E_3 as the original point by coordinate translation, we can get the following lemma by the persistence theory [5, 9, 10], when $B_{12}B_{21} < \dfrac{\omega_0 r_2}{K_2}$ and $s_0 < \min\left\{\dfrac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$.

According to the definition of basic reproduction number in a single population as [5, 11, 12], we define $R_1 = \dfrac{\beta_1 N_1^*}{s_0 + \gamma_1}$ as the basic reproduction number of swine flu transmission in demotic pig population and $R_2 = \dfrac{\beta_{22} N_2^*}{e_2 + \gamma_2 + d_2}$ as the basic reproduction number of swine flu transmission in human population .

Lemma 2. *If $N_1(0) = S_1(0) > 0$, $I_1(0) = 0$ and $I_2(0) > 0$, $\mathbb{R}_+ \times \{0\} \times \mathbb{R}_+^2$ is a invariant set of system (1.2). The trivial equilibrium point E_0 and the boundary equilibrium point E_1, E_2 in model (1.2) are unstable when $B_{12}B_{21} < \dfrac{\omega_0 r_2}{K_2}$ and $s_0 < \min\left\{\dfrac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$, and we have following two cases:*

(a) If $R_2 \leq 1$, the disease-free equilibrium point E_3 of model (1.2) is stable;

(b) If $R_2 > 1$, model (1.2) has a unique equilibrium point E_4 in the interior of $\mathbb{R}_+ \times \{0\} \times \mathbb{R}_+^2$, which is stable, and E_3 is unstable.

Next we focus on the discussion about the existence and the stability of the positive equilibrium point $E_5 = (S_1^*, I_1^*, S_2^*, I_2^*)$. At first, we define $R_s = \max\{R_1, R_2\}$. Then, we get the theorem as the following.

Theorem 1. *If $N_i(0) > 0$ and $I_i(0) > 0$, $i = 1, 2$, $\mathbb{R}_+^4$ is a invariant set of system (1.2). The trivial equilibrium point E_0 and the boundary equilibrium point E_1, E_2 in model (1.2) are unstable when $B_{12}B_{21} < \dfrac{\omega_0 r_2}{K_2}$ and $s_0 < \min\left\{\dfrac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$, and we have following three cases:*

(a) If $R_s \leq 1$, the disease-free equilibrium point E_3 of model (1.2) is stable;

(b) If $R_s > 1$, $R_1 < R_2$ and $R_1 \leq 1$, model (1.2) has a unique equilibrium point E_4 except for E_0, E_1, E_2 and E_3, which is stable, and E_3 is unstable;

(c) If $R_s > 1$ and $R_1 \geq R_2$ (or $R_2 > R_1 > 1$) model (1.2) has a unique equilibrium point E_5 in the interior of $\mathbb{R}_+^4$, which is stable, and E_3 and E_4 are unstable.

Proof. If $R_s \leq 1$, E_4 and E_5 do not exist. Similar to the results of **Lemma 2** (a), the disease-free equilibrium point E_3 of model (1.2) is stable.

Then we consider the results of system (1.2) when $R_s > 1$ and $B_{12}B_{21} < \dfrac{\omega_0 r_2}{K_2}$ and $s_0 < \min\left\{\dfrac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$. At first, we define

$$D = \{(S_1, I_1, S_2, I_2) \big| 0 \leq I_i \leq S_i + I_i \leq N_i^*, i = 1, 2\},$$

$$D_1 = \{(S_1, I_1, S_2, I_2) \big| I_1 = 0 \text{ or } I_2 = 0, 0 \leq S_i + I_i \leq N_i^*, i = 1, 2\},$$

$$D_2 = D \backslash D_1, \widetilde{D_2} = \{(S_1, I_1, S_2, I_2) \big| 0 < I_i \leq S_i + I_i \leq N_i^*, i = 1, 2\}.$$

D_2 and $\widetilde{D_2}$ are forward invariant.

Let Ω^* consists of equilibria E_0, E_1, E_2, E_3 and E_4. These equilibria cannot be chained to each other in D_1. By analyzing the flow in neighborhood of each equilibrium, it is easy to see that Ω^* is isolated in D and D_1 is a uniform strong repeller for $\widetilde{D_2}$.

If $x(t) = (S_1(t), I_1(t), S_2(t), I_2(t))$ stays close to E_2, we have two cases: if $I_1(0) = I_2(0) = 0$, then $I_1(t) = I_2(t) = 0$; if $I_1(0) > 0$ or $I_2(0) > 0$, then $I_2(t) > 0$. Therefore, E_2 is isolated in D. Similarly, we can prove that E_0, E_1 and E_3 are isolated in D.

