J. theor. Biol. (2001) **212,** 169–181
doi:10.1006/jtbi.2001.2365, available online at http://www.idealibrary.com on IDEAL®

Polymorphism Maintenance in Populations with Mixed Random Mating and Apomixis Subjected to Stabilizing and Cyclical Selection

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(*Received on* 20 *December* 2000, *Accepted in revised form on* 30 *May* 2001)

We analysed a diploid population model with a mixed breeding system that includes panmixia and apomixis. Each individual produces a part (*ss*) of its progeny by random mating, the remainder (1-*ss*) being a result of precise copying (vegetative reproduction or apomixis) of the parental genotype. Both constant and periodically varying selection regimes were considered. In the main model, the selected trait was controlled by two diallelic additive or semidominant loci, A/a and B/b, whereas the parameter of breeding system (*ss*) was genotype-independent. A numerical iteration of the evolutionary equations were used to evaluate the proportion (V) of population trajectories converging to internal (polymorphic) fixed points. The results were the following. (a) A complex pattern of dependence of polymorphism stability on interaction among the breeding system, recombination rate, and the genetic architecture of the selected trait emerged. (b) The recombination provided some advantage to sex at intermediate period lengths and strong-to-moderate selection intensities. (c) The complex limiting behavior (CLB) was quite compatible with sexual reproduction, at least within the framework of pure genetic (not including variations in population density) models of multilocus varying selection.

1. Introduction

Understanding the mechanisms of the maintenance of genetic variation remains one of the major issues in evolutionary genetics. This problem is especially difficult for species with mixed breeding systems, like combinations of panmixia with selfing and/or vegetative propagation (apomixis). A temporal variation in the selection regime was considered by many authors to be a factor contributing to mutilocus polymorphism maintenance in panmictic systems (Kirzhner *et al*., 1994, 1995b; Korol *et al*., 1994, 1996; Gimmelfarb, 1998). Many efforts were devoted to analysing the consequences of mixed mating systems (outcrossing with apomixis, selfing with apomixis, outcrossing with selfing, and a combination of outcrossing, selfing, and apomixis) in a constant (Marshal & Weir, 1979; Hastings, 1984; Hamrick *et al*., 1992; Asmussen *et al*., 1998, Overath & Asmussen, 1998) and varying environment (Charlesworth, 1989, 1993; Hedrick, 1998).

An earlier theoretical analysis showed that in organisms with high levels of inbreeding, the conditions for polymorphism stability owing to heterozygote advantage are very restrictive (Hayman, 1953; Workman & Jain, 1966). As expected, predominantly selfing species contain less genetic variation than mixed mating or outcrossing species (Hamrick & Godt, 1989). However, the analysis of two locus selection models with intermediate selfing rates shows that the usual

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expectations about the effect of selfing on polymorphism may not hold in general (Holsinger & Feldman, 1985). In particular, for some ranges of selfing the heterozygosity may increase as the selfing rate is increased.

Using a single-locus model of mixed selfing and random mating, Hedrick (1998) showed that the increase in selfing when there is selection varying over time makes the maintenance of polymorphism much more restrictive, if not impossible altogether. In contrast to outcrossing mixed with selfing, a mixture of outcrossing with vegetative (apomictic) reproduction is known to maintain genetic variation within populations equal to that for pure panmixia or even greater than it (Hamrick & Godt, 1989; Hamrick *et al.*, 1992). Considering the consequences of "imperfect" sex (caused by deviations from pure panmixia) on population adaptation to varying environmental conditions is of special interest for multilocus systems. Very little effort has been devoted to this subject. Among the few existing studies, that of Charlesworth & Charlesworth (1979) should be mentioned. The authors analysed the effect of selfing rate on the evolution of a recombination modifier in a temporarily varying environment. Although a few attempts have been undertaken to analyse the effect of selection, either constant or varying, on polymorphism upon mixed outcrossing and apomixis (e.g. Overath & Asmussen, 1998; Hedrick, 1998), nobody has considered multilocus systems in this context. In the study reported here we addressed this question using computer modeling. In particular, we were interested in the effect of the apomixis level and rate of recombination between the selected loci on polymorphism maintenance, population structure, and mean fitness in a population subjected to temporarily varying selection. Such a formulation was motivated by the interest to consider the evolution of sex and recombination caused by environmental fluctuations (Korol *et al.*, 1994).

2. The Model

We consider a population genetic model with a mixed breeding system that includes panmixia and asexual reproduction (e.g. apomixis or vegetative propagation). Each individual produces part (*ss*) of the progeny by random mating resulting in sex-derived zygotes, the remainder (1-*ss*) being a result of a precise copying of the maternal zygote. Both constant and periodically varying selection regimes were considered. Denote by z^t_{hg} ($z^t_{hg} = z^t_{gh}$; $z^t_{hg} \geqslant 0$) the frequency of zygotes of the (h, g) type; correspondingly, $z^t_{s,hg}$ denotes the frequency of (h, g) type produced by the syngamy of gametes h and g whereas $z^t_{a,hg}$ is the frequency of (h, g) type resulting from copying of the parental genotype. Clearly,

$$\sum_{h,g} (z^t_{s,hg} + z^t_{a,hg}) = 1. \tag{1}$$

The transition to the next generation can be described as follows:

$$x_g^{t+1} = \sum_{i,j} P_{ij,g} z^t_{ij}, \tag{2}$$

$$z_{hg}^{t+1} = w_{hg}[(1 - ss)z^t_{hg} + (ss)x^t_h x^t_g], \tag{3}$$

where $P_{ij,g}$ is the probability of obtaining a gamete of type g from zygote (i, j), and w_{hg} is the fitness of zygote z^t_{hg}. In our model, the fitness of an individual is determined by its genotypic value of the selected trait, u, controlled by two linked trait loci, A/a and B/b:

$$\begin{array}{cccc} & BB & Bb & bb \\ AA & d_a + d_b & d_a + h_b & d_a - d_b \\ Aa & d_b + h_a & h_a + h_b & -d_b + h_a \\ aa & -d_a + d_b & -d_a + h_b & -d_a - d_b \end{array}, \tag{4}$$

where d_a and d_b are the additive effects (with no loss of generality, $0 < d_a, d_b < 1$, $d_a + d_b = 1$ and $d_a/d_b = k$) and h_a and h_b are the dominant effects (here we consider $0 \leqslant h \leqslant 0.5$).

