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Invasive advance of an advantageous mutation: Nucleation theory

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Abstract

For sedentary organisms with localized reproduction, spatially clustered growth drives the invasive advance of a favorable mutation. We model competition between two alleles where recurrent mutation introduces a genotype with a rate of local propagation exceeding the resident's rate. We capture ecologically important properties of the rare invader's stochastic dynamics by assuming discrete individuals and local neighborhood interactions. To understand how individual-level processes may govern population patterns, we invoke the physical theory for nucleation of spatial systems. Nucleation theory discriminates between single-cluster and multi-cluster dynamics. A sufficiently low mutation rate, or a sufficiently small environment, generates single-cluster dynamics, an inherently stochastic process; a favorable mutation advances only if the invader cluster reaches a critical radius. For this mode of invasion, we identify the probability distribution of waiting times until the favored allele advances to competitive dominance, and we ask how the critical cluster size varies as propagation or mortality rates vary. Increasing the mutation rate or system size generates multi-cluster invasion, where spatial averaging produces nearly deterministic global dynamics. For this process, an analytical approximation from nucleation theory, called Avrami's Law, describes the time-dependent behavior of the genotype densities with remarkable accuracy.

Keywords: Critical radius; Ecological invasion; Individual-based models; Preemptive competition; Recurrent mutation; Spatial clustering

1. Introduction

Understanding how localized biotic interactions govern invasion dynamics and an invader's subsequent spatial expansion remains a fundamental challenge in population biology (Levin et al., 1997; Wilson, 1998). Fisher (1937) and Kolmogorov et al. (1937) provided initial insight; they demonstrated how spatially structured dispersal can organize the advance of a favorable mutation. Fisher (1937) approximated the genetic process with a reaction–diffusion equation, and diffusion theory has since served repeatedly to model spatial expansion in ecology, evolution and epidemiology (reviewed by Fife, 1979; Okubo, 1980; Holmes et al., 1994; Murray, 2003). Generalizations of basic reaction–diffusion theory, intended to enhance biological realism, include models with age-dependent birth and death rates (Frantzen and van den Bosch, 2000; Neubert and Caswell, 2000), non-normal dispersal kernels (Kot et al., 1996; see Chesson and Lee, 2005), spatial heterogeneity (Cantrell and Cosner, 1991), and granularity of space or time (Neubert et al., 1995). Most of these analyses neglect demographic stochasticity, which can be important at local introduction of a rare type, to focus on the velocity of a travelling wave propelling an invader's spatial advance (van den Bosch et al., 1990; Caraco et al., 2002; O'Malley et al., in press; see Lewis and Pacala, 2000). Metz et al. (2000) provide a useful guide to biological generalizations of diffusion processes.

Diffusion models sometimes predict velocities of spatial advance with accuracy, from the scale of nearest-neighbor infection (Zadoks, 2000) to biogeographic range expansion (van den Bosch et al., 1992). But travelling waves permit

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infinitely small population densities (van Baalen and Rand, 1998); consequently, the model may fail to capture essential properties of the dynamics of rarity (Durrett and Levin, 1994a), both at introduction and at the edge of an invader's expansion (Ellner et al., 1998; Thomson and Ellner, 2003). An alternative perspective on invasion assumes discrete individuals; individual-based models can directly address the impact of spatially clustered growth on a rare mutation's fate when births and deaths occur as a random process (Claessen and de Roos, 1995; Iwasa et al., 1998; Wei and Krone, 2005; Caraco et al., 2006).

We analyze the spatial dynamics of a two-allele system where discrete individuals compete preemptively. We assume two-way, recurrent mutation in a population propagating clonally; the individual-level assumptions are simple, but the system's behavior can be complex. Mutation, introducing a superior allele, is a rare process, but can potentially occur anywhere in the spatial system. Each introduction initiates a separate cluster of invaders; a cluster may disappear through mortality, or may grow large. Our main results show how patterns in an advantageous mutation's spatial clustering influence the time elapsing until the superior allele replaces the resident. In particular, we present a novel dependence of an inferior allele's "lifetime" on the probabilistic rate of mutation.

