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ON THE DYNAMICS OF A DIFFUSIVE FOOT-AND-MOUTH DISEASE MODEL WITH NONLOCAL INFECTIONS*

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Abstract. Foot-and-mouth disease (FMD) is an acute and highly contagious infectious disease of cloven-hoofed animals. In order to reveal the transmission dynamics and explore effective control measures of FMD, we formulate a diffusive FMD model with a fixed latent period and nonlocal infections. The threshold dynamics of the FMD model are determined by using the basic reproduction number $\mathcal{R}_0$: if $\mathcal{R}_0 < 1$, then the disease-free equilibrium E_0 is globally asymptotically stable; otherwise E_0 is unstable, and there exists an endemic equilibrium E^*. Numerical simulations confirm the theoretical results and suggest that reducing the direct contact rate β_1 and the indirect contact rate β_2 is important in relieving FMD outbreaks. More importantly, we obtain the effect of diffusion on the time from initial values to steady state when $\mathcal{R}_0 > 1$: at a low infection level, the faster the infectious individuals and virus diffuse, the faster the disease reaches the steady state. However, at a high infection level (i.e., the value of $\mathcal{R}_0$ is relatively large), the influence of diffusion on time from initial values to steady state is more complicated, but at least it is certain that the time will be shortened overall. By carrying out some sensitivity analysis of $\mathcal{R}_0(> 1)$ and the equilibrium value of the infectious individuals I^* in terms of β_1 and β_2, it is found that the (β_1, β_2)-plane is divided into two regions by the intersection of two parameter-related surfaces; the sensitivity of $\mathcal{R}_0$ and I^* varies when β_1 and β_2 belong to different regions. When the values of both β_1 and β_2 are very large or very small, β_1 plays a more significant role in the transmission of FMD. These results indicate that stamping out the infected individuals and blocking the epidemic spots and areas are effective in preventing and controlling the spread of FMD.

Key words. foot-and-mouth disease, spatial diffusion, nonlocal infections, basic reproduction number, sensitivity analysis

MSC codes. 35B40, 35K57, 35Q92, 92D30

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1. Introduction.

Foot-and-mouth disease (FMD) is an acute and highly contagious infectious disease with massive socio-economic impact. The disease is an anthropozoonosis caused by viral infection and can affect domestic cloven-hoofed animals, including cattle, swine, sheep, and goats, as well as more than 70 species of wild animals (Alexandersen et al. [1]; Haydon, Kao, and Kitching [21]). Foot-and-mouth disease virus (FMDV), belonging to the small RNA virus *Picornaviridae* family, is the type species of the *Aphthovirus* genus (Doel [10]; Moonen and Schrijver [38]). There are seven strains (A, O, C, Asia 1, and South African Territories 1, 2, and 3)

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which are endemic in different countries worldwide. FMD has been present in almost every part of the world where livestock are kept. More than 100 countries are still affected by FMD worldwide, and distribution of the disease roughly reflects economic development (Grubman and Baxt [19]; OIE [57]).

FMD can be transmitted among herds either by direct or indirect contact. More precisely, FMDV can spread by a wide variety of infection routes, including direct contact between infected animals and susceptible animals; indirect contact with straw or hay that is contaminated by infected animals, with farm vehicles, or milk tankers carrying infected milk, or even with the surgical equipment of veterinary surgeons (Haydon Kao, and Kitching [21]); and through water sources contaminated by excreta and animal products. The airborne spread of FMD has been reported in Donaldson and Alexandersen [11]; airborne virus originates mainly from the exhaled breath of infected animals. FMDV has the potential to spread over borders and seaways under favorable climatic and meteorological conditions (Donaldson [12]; Donaldson et al. [13]; Gloster, Sellers, and Donaldson [17]). Disease signs can appear within 2–3 days after exposure and can last for 7–10 days (Grubman and Baxt [19]). The incubation period is 2–14 days (OIE [57]).

To investigate the transmission dynamics of FMD and to explore effective control strategies, a variety of mathematical models have been proposed (Bailey [3]; Boender et al. [4]; Howey et al. [22]; Keeling [23, 24]; Thornley and France [53]; Zhang, Jin, and Yuan [59]). Moreover, Mushayabasa, Posny, and Wang [41] proposed an ODE model with or without seasonality to study the intrinsic dynamics of FMD. Ferguson, Donnelly, and Anderson [14] presented a mathematical model for the FMD transmission in Great Britain and predicted that culling is more effective than vaccination in controlling the epidemic. There are studies on modeling control strategies for FMD (Ge et al. [16]; Mushayabasa, Bhunu, and Dhlamini [40]). Keeling et al. [25] pointed out that mass prophylactic vaccination could greatly reduce the potential for a major epidemic, and a combination of reactive vaccination and culling might control ongoing epidemics. We refer the reader to Tildesley, Probert, and Woolhouse [54] for a review on various FMD models.

All models mentioned above are nonspatial. However, in reality individuals are nonhomogeneous in space and move randomly, and spatial heterogeneity plays a crucial role in the geographical spread of infectious diseases. It is reported that livestock movement in Great Britain was a crucial factor for the 2001 epidemic of FMD in the UK (Tildesley Probert, and Woolhouse [54]). Green, Kiss, and Kao [18] used the movement data on the network of connections among livestock-holding locations to construct an individual-farm-based model of the initial spread of FMD in Great Britain and performed simulations to show that movements can result in a large nationwide epidemic. Reaction-diffusion equations have been frequently used to model the spatial spread of infectious diseases (Murray [39]; Allen et al. [2]). We refer the reader to Ruan and Wu [45] for a survey on modeling the spatial spread of specific epidemic diseases with animal hosts, including rabies in fox population, dengue, West Nile virus, hantavirus, Lyme disease, and feline immunodeficiency virus, by using reaction-diffusion equations. It should be mentioned that these modeling studies focused on the disease propagation speed that is believed to coincide with the minimal wave speed of traveling wave fronts.

Notice that in the reaction-diffusion equations setting, it is assumed that a given individual interacts only with those living in the same spatial location (i.e., local interaction) at the same time. To model the nonlocal interactions of individuals in one location with individuals in other locations at an earlier time, Britton [5, 6] coined the

concept of spatio-temporal delay (or nonlocal delay). Owing to the mobility of individuals, nonlocal interaction between infectious individuals and susceptible individuals is the key factor that induces spatial transmission of infectious diseases. Earlier studies on the spatio-temporal dynamics of some nonlocal epidemiological models, including the classical Kermack–McKendrick model and the Kendall model described by differential and integral equations, and related references can be found in a review by Ruan [44]. For recent works on nonlocal epidemic models, we refer the reader to Guo, Wang, and Zou [20]; Li and Zou [31]; Liu et al. [33]; Wang and Ma [55]; Wang and Zhao [56]; and Zhao, Wang, and Ruan [61, 62]. These studies focused on traveling wave solutions of the nonlocal epidemic models (Li and Zou [31]; Zhao, Wang, and Ruan [61]), threshold dynamics and asymptotic profiles of steady states for nonlocal models (Guo, Wang, and Zou [20]; Wang and Ma [55]; Wang and Zhao [56]), and threshold dynamics and periodic solutions of nonlocal models with seasonality (Liu et al. [33]; Zhao, Wang, and Ruan [62]).

In this paper, by incorporating the random movement of individuals and considering the nonlocal interactions between susceptible and infectious individuals, we propose an FMD model described by reaction-diffusion equations with spatial diffusion and nonlocal infections. The purpose is to study the threshold dynamics of this diffusive FMD model and to determine which transmission routes have a significant impact on the spatial spread of FMD by sensitivity analysis and numerical simulations.

The paper is organized as follows. In section 2, we construct an FMD transmission model with nonlocal infections and spatial diffusion. In section 3, we study the well-posedness of the model (including existence, uniqueness, positivity, and boundedness of solutions). In section 4, the basic reproduction number ($\mathcal{R}_0$) of the model is calculated by means of the next generation operator. In section 5, we study the threshold dynamics of the model in terms of $\mathcal{R}_0$ and the principal eigenvalue $\overline{\lambda}_0(\tau, S^0)$. Then we use numerical simulations to verify the obtained theoretical results and to explore the impact of diffusion on the spread of FMD when $R_0 > 1$ in section 6. Sensitivity analysis of $\mathcal{R}_0$ and I^* to model parameters is carried out to determine the relative importance of model parameters to disease transmission in section 7. In section 8, we summarize the conclusions and discuss future directions. In section 9, we show that the basic reproduction number is independent of the diffusion coefficients.

2. The diffusive FMD model with nonlocal infections. We propose a diffusive model with nonlocal infections to describe the transmission process of FMD in which two transmission routes are considered: interaction with infected individuals and contact with viruses that exist as aerosols in the environment. For the sake of simplicity, we focus on the one-dimensional spatial domain, denoted by Ω, which is bounded with smooth boundary $\partial\Omega$. To derive the model, we make the following assumptions.

(i) The host population is divided into three groups: susceptible ($S(x,t)$), latent ($L(x,t)$), and infectious ($I(x,t)$) individuals, and the virus load in the environment is denoted by $V(x,t)$.

(ii) There is a latent period (τ) between the moment of being infected and the moment of becoming infectious for animals: cattle (2–4 days), pigs (1–2 days), sheep (about 7 days). A discrete delay is incorporated into the model to take this latent period into account. It is also assumed that exposed individuals in the latent period are not infectious.

(iii) The disease has a fatality rate up to 100 percent for newborn animals, so

TABLE 1
Model parameters.

Parameter	Definition	Unit
μ	recruiting rate	d^{-1}
β_1	infection rate from infective individuals I to susceptible individuals S	d^{-1}
β_2	infection rate from viruses V to susceptible individuals S	d^{-1}
d	removal rate of individuals	d^{-1}
D_S	diffusion coefficient of susceptible individuals (S)	$m^2 \cdot d^{-1}$
D_L	diffusion coefficient of latent individuals (L)	$m^2 \cdot d^{-1}$
D_I	diffusion coefficient of infectious individuals (I)	$m^2 \cdot d^{-1}$
D_V	diffusion coefficient of viruses in the environment (V)	$m^2 \cdot d^{-1}$
r	natural degradation rate of the virus in the environment	d^{-1}
k	discharge quantity of FMDV by infected individuals per unit time	$\log_{10} TCID_{50}$ virus / d

vertical transmission is not considered.

(iv) The mortality rate in adult animals is very low, and the disease-induced mortality rate is ignored.

(v) Based on the fact that individuals in the latent period are also moving around, we combine time delay with diffusion; that is, we use spatial-temporal delay to describe nonlocal infections.

All model parameters are nonnegative constants and are interpreted in Table 1.

