On a stochastic reaction–diffusion system modeling pattern formation on seashells

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Abstract Starting from the Gierer–Meinhardt setting, we propose a stochastic model to characterize pattern formation on seashells under the influence of random space–time fluctuations. We prove the existence of a positive solution for the resulting system and perform numerical simulations in order to assess the behavior of the solution in comparison with the deterministic approach.

Keywords Pattern formation · Stochastic reaction–diffusion equations

Mathematics Subject Classification (2000) 60H15 · 35K57 · 92C15

1 Introduction

Seashells exhibit a huge variety of beautiful, highly complex patterns. This diversity, often within the same species, is one of the reasons making the study of pattern formation on molluscs such an interesting issue. One would like to know whether a single or some few mechanisms are able to generate this wide spectrum of patterns and how this can be explained in a comprehensive way.

Since the seminal paper of Turing (1952), reaction–diffusion systems increasingly became a powerful tool for mathematically describing pattern formation. These model the dynamics of the distribution of chemicals which diffuse within a domain and interact with each other. Accordingly to the Turing approach, patterns arise as a
consequence of one of the involved chemicals activating the pigment production by certain cells and its storing in the skins or shells of animals.

In his work Turing (1952) showed how the interplay between diffusion and nonlinear reactions (the so-called diffusion driven instability) can lead to spatial pattern formation. Since then many examples of systems have been proposed, which are able to explain patterns based on this mechanism. For overviews and comparisons between the models we refer to the works of Murray (1982, 2003).

Meinhardt and Klingler (1987) and Meinhardt (2003) have been concerned with modeling and computer simulations of patterns on seashells, as well as their interpretation in the framework of biochemical processes. Another direction is to investigate the Gierer–Meinhardt system for patterns on molluscs (Gierer and Meinhardt 1972) from a qualitative viewpoint with the aid of dynamical systems methods (see, e.g. Wei and Winter 2001, 2002; Granero-Porati and Porati 1984). This issue has already been mentioned in Meinhardt and Gierer (1974) and used to understand a particular biological problem, namely the chemotactic orientation of a cell. In Wei and Winter (2001, 2002) it is shown that the respective reaction–diffusion system is able to describe under certain conditions the generation of a special kind of patterns, the so-called spikes, while in Granero-Porati and Porati (1984) is evidenced the possibility of time oscillations. The existence of solutions to reaction–diffusion systems has also attracted considerable interest. Thus, Rothe (1984) proved the existence of a global solution based on the method of semigroups of operators and later his result was further improved. A newer result on global solutions to the Gierer–Meinhardt system can be found in Jiang (2006).

Recently, we have shown in Kelkel and Surulescu (2009) the existence of a local weak solution for general initial conditions and parameters upon using an iterative approach and avoiding the usual proof relying on semigroup techniques. Furthermore, a global solution was shown to exist for suitable initial data. In the present paper we make use of the approach in Kelkel and Surulescu (2009) in a stochastic framework, in order to show the existence of a local solution to an adequately constructed stochastic version of the Gierer–Meinhardt system.

Reaction–diffusion systems are mostly deterministic models, meaning that at every time moment the solutions can be inferred from the data. This is actually in contradiction with phenomena happening in nature, where random influences can play an important role. Thus, the parameters of the system depend on the environment, where many different events occur continuously. Due to their complexity the latter can be conceived as random fluctuations. Moreover, the biochemical processes within the shell can also infer stochastic variations. Diffusion and chemical reactions are by their very nature random; it is only by idealising assumptions (like a very large amount of particles and/or motion in a homogeneous medium) that they receive a deterministic description, however these assumptions are rarely realistic.

Motivated by these issues, Ishikawa and Miyajima (2005) proposed a system of stochastic partial differential equations (SPDEs) as an extension of the deterministic Gierer–Meinhardt model. They were only concerned with the numerical simulations of

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1 For a comprehensive introduction to these topics we refer, e.g. to Evans (1999).