Analysis of a multi–patch dynamical model about cattle brucellosis

Juan Zhang¹² Shigui Ruan³ Guiquan Sun²⁴

Xiangdong Sun⁵ Zhen Jin²

¹. School of Mechatronic Engineering North University of China Taiyuan Shan’xi 030051 China; ². Complex Systems Research Center Shanxi University Taiyuan Shan’xi 030006 China; ³. Department of Mathematics University of Miami Coral Gables Fl. 33124-4250 USA; ⁴. School of Mathematical Science Fudan University Shanghai 200433 China; ⁵. The Laboratory of Animal Epidemiological Surveillance China Animal Health & Epidemiology Center Qingdao Shandong 266032 China

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 muti-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 is one of the world’s major zoonotic pathogens known causes infectious abortion in animals and Malta Fever in man. Since many kinds of domestic animals such as sheep cattle dogs pig and so on...
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\(^{22,24}\). In fact, the cow remains an intermittent carrier for years in China\(^{26}\). 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\(^{7-14}\). 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\(^{2}\) 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\(^{19}\) 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 Aineseba et al.\(^{21}\) 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.\(^{19}\) investigated the transmission dynamics of sheep brucellosis in Inner Mongolia Autonomous Region of China. Zhang et al.\(^{22}\) 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 \(N_i\). 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.
susceptible, exposed and infective individuals, the numbers of which at time $t$ in the $i$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 $\theta$ 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 $A_i, \beta_i, \alpha_i, m_i, \delta_i, \mu_i, r_i$ and $w_i$ are all positive constants. $\theta$ 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.

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

(1)

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

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A_i$</td>
<td>The birth number of cattle in $i$th patch per unit time</td>
</tr>
<tr>
<td>$\beta_i$</td>
<td>The infectious cattle-to-susceptible cattle transmission rate in $i$th patch</td>
</tr>
<tr>
<td>$\theta$</td>
<td>Auxiliary parameter</td>
</tr>
<tr>
<td>$\alpha_i$</td>
<td>Brucella in environment-to-susceptible cattle transmission rate in $i$th patch</td>
</tr>
<tr>
<td>$m_i$</td>
<td>Natural elimination rate of cattle in $i$th patch</td>
</tr>
<tr>
<td>$\delta_i$</td>
<td>Clinical outcome rate of the exposed cattle in $i$th patch</td>
</tr>
<tr>
<td>$\mu_i$</td>
<td>Disease-related culling rate of infectious cattle in $i$th patch</td>
</tr>
<tr>
<td>$r_i$</td>
<td>Brucella quantity released by infected cattle in $i$th patch</td>
</tr>
<tr>
<td>$w_i$</td>
<td>Brucella death rate in $i$th patch</td>
</tr>
<tr>
<td>$a_{ji}(j \neq i)$</td>
<td>The immigration rate of the susceptible cattle from $j$th patch to $i$th patch</td>
</tr>
<tr>
<td>$b_{ji}(j \neq i)$</td>
<td>The immigration rate of the exposed cattle from $j$th to $i$th patch</td>
</tr>
<tr>
<td>$c_{ji}(j \neq i)$</td>
<td>The immigration rate of the infectious cattle from $j$th to $i$th patch</td>
</tr>
<tr>
<td>$d_{ji}(j \neq i)$</td>
<td>The immigration rate of brucella in environment from $j$th to $i$th patch</td>
</tr>
<tr>
<td>$- a_{ii}$</td>
<td>The emigration rate of the susceptible cattle in $i$th patch</td>
</tr>
<tr>
<td>$- b_{ii}$</td>
<td>The emigration rate of the exposed cattle in $i$th patch</td>
</tr>
<tr>
<td>$- c_{ii}$</td>
<td>The emigration rate of the infectious cattle in $i$th patch</td>
</tr>
<tr>
<td>$- d_{ii}$</td>
<td>The emigration rate of brucella in environment in $i$th patch</td>
</tr>
</tbody>
</table>

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

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

(2)
Lemma 1 Let $N^* = \frac{A}{m}$ where $A = \sum_{i=1}^{n} A_i$ and $m = \min\{m_i \mid 1 \leq i \leq n\}$ every forward orbit in $R^d$ of system (1) eventually enters $F = \{(S_i \in E_i \in V_i) \in R^d : \sum_{i=1}^{n} (S_i + E_i + I_i) \leq N^* \}$ and $F$ 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.