In order to incorporate the nonlocal delay into the model, we introduce the notion of infection age $a \geq 0$. Let $E(x,t,a)$ be the density of infected individuals at location x and time t with infection age a, including both $L(x,t)$ and $I(x,t)$. A standard argument on structured population and spatial diffusion (see Metz and Diekmann [37]) yields that

$$\frac{\partial E(x,t,a)}{\partial t} + \frac{\partial E(x,t,a)}{\partial a} = D(a)\frac{\partial^2 E(x,t,a)}{\partial x^2} - dE(x,t,a), \quad t,\ a>0,\ x \in \Omega, \tag{2.1}$$

where $D(a)$ is the diffusion rate that depends on the infection age a. We assume that $D(a)$ satisfies the following hypothesis:

$$D(a) = \begin{cases} D_L, & a \in [0,\tau], \\ D_I, & a \in (\tau,\infty). \end{cases}$$

We consider the homogeneous Neumann boundary condition (zero flux)

$$\frac{\partial E(x,t,a)}{\partial n} = 0, \quad x \in \partial\Omega,\ t>0.$$

By the meaning of the latency τ, we obtain that

$$L(x,t) = \int_0^\tau E(x,t,a)da, \quad I(x,t) = \int_\tau^\infty E(x,t,a)da. \tag{2.2}$$

According to the mechanism of disease transmission, we know that new infections (i.e., when the infection age a is equal to zero) originally develop in two ways: direct contact with infectious individuals and indirect contact with viruses in the environment. For convenience, we use the simplest incidence of the mass action law to obtain the following formula:

$$E(x,t,0) = \beta_1 S(x,t)I(x,t) + \beta_2 S(x,t)V(x,t),$$

and we assume that $E(x,t,\infty) = 0$.

Differentiating (2.2) with respect to t and making use of (2.1), we obtain

$$\begin{aligned}\frac{\partial I(x,t)}{\partial t} &= \int_\tau^\infty \frac{\partial E(x,t,a)}{\partial t}da \\ &= \int_\tau^\infty \left[D_I\frac{\partial^2 E(x,t,a)}{\partial x^2} - \frac{\partial E(x,t,a)}{\partial a} - dE(x,t,a)\right]da \\ &= D_I\Delta I(x,t) - dI(x,t) - E(x,t,\infty) + E(x,t,\tau) \\ &= D_I\Delta I(x,t) - dI(x,t) + E(x,t,\tau)\end{aligned} \tag{2.3}$$

and

$$\begin{aligned}\frac{\partial L(x,t)}{\partial t} &= \int_0^\tau \frac{\partial E(x,t,a)}{\partial t}da \\ &= \int_0^\tau \left[D_L\frac{\partial^2 E(x,t,a)}{\partial x^2} - \frac{\partial E(x,t,a)}{\partial a} - dE(x,t,a)\right]da \\ &= D_L\Delta L(x,t) - dL(x,t) - E(x,t,\tau) + E(x,t,0) \\ &= D_L\Delta L(x,t) - dL(x,t) - E(x,t,\tau) + \beta_1 S(x,t)I(x,t) \\ &\quad + \beta_2 S(x,t)V(x,t).\end{aligned} \tag{2.4}$$

By observing (2.3) and (2.4), we can explain the relation between the two compartments $L(x,t)$ and $I(x,t)$, in which $L(x,t)$ progresses to $I(x,t)$ with the rate of $E(x,t,\tau)$.

Next, we determine $E(x,t,\tau)$, which is a solution of system (2.1) at $a=\tau$. By applying the characteristics method, we consider the solutions of system (2.1) along characteristic line $t = a+\xi$, where $\xi \geq 0$. Letting $v(x,\xi,a) = E(x,a+\xi,a)$ for $a \in [0,\tau]$, we have

$$\begin{cases}\dfrac{\partial v(x,\xi,a)}{\partial a} = \left[\dfrac{\partial E(x,t,a)}{\partial t} + \dfrac{\partial E(x,t,a)}{\partial a}\right]_{t=a+\xi} \\ \qquad\qquad = D_L\Delta E(x,a+\xi,a) - dE(x,a+\xi,a) \\ \qquad\qquad = D_L\Delta v(x,\xi,a) - dv(x,\xi,a), \quad a>0, x\in\Omega, \\ \dfrac{\partial v(x,\xi,a)}{\partial n} = 0, \quad a>0, x\in\partial\Omega, \\ v(x,\xi,0) = E(x,\xi,0) = \beta_1 S(x,\xi)I(x,\xi) + \beta_2 S(x,\xi)V(x,\xi), \quad x\in\Omega.\end{cases} \tag{2.5}$$

For the initial-boundary value problem of the parabolic equation (2.5), we have

$$v(x,\xi,a) = \int_\Omega \Gamma(x,y,a)[\beta_1 S(y,\xi)I(y,\xi) + \beta_2 S(y,\xi)V(y,\xi)]dy,$$

where $\Gamma(x,y,a)$ is the fundamental solution of the following system:

$$\begin{cases}\frac{\partial v(x,\xi,a)}{\partial a} = D_L\Delta v(x,\xi,a) - dv(x,\xi,a), & a>0, x\in\Omega, \\ \frac{\partial v(x,\xi,a)}{\partial n} = 0, & a>0, x\in\partial\Omega.\end{cases} \tag{2.6}$$

When $a=\tau$, we obtain

$$\begin{aligned}E(x,t,\tau) &= v(x,t-\tau,\tau) \\ &= \int_\Omega \Gamma(x,y,\tau)[\beta_1 S(y,t-\tau)I(y,t-\tau) + \beta_2 S(y,t-\tau)V(y,t-\tau)]dy.\end{aligned} \tag{2.7}$$

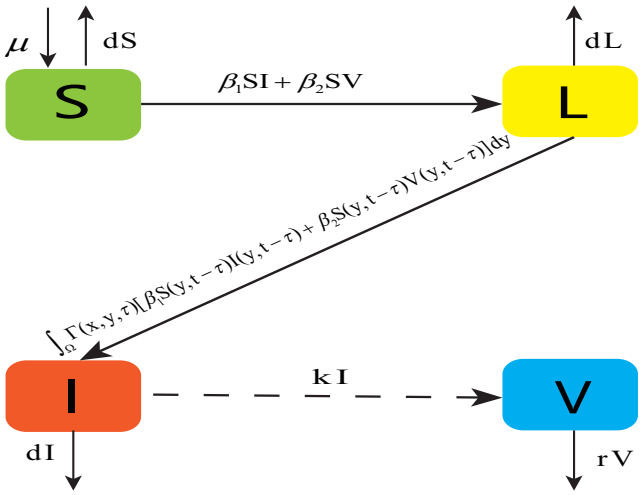

FIG. 2.1. *Transmission diagram of FMD. $S = S(x,t)$, $L = L(x,t)$, $I = I(x,t)$, and $V = V(x,t)$ denote the densities of susceptible, latent, infectious individuals, and virus at location x and time t, respectively. Solid arrows represent the progression of infection and change of each compartment including recruitment, removal, and degradation. Dashed arrows indicate the process by which infectious individuals release viruses.*

The transmission process of FMD is demonstrated in the flowchart (see Figure 2.1).

Substituting (2.7) into (2.3) and (2.4) and combining transmission diagram of FMD (see Figure 2.1), we have the FMD model with diffusion and nonlocal infections:

(2.8)
$$\begin{cases} \dfrac{\partial S(x,t)}{\partial t} = D_S \Delta S(x,t) + \mu - dS(x,t) - \beta_1 S(x,t) I(x,t) - \beta_2 S(x,t) V(x,t), \\ \dfrac{\partial L(x,t)}{\partial t} = D_L \Delta L(x,t) - dL(x,t) + \beta_1 S(x,t) I(x,t) + \beta_2 S(x,t) V(x,t) \\ \qquad\qquad - \displaystyle\int_\Omega \Gamma(x,y,\tau)[\beta_1 S(y,t-\tau) I(y,t-\tau) + \beta_2 S(y,t-\tau) V(y,t-\tau)]dy, \\ \dfrac{\partial I(x,t)}{\partial t} = D_I \Delta I(x,t) - dI(x,t) \\ \qquad\qquad + \displaystyle\int_\Omega \Gamma(x,y,\tau)[\beta_1 S(y,t-\tau) I(y,t-\tau) + \beta_2 S(y,t-\tau) V(y,t-\tau)]dy, \\ \dfrac{\partial V(x,t)}{\partial t} = D_V \Delta V(x,t) + kI(x,t) - rV(x,t), \quad x \in \Omega, \quad t > 0, \\ \dfrac{\partial S(x,t)}{\partial n} = \dfrac{\partial L(x,t)}{\partial n} = \dfrac{\partial I(x,t)}{\partial n} = \dfrac{\partial V(x,t)}{\partial n} = 0, \quad x \in \partial\Omega, \quad t > 0. \end{cases}$$

Because the second equation is decoupled from the other three equations in system

(2.8), we only study the following model:

(2.9)
$$\begin{cases} \dfrac{\partial S(x,t)}{\partial t} = D_S \Delta S(x,t) + \mu - dS(x,t) - \beta_1 S(x,t) I(x,t) - \beta_2 S(x,t) V(x,t), \\ \dfrac{\partial I(x,t)}{\partial t} = D_I \Delta I(x,t) - dI(x,t) \\ \qquad\qquad + \displaystyle\int_\Omega \Gamma(x,y,\tau)[\beta_1 S(y,t-\tau) I(y,t-\tau) + \beta_2 S(y,t-\tau) V(y,t-\tau)]dy, \\ \dfrac{\partial V(x,t)}{\partial t} = D_V \Delta V(x,t) + kI(x,t) - rV(x,t), \quad x \in \Omega,\ t > 0, \\ \dfrac{\partial S(x,t)}{\partial n} = 0, \dfrac{\partial I(x,t)}{\partial n} = 0, \dfrac{\partial V(x,t)}{\partial n} = 0, \qquad x \in \partial\Omega,\ t > 0, \\ S(x,\theta) = \phi_1(x,\theta) \geq 0, I(x,\theta) = \phi_2(x,\theta) \geq 0, V(x,\theta) = \phi_3(x,\theta) \geq 0,\ x \in \Omega, \theta \in [-\tau, 0], \end{cases}$$

where initial value functions $\phi_i(x,\theta)$ $(i = 1,2,3)$ are nonnegative and continuous.

3. Well-posedness. We first introduce some notation on function spaces. Denote $\mathbb{Y} := C(\overline{\Omega}, \mathbb{R})$. Let $\mathbb{X} := C(\overline{\Omega}, \mathbb{R}^3) = \mathbb{Y} \times \mathbb{Y} \times \mathbb{Y}$ be the Banach space associated with the supremum norm $\|u\|_{\mathbb{X}} := \sup_{x \in \overline{\Omega}} \mid u \mid$, where $u = (u_1, u_2, u_3)$ and $|\cdot|$ is the Euclidean norm in $\mathbb{R}^3$. Let $\mathbb{X}^+ := C(\overline{\Omega}, \mathbb{R}^3_+) = \{u > 0, u \in C(\overline{\Omega}, \mathbb{R}^3)\}$ denote the positive cone of $\mathbb{X}$. Define $\mathbb{C}_\tau := C([-\tau, 0], \mathbb{X})$ with the norm $\|\phi\| := \max_{\theta \in [-\tau,0]} \|\phi(\theta)\|_{\mathbb{X}}$. Then $\mathbb{C}_\tau$ is a Banach space. Denote $\mathbb{C}^+_\tau := C([-\tau, 0], \mathbb{X}^+)$. For a given function $u(t) : [-\tau, \sigma) \to \mathbb{X}$ for any $\sigma > 0$, define a pull-back operator by $u_t(\theta) = u(t + \theta)$ for all $\theta \in [-\tau, 0]$.