For E_4 and E_5, we have two cases: (A). $R_1 < R_2$ and $R_1 \leq 1$; (B). $R_1 \geq R_2$ or $R_2 > R_1 > 1$.

(A). $R_1 < R_2$ and $R_1 \leq 1$

If $R_1 < R_2$ and $R_1 \leq 1$, E_5 do not exist. Similar to the results of **Lemma 2** (b), the boundary equilibrium point E_4 of model (1.2) is stable.

(B). $R_1 \geq R_2$ or $R_2 > R_1 > 1$

If $x(t) = (S_1(t), I_1(t), S_2(t), I_2(t))$ stays close to E_4, we have two cases: if $I_1(0) = 0$, then $I_1(t) = 0$; if $I_1(0) > 0$, then $I_1(t) > 0$. Since $(S_1(t), I_1(t), S_2(t), I_2(t))$ satisfying system (1.2) has no invariant subset other than E_4 in its neighborhood. E_4 is isolated in D and a uniform weak repeller for $\widetilde{D_2}$. Therefore, we can prove that E_0, E_1, E_2, E_3 and E_4 are isolated in D.

Using Proposition 4.3 in [5], we can prove that D_1 is a uniform weak repeller for $\widetilde{D_2}$; and using Theorem 4.5 in [5], we can prove that D_1 is a uniform strong repeller for $\widetilde{D_2}$.

Then we get that there exists an $\epsilon > 0$ such that

$$\lim \inf_{t \to \infty} \min\{I_1(t), I_2(t)\} > \epsilon,$$

with $N_i(0) > 0$ and $I_i(0) > 0$, $i = 1, 2$.

Therefore, if $B_{12}B_{21} < \dfrac{\omega_0 r_2}{K_2}$, $s_0 < \min\left\{\dfrac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$ and $R_1 \geq R_2$ ($R_2 > R_1 > 1$), there exists at least one internal equilibrium of system (1.2) [9, 10, 13].

Next, we use Theorem 2 in [11] to discuss the basic reproduction number of system (1.2) .

The Jacobian matrix of (I_1, I_2) is

$$J = \begin{pmatrix} \beta_{11}S_1 - (s_0 + \gamma_1) & 0 \\ \beta_{21}S_2 & \beta_{22}S_2 - (e_2 + \gamma_2 + d_2) \end{pmatrix},$$

Let $J = F - V$, F be the rate of appearance of new infections in compartment I, V be the rate of transfer of individuals out of compartment I. Then, we get

$$F = \begin{pmatrix} \beta_{11}S_1 & 0 \\ \beta_{21}S_2 & \beta_{22}S_2 \end{pmatrix},$$

$$V = diag\begin{pmatrix} s_0 + \gamma_1 \\ e_2 + \gamma_2 + d_2 \end{pmatrix}.$$

We call FV^{-1} be the next generation matrix for the model (1.2) and set $R_s = \rho\left(FV^{-1}\big|_{E_3}\right)$, where $\rho(A)$ denotes the spectral radius of a matrix A.

Then we get

$$R_s = \max\left\{\dfrac{\beta_{11}N_1^*}{s_0 + \gamma_1}, \dfrac{\beta_{22}N_2^*}{e_2 + \gamma_2 + d_2}\right\}.$$

Finally, using Theorem 2 in [11], we can prove Theorem 1.

$\square$

4. Propagating terrace of swine flu

The basic reproduction number is an important threshold value in the research of the epidemic mathematical model, which determines the disease to break out or not. However, it is not sufficient to discuss the breed-slaughter model with interspecific interaction. The main purpose of this paper is to investigate invasion process of infected domestic animal into human habitat. And we construct a propagating terrace linking human habitat E_1 to animal-human coexistent habitat E_3, then to swine flu natural foci E_4 (or E_5), which is divided by certain spreading speeds. The propagating terrace can describe the spatio-temporal continuous change of the transmission of swine flu.

