



# Global behavior of solutions in a Lotka–Volterra predator–prey model with prey-stage structure



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## ABSTRACT

In this paper, the global behavior of solutions is investigated for a Lotka–Volterra predator–prey system with prey-stage structure. First, we can see that the stability properties of nonnegative equilibria for the weakly coupled reaction–diffusion system are similar to that for the corresponding ODE system, that is, linear self-diffusions do not drive instability. Second, using Sobolev embedding theorems and bootstrap arguments, the existence and uniqueness of nonnegative global classical solution for the strongly coupled cross-diffusion system are proved when the space dimension is less than 10. Finally, the existence and uniform boundedness of global solutions and the stability of the positive equilibrium point for the cross-diffusion system are studied when the space dimension is one. It is found that the cross-diffusion system is dissipative if the diffusion matrix is positive definite. Furthermore, cross diffusions cannot induce pattern formation if the linear diffusion rates are sufficiently large.

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## 1. Introduction

A single-species growth model with stage structure consisting of immature and mature stages was developed using a discrete time delay in 1990 in the pioneering paper [1] of Aiello and Freedman. In that paper the authors proved that the model possesses a globally asymptotically stable positive equilibrium point under suitable hypotheses. Questions concerning oscillation and nonoscillation of solutions were addressed analytically and numerically. The effect of the delay on the populations at equilibrium point was also considered. These results were generalized by Aiello, Freedman and Wu [2] to include a monotonically decreasing, state-dependent time delay. In recent years, the stage-structured models have been studied extensively, and many important phenomena have been observed (see e.g. [1–4] and the references therein).

In 2000, Zhang, Chen and Neumann established the following model of two species with stage structure and the relation of predator–prey in [3]:

$$\begin{aligned} \frac{dx_1}{dt} &= \alpha x_2 - r_1 x_1 - \beta x_1 - \eta x_1^2 - \beta_1 x_1 x_3, \\ \frac{dx_2}{dt} &= \beta x_1 - r_2 x_2, \\ \frac{dx_3}{dt} &= x_3(-r + k\beta_1 x_1 - \eta_1 x_3), \end{aligned} \quad (1.1)$$

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where  $x_1$  and  $x_2$  represent the densities of the immature and mature prey species at time  $t$ , respectively.  $x_3$  is the densities of predator species at time  $t$ . The parameters  $\alpha$ ,  $r_1$ ,  $r_2$ ,  $\beta$ ,  $\eta$ ,  $\beta_1$ ,  $r$ ,  $k$  and  $\eta_1$  are positive constants, and their biological meaning can be found in [3].

As in [3], for simplicity, we use the following scaling to (1.1):

$$u = \frac{k\beta_1}{r_2}x_1, \quad v = \frac{k\beta_1}{\beta}x_2, \quad w = \frac{\eta_1}{r_2}x_3, \quad \tilde{t} = r_2t,$$

and still denote  $\tilde{t}$  by  $t$ , then the system (1.1) becomes the form

$$\begin{aligned} \frac{du}{dt} &= av - bu - cu^2 - duw, \\ \frac{dv}{dt} &= u - v, \\ \frac{dw}{dt} &= w(-e + u - w), \end{aligned} \quad (1.2)$$

where

$$a = \frac{\alpha\beta}{r_2^2}, \quad b = \frac{r_1 + \beta}{r_2}, \quad c = \frac{\eta}{k\beta_1}, \quad d = \frac{\beta_1}{\eta}, \quad e = \frac{r}{r_2}.$$

It is obvious that (1.2) has the following three nonnegative equilibria: a trivial equilibrium point  $E_0 = (0, 0, 0)$ , a semi-trivial equilibrium point  $E_1 = (\frac{a-b}{c}, \frac{a-b}{c}, 0)$  if  $a > b$ , and a unique positive equilibrium point  $E_2 = (u_2, v_2, w_2)$  if and only if  $a > b + ce$ , where

$$u_2 = v_2 = \frac{a - b + de}{c + d}, \quad w_2 = \frac{a - b - ce}{c + d}.$$

In [3], the authors obtained the necessary and sufficient conditions for the permanence of two species and the extinction of one species or two species: (i)  $E_2$  is globally asymptotically stable if  $a > b + ce$ ; (ii)  $E_1$  is globally asymptotically stable if  $b < a \leq b + ce$ ; (iii)  $E_0$  is globally asymptotically stable if  $a \leq b$ .