Now, we are in the position to prove the existence and uniqueness of solutions of system (2.9).

Let $T_1(t)$, $T_2(t)$, and $T_3(t)$ be the C_0-semigroups generated by operators $D_S\Delta(\cdot) - d(\cdot)$, $D_I\Delta(\cdot) - d(\cdot)$, and $D_V\Delta(\cdot) - r(\cdot)$ associated with the Neumann boundary conditions, respectively; i.e.,

$$\begin{aligned} (T_1(t)\varphi_1)(x) &= e^{-dt} \int_\Omega \Gamma_1(x,y,t)\varphi_1(y)dy, \\ (T_2(t)\varphi_2)(x) &= e^{-dt} \int_\Omega \Gamma_2(x,y,t)\varphi_2(y)dy, \\ (T_3(t)\varphi_3)(x) &= e^{-rt} \int_\Omega \Gamma_3(x,y,t)\varphi_3(y)dy, \end{aligned}$$

where $\varphi = (\varphi_1, \varphi_2, \varphi_3) \in \mathbb{X}$, and Γ_1, Γ_2, and Γ_3 are the fundamental solutions of the operators $D_S\Delta(\cdot)$, $D_I\Delta(\cdot)$, and $D_V\Delta(\cdot)$ associated with the Neumann boundary conditions, respectively.

Let $A_i : \mathfrak{D}(A_i) \to \mathbb{Y}$ be the infinitesimal generator of $T_i(t), i = 1,2,3$. $T(t) := (T_1(t), T_2(t), T_3(t))$, $A := (A_1, A_2, A_3)$, in which A is the generator of $T(t)$. Then for each $t \geq 0$, $T(t) : \mathbb{X} \to \mathbb{X}$ is a compact and strongly positive operator (Smith [47]). Denote $F = (F_1, F_2, F_3) : \mathbb{C}^+_\tau \to \mathbb{X}$, where

$$\begin{aligned} F_1(\phi)(x) &= \mu - \beta_1\phi_1(x,0)\phi_2(x,0) - \beta_2\phi_1(x,0)\phi_3(x,0), \\ F_2(\phi)(x) &= \int_\Omega \Gamma(x,y,\tau)[\beta_1\phi_1(y,-\tau)\phi_2(y,-\tau) + \beta_2\phi_1(y,-\tau)\phi_3(y,-\tau)]dy, \\ F_3(\phi)(x) &= k\phi_2(x,0) \end{aligned}$$

for any $\phi = (\phi_1, \phi_2, \phi_3) \in \mathbb{C}^+_\tau$.

Then, system (2.9) can be rewritten as the following abstract delay differential equation:

$$\begin{cases} \dfrac{du(t)}{dt} = Au(t) + F(u_t), \quad t > 0, \\ u_0 = \phi \in \mathbb{C}_\tau^+, \end{cases} \tag{3.1}$$

which can be written as the following integral form:

$$u(t) = T(t)\phi + \int_0^t T(t-s)F(u_s)ds,$$

where $u := (S, I, V)$.

LEMMA 3.1. *For each $\phi = (\phi_1, \phi_2, \phi_3) \in \mathbb{C}_\tau^+$, system (2.9) has a unique mild solution $u(t) = u(t, \phi) \in \mathbb{X}^+$ defined on $[0, \sigma)$, where $\sigma = \sigma(\phi) \le \infty$. Furthermore, $u(x, t) = [u(t)](x)$ is a classical solution of (2.9) for all $t > \tau$.*

Proof. For any $\phi = (\phi_1, \phi_2, \phi_3) \in \mathbb{C}_\tau^+$ and $h \ge 0$, it follows that

$$\begin{aligned} &\phi(x,0) + hF(\phi)(x) \\ &= \begin{pmatrix} \phi_1(x,0) + h(\mu - \beta_1\phi_1(x,0)\phi_2(x,0) - \beta_2\phi_1(x,0)\phi_3(x,0)) \\ \phi_2(x,0) + h(\int_\Omega \Gamma(x,y,\tau)[\beta_1\phi_1(y,-\tau)\phi_2(y,-\tau) + \beta_2\phi_1(y,-\tau)\phi_3(y,-\tau)]dy) \\ \phi_3(x,0) + h(k\phi_2(x,0)) \end{pmatrix} \\ &\ge \begin{pmatrix} \phi_1(x,0)(1 - h\beta_1\phi_2(x,0) - h\beta_2\phi_3(x,0)) \\ \phi_2(x,0) \\ \phi_3(x,0) \end{pmatrix}, \ x \in \overline{\Omega}. \end{aligned}$$

The above inequalities imply that $\phi(x,0) + hF(\phi)(x) \in \mathbb{C}_\tau^+$ when h is sufficiently small. Then the following Nagumo condition holds:

$$\lim_{h \to 0^+} h^{-1}\mathrm{dist}(\mathbb{C}_\tau^+, \phi(x,0) + hF(\phi)(x)) = 0.$$

$F(\phi)$ is Lipschitz. In addition, $T(t)$ is a strongly positive semigroup; i.e., $T(t)\mathbb{X}^+ \subset \mathbb{X}^+$, $t \ge 0$. By Theorem 1 in Martin and Smith [35], the proof is completed. ∎

For the scalar reaction-diffusion equation

$$\begin{cases} \dfrac{\partial v(x,t)}{\partial t} = D\Delta v(x,t) + \mu - dv(x,t), \quad x \in \Omega, \ t > 0, \\ \dfrac{\partial v(x,t)}{\partial n} = 0, \quad x \in \partial\Omega, \ t > 0, \end{cases} \tag{3.2}$$

we have the following lemma.

LEMMA 3.2. *System (3.2) has a unique positive steady state μ/d, which is globally asymptotically stable in $\mathbb{Y}$.*

Proof. For any $\phi \in C(\overline{\Omega}, \mathbb{R}_+)$, system (3.2) has a unique solution $v(t, \phi)$ defined on $[0, \infty)$ with $v(0, \phi) = \phi$. Let Φ_t be the solution semiflow associated with (3.2), i.e., $\Phi_t\phi = v(t, \phi)$. Note that $f := \mu - dv(x,t)$ is strictly subhomogeneous; that is, $f(\alpha v) > \alpha f(v)$ for any $\alpha \in (0,1)$ and $v \gg 0$. By Claim 1 in [15], $\Phi_t\phi$ is also strictly subhomogeneous; i.e., $\Phi_t(\alpha\phi) > \alpha\Phi_t\phi$ for any $\alpha \in (0,1)$ and $\phi \gg 0$. And then, from Theorem 2.3.1 in [63], we can obtain that Φ_t has a positive steady state $v^* = \mu/d$ such that the omega limit set $\omega(\phi) = v^* \in \mathbb{Y}$ for any $\phi \in \mathbb{Y}$. Furthermore, it then follows from Theorem 3.4 in [36] that v^* is asymptotically stable, completing the proof. ∎

Recall that Lemma 3.2 is introduced to bound the solutions of system (2.9) using the comparison principle. Further, we obtain global existence of solutions, as shown in the following theorem.

THEOREM 3.3. *For each* $\phi = (\phi_1, \phi_2, \phi_3) \in \mathbb{C}_\tau^+$, *system* (2.9) *has a unique solution* $u(\cdot, t, \phi) \in \mathbb{X}^+$ *defined on* $[0, \infty)$.

Proof. For the equation

$$\begin{cases} \dfrac{\partial S(x,t)}{\partial t} \le D_S \Delta S(x,t) + \mu - dS(x,t), \ \ x \in \Omega, \ t > 0, \\ \dfrac{\partial S(x,t)}{\partial n} = 0, \ \ x \in \partial\Omega, \ t > 0, \end{cases}$$

by Lemma 3.2 and the standard parabolic comparison principle, we know that there exist B_1 and t_1 such that

$$S(x,t,\phi) \le B_1 \quad \forall t \ge t_1, \, x \in \overline{\Omega}, \, \phi \in \mathbb{C}_\tau^+.$$

Denote

$$\overline{S}(t) = \int_\Omega S(x,t)dx, \ \ \overline{I}(t) = \int_\Omega I(x,t)dx, \ \ \overline{V}(t) = \int_\Omega V(x,t)dx.$$

Next, we integrate the first equation of system (2.9) to obtain that

$$\begin{aligned} \frac{d\overline{S}(t)}{dt} &= \mu_0 - d\overline{S}(t) - \int_\Omega (\beta_1 S(x,t)I(x,t) + \beta_2 S(x,t)V(x,t))dx \\ &\le \mu_0 - d\overline{S}(t) - c_1 \int_\Omega S(x,t)[I(x,t) + V(x,t)]dx, \end{aligned}$$

where $c_1 := \min\{\beta_1, \beta_2\}, \mu_0 := \mu|\Omega|$. By the inequality, we have

$$\int_\Omega S(x,t)[I(x,t) + V(x,t)]dx \le \mu_1 - d_0\overline{S}(t) - m_0 \frac{d\overline{S}(t)}{dt},$$

where $\mu_1 \ge \mu_0/c_1, d_0 \le d/c_1, m_0 \le 1/c_1$. Thus,

$$\begin{aligned} \frac{d\overline{I}(t)}{dt} &\le -d\overline{I}(t) + c_2 \int_\Omega S(y, t-\tau)[I(y, t-\tau) + V(y, t-\tau)]dy \\ &\le -d\overline{I}(t) - k_1\overline{S}(t-\tau) - k_2 \frac{d\overline{S}(t-\tau)}{dt} + k_3, \end{aligned}$$

where constants c_2, k_1, k_2, k_3 are all positive. After sorting out the above inequality, we obtain

$$\begin{aligned} \frac{d[\overline{I}(t) + k_2\overline{S}(t-\tau)]}{dt} &\le -d\overline{I}(t) - k_1\overline{S}(t-\tau) + k_3 \\ &= -\frac{k_1}{k_2}[\overline{I}(t) + k_2\overline{S}(t-\tau)] + k_3, \end{aligned}$$

where $d \ge k_1/k_2$. Hence, there exist positive constants k_4 and k_5 such that

$$\overline{I}(t) \le \overline{I}(t) + k_2\overline{S}(t-\tau) \le k_4 e^{-\frac{k_1}{k_2}t} + k_5 \quad \forall t \ge \tau,$$

which implies that $\overline{I}(t)$ is bounded. Similarly, we can integrate the third equation of system (2.9) to obtain

$$\frac{d\overline{V}(t)}{dt} = k\overline{I}(t) - r\overline{V}(t).$$

Thus, $\overline{V}(t)$ is bounded. Therefore, we have

$$\begin{aligned}\frac{\partial I(x,t)}{\partial t} &= D_I \Delta I(t,x) - dI(x,t) + c_3 \int_\Omega \Gamma(x,y,\tau)[I(y,t-\tau) + V(y,t-\tau)]dy \\ &\le D_I \Delta I(t,x) - dI(x,t) + c_3[\overline{I}(t-\tau) + \overline{V}(t-\tau)],\end{aligned}$$

where constant $c_3 > 0$. By the boundedness of $\overline{I}(t)$ and $\overline{V}(t)$, we know that $I(x,t)$ is bounded and thus $V(x,t)$ is also bounded for all $t \ge t_1 + \tau$. According to Lemma 3.1, $\sigma(\phi) = \infty$, which completes the proof. ∎