Clearly, this scheme describes additive control of the selected trait u across the loci with an arbitrary level of dominance within the loci. We assumed stabilizing selection with temporarily varying optimum, so that the fitness $w_{hg}(u)$ of a genotype with trait value u at the moment t is defined by the fitness function

$$w^t(u(h, g)) = F(u(h, g) - U^t), \tag{5}$$

where U^t is the trait optimum selected at the moment t. For example, one can use $F(u(h, g) - U^t) = \exp\{-[u(h, g) - U^t]^2/\sigma\}$.

Two types of selection regimes were considered in this study: (a) constant selection ($U^t \equiv const$), and (b) cyclical selection with the optimum U^t taking consequently four values, U^1, U^2, U^3, and U^4, so that the structure of the period can be represented as $T_p = t_1 + t_2 + t_3 + t_4$, where t_i is the number of generations with optimum being equal to U^i. Within this scheme, we consider two further simplifications: (a) a frequently changing two-state environment with U^1 and U^3 alternating each generation, $t_1 = t_3 = 1$, $t_2 = t_4 = 0$; and (b) a lower frequency trapeziform changes with $t_1 = t_3 = 3, 10, 20, 50$, $t_2 = t_4 = 1$ and $U^1 = U^3$, $U^2 = U^4$. In our numerical examples, the extreme values of the optimum, U_{min} and U_{max} usually coincided with the minimum and maximum of the genotypic values, $U_{min} = -(d_a + d_b) = -1$, $U_{max} = d_a + d_b = 1$).

To analyse the above model, numerical iterations of the dynamic eqns (2) and (3) were employed. Our objective was to analyse the effect of the sexual strategy and recombination rate between the trait loci on polymorphism stability. To that end, for each combination of parameters, we assessed the fate of 500 trajectories with random initial points; the volume of polymorphism attracting domain was calculated as a proportion of interior fixed points. To characterize the effect of the main parameters on the polymorphic equilibria, we also calculated the deviation from Hardy–Weinberg proportion, linkage disequilibrium and trait variance. To allow comparisons across variants (including those between constant and varying selection regimes), the selection intensity was adjusted in such a way as to maintain relative mean fitness in ranges 0.2–0.3, 0.4–0.5, or 0.8–0.9.

3. Results

3.1. CONSTANT ENVIRONMENT

3.1.1. *Unequal Loci with Purely Additive Effects* ($k = d_a/d_b \neq 1$; $h_i = 0$)

We will consider the situation when the double heterozygous genotypes are closest to the selected optimum trait value. The obtained results point to a strong dependence of polymorphism stability (the volume of polymorphism attracting domain, V) and genetic variance of the selected trait (S) on the interaction between the breeding system (ss) and recombination rate (r). In fact, we address this question by considering the dependence of V and S on r for a series of fixed values of ss, and on ss for a series of fixed values of r. A general trend for a lower polymorphism at higher recombination rates is known for purely panmictic systems (i.e. at $ss = 1$, in our terms) (Gregorius, 1991; Kirzhner *et al.*, 1995b; Korol *et al.*, 1996; Gimmelfarb, 1998). The same trend was observed in our analysis for $ss < 1$. Starting from ss values exceeding some critical level ss_0, the volume of polymorphism attracting domain is a decreasing function of r, whereas for $ss \leqslant ss_0$, $V(r) = 1$ (Fig. 1). Similarly, a general trend for a lower polymorphism with an increasing proportion of sexual reproduction was observed: starting from values of r exceeding some critical level r_0, V is a decreasing function of ss, whereas for $r \leqslant r_0$, $V(ss) = 1$ (see Fig. 1). An excess of heterozygotes compared with Hardy–Weinberg proportions was observed, increasing with the deviation from panmixia.

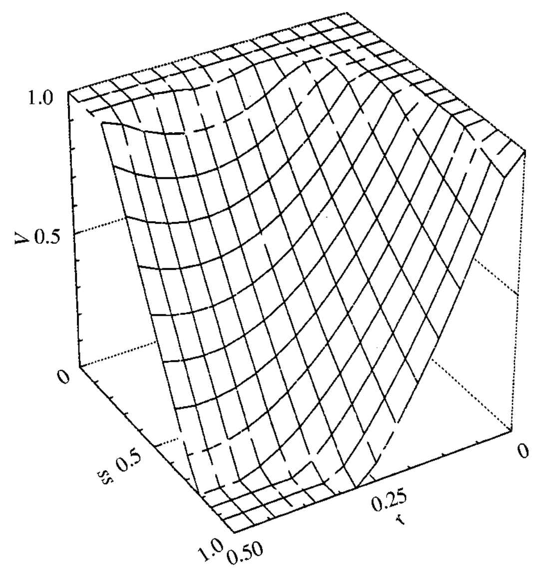


FIG. 1. The dependence of the volume of polymorphism attracting domain on the proportion of panmixia (ss) and recombination rate (r) in a constant environment. The parameter values of the model were defined as follows: $k = 1/4$; $h_a = h_b = 0$; $U^1 = U^2 = U^3 = U^4 = 0.03$; $\sigma = 6$.