Based on the heterogeneity of the population structure and the temporal and spatial continuity of the mammal movement, the population's spatial factor is considered in the spread of swine flu. If the swine flu host populations are distributed differently in space, the diffusion term may change their local population structure, thus change the swine flu epidemic. In order to describe the population invasion process, we set the initial value is zero in the area $x \in (-\infty, -x_0) \cup (x_0, \infty)$. The area of $(-x_0, x_0)$ is the original habitat of N, and N will invade to the area of $x \in (-\infty, -x_0) \cup (x_0, \infty)$ at the spreading speed s [14].
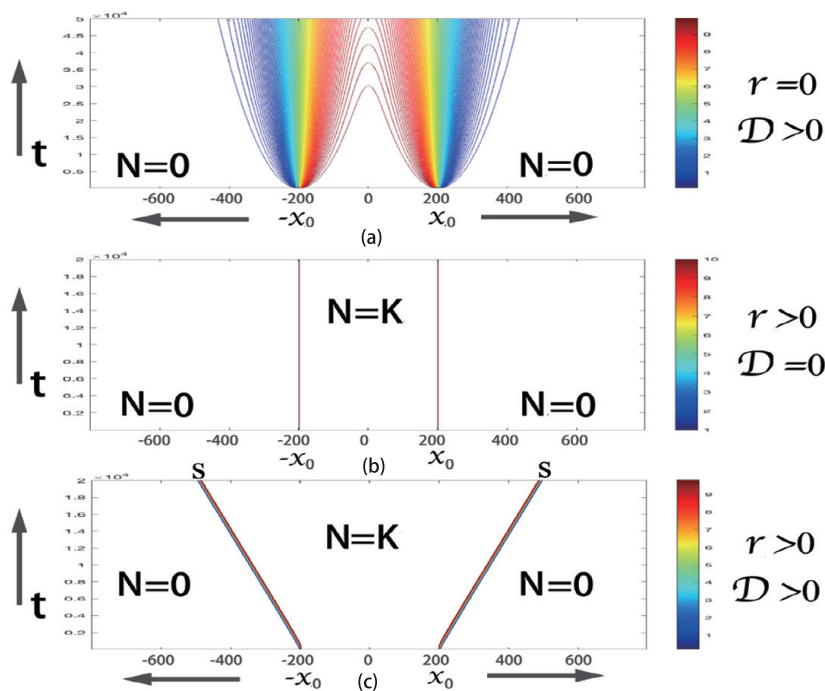

Figure 3. Effect of r and D on the local diffusion of a single population.

The definition of spreading speed of a single population is the positive value s satisfied with the conditions as follows,

$$\lim_{t \to +\infty} \{ \sup_{|x| > ct} N(x, t) \} = 0, \forall c > s$$

and

$$\lim_{t \to +\infty} \inf\{\inf_{|x|<ct} N(x,t)\} > 0, \forall c < s,$$

in the model [4.1]

$$\begin{cases} \frac{\partial N(x,t)}{\partial t} = D\frac{\partial^2 N(x,t)}{\partial x^2} + rN(x,t)(1 - \frac{N(x,t)}{K}), x \in \mathbb{R}, t > 0, \\ N(x,0) = N_0 > 0, x \in [-x_0, x_0], \\ N(x,0) = 0, x \in (-\infty, x_0) \cup (x_0, \infty). \end{cases} \quad (4.1)$$

The biological description of spreading speed s has been shown in the third figure of Figure 3. The value of s approximates the inverse of the slope of the color lines. It is easy to see that the co-effect of diffusion and reproduction leads to the population territory expansion, in which the local diffusion rate D guarantees the population spatial invasion to new areas and the reproduction rate r guarantees its development on occupied areas. The spreading speed of a single population in the model [4.1] is expressed by $s := 2\sqrt{Dr}$ by [14]. However, it is not enough to study the swine flu with more than one host species [15–20]. We redefine the spreading speeds at the human-animal interface, as shown below.

$$s_1 := 2\sqrt{D_1(B_{12}K_2 - s_0)},$$

$$s_2 := \max\left\{2\sqrt{D_1(\beta_{11}N_1^* - s_0 - \gamma_1)}, 2\sqrt{D_2(\beta_{22}N_2^* - e_2 - \gamma_2 - d_2)}\right\}.$$

Due to the participation of two populations, some notations need to be redefined. The notations s and x_0 are replaced by s_i, x_i, with $i = 1, 2$, corresponding to the two swine flu host populations.

Then we construct a propagating terrace linking human habitat E_1 to animal-human coexistent habitat E_3, then to swine flu natural foci E_4 (or E_5), which is divided by certain spreading speeds. The propagating terrace can describe the spatio-temporal continuous change of the transmission of swine flu, which can be show in **Theorem 2**.