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

which can be expanded as follows.

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

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

$$E_0 = (S_1, E_1, E_2, E_3, \cdots, S_n, E_n, V_n).$$

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

$$\mathcal{F} = \begin{pmatrix}
\beta S_i I_i + \theta \beta S_i E_i + \alpha_i S_i V_i \\
0 \\
0 \\
\vdots \\
\beta S_n I_n + \theta \beta S_n E_n + \alpha_n S_n V_n \\
0 \\
0
\end{pmatrix}$$

$$\mathcal{F} = \begin{pmatrix}
m_1 E_1 + \delta_1 E_1 - \sum_{j=1}^{n} b_{ij} E_j \\
-\delta_1 E_1 + (m_1 + \mu_1) I_1 - \sum_{j=1}^{n} c_{ij} I_j \\
-r_1 (E_1 + I_1) + \omega_1 V_1 - \sum_{j=1}^{n} d_{ij} V_j \\
\vdots \\
m_n E_n + \delta_n E_n - \sum_{j=1}^{n} b_{nj} E_j \\
-\delta_n E_n + (m_n + \mu_n) I_n - \sum_{j=1}^{n} c_{nj} I_j \\
-r_n (E_n + I_n) + \omega_n V_n - \sum_{j=1}^{n} d_{nj} V_j
\end{pmatrix}$$

$$\mathcal{F} = \begin{pmatrix}
F_1 \\
0 \\
\vdots \\
0 \\
0 \\
\vdots \\
0
\end{pmatrix}$$

and

$$F = \begin{pmatrix}
F_1 & 0 & \cdots & 0 \\
0 & F_2 & \cdots & 0 \\
\vdots & \vdots & \ddots & \vdots \\
0 & 0 & \cdots & F_n
\end{pmatrix}$$
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\[ V = \begin{pmatrix} V_{11} & V_{21} & \cdots & V_{n1} \\ V_{12} & V_{22} & \cdots & V_{n2} \\ \vdots & \vdots & \ddots & \vdots \\ V_{1n} & V_{2n} & \cdots & V_{nn} \end{pmatrix} \]

where

\[ F_i = \begin{pmatrix} \theta \beta_i S_i^0 & \beta_i S_i^0 & \alpha_i S_i^0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \]

and

\[ V_{ij} \quad (i \neq j) = \begin{pmatrix} -b_{ij} & 0 & 0 \\ 0 & -c_{ij} & 0 \\ 0 & 0 & -d_{ij} \end{pmatrix} \]

The basic reproduction number is \( R_0 = \rho \left( FV^{-1} \right) \). 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:

\[ R_0 = \begin{cases} < 1 & \text{ if } s(M) < 0 \\ > 1 & \text{ if } s(M) > 0 \end{cases} \]

By Theorem 2 in \cite{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

\[ \frac{dS_i}{dt} = A_i - m_i S_i + \sum_{j=1}^{n} a_{ij} S_j \quad 1 \leq i \leq n \]

whose Jacobian matrix is

\[ \left( \begin{array}{cccc} -m_i + a_{i1} & a_{21} & \cdots & a_{ni} \\ a_{12} & -m_2 + a_{22} & \cdots & a_{2i} \\ \vdots & \vdots & \ddots & \vdots \\ a_{1n} & a_{2n} & \cdots & -m_n + a_{nn} \end{array} \right) \]

It is already known that the Jacobian matrix is absolutely diagonally dominant about column and the system (3) has a unique positive equilibrium \( S^0 = (S^0_1, S^0_2, \ldots, S^0_n)^T \). Moreover, \( -m_i + a_{ii} < 0 \quad 1 \leq i \leq n \). 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, \( S^0 \) is globally stable.

