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High genetic variability under the balance between symmetric mutation and fluctuating stabilizing selection

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Summary

We have studied variability maintained in a quantitative trait by the balance between symmetric mutation and direct stabilizing selection with a fluctuating optimum. Using a simulational computer model, we have found that wide fluctuations, such that the range of the optimum changes exceeds the width of the fitness curve, increase the trait variance, often by two or three orders of magnitude, over its value under constant selection. This happens because such fluctuations cause frequent allele substitutions at the loci that control the trait. At any particular moment the variance is increased mostly due to one or several loci where more than one allele is currently common. The data on fluctuating selection in nature are reviewed.

1. Introduction

The maintenance of genetic variability is one of the classical problems in population genetics. In an infinite population, variability may either persist even without mutation or be possible only as the direct result of the mutation process (mutation-independent *v.* mutation-dependent maintenance of variation). In the second case, if invariant stabilizing selection acts directly on a quantitative trait (for discussion of the difference between direct and pleiotropic selection see Kondrashov & Turelli, 1992) and the mutation rate per locus is reasonably low, only one allele is frequent at each locus at a given moment in time (see Barton & Turelli, 1989). Then under invariant Gaussian selection the analytic estimate for the equilibrium genetic variance V in an infinite haploid population is $V_{inv} = 2luS^2$, where l is the number of loci which influence the trait, u is the per locus mutation rate, and S is the width of the fitness curve (the Latter–Bulmer formula: see Barton & Turelli, 1989; Zheng & Cockerham, 1993). Under most realistic parameters V_{inv} is not high. Random drift in a population of a large effective size leads to only a slight decline in V_{inv} (Hill & Keightley, 1988; equation (21a) from Burger *et al.*, 1989; and equation (10) from Houle, 1989).

In contrast, the genetic variance in a population which changes rapidly because of strong directional selection can be high due to permanent allele substitutions (see Kondrashov, 1984; Burger & Lynch, 1995). However, weak directional selection (Turelli, 1988, p. 611; Burger & Lande, 1994) or stabilizing selection with a slightly fluctuating optimum (Barton & Turelli, 1987; Turelli, 1988, p. 613) increases the mutation-dependent genetic variability in a quantitative trait, relative to V_{inv}, only slightly. Here we use computer simulations to study genetic variability under widely fluctuating selection.

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2. Model

A population of n haploid individuals having l loci with alleles 0 and 1 at each was simulated. All these loci were arranged linearly within one chromosome (linkage group). The life cycle is mutation – mating – reproduction – selection with amphimixis, or mutation – reproduction – selection with apomixis. During the mutation process, each allele mutated into the other one with probability u. During apomictic reproduction each individual created one exact copy of itself. With amphimixis, $n/2$ pairs (zygotes) were formed randomly and in each pair recombination occurred, leading to formation of two new haploid individuals. During selection every individual survived with the probability equal to its viability, after which every live individual produced the same number of its exact copies, chosen in such a way that the total number of copies in the population exceeded n slightly. Finally, exactly n individuals were randomly chosen from these copies to start the next generation.

