

Analysis of a multi– patch dynamical model about cattle brucellosis

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Abstract: The dissemination of cattle brucellosis in Zhejiang province of China can be attributed to the transport of cattle between cities within the province. In this paper an n -patch dynamical model is proposed to study the effect of cattle dispersal on brucellosis spread. Theoretically , we analyze the dynamical behavior of the multi-patch model. For the 2-patch submodel , sensitivity analyses of the basic reproduction number R^0 and the number of the infectious cattle in term of model parameters are carried out. By numerical analysis , it is obtained that the dispersal of susceptible cattle between patches and the centralization of infected cattle to the large scale patch can alleviate the epidemic and are in favor of the control of disease in the whole region.

Key words: brucellosis ; cattle ; n -patch model ; dispersal

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1 Introduction

Brucella , one of the world's major zoonotic pathogens known , causes infectious abortion in animals and Malta Fever in man^[1]. Since many kinds of domestic animals , such as sheep , cattle , dogs , pig and so on ,

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can be infected by brucella ,brucellosis usually causes economic devastation on a global scale. China is no exception. In Zhejiang province which locates in the southern China , the livestock breeding , dairy , the leather processing industry have gotten great development. A mass of dairy cows ,beefs , row fur and other animal by-products were taken to trade annually. But it has also brought lots of cattle brucellosis infection^[2,3]. In fact , the cow remains an intermittent carrier for years in China^[4]. For cattle ,transmission of brucella typically occurs through direct contact with brucella carriers or oral contact with aborted foetal material including the bacteria throughout the byre^[4,5]. Bull can spread infection through semen ,but often the disease leads to infertility or arthritis. More detailed information about cattle brucellosis can be seen in [6].

Since Brucellosis caused by brucella is a non-fatal disease , it is often overlooked by the majority of the scientific community. The local government of Zhejiang province has regularly taken detection measures and culled infected cattle immediately. Yet , the data of positive cattle brucellosis in Zhejiang are rising year by year and it has influenced the local economy , even leads to the local prevalence of human brucellosis. From Fig. 1 , we can see that brucellosis has been spreading from north to south in Zhejiang province. So , one of main reasons of the geographical spread of the disease is the transportation of cattle between cities within Zhejiang province. Cattle transportation can cause cross infection of individuals among different regions. Besides , through vehicles and staff movement , it can also lead to the dispersal of brucella surviving in environment. Therefore , public health officials and scientific community should pay more attention to the transmission of cattle brucellosis.

Dynamical systems method is one of the most useful and important tools in studying biological and epidemiological models^[7-13]. Some researches have applied dynamical systems method to study brucellosis^[14-17]. In 1994 ,Gonzalez-Guzman and Naulin^[14] were the first to apply dynamical models to study bovine brucellosis. In 2005 ,besides transmission within sheep and cattle populations ,Zinsstag et al. ^[17] considered the transmission to humans in a dynamical model. The livestock are classified into three subclasses: the susceptible , the seropositive and the immunized. In 2009 ,Xie and Horan^[15] built a simple dynamical model with the susceptible , the infected and the resistant subclasses to discuss brucellosis in the elk and cattle population. In 2010 ,Ainseba et al. ^[16] considered two transmission modes about the ovine brucellosis in their model: direct mode caused by infected individuals and indirect mode related to brucella in the environment. For the transmission of brucellosis in China , there are also some studies^[18-22]. Hou et al. ^[20] investigated the transmission dynamics of sheep brucellosis in Inner Mongolia Autonomous Region of China. Zhang et al. ^[21] and Nie et al. ^[22] established dynamical models about dairy cattle brucellosis in Zhejiang and Jilin Provinces , respectively. According to the spatial spread of disease , there are two types of model we can apply: multi-patch models^[23-30] and reaction-diffusion models^[31-33]. The goal of this paper is to establish an n -patch dynamical model to discuss the effects of cattle dispersal and brucella diffusion on the geographical spread of the disease.

The article is organized as follows. In Sections 2 , we propose an n -patch model about cattle brucellosis with cattle transportation and brucella diffusion , and analyze its dynamical behavior. In section 3 , we apply numerical method to discuss the transmission of the disease between two patches under different conditions. In section 4 , we give a brief discussion.

2 Model and dynamical behavior

There are 11 cities in Zhejiang province , where Hangzhou is the provincial capital. More generally , we propose an epidemic dynamical model with cattle dispersal between n patches. The number of cattle in each patch can be denoted by N_i , $i = 1, 2, \dots, n$. For each patch , the cattle population is divided into three classes:

