Transitions induced by cross-correlated bounded noises and time delay in a genotype selection model

Pei Liu, Li Juan Ning*

College of Mathematics and Information Science, Shaanxi Normal University, Xi’an 710062, China

HIGHLIGHTS

• Genotype selection model interplay with cross-correlated noises and time delay is investigated.
• Transition induced by cross-correlated bounded noises in the systems is observed.
• As time delay increases, probability distribution transfers from unimodal to bimodal.
• The system undergoes a new transition to four stable states for large correlation time.

ARTICLE INFO

Article history:
Received 5 April 2015
Received in revised form 12 June 2015
Available online 8 September 2015

Keywords:
Transitions
Time delay
Bounded noises
Genotype selection model

ABSTRACT

We present a numerical investigation of occurrence of transitions in a genotype selection model with time delay, where two bounded noises are cross-correlated. Stationary probability distribution (SPD) function is obtained. It is found that: the multiplicative bounded noise can facilitate the gene separation and it plays a constructive role in the genetic selection progress, while the additive bounded noise suppresses the gene separation. The strong correlation between noises gives a big chance to one type haploid out of the group. Besides, what is more interesting is that the correlation time $\tau$ can induce a new transitions (i.e., the curve of the SPD changes from unimodal to bimodal, and then to four peaks as the correlation time $\tau$ increases).

© 2015 Elsevier B.V. All rights reserved.

1. Introduction

The influence of noise on nonlinear systems has proved to be of considerable interest in recent years. Noise can play a constructive role in nonlinear systems, which is shown in many experimental facts. These researches include mean first-passage time analysis [1,2], steady-state analysis [3,4], stochastic transitions [5,6], stochastic resonance [7–10] and other effect. Stochastic transitions, as one of the most interesting phenomena induced by noise in random dynamical systems, has become a rapid and hot topic for physics, chemistry, economics and biology [1–10], and is generally characterized with a qualitative change of the SPD, e.g., a transition from unimodal to bimodal distribution or vice versa. In Ref. [11], the authors explored a molecular regulatory systems with three different types noise sources. Result shows that the type of noise determines the strongly attracting steady state or stochastic attractor. In Ref. [12], the authors demonstrated the issue of how intrinsic noise modulates stochastic switching rate using two scenario. Since the roles and benefits of stochastic phenomena in natural systems are starting to be elucidated, it becomes relevant to characterize the features of such stochastic phenomena in terms of the driving fluctuations.

* Corresponding author.
E-mail address: ninglijuan@snnu.edu.cn (L.J. Ning).
Stochastic fluctuations are ubiquitous in any real natural dynamical system. In particular, living organisms are subject to fluctuations (or noise) of distinct origins. At a cellular level, it is a well-known fact that biochemical reactions inside a cell are stochastic events and present inherent randomness. These fluctuations can have disturbing or ordering roles. For instance, noise may act as a trigger for phenotypic variability since the exploration of the phase space through different types of dynamics [13–15]. However, in most of the previous works, the fluctuation was assumed to be Gaussian process, which is unbounded and may reach large values [16,17]. This fact contradicts the very nature of a real physical quantity which is always bounded [18,19]. The conclusions that have been built on Gaussianity assumptions should be reconsidered and a more suitable model for the bounded interference is required. Many experiments in physics, biology, engineering [20], neural networks [21,22], as well as sensory systems [23–25], have proved that the noise source in these systems is general bounded noise. Based on such a consideration, M.F. Dimentiong [26] and W.V. Wedig [27] put forward a versatile model for bounded random processes, by using a sinusoidal function with a constant amplitude, a constant average frequency and a random phase varying as a Wiener process. Meanwhile, another type of bounded noise is well-known as sine-Wiener (SW) noise [19], which induces transitions in different models [19,28,29]. Nevertheless, the investigations of dynamical systems with bounded noise are complicated [19,20,30], and the research in this field is pretty rare so far. In addition, time delay is unavoidable in nature, and the inclusion of time delay term is more reasonable in realistic systems. From the point of physics, time delay, which plays an important role in the dynamical properties of stochastic systems [31,32], usually arises from the finite transport time of matter, energy and information. However, most studies neglect the possible effect caused by time delay. This is mainly because of the difficulty in analytic methods of dealing the non-Markovian nature of the delayed stochastic systems [33,34].

