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Evolution, Vol. 50, No. 3. (Jun., 1996), pp. 1034-1041.

Evolution, 50(3), 1996, pp. 1034–1041

ON PHASE THREE OF THE SHIFTING-BALANCE THEORY

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Abstract.—A common conclusion in several recent publications devoted to the deterministic analysis of the third phase of Wright's shifting-balance theory is that under reasonable conditions phase three should proceed easily. I argue that the mathematical equations analyzed in these papers do not correspond to the biological situation they were meant to describe. I present a more appropriate study of the third phase of the shifting balance. My results show that the third phase can proceed only under much more restricted conditions than the previous studies suggested. Migration should be neither too strong not too weak relative to selection. The higher peak should be sufficiently dominant over the lower peak. Recombination can greatly reduce the plausibility of this phase or completely preclude peak shifts. A very important determinant of the ultimate outcome of the competition between different peaks is the topological structure of the network of demes. Peak shifts in two-dimensional networks of demes are more difficult than in one-dimensional networks. Phase three can be accomplished easiest if it is initiated in one of the peripheral demes.

Key words.—Evolution, mathematical models, shifting-balance theory.

Received January 18, 1995. Accepted June 21, 1995.

A standard result in population genetics theory, which goes back to Fisher (1930), is that selection increases the mean fitness of the population. Presumably, because of epistasis and pleiotropy, the mean fitness has many local "peaks" separated by "adaptive valleys" (Wright 1931, 1980). Natural selection leads a population to a nearby peak. The question is how the population can cross an adaptive valley and reach a higher peak. Wright suggested that this can happen in a population subdivided into many partially isolated groups. In Wright's scenario, a new adaptive combination of genes first stochastically becomes established in a single subpopulation (or, in the continuous version of the theory, in a sufficiently large spatial area) and then takes over the whole population. Two stochastic and one deterministic mechanisms of the latter stage (phase three in Wright's terminology) have been formally studied. Lande (1979, 1985a) considered a situation when a new combination of genes that has stochastically become established in a single subpopulation takes over the whole population as a result of stochastic extinction and colonization. In Barton and Rouhani's (1993) and Rouhani and Barton's (1993) models, the influx of migrants from demes carrying a new combination of genes makes it more likely that the deme will shift to this combination as a result of random fluctuations.

Several recent papers considered the spread of a new combination of genes as a deterministic process (Crow et al. 1990; Barton 1992; Kondrashov 1992; Phillips 1993). Crow et al. (1990) concluded their paper saying that "whatever weaknesses the Wright theory may have, they are not in phase III, (p. 246)." The conclusion section of Phillips (1993) says: "In the end, it is unlikely that phase III is the limiting step in the shifting-balance process in the sense that under reasonable conditions phase III should easily proceed, (p. 1742)." Kondrashov (1992) agreed that a very low migration is sufficient to fix the incoming genotype. Barton (1992) disagreed only about interpretation: "The striking results of Crow et al. are not due to selection in favor of a novel combination of genes, but rather, reflect the power of gene flow over selection . . ." (p. 556) and argued that "the new gene combination spreads not because it is fitter, but because a low rate of immigration can swamp selection, and establish even a deleterious allele" (p. 552). Altogether this seems to have ruled out the pessimism of Haldane (1959) who considered phase three as the weakest point of Wright's theory. It is these four papers and their conclusions that concerns us here.

The basic model analyzed in these papers describes a population subdivided into two subpopulations (demes) connected by migration. The mean fitness has two local maxima, and, initially, one advantageous combination of genes is fixed in one deme and another advantageous combination of genes is fixed in the other deme. This model and its variants were used to argue that very low migration (relative to selection) is sufficient to move the whole system to the higher peak.

There are two assumptions in this model that deserve discussion. The first is that there are only **two** subpopulations initially fixed for different advantageous (combinations of) genes. Presumably, this was considered as a simplified but still representative model for a population subdivided into **many** groups. Let us look at the system of two demes as a whole. The assumption that initially one deme is fixed for one combination of genes and another deme is fixed for a fitter combination of genes implies that in the whole system the fitter genes have already reached the frequency of at least 50%! In models with unidirectional migration, which results from the assumption that one of the demes has much larger size, the initial frequency of the fitter genes in the whole system will be even higher. Obviously, this initial situation is quite different from the usual scenario: one of **many** subpopulations is at a new higher peak, whereas the remaining subpopulations are still at the old peak. In some sense, the interaction between two subpopulations with the specified above initial conditions more closely resembles the second phase (mass selection) of the shifting-balance theory than the third phase. Phase two occurs readily, and this seems to be the reason why the fitter peak took over easily in the previous models.

