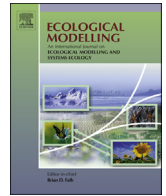




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Dynamic analysis of time fractional order phytoplankton–toxic phytoplankton–zooplankton system

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ABSTRACT

In this paper, we study the dynamics of a time fractional order toxic-phytoplankton–phytoplankton–zooplankton system (TPPZS). Routh–Hurwitz criteria is applied to discuss the stability analysis of biologically feasible equilibrium points for the given system in terms of reproduction numbers (associated with ecological as well as disease phenomena). Local stability properties of the toxic-phytoplankton-free equilibrium are also investigated. Numerical simulations are performed for a hypothetical set of parameter values in support of our analytic results.

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1. Introduction

The dynamics of rapid change of plankton populations (organisms living in water column who cannot swim against a current) is an important area of research in marine plankton ecology. Availability of inorganic nutrients and conducive environment (temperature and salinity levels) give rise to a massive growth of algae. Planktonic bloom formation results in massive cell lysis and rapid disintegration of large planktonic populations. They are found to be a crucial source of energy for many large aquatic organisms such as fish and whales. The importance of plankton for the wealth of the aquatic ecosystem and ultimately for the planet itself is now a days widely recognized. Phytoplankton, an important part of the marine ecosystem, constitute a basis for all aquatic food chains and produce a huge amount of oxygen after absorbing carbon-dioxide from surrounding environments. Marine Phytoplankton are free-floating microscopic plants that are mostly unicellular and produce chemical energy from light. This process is called primary production. Phytoplankton have a critical role in primary production, nutrient cycling, and food webs. The growing phytoplankton population causes rapid increase of biomass due to rapid cell proliferation and almost equally rapid

decrease in populations, separated by some fixed time period. This type of rapid change in phytoplankton population density is known as ‘bloom’. With the accumulation of high level toxic biomass, some of these blooms become noxious to marine ecosystems and human health, and can cause great socioeconomic damage. In view of the difficulty in measuring plankton biomass, mathematical modeling of plankton population has evolved into an important field of investigation for understanding the physical and biological processes related to plankton ecology. Phytoplankton are the food source for numerous other organisms, especially the zooplankton (microscopic animals). Zooplankton grazers can significantly decrease phytoplankton density and serve as a most favorable food source for other aquatic animals. For more details, see the text (Dawes, 1998). Despite the fact that harmful phytoplankton species occur and bloom, the form of definition of a harmful species is qualitative. The issues like identification of such species, the modes and mechanisms for determining harmful effects, and ecophysiological divergence of harmful taxa from species considered to be non-harmful need to be addressed. Also an important investigation relates to the extent to which such blooms impair or disrupt ‘equilibrium’ trophodynamics and whether they fall within the variance in natural catastrophic events that shape the equilibrium. During the recent years, many authors have studied the system between zooplankton and phytoplankton. Although mathematical models to study algae blooms are regarded as traditional, the investigation of these phenomena behind the related mechanism is still in progress.

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Toxin-producing phytoplankton (TPP) are capable of producing some toxic chemicals (Chattopadhyay et al., 2002; Sarkar et al., 2005) and significantly affect the dynamics of phytoplankton and zooplankton (Kirk and Gilbert, 1992; Kozłowski-Suzuki and et, 2003). In recent years, a number of studies have been conducted to investigate the effects of TPP species on the overall dynamics of phytoplankton and zooplankton (Roy et al., 2006; Roy and Chattopadhyay, 2007). In Chowdhury et al. (2008), a mathematical model of non-toxic phytoplankton (NTP) and toxic phytoplankton–zooplankton with constant and variable zooplankton migration is proposed and analyzed. Roy (2009) developed a mathematical model for describing the interaction between a non-toxic and a toxic phytoplankton under a single nutrient. In Yunfei et al. (2010), a phytoplankton–zooplankton model with harvesting is proposed and investigated. In Mukhopadhyay and Bhattacharyya (2006), the authors proposed a nutrient–plankton model in an aquatic environment in the context of phytoplankton bloom. Though the mathematical models to study algae blooms are regarded as classical (Truscott and Brindley, 1994), yet the investigation of these phenomena together with the related mechanisms is still in progress (Freund et al., 2006). The manifestation in new geographic areas and the increase in the number of blooms of both toxic as well as non-toxic algae species are reported in Smayda and Shimizu (1993). In Mukhopadhyay and Bhattacharyya (2006), a nutrient–plankton model in an aquatic environment in the context of phytoplankton bloom is discussed. Models of nutrient–plankton interaction with a toxic substance that inhibits either the growth rate of phytoplankton, zooplankton or both trophic levels are proposed and studied in Janga et al. (2006).

