16

Short-term Changes in the Variance: 1. Changes in the Additive Variance

In artificial selection experiments it seems likely that the effects of linkage disequilibrium will be more important than the slower and less dramatic effects due to changes in gene frequencies — Michael Bulmer (1976a)

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Up to this point, we have been assuming that selection does not significantly change the variance of a trait, at least over the short term (a few generations). This arises from our focus on **directional selection** (direct selection on the mean) and the assumption that a large number of loci, each of small effect, underlie a trait. Under such a genetic architecture, allele frequency changes over the short term can be cumulatively large enough to have a significant effect on the mean but little effect on the variance (Chapter 24). This ignores the fact that selection also generates gametic-phase disequilibrium (LD), even among unlinked loci, which can swiftly and dramatically change the variance even in the absence of *any* allele frequency change. Further, natural and/or artificial selection can act directly on the variance of a trait itself, such as **stabilizing selection** for more uniformity or **disruptive selection** for more extreme phenotypes on either side of the mean. The breeder's equation only considers the change in mean and hence is uninformative on response in these cases.

Both directional and stabilizing selection decrease the phenotypic variance, which generates negative disequilibrium (alleles that increase trait values become negatively correlated within a gamete), reducing σ_A^2. Conversely, disruptive selection increases the phenotypic variance, and this generates positive disequilibrium, inflating the additive variance. This chapter develops the **Bulmer equation**, an analog of the breeder's equation for the change in the additive genetic variance from selection-induced LD. This predicts how changes in LD change h^2, allowing updated values to be substituted into the breeder's equation for more accurate prediction of the response in the mean. It also predicts the short-term change in the variance under stabilizing and disruptive selection. Phenotypic assortative mating also generates disequilibrium, and we can use this machinery to consider the effects of simultaneous assortative mating and selection. Chapter 24 continues this discussion, relaxing many of the infinitesimal assumptions (such as allowing for linkage and a finite number of loci).

Changes in the genetic variance (though either LD or allele frequency change) are not the only route by which selection can alter the phenotypic variance σ_z^2. If there is heritable variation in the environmental variance σ_E^2, this too can respond to selection, resulting in a change in σ_z^2. Short-term response in σ_z^2 through changes in σ_E^2 is examined in Chapter 17.

CHANGES IN VARIANCE DUE TO GAMETIC-PHASE DISEQUILIBRIUM

In the absence of epistasis, gametic-phase disequilibrium does not change the population mean (Chapter 15). However, as pointed out by Lush (1945), it affects the response to selection by introducing correlations between alleles at different loci, altering the additive genetic

variance, even in the absence of any allele-frequency change. To see this, let $a_1^{(k)}$ and $a_2^{(k)}$ be the average effects of the two alleles at locus k from a random individual, where subscript one and two denotes the maternally- and paternally-derived alleles, respectively. Assuming (for now) random mating, there is no covariance between alleles of maternal and paternal origin, so that $\sigma(a_1^{(k)}, a_2^{(j)}) = 0$ for all k and j. However, when gametic-phase disequilibrium is present, there *can* be covariances between alleles at different loci from the *same* parent, so that $\sigma(a_1^{(k)}, a_1^{(j)})$ and $\sigma(a_2^{(k)}, a_2^{(j)})$ can be non-zero. That is, there can be correlations between alleles in any particular gamete. Since σ_A^2 is the variance of the sum of average effects over all loci,

$$\sigma^2\left(\sum_{k=1}^{n}\left(a_1^{(k)}+a_2^{(k)}\right)\right) = 2\sum_{k=1}^{n}\sigma^2\left(a^{(k)}\right) + 4\sum_{k<j}^{n}\sigma\left(a^{(j)}, a^{(k)}\right) \tag{16.1a}$$

$$= 2\sum_{k=1}^{n} C_{kk} + 4\sum_{k<j}^{n} C_{jk} \tag{16.1b}$$

where n is the number of loci and C_{jk} is the covariance between allelic effects at loci j and k (when contributed by the same parent and hence on the same gamete). This decomposes the additive variance as

$$\sigma_A^2 = \sigma_a^2 + d, \tag{16.2}$$

where $\sigma_a^2 = 2\sum C_{kk}$ is the additive variance in the absence of gametic-phase disequilibrium and the disequilibrium contribution $d = 4\sum_{j<k} C_{kj}$ is the covariance between allelic effects at different loci (in terms of the notation used in LW Equation 7.14, $d = \sigma_{A,A}$). The component of the additive genetic variance that is unaltered by changes in gametic-phase disequilibrium, σ_a^2, is often referred to as the **additive genic variance** (or simply the **genic variance**) to distinguish it from the additive *genetic* variance σ_A^2. In the absence of disequilibrium, the genic and genetic variances are equivalent. Negative disequilibrium ($d < 0$) conceals the presence of additional additive variance, with σ_A^2 increasing toward σ_a^2 as the disequilibrium decays. If $d > 0$, additive variance is inflated relative to a random-mating population (i.e., the genic variance) and σ_A^2 decreases towards σ_a^2 as disequilibrium decays. Since $n(n-1)$ terms contribute to d compared to n terms contributing to σ_a^2, gametic-phase disequilibrium can generate large changes in the additive genetic variance even when changes in these individual covariances are all very small.

