

Complex dynamics of multilocus systems subjected to cyclical selection

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ABSTRACT Earlier we have shown that oscillations with a long period (“supercycles”) may arise in two-locus systems experiencing cyclical selection with a short period. However, this mode of complex limiting behavior appeared to be possible for narrow ranges of parameters. Here we demonstrate that a multilocus system subjected to stabilizing selection with cyclically moving optimum can generate ubiquitous complex limiting behavior including supercycles, T-cycles, and chaotic-like phenomena. This mode of multilocus dynamics far exceeds the potential attainable under ordinary selection models resulting in simple behavior. It may represent a novel evolutionary mechanism increasing genetic diversity over long-term time periods.

Constant selection at a single-locus level, as well as multilocus selection-free regimes, cannot produce by themselves complex limiting population genetic behavior (CLB) with an attracting set of a trajectory, consisting of more than one point (1–5). In a continuous two-locus model of constant selection, Akin (6) found some domains of parameter values that can result in autooscillations. Hastings (7) constructed an example demonstrating CLB in a two-locus discrete-time model. Thus, constant selection can produce CLB in population genetic systems. We found that cyclical selection with a short period may induce autooscillations with a long period (“supercycles”; refs. 8 and 9). However, in all of the foregoing two-locus discrete-time systems, CLB is possible for narrow ranges of parameters. Here we demonstrate that in a very natural class of multilocus systems, stabilizing selection with cyclically moving optimum generates CLBs including supercycles, T-cycles, and chaotic-like phenomena.

The Model

We examined the behavior of an infinite population with panmixia, nonoverlapping generations, and several linked diallelic loci, A_i/a_i ($i = 1, L$), affecting the selected trait, u . Consider a genotype g with $u = u(g)$ defined as: $u(g) = \sum u_i(g)$, where the effect of the i th locus of the genotype g is specified as:

$$\begin{aligned} & d_i, \text{ for } A_i A_i \ (d_i > 0), \\ u_i(g) &= d_i h_i, \text{ for } A_i a_i \ (0 \leq h_i \leq 1), \\ & 0, \text{ for } a_i a_i. \end{aligned}$$

Clearly, this scheme describes additive control of the selected trait u across loci with an arbitrary level of dominance within loci. For cyclical selection, the fitness $w_t(u)$ of a genotype with trait value u at the environmental state t is defined by the fitness function

$$w_t(u(g)) = F(u(g) - z_t) = \exp\{-[u(g) - z_t]^2/s^2\},$$

where z_t is the trait optimum selected for at the moment t . This fitness function is widespread in population genetics (for examples, see refs. 9–11). In some cases we use a modification, $F(u(g) - z_t) + \alpha$, where $\alpha > 0$ is a small constant.

The evolutionary equations for the environmental state t can be written in the standard form:

$$x'_m = \sum wt(u(g_{ij}))P_{ij,m}x_i x_j / W, \quad [1]$$

where x and x' are gamete frequencies in adjacent generations; W is the mean fitness; and $P_{ij,m} \geq 0$ is the probability of producing gamete m by a heterozygote g_{ij} that resulted from union of gametes i and j , $\sum P_{ij,m} = 1$. Only single crossovers per chromosome were considered in our model (10). We also assume equal exchange probability across intervals so that the frequency of complementary crossovers for any of the $L - 1$ intervals is $1/2r/(L - 1)$, while noncrossovers appear with frequencies $1/2(1 - r)$. Thus, $P_{ij,m}$ can easily be calculated as a sum of the frequencies of elementary events, resulting in the appearance of haplotype m from the zygote g_{ij} .

The above system was studied numerically, under different types of cyclical selection regimes, conditioned by an ordered set $\{z_1/n_1, z_2/n_2, \dots, z_q/n_q\}$, where z_t is the selected optimum at the t th environmental state, n_t is the longitude of the t th state, and $p = n_1 + n_2 + \dots + n_q$ is the period length.