In Singh et al. (2004), the authors proposed a prey–predator model for the phytoplankton–zooplankton system with the assumption that the viral disease is spreading only among the prey species, and the infected prey is more vulnerable to predation – a natural observation, though the predator feeds on both the susceptible and infected prey. The dynamic behavior of the system is investigated from the point of view of stability and persistence. The model shows that infection can be sustained only above a threshold of the force of infection. Gakhar and Negi (2006) investigated the dynamic behavior of toxin producing phytoplankton and zooplankton. The phytoplankton are divided into two groups, namely, susceptible phytoplankton and infected phytoplankton. Several studies based on field data and experiments show that zooplankton may react to the presence of toxic phytoplankton by reducing its consumption up to the point of starvation. Banerjee and Venturino (2011) proposed a mathematical system to model this situation using a Monod–Haldane response function (Pal et al., 2009). Their results indicate that the underlying mechanism ensures that the toxic phytoplankton group does not drive the zooplankton population toward extinction. For some recent results on the topic, we refer the reader to Javidi and Nyamoradi (2014), Wang et al. (2014), Rehim et al. (2015) and Wang et al. (2015).

Fractional-order calculus, regarded as the generalization of classical integer-order calculus to real or complex order, has gained much popularity from theoretical as well as application viewpoints. There has been much interest in developing the theoretical analysis and numerical methods for fractional differential equations. Fractional differential equations have recently proved to be an effective and valuable modeling tool in various fields of science and engineering. Indeed, we can find numerous applications in polymer rheology, regular variation in thermodynamics, biophysics, blood flow phenomena, aerodynamics, electro-dynamics of complex medium, viscoelasticity, Bode analysis of feedback amplifiers, capacitor theory, electrical circuits, electro-analytical chemistry, biology, control theory, fitting of experimental data, etc. (Samko et al., 1993; Podlubny, 1999; Kilbas et al., 2006; Sabatier et al., 2007; Chang and Nieto, 2009; Lakshmikantham et al., 2009; Bai, 2006). For

further details and examples, we refer the reader to the works in Liang and Zhang (2009), Bai and Lu (2005), Benchohra et al. (2008), El-Sayed et al. (2007), Feng et al. (2011), Lakshmikantham and Vatsala (2008), Ahmad and Nieto (2010), Henderson and Ouahab (2009) and the references cited therein.

Recent works (Ahmed and Elgazzar, 2007; Ahmed et al., 2007; Ding and Ye, 2009; Ye and Ding, 2009) on the qualitative properties and numerical solutions of fractional-order biological models have motivated many investigators and a variety of quality results on the topic are appearing on regular basis. It has been mainly due to the reason that fractional-order equations are naturally related to systems with memory which is a common feature of many biological phenomena. In fact, such equations are closely related to fractals which are abundant in biological systems. Yan and Kou (2012) studied stability properties of a fractional-order differential equation and applied their results to analyze the stability of the equilibria for the model of HIV-1 infection. In Ahmed et al. (2007), the fractional-order predator–prey model and the fractional-order rabies model were investigated. In Ahmed and Elgazzar (2007), a fractional-order model for nonlocal epidemics was investigated and some stability results related to foot-and-mouth disease, SARS and avian flu were obtained. Ding and Ye (2009) and Ye and Ding (2009) introduced some kinds of models for HIV infection and considered the stability properties of the equilibria of the corresponding systems.

Recently, more and more investigators have initiated their research to study the qualitative properties and numerical solutions of fractional-order biological models (Ahmed and Elgazzar, 2007; Ahmed et al., 2007; Ding and Ye, 2009; Ye and Ding, 2009). The main reason is that fractional-order equations are naturally related to systems with memory which exists in most biological systems. Also they are closely related to fractals which are abundant in biological systems. Yan and Kou (2012) have studied stability properties of a fractional-order differential equation and applied their results to analyze the stability of the equilibria for the model of HIV-1 infection.

In Ahmed et al. (2007), the fractional-order predator–prey model and the fractional-order rabies model were investigated to obtain the existence and uniqueness of solutions, the stability of equilibrium points, and numerical solutions for these models. In Ahmed and Elgazzar (2007), the authors studies a fractional-order model for nonlocal epidemics and found some results related to foot-and-mouth disease, SARS and avian flu. Ding and Ye (2009) and Ye and Ding (2009) have also introduced some kinds of models of HIV infection and considered the stability properties of the equilibria of the corresponding systems.

In this manuscript, we investigate a particular issue that would be highlighted under the presentation of the biological background, namely the fact that in presence of toxic phytoplankton, the zooplankton feed them on, what the mechanism is to ensure the toxic phytoplankton group does not drive the zooplankton population toward extinction. For this purpose, we consider the time fractional analog of model problem discussed in Banerjee and Venturino (2011) for phytoplankton–toxic phytoplankton–zooplankton system given by

$$\begin{aligned} \frac{d^\alpha P}{dt^\alpha} &= F_1(P, T, Z) = r_1 P \left(1 - \frac{P}{H_1}\right) - aPT - cPZ, \\ \frac{d^\alpha T}{dt^\alpha} &= F_2(P, T, Z) = r_2 T \left(1 - \frac{T}{H_2}\right) - bPT - TZ, \\ \frac{d^\alpha Z}{dt^\alpha} &= F_3(P, T, Z) = ePZ - TZ - mZ, \end{aligned} \quad (1)$$

$$P(\delta) = P_0 > 0, \quad T(\delta) = T_0 > 0, \quad Z(\delta) = Z_0 > 0,$$

where d^α/dt^α denotes Caputo fractional differential operator of order $\alpha \in (0, 1]$, and $Z(t)$, $P(t)$, $T(t)$ respectively denote the

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