# Sex and Adaptation in a Changing Environment

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ABSTRACT

In this study we consider a mathematical model of a sexual population that lives in a changing environment. We find that a low rate of environmental change can produce a very large increase in genetic variability. This may help to explain the high levels of heritability observed in many natural populations. We also study asexuality and find that a modest rate of environmental change can be very damaging to an asexual population, while leaving a sexual population virtually unscathed. Furthermore, in a changing environment, the advantages of sexuality over asexuality can be much greater than suggested by most previous studies. Our analysis applies in the case of very large populations, where stochastic forces may be neglected.

ALL environments change with time. Understanding how populations respond to change is fundamental for evolutionary biology, agriculture, and conservation. However, this problem has proved resistant to analysis. A truly realistic model must allow for the occurrence of mutations with a wide variety of effects, and it must also allow for large population sizes. Unfortunately, including these factors in a mathematical model introduces profound difficulties into the analysis.

One way that researchers have dealt with the mathematical difficulties is to use computer simulations. Unfortunately, because of the limitations of computer memory and CPU time, computer analysis does not allow consideration of very large populations. As an example, Bürger and Lynch (1995) used computer simulations to study evolutionary dynamics in a changing environment. These authors allowed for genetic mutations with a wide range of effects. However, the largest population considered had only 512 members. In contrast, many natural populations have $>10^9$ members. In addition, the per-allele mutation rate used by Bürger and Lynch ($2 \times 10^{-4}$) was far higher than the rates usually thought to be biologically realistic (Griffiths *et al.* 1996). The high mutation rate may also have been necessitated by computational constraints, as equilibration can be very slow when allelic mutation rates are low.

Many natural populations are very large. With this in mind, some investigators have focused on infinite populations, which should provide very similar results to finite populations of sufficient size. One example is a study by Charlesworth that considered the fate of infinite sexual and asexual populations in a changing environment (Charlesworth 1993). However, to carry out his study, Charlesworth made use of the infinitesimal model (Bulmer 1980). This model assumes that an infinite number of loci control the selected trait and that alleles at each locus have infinitesimal effects. These assumptions are clearly unrealistic, although the analysis does provide some important insights.

In this study, we attempt to make progress toward the formulation of a biologically realistic model of adaptation in a changing environment. Like Charlesworth, we assume that the population is infinite, and we consider both sexual and asexual populations. However, we present a new analysis that allows for consideration of the more realistic situation where a relatively small number of loci control the selected trait, and we also allow for the occurrence of mutations that have substantial effects. We find that the results from this analysis are very different from those of previous studies that have considered small populations and those of previous studies that have used less realistic genetic systems.

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## MODEL AND RESULTS

**Evolution in an unchanging environment:** Consider a population of obligately sexual hermaphrodites that is sufficiently large that stochastic effects can be ignored (*i.e.*, the population is effectively infinite). Each individual is characterized by the value of a phenotypic trait such as height or weight. An individual's measurement on the trait is denoted by $z$. We assume that there is an optimal value of $z$, called $z_{opt}$. The value of $z_{opt}$ does not change over time, and death rate increases with the deviation of $z$ from $z_{opt}$ (thus we have stabilizing selection). In particular, for an individual with phenotypic

value $z$, the probability of dying over a very small period of time, $\Delta t$, is given by $D \cdot \Delta t$. Here, D represents death rate, and it is given by $D = [1 + (z - z_{opt})^2/(2V)]$, where $V > 0$. The value of $V$ is inversely related to the strength of stabilizing selection.

Extensive numerical study shows that, after a sufficiently long period of time has elapsed, the mean value of $D$ tends to settle down to a particular value, which we denote by $\overline{D}_S$ ("S" stands for sexual). Note that for an individual with the optimal phenotype (*i.e.*, $z = z_{opt}$), we have $D = 1$. Thus, in a typical population, where most individuals do not have the optimal phenotype, we have $\overline{D}_S > 1$.

Individuals can produce offspring either by "male effort" (*i.e.*, by providing sperm or pollen) or by "female effort," which involves providing some of the resources necessary for maturation (as in seed production). At any given time, all individuals produce offspring via female effort at the same rate, $B$. Thus, during a very small period of time, $\Delta t$, the probability that a given individual will produce an offspring via female effort is given by $B \cdot \Delta t$. Mating is random, and offspring mature instantaneously. We assume that, at any given instant, births compensate for deaths, so that population density does not change with time. Thus, after equilibration of death rate, we have $B = \overline{D}_S$.

The phenotype of a particular individual is assumed to depend on its "genotypic value," $G$, plus a normally distributed environmental noise component, $\varepsilon$ (thus, $z = G + \varepsilon$). The distribution of $\varepsilon$ is independent of $G$ and has mean zero and standard deviation $V_e$. Without loss of generality, other variables are scaled so that $V_e = 1$. Furthermore, we assume that individuals are diploid with $L$ freely recombining loci determining the value of $G$. Thus, in any individual, there are $2L$ locations within the genome where alleles that influence the value of $G$ occur. These locations are numbered as $i = 1, 2, \ldots, 2L$. The DNA sequence of the allele at location $i$ determines its effect, $x_i$, on the phenotypic character, and $-\infty < x_i < \infty$. The allelic effects combine additively, and thus $G = \Sigma_{i=1}^{2L} x_i$.

Each of an individual's $2L$ alleles is a copy of an allele present in one or the other of the individual's parents. The value of $x_i$ associated with a particular allele is identical to that of the parental allele, unless a mutation occurs during the copying process. The per-allele rate of such mutations is denoted by $\mu$ (where $0 \leq \mu \leq 1$). We make the usual assumptions that mutations to different alleles occur independently and that mutant values of $x_i$ are normally distributed around the parental value (Kimura 1965; Lande 1975; Turelli 1984). When a mutation occurs that alters the allele at location $i$, the probability that the mutant allele has an effect in the infinitesimal interval $y + dy > x_i > y$ is given by $f(y - x^*)\, dy$. Here, $x^*$ is the parental value of $x_i$. $f(y - x^*)$ is given by

$$f(y - x^*) = \left(\frac{1}{\sqrt{2\pi m^2}}\right)\exp\left(\frac{-(y - x^*)^2}{2m^2}\right), \qquad (1)$$

where $m$ is the standard deviation of mutant effects.

What parameter values are reasonable to use for the production of results from the model? At present there is a great deal of debate about this matter. Furthermore, the most realistic choice of parameter values probably depends on which phenotypic trait is under consideration. With this in mind, we produced results for four different sets of parameter values.

Experiments suggest that allelic mutation rates in multicellular organisms are generally on the order of $10^{-5}$ (Griffiths *et al.* 1996). Furthermore, most of the heritable variation for many easy-to-measure traits (*e.g.*, body size) appears to be controlled by <20 loci (Turelli 1984; Bürger *et al.* 1989; Bürger and Lynch 1995; Kearsey and Farquhar 1998). Finally, rough estimates from the data (Turelli 1984; Lynch and Walsh 1998) suggest that, typically, $m^2 \ll 1$, and $V \approx 20$ [$m \approx 0.2$ is often used in published calculations (Turelli 1984; Bürger and Lynch 1995; Lynch *et al.* 1995; Lynch and Walsh 1998)].

The foregoing considerations motivate the calculations made for Table 1, for which we set $L = 10$, $\mu = 10^{-5}$, $m = 0.2$, and $V = 20$. The first row of Table 1 gives the data for an unchanging environment. In this case, the genetic variance within a sexual population, $V_{G,S}$ is quite low ($V_{G,S} = 0.00807$). (The genetic variance is defined as the variance in $G$ values within the population, and the subscript S indicates that the population is sexual.) As a result of the low value of $V_{G,S}$, heritability is also low. As noted previously, the environmental variance is scaled to unity, and thus the heritability ($h_S^2$) is defined by $h_S^2 = V_{G,S}/(1 + V_{G,S})$. In this case, $h_S^2 = 0.00801$.

The parameter values used for Table 1 imply that a very small amount of genetic variance results from newly arisen mutations. This "mutational variance" is equal to $2L\mu m^2$, and for Table 1, $2L\mu m^2 = 8 \times 10^{-6}$. A more realistic number may be closer to $10^{-3}$ (Turelli 1984; Bulmer 1989; Lynch and Walsh 1998). Methods used to calculate the number of loci involved in the control of a phenotypic trait may produce estimates that are much lower than the actual number of loci involved (Kearsey and Farquhar 1998). With this in mind, we produced Table 2, with $L = 1250$, $\mu = 10^{-5}$, $m = 0.2$, and $V = 20$. With these values, the mutational variance is equal to $10^{-3}$. Again, the first row gives the results for an unchanging environment. Note that, in this case, the level of heritability achieved is much higher ($h_S^2 = 0.508$) than what was seen in the first row of Table 1.