Now we consider the following strongly coupled SKT cross-diffusion model

$$\begin{aligned} u_t &= \Delta(d_1u + \alpha_{11}u^2 + \alpha_{12}uv + \alpha_{13}uw) + av - bu - cu^2 - duw, \quad x \in \Omega, \quad t > 0, \\ v_t &= \Delta(d_2v + \alpha_{21}uv + \alpha_{22}v^2 + \alpha_{23}vw) + u - v, \quad x \in \Omega, \quad t > 0, \\ w_t &= \Delta(d_3w + \alpha_{31}uw + \alpha_{32}vw + \alpha_{33}w^2) + w(-e + u - w), \quad x \in \Omega, \quad t > 0, \\ \partial_\eta u(x, t) &= \partial_\eta v(x, t) = \partial_\eta w(x, t) = 0, \quad x \in \partial\Omega, \quad t > 0, \\ u(x, 0) &= u_0(x), \quad v(x, 0) = v_0(x), \quad w(x, 0) = w_0(x), \quad x \in \Omega, \end{aligned} \quad (1.3)$$

which was originally proposed by Shigesada et al. [5] in the case that  $u = v$ . The diffusion terms such as

$$\Delta[D_1(u, v, w)u], \quad \Delta[D_2(u, v, w)v], \quad \Delta[D_3(u, v, w)w]$$

are introduced to describe the situation that individuals are randomly walking and disperse repulsively (Okubo [6]). The biological interpretation is based on Morishita's phenomenological theory of 'environmental density' (Shigesada et al. [5]). This system (1.3) incorporates the movement of individuals subject to the dispersive force characteristic of self- and cross-population pressures. Here  $\Omega \subset \mathbb{R}^n$  is a bounded domain with smooth boundary  $\partial\Omega$  and  $\eta$  is the outward unit normal vector of the boundary  $\partial\Omega$ ,  $\partial_\eta = \partial/\partial\eta$ . The homogeneous Neumann boundary conditions indicate that this system is self-contained with zero population flux across the boundary. The functions  $u_0$ ,  $v_0$ ,  $w_0$  are nonnegative and not identically zero. The constants  $d_1$ ,  $d_2$  and  $d_3$ , called diffusion coefficients, are positive. The coefficients  $\alpha_{ii}$  ( $i = 1, 2, 3$ ) are referred as self-diffusion pressures, and  $\alpha_{ij}$  ( $i \neq j$ ,  $i, j = 1, 2, 3$ ) are cross-diffusion pressures. Self-diffusion implies the movement of individuals from a higher to a lower concentration region. Cross-diffusion expresses the population fluxes of one species due to the presence of the other species. The value of a cross-diffusion coefficient may be positive, negative or zero. The term positive cross-diffusion coefficient denotes the movement of the species in the direction of lower concentration of another species and the negative cross-diffusion coefficient denotes that one species tends to diffuse in the direction of higher concentration of another species. For more details on the biological backgrounds of cross-diffusion model one can see [5].

In recent years, the SKT type cross-diffusion systems have attracted much attention of a great number of investigators and have been successfully developed on the theoretical backgrounds [7–15] (see also the references therein). The above work mainly concentrates on: (1) the instability and stability induced by cross-diffusion, and the existence of nonconstant positive steady-state solutions [7,8]; (2) the global existence of strong solutions [9–11]; (3) the global existence of weak solutions based on semi-discretization or finite element approximation [12,13]; and (4) the asymptotic behavior [14,15].

In this paper, we mainly study three problems for the model (1.3). First, we attempt to discuss the influences of diffusion on stability of the weakly coupled reaction–diffusion system, i.e.  $\alpha_{ij} = 0$ ,  $i, j = 1, 2, 3$ . Second, we use Sobolev embedding

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