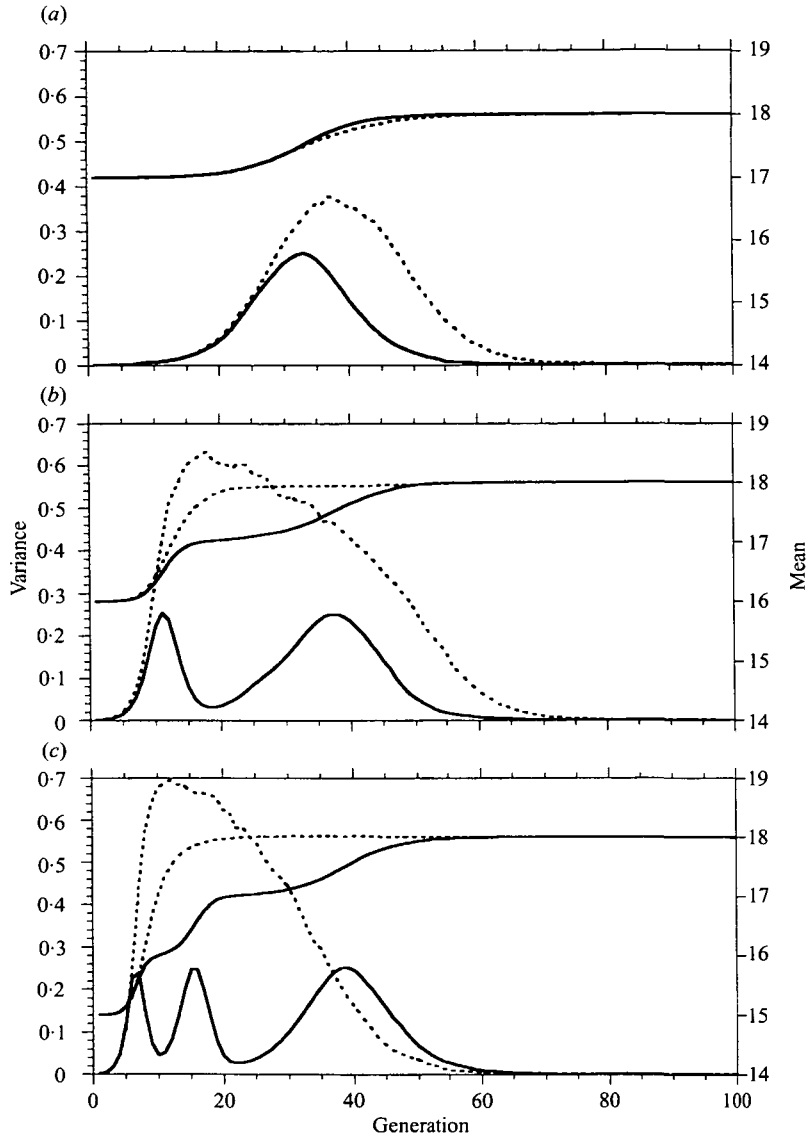

Fig. 1. Dynamics of the mean (increasing curves) and the variance of the quantitative trait during a transition from a 'wrong' to a 'right' equilibrium in the amphimictic (broken lines) and apomictic (continuous lines) population. A transition required substitutions at one (*a*), two (*b*) and three (*c*) loci.

Fitness depended on a single polygenic trait x, the number of 1 alleles at all l loci (we ignored epistasis and phenotypic plasticity: see Bull, 1987; Scheiner, 1993). The populational distribution of x is $p(x)$ with mean μ and variance $V = \sigma^2$. With Gaussian stabilizing selection the fitness of phenotype x is $w(x) = \exp(-(x-o)^2/(2S^2))$, where o is the optimal trait value and S is the width of the fitness curve (Maynard Smith, 1980). With double truncation stabilizing selection (Lewontin 1964), $w(x) = 1$ if $|x-o| \leqslant T$ and 0 otherwise, T being roughly equivalent to S (Maynard Smith, 1988, equation 1).

The value of o was allowed to fluctuate, while S or T remained invariant. With periodical fluctuations, we used

$$o(t) = m + d\sin(2\pi t/\tau), \quad (1)$$

where d is half of the range of fluctuations, m is its centre, t is time in generations, and τ is the period. With random fluctuations, o was incremented each generation by a random variable with the mean 0 and variance v and, if its new value was outside the range $m \pm d$, it was put at its edge. The THINK C programs are available on request.

3. Results

Unless stated otherwise, we used $n = 10000$, $l = 36$, $u = 10^{-5}$, periodically fluctuating Gaussian selection with $m = 18$ and $S = 1{\cdot}5$, and free recombination. When selection fluctuated widely, dynamics of the population converged to the same asymptotic mode after several hundred generations, regardless of its initial state. Under strong selection, i.e. small S and large d, the convergence was faster.

Under constant selection ($d = 0$), an amphimictic population approached an asymptotic state in which one allele at each locus was usually close to fixation, while linkage disequilibria were small. Multiple

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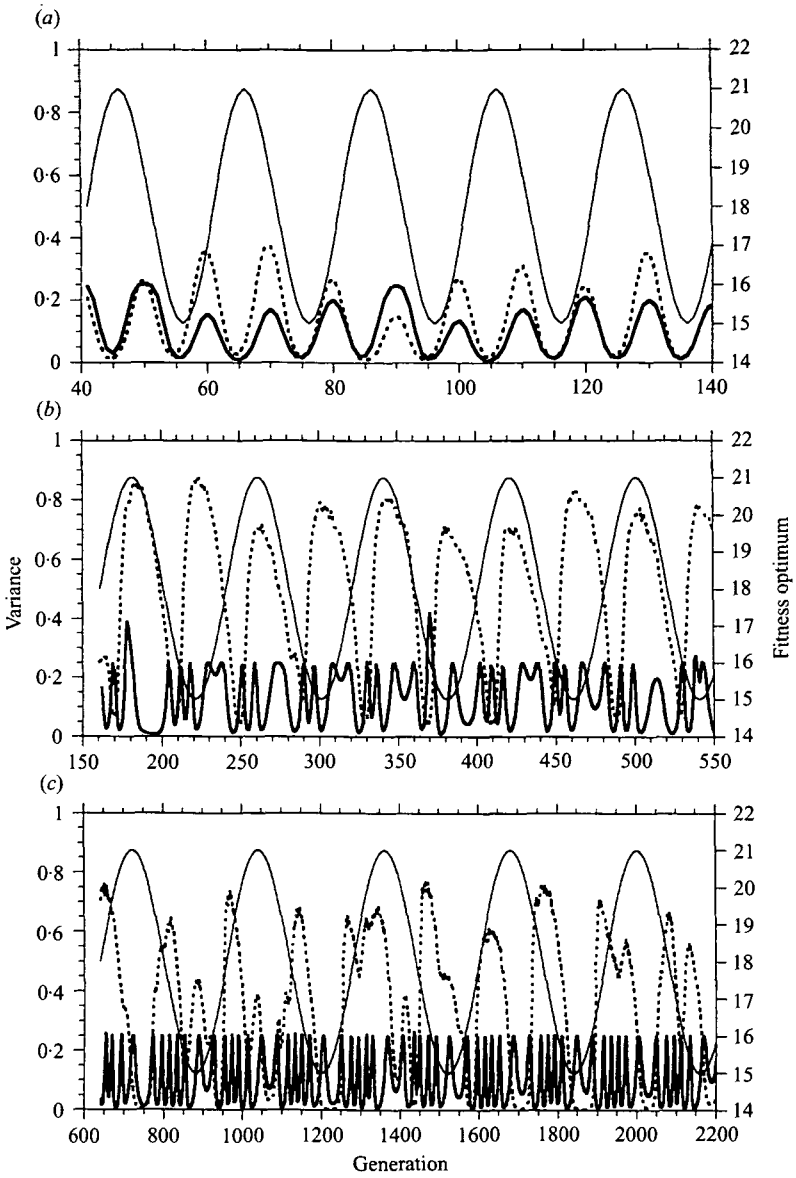