The second assumption concerns the description of mi-

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gration. The above-mentioned authors assumed that a constant migration rate to the initially low fitness deme was different (typically much higher) from a constant migration rate to the initially high-fitness deme. Presumably, the assumption about migration rates in the opposite directions being **constant** and **different** was considered as a reasonable model for Wright's idea about excess emigration from the fitter subpopulation. Let us ask a question: how can migration rates in the opposite directions be different? First, there can be some external (for the population) differences. For example, migration towards the patch occupied by one of the subpopulations can be more difficult because of some physical force (e.g., gravity or wind). Or, the patches themselves can be different with one of them having a higher carrying capacity and, thus, provided everything else is equal, sending more migrants. These situations can be adequately modeled by assuming that migration rates in the opposite directions are **constant** and different but are not related to phase three of the shifting-balance theory. Second, migration rates in the opposite directions can be different because of some internal (for the population) differences. For example, different genotypes can have different tendencies to migrate. This situation, however, is beyond the scope of Wright's theory. What he had in mind is excess emigration from the fitter subpopulation as a consequence of an excess population growth. This mechanism implies that the proportion of new emigrants is not constant but changes in time with changes in the population density and/or fitness. For example, as the initially low-fitness subpopulation approaches the state of the fitter subpopulation, the proportion of new emigrants is supposed to be reduced. As emphasized by Svirezhev and Passekov (1990, ch. 7), to be correct a population genetics model with constant differential migration should include an additional mechanism, which maintains constant sizes of the subpopulations. Without such a mechanism (which in no way appeared in the models that we discuss here), the differences in the migration rates can be attributed only to nongenetical factors. Summarizing, a well-grounded model for the interactions between different peaks should consider many demes simultaneously and either include as a component the dependence of the emigration rate on the population state or assume, as a simplification, that the migration rates in the opposite directions are equal.

The general conclusion of this discussion is that the mathematical equations analyzed in the papers cited above do not correspond to the biological situation they were meant to describe and that the results discussed in these papers are not closely related to the third phase of Wright's shifting-balance theory. In the next section, I shall present a more appropriate study of the third phase of the shifting balance. I shall start with a simple model that assumes that migration rates in the opposite directions are equal and do not depend on the state of demes. Then I consider a model with differential migration rates and population regulation. My results will suggest that the takeover of the higher peak is not as easily achieved as the previous studies lead one to believe. I shall show that both evolutionary factors (selection, recombination, and migration) and the geometrical structure of the population can significantly affect the ultimate outcome of the competition between different peaks.

SINGLE LOCUS PEAK SHIFTS

I consider a population with discrete generations. To simplify the presentation, I shall approximate the corresponding recurrence dynamics equations with differential equations. A standard justification for this approximation is the assumption that both selection and migration are weak. Under this approximation, the exact order of selection and migration does not matter. I start with a single-locus case in which individuals with genotypes **aa**, **aA**, and **AA** have relative fitnesses (viabilities) 1, 1 − S , and 1 + K, respectively (K, S ≥ 0). With this selection scheme, the mean fitness of the population has two local maxima at (two) homozygous states. Let p be the frequency of allele **A**. The rate of change of p under selection in an isolated population (deme) is approximated by

$$\frac{dp}{dt} = 2sp(1 - p)(p - \tilde{P}), \tag{1}$$

where $2s = 2S + K \geq 0$, $\tilde{P} = S/(2S + K) \leq 1/2$. The local dynamics are simple: if initially $p < \tilde{P}$, then the population evolves to the fixation of allele **a**, and if initially $p > \tilde{P}$ the population evolves to the fixation of allele **A**. Thus, the parameter $\tilde{P}$ characterizes the relative dominance of one peak over another: if $\tilde{P} = 0.5$, both peaks have equal domains of attraction, if $\tilde{P} \ll 0.5$, one peak strongly dominates the other. The parameter s describes the overall strength of selection: the larger is its value, the faster the population evolves.

Now let us consider a network of demes, each of which, in general, exchanges a proportion m of its inhabitants with neighboring demes in each generation. A deme at the border of the network has fewer neighboring demes and, as a consequence, exchanges a smaller proportion of its inhabitants (see below). All demes have the same size that is maintained by some sort of population regulation acting independently within each deme, that is, selection is soft (Nagylaki 1992, ch. 6). In this model, the rate of change of the frequency of allele **A** in deme i is (Barton and Rouhani 1991, eq.1):

$$\frac{dp_i}{dt} = 2sp_i(1 - p_i)(p_\iota - \tilde{P}) + m\,\Delta p_i, \tag{2}$$

where Δp_i is related to the pattern of gene flow among demes and depends on the topology of the network (see below). I shall assume that initially one of the demes (deme 0) is fixed for allele **A**, whereas all other demes are fixed for allele **a**:

$$p_i(0) = 1, \quad \text{if } i = 0, \quad p_i(0) = 0, \quad \text{if } i \neq 0. \tag{3}$$

Note that although (2) has three parameters, namely, m, s, and $\tilde{P}$, only the ratio of the first two is important. (To see this one has to divide both sides of (2) by $2s$ and make a variable change to new time $\tau = 2st$.) In what follows, I shall use two parameters: the strength of migration relative to selection, $\epsilon \equiv m/4s$, and the relative advantage of the higher peak, $\tilde{P}$. In the next sections, I shall consider how the ultimate outcome of the dynamics of (2) with initial conditions (3) depends on ϵ, $\tilde{P}$, and on the topology of the network of demes reflected in Δp_i. The previous studies of the third phase of the shifting-balance theory analyzed how the dynamics de-