4. Basic reproduction number. There is a disease-free equilibrium in system (2.9), denoted by $E_0 = (S^0, 0, 0)$, where $S^0 = \mu/d$. Linearizing model (2.9) at the disease-free equilibrium E_0, we obtain

$$\begin{cases} \dfrac{\partial S(x,t)}{\partial t} = D_S \Delta S(x,t) + \mu - dS(x,t) - \beta_1 S^0 I - \beta_2 S^0 V, \\ \dfrac{\partial I(x,t)}{\partial t} = D_I \Delta I(t,x) - dI(x,t) \\ \qquad\qquad + \displaystyle\int_\Omega \Gamma(x,y,\tau)[\beta_1 S^0 I(y,t-\tau) + \beta_2 S^0 V(y,t-\tau)]dy, \\ \dfrac{\partial V(x,t)}{\partial t} = D_V \Delta V(x,t) + kI(x,t) - rV(x,t), \quad x \in \Omega,\ t > 0, \\ \dfrac{\partial S(x,t)}{\partial n} = 0, \dfrac{\partial I(x,t)}{\partial n} = 0, \dfrac{\partial V(x,t)}{\partial n} = 0, \quad x \in \partial\Omega,\ t > 0. \end{cases} \tag{4.1}$$

Then we define the infection operator by

$$H(\varphi)(x) = (H_1(\varphi)(x), H_2(\varphi)(x)) \quad \forall \varphi = (\varphi_2, \varphi_3) \in \mathbb{Y} \times \mathbb{Y},$$

where

$$H_1(\varphi)(x) = \int_\Omega \Gamma(x,y,\tau)[\beta_1 S^0 \varphi_2(y) + \beta_2 S^0 \varphi_3(y)]dy, \quad H_2(\varphi)(x) = k\varphi_2(x).$$

Denote $T^*(t) := (T_2(t), T_3(t))$; then $T^*(t)$ is a strongly positive semigroup such that $T^*(t)(\mathbb{Y}^+ \times \mathbb{Y}^+) \subset \mathbb{Y}^+ \times \mathbb{Y}^+$.

Next, in order to define the basic reproduction number for model (2.9), we assume that the host population and the virus load in the environment are near the disease-free equilibrium E_0. Let $\varphi_2(x), \varphi_3(x)$ be the spatial distributions of initial infected individuals and viruses, respectively; we then see that $([T_2(t)\varphi_2](x), [T_3(t)\varphi_3](x))$ represents the distribution of those infectious individuals and virus at time t. Note that there will be no new infectious individuals infected by $I(x,t)$ at any time $t \in [0,\tau)$, and for $t \ge \tau$, the distribution of new infectious individuals infected by $I(x,t)$ is

$$\int_\Omega \Gamma(x,y,\tau)\beta_1 S^0 [T_2(t-\tau)\varphi_2](y)dy,$$

and the distribution of new infectious individuals infected by $V(x,t)$ is

$$\int_\Omega \Gamma(x,y,\tau)\beta_2 S^0 [T_3(t)\varphi_3](y)dy.$$

Thus, the distribution of total new infectious individuals is

$$\begin{aligned}&\int_\tau^\infty \int_\Omega \Gamma(x,y,\tau)\beta_1 S^0[T_2(t-\tau)\varphi_2](y)dydt + \int_0^\infty \int_\Omega \Gamma(x,y,\tau)\beta_2 S^0[T_3(t)\varphi_3](y)dydt\\ &= \int_0^\infty \int_\Omega \Gamma(x,y,\tau)[\beta_1 S^0[T_2(t)\varphi_2](y) + \beta_2 S^0[T_3(t)\varphi_3](y)]dydt\\ &= \int_0^\infty H_1[T^*(t)\varphi](x)dt.\end{aligned}$$

Similarly, the distribution of total new virus is

$$\int_0^\infty H_2[T^*(t)\varphi](x)dt.$$

It then follows that

$$\mathcal{L}(\varphi) := \int_0^{+\infty} H(T^*(t)\varphi)dt = H\bigg(\int_0^{+\infty}(T^*(t)\varphi)dt\bigg).$$

The next generation operator $\mathcal{L}$ is a compact and strongly positive linear operator (the compactness is obtained by the Arzela–Ascoli theorem, and strong positivity is due to the strong positivity of $T^*(t)$). By the results in Diekmann, Heesterbeek, and Metz [9] and Thieme [51], we define the basic reproduction number for model (2.9) by the spectral radius of $\mathcal{L}$; i.e.,

$$\mathcal{R}_0 := r(\mathcal{L}).$$

Based on the results in Wang and Zhao [56], we can obtain an explicit formula for the basic reproduction number. For any $\epsilon > 0, \varphi \in \mathbb{Y} \times \mathbb{Y}$, define

$$H^\epsilon(\varphi) = \epsilon\varphi + H(\varphi),$$

$$\mathcal{L}_\epsilon(\varphi) = \int_0^{+\infty} H^\epsilon(T^*(t)\varphi)dt = H^\epsilon\left(\int_0^{+\infty}(T^*(t)\varphi)dt\right).$$

Then $\mathcal{L}_\epsilon$ is a compact and strongly positive operator. By the Krein–Rutman theorem, $r(\mathcal{L}_\epsilon) > 0$ is the unique principal eigenvalue. According to $\int_\Omega \Gamma_i(x,y,t)dy = 1, i = 1,2,3$, we have

$$\begin{aligned}T_2(t)\alpha_1 &= \alpha_1 e^{-dt}\int_\Omega \Gamma_2(x,y,t)dy = \alpha_1 e^{-dt},\\ T_3(t)\alpha_2 &= \alpha_2 e^{-rt}\int_\Omega \Gamma_3(x,y,t)dy = \alpha_2 e^{-rt}\end{aligned}$$

for all $\alpha = (\alpha_1,\alpha_2)^{\mathrm{T}} \in \mathbb{R}^2$, and $\int_\Omega \Gamma(x,y,\tau)dy = e^{-d\tau}$. Thus,

$$\mathcal{L}_\epsilon(\alpha) = \int_0^{+\infty} H^\epsilon(T^*(t)\alpha)dt = H^\epsilon\bigg(\int_0^{+\infty} T^*(t)\alpha dt\bigg) = M_\epsilon(\alpha),$$

where $T^*(t)\alpha = (T_2(t)\alpha_1, T_3(t)\alpha_2)$ and

$$M_\epsilon = \begin{bmatrix} \frac{\epsilon + e^{-d\tau}\beta_1 S^0}{d} & \frac{e^{-d\tau}\beta_2 S^0}{r} \\ \frac{\kappa}{d} & \frac{\epsilon}{r} \end{bmatrix}.$$

Letting $\epsilon \to 0^+$ and calculating the eigenvalues of M_ϵ, we obtain that

$$r(M_0) = \frac{e^{-d\tau}\beta_1 S^0}{2d} + \frac{\sqrt{(e^{-d\tau}\beta_1 S^0)^2 + \frac{4\beta_2 S^0 dke^{-d\tau}}{r}}}{2d}.$$

It follows from the uniqueness of the principal eigenvalue of $\mathcal{L}_\epsilon$ that $r(\mathcal{L}_\epsilon) = r(M_\epsilon)$. Moreover, $\mathcal{R}_0 = r(\mathcal{L}) = r(\mathcal{L}_0) = r(M_0)$. Hence, we obtain that

$$\mathcal{R}_0 = \frac{1}{2d^2}\left[e^{-d\tau}\beta_1\mu + \sqrt{(e^{-d\tau}\beta_1\mu)^2 + \frac{4\beta_2\mu k d^2 e^{-d\tau}}{r}}\right]. \tag{4.2}$$

From (4.2), we can see that the basic reproduction number is independent of the diffusion coefficients. We give a proof in section 9. In addition, we know that $\mathcal{R}_0$ is an increasing function of β_1 and β_2. In section 7, we will discuss in detail the dependence of $\mathcal{R}_0$ on some model parameters.

5. Threshold dynamics. In this section, we intend to characterize $\mathcal{R}_0$ in terms of the principal eigenvalue, establish the existence of the endemic equilibrium, and study the stability of the equilibria.

Let $(S, I, V) = e^{\lambda t}(\varphi_1(x), \varphi_2(x), \varphi_3(x))$, where $(\varphi_1(x), \varphi_2(x), \varphi_3(x)) \in \mathbb{X}$. Substituting this into (4.1), we obtain the following eigenvalue problem:

(5.1)
$$\begin{cases} \lambda\varphi_1(x) = D_S\Delta\varphi_1(x) + \mu - d\varphi_1(x) - \beta_1 S^0\varphi_2(x) - \beta_2 S^0\varphi_3(x), \\ \lambda\varphi_2(x) = D_I\Delta\varphi_2(x) - d\varphi_2(x) + e^{-\lambda\tau}\displaystyle\int_\Omega \Gamma(x, y, \tau)[\beta_1 S^0\varphi_2(y) + \beta_2 S^0\varphi_3(y)]dy, \\ \lambda\varphi_3(x) = D_V\Delta\varphi_3(x) + k\varphi_2(x) - r\varphi_3(x), \ x \in \Omega, \quad t > 0, \\ \dfrac{\partial\varphi_1(x)}{\partial n} = 0, \dfrac{\partial\varphi_2(x)}{\partial n} = 0, \dfrac{\partial\varphi_3(x)}{\partial n} = 0, \quad x \in \partial\Omega, t > 0. \end{cases}$$

By the biological meaning of $\mathcal{R}_0$, it is actually independent of the susceptible compartment S. Hence, we have the following nonlocal eigenvalue problem with Neumann boundary conditions:

(5.2)
$$\begin{cases} \lambda\varphi_2(x) = D_I\Delta\varphi_2(x) - d\varphi_2(x) + e^{-\lambda\tau}\displaystyle\int_\Omega \Gamma(x, y, \tau)[\beta_1 S^0\varphi_2(y) + \beta_2 S^0\varphi_3(y)]dy, \\ \lambda\varphi_3(x) = D_V\Delta\varphi_3(x) + k\varphi_2(x) - r\varphi_3(x), \ x \in \Omega, \quad t > 0, \\ \dfrac{\partial\varphi_2(x)}{\partial n} = 0, \dfrac{\partial\varphi_3(x)}{\partial n} = 0, \quad x \in \partial\Omega, t > 0. \end{cases}$$

We consider the following linear nonlocal elliptic eigenvalue problem with Neumann boundary conditions:

(5.3)
$$\begin{cases} \lambda\varphi_2(x) = D_I\Delta\varphi_2(x) - d\varphi_2(x) + \displaystyle\int_\Omega \Gamma(x, y, \tau)[\beta_1 S^0\varphi_2(y) + \beta_2 S^0\varphi_3(y)]dy, \\ \lambda\varphi_3(x) = D_V\Delta\varphi_3(x) + k\varphi_2(x) - r\varphi_3(x), \ x \in \Omega, \ t > 0, \\ \dfrac{\partial\varphi_2(x)}{\partial n} = 0, \dfrac{\partial\varphi_3(x)}{\partial n} = 0, \quad x \in \partial\Omega, t > 0, \end{cases}$$

where the parameters d, k, r, β_1, and β_2 are all positive constants. According to Theorem 7.6.1 in Smith [47], (5.3) has a principal eigenvalue $\lambda_0(\tau, S^0)$ with a strongly positive eigenfunction.