Selection for a Trait Controlled by Additive Loci with Unequal Effects

Following the foregoing assumptions, we put here $h_i = 0.5$ across loci. In all examples presented below the simplest period structure was employed, namely $p = n_1 + n_2$, where $n_1 = 1$ and $n_2 = 1$ correspond to alternative states with selected optima z_1 and z_2 . We have evaluated the multivariate range of parameters resulting in CLB by 10^5 runs of different combinations of model parameters and initial points. We found complex behavior in the majority of systems described by parameter sets $\{d_1 = 1, 0 < d_2, d_3, d_4 < 0.4; 0.2 < s < 0.5; 0.05 < r < 0.2; z_1 = z_{\max} = \sum d_i; \text{ and } z_2 = z_{\min} = 0\}$.

In Fig. 1 we demonstrate different types of CLB as dependent on the ratios of individual effects d_i of the participating loci, recombination rate r , period structure p , and selection intensity s . Computer results without proofs are really only suggestive conjectures; nonetheless, it seems that CLB is very common in multilocus systems (with three and more loci) subjected to strong stabilizing selection with cyclically varying optimum (see Fig. 1a). This is the major distinction from the previous two-locus formulations (7–9) where complex regimes were rather uncommon. Notably, the domain size of starting points of the system's phase space resulting in complex trajectories is also extensive.

The supercycle of Fig. 1b consists of two two-dimensional components that lie in different planes, with two alternative sets of few (three to four) haplotypes predominating in the

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Abbreviation: CLB, complex limiting behavior.

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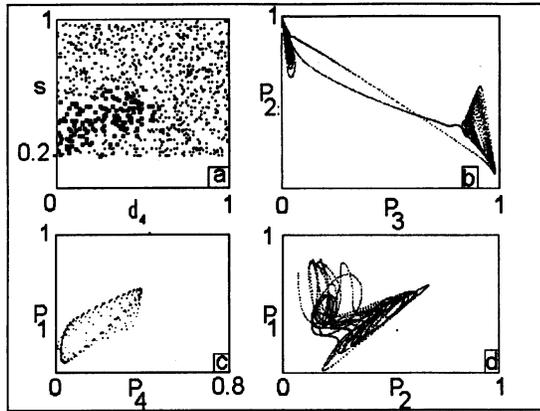


FIG. 1. Complex population trajectories caused by strong cyclical selection for a trait controlled by four additive loci with unequal effects. Here s is the parameter of the fitness function affecting the selection intensity, d_i , and P_i ($i = 1, \dots, 4$) is the additive effect of the i th locus on the selected trait and the frequency of the trait-increasing allele, respectively. Here and in all other figures, the points representing the system phase state are sampled only at times multipliers of p (environmental period lengths). Thus, a full cycle of the environment is marked by the endpoint of the period. The haplotype frequencies at the initial points of the trajectories will be presented below in the following order (1111, 1011, 0111, 0011, 1101, 1001, 0101, 0001, 1110, 1010, 0110, 0010, 1100, 1000, 0100, and 0000), where 1 and 0 at position i ($i = 1, \dots, 4$) stands for A_i and a_i , respectively. The initial points here and in the subsequent figures correspond to $z = z_1$ and are given to a normalizing constant (i.e., the presented coordinates should be divided by their sum). (a) The distribution of systems manifesting complex behavior: s - d_4 plane is presented, with fixed $d_1 = 1$, $d_2 = 0.2$, $d_3 = 0.4$, $\alpha = 0$, and $r = 0.06$. Boldface points correspond to CLBs. (b) An example of supercyclical behavior. The following parameter values were used: $d_1 = 1$, $d_2 = d_3 = d_4 = 0.3$, $s = 0.425$, $\alpha = 0$, $r = 0.22$, $z_1 = 3.8$, and $z_2 = 0$. The initial point in the presented trajectory was (0.002 0.000 0.061 0.006 0.065 0.039 0.098 0.035 0.130 0.174 0.050 0.082 0.018 0.128 0.104 0.007). Then, the range of r resulting in CLB was (0.02–0.32). (c) T-cycles. Parameter values used here were: $d_1 = 3.4$, $d_2 = 1.6$, $d_3 = 0.4$, $d_4 = 0.1$, $s = 1.875$, $r = 0.012$, $z_1 = 11$, $z_2 = 0$, and $\alpha = 10^{-6}$. The initial point here is the same as in previous example. The range of r resulting in CLB was (0.02–0.027). (d) Noncyclical complex trajectory. Parameter values used here: $d_1 = 2.3$, $d_2 = 1.8$, $d_3 = 1.6$, $d_4 = 1.2$, $s = 1.85$, $r = 0.012$, $z_1 = 16.8$, $z_2 = -3$, and $\alpha = 0$. The initial point in the presented trajectory was (0.001855 0.000000 0.061224 0.005566 0.064935 0.038961 0.098330 0.035251 0.129870 0.174397 0.050093 0.081633 0.018553 0.128015 0.103896 0.007421). This noncyclical trajectory was observed only for a very narrow range of r , but other forms of CLB under the foregoing selection regime were found for a wider range of r (0.004–0.014).