The allelic effects $a^{(k)}$ (and hence the genic variance σ_a^2) are altered as allele frequencies change, resulting in a permanent change in σ_A^2. Changes in σ_a^2 due to selection strongly depend on the initial distribution of allelic effects and frequencies (Chapters 5, 25-28), both of which are extremely difficult to estimate. Changes in d, however, are generally less sensitive to the initial distribution of allelic effects (Sorensen and Hill 1982). Any changes in σ_A^2 due to changes in d are *transient* — in the absence of selection, recombination removes disequilibrium and the additive genetic variance σ_A^2 approaches the additive genic variance σ_a^2 as d decays to zero.

Under our (short-term response) assumption that allele frequencies remain effectively constant, changes in σ_A^2 are due entirely to changes in d. Hence, the additive genetic variance in generation t is given by $\sigma_A^2(t) = \sigma_a^2 + d(t)$, with change in (additive) variance $\Delta\sigma_A^2(t) = \Delta d(t)$. Under random mating in the absence of selection, the disequilibrium between pairs of unlinked loci is halved each generation (LW Equation 5.12), halving the covariance between allelic effects,

$$d(t+1) = \frac{d(t)}{2}. \tag{16.3}$$

Countering this, selection tends to generate gametic-phase disequilibrium. Directional selection to change the mean of a character also reduces its variance, generating negative d

(Felsenstein 1965). As shown in Figure 16.1, stabilizing selection reduces the phenotypic variance and creates negative d, while disruptive selection increases the phenotypic variance, generating positive d. Stabilizing and disruptive selection are occasionally referred to as **centripetal** and **centrifugal selection**, respectively (Simpson 1944). How these within-generation changes in the variance translate into between-generation changes has solved for the infinitesimal model by Bulmer (1971, 1974, 1976a, 1980), whose approach is closely followed. Chapter 24 moves beyond the infinitesimal model by considering some of these issues in the presence of both linkage and a finite number of loci. Estimation of the nature and amount of selection acting on the mean and the variance of a character is examined in Chapters 28 and 29.

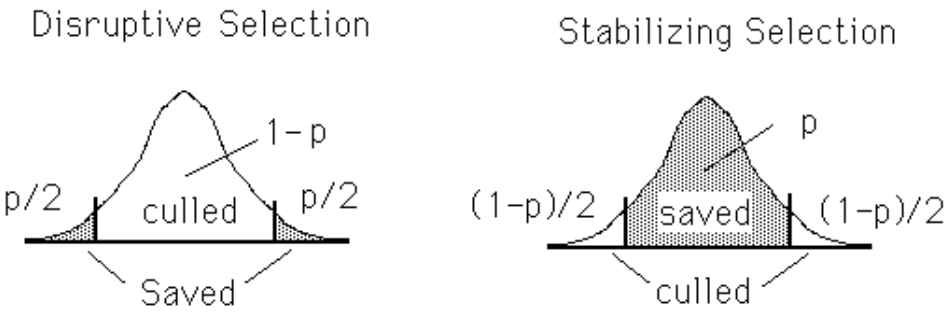


Figure 16.1. Artificial stabilizing and disruptive selection using **double truncation**. In both cases, a fraction p of the population is allowed to reproduce. In stabilizing selection, the central p of the distribution is saved, while under disruptive selection the uppermost and lowermost $p/2$ are saved.

CHANGES IN VARIANCE UNDER THE INFINITESIMAL MODEL

Since allele frequencies remain essentially constant under the infinitesimal model assumptions, the additive genic variance σ_a^2 remains constant and all changes in the additive genetic variance σ_A^2 are due to changes in d. Assuming the population is initially in gametic-phase equilibrium, $\sigma_A^2(0) = \sigma_a^2$, giving $\sigma_A^2(t) = \sigma_a^2 + d(t)$. Let $h^2(t)$ and $\sigma_z^2(t)$ denote the heritability and phenotypic variance before selection in generation t, and h^2 and σ_z^2 be the values of these quantities in the absence of gametic-phase disequilibrium.

Bulmer (1971) has suggested that under the infinitesimal model, gametic-phase disequilibrium does not change the dominance variance. To see this, first note from LW Equation 5.16b that the disequilibrium contribution with a finite number of loci (n) to dominance variance is of order $n^2\,\overline{D}^2$, where $\overline{D}$ is the average pairwise disequilibrium. Under the infinitesimal model, the total disequilibrium (summing over all pairs of loci) remains bounded as the number of loci increases, implying $\overline{D}$ is of order n^{-2} since there are $n(n-1)/2 \approx n^2/2$ pairs of loci contributing to $\overline{D}$. The disequilibrium contribution to dominance variance is thus of order $n^2(n^{-2})^2 = n^{-2}$, which converges to zero in the infinitesimal model limit (as the number of loci $n \to \infty$). There is, however, some delicacy with this argument. In Chapter 24, we show that with strong directional dominance, the amount of inbreeding becomes unbounded as one increases the number of loci to the infinitesimal limit. Likewise, Jorjani et al. (1998) use simulations to show that with a finite number of loci and small population size, changes in disequilibrium (in their case from assortative mating) can significantly change the dominance variance. While we will make the Bulmer assumption of no effect of domi-

nance throughout this chapter, further exploration of the impact of disequilibrium on σ_D^2 is warranted.