LEMMA 5.1. *There is a principal eigenvalue* $\overline{\lambda}_0(\tau, S^0)$ *of* (5.2) *associated with a strongly positive eigenfunction. Moreover,* $\overline{\lambda}_0(\tau, S^0)$ *has the same sign as* $\lambda_0(\tau, S^0)$.

Proof. The proof is similar to those of Theorem 2.2 in Thieme and Zhao [52] and of Lemma 2.4 in Guo, Wang, and Zou [20]. Let $\mathbb{E}_\tau = C([-\tau, 0], \mathbb{Y} \times \mathbb{Y})$, $\mathbb{E}_\tau^+ = C([-\tau, 0], \mathbb{Y}^+ \times \mathbb{Y}^+)$. Define $L = (L_1, L_2) : \mathbb{E}_\tau \to \mathbb{Y} \times \mathbb{Y}$ by

$$\begin{aligned} L_1\phi(x) &= \int_\Omega \Gamma(x, y, \tau)[\beta_1 S^0 \phi_2(y, -\tau) + \beta_2 S^0 \phi_3(y, -\tau)]dy, \\ L_2\phi(x) &= k\phi_2(x, 0), \end{aligned}$$

where $\phi = (\phi_2, \phi_3) \in \mathbb{E}_\tau$. L is a positive operator; i.e., $L(\mathbb{E}_\tau^+) \subset \mathbb{Y}^+ \times \mathbb{Y}^+$. For each $\lambda \in \mathbb{R}$, we define $L_\lambda = (L_{1,\lambda}, L_{2,\lambda}) : \mathbb{Y} \times \mathbb{Y} \to \mathbb{Y} \times \mathbb{Y}$ by

$$\begin{aligned} L_{1,\lambda}\varphi(x) &= L_1(e^{\lambda \cdot}\varphi) = e^{-\lambda\tau} \int_\Omega \Gamma(x, y, \tau)[\beta_1 S^0 \varphi_2(y) + \beta_2 S^0 \varphi_3(y)]dy, \\ L_{2,\lambda}\varphi(x) &= L_2(e^{\lambda \cdot}\varphi) = k\varphi_2(x), \end{aligned}$$

where $\varphi = (\varphi_2, \varphi_3) \in \mathbb{Y} \times \mathbb{Y}$, $e^{\lambda \cdot}\varphi \in \mathbb{E}_\tau$, is defined by

$$(e^{\lambda \cdot}\varphi)(\theta, x) = e^{\lambda\theta}\varphi(x), \quad \theta \in [-\tau, 0], x \in \overline{\Omega}.$$

Let $U(t) : \mathbb{E}_\tau \to \mathbb{E}_\tau, t \geq 0$, be the solution semiflow associated with the abstract delay differential equation

$$\begin{cases} \frac{du}{dt} = \mathcal{A}u(t) + L(u_t), & t > 0, \\ u_0 = \phi \in \mathbb{E}_\tau, \end{cases} \tag{5.4}$$

where $u := (u_1, u_2) = (I, V), \mathcal{A} = (A_2, A_3)$, and let $A_U : \mathfrak{D}(A_U) \to \mathbb{E}_\tau$ be a generator of $U(t)$.

The operator $U(t)$ is strongly positive. In fact, for any $\phi \in \mathbb{E}_\tau^+ \setminus \{(0, 0)\}$, let $u(x, t) = u(t, \phi)(x)$, $x \in \overline{\Omega}, t \geq 0$, be the solution of (5.4); i.e., $u(t, \phi)(x) = U(t)\phi$. Here is the fact that $u(x, t) > 0$ for all $x \in \overline{\Omega}, t > \tau$. Indeed, this argument is based on the following two cases.

Case (i). If $\phi(\cdot, 0) \not\equiv 0$, according to the positivity of L and the parabolic strong maximum principle, we obtain that $u(x, t) > 0$ for all $x \in \overline{\Omega}, t > 0$.

Case (ii). Assume that there exists $\theta_0 \in (0, \tau)$ such that $\phi(\cdot, -\theta_0) \not\equiv 0$. In this case, we first prove that $u(\cdot, \tau - \theta_0) \not\equiv 0$ with the reduction to absurdity. If $u(\cdot, \tau - \theta_0) \equiv 0$, it follows from (5.4) with $t = \tau - \theta_0$ that

$$\begin{cases} \frac{\partial u_1(x, \tau - \theta_0)}{\partial t} = \int_\Omega \Gamma(x, y, \tau)[\beta_1 S^0 u_1(y, -\theta_0) + \beta_2 S^0 u_2(y, -\theta_0)]dy > 0, \\ \frac{\partial u_2(x, \tau - \theta_0)}{\partial t} = 0, \quad \tau > 0, x \in \overline{\Omega}. \end{cases}$$

Since $u(x, t) \geq 0$, for all $x \in \overline{\Omega}$, $t \geq 0$, and $u(x, \tau - \theta_0) \equiv 0$, we have $\frac{\partial u(x, \tau - \theta_0)}{\partial t} \leq 0$, which is a contradiction. Thus, $u(\cdot, \tau - \theta_0) \not\equiv 0$. We show that $u(x, t) > 0$ for all $x \in \overline{\Omega}$, $t > \tau - \theta_0$ again by the positivity of L and the parabolic strong maximum principle. Eventually, we have proved that $u(x, t) > 0$ for all $x \in \overline{\Omega}, t > \tau$ with the combination of cases (i) and (ii).

In addition, $U(t)$ is a compact operator for each $t > \tau$. By the Krein–Rutman theorem, there is a principal eigenvalue of $U(t)$ associated with a strongly positive eigenfunction.

Let $s(A_U) := \sup\{\mathrm{Re}(\lambda) : \lambda \in \sigma(A_U)\}$ be the spectral bound of A_U. The spectral radius $r := \mathrm{spr}(U(t)) = \sup\{|\lambda| : \lambda \in \sigma(U(t))\} > 0$ is the principal eigenvalue of $U(t)$. There is a point spectral value $\overline{\lambda}$ of A_U such that $r = e^{t\overline{\lambda}}$ by the point spectral mapping theorem (Theorem 2.2.4 in Pazy [43]). By means of the compactness of A_U, we know that $\overline{\lambda} \in \mathbb{R}$, $\overline{\lambda} \le s(A_U)$. Moreover, we know the fact that $s(A_U) \in \sigma(A_U)$ and the point spectral mapping theorem (Theorem 2.2.3 in Pazy [43]) indicate $e^{ts(A_U)} \in \sigma(U(t))$. Then, $e^{ts(A_U)} \le r = e^{t\overline{\lambda}}$, which implies that $s(A_U) \le \overline{\lambda}$. Thus, $s(A_U) = \overline{\lambda}$ is a point spectral value of A_U. Let $\psi \in \mathbb{E}_\tau \setminus \{(0,0)\}$ be an eigenvector of A_U associated with $s(A_U)$. Then $U(t)\psi = e^{ts(A_U)} = e^{t\overline{\lambda}}\psi = r\psi$, and we obtain the eigenvector $\psi \in \mathrm{int}(\mathbb{E}_\tau^+)$. Therefore, $s(A_U)$ is the principal eigenvalue of A_U. There is a principal eigenvalue $\overline{\lambda}_0(\tau, S^0)$ of (5.2) associated with a strongly positive eigenfunction. We denote the principal eigenvalue of (5.2) by $\overline{\lambda}_0(\tau, S^0)$.

System (5.3) is the eigenvalue problem of the following system:

$$\begin{cases} \frac{du}{dt} = \mathcal{A}u(t) + L_0 u(t), \quad t > 0, \\ u(0) \in \mathbb{Y} \times \mathbb{Y}. \end{cases} \tag{5.5}$$

It follows that $s(\mathcal{A} + L_0) = \lambda_0(\tau, S^0)$. By the results in Kerscher and Nagel [26], we obtain that $s(A_U) = \overline{\lambda}_0(\tau, S^0)$ has the same sign as $s(\mathcal{A} + L_0) = \lambda_0(\tau, S^0)$. ∎

LEMMA 5.2. *$\mathcal{R}_0 - 1$ has the same sign as $\lambda_0(\tau, S^0)$.*

Proof. The proof follows that of Lemma 2.2 in Wang and Zhao [56]. Define an operator $B := \mathcal{A}^* + H$; then B is a positive perturbation of $\mathcal{A}^*$ and B generates a C_0-semigroup. Hence, B is resolvent positive. By Theorem 3.5 in Thieme [51], we obtain that $s(B)$ has the same sign as $r(-H(\mathcal{A}^*)^{-1}) - 1 = r(\mathcal{L}) - 1 = \mathcal{R}_0 - 1$, where $s(B) = s(\mathcal{A}^* + H) = \lambda_0(\tau, S^0)$, completing the proof. ∎

Next, based on the fact that the sign of the principal eigenvalue of a linear system can determine exponential growth or exponential decay of the solution, we show that $\mathcal{R}_0$ can be regarded as a threshold for persistence or extinction of the disease. Then $\overline{\lambda}_0(\tau, S^0)$ can also be regarded as a threshold of the transmission of the disease by Lemmas 5.1 and 5.2.

THEOREM 5.3. *Let $\mathcal{R}_0$ be defined by* (4.2).