In their computer simulation study, Bürger and Lynch (1995) also chose parameter values that resulted in a mutational variance of $10^{-3}$. However, to do this, they used a moderate number of loci and a very high (and probably unrealistic) rate of mutation ($\mu = 2 \times$

**TABLE 1**

| $\alpha$ | $V_{G,S}$ | $V_{G,A}$ | $h^2_S$ | $h^2_A$ | $\xi_S$ | $\xi_A$ | $\bar{D}_S$ | $\bar{D}_A$ |
|---|---|---|---|---|---|---|---|---|
| $\alpha = 0$ | 0.00807 | 0.00648 | 0.00801 | 0.00644 | 0.000 | 0.000 | 1.03 | 1.03 |
| $\alpha = 0.0001$ | 0.0364 | 0.0133 | 0.0351 | 0.0131 | 0.0726 | 0.176 | 1.03 | 1.03 |
| $\alpha = 0.001$ | 0.114 | 0.0317 | 0.102 | 0.0307 | 0.194 | 0.655 | 1.03 | 1.04 |
| $\alpha = 0.01$ | 0.357 | 0.0862 | 0.263 | 0.0794 | 0.577 | 2.34 | 1.04 | 1.16 |
| $\alpha = \alpha^* = 0.0664$ | 0.883 | 0.208 | 0.469 | 0.172 | 1.52 | 6.39 | 1.10 | 2.05 |
| $\alpha = \alpha^{**} = 0.0779$ | 0.953 | 0.225 | 0.488 | 0.184 | 1.65 | 6.94 | 1.12 | 2.24 |
| $\alpha = 0.1$ | 1.07 | 0.253 | 0.517 | 0.202 | 1.88 | 7.90 | 1.14 | 2.59 |
| $\alpha = 1$ | 3.24 | 0.789 | 0.764 | 0.441 | 6.19 | 25.3 | 2.06 | 17.1 |
| $\alpha = 10$ | 10.1 | ? | 0.910 | ? | 19.8 | ? | 11.1 | ? |

Results from the numerical studies for the various quantities reported after they have reached their long-term stationary values. The data are produced using the methods described in the appendix. The columns marked $V_{G,S}$, $h^2_S$, $\xi_S$, and $\bar{D}_S$ refer to sexual populations, and give, respectively, the genetic variance, the narrow-sense heritability, the difference between the value of the optimum phenotype and the value of the population mean phenotype, and the average death rate. The columns marked $V_{G,A}$, $h^2_A$, $\xi_A$, and $\bar{D}_A$ give these same quantities for asexual populations. Values of $\alpha$ (the rate of environmental change) were set as shown in column 1. Parameters of the model (other than $\alpha$) were set as follows: $L = 10$, $\mu = 10^{-5}$, $m = 0.2$, and $V = 20$. A question mark appears in cases that were too extreme for calculation without very large amounts of computer time. As explained in the appendix, there may be substantial inaccuracy introduced into the calculations when $V_{G,S} > V/2$. Therefore, the data shown for a sexual population with $\alpha = 10$ should be treated with caution.

$10^{-4}$). Presumably, the high mutation rate was required because of computational limitations. For purposes of comparison, we produced Table 3, which presents data produced using parameter values very similar to those used by Bürger and Lynch ($L = 50$, $\mu = 2 \times 10^{-4}$, $m = 0.224$, and $V = 9$).

While it is certainly possible that many phenotypic traits are controlled by a large number of loci, this suggests that mutations typically have pleiotropic effects, affecting more than one trait that is under selection. (Otherwise, an unrealistically large number of loci would be required to influence development of the phenotype.) Furthermore, experimental evidence suggests that pleiotropy is common (Caspari 1952; Wright 1977; Barton and Turelli 1989; Kondrashov and Turelli 1992; Caballero and Keightley 1994; Wagner 1996). In addition, the deleterious side effects caused by pleiotropy seem to be largest for mutations that have a large effect on the trait under study (Barton and Turelli 1989; Caballero and Keightley 1994). Thus, even if the number of loci controlling a trait is relatively large, it may be that mutations that do not have substantial deleterious side effects are rare. Furthermore, such mutations may be associated with relatively low values of $m$. With this in mind, we calculated Table 4, which uses the parameter set $L = 10$, $\mu = 10^{-5}$, $m = 0.1$, and $V = 20$. These sorts of values may be appropriate if mutations that do not have substantial deleterious side effects occur at a small number of loci and have relatively small phenotypic effects. We chose

**TABLE 2**

| $\alpha$ | $V_{G,S}$ | $V_{G,A}$ | $h^2_S$ | $h^2_A$ | $\xi_S$ | $\xi_A$ | $\bar{D}_S$ | $\bar{D}_A$ |
|---|---|---|---|---|---|---|---|---|
| $\alpha = 0$ | 1.03 | 0.137 | 0.508 | 0.120 | 0.000 | 0.000 | 1.05 | 1.03 |
| $\alpha = 0.001$ | 1.80 | ? | 0.643 | ? | 0.0250 | ? | 1.07 | ? |
| $\alpha = 0.01$ | 4.22 | 0.171 | 0.809 | 0.146 | 0.0652 | 1.20 | 1.13 | 1.07 |
| $\alpha = 0.1$ | 13.3 | 0.369 | 0.930 | 0.269 | 0.171 | 5.47 | 1.36 | 1.78 |
| $\alpha = \alpha^* = 0.133$ | 15.3 | 0.417 | 0.938 | 0.294 | 0.193 | 6.40 | 1.41 | 2.06 |
| $\alpha = \alpha^{**} = 0.253$ | 21.2 | 0.557 | 0.955 | 0.358 | 0.258 | 9.10 | 1.56 | 3.11 |
| $\alpha = 1$ | 42.5 | 1.08 | 0.977 | 0.519 | 0.493 | 18.6 | 2.08 | 9.69 |
| $\alpha = 10$ | 129 | 3.33 | 0.992 | 0.769 | 1.57 | 60.2 | 4.30 | 91.6 |

Results from the numerical studies for the various quantities reported after they have reached their long-term stationary values. Parameters of the model (other than $\alpha$) were set as follows: $L = 1250$, $\mu = 10^{-5}$, $m = 0.2$, and $V = 20$. A question mark appears in cases that were too extreme for calculation without very large amounts of computer time. As explained in the appendix, there may be substantial inaccuracy introduced into the calculations when $V_{G,S} > V/2$. Therefore, the data shown for a sexual population with $\alpha \geq 0.1$ should be treated with caution.

**TABLE 3**

| $\alpha$ | $V_{G,S}$ | $V_{G,A}$ | $h_S^2$ | $h_A^2$ | $\xi_S$ | $\xi_A$ | $\bar{D}_S$ | $\bar{D}_A$ |
|---|---|---|---|---|---|---|---|---|
| $\alpha = 0$ | 0.348 | 0.0889 | 0.258 | 0.0817 | 0.000 | 0.000 | 1.07 | 1.06 |
| $\alpha = 0.001$ | 0.457 | ? | 0.314 | ? | 0.0389 | ? | 1.08 | ? |
| $\alpha = 0.01$ | 0.866 | 0.117 | 0.464 | 0.104 | 0.131 | 0.802 | 1.10 | 1.10 |
| $\alpha = 0.1$ | 2.20 | 0.256 | 0.688 | 0.204 | 0.434 | 3.54 | 1.19 | 1.77 |
| $\alpha = \alpha^* = 0.144$ | 2.59 | 0.301 | 0.721 | 0.231 | 0.525 | 4.34 | 1.21 | 2.12 |
| $\alpha = \alpha^{**} = 0.188$ | 2.91 | 0.339 | 0.744 | 0.251 | 0.605 | 5.02 | 1.24 | 2.48 |
| $\alpha = 1$ | 6.19 | 0.750 | 0.861 | 0.429 | 1.48 | 12.1 | 1.52 | 9.14 |
| $\alpha = 10$ | 18.3 | 2.35 | 0.948 | 0.701 | 4.94 | 38.3 | 3.43 | 82.8 |

Results from the numerical studies for the various quantities reported after they have reached their long-term stationary values. Parameters of the model (other than $\alpha$) were set as follows: $L = 50$, $\mu = 2 \times 10^{-4}$, $m = 0.224$, and $V = 9$. A question mark appears in cases that were too extreme for calculation without very large amounts of computer time. As explained in the appendix, there may be substantial inaccuracy introduced into the calculations when $V_{G,S} > V/2$. Therefore, the data shown for a sexual population with $\alpha \geq 1$ should be treated with caution.

these particular values because they facilitate comparison with Table 1, which uses the same parameter values, with one exception (in Table 1, $m = 0.2$).