With this assumption in mind, in the absence of any epistatic variance, genotype $\times$ environment interactions and/or correlations, the phenotypic variance and heritability at generation t become

$$\sigma_z^2(t) = \sigma_E^2 + \sigma_D^2 + \sigma_A^2(t) = \sigma_z^2 + d(t) \tag{16.4a}$$

$$h^2(t) = \frac{\sigma_A^2(t)}{\sigma_z^2(t)} = \frac{\sigma_a^2 + d(t)}{\sigma_z^2 + d(t)} \tag{16.4b}$$

where $\sigma_z^2 = \sigma_z^2(0)$ is the phenotypic variance before selection in the initial (unselected) population. Thus, predicting the value of $d(t)$ is sufficient to predict changes in the variances, and hence the heritability and the response in the mean using $R(t) = h^2(t)S(t)$.

Under the infinitesimal model, genotypic values are normally distributed before selection (Bulmer 1971, 1976b). Recalling $z = G + E$, we see that if the environmental values E are also normally distributed, then the joint distribution of phenotypic and genotypic values is multivariate normal. Hence, from standard statistical theory (e.g., LW Chapter 8), the regression of offspring phenotypic value z_o on parental phenotypes z_m and z_f is linear and homoscedastic, with

$$z_o = \mu + \frac{h^2}{2}(z_m - \mu) + \frac{h^2}{2}(z_f - \mu) + e \tag{16.5a}$$

where

$$\sigma_e^2 = \left(1 - \frac{h^4}{2}\right)\sigma_z^2 \tag{16.5b}$$

The derivation of Equation 16.5 follows from standard multiple regression theory and the correlations between relatives (see Example 6 in LW Chapter 8 for details).

Denote the within-generation change in variance by $\delta(\sigma_z^2) = \sigma_{z^*}^2 - \sigma_z^2$, where z^* refers to a phenotypic value from the selected population. Throughout this chapter we use the notation of δ to distinguish the *within-generation* change of a variable from its *between-generation* change Δ, the latter incorporating the effects of genetic transmission across a generation. Taking variances of both sides of Equation 16.5a and assuming random mating (so that $\sigma(z_f, z_m) = 0$) and identical selection on both sexes, the phenotypic variance among the offspring from selected parents becomes

$$\begin{aligned}
\sigma^2(z_o) &= \frac{h^4}{4}\left[\,\sigma^2(z_m^*) + \sigma^2(z_f^*)\right] + \sigma_e^2 \\
&= \frac{h^4}{2}\left[\,\sigma_z^2 + \delta(\sigma_z^2)\,\right] + \left(1 - \frac{h^4}{2}\right)\sigma_z^2 \\
&= \sigma_z^2 + \frac{h^4}{2}\,\delta(\sigma_z^2)
\end{aligned} \tag{16.6}$$

The change in phenotypic variance in the offspring due to selection on their parents generating disequilibrium is thus $(h^4/2)\,\delta(\sigma_z^2)$. Since there is no change in the environmental, dominance, or genic variances, this change is all in the disequilibrium component d of the additive genetic variance σ_A^2. Combining Equations 16.6 and 16.3 gives the general recursion for changes in the variance under the infinitesimal model with unlinked loci as

$$d(t+1) = \frac{d(t)}{2} + \frac{h^4(t)}{2}\,\delta\left(\sigma_{z(t)}^2\right) \tag{16.7a}$$

This result is due to Bulmer (1971) and implies that the between-generation change in the disequilibrium contribution is

$$\begin{aligned}\Delta d(t) &= \Delta\sigma^2_{z(t)} = \Delta\sigma^2_A(t) \\ &= -\frac{d(t)}{2} + \frac{h^4(t)}{2}\,\delta\left(\sigma^2_{z(t)}\right) \end{aligned} \tag{16.7b}$$

This is the **Bulmer equation** and is variance analogue to the breeder's equation. The first term is the decay due to recombination in the disequilibrium contribution from the previous generation (assuming unlinked loci), while the second term is the amount of new disequilibrium generated by selection that is passed on to the offspring. As with the breeder's equation, this second term is a function of the within-generation change (here δ) and the fraction $h^4/2$ transmitted to the next generation. When loci are linked with recombination fraction c, a larger fraction $(1-c)$ of any previous d remains. Chapter 24 examines the effect of linked loci more detail. Note that if we start from a base population in equilibrium $(d(0) = 0)$, the sign of the within-generation change in the variance equals the sign of d. Selection that *decreases* the phenotypic variance generates negative d, while selection that *inflates* the variance generates positive d. This change in the variance (typically a reduction) due to selection generating disequilibrium is called the **Bulmer effect**. Provided the joint distribution of phenotypic and genotypic values remains multivariate normal, under the infinitesimal model the complete dynamics of the phenotypic distribution are jointly described by the change in the variance (Equation 16.7), while the change in the mean is given by updating the breeder's equation, $R(t) = h^2(t)\,S(t)$. Equation 16.7 makes the further point that if we wish to use variance components to predict the response to selection, we need to start from an *unselected base population*. If a population has experienced recent prior selection, then $d \neq 0$ and hence the change in σ^2_A (and, in turn, the response to selection) cannot be predicted without knowing the value of d in the starting population. Finally, at equilibrium,

$$\widetilde{d} = \widetilde{h}^4\,\widetilde{\delta}(\sigma^2_z) \tag{16.7c}$$

where tilde denotes an equilibrium value.