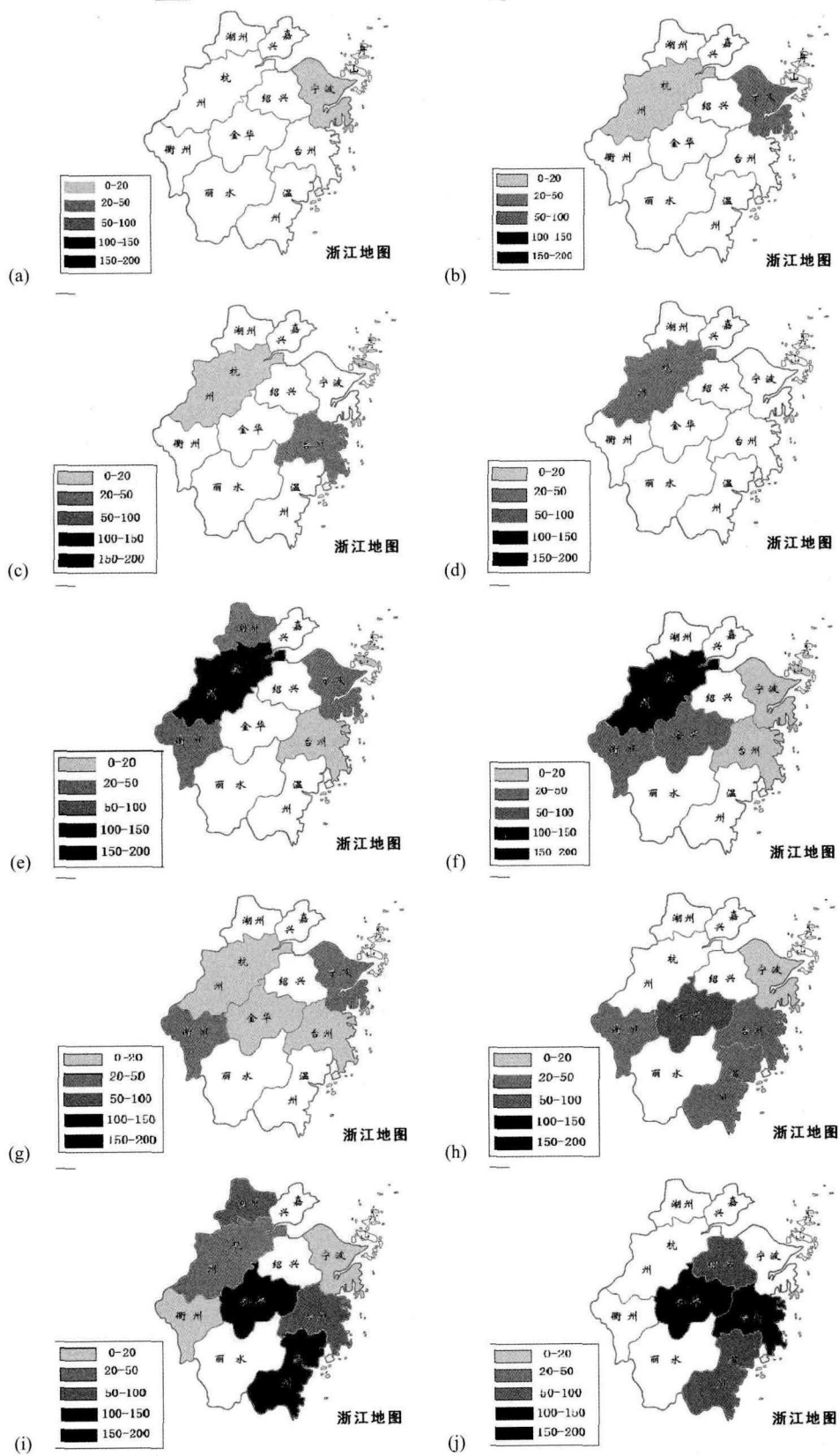


Fig. 1 The distribution of infected dairy cattle in Zhejiang from 2001 to 2010. (a) 2001. (b) 2002. (c) 2003. (d) 2004. (e) 2005. (f) 2006. (g) 2007. (h) 2008. (i) 2009. (j) 2010.

susceptible , exposed and infective individuals , the numbers of which at time t in i th patch are denoted by $S_i(t)$, $E_i(t)$ and $I_i(t)$, respectively. During the infected period , the infected individuals (the exposed and the infectious individuals) discharge brucella into the environment. The quantity of brucella in environment is denoted by $V_i(t)$. Consequently , the susceptible cattle can be infected by contacting with the exposed cattle , the infectious cattle and the brucella in environment. Compared with the infectious individuals , the transmission coefficient of the exposed individuals is relatively smaller. So the auxiliary parameter θ is introduced. The internal relationship of each individual in n patches can be described in the following system and the parameter meanings can be seen in Table 1 , where parameters A_i , β_i , α_i , m_i , δ_i , μ_i , r_i and w_i are all positive constants. θ is a parameter whose value is between 0 and 1. a_{ji} , b_{ji} , c_{ji} and d_{ji} ($j \neq i$) are non-negative constants. a_{ii} , b_{ii} , c_{ii} and d_{ii} are non-positive constants.

$$\begin{cases} \frac{dS_i}{dt} = A_i - \beta_i S_i I_i - \theta \beta_i S_i E_i - \alpha_i S_i V_i - m_i S_i + \sum_{j=1}^n a_{ji} S_j , & 1 \leq i \leq n \\ \frac{dE_i}{dt} = \beta_i S_i I_i + \theta \beta_i S_i E_i + \alpha_i S_i V_i - m_i E_i - \delta_i E_i + \sum_{j=1}^n b_{ji} E_j , & 1 \leq i \leq n \\ \frac{dI_i}{dt} = \delta_i E_i - m_i I_i - \mu_i I_i + \sum_{j=1}^n c_{ji} I_j , & 1 \leq i \leq n \\ \frac{dV_i}{dt} = r_i (E_i + I_i) - w_i V_i + \sum_{j=1}^n d_{ji} V_j , & 1 \leq i \leq n \end{cases} , \quad (1)$$

Table 1 Description of parameters in the model (1).

Parameters	Comments
A_i	The birth number of cattle in i th patch per unit time
β_i	The infectious cattle-to-susceptible cattle transmission rate in i th patch
θ	Auxiliary parameter
α_i	Brucella in environment-to-susceptible cattle transmission rate in i th patch
m_i	Natural elimination rate of cattle in i th patch
δ_i	Clinical outcome rate of the exposed cattle in i th patch
μ_i	Disease-related culling rate of infectious cattle in i th patch
r_i	Brucella quantity released by infected cattle in i th patch
w_i	Brucella death rate in i th patch
$a_{ji} (j \neq i)$	The immigration rate of the susceptible cattle from j th patch to i th patch
$b_{ji} (j \neq i)$	The immigration rate of the exposed cattle from j th to i th patch
$c_{ji} (j \neq i)$	The immigration rate of the infectious cattle from j th to i th patch
$d_{ji} (j \neq i)$	The immigration rate of brucella in environment from j th to i th patch
$-a_{ii}$	The emigration rate of the susceptible cattle in i th patch
$-b_{ii}$	The emigration rate of the exposed cattle in i th patch
$-c_{ii}$	The emigration rate of the infectious cattle in i th patch
$-d_{ii}$	The emigration rate of brucella in environment in i th patch

It is easy to know that there exist the following relationships for the migration rates.

$$\sum_{j=1}^n a_{ij} = \sum_{j=1}^n b_{ij} = \sum_{j=1}^n c_{ij} = \sum_{j=1}^n d_{ij} = 0 , \quad \forall 1 \leq i \leq n. \quad (2)$$

Lemma 1 Let $N^* = \frac{A}{m}$, where $A = \sum_{i=1}^n A_i$ and $m = \min\{m_i, 1 \leq i \leq n\}$, every forward orbit in R_+^{4n} of system (1) eventually enters $\Gamma = \{(S, E, I, V) \in R_+^{4n} : \sum_{i=1}^n (S_i + E_i + I_i) \leq N^*\}$, and Γ is a positively invariant set.

Firstly, we consider the existence and uniqueness of the disease-free equilibrium. Let the right hand side of system (1) be zero and choose $E_i = I_i = V_i = 0$, we can obtain the following system.

$$A_i - m_i S_i + \sum_{j=1}^n a_{ji} S_j = 0, \quad 1 \leq i \leq n.$$

which can be expanded as follows.

$$\begin{pmatrix} -m_1 + a_{11} & a_{21} & a_{31} & \cdots & a_{n1} \\ a_{12} & -m_2 + a_{22} & a_{32} & \cdots & a_{n2} \\ a_{13} & a_{23} & -m_3 + a_{33} & \cdots & a_{n3} \\ \vdots & \vdots & \vdots & \cdots & \vdots \\ a_{1n} & a_{2n} & a_{3n} & \cdots & -m_n + a_{nn} \end{pmatrix} \begin{pmatrix} S_1 \\ S_2 \\ S_3 \\ \vdots \\ S_n \end{pmatrix} = \begin{pmatrix} -A_1 \\ -A_2 \\ -A_3 \\ \vdots \\ -A_n \end{pmatrix}$$