We do not intend to suggest that the data presented in Table 4 represents a complete study of the effects of pleiotropy. Nevertheless, the results are of interest and are likely to give some hint of the outcome of a complete study. The first row shows the data for an unchanging environment. We see that the level of heritability for a sexual population is low ($h_S^2 = 0.00767$). However, this is largely a result of the low mutation rate, not the low value of $m$ (Turelli 1984). Nevertheless, changing the value of $m$ does have a substantial effect when the environment changes over time, as we show below.

**The effect of environmental change:** Let us now modify the model presented above to incorporate a shift in the phenotypic optimum, $z_{opt}$. Say that, at time $t$, the value of the optimum is given by $z_{opt} = \alpha t$, where $\alpha > 0$. In the presence of a steady change in the value of the optimal phenotype, the population tends toward a steady-state situation, where the mean phenotypic value changes at exactly the same rate at the optimum phenotypic value. When the steady state is achieved, the mean phenotypic value does not lie at $z_{opt}$, but lags behind $z_{opt}$ by an amount denoted by $\xi_S$ (*i.e.*, $\xi_S$ is the difference between the optimum and the mean phenotype). At the same time, the genetic variance ($V_{G,S}$), the heritability ($h_S^2$), and the mean death rate ($\bar{D}_S$) all depend on the rate of environmental change ($\alpha$).

Inspection of Table 1 shows that, in a sexual population, altering the rate of environmental change ($\alpha$) can have a very large impact on genetic variance ($V_{G,S}$) and heritability ($h_S^2$). This finding is in accord with analytic approximations, which are presented in Equation A13 of the appendix. Over the range of values of $\alpha$ considered in Table 1 ($0.0001 \leq \alpha \leq 10$), each tenfold increase in $\alpha$ produces about a threefold increase in $V_{G,S}$. As a consequence, the value of $h_S^2$ also increases dramatically with $\alpha$. When $\alpha = 0.0001$, we have $h_S^2 = 0.0351$, which is low in comparison to values typically measured in natural populations (Lande 1975; Turelli 1984; Bulmer 1989). However, when $\alpha > 0.001$, we have $h_S^2 > 0.1$. Thus, as long as the optimum is changing by at least one phenotypic standard deviation every 1000

**TABLE 4**

| $\alpha$ | $V_{G,S}$ | $V_{G,A}$ | $h_S^2$ | $h_A^2$ | $\xi_S$ | $\xi_A$ | $\bar{D}_S$ | $\bar{D}_A$ |
|---|---|---|---|---|---|---|---|---|
| $\alpha = 0$ | 0.00773 | 0.00458 | 0.00767 | 0.00456 | 0.000 | 0.000 | 1.02 | 1.02 |
| $\alpha = 0.0001$ | 0.0320 | 0.00902 | 0.0310 | 0.00894 | 0.0740 | 0.235 | 1.03 | 1.03 |
| $\alpha = 0.001$ | 0.0895 | 0.0216 | 0.0822 | 0.0212 | 0.234 | 0.935 | 1.03 | 1.05 |
| $\alpha = 0.01$ | 0.257 | 0.0596 | 0.204 | 0.0562 | 0.786 | 3.37 | 1.05 | 1.31 |
| $\alpha = \alpha^* = 0.0332$ | 0.448 | 0.104 | 0.310 | 0.0946 | 1.49 | 6.36 | 1.09 | 2.04 |
| $\alpha = \alpha^{**} = 0.0382$ | 0.479 | 0.112 | 0.324 | 0.101 | 1.60 | 6.84 | 1.10 | 2.20 |
| $\alpha = 0.1$ | 0.752 | 0.178 | 0.429 | 0.151 | 2.67 | 11.2 | 1.22 | 4.18 |
| $\alpha = 1$ | 2.28 | ? | 0.695 | ? | 8.79 | ? | 3.01 | ? |

Results from the numerical studies for the various quantities reported after they have reached their long-term stationary values. Parameters of the model (other than $\alpha$) were set as follows: $L = 10$, $\mu = 10^{-5}$, $m = 0.1$, and $V = 20$. A question mark appears in cases that were too extreme for calculation without very large amounts of computer time.

generations, it is possible to produce an appreciable level of heritability with only 10 loci. (We use the word "generation" to denote the average lifetime of a phenotypically optimal individual.)

When the rate of environmental change is increased, the lag of the phenotypic mean behind the phenotypic optimum ($\xi_S$) also increases (see Table 1). As a consequence of the dependence of $\xi_S$ and $V_{G,S}$ on $\alpha$, increases in $\alpha$ produce increases in mean death rate ($\bar{D}_S$). The data in Table 1 also suggest that, with 10 loci under selection, even very high values of $\alpha$ (up to $\alpha = 1$) can be tolerated as long as the species is capable of doubling its birth rate (which is not a severe requirement).

Table 2 shows the effect of environmental change when the number of loci under selection is relatively large ($L = 1250$, with the other parameters set as for Table 1). In this case, the amount of genetic variance and heritability is substantial even in an unchanging environment. However, the effect of changing the environment is similar to what occurs when $L = 10$, in that every tenfold increase in $\alpha$ studied produces about a threefold increase in $V_{G,S}$. Increases in $V_{G,S}$ of a similar magnitude are shown in Tables 3 and 4 for other choices of parameter values. Note that, because of computational constraints, it was not possible to use the entire range of $\alpha$ values found in Table 1 in all of the other tables. Thus, for example, we were unable to run the $\alpha = 0.0001$ case for the parameter values used in Table 2.

Comparing Tables 1 and 2, we see that large numbers of loci generally increase the death rate in a sexual population as long as the rate of environmental change is not too high. This is because many loci lead to a relatively high level of genetic variance. However, for a very high rate of environmental change ($\alpha = 10$), a large number of loci apparently confers an advantage, allowing a much lower death rate than what occurs with 10 loci.

Comparing Tables 1 and 4 leads to the conclusion that a relatively low value of $m$ (the standard deviation of mutant effects) seems to have little impact on the death rate of a sexual population when the rate of environmental change is relatively small. However, for $\alpha \geq 0.1$, the lower value of $m$ used for Table 4 leads to a substantially higher death rate than what is observed in Table 1. Presumably, this is because large-effect mutations that push genotypes toward the optimum are more rare when $m$ is low.

**The effect of asexuality:** So far, we have assumed that all $L$ loci recombine freely. Let us now consider what happens in a population that is identical to the one just described, except that reproduction is asexual so that there is no recombination or segregation. The relevant data are shown in columns 3, 5, 7, and 9 in Tables 1–4, and in Figures 1 and 2. After a sufficiently long period of time has elapsed, the mean death rate of asexuals takes on a value that does not change over time. We denote this value by $\bar{D}_A$. The genetic variance, heritability, and the difference between the phenotypic mean and the optimum phenotype also settle down to steady-state values, denoted by $V_{G,A}$, $h^2_A$, and $\xi_A$, respectively. Analytic approximations for $V_{G,A}$ and $\xi_A$ are given in Equation A5 of the appendix.

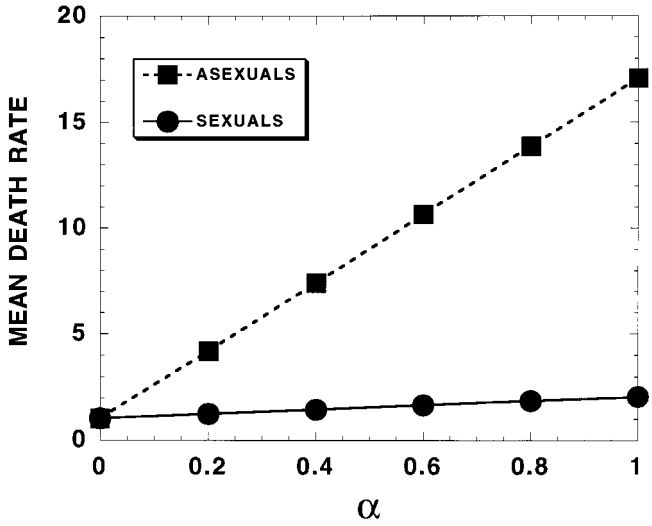


Figure 1.—Effect of the rate of environmental change ($\alpha$) on mean death rate. Circles give the data for sexuals (the $\bar{D}_S$ values), while squares give the data for asexuals (the $\bar{D}_A$ values). For both sexuals and asexuals, parameters were set as follows: $L = 10$, $\mu = 10^{-5}$, $m = 0.2$, and $V = 20$.

Examination of the tables shows that, in a changing environment, asexuals generally have much lower levels of genetic variance and heritability than a sexual population would have in the same circumstances. High heritability facilitates adaptation (Fisher 1930). Thus, it is not surprising to see that the mean phenotype for asexuals generally lags considerably further behind the optimum than does a sexual population in the same circumstances ($\xi_A > \xi_S$). In Figure 2 the distributions of genotypic effects for sexuals and asexuals are plotted as functions of $\alpha$. The difference in widths (variance) of the distributions and the difference in lags are clearly seen.