Recently, the investigations of dynamical actions in genetic selection process have drawn widespread concern due to its wide potential application, such as gene separation, biological evolution, bio-pharmacy and so on. It is necessary to understand selection mechanism and develop relevant strategies to satisfy our human demands. In literatures [35,36], the genotype selection model only driven by multiplicative noise has been studied. It indicates that white multiplicative noise can induce transitions. Zhang and Cao researched the effect of correlated noise on genetic model [37]. The effect of Ornstein–Uhlenbeck noise on genetic has been studied in Refs. [36,38,39], and the effect of a non-Gaussian noise on that model have been investigated in Ref. [40]. F. Castro et al., for first time in Ref. [41], found the reentrance behavior in the genic model, which is subjected to a multiplicative color noise source. All these researches reveal that non-extensive parameter can induce transitions which contributes to gene selection. Environmental fluctuation plays a crucial role in gene selection. Meanwhile, the effect of time delay on a genotype selection model driven by white multiplicative noise has been investigated in Ref. [42], which shows that time delay is an important parameter affecting transitions, and it is helpful to select one type of genes from another type of mixing genes. However, all these works neglected the bounded nature of noise, which is more reasonable for the real physical quantity. Therefore, it is worthy to introduce suitable bounded noise in to a genotype selection progress. Moreover, the synergistic effect of bounded noise with time delay on the genetic selection progress should be further researched.

In this paper, we aim to explore random dynamical behaviors of a genotype selection model with time delay in the present of cross-correlated sine-Wiener (CCSW) noises, which is expected to be a more powerful tool to demonstrate the interactions between the genotype selection system and its surrounding. In particular, we will concern the stochastic transitions induced by CCSW noises and time delay, and its biological interpretations. The paper is organized as follows. Section 2 is devoted to the model with time delay, driven by cross-correlated sine-Wiener noises. In Section 3, based on the SPD of the model, transitions induced by noises and time delay are discussed. In Section 4, we end the paper with concluding remarks.

2. Model and CCSW noises

2.1. Model

We select a haploid group as our object and suppose that each haploid may have gene A or B. The simple genotype selection model can be described as one-variable differential equation [35,36,43],

\[
\dot{x} = \beta - x + \mu x(1 - x),
\]

(1)

where \(x\) is the ratio of the number of gene A to the total number, so \(x \in [0, 1]\). \(\beta\) stand for the mutation rate of gene B, \(\mu \in (0, 1)\). \(\mu\) denote gene selection factor, \(\mu = 1\) means that the selection is completely propitious to gene A haploid, \(\mu = -1\) means that the selection is completely propitious to gene B haploid. No matter how the parameter \(\beta\) or \(\mu\) changes, this equation has only one equilibrium point in the corresponding interval, i.e.,

\[
x_0 = \frac{\mu - 1 + \sqrt{(\mu - 1)^2 + 4\beta\mu}}{2\mu}.
\]

This result indicates that there is no phase transition during the process of gene selection for the deterministic Eq. (1).

Notice that the second term in Eq. (1) represents gene transformation and regeneration. There should be a reaction time of gene number to their surrounding environment fluctuation. Supposing a constant delay time \(\tau_o\), \(x\) item should become \(x(t - \tau_o)\).
Furthermore, environmental variability has been considered an important element that should be included in the modeling of genotype selection system. We notice that the gene select factor $\mu$ can be affected by the extrinsic environment, i.e., the fluctuations generated from extrinsic noise. That is $\mu \rightarrow \mu + \xi(t)$, where $\xi(t)$ is the extrinsic noise. At the same time, this system is affected by viability and intra-specific struggle of the population, etc., which give rise to intrinsic noise, denoted by $\eta(t)$. Therefore, the stochastic differential delayed equation for the system corresponding to Eq. (1) can be rewritten as

$$\dot{x} = \beta - x(t - \tau_x) + \mu x(1 - x) + x(1 - x)\xi(t) + \eta(t),$$

(2)

where $\xi(t)$ and $\eta(t)$ are CCSW noises, and the precise definition will be given below. Fig. 1 depicts the evolution of the stochastic genotype system.