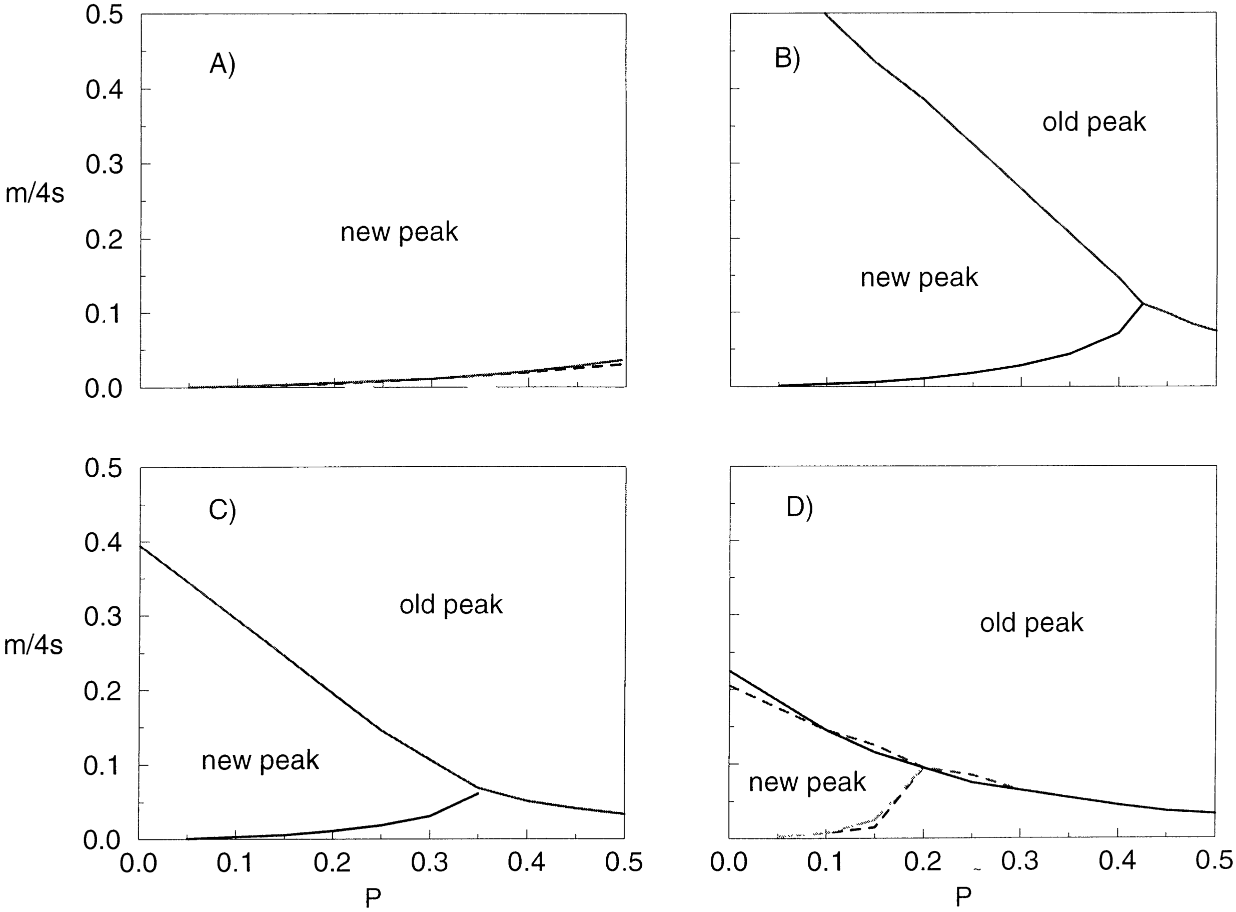

FIG. 1. Regions in parameter space ($m/4s, \tilde{P}$) corresponding to the different outcomes of the peak competition in the one-locus models. (A) Two-deme models with one-way (solid line) and two-way (dashed line) migration. In two-deme models, two different outcomes are possible: the new peak takes over (for parameter values above the corresponding line) or both peaks coexist (for parameter values below the corresponding line). (B) One dimensional stepping-stone model with the fitter deme at the border of the network of demes. (C) One-dimensional stepping-stone model with the fitter deme inside the network of demes. (D) Two dimensional stepping-stone models with four (solid lines) and six (dashed lines) nearest neighbors with the fitter deme inside the network of demes. In multideme models three different outcomes are possible: the old peak takes over (in the area adjacent to the upper border of figures), both peaks coexist (in the area adjacent to the x-axes), or the new peak takes over (in the remaining part of parameter space).

pend on the strength of migration relative to selection. However, the influence of the relative dominance of the higher peak, $\tilde{P}$, on the dynamics was not analyzed in detail and only simple two-deme networks of demes were considered.

Two Demes

To illustrate the difference discussed above between the two-deme models analyzed by Crow et al. (1990), Barton (1992), Kondrashov (1992), and Phillips (1993), and multideme models, I first consider a system of two demes.