Fig. 2. Changes in fitness optimum (thin lines) and genetic variance in the amphimictic (broken lines) and apomictic (continuous lines) population with $d = 3{\cdot}0$ and $\tau = 20$ (*a*), 80 (*b*) and 320 (*c*).

equilibria with different sets of loci where allele 1 is frequent are possible in this situation (Barton, 1986, 1989). If for some equilibrium the number of such loci coincides with or is close to o, the population remained in such a 'right' equilibrium practically indefinitely. In contrast, the population abandoned a 'wrong' equilibrium (where the number of loci with allele 1 frequent was far from o) and switched to a right one relatively fast (Fig. 1). Because all equilibria are locally stable in an infinite population, this was caused by drift. As predicted by Barton (1989, table 1), the variance of the population temporarily occupying a wrong equilibrium was up to several times higher than the variance in a right equilibrium, as described by the Latter–Bulmer formula (data not reported).

Switches between equilibria were accompanied by dramatic temporal increases in the variance (Fig. 1). Because a switch requires substitution of one frequent allele with another one, the peak value of V must be at least $\sim 0{\cdot}25$, the contribution of a locus where alleles 0 and 1 both have frequency 0·5. Such peaks occurred with apomixis where beneficial alleles at different loci substitute inferior alleles successively. With amphimixis the peaks were higher because, even when a switch from a wrong equilibrium to a right one required substitutions at several loci, it occurred as one long leap, with several substitutions occurring simultaneously.

The dynamics of variance under fluctuating selection are shown in Fig. 2. In the amphimictic population, V usually had two high peaks every τ generation. With apomixis, a similar pattern occurred only with $\tau = 20$, where only two substitutions occurred per period, while during longer periods there were more peaks. The heights of these peaks were almost always close to 0·25, with rare higher peaks caused by hitch-hiking and simultaneous substitutions at two loci.

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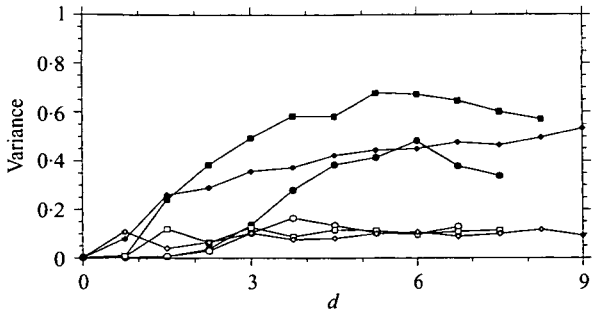

Fig. 3. Arithmetic mean of the genetic variance as a function of d in the amphimictic (filled markers) and apomictic (open markers) population with $\tau = 20$ (circles), 80 (squares) and 320 (diamonds).

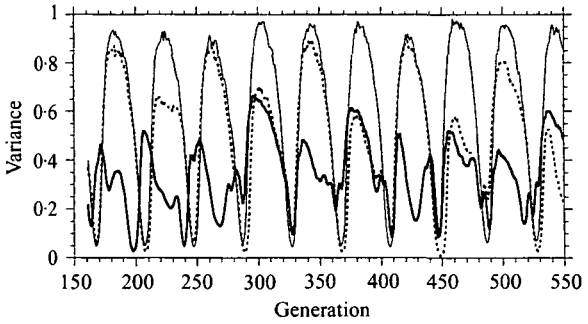

Fig. 5. Changes in genetic variance in the amphimictic population under the same conditions as in Fig. 2*b* with the following deviations: $l = 100$, $m = 50$ (thin line); $l = 36$, $m = 9$ (broken line); $l = 16$, $m = 8$ (thick continuous line).