The lower heritability and larger lags characteristic of asexuals do not mean that their mean death rate will necessarily be larger than in an equivalent sexual population. A large genetic variance may enhance heritability, but it also means that many individuals are far from the phenotypic optimum, and this tends to increase death rates. Thus, for example, in Table 2 (for which $L = 1250$) asexuals have a lower death rate than sexuals when $\alpha = 0.01$. However, for larger values of $\alpha$, the death rate is lower for sexuals. Indeed, for every set of parameter values studied, a sexual population has a much lower death rate than an asexual population when the rate of environmental change ($\alpha$) is sufficiently large.

It is commonly held that asexuals have a twofold fertility advantage (Maynard Smith 1978; Michod and

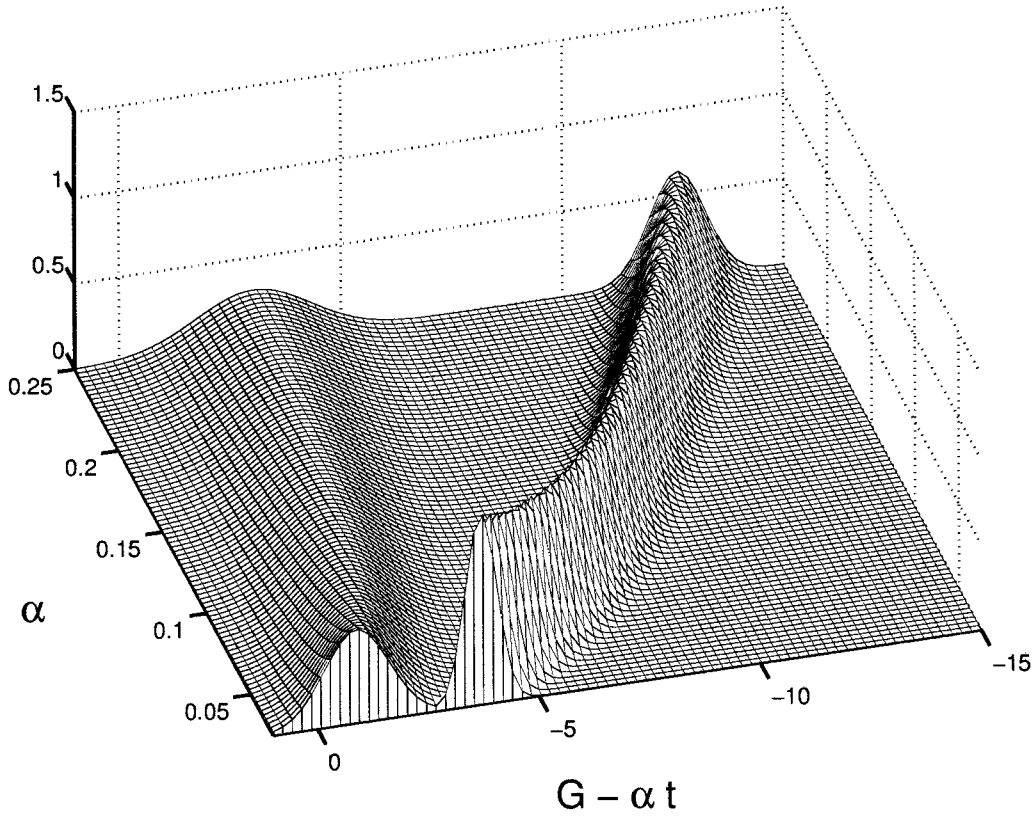


Figure 2.—Genotypic distributions as a function of the rate of environmental change ($\alpha$). A genotype is characterized by its "genotypic value," $G$, which is the mean phenotypic value for individuals with that genotype. The axis labeled $G - \alpha t$ gives the difference between genotypic values and the optimal genotypic value ($\alpha t$). The higher ridge is the peak of the distribution for asexuals, for different values of $\alpha$, while the lower ridge is the peak of the distribution for sexuals. Note that, on average, sexuals are closer to the optimal genotypic value than asexuals, and this difference increases with $\alpha$. Also, both distributions become wider and lower as $\alpha$ increases. For both sexuals and asexuals, parameters were set as follows: $L = 10$, $\mu = 10^{-5}$, $m = 0.2$, $V = 20$. The distributions shown are achieved after a sufficiently long period of time has elapsed.

Levin 1988; Peck *et al.* 1997). If this is so, sexuals should still be able to obtain an overall fitness superiority as long as they live more than twice as long as asexuals ($2\overline{D}_S < \overline{D}_A$) and thus have more than twice as many offsprings as asexuals do over the course of their lifetimes. Therefore, we now describe the conditions under which this inequality is satisfied.

Let $\alpha^*$ represent the rate of environmental change, $\alpha$, for which $\overline{D}_A$ is twice the value that it takes when $\alpha = 0$ (*i.e.*, in an unchanging environment). The value of $\alpha^*$ depends on the various parameters of the model, but it is particularly sensitive to $m$, the standard deviation of mutant effects. If $m$ is small, then mutations that move genotypic values substantially toward the optimum are rare, and this results in a small value of $\alpha^*$. With a large value of $m$, even rapid rates of environmental change can be tolerated, and so $\alpha^*$ is relatively large. Thus, for example, with the parameters used for Table 1 ($L = 10$, $\mu = 10^{-5}$, $m = 0.2$, and $V = 20$) we have $\alpha^* = 0.0664$. Table 4 uses the same parameters as Table 1, except that the value of $m$ is halved to $m = 0.1$. This leads to a halving of the value of $\alpha^*$, to $\alpha^* = 0.0332$. Further investigations (not shown in the tables) show that, if we decrease $m$ to one-fifth of its value in Table 1 ($m = 0.04$), $\alpha^*$ falls by almost five times (to $\alpha^* = 0.0136$).

It is interesting to note that, while $\alpha^*$ is quite sensitive to changes in the value of $m$, it is remarkably insensitive to changes in the allelic mutation rate, $\mu$, as suggested by the analytic approximations found in the appendix (Equation A5). Thus, for example, if $L = 10$, $m = 0.2$, and $V = 20$, then when $\mu = 10^{-6}$ we have $\alpha^* = 0.0555$, which is only 16% lower than the value found in Table 1, for which $\mu$ was 10 times higher.

Were sex to allow perfect adaptation to environmental change, $\overline{D}_S$ would remain unaltered as $\alpha$ is increased. Furthermore, when $\alpha$ is sufficiently close to zero, $\overline{D}_S \approx \overline{D}_A$ for all plausible parameter-value choices that we have studied. Thus, in the case of perfectly adaptable sexuals, $2\overline{D}_S < \overline{D}_A$ will be satisfied when $\alpha$ is just a little larger than $\alpha^*$. In reality, sexuals are not perfectly adaptable. Nevertheless, for the cases we have studied, we find that the value of $\alpha$ that is sufficiently large to induce $2\overline{D}_S < \overline{D}_A$ is typically not greatly in excess of $\alpha^*$, except when the number of loci under selection is very large (as in Table 2). Thus, it seems very likely that only modest conditions must be met for the average lifetime of sexuals to be twice that of asexuals.

We denote the value of $\alpha$ for which $2\overline{D}_S = \overline{D}_A$ as $\alpha^{**}$. In every case we have studied, $2\overline{D}_S < \overline{D}_A$ whenever $\alpha > \alpha^{**}$. We find that, for the parameters used in Table 1, $\alpha^{**} = 0.0779$, which is to say that, to produce a twofold viability advantage for sexuals, the environment must change at a rate that is only 17% faster than the rate that

would be required if sexuals were perfectly adaptable. When the value of $m$ is halved, there is only a 15% difference between $\alpha^*$ and $\alpha^{**}$ (see Table 4). When we decrease the value of $m$ to $m = 0.04$ (and leave the other parameters as in Table 1), we have $\alpha^{**} = 0.0152$, which means that only a 12% difference separates $\alpha^*$ and $\alpha^{**}$. This also means that, in this case, sexuals can gain a twofold advantage when the environment changes by <1.5% of a phenotypic standard deviation per generation.

## DISCUSSION

Taken at face value, the results presented here suggest that sexual populations can maintain a remarkably high level of fitness, even when the environment is changing quite quickly. This conclusion is in sharp contrast with the results of most other studies (but see Kondrashov 1984). One example of the type of results generally found in the literature comes from the study by Bürger and Lynch, who suggested that populations were unlikely to be able to change at a rate >10% of a phenotypic standard deviation per generation (Bürger and Lynch 1995). We find that, with a plausible choice of parameter values, the environment can change at a much faster rate than suggested by Bürger and Lynch without inducing very high death rates in a sexual population. For example, for the parameters chosen for Table 1, $\alpha = 1$ results in a death rate that is only twice what is found in an unchanging environment. When $\alpha = 1$, Table 1 gives a value of $V_{G,S}$ of 3.24, and this means that a phenotypic standard deviation is equal to $\sqrt{3.24 + 1} = 2.06$, and so the environment is changing by about one-half of a phenotypic standard deviation each generation.