Example 16.1. Data of Rendel (1943) suggests stabilizing selection occurs on egg weight in ducks. Of 960 eggs followed, 64.5% hatched. The change in mean egg weight (in grams) after selection was negligible, but the variance showed a significant decrease. The variance before selection was 52.7 (using all 960 eggs), declining to 43.9 after selection (in those eggs that hatched), giving $\delta(\sigma^2_z) = -8.8$. Assuming that the reduction in variance due to gametic-phase disequilibrium is at equilibrium and taking $\widetilde{h}^2_z = 0.60$ (the heritability for egg weight in poultry) gives

$$\widetilde{d} = \widetilde{h}^4\,\widetilde{\delta}(\sigma^2_z) = (0.6)^2(-8.8) = -3.2 \quad \text{and} \quad \widetilde{\sigma}^2_A = \widetilde{h}^2\,\widetilde{\sigma}^2_z = 0.6 \cdot 52.7 = 31.6$$

Assuming the infinitesimal model, if selection is stopped, the additive variance is expected to eventually increase to

$$\sigma^2_A = \sigma^2_a = \widetilde{\sigma}^2_A - \widetilde{d} = 31.6 + 3.2 = 34.8$$

with half this change occuring in one generation (assuming all underlying loci are unlinked). Similarly, $\sigma^2_z = 52.7 + 3.2 = 55.9$ and $h^2 = 34.8/55.9 = 0.62$. (Example from Bulmer 1971.)

Within- and Between-Family Variance Under the Infinitesimal Model

An alternative, and instructive, approach to the phenotypic regression argument leading to Equation 16.7 is to consider the regression of offspring breeding value (A_o) on the breeding values of its parents (A_f, A_m). Under the infinitesimal model, the joint distribution of parental and offspring breeding values before selection is multivariate normal (Bulmer 1971), and Example 7 in Chapter 8 of LW shows that the distribution of breeding values in the offspring of parents with breeding values A_f and A_m is given by the regression

$$A_o = \frac{1}{2}A_m + \frac{1}{2}A_f + e \tag{16.8a}$$

The residual e is the contribution due to segregation, which is normally distributed with mean zero and variance $\sigma_a^2/2 = \sigma_A^2(0)/2$, half the additive genetic variance present in the absence of disequilibrium (Bulmer 1971, Felsenstein 1981, Tallis 1987). Since e is the residual of a regression, it is uncorrelated with both A_f and A_m (LW Chapters 3, 8). Taking variances and assuming random mating (so that A_f and A_m are uncorrelated),

$$\begin{aligned}\sigma_A^2(t+1) = \sigma_{A_o}^2(t+1) &= \sigma^2\left(\frac{A_m(t)}{2} + \frac{A_f(t)}{2}\right) + \sigma_e^2 \\ &= \frac{1}{4}\left(\sigma_{A_m}^2(t) + \sigma_{A_f}^2(t)\right) + \frac{1}{2}\sigma_A^2(0) \\ &= \frac{1}{2}\sigma_{A^*}^2(t) + \frac{1}{2}\sigma_a^2 \end{aligned} \tag{16.8b}$$

where $\sigma_{A^*}^2(t)$ is the variance of the breeding values of the selected parents (with assortative mating, Equation 16.8b has an additional term, $\sigma(A_m^*, A_f^*)/2$, see Equation 16.21b). Equation 16.8b shows that additive variance can be decomposed into a *between-family* component (half the additive *genetic* variance, $\sigma_{A^*}^2(t)/2$) that measures the differences between the mean breeding values of families and a *within-family* component (half the additive *genic* variance, $\sigma_A^2(0)/2 = \sigma_a^2/2$) due to segregation that measures the variation within families. Equations 16.8a and b imply that under the infinitesimal model, ***the within-family additive variance remains constant***. The change in the population additive genetic variance is entirely due to changes in the variance of the mean values of different families. Positive disequilibrium ($d > 0$) increases the between-family component while negative disequilibrium ($d < 0$) decreases it (Reeve 1953).

The within-family variance, $\sigma_a^2/2$, deserves additional comment. This is often called the **Mendelian sampling variance**. Notice that this variance (under the infinitesimal model) is *not* affected by selection, as we assume negligible change in allele frequencies. As we will see shortly, it can be decreased by drift and/or inbreeding. Likewise, with a finite (but large) number of loci σ_a^2 can indeed be affected by selection, but the change per generation is typically very small (Chapter 24). An especially important implication of this constant within-family segregation variance is that it tends to largely restore a normal distribution of breeding values following selection. As Equation 16.8a demonstrates, the distribution of breeding values in the offspring is the sum of two components: the breeding values of the selected parents plus the contribution due to segregation. Even if the distribution of breeding values in the selected parents departs significantly from normality, segregation tends to reduce this departure. Interestingly, Smith and Hammond (1987) found that the short-term deviation from normality is largest when selection is moderate, becoming smaller as selection increases. This can be seen from Equation 16.8a by writing $A_o = A_{mp} + e$, where A_{mp} is the midparental breeding value and e the contribution due to segregation. Under the assumption that e is normally distributed, as selection intensity increases, the variance of

A_{mp} decreases, and more and more of the variance of A_o is accounted for by e, decreasing the departure from normality.