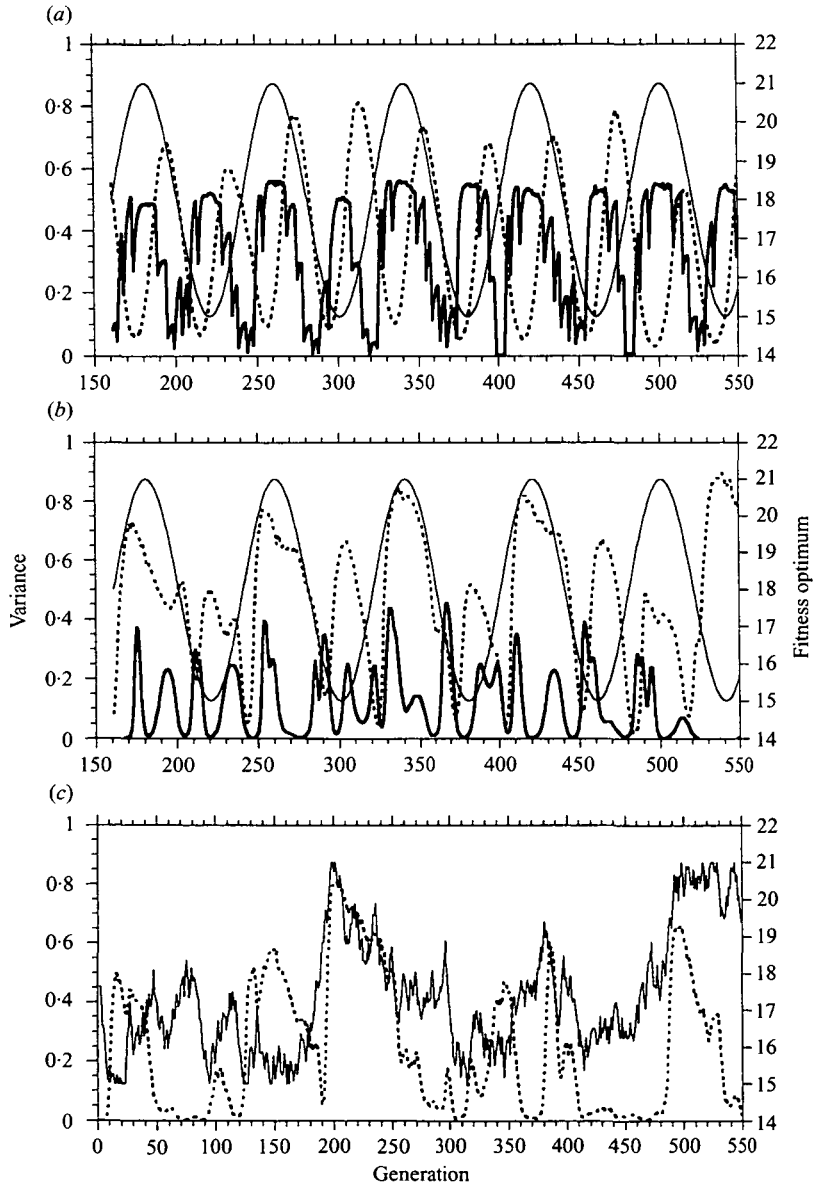

Fig. 4. Changes in fitness optimum (thin lines) and genetic variance in an amphimictic population under the same conditions as in Fig. 2*b* with the following deviations: (*a*) $S = 3{\cdot}0$ (broken line), double truncation selection with $T = 1{\cdot}5$ (continuous line); (*b*) limited recombination with one cross-over per genome (broken line), $u = 10^{-6}$ (continuous line); (*c*) random changes in o (broken line).

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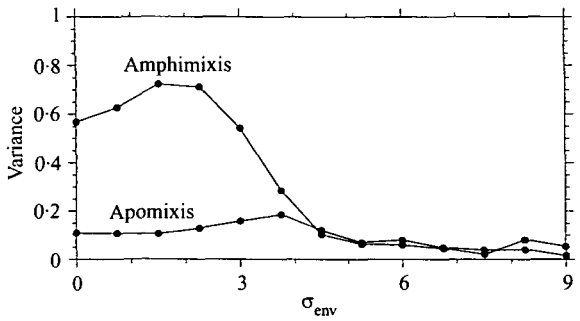

Fig. 6. Arithmetic mean of the genetic variance as the function of the environmental variance under the same parameters as in Fig. 3 ($d = 4{\cdot}5$ and $\tau = 80$).

Figure 3 presents the arithmetic mean of V over time, calculated over 5τ generations starting from the 2τth one, as a function of d. The dramatic rise in V occurred when d became close to S, because then the fitness curves corresponding to different extreme positions of o do not overlap much, and the population must respond by allele substitutions. This rise begins when $d < S$ under $\tau = 320$, while with $\tau = 20$ it begins only when $d \approx 2S$, because with smaller d the population does not respond to frequent fluctuations. Further increase in d led to only a moderate growth of V. With $\tau = 20$ or 80 and high d the population could not evolve fast enough and died out. Similar patterns were observed with various $S > 0{\cdot}3$. Amphimixis and apomixis produced similar results, but with apomixis the mean variance was always below 0·25 (data not reported).

The genic variance, estimated from allele frequencies assuming no linkage disequilibrium, was, in the amphimictic population, only slightly higher than the observed genetic variance, because repulsion linkage disequilibria were not large. In contrast, the genic variance in the apomictic population usually exceeded the genetic variance substantially (data not reported). Actually, the notion of genic variance is not very meaningful with apomixis.