Observing the coefficient matrix and combining Eq. (2), we know that the coefficient matrix is absolutely diagonally dominant about columns. So the above system has a unique untrivial solution and the solution is positive. Thus the corresponding disease-free equilibrium of system (1) is existent and unique, which can be denoted as

$$E_0 = (S_1^0, \rho, \rho, \rho, \dots, S_i^0, \rho, \rho, \rho, \dots, S_n^0, \rho, \rho, \rho).$$

Applying the next generation matrix method, we can present the expression of the basic reproduction number. Define

$$\mathcal{F} = \begin{pmatrix} \beta_1 S_1 I_1 + \theta \beta_1 S_1 E_1 + \alpha_1 S_1 V_1 \\ 0 \\ 0 \\ \vdots \\ \beta_n S_n I_n + \theta \beta_n S_n E_n + \alpha_n S_n V_n \\ 0 \\ 0 \end{pmatrix}, \quad \mathcal{V} = \begin{pmatrix} m_1 E_1 + \delta_1 E_1 - \sum_{j=1}^n b_{j1} E_j \\ -\delta_1 E_1 + (m_1 + \mu_1) I_1 - \sum_{j=1}^n c_{j1} I_j \\ -r_1 (E_1 + I_1) + w_1 V_1 - \sum_{j=1}^n d_{j1} V_j \\ \vdots \\ m_n E_n + \delta_n E_n - \sum_{j=1}^n b_{jn} E_j \\ -\delta_n E_n + (m_n + \mu_n) I_n - \sum_{j=1}^n c_{jn} I_j \\ -r_n (E_n + I_n) + w_n V_n - \sum_{j=1}^n d_{jn} V_j \end{pmatrix},$$

$$F = \begin{pmatrix} F_1 & 0 & \cdots & 0 \\ 0 & F_2 & \cdots & 0 \\ \vdots & \vdots & \cdots & \vdots \\ 0 & 0 & \cdots & F_n \end{pmatrix},$$

and

$$V = \begin{pmatrix} V_{11} & V_{21} & \cdots & V_{n1} \\ V_{12} & V_{22} & \cdots & V_{n2} \\ \vdots & \vdots & \cdots & \vdots \\ V_{1n} & V_{2n} & \cdots & V_{nn} \end{pmatrix},$$

where ,

$$F_i = \begin{pmatrix} \theta\beta_i S_i^0 & \beta_i S_i^0 & \alpha_i S_i^0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, V_{ij(i \neq j)} = \begin{pmatrix} -b_{ij} & 0 & 0 \\ 0 & -c_{ij} & 0 \\ 0 & 0 & -d_{ij} \end{pmatrix},$$

and

$$V_{ii} = \begin{pmatrix} m_i + \delta_i - b_{ii} & 0 & 0 \\ -\delta_i & m_i + \mu_i - c_{ii} & 0 \\ -r_i & -r_i & w_i - d_{ii} \end{pmatrix}.$$

The basic reproduction number is $R_0 = \rho(FV^{-1})$. Defining $M = F - V$ and $s(M) := \max\{\text{Re}\lambda : \lambda \text{ is an eigenvalue of } M\}$, we have the following result.

Lemma 2 There hold two equivalences^[34] :

$$R_0 < 1 \Leftrightarrow s(M) < 0, \quad R_0 > 1 \Leftrightarrow s(M) > 0. \tag{3}$$

By Theorem 2 in [34] , the disease-free equilibrium E_0 is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$. Now we further investigate the global dynamical behavior of E_0 .

Firstly , we consider the auxiliary system

$$\frac{dS_i}{dt} = A_i - m_i S_i + \sum_{j=1}^n a_{ji} S_j, \quad 1 \leq i \leq n, \tag{4}$$

whose Jacobian matrix is

$$\begin{pmatrix} -m_1 + a_{11} & a_{21} & a_{31} & \cdots & a_{n1} \\ a_{12} & -m_2 + a_{22} & a_{32} & \cdots & a_{n2} \\ a_{13} & a_{23} & -m_3 + a_{33} & \cdots & a_{n3} \\ \vdots & \vdots & \vdots & \cdots & \vdots \\ a_{1n} & a_{2n} & a_{3n} & \cdots & -m_n + a_{nn} \end{pmatrix}.$$

It is already known that the Jacobian matrix is absolutely diagonally dominant about column and the system (3) has a unique positive equilibrium $S^0 = (S_1^0, S_2^0, S_3^0, \dots, S_n^0)^T$. Moreover , $-m_i + a_{ii} < 0, 1 \leq i \leq n$. So , all eigenvalues of the Jacobian matrix have negative real parts which imply that S^0 is locally stable. Since system (4) is a linear system , equilibrium S^0 is globally stable.

Theorem 1 When $R_0 < 1$, the disease-free equilibrium E_0 of system (1) is globally asymptotically stable in Γ .

Proof Now , we only need to prove the global attraction of the disease-free equilibrium. Because $R_0 < 1$, then $s(M) < 0$. For small enough η , $s(M + M_\eta) < 0$, where

$$M_\eta = \begin{pmatrix} M_1 & 0 & \cdots & 0 \\ 0 & M_2 & \cdots & 0 \\ \vdots & \vdots & \cdots & \vdots \\ 0 & 0 & \cdots & M_n \end{pmatrix}, M_i = \begin{pmatrix} \theta\beta_i \eta & \beta_i \eta & \alpha_i \eta \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} (i = 1 \cdots n).$$

It is obvious to know that

$$\frac{dS_i}{dt} \leq A_i - m_i S_i + \sum_{j=1}^n a_{ji} S_j, \quad 1 \leq i \leq n. \tag{5}$$

Then the following auxiliary system is introduced.

$$\frac{dS_i}{dt} = A_i - m_i S_i + \sum_{j=1}^n a_{ji} S_j, \quad 1 \leq i \leq n, \tag{6}$$

The positive equilibrium S^0 of system (6) has been proved to be globally stable. So, for η , there exists T such that $\forall t > T, S(t) \leq S^0 + \eta$, where $S(t) = (S_1(t), \dots, S_n(t))$. Thus, we obtain the following system.

$$\begin{aligned} \frac{dE_i}{dt} &\leq \beta_i (S_i^0 + \eta) I_i + \theta \beta_i (S_i^0 + \eta) E_i + \alpha_i (S_i^0 + \eta) V_i - m_i E_i - \delta_i E_i + \sum_{j=1}^n b_{ji} E_j, \quad 1 \leq i \leq n, \\ \frac{dI_i}{dt} &= \delta_i E_i - m_i I_i - \mu_i I_i + \sum_{j=1}^n c_{ji} I_j, \quad 1 \leq i \leq n, \\ \frac{dV_i}{dt} &= r_i (E_i + I_i) - w_i V_i + \sum_{j=1}^n d_{ji} V_j, \quad 1 \leq i \leq n. \end{aligned}$$

Because $s(M + M_\eta) < 0$, the solution of the right side system tends to zero as t goes to infinity, which implies $\lim_{t \rightarrow \infty} E_i(t) = \lim_{t \rightarrow \infty} I_i(t) = \lim_{t \rightarrow \infty} V_i(t) = 0, 1 \leq i \leq n$. By the theory of asymptotic autonomous systems^[35], it is also known that $S(t) \rightarrow S^0$ as $t \rightarrow \infty$. Then E_0 is globally attractive when $R_0 < 1$.