The derivation of Equations 16.7 and 16.8a requires the assumption that breeding values remain normally distributed. Selection and/or assortative mating, however, cause the population to deviate from normality by creating gametic-phase disequilibrium that generates skew and kurtosis in the distribution of breeding values (Chapter 24). If selection changes the distribution of breeding values away from normality, the parent-offspring regression may no longer be linear and homoscedastic. Consequences of departures from linearity were briefly discussed in Chapter 13 and developed more fully in Chapter 24. For example, heteroscedasticity of the residuals implies that the residual variance σ_e^2 may depend on the actual parental values chosen, which greatly complicates matters. The within-family variance in such cases is no longer a constant independent of the parental breeding values, potentially reducing the effectiveness of segregation in restoring normality. In all discussions that follow, we assume that these departures from normality can be ignored. Chapter 24 works at relaxing these assumptions.

Accounting For Inbreeding and Drift

The effects of drift and regular inbreeding are easily accommodated under the infinitesimal model (Verrier et al. 1989). The segregation variation (the variance in the residual e in Equation 16.8a) is just half the additive genic variance of the parents. When genetic drift is present, the genic variance in generation t becomes

$$\sigma_a^2(t) = \sigma_a^2(0)\left(1 - \frac{1}{2N_e}\right)^t, \tag{16.9a}$$

while Keightley and Hill (1987) show that drift modifies the disequilibrium by

$$\Delta d(t) = -\frac{d(t)}{2}\left(1 + \frac{1}{N_e}\right) - \frac{1}{2}\left(1 - \frac{1}{N_e}\right)\kappa h^2(t)\sigma_A^2(t) \tag{16.9b}$$

where κ is the fractional reduction in variance following selection (see Equation 16.10). When population size is finite, the variance in any particular generation can be computed by jointly iterating Equations 16.9a and b. Using these updated values for the additive variance and heritability, one can then use the breeder's equation to predict the change in mean.

Similarly, when the parents are inbred, the segregation variance is also correspondingly reduced. Segregation variance in parents arises from segregation of alleles in heterozygotes. As parents become more inbred, the amount of heterozygotes, and hence segregation, decreases. Assuming no correlation between the parents, the within-family segregation variance under inbreeding is

$$\frac{\sigma_a^2(t)}{2} = \frac{\sigma_a^2(0)}{2}\left[1 - \frac{f_m(t) + f_f(t)}{2}\right], \tag{16.9c}$$

where f_m and f_f denote the average amount of inbreeding in selected male and female parents. The additive variance recursion equation under the infinitesimal model assumptions becomes

$$\sigma_A^2(t+1) = \frac{1}{4}\left[\sigma_{A_m^*}^2(t) + \sigma_{A_f^*}^2(t)\right] + \frac{\sigma_a^2(0)}{2}\left[1 - \frac{f_m(t) + f_f(t)}{2}\right] \tag{16.9d}$$

The above results for the reduction in σ_a^2 under inbreeding apply to the case of only additive variance. When nonadditive variance is present, the changes in additive variance under inbreeding are potentially much more complex (Chapter 12).

CHANGES IN VARIANCE UNDER TRUNCATION SELECTION

Provided the normality assumptions of the infinitesmal model hold, the changes in variance under any selection model can be computed by obtaining the within-generation change in the phenotype variance, $\delta(\,\sigma^2_{z(t)}\,)$, and applying Equation 16.7. In the general case, this requires numerical iteration to obtain the equilibrium heritiability and genetic variance. However, in many cases phenotypic variance after selection can be written as

$$\sigma^2_{z^*} = (1-\kappa)\,\sigma^2_z \tag{16.10a}$$

implying

$$\delta\left(\sigma^2_z\right) = \sigma^2_{z^*} - \sigma^2_z = -\kappa\,\sigma^2_z \tag{16.10b}$$

where κ is a constant independent of the variance. When Equation 16.10 holds (implying that selection generates a constant proportional reduction in variance), simple analytic solutions for the equilibrium variances and heritability can be obtained. Truncation selection — both as we have defined it for directional selection (Chapter 13) and **double truncation** giving disruptive or stabilizing selection (Figure 16.1) — satisfies Equation 16.10. As shown in Table 16.1, for truncation selection on a normally-distributed phenotype, κ is strictly a function of the fraction p of the population saved and the type of truncation selection used.

Table 16.1. Changes in the phenotypic variance under the various schemes of single- and double-truncation given in Figure 16.1. Assuming the character is normally distributed before selection, the phenotypic variance after selection is given by $\sigma^2_{z^*} = (1-\kappa)\,\sigma^2_z$, where κ is a function of the fraction p of individuals saved. Here φ denotes the unit normal density function and $x_{[p]}$ satisfies $\Pr(U \le x_{[p]}) = p$ (equivalently, $\Pr(U > x_{[1-p]}) = p$) where U is a unit normal random variable. Finally, $\overline{i}$ is the selection intensity and is also a function of p (Equation 14.3a). While first presented in the quantitative genetics literature by Bulmer (1976a), derivations for these expressions can be found in Johnson and Kotz (1970a).