One-Way Migration from the Fitter Deme.—In this case, deme 0, which is fixed for allele **A**, does not change its state. The allele frequency dynamics in deme 1 are described by (2) with $\Delta p_1 = 1 - p_1$:

$$\frac{dp_1}{dt} = 2sp_1(1 - p_1)(p_1 - \tilde{P}) + m(1 - p_1). \qquad (4)$$

Discrete time analogues of this equation have been studied. Barton (1992) considered a case of symmetric peaks, that is, $\tilde{P} = 0.5$. In Kondrashov's (1992) model parameters s and $\tilde{P}$ were connected by the equality $s\tilde{P} = 1$. The behavior of (4) is trivial if:

$$\epsilon \equiv m/4s > \epsilon^* \equiv \tilde{P}^2/8, \qquad (5)$$

the new peak takes over and allele **A** becomes fixed in the whole system. If the inequality in (5) is reversed, the new peak is not able to take over, and the first deme remains polymorphic indefinitely. Figure 1A shows that the critical ratio of the rates of migration and selection, ϵ^*, is small and increases with increasing $\tilde{P}$.

Two-Way Migration.—In this case, allele frequencies in both demes change. To describe the dynamics, one needs two equations in the form (2) with

$$\Delta p_0 = p_1 - p_0, \qquad \Delta p_1 = p_0 - p_1. \qquad (6)$$

A partial case (with $\tilde{P} = 0.5$) of this dynamic system was discussed by Karlin and McGregor (1972) and Barton and Rouhani (1991). The possible outcomes in this model are fixation of allele **A** (for large ϵ) or maintenance of genetic variability with allele **A** dominating in deme 0 and allele **a** dominating in deme 1 (for small ϵ). The critical value of ϵ, that is, the value that separates these two regimes, depends on $\tilde{P}$. Dependence of the critical value of ϵ on $\tilde{P}$ can be approximated using a small-parameter method, which has proved to be very useful in studies of migration effects (Svirezhev 1968; Karlin and McGregor 1972; Svirezhev and Logofet 1983, ch. 8.5; Svirezhev and Passekov 1990, ch. 7). However, instead of presenting the corresponding formulae, here and in what follows, I approximate the critical values of ϵ by solving the dynamics equations numerically. There are two reasons for this. The first is that the resulting formulae are cumbersome, and the best way to understand what they describe is to present them graphically. The second reason is that the analyzed system is one of rare cases of dynamic systems whose behavior can be effectively studied using numerical simulations. Its dynamics are well understood, and it has only two parameters (or three in the models studied in the last section). The numerical analysis is at least as informative as possible analytical approaches, yet it requires less effort. An approximation for the dependence of the critical value of ϵ on $\tilde{P}$ for the two-deme model with two-way migration was determined numerically and is presented in Figure 1A. Comparison of the two curves in Figure 1A shows that although reverse migration changes critical value of ϵ, the effect is not dramatic. With only two demes and with initial conditions (3), very small migration rate (relative to selection) is sufficient to move the whole system to the higher peak. This conclusion is in accord with that one of Crow et al. (1990), Barton (1992), Kondrashov (1992), and Phillips (1993).

MULTIDEME MODELS

As was argued above, models with only two demes are inappropriate for analyzing the third phase of the shifting-balance theory. In what follows, I shall consider different networks of demes linked by migration. As before, I shall assume that initially one of the demes (deme 0) is fixed for allele **A**, whereas all other demes are fixed for allele **a**. What will happen as migration starts to interact with selection? There are three possible outcomes. First, the fitter peak can take over and spread over the whole system. Second, there can be a balance between selection and migration such that deme 0 will stay at a state close to the fixation of allele **A**, whereas remaining demes will stay at states close to the fixation of allele **a**. These two outcomes occurred in the two-deme models considered above. With many demes, however, it is also possible that migration from other demes will overcome selection at deme 0 and move the whole system back to the lower peak. What eventually happens depends on the parameters of the model and, equally importantly, on the configuration of demes.

Before proceeding with a description of specific models and results, three observations that are common to these multideme models should be mentioned. The first is that if the new peak takes over, it happens in the form of a traveling wave of alleles. The second is that in general it takes a very short time (fewer than 100 generations) to approach very closely the appropriate asymptotic solution (that is, the traveling wave of alleles, the cline, or the monomorphic equilibrium corresponding to the old peak). The third is that the exact number of demes in the network does not seem to be very important provided it is not too small. The second and the third observations greatly simplify numerical analysis.

One-Dimensional Stepping-Stone Models

I start with a network of linearly arranged demes with migration only between nearest neighbors (at the rate $m/2$), that is, the one-dimensional stepping-stone model. I shall consider two different initial configurations of demes.

Deme 0 at the Border.—If the fitter deme happens to be at the border of a species range, the allele frequency dynamics are described by (2) with

$$\Delta p_0 = (p_1 - p_0)/2, \tag{7A}$$

$$\Delta p_1 = (p_{i-1} + p_{i-1} - 2p_i)/2, \qquad i = 1, 2, \ldots . \tag{7B}$$

These equations imply that the deme at the border receives migrants only from one neighbor, whereas other demes receive migrants from two neighbors with the rate $m/2$ from each. Figure 1B shows areas of parameter space determined numerically that correspond to the three possible outcomes of the dynamics. Two points concerning this figure are interesting. The first is that the higher peak takes over only for much more restricted parameter combinations (compare with Fig. 1A). The second point is that this never happens if $\tilde{P}$, which characterizes the relative dominance of one peak over another, is greater than some critical value (about 0.42). The latter observation means that for the system to move through phase three, the higher peak must be sufficiently dominant over the lower peak. For example, if relative fitnesses of genotypes **aa** and **aA** are 1.0 and 0.9, respectively, relative fitness of genotype **AA** must be larger than 1.04. This is in contrast to Barton (1992) who argued that even the less adaptive peak can easily take over.

