Global stability in diallelic migration–selection models

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A B S T R A C T

For diallelic migration–selection models in continuous time with arbitrary migration in either discrete or continuous space, a sufficient condition for the existence of a globally asymptotically stable equilibrium is established. As a special case, this condition includes concavity of the mean selection coefficient.

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1. Introduction

We consider a gene at a single locus with two alleles A_1 and A_2. We posit weak selection and use a continuous-time approximation. The genetic structure of the population is measured by the relative frequencies p and $1 - p$ of A_1 and A_2, respectively. Unless they are close to extinction, populations are usually distributed in space. They occupy a habitat within which they undergo selection and migration. Therefore, it is desirable to study the evolution of gene frequencies under different migration–selection schemes. For recent general reviews of this subject, consult Bürger [4], Lou et al. [21], and Nagylaki and Lou [28].

Let r_{ij} $(= r_{ji})$ for $i, j = 1, 2$ designate the selection coefficient (sometimes called Malthusian fitness) of the genotype $A_i A_j$ (among which $A_1 A_1$ and $A_2 A_2$ are called homozygotes, and $A_1 A_2$ heterozygote). Then the selection coefficient of allele A_i is

$$r_i = r_{i1}p + r_{i2}(1 - p),\tag{1.1}$$

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and the mean selection coefficient of the population is

$$\bar{r} = r_1 p + r_2(1-p)$$
$$= r_{11}p^2 + 2r_{12}p(1-p) + r_{22}(1-p)^2 . \tag{1.2}$$

Under selection the frequency of A_1 changes according to

$$\dot{p} = p(r_1 - \bar{r}) = p(1-p)s(p) , \tag{1.3}$$

where

$$s(p) = r_{12} - r_{22} + (r_{11} + r_{22} - 2r_{12})p . \tag{1.4}$$

If every r_{ij} is frequency independent, then from (1.2) and (1.4) we see that the mean selection coefficient $\bar{r}$ is a concave function of p if and only if

$$r_{11} + r_{22} - 2r_{12} \leq 0 , \quad \text{i.e.,} \quad s'(p) \leq 0 . \tag{1.5}$$

The inequality (1.5) includes the following cases:

(A) $r_{12} = \frac{1}{2}(r_{11} + r_{22})$: the alleles A_1 and A_2 contribute additively to the fitness of the genotypes, this is called *no dominance*; s is independent of p.

(B) $r_{12} > r_{11}, r_{22}$: the heterozygote is fitter than both homozygotes, this is called *overdominance*.

(C) $r_{12} = \max\{r_{11}, r_{22}\}$ and $r_{11} \neq r_{22}$: the heterozygote behaves the same as the fitter of the homozygotes, the fitter allele is *completely dominant*.

(D) $\frac{1}{2}(r_{11} + r_{22}) < r_{12} < \max\{r_{11}, r_{22}\}$: the fitness of the heterozygote is between those of the homozygotes and closer to the fitter of them, the fitter allele is *partially dominant*.

In cases (A), (C), and (D), the selection function $p(1-p)s(p)$ does not change sign for $p \in (0,1)$, and therefore *selection is directional*. This is not the case for (B).

The main purpose of this paper is to establish a sufficient condition for the existence of a globally asymptotically stable equilibrium. In particular, this condition includes concavity of the mean selection coefficient. In fact, following Fleming [10] and Hess and Weinberger [15], for both discrete demes and continuous space, we investigate a more general situation: we replace $p(1-p)$ in (1.3) by a general function $f(p)$ that satisfies

$$f \in C^1[0,1], \quad f(0) = f(1) = 0, \quad f(p) > 0 \quad \text{in } (0,1) , \tag{1.6a}$$

$$f' \text{ is strictly decreasing, i.e., } f \text{ is strictly concave on } [0,1]. \tag{1.6b}$$

We prove also that under certain conditions, a sufficiently high ratio of the strength of selection to that of migration leads to a stable equilibrium where both alleles coexist everywhere in space.

We treat the discrete-space model (2.1) in Section 2; in Theorem 2.3 we establish global asymptotic stability. For the case of discrete time, Eyland [8] analyzed two demes with no dominance under a weak-selection, weak-migration assumption; Campbell [5], based on Karlin and Campbell [17], sketched a proof for global asymptotic stability under the assumption of submultiplicative fitnesses, which corresponds to the concavity of the mean selection coefficient in continuous time. Since the continuous-time model is a limiting case of the discrete-time model, one expects strong similarity between their properties; our results and the above literature confirm this. Proposition 2.7 and Remarks 2.6, 2.8, and 2.9 demonstrate that if