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Stationary Distribution and Extinction of Stochastic Beddington-DeAngelis Predator-prey Model with Distributed Delay

Mingyu Song[1], Wenjie Zuo[1,†], Daqing Jiang[1,2] and Tasawar Hayat[2]

Abstract In this paper, we consider the dynamics of the stochastic Beddington-DeAngelis predator-prey model with distributed delay. First, we adopt the linear chain technique to transfer the stochastic system with strong kernel into an equivalent degenerated stochastic system made up four equations. Then we give the existence and uniqueness of the global positive solution. Next, sufficient conditions for persistence and extinction of two species are obtained. Particularly, the existence of the stationary distribution is established by constructing a suitable Lyapunov function. Finally, numerical simulations illustrate our theoretical results. It shows that the system still maintains the stability for the smaller white noises, but the stronger white noises will lead to the extinction of one or two species.

Keywords stochastic Beddington-DeAngelis predator-prey model, Distributed delay, Stationary distribution, Extinction.

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1. Introduction

Predator-prey systems describing the dynamic relationship between two species have long been and will continue to be the focus in an existing ecosystem. Predator-dependent functional response is the significant component describing the predator-prey relationship (see [1–3]). Particularly, the Beddington-DeAngelis functional response plays an important role in feeding over a range of predator-prey abundances [4–7]. Cantrell et al. [8] and Hwang [9] studied a classical predator-prey system with Beddington-DeAngelis response as follows:

$$\begin{aligned} \frac{dx}{dt} &= b_1 x\left(1-\frac{x}{k}\right)-\frac{a_{12}xy}{m_1+m_2x+m_3y}, \\ \frac{dy}{dt} &= -b_2 y+\frac{a_{21}xy}{m_1+m_2x+m_3y}, \end{aligned} \tag{1.1}$$

where $x(t)$ and $y(t)$ denote the prey and predator densities at time t respectively. And b_1 and k are intrinsic growth rate of the prey and carrying capacity of the envi-

[†]the corresponding author. Email address: zuowjmail@163.com(W. Zuo)
[1]College of Science, Key Laboratory of Unconventional Oil Gas Development, China University of Petroleum (East China), Qingdao, Shandong 266580, China
[2]Nonlinear Analysis and Applied Mathematics (NAAM)-Research Group, Department of Mathematics, Quaid-I-Azam University, Islamabad, 44000, Pakistan

ronment in the absence of predator, b_2 is the death rate of the predator. The predator consumes the prey with Beddington-DeAngelis functional response $\frac{a_{12}xy}{m_1+m_2x+m_3y}$ and contributes to its growth rate $\frac{a_{21}xy}{m_1+m_2x+m_3y}$. All parameters are assumed to be positive.

It is known that [8, 9] , if $b_2 \geq \frac{a_{21}k}{m_1+km_2}$, then system (1.1) has two boundary equilibria $(0,0),(k,0)$. And $(k,0)$ is globally asymptotically stable. If $0 < b_2 < \frac{a_{21}k}{m_1+km_2}$, then system (1.1) has three nonnegative equilibria $(0,0)$, $(k,0)$ and (x_*, y_*), where (x_*, y_*) is positive and satisfies the following equation:

$$\frac{b_1a_{21}}{m_3ka_{12}}x_*^2 - \left(b_2m_2 + \frac{b_1a_{21}}{m_3a_{12}} - a_{21}\right)x_* - b_2m_1 = 0,$$
$$y^* = \frac{(a_{21} - b_2m_2)x^* - b_2m_1}{b_2m_3}.$$

And the local and global asymptotic stabilities of (x_*, y_*) coincide.

On the other hand, the growth of biological organisms may depend on the population density of previous time. Distributed delay has been widely introduced into equations used in mathematical biology (see [10–13]). Some authors (see e.g. [10,14]) studied the stability and the bifurcation of a predator-prey model with distributed delay. A classical Beddington-DeAngelis predator-prey system with distributed delay is as follows:

$$\begin{cases} \dfrac{dx}{dt} = b_1x\left(1-\frac{x}{k}\right) - \frac{a_{12}xy}{m_1+m_2x+m_3y}, \\ \dfrac{dy}{dt} = -b_2y + a_{21}\int_{-\infty}^{t}\frac{K(t-s)x(s)y(s)}{m_1+m_2x(s)+m_3y(s)}ds. \end{cases} \tag{1.2}$$

In addition, in the natural environment, the growth rate of biological population is inevitably affected by white noises. In some cases, white noise will have a huge impact on the size of the biological population and the evolution of biological population. Some researchers [15–18] studied stationary distribution and extinction of a kind of predator-prey model with stochastic disturbance.

In this article, we assume that the intrinsic growth rates b_1 and b_2 of the prey and the predator are disturbed with:

$$b_1 \to b_1 + \alpha_1\dot{B}_1(t),\ b_2 \to b_2 + \alpha_2\dot{B}_2(t),$$

where $B_1(t)$, $B_2(t)$ are independent Brownian motion, α_1^2 and α_2^2 represent the intensity of the white noises, respectively. Then system (1.2) can be transformed into the following stochastic model:

$$\begin{cases} dx = \left(b_1x\left(1-\frac{x}{k}\right) - \frac{a_{12}xy}{m_1+m_2x+m_3y}\right)dt + \alpha_1xdB_1(t), \\ dy = \left(-b_2y + a_{21}\int_{-\infty}^{t}\frac{K(t-s)x(s)y(s)}{m_1+m_2x(s)+m_3y(s)}ds\right)dt - \alpha_2ydB_2(t). \end{cases} \tag{1.3}$$

We focus on two well-known ones: the strong kernel and the weak kernel, respectively, represented by

$$(1)\ K(t) = \sigma^2te^{-\sigma t}\ ,\ (2)\ K(t) = \sigma e^{-\sigma t}.$$

These two kinds of kernels have been widely used in many fields of biological system, such as population system [19], neutral network [20, 21] and epidemiology [22].