Directional Truncation Selection: Uppermost (or lowermost) p saved

$$\kappa = \frac{\varphi\left(x_{[1-p]}\right)}{p}\left(\frac{\varphi\left(x_{[1-p]}\right)}{p} - x_{[1-p]}\right) = \overline{i}\,\left(\overline{i} - x_{[1-p]}\right) \tag{16.11a}$$

Stabilizing Truncation Selection: Middle fraction p of the distribution saved

$$\kappa = \frac{2\,\varphi\left(x_{[1/2+p/2]}\right)\,x_{[1/2+p/2]}}{p} \tag{16.11b}$$

Disruptive Truncation Selection: Uppermost and lowermost $p/2$ saved

$$\kappa = -\frac{2\,\varphi\left(x_{[1-p/2]}\right)\,x_{[1-p/2]}}{p} \tag{16.11c}$$

Suppose selection is such that Equation 16.10a is satisfied. We allow for differential selection on the sexes by letting the variance after selection in mothers and fathers be $\sigma^2(z^*_m) = (1-\kappa_m)\sigma^2_z$ and $\sigma^2(z^*_f) = (1-\kappa_f)\sigma^2_z$, respectively. If parental phenotypes are uncorrelated (i.e., random mating),

$$\sigma^2_{z^*(t)} = \frac{\sigma^2\left[\,z^*_f(t)\,\right]}{2} + \frac{\sigma^2\left[\,z^*_m(t)\,\right]}{2} = (1-\kappa)\,\sigma^2_z(t) \tag{16.12a}$$

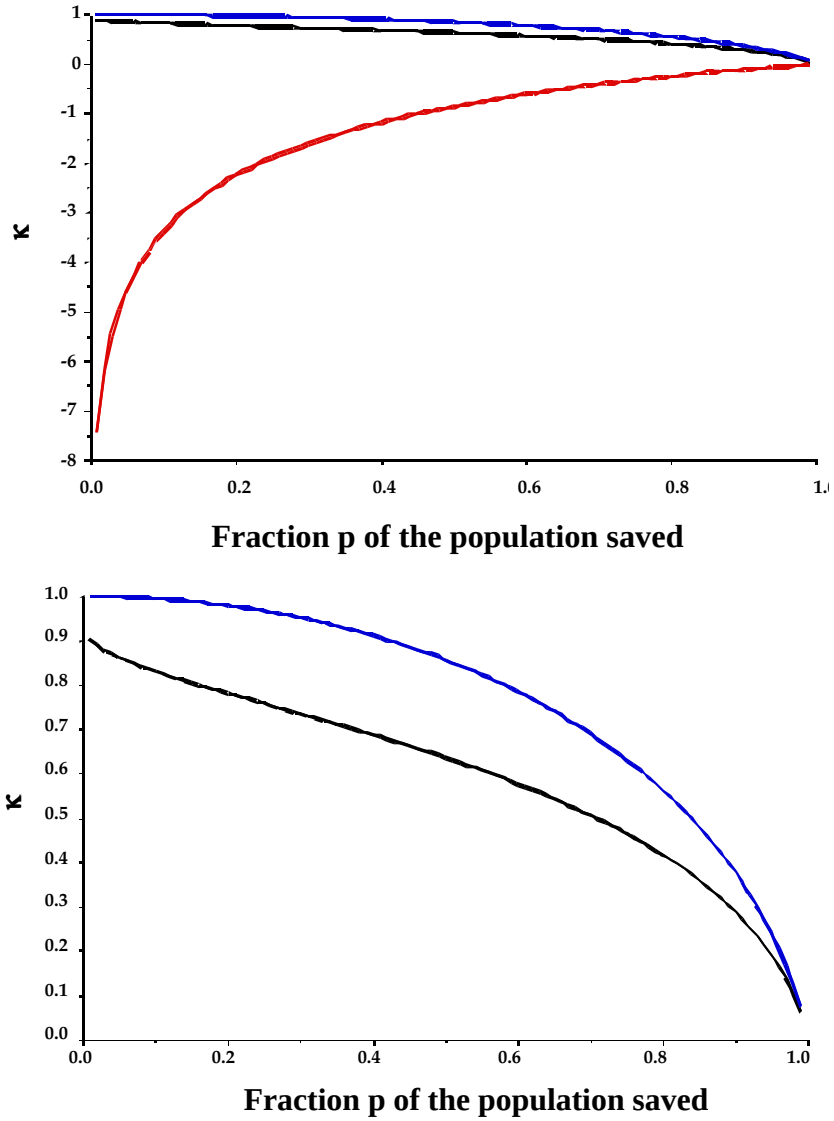


Figure 16.2 The fractional reduction κ of phenotypic variance removed by truncation selection (Figure 16.1) as a function of the fraction p of individuals saved. Following selection, the new variance is $(1-\kappa)\sigma_z^2$. **Top**: The lowest-most curve (values of $\kappa < 0$) corresponds to disruptive selection (and hence an *increase* in the variance, $\sigma_{z^*}^2 > \sigma_z^2$), while the upper two curves ($\kappa > 0$) correspond to directional (middle curve) and stabilizing selection (upper curve) and hence a decrease in the variance, $\sigma_{z^*}^2 < \sigma_z^2$. **Bottom**: Closeup for directional (lower curve) and stabilizing selection (upper curve).