Define

$$\begin{aligned} X &= \{ (S_1, E_1, I_1, V_1, \dots, S_n, E_n, I_n, V_n) : S_i \geq 0, E_i \geq 0, I_i \geq 0, V_i \geq 0, i = 1, \dots, n \}, \\ X_0 &= \{ (S_1, E_1, I_1, V_1, \dots, S_n, E_n, I_n, V_n) \in X : E_i > 0, I_i > 0, V_i > 0, i = 1, \dots, n \}, \\ \partial X_0 &= X \setminus X_0. \end{aligned}$$

Considering the auxiliary system

$$\frac{dS_i}{dt} = A_i - \beta_i S_i \epsilon - \theta \beta_i S_i \epsilon - \alpha_i S_i \epsilon - m_i S_i + \sum_{j=1}^n a_{ji} S_j, \quad 1 \leq i \leq n. \tag{7}$$

For system (7), similar as system (4), there exists a unique positive equilibrium $S^0(\epsilon)$ and it is global asymptotically stable. By the implicit function theorem, it follows that $S^0(\epsilon)$ is continuous in term of ϵ . For given τ , we can restrict ϵ small enough such that $S^0(\epsilon) \geq S^0 - \tau$ for all $t > T_1$.

Theorem 2 When $R_0 > 1$, there exists positive constant ϵ such that when $\| (E_i(0), I_i(0), V_i(0)) \| < \epsilon$ for $(S_i(0), E_i(0), I_i(0), V_i(0)) \in X_0$,

$$\limsup_{t \rightarrow \infty} \max_i \| (E_i(t), I_i(t), V_i(t)) \| > \epsilon, \quad i = 1, \dots, n. \tag{8}$$

Proof Because $R_0 > 1, s(M) > 0$. So, for small enough $\tau, s(M - M_\tau) > 0$, where

$$M_\tau = \begin{pmatrix} M_1 & 0 & \dots & 0 \\ 0 & M_2 & \dots & 0 \\ \vdots & \vdots & \dots & \vdots \\ 0 & 0 & \dots & M_n \end{pmatrix}, M_i = \begin{pmatrix} \theta \beta_i \tau & \beta_i \tau & \alpha_i \tau \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} (i = 1 \dots n).$$

Now we proceed by contradiction to prove the above conclusion. Suppose, there exist ϵ and $T > 0$ such that $E_i(t) < \epsilon, I_i(t) < \epsilon$ and $V_i(t) < \epsilon, i = 1 \dots n$ for all $t > T$. Then for all $t > T$, we can have that

$$\frac{dS_i}{dt} > A_i - \beta_i S_i \epsilon - \theta \beta_i S_i \epsilon - \alpha_i S_i \epsilon - m_i S_i + \sum_{j=1}^n a_{ji} S_j, \quad 1 \leq i \leq n. \tag{9}$$

For the right side system, there exists a unique positive equilibrium $S^0(\epsilon)$ which is global asymptotically stable. There exists a large enough $T_1 > T$ such that $S(t) \geq S^0(\epsilon)$. Because $S^0(\epsilon) \geq S^0 - \tau, S(t) \geq S^0 - \tau$ for

all $t > T_1$. Thus , there holds

$$\begin{aligned} \frac{dE_i}{dt} &\geq \beta_i(S_i^0 - \tau)I_i + \theta\beta_i(S_i^0 - \tau)E_i + \alpha_i(S_i^0 - \tau)V_i - m_iE_i - \delta_iE_i + \sum_{j=1}^n b_{ji}E_j , \quad 1 \leq i \leq n , \\ \frac{dI_i}{dt} &= \delta_i E_i - m_iI_i - \mu_iI_i + \sum_{j=1}^n c_{ji}I_j , \quad 1 \leq i \leq n , \\ \frac{dV_i}{dt} &= r_i(E_i + I_i) - w_iV_i + \sum_{j=1}^n c_{ji}V_j , \quad 1 \leq i \leq n . \end{aligned}$$

Because $s(M - M_\tau) > 0$, $I_i(t) \rightarrow \infty$, $E_i(t) \rightarrow \infty$, $V_i(t) \rightarrow \infty$ as $t \rightarrow \infty$, $i = 1 \cdots n$, which is a contraction. So , inequality (8) is well-founded.

Theorem 3 When $R_0 > 1$, system (1) admits at least one positive equilibrium , and there exists positive constant ϵ such that every solution of (1) with $(S_i(0) , E_i(0) , I_i(0) , V_i(0)) \in X_0$ satisfies

$$\min\{\liminf_{t \rightarrow \infty} E_i(t) , \liminf_{t \rightarrow \infty} I_i(t) , \liminf_{t \rightarrow \infty} V_i(t)\} \geq \epsilon , \quad i = 1 , \dots , n . \tag{10}$$

Proof Firstly , we show that system (1) is uniformly persistent with respect to $(X_0 , \partial X_0)$. It is easy to know that both X and X_0 are positively invariant and ∂X_0 is relatively closed in X . Moreover , from Lemma 1 , system (1) is point dissipative. Set $M_\partial = \{(S(0) , E(0) , I(0) , V(0)) : (S(t) , E(t) , I(t) , V(t)) \in \partial X_0 , \forall t \geq 0 , i = 1 , \dots , n\}$, where $S(t) = (S_1(t) , \dots , S_n(t))$, $E(t) = (E_1(t) , \dots , E_n(t))$, $I(t) = (I_1(t) , \dots , I_n(t))$, $V(t) = (V_1(t) , \dots , V_n(t))$. It is needed to show that

$$M_\partial = \{(S(t) , \rho , \dots , \rho) : S(t) \geq 0\} . \tag{11}$$

Noting that

$$\{(S(t) , \rho , \dots , \rho) : S(t) \geq 0\} \subseteq M_\partial , \tag{12}$$

we only need to prove

$$M_\partial \subseteq \{(S(t) , \rho , \dots , \rho) : S(t) \geq 0 , i = 1 , \dots , n\} . \tag{13}$$