Let us consider now in more detail the polymorphic states of the system. Although the case $ss = 0$ (pure asexual propagation) formally also gives $V(r) = 1$ for all r, this polymorphism is "phenotypically neutral" (for the chosen model parameters and selected optimum). Only double heterozygotes are represented in the steady state (hence $p_a = p_b = 0.5$) with arbitrary proportions of linkage and repulsion phase genotypes (hence D_{ab} takes any arbitrary value for the interval $(-0.25, 0.25)$ depending on the initial point). With small deviations of ss and r from zero, instead of the foregoing neutral polymorphism, two stable polymorphic points appear with very similar allele frequencies and opposite signs of D_{ab}. As one could expect, such a situation is also characteristic of systems with larger ss but tight linkage. In other words, within the class of "low mixing" systems, close linkage and a high proportion of asexual progeny seem to affect polymorphism similarly. For both loci, a strong excess of heterozygotes over the expected Hardy–Weinberg level is observed for both types of polymorphic fixed points. With higher mixing (increased $ss \cdot r$), the proportion of trajectories converging to $D_{ab} < 0$ increases at the expense of those that converge to $D_{ab} > 0$, with the total amount of polymorphism $V(ss,r)$ remaining 100%; a further increase in $ss \cdot r$ results in the failure of polymorphism. Clearly, the steady states with opposite signs of D_{ab} differ with respect to the trait variance: higher S is associated with $D_{ab} > 0$. It is noteworthy that with increasing mixing, the mean fitness decreases for both types of the polymorphic steady states, with changes in the breeding system playing a much larger role than that of the recombination rate. With increasing selection intensity, both the condition $V(ss, r) = 1$ and simultaneous stability of $D_{ab} > 0$ and $D_{ab} < 0$ are retained at greater values of $ss \cdot r$.

For all systems polymorphic at both loci, the increase in $ss \cdot r$ results in an increase in the variance S of the selected trait at both steady states (with $D_{ab} < 0$ and $D_{ab} > 0$) and decrease of deviations from Hardy–Weinberg equilibrium. Note that the aforementioned tendency for S to grow with $ss \cdot r$ is caused by different mechanisms for $D_{ab} < 0$ and $D_{ab} > 0$: by the appearance of coupling haplotypes in the first case, and by a joint effect of a reduction in S at larger $ss \cdot r$ and increasing S caused by the movement of the polymorphic fixed point toward the center ($p_a \to 0.5$ and $p_b \to 0.5$) in the second case. Consequently, at higher $ss \cdot r$ the proportion of haplotypes AB and ab is closer to 1 : 1.

3.1.2. *Equal Loci with Semidominant Effects* ($k = 1$, $h_i \neq 0$)

Small deviations from a pure additive scheme result in stable polymorphism maintenance which increases with linkage intensity and proportion of apomixis, and to some extent with h_i. A further increase in h_i is associated with a decrease in the proportion of polymorphic trajectories, and finally, total absence of polymorphism.

3.1.3. *Unequal Loci with Semidominant Effects* ($k \neq 1$, $h_i \neq 0$)

The behavior of this system is quite similar to that of the additive one (with all $h_i = 0$). The only difference is that a deviation from a purely additive effect seems to be an additional factor contributing to polymorphism maintenance.

3.2. CYCLICAL SELECTION

The foregoing examples can easily be extended to include varying selection regimes with abundant polymorphisms. However, in order to reveal the protective role of a changing environment in polymorphism maintenance, it is preferable to consider such varying selection patterns that do not include constant selection components alone that are able to produce stable polymorphism (or do include them, but as minor components) (Korol *et al.*, 1996).

3.2.1. *Unequal Loci with Purely Additive Effects* ($k = d_a/d_b \neq 1$; $h_i = 0$)

The main aspects of the dependence of polymorphism on ss and r caused by weak-to-moderate cyclical selection remain similar to those in constant selection. This concerns the existence of two polymorphic limiting movements (forced oscillations with period length equal to the environmental period) with $D_{ab} < 0$ and $D_{ab} > 0$ along the period (Fig. 2). For purely panmictic systems ($ss = 1$) the last result, i.e. the constancy of sign(D) along the limiting trajectory, was earlier proved analytically for the class of log-convex/log-concave fitness functions (to which the examples of

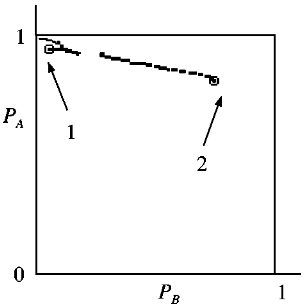


FIG. 2. Two polymorphic fixed points with opposite signs of linkage disequilibrium D_{ab}. The parameter values of the model were defined as follows: $t_1 = t_3 = 10$, $t_2 = t_4 = 1$; $k = 1/4$; $h_a = h_b = 0$; $U^1 = 1$; $U^2 = U^4 = 0$; $U^3 = -1$; $\sigma = 1.4$; $ss = 0.008$; $r = 0.009$. Note that $D_{ab} > 0$ at point 1 and $D_{ab} < 0$ at point 2.

this study also belong) (Kirzhner *et al.*, 1995a). Therefore, our numerical results indicate that the foregoing theory holds, in fact, for a broader class of genetic systems, e.g. mixed random mating and apomixis. Note that the two limiting trajectories (with $D_{ab} < 0$ and $D_{ab} > 0$) also differ for allele frequencies at both loci across the period, in contrast to the constant selection regime, where the allele frequencies at the alternative fixed points (with $D_{ab} < 0$ and $D_{ab} > 0$) coincide. Similar to the results for a constant selection regime, at pure apomixis ($ss = 0$) we obtain a "phenotypically neutral" polymorphism with only double heterozygotes presented in the population.

With increasing intensity of selection, the effects of apomixis and recombination rate on polymorphism maintenance are more complicated and depend on the period length. In particular, at very short and very long periods, the proportion of polymorphic limiting trajectories V is a decreasing function of both ss and r. A different pattern is observed at intermediate period lengths. When outbreeding predominates ($ss \sim 1$), V is a decreasing function of r, corroborating the results obtained by other authors (Gregorius, 1991; Kirzhner *et al.*, 1994, 1995b; Korol *et al.*, 1996; Gimmelfarb, 1998). With increasing proportion of apomixis, maximum $V(r)$ moves toward intermediate and then maximal values of recombination rate. This actually means that the intermediate values of $ss \cdot r$ provide maximum polymorphism (Fig. 3).