where

$$\kappa = \frac{\kappa_f + \kappa_m}{2} \tag{16.12b}$$

The within-generation change in the variance due to selection becomes

$$\delta(\sigma_{z(t)}^2) = -\kappa\,\sigma_z^2(t) = -\kappa\,\frac{\sigma_A^2(t)}{h^2(t)} \tag{16.12c}$$

where we have used the identity $\sigma_z^2 = \sigma_A^2/h^2$. Substituting Equation 16.12c into Equation 16.7a recovers the result of Bulmer (1974),

$$d(t+1) = \frac{d(t)}{2} - \frac{\kappa}{2}\, h^2(t)\, \sigma_A^2(t) = \frac{d(t)}{2} - \frac{\kappa}{2}\, \frac{[\,\sigma_a^2 + d(t)\,]^2}{\sigma_z^2 + d(t)} \tag{16.12d}$$

with last step following from $h^2\sigma_A^2 = (\sigma_A^2/\sigma_z^2)\sigma_A^2 = \sigma_A^4/\sigma_z^2$. At equilibrium, $\widetilde{d} = -\kappa\, \widetilde{h}^2\, \widetilde{\sigma}_A^2$. Since $\widetilde{\sigma}_A^2 = \sigma_a^2 + \widetilde{d}$ and $\widetilde{h}^2 = (\sigma_a^2 + \widetilde{d})/(\sigma_z^2 + \widetilde{d})$, we have

$$\widetilde{d} = -\kappa\, \frac{(\,\sigma_a^2 + \widetilde{d}\,)^2}{\sigma_z^2 + \widetilde{d}}$$

This is a quadratic equation in $\widetilde{d}$ which has one admissible solution (the constraint being that $\widetilde{\sigma}_A^2 \geq 0$). Solving gives

$$\widetilde{\sigma}_A^2 = \sigma_z^2\, \theta, \quad \text{where} \quad \theta = \frac{2h^2 - 1 + \sqrt{1 + 4h^2(1-h^2)\kappa}}{2(1+\kappa)} \tag{16.13a}$$

Since $\widetilde{\sigma}_A^2 - \sigma_A^2 = \widetilde{d}$, we can write

$$\widetilde{\sigma}_z^2 = \sigma_z^2 + (\widetilde{\sigma}_A^2 - \sigma_A^2) = \sigma_z^2(1 + \theta - h^2) \tag{16.13b}$$

It follows that the equilibrium heritability is

$$\widetilde{h}^2 = \frac{\widetilde{\sigma}_A^2}{\widetilde{\sigma}_z^2} = \frac{\theta}{1 + \theta - h^2} \tag{16.13c}$$

We can also (Gomez-Raya and Burnside 1990) express the equilibrium heritability as

$$\widetilde{h}^2 = \frac{-1 + \sqrt{1 + 4h^2(1-h^2)\kappa}}{2\,\kappa\,(1 - h^2\,)} \tag{16.13d}$$

Figure 16.3 plots the equilibrium heritability as a function of κ and the initial heritability in the absence of any disequilibrium.

Changes in a Correlated Character

Suppose the joint distribution of phenotypic values for our trait under selection z and two other correlated traits x and y is multivariate normal. If the within-generation change in the phenotypic values of z is given by Equation 16.10, then classic results (Pearson 1903) for the multivariate distribution imply that the variance in x following selection on (only) z is given by

$$\sigma^2(x^*) = (1 - \kappa\, \rho_{x,z}^2)\sigma^2(x) \tag{16.14a}$$

implying

$$\delta\left[\sigma^2(x)\,\right] = -\kappa\, \rho_{x,z}^2\, \sigma^2(x) \tag{16.14b}$$

where $\rho_{x,z}$ is the phenotypic correlation between traits x and z. If selection reduces the variance in z ($0 < \kappa < 1$), then the variance in any correlated character is also reduced, *independent* of the sign of the correlation (as change is a function of ρ^2). Likewise, the covariance between x and y following selection on z is given by

$$\sigma(x^*, y^*) = \sigma(x,y) - \kappa\, \frac{\sigma(x,z)\sigma(y,z)}{\sigma_z^2}, \tag{16.14c}$$

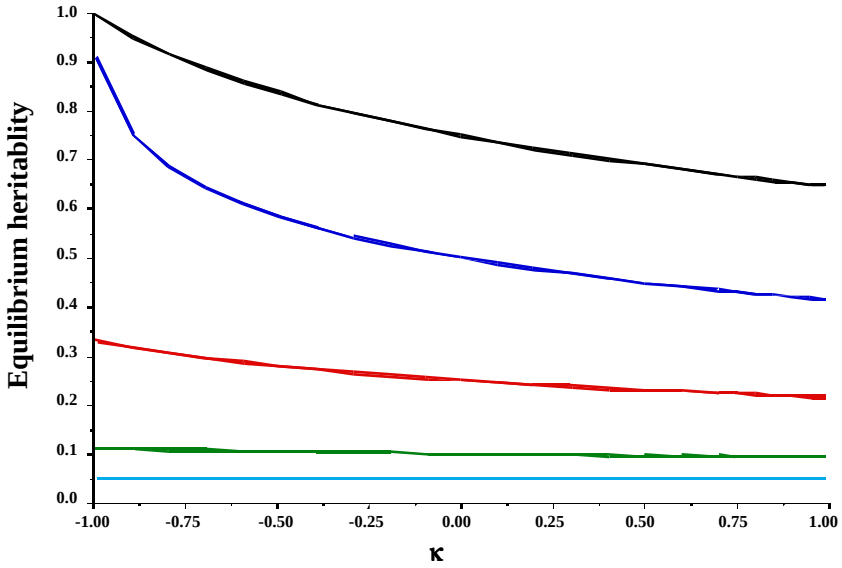


Figure 16.3. Equilibrium h^2 values as a function of κ (recall that $1-\kappa$ is the fraction of variance following selection) initial heritability h^2. Curves (from top to bottom) correspond to h^2 values of 0.75 (upper curve), 0.5, 0.25, 0.1, and 0.05 (lower curve). Note for $\kappa < 0$ that the variance is *increased* by selection (as occurs with disruptive selection) and the equilibrium h^2 is greater than its initial value.