Suppose not. Assume $(S(0) , E(0) , I(0) , V(0)) \in M_\partial$. There exist an $i_0 (1 \leq i_0 \leq n)$ and a t_0 such that $(E_{i_0}(t_0) , I_{i_0}(t_0) , V_{i_0}(t_0))^T > 0$. Then we can separate $\{1 , \dots , n\}$ into two sets Q_1 and Q_2 such that

$$\begin{aligned} (E_i(t_0) , I_i(t_0) , V_i(t_0))^T &= 0 , \quad \forall i \in Q_1 , \\ (E_i(t_0) , I_i(t_0) , V_i(t_0))^T &> 0 , \quad \forall i \in Q_2 . \end{aligned}$$

It is easy to know that Q_1 and Q_2 are not empty. For $i \in Q_2$, without loss of generality , we assume $E_i(t_0) > 0$, $I_i(t_0) = V_i(t_0) = 0$. From the equations $I_i'(t_0) = \delta_i E_i(t_0) > 0$ and $V_i'(t_0) = r_i E_i(t_0) > 0$, we can know that there is a small enough $\epsilon_0 > 0$ such that $E_i(t) > 0$, $I_i(t) > 0$, $V_i(t) > 0$, $i \in Q_2$ for $t_0 < t < t_0 + \epsilon_0$. For $j \in Q_1$, we have $E_j'(t_0) \geq b_{ji} E_i(t_0) > 0$. So , there exists $\epsilon_1 > 0$ such that $E_j(t) > 0$, $j \in Q_1$ for $t_0 < t < t_0 + \epsilon_1$. Similarly , there exists $\epsilon_2 > 0$ such that $I_j(t) > 0$, $V_j(t) > 0$, $j \in Q_1$ for $t_0 < t < t_0 + \epsilon_2$. These mean that $(S(t) , E(t) , I(t) , V(t)) \notin \partial X_0$ for $t_0 < t < t_0 + \hat{\epsilon}$, $\hat{\epsilon} = \min\{\epsilon_0 , \epsilon_1 , \epsilon_2\}$, which contradicts the assumption that $(S(0) , E(0) , I(0) , V(0)) \in M_\partial$. So , the equality (11) holds. Moreover , from Theorem 2 , it can be known that E_0 is an isolated invariant set in X and $W^s(E_0) \cap X_0 = \emptyset$. E_0 is the only fixed point and acyclic in ∂X_0 . By Theorem 4.3 in [36] and in Theorem 4.6^[37] , we can conclude that system (1) is uniformly persistent with respect to $(X_0 , \partial X_0)$.

By Theorem 2.4 in [38] , system (1) has an equilibrium $(S^* , E^* , I^* , V^*) \in X_0$ where $S(t) = (S_1^* , \dots , S_n^*)$, $E(t) = (E_1^* , \dots , E_n^*)$, $I(t) = (I_1^* , \dots , I_n^*)$, $V(t) = (V_1^* , \dots , V_n^*)$. From $A_i - \beta_i S_i I_i - \theta\beta_i S_i E_i - \alpha_i S_i V_i - m_i S_i + \sum_{j=1}^n a_{ji} S_j = 0$ and $A_i > 0$, $i = 1 , \dots , n$, we know $S^* > 0$. Then (S^* , E^* , I^* , V^*) is a positive equilibrium of system (1).

3 Application to two patches

In this section , for simplicity , assuming $n = 2$, we perform numerical simulation to study the effects of cattle dispersal on brucellosis transmission. Let $a_{12} = -a_{22}$, $a_{21} = -a_{11}$, $b_{12} = -b_{22}$, $b_{21} = -b_{11}$, $c_{12} = -c_{22}$, $c_{21} = -c_{11}$, $d_{12} = -d_{22}$, $d_{21} = -d_{11}$. Then system (1) reduces to

$$\left\{ \begin{aligned} \frac{dS_1}{dt} &= A_1 - \beta_1 S_1 I_1 - \theta \beta_1 S_1 E_1 - \alpha_1 S_1 V_1 - m_1 S_1 - a_{12} S_1 + a_{21} S_2 \\ \frac{dE_1}{dt} &= \beta_1 S_1 I_1 + \theta \beta_1 S_1 E_1 + \alpha_1 S_1 V_1 - m_1 E_1 - \delta_1 E_1 - b_{12} E_1 + b_{21} E_2 \\ \frac{dI_1}{dt} &= \delta_1 E_1 - m_1 I_1 - \mu_1 I_1 - c_{12} I_1 + c_{21} I_2 \\ \frac{dV_1}{dt} &= r_1 (E_1 + I_1) - w_1 V_1 - d_{12} V_1 + d_{21} V_2 \\ \frac{dS_2}{dt} &= A_2 - \beta_2 S_2 I_2 - \theta \beta_2 S_2 E_2 - \alpha_2 S_2 V_2 - m_2 S_2 - a_{21} S_2 + a_{12} S_1 \\ \frac{dE_2}{dt} &= \beta_2 S_2 I_2 + \theta \beta_2 S_2 E_2 + \alpha_2 S_2 V_2 - m_2 E_2 - \delta_2 E_2 - b_{21} E_2 + b_{12} E_1 \\ \frac{dI_2}{dt} &= \delta_2 E_2 - m_2 I_2 - \mu_2 I_2 - c_{21} I_2 + c_{12} I_1 \\ \frac{dV_2}{dt} &= r_2 (E_2 + I_2) - w_2 V_2 - d_{21} V_2 + d_{12} V_1 \end{aligned} \right. \quad (14)$$

For system (14) , it is easy to calculate that its disease-free equilibrium is $P^0 = (S_1^0, 0, 0, 0, S_2^0, 0, 0, 0)$,

where $S_1^0 = \frac{A_1(m_2 + a_{21}) + a_{21}A_2}{(m_1 + a_{12})(m_2 + a_{21}) - a_{12}a_{21}}$ and $S_2^0 = \frac{A_2(m_1 + a_{12}) + a_{12}A_1}{(m_1 + a_{12})(m_2 + a_{21}) - a_{12}a_{21}}$. And $R_0 = \rho(FV^{-1})$, where

$$F = \begin{pmatrix} F_1 & 0 \\ 0 & F_2 \end{pmatrix}, V = \begin{pmatrix} V_{11} & V_{21} \\ V_{12} & V_{22} \end{pmatrix}.$$

Also , we can obtain the basic reproduction numbers R_1, R_2 of two patches under the situation that there exists no migration of cattle and the diffusion of brucella between them as follows.

$$R_1 = \frac{A_1 \beta_1 \theta}{m_1(\delta_1 + m_1)} + \frac{A_1 \beta_1 \delta_1}{m_1(\delta_1 + m_1)(m_1 + \mu_1)} + \frac{A_1 \alpha_1 r_1 (m_1 + \delta_1 + \mu_1)}{m_1 w_1 (\delta_1 + m_1)(m_1 + \mu_1)}$$

$$R_2 = \frac{A_2 \beta_2 \theta}{m_2(\delta_2 + m_2)} + \frac{A_2 \beta_2 \delta_2}{m_2(\delta_2 + m_2)(m_2 + \mu_2)} + \frac{A_2 \alpha_2 r_2 (m_2 + \delta_2 + \mu_2)}{m_2 w_2 (\delta_2 + m_2)(m_2 + \mu_2)}$$

Now , we mainly have a look at the effect of some parameters and population scales on the basic reproduction number and the number of the infected individuals , respectively.