population. With an exception of a small domain close to the border set, any arbitrary initial point results in a trajectory converging to this supercycle. In the example of T-cycles shown in Fig. 1c, the limiting motion is two-dimensional, although the full system is clearly 16-dimensional. Even a more complex noncyclical trajectory is presented in Fig. 1d. This limiting chaotic-like motion belongs to an eight-dimensional plane. A small perturbation of the coordinates of the initial point leads to an increasing divergence of the resulting trajectory with time as compared to the initial (nondisturbed) one. Some other two-dimensional projections could be found where the trajectories look like chaotic attractor. In the projection shown in Fig. 2, one could see two domains of attraction; consequent switching of the trajectory between these domains appears to be nonregular.

Selection for a Trait Controlled by Dominant Loci

We consider here the same model, but assume that the selected trait is controlled by dominant loci ($h_i = 1$) with equal effects.

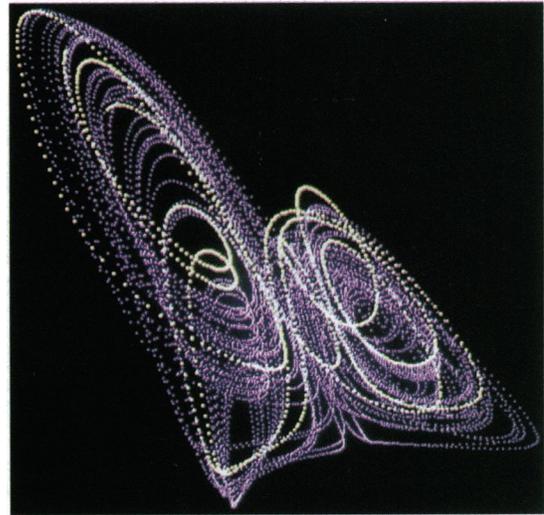


FIG. 2. Chaotic-like attractor The same system as in Fig. 1d is presented here, but projected to another plane. The boldface points correspond to the last portion of the trajectory.

In all examples presented in Fig. 3, the period structure was $p = n_1 + n_2 + n_3 + n_2$, where $n_1 = n_2 = n_3 = 2$ correspond to alternative states with selected optima z_1 , z_2 , and z_3 , respectively; $\alpha = 0$. Here we also evaluated the range of parameters resulting in CLB. Depending on the triads (z_1 , z_2 , and z_3), CLB in this system could be found for any r and s from the range $\{0.5 < s < 0.7$ and $0.01 < r < 0.05\}$. On the other hand, with the