(i) *If $\mathcal{R}_0 < 1$, then the disease-free equilibrium E_0 of system* (2.9) *is globally asymptotically stable.*

(ii) *If $\mathcal{R}_0 > 1$, then the disease-free equilibrium E_0 of system* (2.9) *is unstable, whereas there exists $\delta > 0$ such that any nonnegative solution with $\phi_2(0) \not\equiv 0$ and $\phi_3(0) \not\equiv 0$ satisfies*

$$\liminf_{t\to\infty} I(x,t) \ge \delta, \quad \liminf_{t\to\infty} V(x,t) \ge \delta$$

uniformly for all $x \in \overline{\Omega}$. Furthermore, system (2.9) *has an endemic equilibrium E^*.*

Proof. The idea of the proof mainly comes from Theorem 3.1 in Guo, Wang, and Zou [20] and Theorem 3.4 in Wang and Zhao [56]. In the case where $\mathcal{R}_0 < 1$, we can see that $\lambda_0(\tau, S^0) < 0$ by Lemma 5.2. Then by Lemma 5.1, we obtain that $\overline{\lambda}_0(\tau, S^0) < 0$. There exists ε_0 sufficiently small such that $\overline{\lambda}_0(\tau, S^0 + \varepsilon_0) < 0$. And

there exists $T > 0$ such that $S(x,t) \le S^0 + \varepsilon_0$ for all $t \ge T$. Thus, we obtain that

$$\begin{cases} \dfrac{\partial I(x,t)}{\partial t} \le D_I \Delta I(x,t) - dI(x,t) \\ \qquad\qquad + \displaystyle\int_\Omega \Gamma(x,y,\tau)[\beta_1(S^0+\varepsilon_0)I(y,t-\tau) + \beta_2(S^0+\varepsilon_0)V(y,t-\tau)]dy, \\ \dfrac{\partial V(x,t)}{\partial t} \le D_V \Delta V(x,t) + kI(x,t) - rV(x,t), \quad x \in \overline{\Omega}, \quad t \ge T. \end{cases}$$

There exists a strongly positive eigenfunction $\varphi(x) = (\varphi_2(x), \varphi_3(x))$ corresponding to $\overline{\lambda}_0(\tau, S^0 + \varepsilon_0)$. For any given initial value function $\phi = (\phi_1, \phi_2, \phi_3) \in \mathbb{C}_\tau^+$, there exists $\overline{\alpha} > 0$ such that $(I(x,t,\phi), V(x,t,\phi)) \le \overline{\alpha} e^{\overline{\lambda}_0(\tau, S^0+\varepsilon_0)t}(\varphi_2(x), \varphi_3(x))$ for all $t \in [T-\tau, \infty)$ by the comparison principle. Therefore, $\lim_{t\to\infty}(I(x,t,\phi), V(x,t,\phi)) = (0,0)$ for all $x \in \overline{\Omega}$ and then according to Thieme [50], we have $\lim_{t\to\infty} S(x,t,\phi) = S^0$ for all $x \in \overline{\Omega}$, which shows that E_0 is globally attractive when $\mathcal{R}_0 < 1$. We also know that E_0 is locally asymptotically stable when $\mathcal{R}_0 < 1$. Let λ be any given eigenvalue of the nonlocal eigenvalue problem associated with system (5.2); then it follows that $\mathrm{Re}\lambda \le \overline{\lambda}_0(\tau, S^0) < 0$. Consequently, E_0 is locally stable, and thus (i) is proved completely.

In the case when $\mathcal{R}_0 > 1$, (5.2) has at least an eigenvalue with positive real part. Then we know that E_0 is unstable. In the following we use the persistence theory in Smith and Zhao [48] to show the uniform persistence of system (2.9). Define

$$\mathbb{W}_0 := \{\phi = (\phi_1, \phi_2, \phi_3) \in \mathbb{C}_\tau^+ : \phi_2(\cdot, 0) \not\equiv 0 \ \text{ and } \ \phi_3(\cdot, 0) \not\equiv 0\}$$

and

$$\partial\mathbb{W}_0 := \mathbb{C}_\tau^+ \backslash \mathbb{W}_0 = \{\phi = (\phi_1, \phi_2, \phi_3) \in \mathbb{C}_\tau^+ : \phi_2(\cdot, 0) \equiv 0 \ \text{ or } \ \phi_3(\cdot, 0) \equiv 0\}.$$

Denote $\Phi(t) : \mathbb{C}_\tau^+ \to \mathbb{C}_\tau^+$ as the solution semiflow of system (2.9); i.e., $(\Phi(t)\phi)(x,\theta) = u(x, t+\theta, \phi)\, \forall x \in \overline{\Omega}, t \ge 0, \theta \in [-\tau, 0]$. Let

$$M_\partial := \{\phi \in \partial\mathbb{W}_0 : \Phi(t)\phi \in \partial\mathbb{W}_0\, \forall t \ge 0\}.$$

We can see that M_∂ is nonempty based on the fact that $\Phi(t)\mathbb{W}_0 \subseteq \mathbb{W}_0$ when $\phi \in \mathbb{W}_0$. Let $w(\phi)$ be the omega limit set of the orbit of $\Phi(t)$ through $\phi \in \mathbb{C}_\tau^+$. Next, we prove $w(\phi) = \{(S^0, 0, 0)\}\, \forall \phi \in M_\partial$.

For given $\phi \in M_\partial$, we have $I(\cdot, t, \phi) \equiv 0$ or $V(\cdot, t, \phi) \equiv 0$. In the case when $I(\cdot, t, \phi) \equiv 0\, \forall t \ge 0$, it is easy to obtain that $\lim_{t\to\infty} V(\cdot, t, \phi)) = 0$ and then $\lim_{t\to\infty} S(\cdot, t, \phi)) = S^0$. The same is true for the case when $V(\cdot, t, \phi) \equiv 0$. Therefore, $w(\phi) = \{(S^0, 0, 0)\}\, \forall \phi \in M_\partial$.

Define a continuous function $p : \mathbb{C}_\tau^+ \to \mathbb{R}^+$ by

$$p(\phi) := \min\{\min_{x\in\overline{\Omega}} \phi_2(x, 0), \min_{x\in\overline{\Omega}} \phi_3(x, 0)\}\, \forall \phi \in \mathbb{C}_\tau^+.$$

It is obvious that $p^{-1}(0, \infty) \subseteq \mathbb{W}_0$ and $p(\phi)$ has the following property: if $p(\phi) > 0$ or $\phi \in \mathbb{W}_0$ with $p(\phi) = 0$, then $p(\Phi(t)\phi) > 0\, \forall t > 0$. According to the above analysis, p is a generalized distance function for the solution semiflow $\Phi(t)$. We also know that $w(\phi)$ is an isolated invariant set in $\mathbb{C}_\tau^+$ by Lemma 3.3 in Wang and Ma [55] and $W^s(S^0, 0, 0) \bigcap p^{-1}(0, \infty) = \emptyset$, where $W^s(S^0, 0, 0)$ is the stable manifold of $(S^0, 0, 0)$. Moreover, there is no cycle in M_∂ from $(S^0, 0, 0)$ to $(S^0, 0, 0)$. In the end, we can

prove that $U(t)$ has a compact global attractor for $t \geq 0$ referring to Theorem 2.1 in Guo, Wang, and Zou [20]. By Theorem 3 in Smith and Zhao [48], we obtain that there exists $\delta > 0$ such that $\min\{p(\psi) : \psi \in w(\phi)\} > \delta \, \forall \phi \in \mathbb{W}_0$, which implies $\liminf_{t\to\infty} I(x,t) \geq \delta$, $\liminf_{t\to\infty} V(x,t) \geq \delta$ uniformly for all $x \in \overline{\Omega}$. Hence, system (2.9) has an endemic equilibrium E^* by Theorem 4.7 in Magal and Zhao [34]. The proof of (ii) is completed. ∎

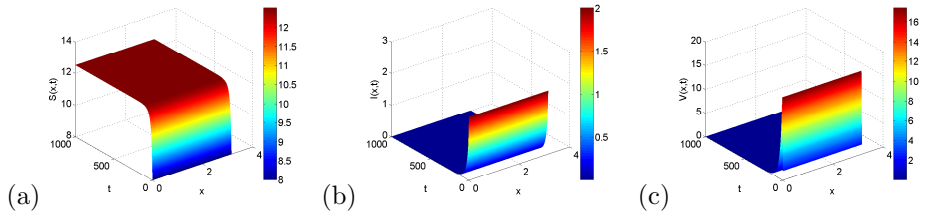

FIG. 6.1. *Numerical simulations on the asymptotic behavior of solutions to system* (3.1) *when* $\mathcal{R}_0 < 1$. (a) $S(x,t)$; (b) $I(x,t)$; (c) $V(x,t)$. *The parameter values are* $k = 4$, $r = 0.3$, $d = 0.08$, $\mu = 1$, $\tau = 6$, $\beta_1 = 0.001$, $\beta_2 = 0.0003$, $D_S = 0.05$, $D_I = 0.001$, $D_V = 0.1$, $D_L = 0.04$.

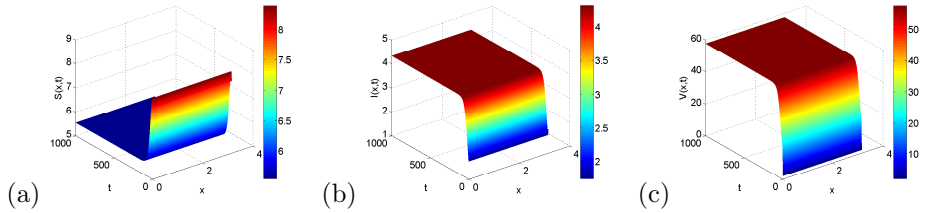

FIG. 6.2. *Numerical simulations on the asymptotic behavior of solutions to system* (3.1) *when* $\mathcal{R}_0 > 1$. (a) $S(x,t)$; (b) $I(x,t)$; (c) $V(x,t)$. *The parameter values are* $k = 4$, $r = 0.3$, $d = 0.08$, $\mu = 1$, $\tau = 6$, $\beta_1 = 0.01$, $\beta_2 = 0.001$, $D_S = 0.05$, $D_I = 0.001$, $D_V = 0.1$, $D_L = 0.04$.