Mutation–selection balance in a quantitative trait under fluctuating selection depends on many factors. Although it is impossible to cover all possibilities, we have considered the effects of some deviations from our standard set of parameters (Fig. 4). Apparently, the results reported above are robust and do not change much after moderate changes in parameters. In addition, three extra factors were studied in some detail.

The number of loci which control the trait is not too important, although the variance grows with it slowly (Fig. 5). Apparently, the only thing which matters is that enough loci must be available for mutations that are currently favourable. Thus, with $l = 36$ and $m = 9$, the heights of peaks that correspond to the times of decline or increase in o were close to those with $l = 16$ or $l = 100$, respectively.

The effect of environmental variance was also straightforward (Fig. 6). Here the phenotype of an individual is determined as the sum of its breeding value x (used before) and a random variable having Gaussian distribution with the mean 0 and variance σ^2_{env}. With small σ^2_{env} the genetic variance was, as before, much higher than what is expected under invariant selection. However, when σ^2_{env} gets so large that d becomes smaller than $\sqrt{(S^2+\sigma^2_{env})}$, the genetic variance becomes closer to its values expected for the corresponding $S^2+\sigma^2_{env}$ under constant selection (equation 8 from Charlesworth, 1993). This generalizes the results of Fig. 3, and confirms that $S^2+\sigma^2_{env}$ describes the strength of stabilizing selection on breeding values (Turelli, 1984).

The data obtained when alleles with all contributions were possible, instead of just 0 and 1, are presented in Fig. 7. A mutation incremented the contribution on an allele by a Gaussian random variable (Turelli, 1984) with the average 0 and variance 1·0. This led to less regular changes of variance with time. In particular, peaks higher than 0·25 routinely occurred even with apomixis, due to substitutions involving pairs of alleles whose contributions differ by more than 1 (compare Figs. 7*a* and 2*b*). However, the dependence of the mean variance on d was very similar to that in the case of two alleles (Figs. 7*b* and 3).

4. Discussion

The main result of our simulations is that when genetic variance is maintained by the balance between mutations and direct stabilizing selection, wide fluctuations of the fitness optimum such that $d > \sqrt{(S^2+\sigma^2_{env})}$, lead to a much higher average genetic variance than constant selection. With only two alleles, 0 and 1, at least two factors can contribute to this effect. First, because o moves, a population frequently finds itself in a 'wrong' equilibrium (see Results), which leads to a higher V (Barton, 1986). Second, when o moves too far away, the population follows it, switching to a new equilibrium, which causes a dramatic temporary increase in V (Fig. 1). Such switches can occur permanently if selection changes fast, leading to a high average V. Of course, if selection fluctuates too frequently, the population may fail to respond and stay in the same equilibrium, which would lead to only a modest increase in variance. However, because a switch to a new equilibrium can occur rapidly, even $\tau = 20$ can already generate a high variance (Figs. 2 and 3).

Substitutions are the leading variance-increasing factor, because V in a population in a wrong equilibrium, although increased, is much lower than what we observed (compare Figs. 2 and 3 with Barton, 1989, table 1). With haploid selection, $l = 36$, $S = 1{\cdot}5$, and $u = 10^{-5}$, where the Latter–Bulmer formula predicts $V_{inv} = 2luS^2 \approx 0{\cdot}001$, the average variance under $d > S$ was ~ 3 orders of magnitude higher (Fig.

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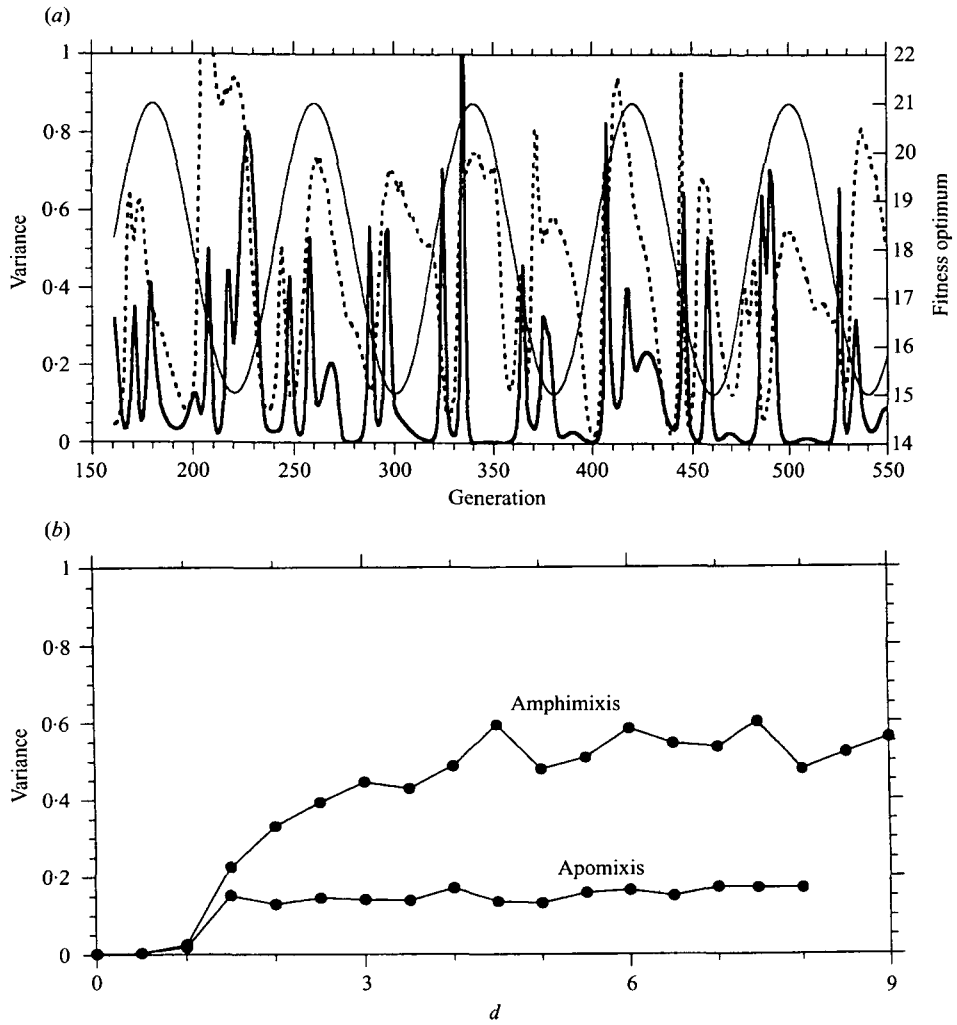