Theorem 2. *For system* (1.1), *if* $B_{12}B_{21} < \dfrac{\omega_0 r_2}{K_2}$,$B_{21}N_1^* < r_2$ *and* $s_0 < \min\left\{\dfrac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$, *the initial conditions satisfy that* $0 < S_1(x,0) < N_1^*$, $x \in [-x_1, x_1]$; $S_1(x,0) = 0$, $x \in (-\infty, x_1) \cup (x_1, \infty)$, *for some* $x_1 > 0$; $0 < I_1(x,0) < N_1^*$, $x \in [-x_2, x_2]$; $I_1(x,0) = 0$, $x \in (-\infty, x_2) \cup (x_2, \infty)$, *for some* $x_2 > 0$; $S_2(x,0) = K_2$, $I_2(x,0) = 0$, $x \in \mathbb{R}$.
We set

$$s_1 := 2\sqrt{D_1(B_{12}K_2 - s_0)}, s_2 := \max\left\{2\sqrt{D_1(\beta_{11}N_1^* - s_0 - \gamma_1)}, 2\sqrt{D_2(\beta_{22}N_2^* - e_2 - \gamma_2 - d_2)}\right\}.$$

Suppose that $s_1 > s_2$, $x_1 > x_2$, *then there are three cases about the invasion process as following:*
(a) $R_s \le 1$,

$$\lim_{t \to +\infty} \sup_{|x|>ct} \{|S_1(x,t)| + |I_1(x,t)| + |S_2(x,t) - K_2| + |I_2(x,t)|\} = 0, \quad \forall c > s_1,$$

$$\lim_{t \to +\infty} \sup_{|x|<ct} \left\{\left|S_1(x,t) - N_1^*\right| + |I_1(x,t)| + \left|S_2(x,t) - N_2^*\right| + |I_2(x,t)|\right\} = 0, \quad \forall c < s_1.$$

The system (1.1) *forms a propagating terrace, linking* E_1 *to* E_3.

(b) If $R_s > 1$, $R_1 < R_2$ and $R_1 \leq 1$,

$$\lim_{t \to +\infty} \sup_{|x|>ct} \{|S_1(x,t)| + |I_1(x,t)| + |S_2(x,t) - K_2| + |I_2(x,t)|\} = 0, \quad \forall c > s_1,$$

$$\lim_{t \to +\infty} \sup_{c_2t<|x|<c_1t} \left\{ \left|S_1(x,t) - N_1^*\right| + |I_1(x,t)| + \left|S_2(x,t) - N_2^*\right| + |I_2(x,t)| \right\} = 0, \quad \forall s_2 < c_2 < c_1 < s_1,$$

$$\lim_{t \to +\infty} \sup_{|x|<ct} \left\{ \left|S_1(x,t) - N_1'\right| + |I_1(x,t)| + \left|S_2(x,t) - S_2'\right| + \left|I_2(x,t) - I_2'\right| \right\} = 0, \quad \forall c < s_2.$$

The system (1.1) *forms a propagating terrace, linking E_1 to E_3, then to E_4.*

(c) If $R_s > 1$ and $R_1 \geq R_2$ (or $R_2 > R_1 > 1$),

$$\lim_{t \to +\infty} \sup_{|x|>ct} \{|S_1(x,t)| + |I_1(x,t)| + |S_2(x,t) - K_2| + |I_2(x,t)|\} = 0, \quad \forall c > s_1,$$

$$\lim_{t \to +\infty} \sup_{c_2t<|x|<c_1t} \left\{ \left|S_1(x,t) - N_1^*\right| + |I_1(x,t)| + \left|S_2(x,t) - N_2^*\right| + |I_2(x,t)| \right\} = 0, \quad \forall s_2 < c_2 < c_1 < s_1,$$

$$\lim_{t \to +\infty} \sup_{|x|<ct} \left\{ \left|S_1(x,t) - S_1^*\right| + \left|I_1(x,t) - I_1^*\right| + \left|S_2(x,t) - S_2^*\right| + \left|I_2(x,t) - I_2^*\right| \right\} = 0, \quad \forall c < s_2.$$

The system (1.1) *forms a propagating terrace, linking E_1 to E_3, then to E_5.*

Proof. The epidemic of swine flu originates in the interaction between humans and domestic animals in the breeding process, so the breaking out of swine flu would lag behind this process. Therefore, we first confirm the propagating terrace linking E_1 and E_3.

The breed-slaughter system without swine flu transmission can be transferred to model (4.2).

$$\begin{cases} \frac{\partial N_1(x,t)}{\partial t} = D_1 \frac{\partial^2 N_1(x,t)}{\partial t^2} + (B_{12}N_2(x,t) - \omega_0 N_1(x,t))N_1(x,t) - s_0 N_1(x,t), \\ \frac{\partial N_2(x,t)}{\partial t} = D_2 \frac{\partial^2 N_2(x,t)}{\partial t^2} + r_2(1 - \frac{N_2(x,t)}{K_2})N_2(t) + B_{21}N_1(x,t)N_2(x,t). \end{cases} \tag{4.2}$$

Let (N_1, N_2) be a solution to system (4.2) with the initial condition $0 < N_1(x,0) < N_1^*$, $x \in [-x_1, x_1]$; $N_1(x,0) = 0$, $x \in (-\infty, x_1) \cup (x_1, \infty)$, for some $x_1 > 0$; $N_2(x,0) = K_2$, $x \in \mathbb{R}$.