To address the system's population-level behavior, we invoke the theory for homogeneous nucleation of spatial systems (Kolmogorov, 1937; Johnson and Mehl, 1939; Avrami, 1940). Nucleation theory offers novel characterizations of the genetic or ecological clustering found in populations with locally structured interactions (Gandhi et al., 1999; Korniss and Caraco, 2005). Expanding upon our preliminary analysis (Yasi et al., in press), we apply nucleation theory to the spread of an advantageous mutation. Foremost, we want to predict the time-dependent, global genotype densities, which are driven by locally clustered growth of the favored allele. To do so, we employ a powerful approximation, called Avrami's Law (Ishibashi and Takagi, 1971; Rikvold et al., 1994; Korniss et al., 1999; Ramos et al., 1999) that describes our simulated mutation-selection dynamics quite accurately. We offer some new predictions about temporal behavior of spatially structured competitive systems, and suggest a framework for developing new ideas concerning spatially explicit invasion dynamics.

In Section 2, we describe the details of our model. Section 3 examines conditions for equilibrium behavior, and the transitions between equilibria. To emphasize the impact of spatial structure, we compare equilibrium phase transitions observed in simulation to the model's mean-field (MF) approximation and its pair approximation (PA). We relegate details of the MF analysis, and some results on approach to population extinction, to Appendix A. We analyze a PA in Appendix B. Section 4 contrasts single-cluster and multi-cluster invasion processes, motivating the application of nucleation theory in Section 5. In Section 6, we use the theory to interpret the simulated dynamics. Section 7 summarizes our results and discusses further applications of nucleation theory in evolutionary ecology.

2. Spatial model

We consider an $L \times L$ lattice with periodic boundaries; a lattice site represents the minimal level of local resources required to sustain a single organism. Hence each site is either empty or occupied by one haploid individual (a resident or an invader). The local occupation numbers at site $\mathbf{x}$, $n_g(\mathbf{x}) = 0,1$; $g = 1,2$, count the number of resident and invader genotypes, respectively.

Competition for space is preemptive (Amarasekare, 2003; Shurin et al., 2004; Tainaka et al., 2004); an individual of either genotype may propagate clonally only if one or more of the δ nearest neighboring sites is empty. Specifically, if site $\mathbf{x}$ is empty, that site is colonized by allele g at total probabilistic rate $\alpha_g\eta_g(\mathbf{x})$. α_g is the per-individual propagation rate of allele g. $\eta_g(\mathbf{x})$ is the density of allele g on $\sigma(\mathbf{x})$, the set of nearest neighbors of site $\mathbf{x}$. Since the size of the interaction neighborhood is $|\sigma(\mathbf{x})| = \delta$, we have

$$\eta_g(\mathbf{x}) = (1/\delta) \sum_{\mathbf{x}' \in \sigma(\mathbf{x})} n_g(\mathbf{x}'). \tag{1}$$

Most of our analyses below take $\delta = 4$, the four nearest neighbors on a square lattice. Unless noted explicitly in the figures, results are for $\delta = 4$. To test the robustness of some of our findings, we also considered neighborhood sizes $\delta =$ 8 and 12.

When the invader allele has a reproductive advantage, $\alpha_2 > \alpha_1$; we shall assume this condition holds when we analyze invasion with nucleation theory (Sections 4–6). We assume two-way, recurrent mutation. Each individual of genotype g independently mutates to genotype $(1+|g-2|)$ at constant probabilistic rate ϕ_g. Finally, each individual carrying allele g suffers mortality at probabilistic rate μ_g.

We have a particular interest in the way clonal propagation, through direct effects on cluster-size dynamics, drives competition between populations (O'Malley et al., 2005). Therefore, we let $\mu_1 = \mu_2 = \mu$, and $\phi_1 = \phi_2 = \phi$. The sole difference between genotypes is the difference in propagation rates. We summarize the local transition rates for an arbitrary site $\mathbf{x}$ as

$$0 \overset{\alpha_1\eta_1(\mathbf{x})}{\rightarrow} 1, \quad 0 \overset{\alpha_2\eta_2(\mathbf{x})}{\rightarrow} 2, \quad 1 \overset{\mu}{\rightarrow} 0, \quad 2 \overset{\mu}{\rightarrow} 0, \quad 1 \overset{\phi}{\leftrightarrow} 2, \tag{2}$$

where 0,1,2 indicates whether the site is empty, occupied by the resident genotype, or occupied by the invader genotype, respectively. We list the paper's symbols in Table 1.

3. Equilibrium phase diagram

Although this paper focuses on the dynamics of an advantageous allele's invasion, it is instructive to begin with a general picture of the model's underlying equilibrium phases. Our assumptions imply strong spatial clustering of the invasion process. Therefore, both MF