Fig. 7. Genetic variance when alleles can have arbitrary effects (see text). (*a*) Changes in fitness optimum (thin line) and genetic variance in the amphimictic (broken lines) and apomictic (continuous lines) population under the same conditions as in Fig. 2 ($\tau = 80$). (*b*) Arithmetic mean of the genetic variance as the function of d under the same parameters as in Fig. 3 ($\tau = 80$).

3), while with $u = 10^{-6}$ the relative increase was even greater.

While with apomixis the average V is always below 0·25, because substitutions usually occur successively, with amphimixis V can be even higher, due to simultaneous substitutions (Figs. 2 and 3), and was sometimes only several times lower than $0{\cdot}25l$, the highest variance possible under linkage equilibrium. Both deterministic (repulsion linkage disequilibria created by selection) and stochastic (initial absence, in a finite population, of very rare genotypes carrying multiple beneficial allele: see Maynard Smith, 1978) factors led to successive substitutions with apomixis in our simulations.

The situation may be even simpler if alleles with all contributions are possible, because in this case apparently there is a unique equilibrium under constant selection, in which an allele with the contribution o/l is close to fixation at every locus (Turelli, 1984). Still, responding to widely fluctuating selection requires frequent allele substitutions (Fig. 7), which cause increased genetic variance. Thus, a dramatic increase in genetic variance due to widely fluctuating selection does happen under a variety of realistic assumptions.

The increase in variance was significantly higher with amphimixis than with apomixis, unless S was smaller than $\sim 0{\cdot}3$. With such small S substitutions occurred successively even with amphimixis (data not reported). Such values of S seem unlikely, because the width of fitness function usually exceeds the magnitude of the typical change introduced by one mutation (Turelli, 1984; note that we measure our trait in the units of such change).

We assumed equal and additive contributions of different loci to a quantitative trait. In this case, without mutation variability is not maintained by direct frequency-independent selection. This is true for both constant (Lewontin, 1964; Lande, 1975; Rutchman, 1994) and fluctuating (Lande, 1977; Bull, 1987) selection, although in the second, but not the first, case the genetic load usually decreases when

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variability grows, and the alleles for recombination can be selected for because they increase the genetic variance if some variability exists (see Kondrashov & Yampolsky, 1996). However, mutation-independent maintenance of variability is possible under constant selection in the diplophase in the case of unequal or non-additive contributions of different loci (see Gavrilets, 1993; Gavrilets & Hastings, 1994*a*, *b*) or overdominance (Korol & Preygel, 1989; Lorenzi *et al.*, 1989). Fluctuating selection, even haploid, can maintain variability, although apparently the range of parameters where this happens is very narrow (Kirzhner *et al.*, 1995*a*, *b*), unless generations overlap (Ellner & Hairston, 1994). Frequency dependence (Slatkin, 1979) and genotype–environment interactions in a heterogeneous environment (Gillespie & Turelli, 1989) can also maintain variability. Thus, the importance of mutation-dependent variability is not clear. Even if it is important, stabilizing selection may be only an apparent phenomenon caused by pleiotropy (see Kondrashov & Turelli, 1992), in which case it probably cannot fluctuate.

Thus, the estimates of genetic variance maintained by the balance between mutations and direct invariant stabilizing selection are completely irrelevant when selection fluctuates widely, relatively to the width of the fitness function. If this balance is important for the maintenance of genetic variability in nature, we can expect a higher variance in populations living under fluctuating conditions, provided that the variance caused by one or several loci where at least two alleles are frequent exceeds the variance generated by rate alleles at many loci according to the Latter–Bulmer formula (Turelli, 1984). At any given moment of time this extra variance in a quantitative trait should be caused only by the loci where substitutions currently proceed, i.e. high variance in traits under fluctuating selection should be oligogenic, although the identity of the genes that contribute most to it changes permanently.