2.2. CCSW noises

$\xi(t)$ and $\eta(t)$ are given by two SW noises firstly $[19]$,

$$\xi(t) = D \sin \left( \frac{2}{\tau_1} w_1(t) \right),$$

(3)

$$\eta(t) = Q \sin \left( \frac{2}{\tau_2} w_2(t) \right),$$

(4)

here $\tau_1$ and $\tau_2$ are the correlation times of $\xi(t)$ and $\eta(t)$, respectively; $D$ and $Q$ are noise intensities of them, $D \geq 0$ and $Q \geq 0$; $w_1(t)$ and $w_2(t)$ are two standard Wiener processes cross-correlated. Using the properties of the Wiener process and the Euler representation of the sine function, one can obtain the statistical properties of the CCSW noises $[3,44]$. As $t \geq s$, we have

$$\langle \xi(t) \rangle = \langle \eta(t) \rangle = 0,$$

(5)

$$\langle \xi(t) \xi(s) \rangle = \frac{D^2}{2} \exp \left( -\frac{t - s}{\tau_1} \right) \left[ 1 - \exp \left( -\frac{4s}{\tau_1} \right) \right],$$

(6)

$$\langle \eta(t) \eta(s) \rangle = \frac{Q^2}{2} \exp \left( -\frac{t - s}{\tau_2} \right) \left[ 1 - \exp \left( -\frac{4s}{\tau_2} \right) \right],$$

(7)

$$\langle \xi(t) \eta(s) \rangle = \langle \xi(s) \eta(t) \rangle = \frac{\lambda DQ}{2} \exp \left( -\frac{t - s}{\tau_3} \right) \left[ 1 - \exp \left( -\frac{4s}{\tau_3} \right) \right],$$

(8)

where $\tau_3$ and $\lambda$ are the cross-correlation time and cross-correlation intensity between noises, $\lambda \in [-1, 1]$ and $\tau_3 \geq 0$, respectively. It should be noted that the correlation time $\tau_3$ must be zero when intensity $\lambda$ is 0.

3. Transitions and discussions

The approximate Fokker–Planck equation corresponding to Eq. (2) can be obtained by the approach of Ref. [19]. Nevertheless, we have to resort to numerical methods to achieve the solutions since the analytical solution cannot be obtained $[19,28]$. In order to study the transitions in the system, SPD is simulated from Eq. (2).
3.1. Algorithm

Generally, owing to the cross-correlated noises cannot be treated directly, it is necessary to make a transformation, i.e., a stochastic equivalent scheme [3,45]. For simplification, we let all the correlation times to take the same value $\tau$ (i.e., $\tau_1 = \tau_2 = \tau_3 = \tau$ for $\lambda \neq 0$; $\tau_1 = \tau_2 = \tau$ and $\tau_3 = 0$ for $\lambda = 0$). Besides, we set $\mu = 0$, $\beta = \frac{1}{2}$, as was done previously by all authors [39–41]. Supposing in the initial environment, the probability of gene A mutate into gene B or vice versa is equal (i.e., $\beta = 1/2$), and the gene selection is fair to both gene A and B haploid (i.e., neither propitious to gene A nor to gene B, so $\mu = 0$). Here, the CCSV noises are obtained by the following transformations,

$$\xi(t) = D \sin \left( \sqrt{\frac{2}{\tau}} w_\alpha(t) \right),$$

$$\eta(t) = Q \lambda \sin \left( \sqrt{\frac{2}{\tau}} w_\alpha(t) \right) + Q \sqrt{1 - \lambda^2} \sin \left( \sqrt{\frac{2}{\tau}} w_\beta(t) \right),$$

where, though the form of Eq. (9) is the same as Eq. (3), $w_\alpha(t)$ and $w_\beta(t)$ are two independent standard Wiener processes. Refs. [44,45] have verified that the transformation do not change the statistical properties of Eqs. (5)–(8). By substituting Eqs. (9) and (10) for Eqs. (3) and (4), we integrate Eq. (2) with the Box–Muller algorithm for generating the increment of standard Wiener process, i.e., a Gaussian white noise unitary intensity, and the Euler forward procedure [46]. The value $x(t + \Delta t)$ is generated from the value $x(t)$ (i.e., $x$):