6. Numerical simulations. In this section, we carry out some numerical simulations to verify the theoretical results obtained in previous sections. For convenience, let $\Omega = (0, \pi)$. Moreover, select the initial functions as follows:

$$\begin{aligned}
\phi_1(x,\theta) &= 8 + 10^{-6}\sin(x)\cos(\theta),\\
\phi_2(x,\theta) &= 2 + 10^{-6}\sin(x)\cos(\theta),\\
\phi_3(x,\theta) &= 2 + 10^{-6}\sin(x)\cos(\theta),
\end{aligned}$$

where $x \in \overline{\Omega}, \theta \in [-\tau, 0]$, and we have

$$\Gamma(x,y,\tau) = e^{-d\tau}\left(\frac{1}{\pi} + \frac{2}{\pi}\sum_{n=1}^{\infty} e^{-n^2 D_L \tau}\cos nx \cos ny\right).$$

The parameter k represents the excretion of airborne FMD virus, and we take $k = 4$ according to [49]. FMDV does not tolerate high temperature and can survive only 3 days in the summer; however, it can survive over the winter. So the natural decay rate of FMDV in the environment is taken as $r = 0.3$. According to the epidemiological characteristics of FMD, take $\tau = 6$. For illustrative purposes, choose $\mu = 1, d = 0.08$. Moreover, fix $D_S = 0.05, D_L = 0.04, D_I = 0.001, D_V = 0.1$, which means that

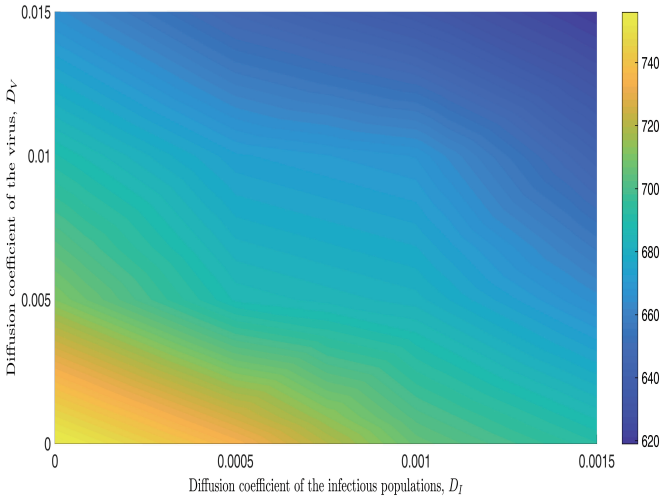

FIG. 6.3. *The effect of D_I, D_V on time from initial values to the endemic equilibrium. Fixing $k = 4$, $r = 0.3$, $d = 0.08$, $\mu = 1$, $\tau = 6$, $\beta_1 = 0.01$, $\beta_2 = 0.001$, we obtain $\mathcal{R}_0 = 1.717$. Setting diffusion coefficients $D_S = 0.01$, $D_L = 0.01$, and $D_I \in [0, 0.0015]$, $D_V \in [0, 0.015]$, the time from initial values to the steady state is shortened with the increase of the diffusion coefficient. The colorbar on the right represents time.*

the mobility of susceptible and latent individuals is greater than that of infectious individuals, and virus can diffuse faster. We make a remark on the choice of these diffusion coefficients.

REMARK 6.1. *The choice of diffusion coefficients is based on some quantitative relationships between compartments; that is, we assume that the virus spreads more quickly than all individuals and the infectious individuals disperse more slowly than other individuals. Thus, we choose the virus diffusion coefficient to be one order of magnitude higher than the others; those of the susceptible and latent individuals are one order of magnitude, and that of the infected individuals is one order of magnitude lower.*

Figure 6.1 reveals that the disease-free equilibrium E_0 of system (2.9) is globally asymptotically stable when $\mathcal{R}_0 = 0.672103 < 1$, which is consistent with the conclusion in Theorem 5.3(i). When $\mathcal{R}_0 = 1.717455 > 1$, we can observe that the solution of (2.9) tends to an equilibrium (see Figure 6.2). It also illustrates the uniform persistence of system (2.9) as in Theorem 5.3(ii).

Furthermore, we simulate the effect of diffusion on the time from initial values to the steady state when $\mathcal{R}_0 > 1$. We take initial value functions as $\phi_1(x, \theta) = 8 + \sin(x)\cos(\theta)$, $\phi_2(x, \theta) = 2 + \sin(x)\cos(\theta)$, $\phi_3(x, \theta) = 2 + \sin(x)\cos(\theta)$. The result shows that at a low infection level, the faster the infectious individuals and virus diffuse, the faster the disease reaches a steady state (see Figure 6.3). However, at a high infection level (i.e., the value of $\mathcal{R}_0$ is relatively large), the influence of diffusion on time from initial values to a steady state is more complicated, but at least it is certain that the time will be shortened overall.

In addition, fixing $k = 4$, $r = 0.3$, $d = 0.08$, $\mu = 1$, $\tau = 6$, $D_S = 0.05$, $D_I = 0.001$, $D_V = 0.1$, $D_L = 0.04$, we explore the impact of β_1 and β_2 on the spread of the disease.

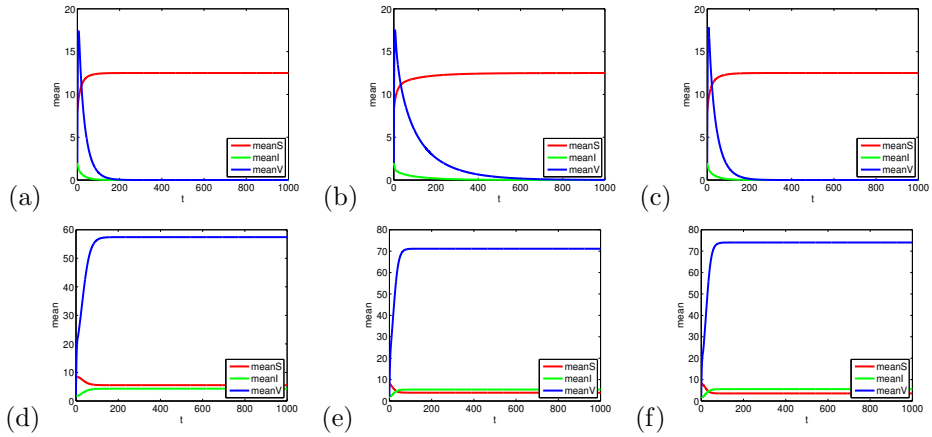

FIG. 6.4. *Plots of the mean values of* $S(x,t), I(x,t), V(x,t)$*, where the fixed parameter values are* $k = 4,\ r = 0.3,\ d = 0.08,\ \mu = 1,\ \tau = 6,\ D_S = 0.05,\ D_I = 0.001,\ D_V = 0.1,\ D_L = 0.04$. (a) $\beta_1 = 0.001, \beta_2 = 0.0003, \mathcal{R}_0 = 0.672103$. (b) $\beta_1 = 0.001, \beta_2 = 0.0006, \mathcal{R}_0 = 0.929147$. (c) $\beta_1 = 0.002, \beta_2 = 0.0003, \mathcal{R}_0 = 0.726040$. (d) $\beta_1 = 0.01, \beta_2 = 0.001, \mathcal{R}_0 = 1.717455$. (e) $\beta_1 = 0.02, \beta_2 = 0.001, \mathcal{R}_0 = 2.458133$. (f) $\beta_1 = 0.01, \beta_2 = 0.002, \mathcal{R}_0 = 2.160316$.

In the case when $\mathcal{R}_0 < 1$, we take three sets of parameter values. Under three different cases, changes of the mean numbers of $S(x,t), I(x,t), V(x,t)$ are simulated, respectively. Observing Figures 6.4(a) and 6.4(b), we find that as β_2 changes, the mean numbers of both $V(x,t)$ and $I(x,t)$ decrease more slowly. Comparing Figure 6.4(a) with Figure 6.4(c), we see that the increase of β_1 has little effect on the mean numbers of $I(x,t)$ and $V(x,t)$. These indicate that the air infection rate β_2 makes the disease go extinct more slowly than the direct contact infection rate β_1 when $\mathcal{R}_0 < 1$.

Similarly, when $\mathcal{R}_0 > 1$ we take three sets of parameter values to simulate the changes of the mean numbers of $S(x,t), I(x,t)$, and $V(x,t)$. Comparing Figure 6.4(d) with Figure 6.4(e), we observe that the mean number of $V(x,t)$ increases to nearly 70, whereas the change of $I(x,t)$ is not obvious as β_1 increases. By comparing Figure 6.4(d) with Figure 6.4(f), we obtain similar results when β_2 increases. In conclusion, we cannot determine which of the two transmission rates, β_1 and β_2, has a more significant impact on the spread of the disease. Hence, we apply sensitivity analysis to discuss the relative importance of model parameters to the disease transmission in next section.

7. Sensitivity analysis. In this section, we discuss the sensitivity of $\mathcal{R}_0$ and I^* to model parameters β_1 and β_2, respectively, for the case when $\mathcal{R}_0 > 1$. The normalized forward sensitivity index of a variable to a parameter is the ratio of the relative change in the variable to the relative change in the parameter. Specifically, the normalized forward sensitivity index of a variable u that depends differentiably on a parameter p is defined by (Chitnis, Hyman, and Cushing [7])

$$\Upsilon_p^u := \frac{\partial u}{\partial p} \times \frac{p}{u}. \tag{7.1}$$

Now, we consider the sensitivity of $\mathcal{R}_0$ to the parameters β_1 and β_2 in order to determine which one has a more significant impact on $\mathcal{R}_0$. By (7.1), we compute the

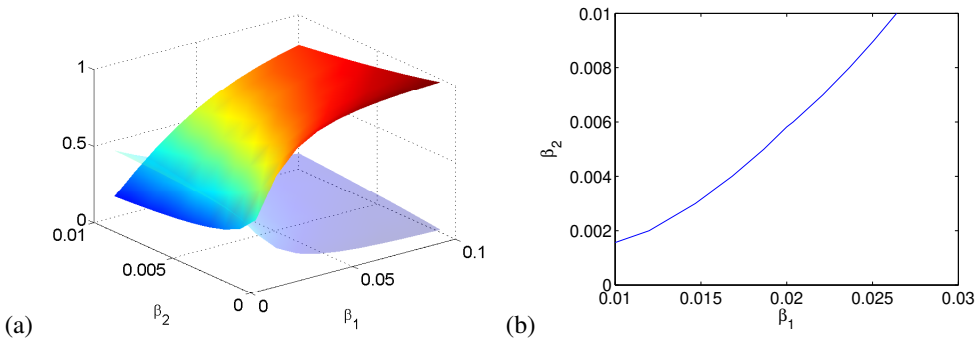

FIG. 7.1. *Sensitivity of $\mathcal{R}_0$ to β_1 and β_2.* (a) *The opaque surface presents the sensitivity of $\mathcal{R}_0$ to β_1, while the transparent one shows the sensitivity of $\mathcal{R}_0$ to β_2 in the (β_1, β_2)-plane.* (b) *The intersection of the two surfaces in* (a).

sensitivity index of $\mathcal{R}_0$ to β_1 and β_2 (denoted by $\Upsilon_{\beta_1}^{\mathcal{R}_0}$ and $\Upsilon_{\beta_2}^{\mathcal{R}_0}$) directly:

$$\Upsilon_{\beta_1}^{\mathcal{R}_0} = \frac{e^{-d\tau}\beta_1\mu}{\sqrt{(e^{-d\tau}\beta_1\mu)^2 + \frac{4\beta_2\mu k d^2 e^{-d\tau}}{r}}},$$

$$\Upsilon_{\beta_2}^{\mathcal{R}_0} = \frac{2d^2\mu k\beta_2 e^{-d\tau}}{\sqrt{(e^{-d\tau}\beta_1\mu)^2 + \frac{4\beta_2\mu k d^2 e^{-d\tau}}{r}}\, r(e^{-d\tau}\beta_1\mu + \sqrt{(e^{-d\tau}\beta_1\mu)^2 + \frac{4\beta_2\mu k d^2 e^{-d\tau}}{r}})}.$$

Now choose the same given parameter values as in the above numerical simulations; i.e., take $D_S = 0.05, D_I = 0.001, D_V = 0.001, D_L = 0.04, \mu = 1, k = 4, r = 0.3, d = 0.08, \tau = 6$, and let β_1, β_2 vary.