Example 1 When all the parameter values are same between two patches and the dispersal rates of each subpopulation from one patch to the other are taken as the same. Assume that $A_1 = A_2 = 13000$; $m_1 = m_2 = 0.25$; $\delta_1 = \delta_2 = 6$; $\mu_1 = \mu_2 = 0.85$; $r_1 = r_2 = 5$; $w_1 = w_2 = 6$; $a_{12} = a_{21} = b_{12} = b_{21} = c_{12} = c_{21} = d_{12} = d_{21} = 0.1$; $\beta_1 = \beta_2 = 2.1 \times 10^{-6}$; $\theta = 0.5$.

(1) If $\alpha_1 = \alpha_2 = 2.2 \times 10^{-5}$, $R_0 = R_1 = R_2 = 1.0886$. In this case , the brucellosis in two patches will become endemic with time (see Fig. 2).

(2) If $\alpha_1 = \alpha_2 = 1.8 \times 10^{-5}$, $R_0 = R_1 = R_2 = 0.9096$. In this case , the infectious cattle in two patches will disappear with time (see Fig. 3).

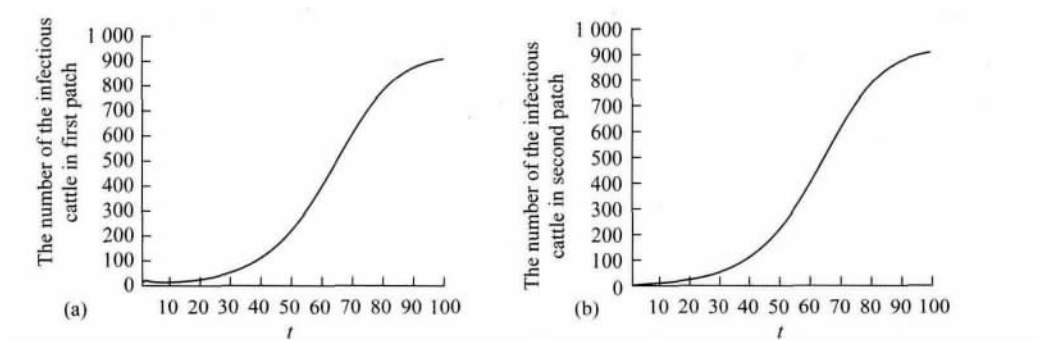


Fig. 2 The number of the infectious cattle with time. (a) in the first patch. (b) in the second patch. The initial values will be taken as $S_1(0) = 40000$, $E_1(0) = 7$, $I_1(0) = 12$, $V_1(0) = 100$, $S_2(0) = 40000$, $E_2(0) = I_2(0) = V_2(0) = 0$.

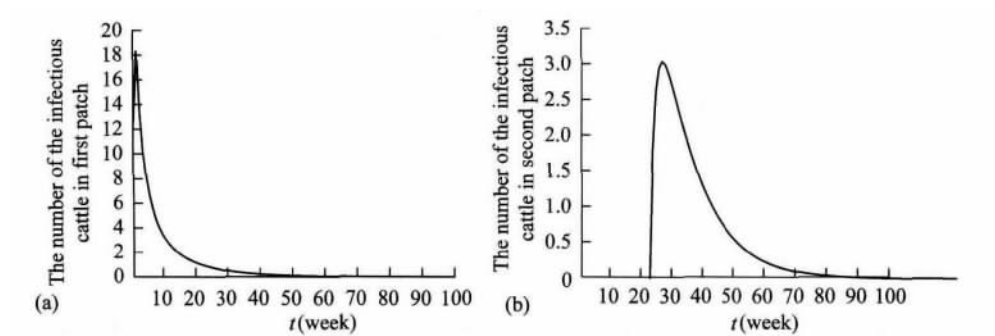


Fig. 3 The number of the infectious cattle with time. (a) in the first patch. (b) in the second patch. $S_1(0) = 40000$, $E_1(0) = 7$, $I_1(0) = 12$, $V_1(0) = 100$, $S_2(0) = 40000$, $E_2(0) = I_2(0) = V_2(0) = 0$.

Figs. 2 and 3 confirm that the basic reproduction number R_0 is the transmission threshold of brucellosis in two patches. Besides , the sensitivity of the basic reproduction number R_0 in term of β_1 , α_1 , A_1 , a_{12} , b_{12} , c_{12} , d_{12} can be seen in Fig. 4. From Fig. 4 , we know that R_0 will increase with the increase of A_1 . Comparing with β_1 , the effect of α_1 on R_0 is larger. What is interesting is that the transport of susceptible cattle can reduce R_0 , which implies that the dispersal of susceptible cattle can relief the transmission situation of brucellosis in the whole region. However , the transport of the infected cattle or the diffusion of brucella has no influence on R_0 .

Example 2 When the numbers of cattle in two patches are different , the disease situation will be different from Example 1. Assume that the number of cattle in the first patch is larger than the second patch. $A_1 = 20000$; $A_2 = 10000$; $m_1 = m_2 = 0.25$; $\delta_1 = \delta_2 = 6$; $\mu_1 = \mu_2 = 0.85$; $r_1 = r_2 = 5$; $w_1 = w_2 = 6$; $\beta_1 = \beta_2 = 2.1 \times 10^{-6}$; $\theta = 0.5$; $\alpha_1 = \alpha_2 = 2.2 \times 10^{-5}$.

(1) If the dispersal rate of the first patch is smaller than the second patch , $a_{12} = b_{12} = c_{12} = d_{12} = 0.3$, $a_{21} = b_{21} = c_{21} = d_{21} = 0.1$. In this case , $R_0 = 1.1785$, $R_1 = 1.3993$, $R_2 = 0.6997$ (see Fig. 5).

(2) If the dispersal rate of the first patch is larger than the second patch , $a_{12} = b_{12} = c_{12} = d_{12} = 0.1$, $a_{21} = b_{21} = c_{21} = d_{21} = 0.3$. In this case , $R_0 = 1.4059$, $R_1 = 1.3993$, $R_2 = 0.6997$ (see Fig. 6).

From Figs. 5 and 6 , we can see that the patch whose dispersal rate is bigger , the number of infectious cattle will be smaller. For the patch that has larger cattle population , the emigration of susceptible cattle can reduce R_0 , see Fig. 7. However , the emigration of the brucella carriers and the diffusion of brucella can increase

R_0 . For the patch that has smaller cattle population, the emigration of all subpopulation can reduce R_0 .

