SYMPATRIC SPECIATION IN SEXUAL POPULATIONS

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Speciation is the dominant mode for the origin of new species, which is one of the core problems of evolutionary biology. Recently, several empirical studies put forward disruptive sexual selection as an important driving force of sympatric speciation. Theoretical sexual-selection models are based on competition for mates, creating differential fitness depending on the individuals displaying traits or preferences. Here we propose a model for sympatric speciation using mechanisms as sexual selection, competition and different pregnancy periods, acting on a population living in a two-dimensional lattices. We expect to find out which of these conditions are necessary for the empirical patterns of sympatric speciation to arise.

Keywords: sympatric speciation, fitness, reproductive isolation, assortative mating

1. Introduction

The idea that natural selection can cause speciation through the ecological interactions of organisms with their environment dates back to Darwin himself1. Given the remarkable changes in science and technology during the past 145 yr, how new species are formed is still a fundamental problem in biology2,3,4,5.

Speciation usually occurs when a pre-existing population is suddenly divided into two or more isolated subpopulations by a geographical barrier. When reproductive isolation makes the gene pools of the subpopulations sufficiently diverge, the inter-breeding among the subpopulations will not occur even after a secondary contact (as the barrier removed). As a result, new species have been formed.

Despite theoretical difficulties to show convincingly how speciation might occur without geographical separation6, there is however, mounting evidence7,8,9,10,11 that speciation might have emerged in sympatry (without physical isolation). Ex-
amples like the cichlids in lake Victoria or many migratory birds, do not seem to fit the basic requirement of long periods of geographical isolation needed for allopatric speciation. Laboratory experiments have also shown that in principle, sympatric speciation is possible\textsuperscript{22}. Understanding how sympatric speciation can be driven, has thus attracted much theoretical effort. However, some early works showed that finding a biologically reasonable and robust model seems not to be an easy subject\textsuperscript{10,16}.

The most straightforward scenario for sympatric speciation requires disruptive selection favoring two substantially different phenotypes, followed by the elimination of all intermediate phenotypes. In sexual populations, the stumbling block preventing sympatric speciation is that mating between divergent ecotypes constantly scrambles gene combinations, creating organisms with intermediate phenotypes. However, this mixing can be prevented if there is assortative\textsuperscript{11} instead of random mating, i.e., mating of individuals that are phenotypically similar. It can be based on ecologically important traits such as body size\textsuperscript{23} or on marker traits that co-vary with ecological traits (such as coloration or breeding behavior\textsuperscript{28}).

The present paper reports on a simple, explicit individual-based genetic model to address the challenging problem of sympatric speciation using mechanisms as sexual selection, competition and different pregnancy periods, acting on a population living in a two dimensional lattices. We expect to find out which of these conditions are necessary for the empirical patterns of sympatric speciation to arise.

2. The model

The model employed in this paper is a nine-locus haploid model under a sexual population with overlapping generations. Each individual lives on a given site \((x, y)\) of a square lattice\((250 \times 250)\) and, at every time-step, has a probability \(p_w\) to move to 1- or 2-distance neighboring site. The genotype of an individual is represented by a 81-bit string, which is divided into 9 genes (9 bits each) counterpart with the 9 loci. Every bit of phenotype string will be calculated from a 9-bit gene, i.e. there are 9 bits in the phenotype string. The first 5 bits in the phenotype string are the phenotypic trait to fit with the environment, the fitness of the individual to the environment will be calculated by Hamming distance between the phenotypic trait and a 5-bit string which is represent the ecological character of the environment (we set the simplified form with bit string “11111”), which is ranging from 0 to 5. The rest 4 bits is preparing for the female-preference (sexual trait). When a female meets a male, she check the hamming distance (HD) of the 4-bit sexual trait string, when HD is ranging from 0 to 4, the probability of the male chosen by the female to mate will decrease by exponential law. If they mate, the number of their offspring will be determined by the function of the fitness of them. The genotype of the offsprings will be randomly chosen gene by gene from their parents, and there is a mutation rate about 0.003 to 0.001. Then the offsprings will be dispersed around the parents in the 1- or 2-distance neighbor.
3. Simulation results

The simulation starts with 500 individuals, half males and half females, all individuals have the same genotype and phenotype; then the simulation runs for 6000 time steps.

![Graph showing simulation results](image)

Fig. 1. Random mating strategy.

When the female mate the male without preference, there isn’t speciation. While if the there is restrict to the mating process, sympatric speciation will be occur. The result is agree with the other work that, disruptive sexual selection is one of the precondition of sympatric speciation.

4. Conclusions

Female assortative mating strength is an important prerequisite to sympatric speciation, and its value will determine whether the species can be divided or not.

We hope that this article will both provide a context for sympatric speciation and stimulate others to apply this point of view when considering how sympatric speciation occurs.

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Fig. 2. Random mating strategy. At the end of the simulation, time 6000.
Fig. 3. Random mating strategy. The population evolution plotting by phenotype.
Fig. 4. Same phenotype mating strategy.
Fig. 5. Same phenotype mating strategy. At the end of the simulation, time 6000.
Fig. 6. Same phenotype mating strategy. The population evolution plotting by phenotype.
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References