Extreme caution should be exercised before accepting the conclusion that natural populations are much more able to deal with environmental change than previously realized. Our knowledge of the genetic systems underlying quantitative traits is very incomplete (Barton and Turelli 1989; Bulmer 1989). Before firm conclusions can be made, experimentalists must learn much more about pleiotropy, genetic constraints, population structure, and effective population size, and more must be done to incorporate these factors into models. We discuss some of these complications below.

We find that low rates of environmental change (*e.g.*, $\alpha = 0.01$) can induce a very large increase in genetic variation in comparison with the case of an unchanging environment ($\alpha = 0$). This finding may help to explain the high levels of heritability and genetic variation commonly found in natural populations. High heritability has been a puzzle because the best current estimates of the relevant genetic parameter values suggest that low heritability is likely when environments do not change over time (Turelli 1984; Bulmer 1989). However, our finding about the impact of low rates of environmental change is another case in which our results appear, at least at first glance, to contradict previously published results, which have generally suggested that rapid changes in the environment are required to induce such large increases in genetic variation (Bürger and Lynch 1995; Kondrashov and Yampolsky 1996).

What accounts for the differences between our results and those of previous studies of the effects of environmental change? To address this question, it is useful to develop an intuitive understanding of the relationship between environmental change and genetic variation in our model. Recall that, when the optimum changes over time, the phenotypic mean value tends to lag behind the optimum value. As a result of this lag, a subclass of mutations is beneficial as they tend to bring phenotypes closer to the optimum. When these beneficial mutations occur, some of the resulting mutant alleles rise in frequency. However, once the optimum has moved further, new alleles become beneficial, and alleles that were once beneficial become deleterious and fall in frequency. This "turnover" of alleles is very different to what apparently occurs in large populations in an unchanging environment, where a single allele can become common and all other alleles remain rare forever (Turelli 1984). Our calculations show that the turnover in allele frequencies induced by environmental change can generate very substantial genetic variability.

The idea that environmental change can lead to an increase in genetic variation is in accord with much of the experimental literature (*e.g.*, see pp. 200–202 in Bell 1997). However, environmental change does not always induce an increase in genetic variation, presumably because of small experimental population sizes combined with strong selection (see below). Despite the plausibility of a relationship between environmental change and genetic variation, a number of key studies have assumed that the amount of genetic variation is independent of the rate of environmental change (Lynch *et al.* 1991; Charlesworth 1993; Lynch and Lande 1993). This assumption can be justified a number of ways. For example, Charlesworth (1993) considers a genetic system that follows the assumptions of the infinitesimal model (Bulmer 1980). This implies that gene frequencies do not undergo any substantial change as a result of environmental fluctuations, and as a consequence, genetic variance does not increase with the rate of environmental change. The infinitesimal model assumes an infinite number of loci, each of which has infinitesimal effects. We feel that these assumptions are much less realistic than the ones made in the model presented here.

A study that did make similar assumptions to ours was carried out by Bürger and Lynch (1995). In accord with our results, Bürger and Lynch found that a changing environment can increase genetic variance. However, the increases in variance reported by Bürger and

Lynch were much smaller than those reported here. This is true even for the parameter values used in Table 3, which are very similar to those used by Bürger and Lynch.

The main reason for the differences between our results and those of Bürger and Lynch seems clear. As stated above, Bürger and Lynch relied on simulation methods, and thus they were unable to consider large population sizes (the largest population size used was 512). They did, however, observe that, as population size increases, there is also an increase in the degree to which environmental change enhances genetic variation. With this in mind, we strongly suspect that the main difference between our results and those of Bürger and Lynch is accounted for by the difference in population size.

To facilitate comparison with other studies, we used a Gaussian function for our distribution of mutant effects. There is, however, some evidence that a more leptokurtic function is more appropriate for this purpose (Mukai *et al.* 1972; Mackay *et al.* 1992; Ohta 1992; Keightley 1994). For this reason, some researchers have used a "reflected gamma" distribution, with parameter 1/2 (Keightley and Hill 1987, 1988). We carried out some preliminary studies using this sort of function, and we find that the change makes very little difference to the outcome of evolution for a sexual population. For an asexual population, the change to a reflected gamma has a more substantial effect, allowing somewhat higher levels of heritability ($h_A^2$), smaller lags ($\xi_A$), and lower death rates ($\overline{D}_A$) in comparison to what is obtained with a Gaussian mutation function. However, the differences caused by switching from one mutation function to another are not very large, and we would reach the same qualitative conclusions with either function.

We assumed that the population is so large that stochastic effects can be ignored. This means that, effectively, the population has infinite size. Thus, there is always a supply of mutations that tend to move genotypes in the direction of the optimum. With this in mind, it is worth asking whether any natural populations are likely to be large enough to exhibit the sort of behavior reported here. Unfortunately, we have not yet been able to develop methods that allow us to address this question directly. However, it is possible to make a few relevant observations.

Consider, for example, the 7th row of Table 1, corresponding to $\alpha = 0.1$. This row shows that, in a very large sexual population, the average population member has a phenotype that deviates from the optimal phenotype by 1.88 environmental standard deviations. This implies that the average allelic effect deviates from the optimum allelic effect by $1.88/(2L) = 1.88/20 = 0.0940$ environmental standard deviations. Thus, the distance between the average effect and the optimum is less than one-half of the standard deviation of mutant effects ($m = 0.2$). In addition, from the value of $V_{G,S}$ given in Table 1 ($V_{G,S} = 1.07$), we can calculate that the standard deviation of allelic effects is equal to 0.231. Thus, a large percentage ($\sim$34%) of alleles are actually in advance of the optimum. These alleles are suboptimal, but many of them will become closer to optimal in the next generation, after the value of the optimum phenotype has changed. These considerations suggest that an extremely large population size would not be necessary to produce effects that are roughly similar to those reported in the 7th row of Table 1 for a sexual population. We would guess that a population size of $\sim$10 times the inverse of the allelic mutation rate would be sufficient (*i.e.*, a population with $\sim 10^6$ members).

The situation is very different under asexuality. Consider, once again, the 7th row of Table 1. Note that, for asexuals, the optimum is nearly eight environmental standard deviations away from the phenotypic optimum. Furthermore, the standard deviation in genotypic values ($\sqrt{V_{G,A}}$) is only about half of one environmental standard deviation. This means that some extremely rare mutations are strongly beneficial. For example, mutations that would bring an average genotype to (or beyond) the optimum occur to $\sim$1 newly produced genome in $10^{20}$. Nevertheless, this does not imply that very rare mutations are necessary for adaptation. We recalculated the results for the 7th row of Table 1 using a "truncated normal" distribution, which is very similar to a standard normal distribution, except that no mutations occur that alter allelic effects by more than $2m$. Thus, rare and extreme mutations are excluded. We found that the truncated normal distribution made an asexual population less adaptable, but the impact was not as large as one might expect. In particular, the truncated normal distribution resulted in an elevation of $\overline{D}_A$ by 28%, to $\overline{D}_A = 3.32$. Other things being equal, imposition of the truncated normal distribution resulted in smaller changes for smaller values of $\alpha$, and larger changes resulted for larger values of $\alpha$. The changes produced by the truncated normal distribution were generally much smaller for a sexual population as compared to an otherwise-equivalent asexual population. Thus, unrealistically large populations may not be necessary for the survival of sexual or asexual populations when the environment changes relatively quickly. Additional work is required to clarify this issue.

In the effectively infinite population studied here, a population, whether sexual or asexual, can always keep pace with a shifting optimum. If the optimum moves quickly, the population mean may fall well behind. However, once there is sufficient separation between the optimum and the population mean, mutations that move phenotypes substantially in the direction of the optimum will be strongly favored by selection. Once the strength of selection on these beneficial mutations is sufficiently strong, the population mean can change at the same rate as the optimum.

In a real and finite population, the necessary mutations may not always be available. Thus, it is possible for a changing optimum to outrun the population, in the sense that the difference between the optimum and the population mean may increase each generation, leading to a long-term decrease in fitness and finally to extinction of the population. In light of the results presented here, we feel certain that the rate of environmental change sufficient for the optimum to outrun the population will typically be much smaller for asexual populations than in the case of sexuality.