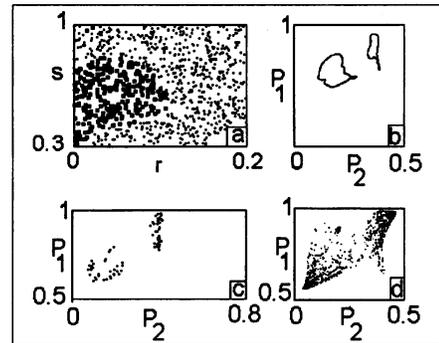


FIG. 3. Complex trajectories caused by strong cyclical selection for a trait controlled by four equal dominant loci. Parameters are as defined in Fig. 1. (a) The distribution of systems manifesting complex behavior: s - r plane is presented, with fixed $z_1 = 4.2$, $z_2 = 2.4$, and $z_3 = 0$. Boldface points correspond to CLBs. (b) T-cycle-like dynamics. The parameters used in this case were: $s = 0.7$, $r = 0.05$, $z_1 = 4.0$, $z_2 = 2.4$, and $z_3 = 0$. The initial point in the presented trajectory was (0.000 0.000 0.000 0.001 0.000 0.006 0.017 0.295 0.000 0.001 0.002 0.122 0.004 0.180 0.350 0.015). Then, the range of r resulting in CLB was (0.001–0.07). Within this range of r , beside the presented type of CLB, we also observed T-cycles and chaotic-like behavior. (c) A long T-cycle. Parameter used were: $s = 0.5$, $r = 0.03$, $z_1 = 4.0$, $z_2 = 2.2$, and $z_3 = 0$. The initial point in the presented trajectory was (0.000 0.000 0.004 0.000 0.002 0.012 0.315 0.000 0.000 0.001 0.088 0.003 0.183 0.386 0.001). The range of r resulting in CLB was (0.01–0.04). Within this range, beside the presented long T-cycles, we observed also short T-cycles (say, 2-cycles). (d) Chaotic-like behavior. This CLB can be obtained by a small change of the selection regime presented in Fig. 3c: here $z_3 = 0.1$ but all other parameters remain the same. The conclusion about chaotic-like regime is derived from the foregoing criterion of trajectory divergence caused by perturbation of the initial point. The initial point in the presented trajectory was (0.000 0.000 0.000 0.001 0.000 0.001 0.013 0.331 0.000 0.000 0.002 0.180 0.001 0.075 0.388 0.008). The range of r resulting in CLB was (0.01–0.05). Within this range, T-cycles were also observed.

indicated ranges of r and s , the range of z_i resulting in CLB was also rather wide: $\{3.4 < z_1 < 4.4; 1.8 < z_2 < 2.4; \text{ and } -1 < z_3 < 1\}$ (Fig. 3a).

It should be stressed that more than one mode of CLB could be common for one dominant system, the observed trajectory being dependent on the initial point. The main difference of the regimes produced by this assumption is that T-cycles and chaotic-like behavior are the common modes of the manifested CLB (Fig. 3 b-d).

The attractor set shown in Fig. 3b consists of two "circles" that lie in a four-dimensional plane. The phase point jumps every following environmental period from one circle to another, so that we have here $T = 2$. However, these consequent landings of both circles occur each moment at a new position, so that the entire circle appears to be the limiting set. The described mode of CLB (short T-cycles undergoing slow superoscillations) is very characteristic of the considered models with equal dominant genes. It is noteworthy that the small variation of parameters may result in a two-point attractor (two-cycle). Thus, here, for the first time, we found a supercyclical behavior with a short period. Long supercycles could also be easily found (see Fig. 3c). Although the limiting set of this system is rather complex, it belongs to a four-dimensional plane, as in the foregoing examples.

Recombination rate (r) is an important parameter affecting the observed modes of the system behavior. To illustrate this point, we present a series of examples of the system trajectories that start from one initial point with different values of r (Fig. 4A). Bifurcation diagram for the initial part of changes in r