Much of the data on the genetic variability at individual loci has been obtained by protein electrophoresis, although the role of these loci in determining phenotypic traits is usually obscure. The populations from supposedly stable underground and cave habitats appear to have low variabilities (for a review see Nevo *et al.*, 1984). However, this trend is not universal: tropical and deep sea species are usually highly variable, despite the apparent stability of their environments (Nei & Graur, 1984; Nevo *et al.*, 1984). In any case, the differences are much smaller than those observed in our study. Besides, it is difficult to determine conclusively whether selection in a particular population fluctuates (Endler, 1986). Beardmore & Levine (1963) and Mackay (1980, 1981) observed a higher genetic variance in quantitative traits in artificial populations of *Drosophila* in a temporarily fluctuating environment, but the increase was not large.

Populations of many freshwater plankton invertebrates are particularly likely to experience fluctuating selection with periods in the range of tens of generations, because temperature, food abundance and the presence of predators change dramatically over the course of a year. In *Daphnia* selection was shown to change direction during a season (Carvalho & Crisp, 1987; Lynch, 1987). However, this does not necessarily translate into swift changes in the genetic structure of the population. Instead, some plankton organisms show remarkable seasonal phenotypic plasticity in morphology (Havel, 1985; Parejko & Dodson, 1991), reproductive traits (Threlkeld, 1987; Yampolsky & Ebert, 1994) and overall gene expression (Lee, 1984). There is no evidence that plankton organisms have unusually higher levels of genetic variability.

Thus, currently there is no indication that widely fluctuating selection in quantitative traits is a common phenomenon. However, the matter is not closed, and potential implications of such selection make it worth studying. In particular, it seems that fluctuating selection in quantitative traits can play a role in the maintenance of amphimixis and recombination only under conditions which lead to a large increase in the genetic variance, compared with invariant selection (see Kondrashov & Yampolsky, 1996). This increase can help to detect such selection when it exists.

References

Barton, N. H. (1986). The maintenance of polygenic variation through a balance between mutation and stabilizing selection. *Genetical Research* **47**, 209–216.

Barton, N. H. (1989). The divergence of a polygenic system subject to stabilizing selection, mutation and drift. *Genetical Research* **54**, 59–77.

Barton, N. H. & Turelli, M. (1987). Adaptive landscapes, genetic distance and the evolution of quantitative characters. *Genetical Research* **49**, 157–173.

Barton, N. H. & Turelli, M. (1989). Evolutionary quantitative genetics: how little do we know? *Annual Review of Genetics* **23**, 337–370.

Beardmore, J. A. & Levine, L. (1963). Fitness and environmental variation. I. Study of some polymorphic populations of *Drosophila pseudoobscura*. *Evolution* **17**, 121–129.

Bull, J. J. (1987). Evolution of phenotypic variance. *Evolution* **41**, 303–315.

Burger, R. & Lande, R. (1994). On the distribution of the mean and variance of a quantitative trait under mutation–selection–drift balance. *Genetics* **138**, 901–912.

Burger, R. & Lynch, M. (1995). Evolution and extinction in a changing environment: a quantitative-genetic analysis. *Evolution* **49**, 151–163.

Burger, R., Wagner, G. P. & Stettinger, F. (1989). How much heritable variation can be maintained in finite populations by mutation–selection balance? *Evolution* **43**, 1748–1766.

Carvalho, G. R. & Crisp, D. J. (1987). The clonal ecology of *Daphnia magna* Crustacea: Cladocera). I. Temporal changes in the clonal structure of a natural population. *Journal of Animal Ecology* **56**, 453–468.

