Available online at www.sciencedirect.com

SCIENCE DIRECT®

Physica A 369 (2006) 612–618

PHYSICA A

www.elsevier.com/locate/physa

Phase transition in a mean-field model for sympatric speciation

V. Schwämmle, K. Luz-Burgoa, J.S. Sá Martins, S. Moss de Oliveira*

Instituto de Física, Universidade Federal Fluminense, Campus da Praia Vermelha, Boa Viagem, Niterói, 24210-340, RJ, Brazil

Received 2 June 2005; received in revised form 13 January 2006
Available online 23 February 2006

Abstract

We introduce an analytical model for population dynamics with intra-specific competition, mutation and assortative mating as basic ingredients. The set of equations that describes the time evolution of population size in a mean-field approximation may be decoupled. We find a phase transition leading to sympatric speciation as a parameter that quantifies competition strength is varied. This transition, previously found in a computational model, occurs to be of first order.
© 2006 Elsevier B.V. All rights reserved.

Keywords: Speciation; Sympatry; Mean-field

---

1. Introduction

The dynamics that generate the rich and diverse structure of the living world is still one of the greatest puzzles in science. Why and how the primitive living organisms gave birth to the immense variety of species in our environment is still a matter of debate and research to our days. The theory of biological evolution, the paradigm that guided the rapid growth of our knowledge about the microscopics (e.g. the behaviour of individuals in a population) of life and the development of all the dazzling techniques and possibilities of genetical engineering, has yet to answer some simple and rather basic questions. One of these stands out as a crucial difficulty: the issue of sympatric speciation.

If a single-species population is somehow split into two separate groups—by the establishment of some geographical barrier, say—uncorrelated genetic drift in these non-mating populations may eventually lead to differentiation. This process is called allopatric speciation and is reasonably well understood. The same cannot be said about the branching of a single population into two distinct species without the appearance of an external barrier dividing the original group: sympatric speciation. Until recently, the possibility of such a process was still under debate, but observations of micro-evolution [1] and the development of theoretical frameworks [2–4] have established it as a valid conjecture in the last years, turning sympatric speciation into one of the favourite themes of research in modern evolutionary theory [5–7].

A variety of theoretical models have been proposed to explain sympatric speciation, from analytical mean-field type ones to more realistic individual-based models. Computational representations based on variations

---

*Corresponding author.
E-mail address: suzana@if.uff.br (S.M. de Oliveira).

doi:10.1016/j.physa.2006.01.076

of the Penna model for biological ageing [8], popular amongst physicists working on the statistical mechanical aspects of evolutionary theory, belong to this latter class. Previous work on such representations have shown that sympatric speciation appears when driven by a change in the character of the distribution of ecological resources, as suggested by some biologists [3]. From this perspective, sympatric speciation appears as a transition between two different organisations of some population. In our present work, we develop a variation that allows a mean-field approximation with analytical solution, in which the nature of this transition may be further discussed.

The computational model has intra-specific competition, mutations and assortative mating as its sole ingredients. The mean-field approximation leads to a set of simple equations that reproduces some of the features of individual-based models, and whose solutions show a clear signature of the above-mentioned phase transition.

2. The computational model

We take as starting point the sexual version of the Penna model, as described for instance in Refs. [9,10]. In addition to the age-structured pair of bit-strings that represents the genome for purposes of ageing analysis, each individual carries an extra pair of non-structured bit-strings of 32 bits each, that encodes a genetically acquired phenotype trait, as already published in Ref. [11]. This extra pair of genetic material is inherited with the same dynamics of the age-structured pair, involving a meiotic cycle with crossing and recombination of each parent's bit-strings. The trait for a particular individual is obtained by counting the number of loci in the non-structured pair where the allele 1 is either homozygous or dominant, and is an integer in the interval $[0, 32]$ which determines the individual's survival probability and its mating preferences. The positions where the allele 1 is dominant are chosen randomly at the beginning of the simulation and are the same for all individuals. According to this number, the population is divided into three groups (subpopulations). We will follow the dynamical evolution of the size of the three subpopulations independently (P_1 for the one with small values of the phenotype trait, P_2 for the one with large values, and P_i for the intermediate one). The survival probability is $1 - V$, where V is the so-called (modified) Verhulst factor. This factor has a resource-size parameter, the carrying capacity C, and represents a mean-field competition for the ecological resources of the environment. It has a different value for each one of the three subpopulations, representing different levels of competition for those resources

$$V_{P_{1,2}} = \frac{P_{1,2} + P_i}{C}, \quad V_{P_i} = \frac{x(P_1 + P_2) + P_i}{C}, \tag{1}$$

where we set $C = 100,000$. The intermediate subpopulation P_i competes with a fraction x of the sum of the subpopulations with extreme values of the phenotype trait, and this fraction will drive the speciation phase transition. Each of the subpopulations 1 and 2 competes only with itself and with the intermediate one. This variation of the Verhulst factor has previously been used in a study of sympatric speciation in food webs [12]. A genetic trait, encoded by a single bit and subject to mutation, determines female selectivity in mating. This trait is initially set to zero: every female selects a mating partner randomly. Observe that due to mutations the offspring of a selective female may be non-selective and vice versa. Mating preference also depends on the value of the phenotype trait. A selective female of population P_1 or P_2 chooses to mate, among a set of A males from its own subpopulation, the one with the most extreme value of the phenotype trait. A selective female of population P_i chooses randomly to act as one of the above. Any non-selective female mates randomly. The number A of available males is a measure of the female's selectivity degree: the larger A is, more selective is the female.

3. Results of the computational model

We focus on the identification of the phase transition already mentioned. Fig. 1 compares the final states of simulations carried out with extreme values of x with the one at the transition point $x = 0.5$. In all cases, $A = 50$, the mutation probability at birth of a locus of the phenotype trait is 0.01, and total time equals 100,000 MC steps. Speciation is well observed for $x = 1$, where complete reproductive isolation leads to the