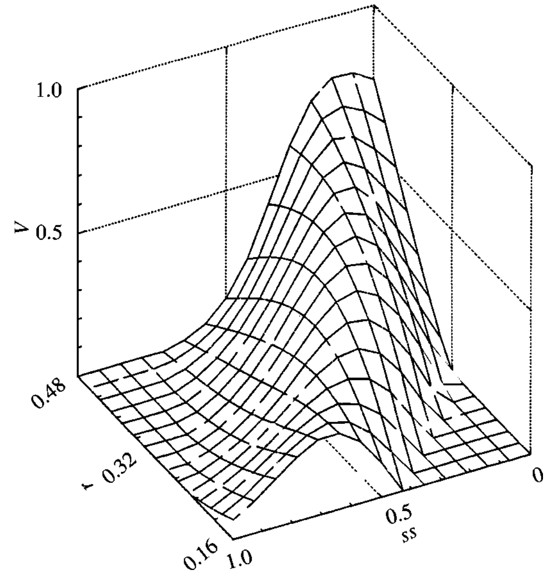


FIG. 3. The dependence of volume of polymorphism attracting domain on the proportion of panmixia (ss) and recombination rate (r) upon strong-to-moderate cyclical selection. The parameter values of the model were defined as follows: $t_1 = t_3 = 10$, $t_2 = t_4 = 1$; $k = 1/4$; $h_a = h_b = 0$; $U^1 = 1$; $U^2 = U^4 = 0$; $U^3 = -1$; $\sigma = 0.9$.

Similar to the foregoing $V(r,ss)$ patterns, the effect of mixing $ss \cdot r$ on other characteristics of population dynamics also depends on the period length T and its interaction with the selection intensity. For small T, increasing $ss \cdot r$ resulted in an increase in trait variance, for any intensity of selection. As expected, changes in the variance of the selected trait along the period are small for short periods, for any ss and r. This variation increases with period length and $ss \cdot r$ (mainly owing to the reduction of the minimum trait variance).

Within the framework of adaptation to varying conditions, it is of great interest to compare outbreeding with different deviations from pure sexual reproduction, including the considered form of partial apomixis mixed with outbreeding. It transpired that with weak cyclical selection, an increase of $ss \cdot r$ resulted in a decrease in the geometric mean fitness W averaged over the period, for any period length. In other words, a weak fluctuating selection does not make mixing advantageous (in terms of mean fitness). The same conclusion is obtained using a related criterion, namely the deviation of the mean value of the selected trait from the temporarily varying optimum. Somewhat different results will be obtained for a moderate-to-strong cyclical selection. Like

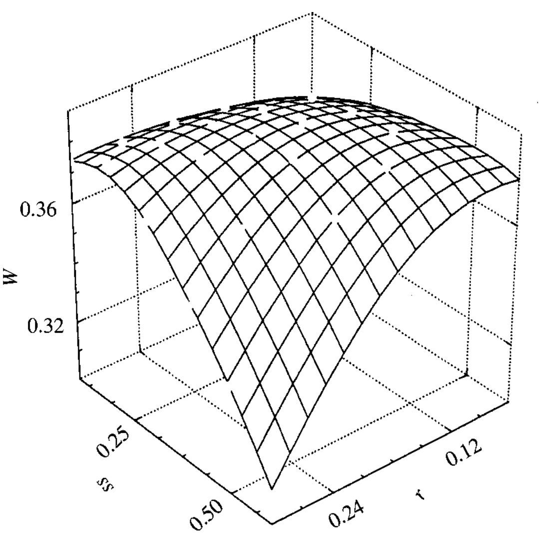


FIG. 4. The dependence of mean fitness on the proportion of panmixia (*ss*) and recombination rate (*r*) in a cyclical environment, at strong-to-moderate selection intensity. The parameter values of the model were: $t_1 = t_3 = 10$, $t_2 = t_4 = 1$; $k = 1/4$; $h_a = h_b = 0$; $U^1 = 1$; $U^2 = U^4 = 0$; $U^3 = -1$; $\sigma = 0.9$.

the size of polymorphism attracting domain V, the effects of apomixis and recombination rate on mean fitness W depend on the period length. At very short and very long periods W is a decreasing function of *ss* and r. At intermediate period lengths, W is a non-monotonic function of *ss* and r. When outbreeding predominates (i.e., $ss \sim 1$), W is a decreasing function of r, whereas with increasing proportion of apomixis, maximum of $W(r)$ moves toward intermediate values of recombination. This actually means that the intermediate values of $ss \cdot r$ provide maximum mean fitness (Fig. 4). This pattern indicates that strong selection may favor an intermediate level of mixing at moderate frequencies of environmental fluctuations.

3.2.2. *Equal Loci with Semidominant Effects* ($k = d_a/d_b = 1$, $h_i \neq 0$)

Like inequality in the effects of loci on the selected trait, semi-dominance contributes to polymorphism maintenance. Under a strong selection regime, polymorphism increased with linkage intensity and the proportion of apomixis. With moderate selection, maximum polymorphism was observed at intermediate values of *ss* whereas the effect of recombination was negative. Asymmetry in the dominance deviations may have a higher protective effect on polymorphism compared to equal dominance situations.

3.2.3 *Unequal Loci with Semidominant Effects* ($k = d_a/d_b \neq 1$, $h_i \neq 0$)

The behavior of this system is quite similar to that of the additive one with unequal loci. The only difference is that a deviation from a purely additive effect seems to be a much less efficient mechanism for polymorphism protection than a deviation from the equal effect of purely additive loci. However, when both mechanisms are presented, their joint effect exceeds the separate contributions. Consequently, for small h_a and/or h_b and $k = d_a/d_b \neq 1$, $V(ss, r) = 1$ is maintained in a wider range of *ss* and r values compared with either: (i) $k = 1$ combined with $h_a \neq 0$ or $h_b \neq 0$, or (ii) $k \neq 1$ combined with $h_a = h_b = 0$. Higher h values may have an opposite effect, resulting in narrower ranges of *ss* and r compatible with polymorphism.