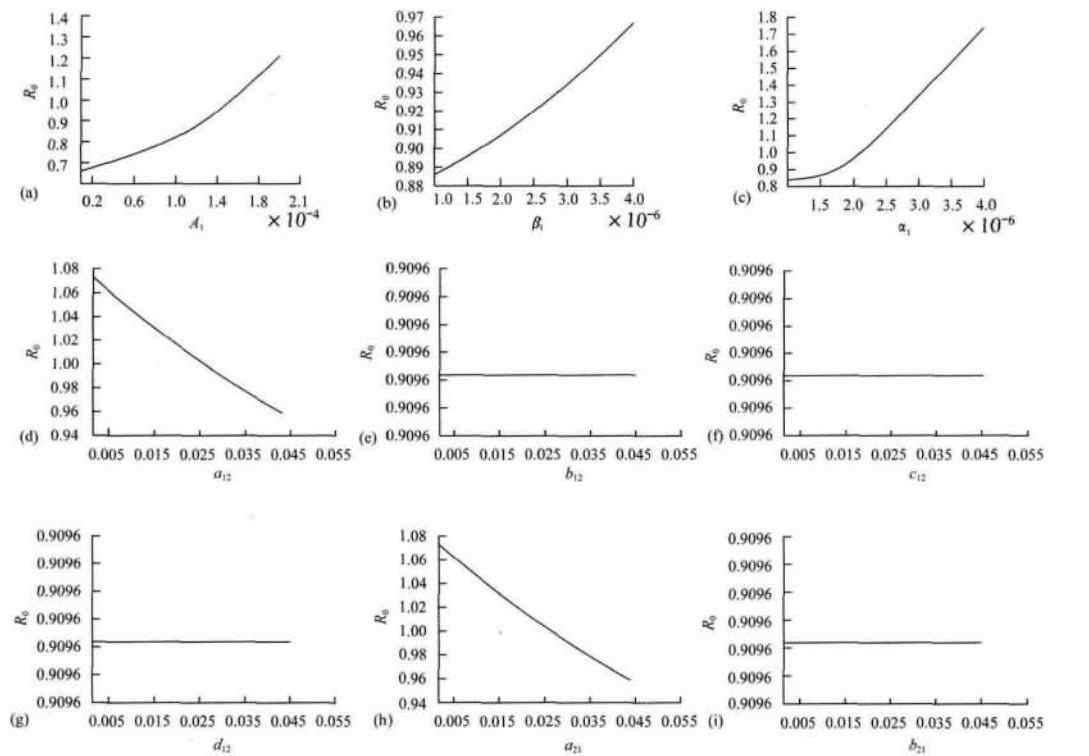


Fig. 4 R_0 in term of parameters $A_1, \beta_1, \alpha_1, a_{12}, b_{12}, c_{12}, d_{12}, a_{21}, b_{21}$.

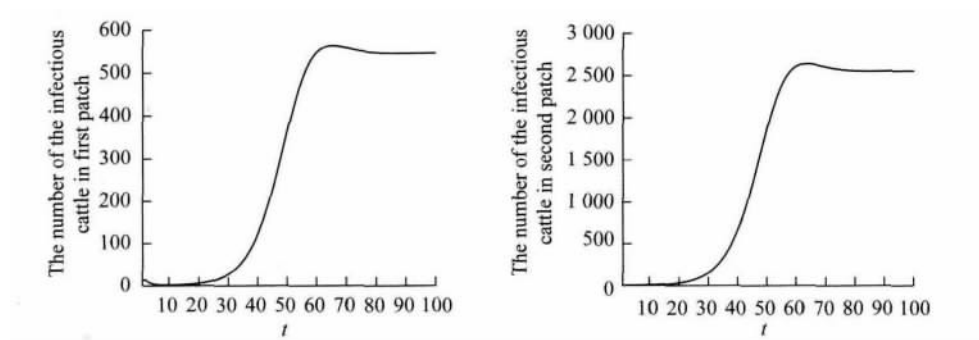


Fig. 5 The number of the infectious cattle with time. (a) in the first patch. (b) in the second patch.

The initial values will be taken as $S_1(0) = 40000, E_1(0) = 7, I_1(0) = 12, V_1(0) = 100,$
 $S_2(0) = 20000, E_2(0) = I_2(0) = V_2(0) = 0.$

Example 3 We need to know that when the basic reproduction numbers R_1 and R_2 of two patches are both less than 1, what is about R_0 ? The parameter values are the same as Example 2 except for α_1 and α_2 . Assume $\alpha_1 = \alpha_2 = 1.8 \times 10^{-5}$.

(1) If the dispersal rate of the first patch is larger than the second patch, $a_{12} = b_{12} = c_{12} = d_{12} = 0.3,$
 $a_{21} = b_{21} = c_{21} = d_{21} = 0.1$. In this case, $R_0 = 0.9548, R_1 = 0.9096, R_2 = 0.6997$. The brucellosis in two patches will disappear with time. (see Fig. 8)

(2) If the dispersal rate of the first patch is larger than the second patch, $a_{12} = b_{12} = c_{12} = d_{12} = 0.1,$
 $a_{21} = b_{21} = c_{21} = d_{21} = 0.3$. In this case, $R_0 = 1.0233, R_1 = 0.9096, R_2 = 0.6997$. The infectious disease in two patches will become endemic with time. (see Fig. 9)

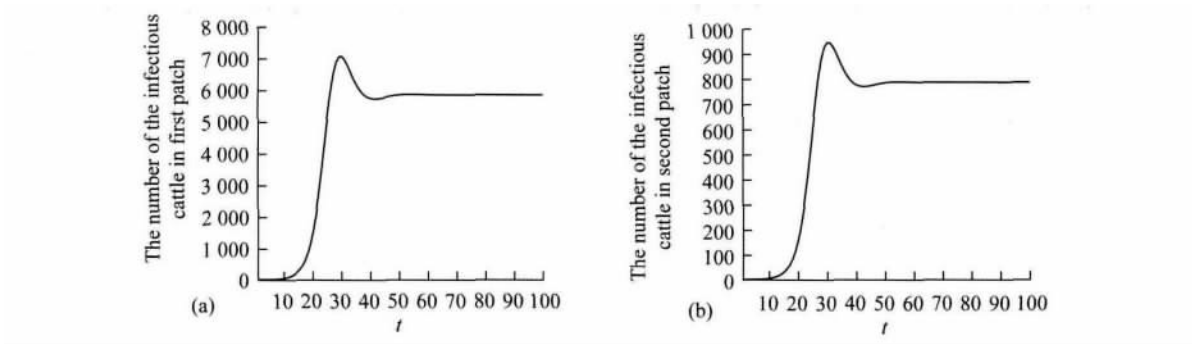


Fig. 6 The number of the infectious cattle with time. (a) in the first patch. (b) in the second patch.

The initial values will be taken as $S_1(0) = 40000$ $E_1(0) = 7$ $I_1(0) = 12$ $V_1(0) = 100$ $S_2(0) = 20000$ $E_2(0) = I_2(0) = V_2(0) = 0$.