What accounts for the difference between the behavior of sexual and asexual populations that was observed in this study? There are a variety of roughly equivalent ways to answer this question, but perhaps the most straightforward explanation was put forward by James Crow (1992). Crow pointed out that, in the absence of new mutations, the mean of an asexual population cannot change beyond the genotypic value of the individual with the most extreme genotype in the current population. On the other hand, in the absence of mutation, a sexual population may be able to evolve far beyond the phenotype of any individual present in the population by combining rare alleles drawn from different individuals. The situation is similar when mutations are allowed to occur. Furthermore, mutations that push genotypes toward the optimum will tend to be lost in an asexual population unless they occur in one of the few individuals that has a genotype closest to the optimum (Fisher 1930; Manning and Thompson 1984; Peck 1994). This is not the case in a sexual population. Even if a beneficial mutation occurs in a very unfit individual, it can escape from the genetic context in which it arose through mating and recombination, and it can thus contribute to the long-term adaptation of the population.

A study by Charlesworth (mentioned above) shows that a sexual population can obtain a large advantage over asexuals in a changing environment, even if environmental change is not very fast (Charlesworth 1993). This finding is in qualitative agreement with our results. However, Charlesworth made use of the infinitesimal model, and as we have explained, this model is quite unrealistic despite its advantages. Furthermore, the substantial advantage of sex shown by Charlesworth vanishes for many plausible parameter choices. For example, the advantage is very small (or absent) if mutations affecting the trait are sufficiently rare. We also note that our results are related to studies of pure directional selection (Hill 1982; Bürger 1993). However, these studies are very different from ours, as they make the assumption that no optimum phenotype exists.

Our results suggest a number of ways that sexual populations might be maintained despite competition from asexual populations. First, this could happen if multiple traits are subject to changing optima. We expect that, if the number of these traits is sufficiently large, then a very low rate of change in the optimum for each trait will be all that is required to overcome the "twofold cost of sex" (Maynard Smith 1978; Charlesworth 1993; Peck *et al.* 1997). Second, sex might be maintained if only a single trait is subject to a changing optimum as long as the rate of environmental change is sufficiently swift. Furthermore, as we have seen, the rate of change required may be very modest as long as $m$ is small. In fact, the relevant value of $m$ in typical real-world situations may be very low. This is because many large-effect mutations have substantial deleterious side effects, and thus they should not be considered when $m$ is calculated (Barton and Turelli 1989; Caballero and Keightley 1994).

Finally, even with a large value of $m$ and a single trait subject to a shifting optimum, sex might be maintained by occasional catastrophes, where the rate of environmental change temporarily rises to a level that would doom any population were it to go on unabated. Our results show that a long period of very slow environmental change can lead to much higher levels of heritability in a sexual population, as compared to an asexual population. If a period of very slow change is followed by a catastrophe, this heritability difference could easily lead to the extinction of asexuals. With their greater genetic variability, sexuals can adapt more quickly to the environmental change, and thus they may survive the catastrophe.

Our results do not represent a definitive analysis of the process whereby populations adapt to changing environments. Such an analysis must await more data on the genetics underlying quantitative traits, more sophisticated mathematical techniques, and much more powerful computers. Nevertheless, the work presented here should bring closer the day when we understand how organisms deal with the challenge of a changing world.

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## LITERATURE CITED

Barton, N. H., and M. Turelli, 1989 Evolutionary quantitative genetics: how little do we know? Annu. Rev. Genet. **23:** 337–370.

Bell, G., 1997 *Selection: The Mechanism of Evolution*. Chapman and Hall, New York.

Bulmer, M., 1980 *The Mathematical Theory of Quantitative Genetics*. Clarendon Press, Oxford.

Bulmer, M. G., 1989 Maintenance of genetic variability by mutation-selection balance: a child's guide through the jungle. Genome **31:** 761–767.

Bürger, R., 1993 Predictions of the dynamics of a polygenic character under directional selection. J. Theor. Biol. **162:** 487–513.

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

Bürger, R., G. P. Wagner and F. Stettinger, 1989 How much heritable variation can be maintained in finite populations by mutation-selection balance? Evolution **43:** 1748–1766.

Caballero, A., and P. D. Keightley, 1994 A pleiotropic nonaddi-

tive model of variation in quantitative traits. Genetics **138:** 883–900.
Caspari, E., 1952 Pleiotropic gene action. Evolution **6:** 1–18.
Charlesworth, B., 1993 Directional selection and the evolution of sex and recombination. Genet. Res. **61:** 205–224.
Crow, J. F., 1992 An advantage of sexual reproduction in a rapidly changing environment. J. Hered. **83:** 169–173.
Fisher, R. A., 1930 *The Genetical Theory of Natural Selection*. Clarendon Press, Oxford.
Griffiths, A. J. F., J. H. Miller, D. T. Suzuki, R. C. Lewontin and W. M. Gelbart, 1996 *An Introduction to Genetic Analysis*. W. H. Freeman, New York.
Hill, W. G., 1982 Rate of change in quantitative traits from fixation of new mutations. Proc. Natl. Acad. Sci. USA **79:** 142–145.
Kearsey, M. J., and A. G. L. Farquhar, 1998 QTL analysis in plants: where are we now. Heredity **80:** 137–142.
Keightley, P. D., 1994 The distribution of mutation effects on viability in *Drosophila melanogaster*. Genetics **138:** 1315–1322.
Keightley, P. D., and W. G. Hill, 1987 Directional selection and variation in finite populations. Genetics **117:** 573–582.
Keightley, P. D., and W. G. Hill, 1988 Quantitative genetic variability maintained by mutation-stabilizing selection balance in finite populations. Genet. Res. **52:** 33–43.
Kimura, M., 1965 A stochastic model concerning the maintenance of genetic variability in quantitative characters. Proc. Natl. Acad. Sci. USA **54:** 731–736.
Kondrashov, A. S., 1984 Rate of evolution in a changing environment. J. Theor. Biol. **107:** 249–260.
Kondrashov, A. S., and M. Turelli, 1992 Deleterious mutations, apparent stabilizing selection and the maintenance of quantitative variation. Genetics **132:** 603–618.
Kondrashov, A. S., and L. Y. Yampolsky, 1996 High genetic variability under the balance between symmetric mutation and fluctuating stabilizing selection. Genet. Res. **68:** 157–164.
Lande, R., 1975 The maintenance of genetic variability by mutation in a polygenic character with linked loci. Genet. Res. **26:** 221–236.
Lovitt, W. V., 1924 *Linear Integral Equations*. McGraw-Hill, New York.
Lynch, M., and R. Lande, 1993 Evolution and extinction in response to environmental change, pp. 234–250 in *Biotic Interactions and Global Change*, edited by P. M. Kareiva, J. G. Kingsolver and R. B. Huey. Sinauer, Sunderland, MA.
Lynch, M., and B. Walsh, 1998 *Genetics and Analysis of Quantitative Traits*. Sinauer, Sunderland, MA.
Lynch, M., W. Gabriel and A. M. Wood, 1991 Adaptive and demographic responses of plankton populations to environmental change. Limnol. Oceanog. **36:** 1301–1312.
Lynch, M., J. Connery and R. Bürger, 1995 Mutation accumulation and the extinction of small populations. Am. Nat. **146:** 489–518.
Mackay, T. F. C., R. F. Lyman and M. S. Jackson, 1992 Effects of *P* element insertions on quantitative traits in *Drosophila melanogaster*. Genetics **130:** 315–332.
Manning, J. T., and D. J. Thompson, 1984 Muller's ratchet and the accumulation of favourable mutations. Acta Biotheor. **33:** 219–225.
Maynard Smith, J., 1978 *The Evolution of Sex*. Cambridge University Press, Cambridge, United Kingdom.
Michod, R. E., and B. R. Levin, 1988 *The Evolution of Sex: An Examination of Current Ideas*. Sinauer, Sunderland, MA.
Mukai, T. S., S. J. Chigusa, L. E. Mettler and J. F. Crow, 1972 Mutation rate and dominance of genes affecting viability in *Drosophila melanogaster*. Genetics **72:** 339–355.
Ohta, T., 1992 The nearly neutral theory of molecular evolution. Annu. Rev. Ecol. Syst. **23:** 263–286.
Peck, J. R., 1994 A ruby in the rubbish: beneficial mutations, deleterious mutations and the evolution of sex. Genetics **137:** 597–606.
Peck, J. R., G. Barreau and S. C. Heath, 1997 Imperfect genes, Fisherian mutation and the evolution of sex. Genetics **145:** 1171–1199.
Turelli, M., 1984 Heritable genetic variation via mutation-selection balance: Lerch's zeta meets the abdominal bristle. Theor. Popul. Biol. **25:** 138–193.
Wagner, G. P., 1996 Apparent stabilizing selection and the maintenance of neutral genetic variation. Genetics **143:** 617–619.
Waxman, D., and J. R. Peck, 1998 Pleiotropy and the preservation of perfection. Science **279:** 1210–1213.
Wright, S., 1977 *Evolution and the Genetics of Populations*, Vol. 3. University of Chicago Press, Chicago.