If $B_{12}B_{21} < \frac{\omega_0 r_2}{K_2}$ and $s_0 < \min\left\{\frac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$, we claim that $(N_1(x,t), N_2(x,t)) \in \Sigma$, $\forall x \in \mathbb{R}, t \in [0, \infty)$, where

$$\Sigma := \{(N_1, N_2) \in [0, N_1^*] \times [0, N_2^*] : B_{12}N_2(x,t) - \omega_0 N_1(x,t) - s_0 \geq 0, r_2(1 - \frac{N_2(x,t)}{K_2}) + B_{21}N_1(x,t) \geq 0\}.$$

By the strong maximum principle, $N_1 \geq 0$ for $t > 0$. Then we get

$$\frac{\partial N_2(x,t)}{\partial t} \geq D_2 \frac{\partial^2 N_2(x,t)}{\partial t^2} + r_2(1 - \frac{N_2(x,t)}{K_2})N_2(x,t).$$

By a comparison, $N_2 \geq X$, where X is the solution to

$$\begin{cases} \frac{\partial X(x,t)}{\partial t} = D_2 \frac{\partial^2 X(x,t)}{\partial t^2} + r_2(1 - \frac{X(x,t)}{K_2})X(x,t), \\ X(x,0) = N_2(x,0). \end{cases} \tag{4.3}$$

Then we get the result

$$\lim_{t \to +\infty} \inf N_2(x,t) \geq \lim_{t \to +\infty} \inf X(x,t) = K_2.$$

Set $u := N_1$ and $v := N_2 - K_2$. Then $\frac{\partial N_2(x,t)}{\partial t}$ can be rewritten as

$$\frac{\partial v(x,t)}{\partial t} = D_2 \frac{\partial^2 v(x,t)}{\partial t^2} - r_2 \frac{v(x,t)}{K_2}(v(x,t) + K_2) + B_{21}u(x,t)(v(x,t) + K_2).$$

Due to $u = N_1 \in [0, N_1^*]$ and $v = N_2 - K_2 \geq 0$ then

$$\frac{\partial v(x,t)}{\partial t} \leq D_2 \frac{\partial^2 v(x,t)}{\partial t^2} - (r_2 - B_{21}N_1^*)v(x,t) + B_{21}K_2 u(x,t).$$

By the strong maximum principle, if follows that $v \leq Y$ in $\mathbb{R} \times [0, \infty)$, where Y is the solution to

$$\begin{cases} \frac{\partial Y(x,t)}{\partial t} = D_2 \frac{\partial^2 Y(x,t)}{\partial t^2} - (r_2 - B_{21}N_1^*)Y(x,t) + B_{21}K_2 u(x,t), \\ X(x,0) = 0, x \in \mathbb{R}. \end{cases} \tag{4.4}$$

Then we have

$$Y(x,t) = B_{21}K_2 \int_0^t \left\{ e^{-(r_2 - B_{21}N_1^*)(t-s)} \int_{\mathbb{R}} e^{-(x-y)^2/[4(t-s)]} u(y,s) dy \right\} ds.$$

Given $\epsilon > 0$, we choose $\delta > 0$ small enough such that $2\sqrt{D_1(B_{12}K_2 - s_0 + B_{12}\delta)} < s_1 + \epsilon$.

For this δ, we claim that there is $\tau \gg 1$ such that $Y(x,t) < \delta + Mu(x,t)$, $\forall x \in \mathbb{R}$, $t \geq \tau$, for some positive constant M. Then it follows that N_1 satisfies

$$\frac{\partial N_1(x,t)}{\partial t} \leq D_1 \frac{\partial^2 N_1(x,t)}{\partial t^2} + (B_{12}K_1 - s_0 + B_{12}\delta - (B_{12}M + \omega_0)N_1(x,t))N_1(x,t).$$

Therefore, according to the comparison principle and the definition of spreading speed [14–16, 19, 21], for any $c \in (2\sqrt{D_1(B_{12}K_2 - s_0 + B_{12}\delta)}, s_1 + \epsilon)$, it follows that $\lim_{t \to +\infty} \sup_{|x| > ct} N_1(x,t) = 0$, and then $\lim_{t \to +\infty} \sup_{|x| > ct} N_2(x,t) = K_2$.