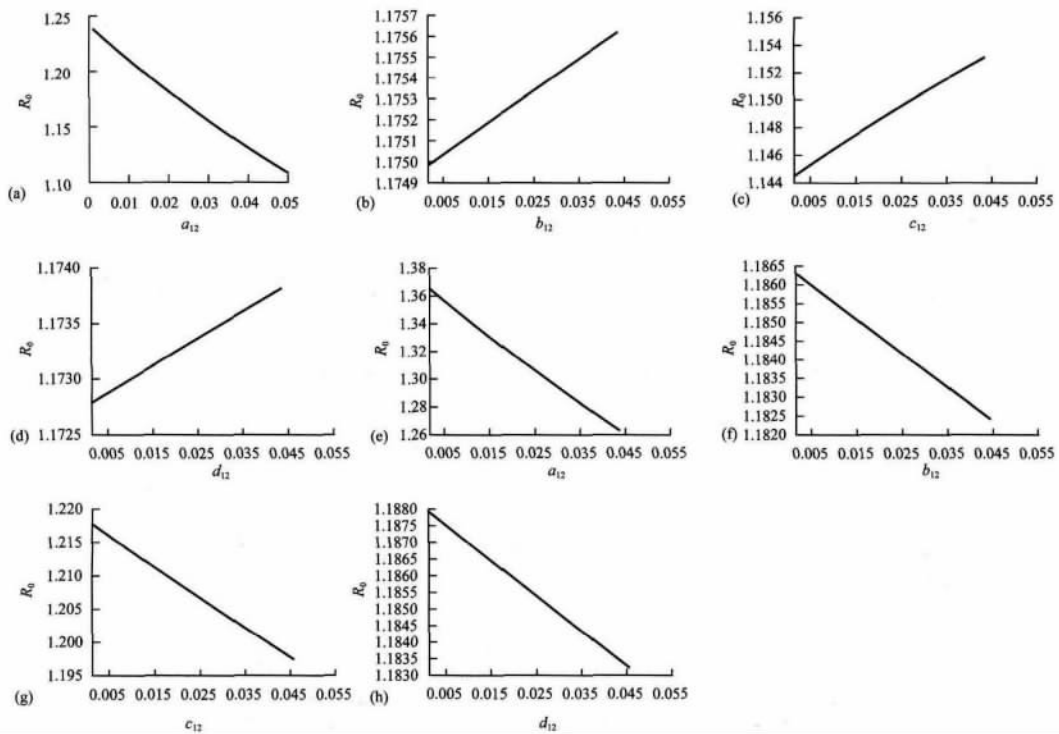


Fig. 7 R_0 in term of parameters a_{12} b_{12} c_{12} d_{12} a_{21} b_{21} c_{21} d_{21} .

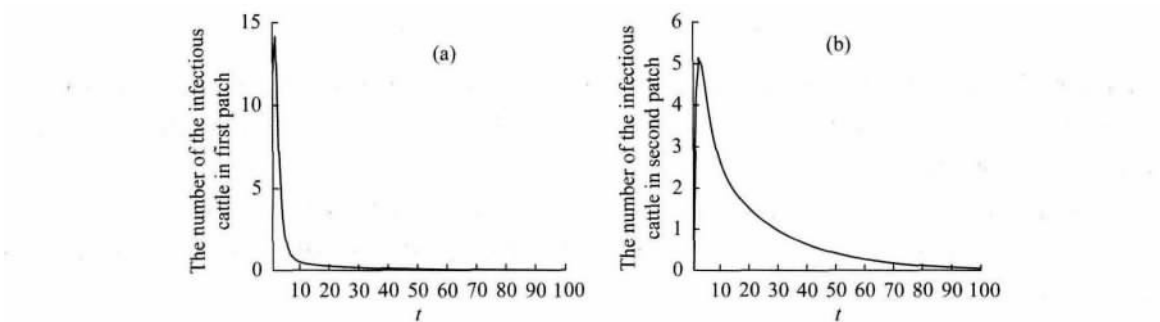


Fig. 8 The number of the infectious cattle with time. (a) in the first patch. (b) in the second patch.

The initial values will be taken as $S_1(0) = 40000$ $E_1(0) = 7$ $I_1(0) = 12$ $V_1(0) = 100$ $S_2(0) = 20000$ $E_2(0) = I_2(0) = V_2(0) = 0$.

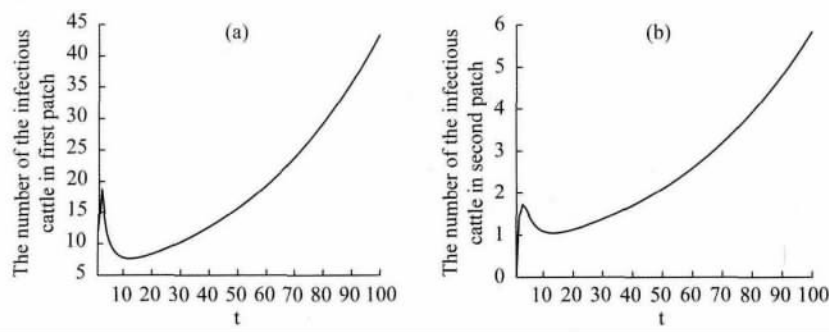


Fig. 9 The number of the infectious cattle with time. (a) in the first patch. (b) in the second patch.

The initial values will be taken as $S_1(0) = 40000$, $E_1(0) = 7$, $I_1(0) = 12$, $V_1(0) = 100$,
 $S_2(0) = 20000$, $E_2(0) = I_2(0) = V_2(0) = 0$.

From Figs. 8 and 9, we can see that if the basic reproduction numbers of two patches without cattle and brucella dispersal are less than 1, with the change of dispersal rates between patches, the basic reproduction number in the whole region will be variable. It can be less than 1, also can be more than 1 as the dispersal rates increase.

4 Discussion

For Zhejiang province of China, the recent prevalence of brucellosis in cattle is believed to be caused by the transportation of cattle and brucella between cities in Zhejiang province. In this article, we applied an n -patch dynamical model to study the effect of dispersal of cattle and brucella on the spatial transmission of brucellosis. Firstly, we analyzed the dynamical behavior of the model. More specifically, assuming $n = 2$, we carried out the sensitivity analysis of the basic reproduction number and the number of the infectious cattle in term of different parameter values. Finally, it is obtained that the dispersal of the susceptible cattle can relief the spread of brucellosis in the whole region. However, the emigration of the brucella carriers or the diffusion of brucella in patch whose raising quantity of cattle is larger can increase R_0 . On the contrary, the emigration of the brucella carriers or the diffusion of brucella in patches where the amount of live cattle is smaller can reduce R_0 . In summary, the dispersal of the susceptible population of each patch and the centralization of the infected cattle to the patches where the breeding scale is bigger are in favor of the controlling of the disease.

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