3.3. WHEN IS MORE MIXING ADVANTAGEOUS?

The foregoing results (summarized briefly in Fig. 5) allowed us to conclude that at some range of selection intensities and period lengths, an increased proportion of panmixia is advantageous (in terms of higher mean fitness W). The fact that the optimum value of *ss* (resulting in maximum W) depends on the recombination rate, seems to indicate that this advantage is due to recombination and segregation rather than to segregation itself. In order to discriminate between these two aspects of sex, let us first consider situations where only the segregation components exist, i.e. let the selected trait be dependent on only one locus, with the same total effect as was characteristic of the two-locus system. We were unable to find any combination of parameters that resulted in an intermediate optimum for *ss*: $W(ss)$ appeared to be a decreasing function of *ss*. The next step was to test whether this result is inherited from such two-locus systems where recombination has a very limited ability to produce variation. Namely, we considered two-locus systems with highly asymmetric effects, i.e. with $k = d_a/d_b \ll 1$. This allowed us to demonstrate the advantage of sex as a continuous function of k. Compared with systems with less diverging

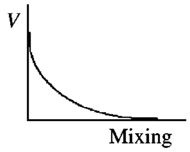
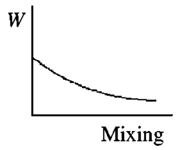
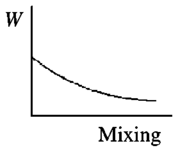
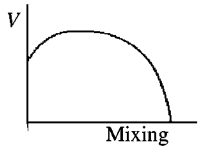
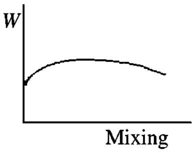
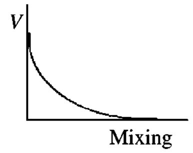
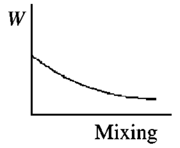
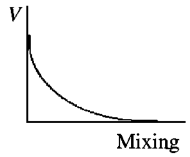
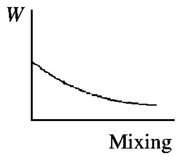
	$V(ss,r)$	$W(ss,r)$
Short period		
Any selection intensity		
Intermediate period		
Strong selection		
Moderate selection		
Weak selection		
Long period		
Any selection intensity		

FIG. 5. A summary of the effect of two-locus cyclical selection on polymorphism (V) and mean fitness (W) as dependent on the level of mixing (due to increasing level of sexual reproduction and/or recombination rate).

effects of contributing loci (i.e. with k closer to 1), an increasing asymmetry (smaller k) reduces the advantage of sex, and starting from some small k only the disadvantage of sex was observed, with W being taken as the criterion (Fig. 6). This analysis means that it is the recombination that gives some advantage to sex at intermediate period lengths and strong-to-moderate selection intensities. With no recombination, sex (syngamy and segregation) becomes useless, at least in the formulation presented.

In the same context, we also considered models with three linked unequal loci, A/a, B/b and C/c, with purely additive effects d_a, d_b and d_c. The increasing of the fitness function with ss and r for intermediate period lengths and strong-to-moderate selection could be observed on a three-locus level as well. However, it emerged that for trajectories converging to limiting polymorphic points, mean fitness is an increasing function of r and ss for a narrower range of these parameters compared with those in two-locus systems (for the same period lengths and selection intensities).

3.4. ENVIRONMENT FOLLOWING A MARKOVIAN CHAIN

The above results on the effect of mixing (ss and r) on polymorphism stability and mean fitness concern a deterministically varying environment. It is interesting to test their robustness with respect to violation of the strong periodicity of the selection regime. To address this question we employed a Markov chain model for environmental variation, by using transition matrices that result in the same average characteristics as the corresponding deterministic models. We suppose that the transition from one environmental state to another is determined by some probability that depends only on these two states. If the cyclical regime included t_1 generations in the first environmental state and t_2 generations in the second state, then for the corresponding chain we define the transition matrix as

$$\begin{bmatrix} 1-c & c \\ d & 1-c \end{bmatrix}, \quad 0 < c, d < 1.$$

In the Markovian model, the ratios $1/c$ and $1/d$, respectively, characterizing the mean time of first attaining state 2 from state 1, and vice versa, can be considered as analogs of t_1 and t_2 values of the cyclical environment. To obtain a Markovian analogue of the main foregoing results obtained for a strictly deterministic environmental variation, an additive system with unequal gene effects was used ($k = 1/4$) with transition probabilities corresponding to three period lengths with $t_1 = t_2 = 3, 10, 20$. The obtained patterns of polymorphism maintenance fully corroborated the conclusions reached for deterministic variations. Nevertheless, the dependence of mean fitness on mixing parameters (r and ss) in Markovian environment differs from the aforementioned patterns for the cyclical environment:

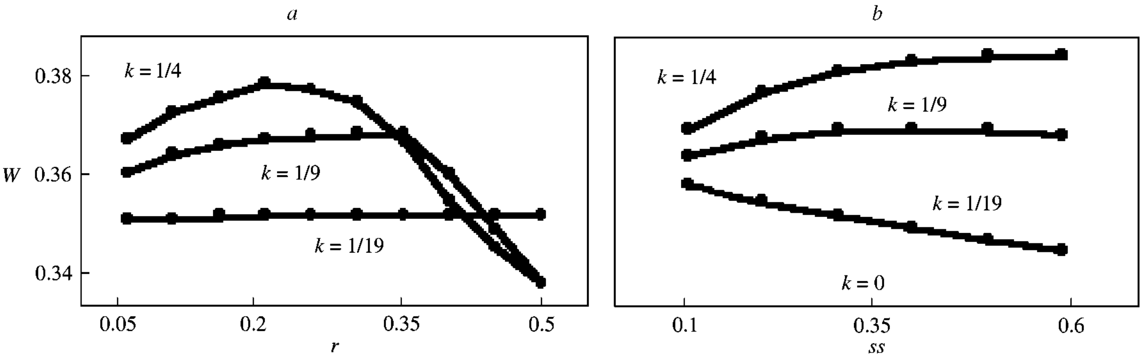


FIG. 6. The dependence of mean fitness on the proportion of panmixia (*ss*) and recombination rate (*r*) for different ratios of gene effects in the cyclical environment. (a) the effect of recombination rate (at $ss = 0.3$); (b) the effect of proportion of panmixia (at $r = 0.1$). Other parameter values: $t_1 = t_3 = 10, t_2 = t_4 = 1$; $k = 1/4$; $h_a = h_b = 0$; $U^1 = 1$; $U^2 = U^4 = 0$; $U^3 = -1$; $\sigma = 0.9$.

the existence of intermediate “optimal” values of *r* and *ss* was found here only under stronger selection and slower environmental changes (not shown).

3.5. CYCLES

We found earlier that a simple cyclical selection for a trait controlled by multiple additive, dominant, or semidominant loci can result in extremely complex limiting behavior (CLB) (Kirzhner *et al.*, 1995c, 1996; Korol *et al.*, 1998). The recombination rate proved as a key factor affecting the mode of CLB and the very existence of CLB (Kirzhner *et al.*, 1995c, 1996; Korol *et al.*, 1998). The foregoing results on CLB were obtained for purely panmictic models. Therefore, we considered it both interesting and instructive to analyse our model with mixed pamixia and apomixis. In particular, we wished to address the following questions: (i) Are CLBs robust to any deviation from panmixia, and how large can these deviations be? (ii) In case of robustness, how will the system’s behavior depend on recombination? (iii) Do systems that display CLB for a mixed breeding system but not for pure panmixia exist? (iv) How attractive are the CLB attractors, i.e. how large is the proportion of trajectories displaying CLB? The following examples answer these questions.

3.5.1. *Example* 1

The selected system consisted of three equal semi-dominant loci. The parameters of the model were $d_a = d_b = d_c = 1$; $h_a = h_b = 0.65$, $h_c = 0.7$; $r_1 = 0.004$; $r_2 = 0.001$; $U^1 = 3.3$; $U^2 = U^4 = 0$; $U^3 = 0.3$; $\sigma = 0.86$, $t_1 = t_3 = 1$, $t_2 = t_4 = 0$. For pure panmixia ($ss = 1$) a rather simple supercycle was observed. A small disturbance of panmixia ($ss = 0.98$) did not change the fact itself of CLB, although the amplitude and period of the supercycle increased several times. A further deviation from panmixia ($ss < 0.98$) resulted in loss of polymorphism. In this example, CLB, when it exists at all, is globally stable. It is noteworthy that with a smaller recombination rate r_1, the CLB existence is compatible only with a smaller deviation from panmixia (so that at $r_1 = 0.001$ and $r_2 = 0.001$ CLB can be observed only for full panmixia). An opposite change in r_1 (from 0.004 to 0.008) increases the range of deviations for panmixia where CLB can be observed, whereas with increased r_2 (e.g. from 0.001 to 0.004–0.005) CLB can be observed at a wider range of *ss* (but it disappears for pure panmixia).

3.5.2. *Example* 2

The selected system consisted of three equal semi-dominant loci. The parameters of the model were $d_a = d_b = d_c = 1$; $h_a = h_b = 0.64$, $h_c = 0.7$; $r_1 = r_2 = 0.0001$; $U^1 = 3.67$; $U^2 = U^4 = 0$; $U^3 = 0.03$; $\sigma = 1.35$; $t_1 = t_3 = 1$, $t_2 = t_4 = 0$. With $ss = 0.9$ a supercycle with a period approximately equal to 1200 environmental periods was found. Here, 90% of the trajectories starting from 100 different points converged to the limiting supercycle and 10% of the limiting trajectories