Because of the arbitrariness of ϵ, we get

$$\lim_{t \to +\infty} \sup_{|x| > ct} \{|N_1(x,t)| + |N_2(x,t) - K_2|\} = 0, \forall c > s_1.$$

Thus, if the swine flu does not break out, namely $R_s \leq 1$, for system (1.1),

$$\lim_{t \to +\infty} \sup_{|x| > ct} \{|S_1(x,t)| + |I_1(x,t)| + |S_2(x,t) - K_2| + |I_2(x,t)|\} = 0, \quad \forall c > s_1.$$

Then we set $U := N_1^* - N_1$ and $V := N_2^* - N_2$. Similar to the proof before, we can get

$$\lim_{t \to +\infty} \sup_{|x| < ct} \{|N_1(x,t) - N_1^*| + |N_2(x,t) - N_2^*|\} = 0, \quad \forall c < s_1.$$

If $R_s \leq 1$, for system (1.1),

$$\lim_{t \to +\infty} \sup_{|x| < ct} \{|S_1(x,t) - N_1^*| + |I_1(x,t)| + |S_2(x,t) - N_2^*| + |I_2(x,t)|\} = 0, \quad \forall c < s_1.$$

Next we consider the propagating terrace linking E_3 to (E_4 or E_5). Let (S_1, I_1, S_2, I_2) be a solution to system (1.1) with the initial condition $S_1(x, 0) = N_1^*$, $S_2(x, 0) = N_2^*$, $I_2(x, 0) = 0$, $x \in \mathbb{R}$. $I_1(x, 0) > 0$, $x \in [-x_2, x_2]$; $I_1(x, 0) = 0$, $x \in (-\infty, x_2) \cup (x_2, \infty)$, for some $x_2 > 0$.

If $B_{12}B_{21} < \dfrac{\omega_0 r_2}{K_2}$ and $s_0 < \min\left\{\dfrac{\omega_0 r_2}{B_{21}}, B_{12}K_2\right\}$, we claim that $(S_1(x, t)+I_1(x, t), S_2(x, t)+I_2(x, t)) \in \Sigma$, $\forall x \in \mathbb{R}, t \in [0, \infty)$.

For the spreading speed when $R_s > 1$, comparison principle and strong maximum principle are no longer applicable due to the complexity of system (1.1). However, we can calculate the minimum wave speed from largest eigenvalue of its linearized system at E_3 as [22] to link E_3 and E_4 (or E_5).

For the following eigenvalue problem

$$\frac{1}{\lambda}A_\lambda \eta_\lambda = c\eta_\lambda,$$

where

$$A_\lambda = diag(D_i\lambda^2) + J\big|_{E_3}.$$

J is the jacobian matrix,

$$J = \begin{pmatrix} B_{12}N_2 - 2\omega_0 N_1 - s_0 - \beta_{11}I_1 & -\beta_{11}S_1 + \gamma_1 & B_{12}N_1 & 0 \\ \beta_{11}I_1 & \beta_{11}S_1 - (s_0 + \gamma_1) & 0 & 0 \\ B_{12}N_2 & -\beta_{21}S_2 & r_2(1 - 2\frac{N_2}{K_2}) + B_{21}N_1 - (\beta_{21}I_1 + \beta_{22}I_2) & -\beta_{22}S_2 + \gamma_2 \\ 0 & \beta_{21}S_2 & \beta_{21}I_1 + \beta_{22}I_2 & \beta_{22}S_2 - (e_2 + \gamma_2 + d_2) \end{pmatrix}.$$

For $\lambda \geq 0$, the eigenvalues of the matrix

$$A_\lambda = \begin{pmatrix} D_1\lambda^2 - \omega_0 N_1^* & -\beta_{11}N_1^* + \gamma_1 & B_{12}N_1^* & 0 \\ 0 & D_1\lambda^2 + \beta_{11}N_1^* - (s_0 + \gamma_1) & 0 & 0 \\ B_{12}N_2^* & -\beta_{21}N_2^* & D_2\lambda^2 - r_2\frac{N_2^*}{K_2} & -\beta_{22}N_2^* + \gamma_2 \\ 0 & \beta_{21}N_2^* & 0 & D_2\lambda^2 + \beta_{22}N_2^* - (e_2 + \gamma_2 + d_2) \end{pmatrix}.$$

are $D_1\lambda^2 + \beta_{11}N_1^* - (s_1 + \gamma_1)$, $D_2\lambda^2 + \beta_{22}N_2^* - (e_2 + \gamma_2 + d_2)$ and other two impossible results, which cannot define positive wave speed.