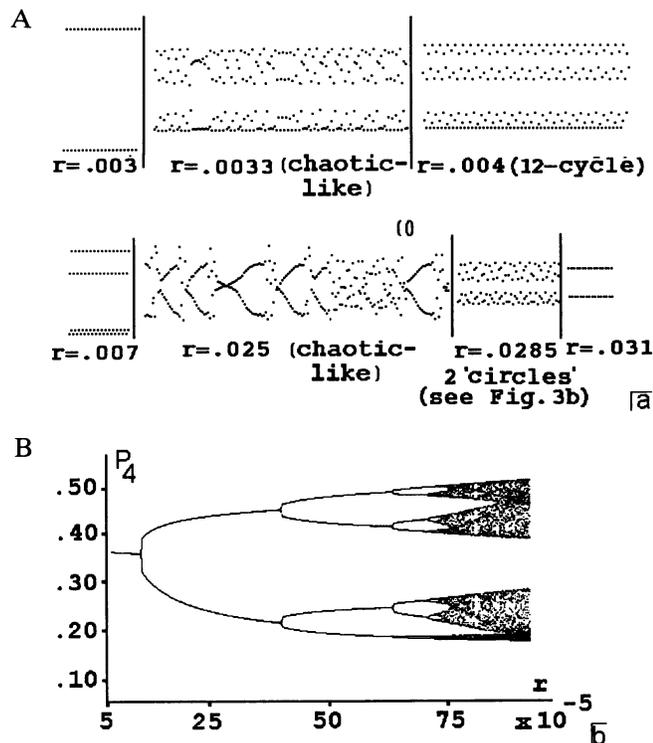


FIG. 4. Changes in the limiting system behavior that resulted from successive changes of recombination rate. The behavior of a system with four equal dominant loci ($h_i = 1$) is shown here, with parameters $s = 0.5$, $z_1 = 3.8$, $z_2 = 2.0$, and $z_3 = 0.6$. (A) Starting from the same initial point, we obtain a series of different CLBs for different intervals of r . The frequency of one-allele at one of the two marginal loci is presented as a time series; each fragment presented in the figure was obtained after 1000 environmental periods. The initial point here is the same as that in Fig. 1d. (B) Bifurcation diagram for the initial part of changes in r values. The initial point was (0.000000 0.000000 0.000000 0.000010 0.000000 0.000013 0.000000 0.358222 0.000000 0.000010 0.000000 0.275081 0.000000 0.000016).

demonstrates a standard picture of period doubling, resulting in a chaotic-like dynamics (Fig. 4B).

Probably, the mechanism generating CLB in a population system with equal dominant loci is somehow different from those with nonequal additive loci. A combination of the considered two groups of models, nonequal additive genes and equal dominant genes, results in a general case of nonequal semidominant genes. Our analysis indicates that in such systems it is much easier to find supercyclical regimes with rather high mean fitness (e.g., up to 0.3–0.4).

Strong Selection, Blocks of Genes, and Complex Trajectories

The selection model considered in this paper is a standard one in population genetics (for examples see refs. 11–13). Nevertheless, its potential to manifest en masse such a complex dynamic pattern as autooscillations or chaotic-like behavior is described here for the first time. The biological relevance of these findings depends on (i) how real are the parameter sets which result in CLB, and (ii) whether the required intensity of selection and resulting mean fitness are compatible with the reproductive capabilities of real populations. Both questions can be answered positively. The range of the ratios of gene effects, dominance ratios, and rates of recombination in our numerical examples (see Figs. 1–4) seem to be quite realistic.

But what about the mean fitness? It is true that in the case of nonequal additive genes, very low mean fitness characterizes a significant part of complex trajectories. Nevertheless, variants with realistic, but very low, mean fitness (e.g., 0.03–0.15) are not uncommon. In case of dominant gene action, the majority of situations with CLB lies in the fitness range of 0.03–0.3. Moreover, in the general model, combining the basic models of sections 2 and 3, it is easy to find supercyclical regimes with rather high mean fitness (up to 0.4), which is compatible even with the relatively low reproductive capacities of many reptiles, birds, and mammals, let alone organismal groups with higher reproduction rates—i.e., most living organisms.

An important question immediately follows about real selection intensities in natural populations. Ford (14) was among the first who demonstrated that strong selection may be quite a common phenomenon in nature. Moreover, the whole concept of the evolution of coadapted blocks of genes is based on the assumption that strong selection and tight linkage are the major factors maintaining these blocks intact (for example, see ref. 15). Many examples of polymorphic coadapted gene blocks are well known (reviewed in refs. 14–17).

The results of this research program reveal a new broad class of relatively simple genetic systems manifesting extremely complex dynamic patterns. This may have important consequences for evolutionary theory, showing that complex behavior may arise even in single species genetic systems without frequency- and/or density-dependent selection. Moreover, the revealed phenomenon might be considered a novel evolutionary mechanism that can assist, in combination with mutation, in long-term maintenance of genetic variation. Thus, it can substantially contribute to the standing biodiversity over evolutionary time.

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