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## APPENDIX

**Asexual population:** Consider an effectively infinite population of diploid asexual organisms that evolve in continuous time and have alleles with continuous effects (Kimura 1965). During the life of an organism, the processes of viability selection and offspring production occur. Mutations in offspring are taken to occur at the time of birth and offspring are assumed to mature instantaneously to adulthood. Selection occurs on a single phenotypic trait that is controlled by $2L$ alleles located at $L$ loci. The probability that one or more of the alleles in an offspring differ from those of its parent is $\simeq 2L\mu$ (assumed $\ll 1$), where $\mu$ is the allelic mutation rate. It is highly unlikely that more than one allele in an offspring suffers a mutation, so the distribution of mutant effects is accurately taken to be that of a single allele.

The genotypic value of the trait, $G$, is continuous and runs from $-\infty$ to $\infty$. The equation for the distribution of $G$ at time $t$, namely $\Phi_A(G,t)$, is obtained from the limit of discrete time and discrete genotypic effects and an equation similar to that found by Kimura (1965) is obtained. In contrast to Kimura's procedure, however, we explicitly regulate the total population density, so it remains constant in time. This is achieved by having a genotype-independent birth rate that is equal to the mean death rate.

The focus of this work is the effect of a changing environment. To incorporate a constantly changing environment into the calculation, the death rate of individuals with genotypic value $G$ at time $t$ is taken to be $D(G - \alpha t)$, with $\alpha$ the constant rate of change of the optimal phenotype and $D(G)$ the death rate in a static environment. $\Phi_A(G,t)$ is found to obey

$$\frac{\partial \Phi_A(G,t)}{\partial t} = [(1 - 2L\mu)\bar{D}_A(t) - D(G - \alpha t)]\, \Phi_A(G,t) + 2L\mu \bar{D}_A(t) \int_{-\infty}^{\infty} f(G - Y)\Phi_A(Y,t)dY. \quad \text{(A1)}$$

Here $\bar{D}_A(t) = \int_{-\infty}^{\infty} D(G - \alpha t)\Phi_A(G,t)dG$ is the mean death rate at time $t$ and $f(G)$ is given in Equation 1. The regulation of population density results in $\bar{D}_A(t)$ appearing as a factor of the final term in Equation A1.

The form of the death rate follows from the assumption, made in the main text, that individuals in a static environment have a death rate that depends quadratically on phenotypic value $z$. As a consequence, when the phenotypic death rate is averaged over the environmental effect (a Gaussian random variable that is inde-

pendent of $G$ and has mean zero and variance $V_e$), the death rate of individuals with genotypic value $G$ at time $t$ is $D(G - \alpha t)$, where $D(G) = 1 + V_e/(2V) + G^2/(2V)$. In what follows, we scale variables so that, without loss of generality, $V_e = 1$.

After a transient period in a constantly changing environment, numerical evidence indicates that $\Phi_A(G,t)$ settles down to a steady-state tracking solution—one that continuously follows, without change of shape, the optimal genotypic value. Such a solution depends on $G$ and $t$ only in the combination $G - \alpha t$ and it is useful to write

$$\Phi_A(G,t) = \psi_A(G - \alpha t). \tag{A2}$$

Substituting Equation A2 into Equation A1 and changing the variable to $G' = G - \alpha t$ leads to an equation for $\psi_A(G')$. For typographical simplicity we omit all primes and obtain

$$-\alpha \frac{d\psi_A(G)}{dG} = [(1 - 2L\mu)\bar{D}_A - D(G)]\,\psi_A(G) + 2L\mu\bar{D}_A \int_{-\infty}^{\infty} f(G - Y)\psi_A(Y)dY, \tag{A3}$$

where $\bar{D}_A = \int_{-\infty}^{\infty} D(G)\psi_A(G)dG$.

When $\alpha = 0$ we arrive at the equation for the equilibrium distribution in a static environment. Let $V_s = VD(0)$. If $2L\mu V_s/m^2 \ll 1$, the distribution may be found in the "house of cards" approximation (Turelli 1984): $\psi_A(G) \equiv \Phi_A(G) \approx 4L\mu V_s f(G)/(G^2 + \beta^2)$, $\beta = 4\pi L\mu V_s/\sqrt{2\pi m^2}$. This distribution has a mean of zero and an approximate variance of $4L\mu V_s$. Alternatively, if $2L\mu V_s/m^2 \gg 1$, $\Phi_A(G)$ is approximately Gaussian, with mean zero and variance $\sqrt{2L\mu V_s m^2}$. This result is derived using a similar approach to that of Kimura (1965).

When the environment changes ($\alpha \neq 0$) the foregoing mutation selection balance results may be changed significantly because the "environmental force" in Equation A3, $-\alpha d\psi_A(G)/dG$, need not be small compared with the mutation contribution, $2L\mu\bar{D}_A \int_{-\infty}^{\infty} f(G - Y)\psi_A(Y)dY$.

Generally, the solution of Equation A3 has to satisfy

$$\psi(G) \geq 0, \quad \int_{-\infty}^{\infty} \psi(G)dG = 1 \tag{A4}$$

as follows from $\Phi_A(G,t)$ being a probability density. Numerical evidence supports the assumption that the solution of Equation A3 with these properties is unique.

Let $E_A(\mathrm{Var}_A)$ denote the expectation operator (variance) for the asexual population. For tracking solutions, $\xi_A$ denotes the lag of the mean genotypic value behind the value of the optimum and is defined by $E_A(G) = \alpha t - \xi_A$. In terms of $\psi_A(G)$, $\xi_A = -\int_{-\infty}^{\infty} G\psi_A(G)dG$ and the variance of genotypic effects is $V_{G,A} = \int_{-\infty}^{\infty} [G - (-\xi_A)]^2\,\psi_A(G)dG$. The mean death rate following from these is $\bar{D}_A = 1 + 1/(2V) + (V_{G,A} + \xi_A^2)/(2V)$ (recall that we use units where $V_e = 1$). Because there is no epistasis or dominance in the model, the narrow sense heritability is the ratio of genotypic to phenotypic variance: $h_A^2 = V_{G,A}/(V_{G,A} + 1)$. Tables 1–4 contain results following from the numerical solution of Equation A3. The numerical results are complemented by an analytical approximation that applies for asexuals when $L\mu V/m^2 \ll 1$:

$$\xi_A \simeq \sqrt{\alpha V/m}\left[8\ln\left(\frac{m^2}{4L\mu V}\right)\right]^{1/4},$$
$$V_{G,A} \simeq \sqrt{\alpha m V}\left[8\ln\left(\frac{m^2}{4L\mu V}\right)\right]^{-1/4}. \tag{A5}$$

These approximations exhibit the general dependencies of the lag, $\xi_A$, and the genetic variance, $V_{G,A}$, on parameters in the problem. In particular, they indicate that as far as the rate of optimum shift, $\alpha$, is concerned, both the lag and the genetic variance are proportional to $\sqrt{\alpha}$. Furthermore, the approximations show that $\xi_A$ and $V_{G,A}$ exhibit a strikingly weak dependence on the mutation rate, $\mu$.

**Derivation of approximate results:** The derivation given in this section is somewhat technical and may be omitted at a first reading. To begin, we introduce a parameter $\Theta$ defined by $\Theta^2 = 2V[(1 - 2L\mu)\,\bar{D}_A - D(0)]$. When $\alpha = 0$, $\Theta^2$ is negative (Waxman and Peck 1998). A changing environment modifies the balance of evolutionary forces and allows the new possibility that $\Theta^2$ is positive. We estimate that for $L\mu V/m^2 \ll 1$, $\Theta^2$ becomes positive at an $\alpha$ of order $\alpha_0 \overset{\text{def}}{\equiv} 27(2L\mu)^3V^2m^{-3}$. Here we assume that $\alpha$ is sufficiently large that $\Theta^2 > 0$. Furthermore, we take $\Theta$ itself to be positive.

Next we assume that the smallness of the trait mutation rate, $2L\mu$, means that at almost all $G$ where $\psi_A(G)$ is appreciable, the environmental term $-\alpha d\psi_A(G)/dG$ in Equation A3 dominates the mutation contribution $2L\mu\bar{D}_A \int_{-\infty}^{\infty} f(G - Y)\psi_A(Y)dY$. We thus neglect the latter term where $\psi_A(G)$ is appreciable, in which case $-\alpha V d\psi_A(G)/dG \approx \frac{1}{2}(\Theta^2 - G^2)\psi_A(G)$. Only in the vicinity of $G = -\Theta$ is $\psi_A(G)$ appreciable, because it has a maximum at this point. Approximating $\frac{1}{2}(\Theta^2 - G^2)$ by $\Theta(\Theta + G)$ yields a Gaussian approximation for $\psi_A(G)$: $\psi_A(G) \approx \sqrt{\Theta/(2\pi\alpha V)}\,\exp[-(\Theta/(2\alpha V))(G + \Theta)^2]$. This is a distribution with a lag of $\xi_A = \Theta$ and a variance of $V_{G,A} = \alpha V/\Theta$.