Deme 0 Inside.—If the fitter deme happens to be inside the network of demes, the allele frequency dynamics are described by (2) with Δp_i in the form (7B) for all demes, which I specify using index $i = 0, \mp 1, \mp 2, \ldots$. Figure 1C corresponds to this case. One can see that the area of parameter combinations necessary for the third phase to take place dwindles further. Under these conditions, the peak shift never happens if $\tilde{P} > 0.35$. For example, if relative fitnesses of genotypes **aa** and **aA** are 1.0 and 0.9, respectively, the peak shift never happens unless relative fitness of genotype **AA** is larger than 1.09. Comparison of Figure 1B with Figure 1C shows that phase three can be accomplished easier if it is initiated in a peripheral deme (cf. Mayr 1963).

Two-Dimensional Stepping-Stone Models

Most species are found in two-dimensional habitats, not one-dimensional habitats. As a simple example, let us consider a network of demes arranged at the nodes of a square lattice. Now one needs two indices, say i and j, to specify a deme, $i, j = 0, \mp 1, \mp 2, \ldots$. Appropriate initial conditions in this case are $p_{0,0} = 1$ and $p_{i,j} = 0$ for all other demes. Each deme inside this network has four neighbors and exchanges a proportion $m/4$ of its inhabitants with each of them. The allele frequency dynamics are described by (2) with

$$\Delta P_{i,j} = (p_{i-1,j} + p_{i+1,j} + p_{i,j-1} + p_{i,j+1} - 4p_i)/4,$$

$$i = 0, \mp 1, \mp 2, \ldots. \tag{8}$$

Figure 1D presents parameter space both for this model and for a network of demes arranged on a hexagonal lattice as well. In the latter case, each deme inside the network has six neighbors. One can see that the area of possible parameter combinations necessary for the third phase dwindles further. Now the peak shift never happens if $\tilde{P} > 0.2$. For example, if relative fitnesses of genotypes **aa** and **aA** are 1.0 and 0.9, respectively, the peak shift never happens unless relative fitness of genotype **AA** is larger than 1.30. Note also that differences between the model with four neighbors and the model with six neighbors are not very large. Comparison of Figure 1D with Figure 1C shows that phase three can be accomplished easier in one-dimensional networks of demes than in two-dimensional networks. Increasing the dimensionality of the network from one to two dimensions increases the ease with which a higher peak can be swamped by migration. A similar observation was made by Nagylaki (1975) in analyzing models with spatially varying selection.

TWO-LOCUS PEAK SHIFTS

The analysis in the preceding sections was restricted to the single-locus case. If there are several loci underlying fitness, then recombination will destroy adaptive combinations of genes and may make the third phase of the shifting-balance more difficult. Crow et al. (1990) and Phillips (1993) concluded that this is not the case, but their studies were limited to a two-deme case and some specific fitness schemes. What can happen in other situations? To get some insight into this question, I consider a simple two-locus model. I assume that there are two diallelic loci with alleles **A** and **a** at the first locus and alleles **B** and **b** at the second locus. Let r be the recombination rate ($0 \leq r \leq 0.5$ with $r = 0$ if there is no recombination, and $r = 0.5$ if the loci are unlinked). The fitness of genotype **AABB** is 1 + K, the fitness of genotype **aabb** is 1, whereas all other genotypes have reduced fitness $1 - S$, $K, S > 0$ (see Table 1). In principle, there are many different ways to assign fitnesses to "intermediate" genotypes (see Crow et al. 1990; Phillips, 1993). The reason the form presented in Table 1 was chosen is that it simplifies the comparison with the one-locus case: with no recombination and with initial conditions specified below this two-locus model reduces to the one-locus model studied above.

TABLE 1. Relative fitnesses in the two-locus model.

	BB	**Bb**	**bb**
AA	$1 + K$	$1 - S$	$1 - S$
Aa	$1 - S$	$1 - S$	$1 - S$
aa	$1 - S$	$1 - S$	1

Let index k = 1, 2, 3, 4 correspond to the gametes **AB, Ab, aB** and **ab**, respectively, and x_k be the frequency of gamete k. The rate of change of x_k under selection and recombination in an isolated population (deme) is approximated by the standard equation

$$\frac{dx_k}{dt} = (w_k - \bar{w})x_k \mp rw_{AaBb}D, \qquad k = 1, 2, 3, 4, \tag{9}$$

where $D = x_1x_4 - x_2x_3$ is the standard linkage disequilibrium, and w_{AaBb} is the fitness of a heterozygote at both loci (for fitnesses as in Table 1, $w_{AaBb} = 1 - S$). $\bar{w}$ is the mean fitness of the population, and w_k is the induced fitness of gamete k (for example, $w_1 = w_{AABB}\,x_1 + w_{AABb}\,x_2 + w_{AaBB}\,x_3 + w_{AaBb}\,x_4$). In (9), the sign is minus for i=1 and 4 and is plus for i = 2 or 3.