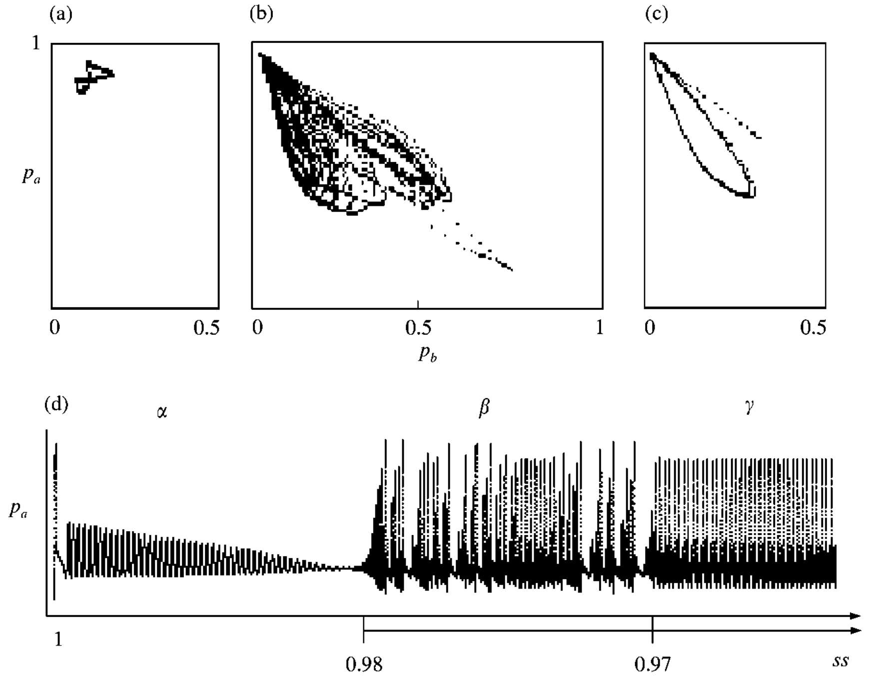


FIG. 7. Complex dynamic patterns caused in a three-locus system subjected to frequent two-state environmental oscillations of selection coefficients. The parameters of the model were: $t_1 = t_3 = 1$, $t_2 = t_4 = 0$; $d_a = d_b = d_c = 1$, $h_a = h_b = 0.64$, $h_c = 0.7$; $r_1 = r_2 = 0.001$; $U^1 = 3.67$; $U^2 = U^4 = 0$; $U^3 = 0.03$; $\sigma = 1.35$. (a) a globally stable supercycle at full panmixia ($ss = 1$); chaos-like behavior at $ss = 0.99$; (c) a supercycle at $ss = 0.97$; complex dynamic pattern bifurcation with a proportion of panmixia (ss) as the bifurcation parameter (α—supercyclical movement, β—chaotic like behavior, γ—supercycle). Note, that the scale of scanning along ss was different for the part α compared with that of $\beta + \gamma$.

converged to an interior fixed point. By contrast, for full panmixia, 80% trajectories converged to the fixed point and only 20% to CLB. Therefore, a deviation from panmixia may promote CLB.

As in the previous example, the pattern of limiting dynamics may strongly depend on linkage intensity. In particular, with a ten-fold increase in recombination compared with the initial values ($r_1 = r_2 = 0.0001 \rightarrow 0.001$), an opposite effect of deviation from panmixia was observed. Out of 100 trajectories starting from random interior points, the following distribution of the resulting limiting trajectories was obtained for different ss: (1) at $ss = 1$, a globally stable supercycle; (2) at $ss = 0.98$, about 97% chaos-like CLBs and only 3% limiting cycles with a very small period; (3) at $ss = 0.97$, two supercycles that together attracted 100% of the trajectories; (4) at $ss = 0.95$–0.94, one of the supercycles degenerated into an interior fixed point whereas the other one attracted 50% of the trajectories. In particular, the chaos-like movements were tested with respect to small disturbances ($< 10^{-7}$) of the coordinates of initial points; already after 5000 environmental cycles most of the coordinates of the trajectories diverged by 1–3 orders of magnitude from the non-disturbed movements (Fig. 7).

3.5.3. *Example* 3

The selected system consisted of three equal semi-dominant loci. The parameters of the model were $d_a = d_b = d_c = 1$; $h_a = h_b = 0.64$, $h_c = 0.7$; $r_1 = 0.0001$; $r_2 = 0.001$; $U^1 = 2.8$; $U^2 = U^4 = 0$; $U^3 = 0.8$; $\sigma = 0.88$; $t_1 = t_3 = 1$, $t_2 = t_4 = 0$. At $ss = 1$, this system displayed only damping oscillations converging to an interior fixed point. With a deviation from panmixia ($ss < 1$) the decrement of oscillations increased. For $ss \in [0.90, 0.92)$ chaos-like CLB was found (with 70% of the trajectories displaying this dynamic pattern and 30% converging to an interior fixed point via damping oscillations). With a further deviation from panmixia ($0.88 < ss < 0.9$), the proportion of chaotic-like CLB fell to about 10%, 70%

converged to a supercycle, and 20% converged to an interior fixed point via damping oscillations. At $ss \sim 0.873$, already 95% of the trajectories converged to supercycle and 5% to the polymorphic point and starting from $ss \leqslant 0.87$, all trajectories converged to the polymorphic point (via damping oscillations).

4. Discussion

4.1. EFFECT OF THE GENETIC SYSTEM ON POLYMORPHISM

The obtained results point to a complex pattern of dependence of polymorphism stability on interaction among the breeding system, recombination rate, and the genetic architecture of the selected trait. A general trend for a lower polymorphism at high recombination rates is known for purely panmictic systems with additive selection. The same trend was manifested in our model at $ss \sim 1$.

In a constant environment, we found that the potential for maintaining polymorphism increased with the level of apomixis. Our computer simulations of two-locus systems corroborated the analytical results obtained earlier for single-locus systems (Bayer 1989; Hamrick *et al.*, 1992; Overath & Asmussen, 1998). For pure panmixia, polymorphism stability is usually a decreasing function of the recombination rate (Korol *et al.*, 1994, 1996; Burger & Gimelfarb, 1999). Here we found that with increasing deviation from panmixia, recombination may become a positive factor in polymorphism maintenance (see Fig. 1).

In a temporally varying environment, we found that higher polymorphism was characteristic of *intermediate* values of ss and r. Other parameters, like the ratio of additive effects (d_a/d_b) on the selected trait, and the dominance effects (h_a and h_b), may cause a simplification of this nonmonotonic dependence by shifting the optimum. The foregoing tendencies were manifested at both constant and cyclically varying selection. Our modeling showed that for most combinations of r and ss, varying selection was a more powerful factor of polymorphism maintenance than constant selection, corroborating the results obtained for pure panmixia (Korol *et al.*, 1994, 1996). The obtained patterns of polymorphism maintenance in Markovian environment fully confirmed the conclusions reached for deterministic cyclical variations.

4.2. ANALYSIS OF EQUILIBRIUM STRUCTURE

It was found earlier that a single-locus constant selection can maintain polymorphism under mixed random mating and apomixis or mixed selfing and outcrossing. This requires an overdominant selection (Overath & Asmussen, 1998). Likewise, in diploid two-locus panmictic models in a constant environment, a globally stable polymorphism is possible only for overdominant selection (Bodmer & Felsenstein, 1967; Hastings, 1981; Gavrilets & Hastings, 1994). Earlier, for cyclical selection, we numerically showed that in panmictic systems polymorphism stability is usually associated with overdominance, but the local stability of polymorphism cannot be excluded even if geometric mean fitnesses of all double homozygotes averaged over the period are higher than those of all heterozygotes (Korol *et al.*, 1996).

In our current numerical analysis of genetic models with a mixed breeding system that includes panmixia and asexual reproduction, stable polymorphism, if it exists at all, is associated with overdominant selection.