Thus, the minimum wave speed can be defined as follows, which can be divided the propagating terrace, linking E_3 to E_4 (or E_5).

$$s_2 = \max\left\{\inf_{\lambda>0} \frac{D_1\lambda^2 + \beta_{11}N_1^* - (s_0 + \gamma_1)}{\lambda}, \inf_{\lambda>0} \frac{D_2\lambda^2 + \beta_{22}N_2^* - (e_2 + \gamma_2 + d_2)}{\lambda}\right\}$$

$$= \max\left\{2\sqrt{D_1(\beta_{11}N_1^* - s_0 - \gamma_1)}, 2\sqrt{D_2(\beta_{22}N_2^* - e_2 - \gamma_2 - d_2)}\right\}.$$

If $R_s > 1$, there are two cases: (A). $R_1 < R_2$ and $R_1 \leq 1$; (B). $R_1 \geq R_2$ or $R_2 > R_1 > 1$.

(A). If $R_1 < R_2$ and $R_1 \leq 1$, then E_5 does not exist. $s_2 = 2\sqrt{D_2(\beta_{22}N_2^* - e_2 - \gamma_2 - d_2)}$, then we get

$$\lim_{t\to+\infty} \sup_{|x|>c_2t+x_2} \left\{\left|S_1(x, t) - N_1^*\right| + |I_1(x, t)| + \left|S_2(x, t) - N_2^*\right| + |I_2(x, t)|\right\} = 0, \quad \forall c > s_2,$$

$$\lim_{t\to+\infty} \sup_{|x|<ct+x_2} \left\{\left|S_1(x, t) - N_1'\right| + |I_1(x, t)| + \left|S_2(x, t) - S_2'\right| + \left|I_2(x, t) - I_2'\right|\right\} = 0, \quad \forall c < s_2.$$

Combining the results before, linking E_1 to E_3, then

$$\lim_{t\to+\infty} \sup_{|x|>ct+x_1} \{|S_1(x,t)| + |I_1(x,t)| + |S_2(x,t) - K_2| + |I_2(x,t)|\} = 0, \quad \forall c > s_1,$$

$$\lim_{t\to+\infty} \sup_{c_2t+x_2<|x|<c_1t+x_1} \left\{\left|S_1(x,t) - N_1^*\right| + |I_1(x,t)| + \left|S_2(x,t) - N_2^*\right| + |I_2(x,t)|\right\} = 0, \quad \forall s_2 < c_2 < c_1 < s_1,$$

$$\lim_{t\to+\infty} \sup_{|x|<ct+x_2} \left\{\left|S_1(x,t) - N_1'\right| + |I_1(x,t)| + \left|S_2(x,t) - S_2'\right| + \left|I_2(x,t) - I_2'\right|\right\} = 0, \quad \forall c < s_2.$$

The system (1.1) forms a propagating terrace, linking E_1 to E_3, then to E_4.

(B). If $R_1 \geq R_2$ or $R_2 > R_1 > 1$, set $s_2 = \max\left\{2\sqrt{D_1(\beta_{11}N_1^* - s_0 - \gamma_1)}, 2\sqrt{D_2(\beta_{22}N_2^* - e_2 - \gamma_2 - d_2)}\right\}$. then we get

$$\lim_{t\to+\infty} \sup_{|x|>ct+x_1} \{|S_1(x,t)| + |I_1(x,t)| + |S_2(x,t) - K_2| + |I_2(x,t)|\} = 0, \quad \forall c > s_1,$$

$$\lim_{t\to+\infty} \sup_{c_2t+x_2<|x|<c_1t+x_1} \left\{\left|S_1(x,t) - N_1^*\right| + |I_1(x,t)| + \left|S_2(x,t) - N_2^*\right| + |I_2(x,t)|\right\} = 0, \quad \forall s_2 < c_2 < c_1 < s_1,$$

$$\lim_{t\to+\infty} \sup_{|x|<ct+x_2} \left\{\left|S_1(x,t) - S_1^*\right| + \left|I_1(x,t) - I_1^*\right| + \left|S_2(x,t) - S_2^*\right| + \left|I_2(x,t) - I_2^*\right|\right\} = 0, \quad \forall c < s_2.$$

The system (1.1) forms a propagating terrace, linking E_1 to E_3, then to E_5.