Let us consider a network of demes, each of which, in general, exchanges a proportion m of its inhabitants with neighboring demes in each generation. Let $x_{k,i}$ be the frequency of gamete k in deme i. I shall assume that initially one of the demes (deme 0) is fixed for gamete **AB**, whereas all other demes are fixed for gamete **ab**:

$$x_{1,i}(0) = 1, \qquad \text{if } i = 0,\ x_{4,i}(0) = 1, \qquad \text{if } i \neq 0. \tag{10}$$

This model has an additional parameter, the recombination rate r. In the figures below, I shall use the rate of recombination relative to the strength of selection, $R = r/4s$. With absolute linkage, that is, if $R = 0$, and with initial conditions (10), there are only two types of gametes, **AB** and **ab**, and the system is equivalent to the one-locus two-allele system analyzed in the previous section. The latter can be used as a reference point to evaluate the effects of recombination. Figure 2A presents parameter space for a one-dimensional stepping-stone model in which deme 0 is at the border of the network of demes. One can see that recombination reduces the possibility of phase three significantly. Figure 2B presents parameter space for a two-dimensional network of demes located at the nodes of a hexagonal lattices in which deme 0 is inside the network of demes. For $R = 1$ or $R = 10$, this figure looks similar to Figure 1A: there are only two different regions. As in Figure 1A the smallest region corresponds to migration-selection balance. However, in the area above the corresponding line the whole systems moves back to the lower peak. This means that independently of $\tilde{P}$ if $R = 1$ or $R = 10$, the takeover of the higher peak never happens.

In general, the results of this and preceding sections show that the optimism of the previous authors about the possibility of the third phase of the shifting-balance is unjustified. The third phase can happen only under much more restricted conditions than previous studies lead one to believe. The models used above, however, do not use Wright's idea about excess emigration from the fitter demes. Wright imagined that an increase in fitness of a deme results in increasing the number of individuals within this deme that, in turn, results in increasing the emigration **from** the fitter deme. Excess emigration from the fitter deme should be more favorable for the third phase of the shifting-balance theory. In the next section, I use a simple model of density-dependent selection to evaluate how strong this effect could be.

PEAK SHIFTS UNDER DENSITY DEPENDENT SELECTION

In this section, I consider a simple one-locus two-allele model of weak density-dependent selection acting on a population with overlapping generations. (For reviews of models of density-dependent selection see Roughgarden 1979; Ginzburg 1983.) I assume that fitness depends both on genotype

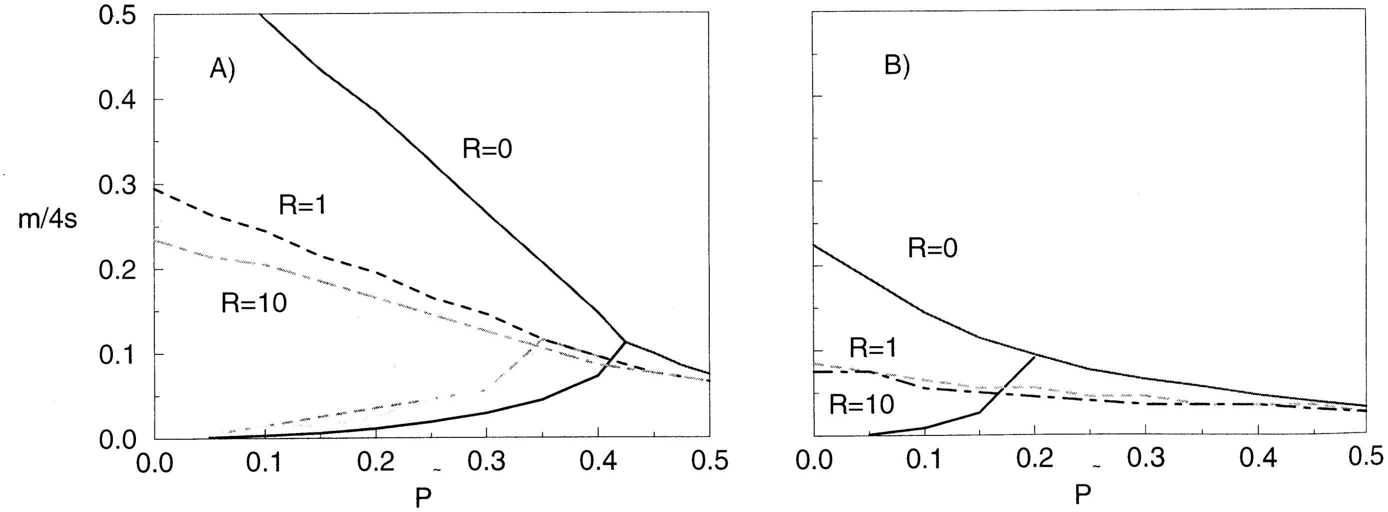

FIG. 2. Regions in parameter space ($m/4s, \tilde{P}$) corresponding to the different outcomes of the peak competition in the two-locus models. (A) One dimensional stepping-stone models with the fitter deme at the border of the network of demes. (B) Two-dimensional stepping-stone models with six nearest neighbors with the fitter deme inside the network of demes. The cases of $R = 0$, $R = 1$, and $R = 10$ are described using solid, dashed, and dashed-dotted lines, respectively. In the one-dimensional stepping-stone models three possible outcomes are possible. In the two dimensional stepping-stone models for $R = 1$ and $R = 10$ only two outcomes are possible: both peaks coexist (in the area adjacent to the x-axes) or the old peak takes over (in the remaining part of parameter space).