$$x(t + \Delta t) = x + \left( \frac{1}{2} - x \left( t - \frac{\tau_\alpha}{\Delta t} \right) \right) \Delta t + D\lambda(1 - x)X_1(t)\Delta t$$

$$+ Q[\lambda X_1(t) + \sqrt{1 - \lambda^2} X_2(t)]\Delta t + \frac{1}{2}[D(1 - 2x)X_1(t)]$$

$$\times \{D\lambda(1 - x)X_1(t) + Q[\lambda X_1(t) + \sqrt{1 - \lambda^2} X_2(t)]\} \Delta t^2,$$

where

$$X_1(t) = \sin \left( \sqrt{\frac{2}{\tau}} w_\alpha(t) \right),$$

$$X_2(t) = \sin \left( \sqrt{\frac{2}{\tau}} w_\beta(t) \right),$$

in which

$$w_\alpha(t) = w_\alpha(t - \Delta t) + \sqrt{-2\Delta t \cdot \ln(a)} \cdot \cos(2\pi b),$$

$$w_\beta(t) = w_\beta(t - \Delta t) + \sqrt{-2\Delta t \cdot \ln(c)} \cdot \cos(2\pi d).$$

$a$, $b$, $c$, and $d$ are independent uniform distribution in $[0, 1]$.

For each value of the noise parameters and the time delay, SPD is calculated as an ensemble average of independent realizations. Every realization is obtained by Eqs. (11)–(15) and spans $8 \times 10^3$ integration steps (the initial value $x(t \leq 0) \in (0, 0.1)$, $w_\alpha(t \leq 0) = w_\beta(t \leq 0) = 0$, and the integration step $\Delta t = 0.01$). The results are presented as follows.

3.2. Numerical simulation results and discussions

The SPD, as a function of $x$ for different values of the correlation time $\tau$, is plotted in Fig. 2. Firstly, the curves are symmetrically located at two sides of $x = 0.5$, that is due to the selection factor $\mu = 0$. Secondly, unimodal SPD becomes bimodal structure, and then evolves into four peaks structure as $\tau$ increases. Furthermore, the height of the two peaks in the middle decreases slightly while that in the two sides increases; the position of the left peak is shifted to $x = 0$ while that of the right peak is shifted to $x = 1$ gradually with increasing $\tau$, which indicates the environmental selection yields a high probability for one of the two gene A and B. In this case, it is easy to select one type haploid from the group since the other type haploid number can be neglected with regard to the selected type number. On the other hand, from the Fig. 2 we can know that the correlation time can induce a new transition to four stable states for large value of the correlation time. Nevertheless, the dynamic behavior is different from the reentrance transitions showed in Ref. [41].

In Fig. 3, we discuss the effect of multiplicative bounded noise intensity on the SPD. It is clear that the curve of SPD is symmetric, and it is presented the same tendency with the variable $D$ in both Fig. 3(a) and (b). For a small value of $D$, the curve shows a single peak, which manifests that environment selection gives the same chance to both the gene A haploid
Fig. 2. The SPD as a function of $x$ for $\tau_\alpha = 0.01, D = 0.5, Q = 0.4, \lambda = 0.3$ with $\tau = 0.2, 0.5, 1.5, 3, 6, 10$.

Fig. 3. The SPD as a function of $x$ for $\tau_\alpha = 0.01, \tau = 0.3$ with (a) $Q = 0.4, \lambda = 0.2; D = 0.08, 0.8, 1.5, 2.5, 3.5, 5$, and (b) $Q = 0, \lambda = 0; D = 0.8, 1.5, 2.5, 3.5, 5$.

and the gene B haploid under this condition, and it is difficult to select one haploid from the group. The height of the single peak decreases with increasing $D$. As $D$ further increases, the single peak vanishes and becomes to double peaks. The height of the two peaks increases and the distance between them becomes larger with $D$. The left peak is near the position $x = 0$ while the right one is near the position $x = 1$, showing that environment selection gives a large selection advantage to either gene A or B. Though their tendencies of the SPD are similar, the height of peaks in Fig. 3(b) is always much larger than that in Fig. 3(a) corresponding to the same value of $D$. Besides, we can find that there is an equal critical value of $D$ in both Fig. 3(a) and (b), near which a transition appears. It reveals that multiplicative bounded noise plays a dominated role for the process of gene selection, and in this case the selection regulation is weakly affected by additive bounded noise.