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

**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 \( \eta \), \([M + M_\eta] < 0\), where

\[ M_\eta = \begin{pmatrix} M_1 & 0 & \cdots & 0 \\ 0 & M_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & M_n \end{pmatrix} \]

It is obvious to know that

\[ M_i = \begin{pmatrix} \theta \beta_i \eta & \beta_i \eta & \alpha_i \eta \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \]
\[
\frac{dS_i}{dt} = A_i - m_i S_i + \sum_{j=1}^{n} a_{ji} S_j, \quad 1 \leq i \leq n.
\]

Then the following auxiliary system is introduced.
\[
\frac{dS_i}{dt} = A_i - m_i S_i + \sum_{j=1}^{n} a_{ji} S_j, \quad 1 \leq i \leq n\]
(6)

The positive equilibrium \( S^0 \) of system (6) has been proved to be globally stable. So there exists \( T \) such that \( \forall \ t \geq T \), \( S(t) \leq S^0 + \eta \), where \( S(t) = \{S_i(t) \mid 1 \leq i \leq n\} \). Thus we obtain the following system.
\[
\begin{align*}
\frac{dE_i}{dt} &\leq \beta_i(S_{i0} + \eta) I_i + \theta \beta_i(S_{i0} + \eta) E_i + \alpha_i(S_{i0} + \eta) V_i - m_i E_i - \delta_i E_i + \sum_{j=1}^{n} b_{ji} E_j; \quad 1 \leq i \leq n
\
\frac{dI_i}{dt} &= \delta_i E_i - m_i I_i - \mu_i I_i + \sum_{j=1}^{n} c_{ji} I_j, \quad 1 \leq i \leq n
\
\frac{dV_i}{dt} &= r_i (E_i + I_i) - w_i V_i + \sum_{j=1}^{n} d_{ji} V_j, \quad 1 \leq i \leq n.
\end{align*}
\]

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

Define
\[
X = \{ (S_i E_i V_i \cdots S_i E_i V_i) : S_i \geq 0, E_i \geq 0, V_i \geq 0 \mid i = 1 \cdots n \}
\]
\[
X_0 = \{ (S_i E_i V_i \cdots S_i E_i V_i) \in X : E_i > 0, V_i > 0 \mid i = 1 \cdots n \}
\]
\[
\partial X_0 = X \setminus X_0.
\]

Considering the auxiliary system
\[
\frac{dS_i}{dt} = A_i - \beta S_i e - \theta \beta S_i e - \alpha S_i e - m_i S_i + \sum_{j=1}^{n} a_{ji} S_j, \quad 1 \leq i \leq n.
\]
(7)

For system (7) there exists a unique positive equilibrium \( S^0(\epsilon) \) and it is globally asymptotically stable. By the implicit function theorem, it follows that \( S^0(\epsilon) \) is continuous in \( \epsilon \). For given \( \tau \) we can restrict \( \epsilon \) small enough such that \( s(M + M_n) \geq s(M^0 - \tau) \) for all \( t > T_1 \).

**Theorem 2** When \( R_0 > 1 \) there exists positive constant \( \epsilon \) such that when \( \| (E_i(0) V_i(0) V_j(0)) \| < \epsilon \) for \( (S_i(0) E_i(0) V_i(0) V_j(0)) \in X_0 \),
\[
\limsup_{t \to \infty} \| (E_i(t) V_i(t) V_j(t)) \| > \epsilon \mid i = 1 \cdots n.
\]
(8)

**Proof** Because \( R_0 > 1 \), \( \tau(M) > 0 \). So for small enough \( \epsilon \), \( \tau(M + M_n) > 0 \) where
\[
M_n = \begin{pmatrix}
M_1 & 0 & \cdots & 0 \\
0 & M_2 & \cdots & 0 \\
\vdots & \vdots & \ddots & \vdots \\
0 & 0 & \cdots & M_n
\end{pmatrix}, \quad M_i = \begin{pmatrix}
\theta \beta_i & \beta_i \tau & \alpha_i \\
0 & 0 & 0 \\
0 & 0 & 0
\end{pmatrix}, \quad i = 1 \cdots n.
\]