and on the population size, N. The dynamics of the frequency of allele **A** and the population size in a single population are approximated by the standard system of differential equations

$$\frac{dp}{dt} = p(w_A - \bar{w}), \tag{11A}$$

$$\frac{dN}{dt} = \bar{w}N, \tag{11B}$$

where w_A is the induced (Malthusian) fitness of allele **A**, and $\bar{w}$ is the mean (Malthusian) fitness of the population (Fisher 1930). I assume that Malthusian fitness decreases linearly with increasing in the population size N (see Table 2 where all αs and βs are assumed to be positive). The dynamics of this system are well understood (Roughgarden 1979; Ginzburg 1983). The population always evolves to an equilibrium with a finite population size. An initially monomorphic population grows according to the logistic curve and equilibrates at a population size equal to the corresponding "carrying capacity" $K \equiv \alpha/\beta$. For example, a population monomorphic for allele **a** reaches a stable population size $K_{aa} \equiv \alpha_{aa}/\beta_{aa}$. The outcome of the evolution of an initially polymorphic population depends on the relation among "carrying capacities" Ks. If $K_{Aa} > K_{aa}, K_{AA}$, the population evolves to a stable polymorphic state. If $K_{AA} > K_{Aa} > K_{aa}$ or $K_{AA} < K_{Aa} < K_{aa}$, the population evolves to the fixation of allele **A** or **a**, respectively. If the heterozygote has the lowest "carrying capacity," that is, if $K_{Aa} < K_{aa}, K_{AA}$, the system has two stable equilibria, and the eventual outcome depends on initial conditions. At one equilibrium, allele **A** is fixed and the population size is K_{AA}. At the other equilibrium, allele **a** is fixed and the population size is K_{aa}. The last situation represents a possible candidate for analyzing the third phase of the shifting-balance theory.

TABLE 2. Malthusian fitnesses in the model of density-dependent selection.

Genotype	Fitness
AA	$\alpha_{AA} - \beta_{AA}N$
Aa	$\alpha_{Aa} - \beta_{Aa}N$
aa	$\alpha_{aa} - \beta_{aa}N$

To simplify the analysis, I shall assume that $\beta_{AA} = \beta_{Aa} = \beta_{aa} = \beta$. Expressing the population size in the units of K_{aa}, that is, using a new variable, normalized population size $n = N/K_{aa}$, one can rewrite (11) as

$$\frac{dp}{dt} = f(p) \equiv (\alpha_{aa})2sp(1 - p)(p - \tilde{P}), \tag{12A}$$

$$\frac{dn}{dt} = g(n) \equiv (\alpha_{aa})(1 + 2sp(p - 2\tilde{P}) - n)n, \tag{12B}$$

where

$$2s = (K_{AA} - 2K_{Aa} + K_{aa})/K_{aa}$$

and

$$\tilde{P} = (K_{aa} - K_{Aa})/(K_{AA} - 2K_{Aa} + K_{aa}).$$

Note that the right-hand side of (12A) is similar to that one in Equation (1). As before, parameter $\tilde{P}$ characterizes the relative advantage of one peak over another: if initially $p < \tilde{P}$, then the population evolves to the fixation of allele **a** and the population size K_{aa}, and if initially $p > \tilde{P}$, the population evolves to the fixation of allele **A** and the population size K_{AA}.

In a network of demes connected by migration, the rate of change of the frequency of allele **A** and of the normalized population size in deme i are