4.3. WHAT CAUSES THE ADVANTAGES OR DISADVANTAGES OF SEX? SEGREGATION VS. RECOMBINATION

In a constant environment, the mean fitness is expected to be a decreasing function of mixing (Fisher, 1930; Lewontin, 1971). Our computer simulations fully confirmed this expectation for all ranges of ss and r. In a temporally varying environment, selection on quantitative traits may lead to an advantage for sexual recombination (Maynard Smith, 1980, 1988a, b; Korol & Preygol, 1989; Bergman & Feldman, 1990; Charlesworth, 1993; Korol *et al.*, 1990; Kondrashov & Yampolsky, 1996; Otto & Michalakis, 1998). There is evidence from artificial selection experiments that a response to the directional selection on a trait is frequently associated with a correlated increase in the recombination rate (Flexon & Rodell, 1982; Gorodetsky *et al.*, 1990; Korol *et al.*, 1994; Korol & Iliadi, 1994; Korol, 1999).

In our model with the mixed breeding system, we found that in the cyclical varying environment, weak fluctuating selection did not make mixing advantageous (in terms of mean fitness). The same conclusion was drawn with the use of a related criterion, the deviation of mean value of the selected trait from the temporarily varying optimum. Somewhat different results were obtained for moderate-to-strong cyclical selection. As with the size of polymorphism attracting domain V, the effects of apomixis and recombination rate on mean fitness W depend on the period length. At very short and very long periods, W is a decreasing function of ss and r. At intermediate period lengths, W is a non-monotonic function of ss and r. When outbreeding predominates ($ss \sim 1$), W is a decreasing function of r whereas with an increasing proportion of apomixis maximum $W(r)$ moves toward intermediate r and then to the maximal values of recombination. This actually means that the intermediate values of $ss \cdot r$ provide maximum mean fitness (see Fig. 3). This pattern indicates that a strong selection may favor an intermediate level of mixing at moderate frequencies of environmental fluctuations.

That the optimum value of ss (resulting in maximum W) depends on the recombination rate seems to indicate that this advantage is due to recombination and segregation rather than to segregation itself. To discriminate between these two aspects of sex, let us first consider situations where only the segregation component exists, i.e. let the selected trait be dependent on only one locus, with the same total effect as was characteristic of the two-locus system. We were unable to find any combination of parameters that resulted in intermediate optima for ss: $W(ss)$ appeared to be a decreasing function of ss. The next step was to test whether this result was inherited from two-locus systems where recombination has a very limited ability to produce variation. Namely, we considered two-locus systems with highly asymmetric effects, i.e. with $k = d_a/d_b \ll 1$. This allowed us to show the advantage of sex as a continuous function of k (see Fig. 5). Compared with systems with comparable effects of the contributing loci (large k), an increasing asymmetry (smaller k) reduced the advantage of sex, and starting from some small k, only the disadvantage of sex was observed (with W serving as the criterion). This analysis means that it is the recombination that provides some advantage to sex at intermediate period lengths and strong-to-moderate selection intensities. With no recombination, sex (segregation and syngamy) becomes useless, at least in the formulation presented.

4.4. HOW DOES SEX AFFECT COMPLEXITY?

Temporally varying selection is considered as one of the potential mechanisms of evolution of sex. We found earlier that cyclical selection for a trait controlled by multiple additive, dominant, or semidominant loci with a short period may induce auto-oscillations with a long period ("supercycles") and chaos-like phenomena (Kirzhner *et al*., 1995c, 1996; Korol *et al*., 1998). This selection can result in extremely complex limiting behavior (CLB) of diploid and haploid population trajectories (Kirzhner *et al*., 1994, 1995b, c, 1996; Korol *et al*., 1998). Such behavior was observed for a broad range of system parameters.

One of the key factors affecting the mode (CLB) of population trajectories is the recombination rate. The foregoing results on CLB were obtained for pure panmictic models. Therefore, it was interesting to analyse how the proportion of sexually derived progeny affected CLB. We demonstrated that CLB may arise in mixed breeding systems (panmixia combined with apomixis) experiencing stabilizing selection with cyclically varying optima over a short period. Our CLB included "supercycles" and more complex attractors. It is worth mentioning that we were unable to find two locus examples of CLB for both panmictic and mixed (panmixia with apomixis) breeding systems.

The main source of complex dynamic patterns in population genetics is frequency-dependent selection in single (Charlesworth, 1971; Roughgarden, 1971; Loeschcke & Christiansen, 1984; Altenberg, 1991) and two- or multiple-species interactions (May & Anderson, 1983; Bell & Maynard Smith, 1987; Preygel & Korol, 1990; Hamilton, 1993; Korol *et al*., 1994; Kirzhner *et al*., 1998). One of the generalizations derived recently from a study of single-locus ecological–genetic models with restricted mixing was that sex *reduces* the likelihood of complex dynamics and chaos (Ruxton, 1995). Ruxton's single-locus model could deal with only a very restricted aspect of sex, meiotic segregation and syngamy. However, sexual reproduction includes one more major component: genetic recombination. The foregoing conclusion of Ruxton corresponds indirectly to our results presented in previous papers on cyclical selection obtained for purely panmictic multilocus systems (Kirzhner *et al.*, 1996; Korol *et al.*, 1998): CLB were more frequently observed at lower rates of recombination. Now, we can use a deviation from full panmixia to continue this discussion. It appeared that some of the supercycles observed at small proportions of apomixis vanished at full panmixia. On the other hand, some of the CLBs found for panmictic systems resisted only small deviations from panmixia. Recombination also plays an important role. At larger r, higher deviations from panmixia were compatible with CLB and vice versa, at small r CLBs were observed only for pure panmixia or for very small deviations from it. All in all, the possibility to display CLB seems to depend on the "level of mixing", something like $ss \cdot r$. We can conclude that complex dynamics is quite compatible with sexual reproduction, at least within the framework of pure genetic models (not including variations in population density) of multilocus varying selection.

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