Combining Figure 7.1(a) with Figure 7.1(b), we can see that when the two parameters lie on the left of the intersection in the (β_1, β_2)-plane, the sensitivity of $\mathcal{R}_0$ to β_2 is higher than that of $\mathcal{R}_0$ to β_1; when the two parameters lie on the intersection curve, the sensitivity of $\mathcal{R}_0$ to β_1 is equal to that of $\mathcal{R}_0$ to β_2; when the two parameters lie on the right of the intersection in the (β_1, β_2)-plane, the sensitivity of $\mathcal{R}_0$ to β_1 is always higher than that of $\mathcal{R}_0$ to β_2. These demonstrate that the sensitivity of $\mathcal{R}_0$ to β_1 and β_2 varies with the infection coefficients lying in different regions. It is worth noting that the effect of β_1 on $\mathcal{R}_0$ is greater than that of β_2 when the values of β_1 and β_2 are very large or very small. From the biological perspective, direct contact infection has a more significant impact on the outbreak of FMD. Thus, to control the transmission of the disease the direct contact infection rate β_1 needs to be decreased significantly.

Next we consider the sensitivity of the equilibrium value of infectious individuals I^* to parameters β_1 and β_2. Since I^* has no specific expression, we use the method mentioned in Kong, Salceanu, and Wang [27] to calculate approximately the sensitivity index of I^* with respect to parameters β_1 and β_2. The specific formula is given as follows:

$$\Upsilon_{\beta_i}^{I^*} := \frac{I^*(1.01\beta_i) - I^*(0.99\beta_i)}{0.02I^*(\beta_i)}, \quad i = 1, 2. \tag{7.2}$$

From Figure 7.2(a), we first observe that the sensitivity index is positive, which means that I^* and β_1, β_2 all present the positive correlations. Second, we find that the

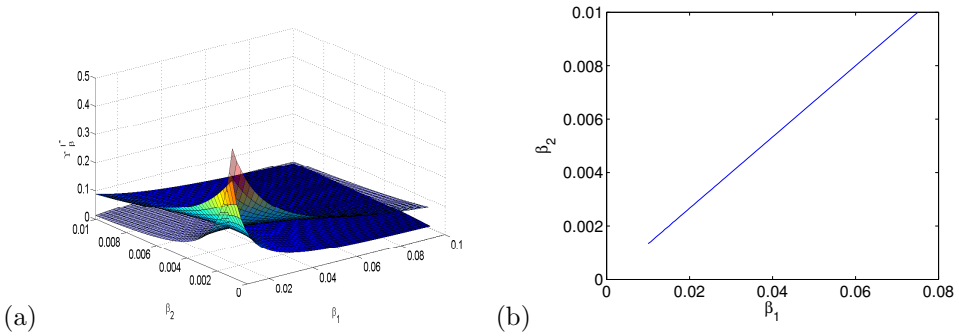

FIG. 7.2. *Sensitivity of I^* to β_1 and β_2.* (a) *The opaque surface shows the sensitivity of I^* to β_1, while the transparent one represents the sensitivity of I^* to β_2 in the (β_1, β_2)-plane.* (b) *The curve is the intersection of the two surfaces in* (a).

sensitivity of I^* to β_1 and β_2 declines with the increasing of β_1 and β_2, respectively. In Figure 7.2(b), I^* is more sensitive to β_1 when the two parameters lie on the left of the intersection in the (β_1, β_2)-plane. Thus, we can reduce the value of β_1 to lower the ultimate scale of the disease. I^* is more sensitive to β_2 when the two parameters lie on the right of the interaction in the (β_1, β_2)-plane. In this case, we can decrease the value of β_2 to reduce the ultimate scale of the disease. Once again, the sensitivity of I^* to β_1 and β_2 varies with the infection coefficients belonging to different regions.

8. Discussion. It has been reported that livestock movement is a crucial factor for the spatial spread of FMD, and there is a latent period between the moment of being infected and the moment of becoming infectious for animals. However, infectious animals in the present location x at the present time t were normally exposed in another location y at an earlier time $t - \tau$, and transmission happens continuously in the process of movement. In other words, nonlocal infection occurs in the transmission of FMD. In order to understand the spatio-temporal transmission dynamics of FMD and explore effective prevention and control measures, we proposed a diffusive FMD model with nonlocal infections (spatio-temporal delays) and obtained the basic reproduction number $\mathcal{R}_0$, a threshold in determining whether the disease will die out or become endemic. We showed that if $\mathcal{R}_0 < 1$ (or $\overline{\lambda}_0(\tau, S^0) < 0$), then FMD will disappear; otherwise, FMD will persist. Numerical simulations were performed to verify the theoretical results.

It is known that FMD can be transmitted by direct contact between infected animals and susceptible animals, as well as indirect contact with straw or hay that is contaminated by infected animals, with farm vehicles or milk tankers carrying infected milk, or even the surgical equipment of veterinary surgeons. It is not clear which contact route has a more significant impact on the transmission of the disease. Our numerical simulations in section 6 on the mean numbers of $S(x,t)$, $I(x,t)$, and $V(x,t)$ cannot determine which of the two transmission rates, β_1 (direct) or β_2 (indirect), has a more significant impact on the spread of the disease. Also, we studied the impact of diffusion on the spread of FMD in the case when $R_0 > 1$. In section 7, we performed sensitivity analysis of the basic reproduction number $\mathcal{R}_0(> 1)$ and the equilibrium value of the infectious individuals I^* in terms of β_1 and β_2. It is found that the (β_1, β_2)-plane is divided into two regions by the intersection of two parameter-related

surfaces; the sensitivity of $\mathcal{R}_0$ and I^* to β_1 and β_2 varies when the infection coefficients belong to different regions.

These results demonstrate that both the direct and indirect transmission routes have a significant impact on the transmission of the disease. Hence, a combination of strategies aimed at preventing and controlling both direct and indirect transmission is needed for FMD. When the disease prevails ($\mathcal{R}_0 > 1$), stamping out the infected individuals from the infected areas and blocking the epidemic spots and areas to cut off contact with outside animals are effective prevention and control measures. Moreover, thoroughly disinfecting the polluted environment to prevent the spread of pathogens is important to prevent indirect spread of the disease. In addition, we obtain the impact of diffusion on the spread of disease in the case of $\mathcal{R}_0 > 1$. Specifically, at a low infection level (i.e., the value of $\mathcal{R}_0$ is relatively small), the faster infectious individuals and virus diffuse, the faster the disease reaches the steady state.

Regarding environment transmission, we would like to mention that FMDV has the potential to spread over long distances under favorable climatic and meteorological conditions (Donaldson [12]; Gloster, Sellers, and Donaldson [17]), and it is reported that the spread of the virus exceeds 250km (Donaldson et al. [13]). Taking this into account, it will be interesting to consider nonlocal diffusion of the virus in the FMD model. With respect to the theoretical analysis of nonlocal diffusion problems including epidemic models with nonlocal diffusion, we refer the reader to Kot, Lewis, and van den Driessche [28]; Lee et al. [30]; Zhao and Ruan [60]; and Xu, Li, and Ruan [58]. In addition, we can consider the influence of wind on the spread of FMD (Cui, Lam, and Lou [8]; Kuto, Matsuzawa, and Peng [29]). Moreover, incorporating FMD data into the mathematical model is likely to predict the scale of the disease outbreak and provide effective control measures more precisely.

Diffusion is the collective behavior of passive random Brownian motions of individuals (originally, particles in chemistry or physics). However, the movement of living organisms includes both cognitive movement with memory and random movement. Recently, Shi, Shi, and Wang [46] studied the diffusive movement with cognitive memory of a single species. The idea can be modified and applied to epidemic models like the diffusive FMD model (2.9). This theoretical approach provides much more realistic results and induces intriguing mathematical challenges.

9. Appendix. $\mathcal{R}_0^{PDE} = \mathcal{R}_0^{ODE}$ in homogeneous environment. We first consider the following system:

$$\begin{cases} \dfrac{\partial U}{\partial t} = D\Delta U + \lambda FU - VU, \quad x \in \Omega, \lambda \in (0,\infty),\ t > 0, \\ \dfrac{\partial U}{\partial \vec{n}} = 0, \quad x \in \partial\Omega,\ t > 0, \end{cases} \tag{9.1}$$

where $U = (u_1, u_2, \ldots, u_m)^T$ denotes all the infected compartments, $D = \mathrm{diag}(D_1, D_2, \ldots, D_m)$ represents the diffusion matrix, and F, V are $m \times m$ matrices. Let $\widetilde{\mathcal{R}}_0(\lambda) = \lambda\widetilde{\mathcal{R}}_0$ be the basic reproduction number of (9.1), where $\widetilde{\mathcal{R}}_0$ is the basic reproduction number of (9.1) with $\lambda = 1$.

Consider the following ODE system:

$$\frac{dW}{dt} = \lambda FW - VW, \quad t > 0, \tag{9.2}$$

where F, V are $m \times m$ constant matrices. Let $\mathcal{R}_0(\lambda)$ be the basic reproduction number of system (9.2), where $\mathcal{R}_0$ is the basic reproduction number of (9.2) with $\lambda = 1$.

We prove that when $F(x) = F,\ V(x) = V$, the claim $\widetilde{\mathcal{R}_0} = \mathcal{R}_0$ holds; that is, $\widetilde{\mathcal{R}_0}$ in a homogeneous environment is the same as that of ODEs, and then, the number is independent of the diffusion.

Let Φ_t^λ, Ψ_t^λ be the solution map of system (9.1) and (9.2), respectively. It is easy to prove that for each $t > 0$, Φ_t^λ, Ψ_t^λ are compact and strongly positive operators. Let $r(\Phi_t^\lambda), r(\Psi_t^\lambda)$ be the spectral radius of Φ_t^λ, Ψ_t^λ, respectively. By the Krein–Rutman theorem [42], it follows that $r(\Phi_t^\lambda)$ is a simple eigenvalue of Φ_t^λ associated with a strongly positive eigenvector $\widetilde{\phi}$, and $r(\Psi_t^\lambda)$ is a simple eigenvalue of Ψ_t^λ associated with a strongly positive eigenvector ϕ.

Note that solutions of system (9.2) are also solutions of system (9.1) subject to the Neumann boundary condition. Let $W(t, \phi)$ be the solution of system (9.2). By the uniqueness of the principal eigenvalue, we have that $\phi = \widetilde{\phi}$. So,

$$r(\Phi_t^\lambda) = r(\Psi_t^\lambda). \tag{9.3}$$

According to Liang, Zhang, and Zhao [32], let $\widetilde{U}(t, s)$ and $\widetilde{W}(t, s)$ be the evolution operators of systems (9.1) and (9.2), respectively; then it can be seen that

$$\begin{cases} r(\widetilde{U}(t,0)) = r(\Phi_t^\lambda) = \widetilde{\mathcal{R}_0}, \\ r(\widetilde{W}(t,0)) = r(\Psi_t^\lambda) = \mathcal{R}_0. \end{cases} \tag{9.4}$$

Combining (9.3) and (9.4), we obtain $\widetilde{\mathcal{R}_0} = \mathcal{R}_0$.

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