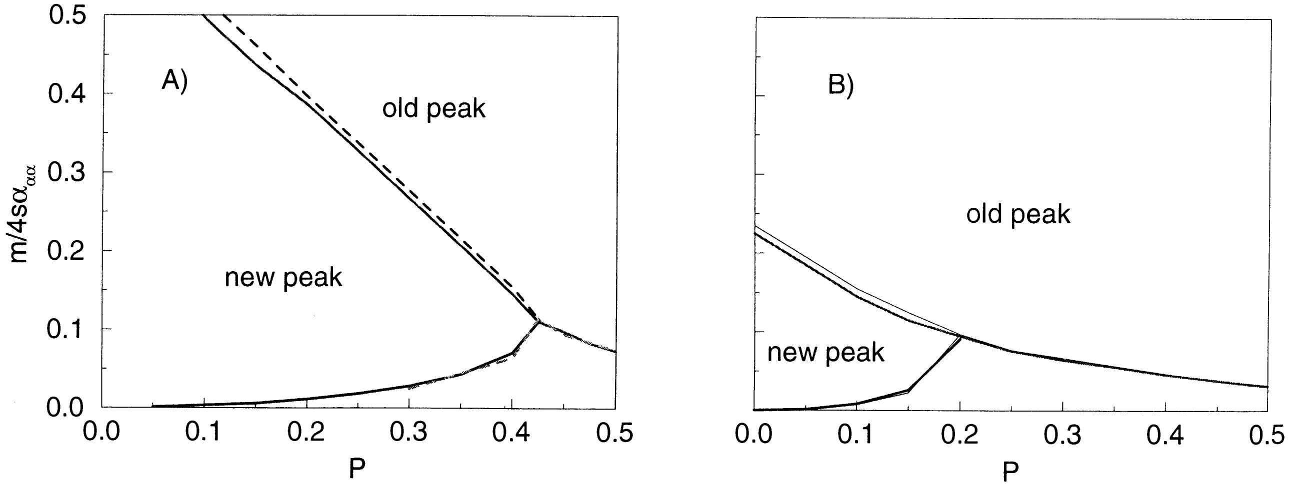

FIG. 3. Comparison of regions in parameter space ($m/4s\ \alpha_{aa},\tilde{P}$) corresponding to the different outcomes of the peak competition in one-locus models without (solid lines) and with (dashed lines) differential migration. In the models with differential migration, $s = 0.1$. (A) One-dimensional stepping-stone models with the fitter deme at the border of the network of demes. (B) Two-dimensional stepping-stone models with six nearest neighbors with the fitter deme inside the network of demes.

$$\frac{dp_i}{dt} = f(p_i) + m\ \Delta p_i, \tag{13A}$$

$$\frac{dn_i}{dt} = g(n_i) + m\ \Delta n_i. \tag{13B}$$

Here m is a (constant) probability that an individual from a "typical" deme leaves its deme. Δp_i and Δn_i are related to the pattern of flows of genes and individuals among demes and depend on the topology of the network. The formulae for Δn_i are standard. For example, in the case of two demes

$$\Delta n_0 = n_1 - n_0, \qquad \Delta n_1 = n_0 - n_1, \tag{14}$$

that is, this is just the difference of the normalized population sizes. The terms Δp_i are more complicated. In the case of two demes

$$\Delta p_0 = (p_1 - p_0)\frac{n_1}{n_0}, \qquad \Delta p_1 = (p_0 - p_1)\frac{n_0}{n_1} \tag{15}$$

(Svirezhev and Passekov 1990, ch. 7). In general, the contribution of migration between demes i and j into Δp_i is proportional to $(p_j - p_i)\ n_j/n_i$. Note that if the sizes of both populations are equal, that is, $n_1 = n_0$, then (15) reduces to (6). In general, however, the ratio of sizes is different from one and changes in time. The system (13–15) of two demes linked by migration was analyzed in (Svirezhev and Passekov 1990, ch. 7). In the model described by equations (12–13), a deme that has higher fitness has a larger size and sends more migrants as well.

In presenting numerical results, I shall use three parameters: s, the relative advantage of the higher peak, $\tilde{P}$, and the parameter $\varepsilon \equiv m/(4s\alpha_2)$ that is equivalent to ϵ in the models considered in the previous sections. Figure 3 compares regions in parameter space corresponding to the different outcomes of the dynamics in models with density-dependent selection (and, hence, with differential migration) with those in the case of density-independent selection where migration was uniform. The latter are exactly the same as those found in the section titled "Single Locus Peak Shift" assuming that all demes have the same constant size. Figure 3A describes a one-dimensional stepping stone model. Similar comparisons are done in Figure 3B for a two-dimensional stepping stone model. One can see that differential migration does not introduce much difference.

DISCUSSION AND CONCLUSION

Altogether the results described here seem to be consistent with Haldane's (1959) intuition about the difficulties with phase three. These results show that the third phase of the shifting-balance theory can proceed only under much more restricted conditions than the previous studies (Crow et al. 1990; Barton 1992; Kondrashov 1992; Phillips 1993) suggested. Migration should be neither too strong no too weak relative to selection for this phase to proceed. The higher peak should be sufficiently dominant over the lower peak. This is in contrast to Barton (1992) who argued that a very low migration rate can spread the new gene combination even if it is deleterious. Contrary to what Crow et al. (1990) and Phillips (1993) concluded, recombination can greatly reduce the plausibility of this phase. In two-dimensional models, recombination can completely preclude peak shifts. Excess emigration that results from excess population growth does facilitate phase three but not significantly (cf, Barton 1992, p. 555). A very important determinant of the ultimate outcome of the competition between different peaks is the topological structure of the network of demes. Analysis given in this paper demonstrates extreme dependence of the outcome of the peak competition on the number of neighboring demes. This property is shared by stochastic models of peak shifts (e.g., Lande 1985a,b, 1986; Rouhani and Barton 1987, 1993; Barton and Rouhani 1991, 1993) in which the outcome of the peak competition strongly depends on the neighborhood size. The importance of the topological structure of the network of demes reflects the power of gene flow over selection (Barton 1992, p. 556). Peak shifts in two-dimensional networks of demes are more difficult than in one-dimensional networks. Increasing the dimensionality of the network from one to two dimensions increases the ease with which a higher peak can be swamped by migration. A similar observation was made by Nagylaki (1975) in analyzing models with spatially varying selection. Phase three can be accomplished easiest if it is initiated in one of the peripheral demes (cf, Mayr 1963) that presumably have fewer number of neighboring demes.

ACKNOWLEDGMENTS

I thank N. Barton, J. Braverman, B. Costantino, J. Crow, A. Hastings, and M. Turelli for helpful discussions and/or comments on the manuscript. This work was supported by Public Health Service Grant R01 GM 32130 to A. Hastings.

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