So far the parameter $\Theta$ is unknown but an approximation for $\Theta$ can be derived by writing Equation A3 as the integral equation

$$\psi_A(G) - 2L\mu\bar{D}_A \int_{-\infty}^{\infty} R(G,Y)\psi_A(Y)dY = 0, \tag{A6}$$

where $R(G,Y) = (1/\alpha)\int_G^{\infty} \exp(-[H(G) - H(X)]/\alpha) \cdot f(X - Y)dX$ and $H(G) = [\Theta^2 G - G^3/3]/(2V)$. An approximate equation can be obtained by expanding the Fredholm determinant associated with Equation A6. The simplest nontrivial approximation keeps only terms up to linear order in $R$ and yields (Lovitt 1924)

$$1 - 2L\mu\bar{D}_A \int_{-\infty}^{\infty} R(G,G)dG \approx 0. \tag{A7}$$

For $\alpha \to 0$, it may be shown that the value of $\Theta^2$ obtained from this equation coincides with the house of cards approximation (Turelli 1984), thereby indicating that the approximation holds when $L\mu V/m^2 \ll 1$.

After some manipulations, we find that Equation A7 can be written as

$$1 - 4\overline{D}_A \frac{L\mu V}{m^2} K\left(\frac{\alpha V}{m^3}, \frac{\Theta}{m}\right) \approx 0,$$

$$K(\lambda,q) = \int_0^\infty \exp\left[-\lambda^2\left(\frac{x^6}{24} + \frac{x^4}{2}\right) + q^2\frac{x^2}{2}\right]dx. \quad \text{(A8)}$$

To make further progress, we make the crude approximation of keeping only the leading $\Theta$ dependence of $\ln(K(\alpha V/m^3, \Theta/m))$. After some work, we find, $\ln(K(\alpha V/m^3, \Theta/m)) = \Theta^4 m^2/(8\alpha^2 V^2) + \ldots$; thus Equation A8 yields $\Theta^4 m^2/(8\alpha^2 V^2) \approx \ln(m^2/(4\overline{D}_A L\mu V))$. It is clear that among other things, various logarithmic corrections have been omitted to obtain this result, and in this spirit, we drop the factor $\overline{D}_A$ within the argument of the logarithm, thereby allowing $\Theta$ to be given in terms of known quantities: $\Theta \approx \sqrt{\alpha V/m}\,[8\ln(m^2/(4L\mu V))]^{1/4}$. Analytical approximations for $\xi_A$ and $V_{G,A}$ then follow from this formula for $\Theta$.

Last, we note that the Gaussian distribution predicts $V_{G,A} \times \xi_A = \alpha V$ and this approximately applies when $\alpha$ is not too small ($\alpha > 0.001$).

**Sexual population:** Consider an effectively infinite population of diploid sexual organisms with $L$ unlinked loci that undergo random mating. The death rate for individuals with genotypic value $G$ at time $t$ is, as for asexuals in a constantly changing environment, $D(G - \alpha t)$.

We assume the population has achieved a steady-state tracking distribution, with $G - \alpha t$ having a time-independent distribution. To proceed further, we neglect correlations of genes both across and between loci. We estimate both types of correlations to be comparable in magnitude and Bulmer's analysis of between-loci correlations (Bulmer 1989) indicates that correlation effects are small when $V_{G,S} \ll V$. Results presented in the tables, which are consistent with the neglect of correlations, yield genetic variances satisfying $V_{G,S} \ll V$. Results for which this inequality does not hold, *e.g.*, those yielding $V_{G,S} \geq V/2$, are included for aid of comparison, but the reader should note that they may require significant corrections due to neglected correlations.

The neglect of correlations leads to all $2L$ alleles under selection having independent and identical distributions. In particular this means that for all values of the allelic location, $i$, the combination $x_i - \alpha t/(2L)$ has a time-independent distribution. For the mean and variance of this quantity, we write $M_1 = E_S(x_i - \alpha t/(2L))$, $V_1 = \mathrm{Var}_S\,(x_i - \alpha t/(2L)$, where $E_S(\mathrm{Var}_S)$ denotes the expectation operator (variance) for the sexual population.

Each allele may be treated as that of a single haploid locus existing in an averaged genetic background composed of the remaining alleles. The background quantities are present in a nontrivial way and we give some details of the calculations. Consider, *e.g.*, those individuals with an allele at location $i$ with effect $x_i$ at time $t$. Their death rate follows by averaging $D(G - \alpha t)$ over the genetic background and yields the death rate $D_S(x_i - \alpha t/(2L) + (2L - 1)M_1)$, where

$$D_S(x) \overset{\text{def}}{\equiv} \left(1 + \frac{1}{2V}\right) + \frac{(2L-1)V_1}{2V} + \frac{x^2}{2V}. \quad \text{(A9)}$$

The distribution of allelic effects at location $i$, written as $\Phi_{S,1}(x_i,t)$, satisfies the one-locus haploid equation

$$\frac{\partial\Phi_{S,1}(x_i,t)}{\partial t} = \left[(1-\mu)\overline{D}_S - D_S\left(x_i - \frac{\alpha t}{2L} + (2L-1)M_1\right)\right] \cdot \Phi_{S,1}(x_i,t) + \mu\overline{D}_S \int_{-\infty}^{\infty} f(x_i - y)\Phi_{S,1}(y,t)dy,$$

where

$$\overline{D}_S = \int_{-\infty}^{\infty} D_S\left(x_i - \frac{\alpha t}{2L} + (2L-1)M_1\right)\Phi_{S,1}(x_i,t)dx_i,$$

a quantity independent of time.

By virtue of being a tracking solution, $\Phi_{S,1}(x_i,t)$ depends on $x_i$ and $t$ only in the combination $x_i - \alpha t/2L$ and we write

$$\Phi_{S,1}(x_i,t) = \psi_S\left(x_i - \frac{\alpha t}{2L} + (2L-1)M_1\right). \quad \text{(A11)}$$

Changing the variable to $x = x_i - \alpha t/(2L) + (2L - 1)M_1$ in Equation A10 yields

$$-\frac{\alpha}{2L}\frac{d\psi_S(x)}{dx} = [(1-\mu)\overline{D}_S - D_S(x)]\,\psi_S(x) + \mu\overline{D}_S\int_{-\infty}^{\infty} f(x-y)\psi_S(y)dy. \quad \text{(A12)}$$

The lag of the mean genotypic value behind the fitness optimum, $\xi_S$, is defined by $E_S(G) = \alpha t - \xi_S$. In terms of $\psi_S(x)$ we have $\xi_S = -E_S(G - \alpha t) = -\int_{-\infty}^{\infty}[x_i - \alpha t/(2L) + (2L-1)M_1]\,\Phi_{S,1}(x_i,t)dx_i = -\int_{-\infty}^{\infty} x\psi_S(x)dx$. Similarly, the total genotypic value for the sexuals is $V_{G,S} = \mathrm{Var}_S\,(\Sigma_{i=1}^{2L}x_i) = 2LV_1$ and $V_1 = \int_{-\infty}^{\infty}[x - (-\xi_S)]^2\,\psi_S(x)dx$. The mean death rate and narrow sense heritability are $\overline{D}_S = 1 + 1/(2V) + (V_{G,S} + \xi_S^2)/(2V)$, $h_S^2 = V_{G,S}/(V_{G,S} + 1)$. Tables 1–4 contain results following from the numerical solution of Equation A12. These are complemented by analytical approximations that follow from the same methods as those used for the asexuals. The approximations apply when $\mu V/m^2 \ll 1$: a fairly unrestrictive condition. The approximations for sexuals can be obtained from the asexual results of Equation A5 by the replacements $\xi_S = \xi_A(\alpha \to \alpha/(2L), \mu \to \mu/(2L))$, $V_{G,S} = 2L \cdot V_{G,A}(\alpha \to \alpha/(2L), \mu \to \mu/(2L))$, as follows from comparing Equations A12 and A3:

$$\xi_S \simeq \sqrt{\alpha V/(2Lm)}\left[8\ln\left(\frac{m^2}{2\mu V}\right)\right]^{1/4},$$

$$V_{G,S} \simeq \sqrt{2L\alpha mV}\left[8\ln\left(\frac{m^2}{2\mu V}\right)\right]^{-1/4}. \quad \text{(A13)}$$

As for asexuals, the approximations indicate that both the lag and the genetic variance are proportional to $\sqrt{\alpha}$ and there is a very weak dependence on the mutation rate, $\mu$. Also, as for asexuals, the approximations yield the relation $V_{G,S} \times \xi_S = \alpha V$, which approximately applies when $\alpha$ is not too small ($\alpha > 0.001$).

The distribution of genotypic effects, $\Phi_S(G,t)$ is approximately Gaussian, because $G$ is the sum of $2L$ approximately independent Gaussian random variables with identical distributions.