Now we proceed by contradiction to prove the above conclusion. Suppose there exist \( \epsilon \) and \( T > 0 \) such that \( E_i(t) < \epsilon \mid I_i(t) < \epsilon \) and \( V_i(t) < \epsilon \mid i = 1 \cdots n \) for all \( t > T \). Then for all \( t > T \) we can have that
\[
\frac{dS_i}{dt} > A_i - \beta S_i e - \theta \beta S_i e - \alpha S_i e - m_i S_i + \sum_{j=1}^{n} a_{ji} S_j, \quad 1 \leq i \leq n.
\]
(9)

For the right side system there exists a unique positive equilibrium \( S^0(\epsilon) \) which is globally 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 $t > T_i$. Thus there holds
\[
\frac{dE_i}{dt} \geq \beta(E_i - \tau)I_i + \theta\beta(S_i^0 - \tau)E_i + \alpha(S_i^0 - \tau) V_i - m_i E_i - \delta E_i + \sum_{j=1}^n b_{ij} E_j \quad 1 \leq i \leq n
\]
\[
\frac{dl_i}{dt} = \delta E_i - m_i l_i - \mu I_i + \sum_{j=1}^n c_{ij} l_j \quad 1 \leq i \leq n
\]
\[
\frac{dV_i}{dt} = r_i(E_i + l_i) - \omega_i V_i + \sum_{j=1}^n c_{ij} V_j \quad 1 \leq i \leq n.
\]
Because $s(M - M_j) > 0$ for all $t \to \infty$ and $E_i(t) \to \infty$ as $t \to \infty$, 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 $\varepsilon$ such that every solution of (1) with $\left(S_i(0) \cap E_i(0) \cap V_i(0)\right) \in X_0$ satisfies
\[
\min \{\lim \inf E_i(t) \cap \lim \inf l_i(t) \cap \lim \inf V_i(t)\} \geq \varepsilon \quad i = 1\cdots n.
\]

**Proof** Firstly we show that system (1) is uniformly persistent with respect to $(X_0 \cup \partial X_0)$. It is easy to know that both $X$ and $X_0$ are positively invariant and $\partial X_0$ is relatively closed in $X$. Moreover from Lemma 1 system (1) is point dissipative. Set $M_j = \{(S_i(0) \cap E_i(0) \cap V_i(0)) : (S_i(t) \cap E_i(t) \cap V_i(t)) \in \partial X_0 \}$ $\forall t \in [0, \infty)$ where $S_i(t) = (S_i(t) \cap E_i(t) \cap V_i(t))$. It is needed to show that
\[
M_j = \{(S_i(t) \cap E_i(t) \cap V_i(t)) : S_i(t) \neq 0\}.
\]
Noting that
\[
\{(S_i(t) \cap E_i(t) \cap V_i(t)) : S_i(t) \geq 0\} \subset M_j
\]
we only need to prove
\[
M_j \subset \{(S_i(t) \cap E_i(t) \cap V_i(t)) : S_i(t) \geq 0\} = \overline{M}_j.
\]
Suppose not. Assume $(S_i(0) \cap E_i(0) \cap V_i(0)) \in M_j$. There exist an $i_0(1 \leq i_0 \leq n)$ and a $t_0$ such that $(E_{i_0}(t_0) \cap V_{i_0}(t_0)) \cap V_i(t_0) \neq 0$. Then we can separate $\{1\cdots n\}$ into two sets $Q_l$ and $Q_2$ such that
\[
\begin{aligned}
E_i(t_0) \cap V_i(t_0) &\neq 0 \quad \forall i \in Q_1, \\
E_i(t_0) \cap V_i(t_0) &\neq 0 \quad \forall i \in Q_2.
\end{aligned}
\]
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 $E_i(t_0) > 0$ and $V_i(t_0) = 0$. From the equations $I_i(t_0) = \delta E_i(t_0) > 0$ and $V_i(t_0) = r_i E_i(t_0) > 0$ we can know that there is a small enough $\varepsilon_2 > 0$ such that $E_i(t) > 0 \forall i \in Q_2$ for $t_0 < t < t_0 + \varepsilon_2$. For $j \in Q_1$ we have $E_j(t_0) > 0$ and $E_j(t_0) > 0$. So there exists $\varepsilon_2 > 0$ such that $E_i(t) > 0 \forall i \in Q_1$ for $t_0 < t < t_0 + \varepsilon_2$. Similarly there exists $\varepsilon_2 > 0$ such that $I_i(t) > 0 \forall i \in Q_1$ for $t_0 < t < t_0 + \varepsilon_2$. These mean that $(S_i(t) \cap E_i(t) \cap V_i(t)) \neq \partial X_0$ for $t_0 < t < t_0 + \varepsilon_2$ and hence which contradicts the assumption that $(S_i(0) \cap E_i(0) \cap V_i(0)) \in M_j$. So the equality (11) holds. Moreover from Theorem 2 it can be known that $E_0$ is an isolated invariant set in $X$ and $W(E_0) \cap X_0 = \emptyset$. $E_0$ is the only fixed point and acyclic in $\partial X_0$.