□

5. Simulations

If $s_1 > s_2$, $x_1 > x_2$ and $R_s > 1$, $R_1 > R_2 > 1$, then in Figure 4, the blue area represents the original habitat area of humans at the population size of E_1. After domesticating pigs, the red part will be shared with the two species at E_3. While after swine flu transmitting between domestic pigs and humans, the internal red part will be shared again with two populations at E_5 with swine flu transmission. It is a biological description of propagating terrace of humans with swine flu transmission, which is the local spacial variation of the population.
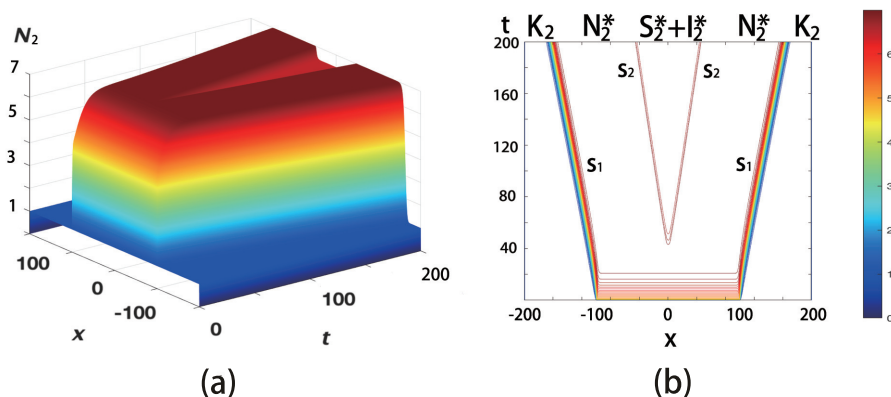

Figure 4. If $R_s > 1$, $R_1 > R_2 > 1$, the propagating terrace from E_1 to E_3, then to E_5. (a): The simulation of N_2; (b): Contour line of N_2.

If $s_1 > s_2$, $x_1 > x_2$ and $R_s \leq 1$, then in Figure 5, the blue area represents the original habitat area of humans at the population size of E_1. After domesticating pigs, the red part will be shared with the two species at E_3. Because $R_s \leq 1$, there is no swine flu transmission during the breed and slaughter process. Then the propagating terrace links unstable equilibrium E_1 and stable equilibrium E_2.
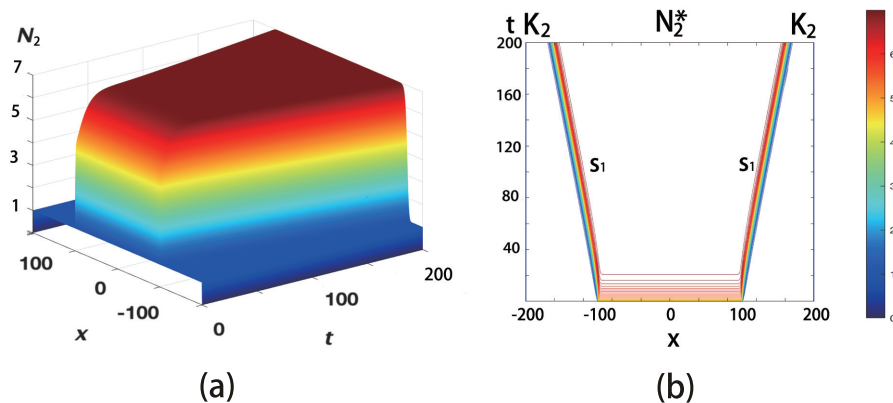

Figure 5. If $R_s \leq 1$, the propagating terrace from E_1 to E_3. (a): The simulation of N_2; (b): Contour line of N_2.

6. Discussions

We establish a new swine flu mathematical model to reflect the dynamic process of swine flu transmission with interspecific action between domestic pigs and humans, in which the roles of different species will no longer be at the same level. Domestic pigs cannot survive independently without human beings, but human beings can still survive well without the supply of pork. By our new swine flu model, we find that the human-animal interface has promoted the cross-species transmission of swine flu and resulted in the prevalence of flu in humans. In addition, the threshold values of population development and disease transmission are also discussed in order to provide a scientific basis for future health decision makers in swine flu prevention and control. We propose the zoonotic basic reproduction number R_s, which is more applicable to the study of swine flu transmission. Then, it is analyzed that the spreading speed of different species forming propagating terraces is influenced by the intrinsic growth rate r and diffusion rate D.

In this paper, the equilibrium points of the model are calculated and we analyze the existence of the equilibrium points by the persistence theory. Then we discuss their stability by the basic reproduction number. In addition, after redefining the spreading speed, we divide the propagating terrace with two populations, which is an unprecedented task. We concern with the invasion process of infected domestic animals into the habitat of humans. Under certain conditions as in Theorem 2, we construct a propagating terrace linking human habitat to animal-human coexistent habitat, then to swine flu natural foci, which is divided by spreading speeds.

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Conflict of interest

The authors declared that they have no conflicts of interest to this work.

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