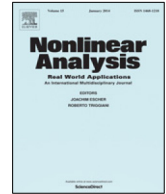




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Global dynamics of a West Nile virus model in a spatially variable habitat

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ABSTRACT

In this paper, we investigate a mathematical model that describes the transmission dynamics of West Nile virus (WNV) associated with the mosquito–bird population in a continuous bounded habitat. Our model is given by a spatial reaction–diffusion system with the zero-flux condition on the boundary, which is motivated by the models in the previous works of Wonham et al. (2004) and Lewis et al. (2006). By using the comparison theorem and the theory of uniform persistence, we show that the global dynamics of the model can be determined by two indices, mosquito reproduction number and infection invasion threshold.

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1. Introduction

West Nile virus (WNV) is an emerging mosquito-borne virus in North America. It was initially detected in New York City in 1999 and spread rapidly across the USA and Canada, and into Latin America and the Caribbean (see, e.g., [1,2]). Birds are known to be the natural reservoir of WNV, which is transmitted from bird to bird by mosquitoes. Mosquitoes become carriers when they feed on infected birds, and infected mosquitoes transmit the virus to birds when biting susceptible birds to take blood meals. It is likely that humans and other mammals are dead-end hosts since they can be infected by infectious mosquitoes, but

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they do not transmit the disease (see, e.g., [1,3]). Wonham et al. [4] focused on the shorter-term dynamics of a single season, and they proposed a system of ordinary differential equations modeling the interactions of female mosquitoes (vectors) and birds (reservoirs). Lewis et al. [5] further extended the model in [4] to include spatial factors, where they also assumed that removed birds can return to the susceptible class. The system in [5] takes the form of reaction–diffusion equations in the one dimensional whole space $\mathbb{R} = (-\infty, \infty)$, and the main concern is the existence of traveling wave fronts and the propagation of WNV.

In reality, the habitat of a host population is bounded and it is natural to model the transmission of WNV in a spatially bounded habitat. We intend to modify the model in [5] and investigate a reaction–diffusion system in a spatially bounded domain. Let $\Omega \subset \mathbb{R}^n$ be a spatial habitat with the smooth boundary $\partial\Omega$ and ν be the outward normal to $\partial\Omega$. Following [4–6], we divide the female mosquito population into uninfected (L_{V1}) and infected (L_{V2}) larval, susceptible (S_V), exposed (E_V) and infective (I_V) classes, respectively; we also divide the bird population into susceptible (S_R), infective (I_R) and removed (R_R) groups, respectively. We assume that all populations remain confined to the region Ω for all time, and supplement the Neumann boundary conditions to our equations. Then we consider

$$\left\{ \begin{aligned} \frac{\partial L_{V1}}{\partial t} &= b_V(x) (S_V + E_V + (1 - q)I_V) \left(1 - \frac{L_{V1} + L_{V2}}{K(x)} \right) \\ &\quad - m_V(x)L_{V1} - d_L(x)L_{V1}, \quad x \in \Omega, \quad t > 0, \\ \frac{\partial L_{V2}}{\partial t} &= qb_V(x)I_V \left(1 - \frac{L_{V1} + L_{V2}}{K(x)} \right) - m_V(x)L_{V2} - d_L(x)L_{V2}, \quad x \in \Omega, \quad t > 0, \\ \frac{\partial S_V}{\partial t} &= D_V \Delta S_V - \alpha_V(x)\beta_R(x) \frac{I_R}{S_R + I_R + R_R} S_V \\ &\quad + m_V(x)L_{V1} - d_V(x)S_V, \quad x \in \Omega, \quad t > 0, \\ \frac{\partial E_V}{\partial t} &= D_V \Delta E_V + \alpha_V(x)\beta_R(x) \frac{I_R}{S_R + I_R + R_R} S_V - (\kappa_V(x) + d_V(x))E_V, \quad x \in \Omega, \quad t > 0, \\ \frac{\partial I_V}{\partial t} &= D_V \Delta I_V + m_V(x)L_{V2} + \kappa_V(x)E_V - d_V(x)I_V, \quad x \in \Omega, \quad t > 0, \\ \frac{\partial S_R}{\partial t} &= D_R \Delta S_R + \Lambda_R(x) - \alpha_R(x)\beta_R(x) \frac{S_R}{S_R + I_R + R_R} I_V \\ &\quad + \eta_R(x)R_R - d_R(x)S_R, \quad x \in \Omega, \quad t > 0, \\ \frac{\partial I_R}{\partial t} &= D_R \Delta I_R + \alpha_R(x)\beta_R(x) \frac{S_R}{S_R + I_R + R_R} I_V - (\gamma_R(x) + d_R(x) + \delta_R(x)) I_R, \quad x \in \Omega, \quad t > 0, \\ \frac{\partial R_R}{\partial t} &= D_R \Delta R_R + \gamma_R(x)I_R - \eta_R(x)R_R - d_R(x)R_R, \quad x \in \Omega, \quad t > 0, \\ \frac{\partial \tilde{W}_V}{\partial \nu} &= \frac{\partial \tilde{W}_R}{\partial \nu} = 0, \quad x \in \partial\Omega, \quad t > 0, \quad \tilde{W} = S, E, I, \quad \tilde{W} = S, I, R. \end{aligned} \right. \tag{1.1}$$

Here, it is assumed that larval mosquitoes do not diffuse, and the diffusion rates for adult mosquitoes and birds are denoted by D_V and D_R , respectively; $b_V(x)$ represents the birth rate of larvae; $K(x)$ represents the carrying capacity of larval mosquitoes; q represents the probability of vertical transmission; $m_V(x)$ represents maturation rate of mosquitoes; $d_L(x)$, $d_V(x)$ and $d_R(x)$ represent the (natural) death rates of larvae, adult mosquitoes and birds, respectively; $\delta_R(x)$ is the disease-induced mortality rate of birds; $\Lambda_R(x)$ is the recruitment rate of susceptible birds; $\alpha_V(x)$ and $\alpha_R(x)$ represent WNV transmission probability per bite to mosquitoes and birds, respectively; $\beta_R(x)$ is the biting rate of mosquitoes on birds; $\kappa_V(x)$ represents the incubation rate of virus in mosquitoes; $\gamma_R(x)$ represents bird recovery rate from WNV; $\eta_R(x)$ stands for the rate of immunity loss of birds. In this paper, we always assume that all space dependent parameters in (1.1) are continuous and strictly positive.

In our model (1.1), we only consider the mosquito–bird cycle, and we extend the system in [5] to include the vertical transmission of mosquitoes (see, e.g., [6]) as well as the disease-induced mortality rate of birds.

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