By Theorem 4.3 in [36] and in Theorem 4.6 [37] we can conclude that system (1) is uniformly persistent with respect to $(X_0 \cup \partial X_0)$. By Theorem 2.4 in [38] system (1) has an equilibrium $(S \cap E^* \cap V^* \cap V^*) \in X_0$ where $S(t) = (S_1^* \cdots S_n^*) \cap E(t) = (E_1^* \cdots E_n^*) \cap I(t) = (I_1^* \cdots I_n^*) \cap V(t) = (V_1^* \cdots V_n^*)$. From $A_i - \beta S_i I_i - \theta \beta S_i E_i - \alpha E_i V_i - m_i S_i + \sum_{j=1}^n c_{ij} S_j = 0$ and $A_i > 0$ it is easy to see that $I^* > 0$. Then $(S \cap E^* \cap V^* \cap V^*)$ is a positive equilibrium of system (1).
3 Application to two patches

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

$$
\begin{align*}
\frac{dS_i}{dt} & = A_i - \beta_i S_i I_i - \theta \beta_i S_i E_i - \alpha_i S_i V_i - m_i S_i - a_{12} S_i + a_{21} S_2 \\
\frac{dE_i}{dt} & = \beta_i S_i I_i + \theta \beta_i S_i E_i + \alpha_i S_i V_i - m_i E_i - \delta_i E_i - b_{12} E_1 + b_{21} E_2 \\
\frac{dI_i}{dt} & = \delta_i E_i - m_i I_i - \mu_i I_i - c_{12} I_1 + c_{21} I_2 \\
\frac{dV_i}{dt} & = r_i (E_i + I_i) - w_i V_i - d_{12} V_i + d_{21} V_2 \\
\frac{dS_2}{dt} & = A_2 - \beta_2 S_2 I_2 - \theta \beta_2 S_2 E_2 - \alpha_2 S_2 V_2 - m_2 S_2 - a_{21} S_2 + a_{12} S_1 \\
\frac{dE_2}{dt} & = \beta_2 S_2 I_2 + \theta \beta_2 S_2 E_2 + \alpha_2 S_2 V_2 - m_2 E_2 - \delta_2 E_2 - b_{12} E_1 + b_{21} E_1 \\
\frac{dI_2}{dt} & = \delta_2 E_2 - m_2 I_2 - \mu_2 I_2 - c_{21} I_2 + c_{12} I_1 \\
\frac{dV_2}{dt} & = r_2 (E_2 + I_2) - w_2 V_2 - d_{21} V_2 + d_{12} V_1
\end{align*}
$$