In Figs. 4 and 5, the effect of additive bounded noise on the SPD is investigated. It can be seen that the curve of SPD is symmetric and the height of the peaks decreases with increasing $Q$. For a small $Q$, Fig. 4 displays a bimodal SPD structure and the distance between the two peaks becomes smaller gradually. When variable $Q$ exceeds a certain threshold value (about $Q = 0.3$), the SPD changes from two peaks to one peak. Comparing Fig. 4 with Fig. 5, we find that the SPD changes in an opposite way. For a small value of $Q (Q = 0.01)$, the curve of the SPD shows a unimodal structure and the only peak is quite sharp in Fig. 5(a). When $Q$ exceeds a certain threshold value (about $Q = 0.02$), the SPD changes from one peak to two peaks. Moreover, the height of the peaks decrease and the distance between the two peaks becomes bigger with increasing $Q$ in Fig. 5(b). Based on the analysis above, we can conclude that the synergistic effect of multiplicative noise and additive
noise can facilitate the gene separation when $Q$ is small, and restrain the gene separation when $Q$ is relatively big. Finally, we must notice that the SPD almost evolves into a straight line under the condition of Fig. 3 or Fig. 5(b) when the value of $Q$ is big enough (about $Q > 0.5$), which means the mechanism of genetic selection is invalid.

Fig. 6 presents the SPD as a function of $x$ for different values of correlation intensity between noises. It is revealed that unimodal SPD located at $x = 0.5$ becomes bimodal structure that has two maximum with increasing $|\lambda|$. When $\lambda = 0$, that is the fluctuations from internal and external environment independent mutually, the curve has a single peak. When $\lambda > 0$, that is positive correlation between noises, there is a critical value of $\lambda = 0.25$ in Fig. 6(a), near which a transition occurs. When $\lambda < 0$, that is negative correlation between noises, there is a transition next to $\lambda = −0.5$ in Fig. 6(b). Therefore, we can conclude that an increase of the correlation degree makes it possible to separate one type haploid from a haploid group.

In Fig. 7, the SPD is depicted as a function of $x$ for different values of time delay. When $\tau_\alpha = 0$, namely no time delay, the curve gives one peak region about $x$ in $[0.4, 0.6]$. Its peak position is at $x = 0.5$, which means the selection is fair to both gene A haploid and B haploid. As $\tau_\alpha$ increases, the peak at $x = 0.5$ vanishes gradually and finally becomes a bimodal structure. Moreover, the position of the two peaks hardly has any change and the height of them decreases with increasing $\tau_\alpha$. From Fig. 7, we can see that the time delay can induce transition from one peak to double peaks. This conclusion is in accord with that in Ref. [42].
4. Conclusion

We studied the occurrence of transitions in the genetic selection system. In this model, two correlative bounded noises are introduced to imitate the environmental fluctuations on both the gene mutation factor and the gene selection factor. Time delay is used to represent the reaction time of gene transformation and regeneration. Numerically we have shown the transitions induced by time delay and CCSW noises. By virtue of simulation, we have studied the effect of all system parameters on the SPD. The multiplicative bounded noise can break the single peak state to the double peak state whether the additive noise exists or not. The influence of the additive noise on the SPD is opposite when the multiplicative is present or absent. It shows the multiplicative noise plays a dominated role in the selection process. Yet, when the intensity of additive noise increases to a relative big value, it plays a diffusing role in the process no matter the multiplicative noise exists or not, which causes the probability distribution to a uniform distribution. Finally, we have drawn the conclusion that time delay, the correlation time and correlation intensity between the two noises can induce transitions.

Our results may be helpful for explaining basic mechanisms of the genetic selection process. However, we must honestly stress that our stochastic model is speculative and it needs experimental confirmations. Moreover, for biological evolution or producing gene order, more interference and more complicated fluctuation must be involved in the dynamical system. Hence, the multivariate model with delays and noises should be introduced to address the issue in depth.


Acknowledgments

This work was supported by National Natural Science Foundation of China under grant Nos. 11202120 and 61273311, the Fundamental Research Funds for the Central Universities under Nos. GK201302004 and GK201502007.

References