Charlesworth, B. (1993). Directional selection and the

evolution of sex and recombination. *Genetical Research* **61**, 205–224.
Ellner, S. & Hairston, N. G., Jr (1994). Role of overlapping generations in maintaining genetic variation in a fluctuating environment. *American Naturalist* **143**, 403–417.
Endler, J. A. (1986). *Natural Selection in the Wild*. Princeton, NJ: Princeton University Press.
Gavrilets, S. (1993). Equilibria in an epistatic viability model under arbitrary strength of selection. *Journal of Mathematical Biology* **31**, 397–410.
Gavrilets, S. & Hastings, A. (1994*a*). Maintenance of multilocus variability under strong stabilizing selection. *Journal of Mathematical Biology* **32**, 287–302.
Gavrilets, S. & Hastings, A. (1994*b*). Dynamics of genetic variability in two-locus models of stabilizing selection. *Genetics* **138**, 519–532.
Gillespie, J. H. & Turelli, M. (1989). Genotype–environment interactions and the maintenance of polygenic variation. *Genetics* **121**, 129–138.
Havel, J. E. (1985). Cyclomorphosis of *Daphnia pulex* spined morphs. *Limnology and Oceanography* **30**, 853–861.
Hill, W. G. & Keightley, P. D. (1988). Interrelations of mutation, population size, artificial and natural selection. In *Proceedings of the Second International Conference on Quantitative Genetics* (ed. B. S. Weir, E. J. Eisen, M. M. Goodman & G. Namkoong), pp. 57–70. Sunderland: Sinauer.
Houle, D. (1989). The maintenance of polygenic variation in finite populations. *Evolution* **43**, 1767–1780.
Kirzhner, V. M., Korol, A. B., Ronin, Y. I. & Nevo, E. (1994). Cyclical behavior of genotype frequencies in a two-locus population under fluctuating haploid selection. *Proceedings of the National Academy of Sciences of the USA* **91**, 11432–11436.
Kirzhner, V. M., Korol, A. B. & Ronin, Y. I. (1995). Cyclical environmental changes as a factor maintaining genetic polymorphism. I. Two-locus haploid selection. *Journal of Evolutionary Biology* **8**, 93–120.
Kondrashov, A. S. (1984). Rate of evolution in a changing environment. *Journal of Theoretical Biology* **107**, 249–260.
Kondrashov, A. S. & Turelli, M. (1992). Deleterious mutations and apparent stabilizing selection in quantitative traits. *Genetics* **132**, 603–618.
Kondrashov, A. S. & Yampolsky, L. Yu. (1996). Evolution of amphimixis and recombination under fluctuating genetic selection in one and many traits. *Genetical Research* **68**, 165–173.
Korol, A. B. & Preygel, I. A. (1989). The increase of recombination in the multilocus system under changing environment. *Genetika* **25**, 923–931 (in Russian).
Lande, R. (1975). The maintenance of genetic variability by mutation in a polygenic character with linked loci. *Genetical Research* **26**, 221–235.
Lande, R. (1977). The influence of the mating system on the maintenance of genetic variability in polygenic characters. *Genetics* **86**, 485–498.
Lee, L. W. (1984). Environmentally controlled phenotypic plasticity of morphology and polypeptide expression in two populations of *Daphnia pulex* (Crustacea: Cladocera). *Oecologia (Berlin)* **63**, 207–214.
Lewontin, R. C. (1964). The interaction of selection and linkage. II. Optimum models. *Genetics* **50**, 757–782.
Lorenzi, R., Zonta, L. A. & Jayakar, S. D. (1989). Quantitative traits and temporally variable selection: two-locus models. *Journal of Genetics* **68**, 29–42.
Lynch, M. (1987). The consequences of fluctuating selection for isozyme polymorphisms in *Daphnia*. *Genetics* **115**, 657–670.
Mackay, T. F. C. (1980). Genetic variance, fitness, and homeostasis in varying environment: an experimental check of the theory. *Evolution* **34**, 1219–1222.
Mackay, T. F. C. (1981). Genetic variation in varying environments. *Genetical Research* **37**, 79–83.
Maynard Smith, J. (1978). *The Evolution of Sex*. Cambridge: Cambridge University Press.
Maynard Smith, J. (1980). Selection for recombination in a polygenic model. *Genetical Research* **35**, 269–277.
Maynard Smith, J. (1988). Selection for recombination in a polygenic model: the mechanism. *Genetical Research* **51**, 59–63.
Nei, M. & Graur, D. (1984). Extent of protein polymorphism and the neutral mutation theory. *Evolutionary Biology* **17**, 73–118.
Nevo, E., Beiles, A. & Ben-Shlomo, R. (1984). The evolutionary significance of genetic diversity: ecological, demographic and life history correlates. *Lecture Notes in Biomathematics* **53**, 13–213.
Parejko, K. & Dodson, S. I. (1991). The evolutionary ecology of an antipredator reaction norm: *Daphnia pulex* and *Chaoborus americanus*. *Evolution* **45**, 1665–1674.
Rutchman, D. H. (1994). Dynamics of the two-locus haploid model. *Theoretical Population Biology* **45**, 167–176.
Scheiner, S. M. (1993). Genetics and evolution of phenotypic plasticity. *Annual Review of Ecology and Systematics* **24**, 35–68.
Slatkin, M. (1979). Frequency- and density-dependent selection on a quantitative character. *Genetics* **93**, 755–771.
Threlkeld, S. T. (1987). *Daphnia* life history strategies and resource allocation patterns. *Memorie dell'Istituto Italiano di Idrobiologia* **45**, 353–366.
Turelli, M. (1984). Heritable genetic variation via mutation–selection balance: Lerch's zeta meets the abdominal bristle. *Theoretical Population Biology* **25**, 138–193.
Turelli, M. (1988). Population genetic models for polygenic variation and evolution. In *Proceedings of the Second International Conference on Quantitative Genetics* (ed. B. S. Weir, E. J. Eisen, M. M. Goodman & G. Namkoong), pp. 601–608. Sunderland: Sinauer.
Yampolsky, L. Yu. & Ebert, D. (1994). Variation and plasticity of biomass allocation in *Daphnia*. *Functional Ecology* **8**, 435–440.
Zeng, Z.-B. & Cockerham, C. C. (1993). Mutation models and quantitative genetic variation. *Genetics* **133**, 729–736.