For system (14) it is easy to calculate that its disease-free equilibrium is $P^0 = (S^0_i, S^0_2, E^0, I^0, V^0)$, where $S^0_i = \frac{A_i (m_i + a_{1i} + a_{2i} A_2)}{m_i + a_{1i} + a_{2i}}$ and $S^0_2 = \frac{A_2 (m_i + a_{12} + a_{22} A_2)}{m_i + a_{12} + a_{22}}$. And $R_0 = \rho(FV^{-1})$, where

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

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

$$
R_i = \frac{A_i \beta_i \theta}{m_i (\delta_i + m_i)} + \frac{A_i \beta_i \delta_i}{m_i (\delta_i + m_i)} + \frac{A_i \alpha_i r_i (m_i + \delta_i + \mu_i)}{m_i w_i (\delta_i + m_i) (m_i + \mu_i)},
$$

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

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 $A_1 = A_2 = 13000$; $m_1 = m_2 = 0.25$; $\delta_1 = \delta_2 = 0.6$; $\mu_1 = \mu_2 = 0.85$; $r_1 = r_2 = 5$; $w_1 = w_2 = 6$; $a_{12} = a_{21} = b_{12} = b_{21} = c_{12} = c_{21} = d_{12} = d_{21} = 0.1$; $\beta_1 = \beta_2 = 2.1 \times 10^{-6}$; $\theta = 0.5$.

(1) If $\alpha_1 = \alpha_2 = 2.2 \times 10^{-7}$, $R_0 = R_1 = R_2 = 1.0886$. In this case the brucellosis in two patches will become endemic with time (see Fig. 2).
(2) If $\alpha_1 = \alpha_2 = 1.8 \times 10^{-5}$ then $R_0 = R_1 = R_2 = 0.9096$. In this case the infectious cattle in two patches will disappear with time (see Fig. 3).

\[
S_0(0) = 40000; E_0(0) = 7; I_0(0) = 12; V_0(0) = 100;
\]
\[
S_1(0) = 40000; E_1(0) = I_1(0) = V_1(0) = 0.
\]

\[
S_1(t) = 40000; E_1(t) = I_1(t) = V_1(t) = 0.
\]

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 $\beta_1 \alpha_4 A_4 a_12; b_12; c_12; d_12$ can be seen in Fig. 4. From Fig. 4 we know that $R_0$ will increase with the increase of $A_1$. Comparing with $\beta_1$ the effect of $\alpha_1$ 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 relieve 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. $A_1 = 20000; A_2 = 10000; m_1 = m_2 = 0.25; \delta_1 = \delta_2 = 6; \mu_1 = \mu_2 = 0.85; r_1 = r_2 = 5; w_1 = w_2 = 6; \beta_1 = \beta_2 = 2.1 \times 10^{-5}; \theta = 0.5; \alpha_1 = \alpha_2 = 2.2 \times 10^{-5}.$

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

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

$R_0$ in term of parameters $A_1, B_1, D_1, D_{12}, D_{11}, D_{21}, D_{22}, D_{21}$.

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 $\alpha_1$ and $\alpha_2$. 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 $a_{12} = b_{12} = c_{12} = d_{21} = 0.3, a_{21} = b_{21} = c_{21} = d_{21} = 0.1$. 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 $a_{12} = b_{12} = c_{12} = d_{21} = 0.1, a_{21} = b_{21} = c_{21} = d_{21} = 0.3$. 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)
The initial values will be taken as $S_1(0) = 40000$, $E_1(0) = 7$, $I_1(0) = 12$, $V_1(0) = 100$, $S_2(0) = 20000$, $E_2(0) = I_2(0) = V_2(0) = 0$. 

$R_0$ in terms of parameters $a_{12}, b_{12}, c_{12}, d_{12}, a_{21}, b_{21}, c_{21}, d_{21}$. 

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

Fig. 7 $R_0$ in terms 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.
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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 terms of different parameter values. Finally, it is obtained that the dispersal of the susceptible cattle can relieve 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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(Zhenzhen Feng)