giving the within-generation change in this covariance as

$$\delta\left[\,\sigma(x,y)\,\right] = -\kappa\,\frac{\sigma(x,z)\sigma(y,z)}{\sigma_z^2}. \tag{16.14d}$$

These results will prove useful in Volume 3 when we consider the Bulmer effect for multivariate traits, such as selection on an index or using BLUP.

Directional Truncation Selection: Theory

Directional truncation results in a reduction in the phenotypic variance following selection, generating negative d and a corresponding reduction in both the additive variance and heritability. When the trait is normally-distributed, recalling LW Equation 2.15 and our Equation 14.3a gives

$$\sigma_{z^*}^2 = \left[\,1 - \overline{\imath}\,\left(\overline{\imath} - x_{[1-p]}\right)\,\right]\,\sigma_z^2 \tag{16.15a}$$

and hence

$$\kappa = \overline{\imath}\,\left(\overline{\imath} - x_{[1-p]}\right) \tag{16.15b}$$

The stronger the selection (i.e., the smaller the value of p and hence the larger the value of $\overline{\imath}$), the larger the disequilibrium generated and the greater the reduction in additive variance. Since the response to selection depends on the additive genetic variance in the selected *parents*, the response to selection in the first generation is unaffected (assuming the parents from the base population are in gametic-phase equilibrium). However, in the next two or three generations, essentially all of the reduction in h^2 due to buildup of negative d occurs, after which heritability remains constant (see Example 16.2). Equations 16.13a-d

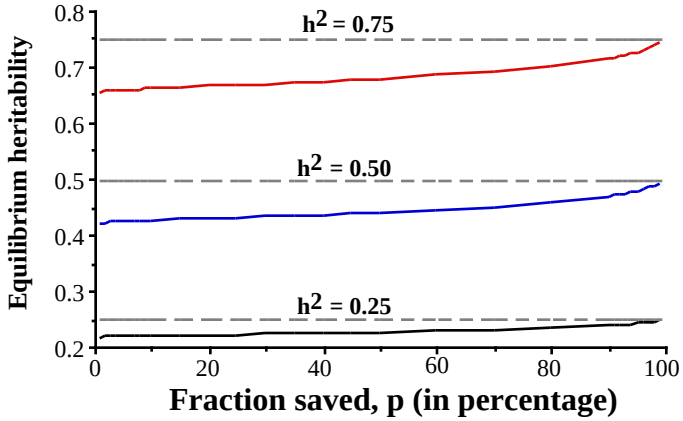


Figure 16.4. Equilibrium heritability values under directional (truncation) selection as a function of the fraction p saved and the initial heritability h^2. The three curves correspond to initial heritability values of 0.75, 0.5, and 0.25.

give the equilibrium (or **asymptotic**) variances and heritabilites. The ratio of the asymptotic to initial (assuming $d = 0$) rates of response is given by

$$\frac{\widetilde{R}}{R(0)} = \frac{\overline{\imath}\,\widetilde{h}\,\widetilde{\sigma}_A}{\overline{\imath} h(0)\,\sigma_A(0)} = \sqrt{\frac{\widetilde{h}^2}{h^2(0)\,[\,1 + \kappa\,\widetilde{h}^2\,]}} \tag{16.16}$$

as obtained by Gomez-Raya and Burnside (1990). As shown in Figure 16.4, the reduction in heritability is greatest when selection is strongest (i.e., when the fraction saved p is small) and heritability is high.

Example 16.2. Suppose directional truncation selection is performed (equally on both sexes) on a normally distributed character with $\sigma_z^2 = 100$, $h^2 = 0.5$, and $p = 0.20$ (the upper 20 percent of the population is saved). To find the value $z_{[0.8]}$ that satifies $\Pr(U \le z_{[0.8]}) = 0.8$, we use the **R** command **`qnorm(0.8)`** which returns a value of 0.84. Likewise, evaluating the unit normal density function at $z = 0.84$ (**`dnorm(0.84)`** in **R**) gives $\varphi(0.84) = 0.2803$, so that Equation 14.3a gives

$$\overline{\imath} = \varphi(0.84)/p = 0.2803/0.20 = 1.402.$$

From Equation 16.15b, the fraction of variance removed by selection is

$$\kappa = \overline{\imath}\,\left(\overline{\imath} - x_{[0.8]}\right) = 1.402\,(1.402 - 0.84) = 0.787.$$

Equation 16.12d becomes

$$d(t+1) = \frac{d(t)}{2} - 0.394\,\frac{[\,50 + d(t)\,]^2}{100 + d(t)}.$$

Starting selection in generation 0 on a base population in gametic-phase equilibrium, $d(0) = 0$, iteration of this expression yields

Generation	0	1	2	3	4	5	∞
$d(t)$	0.00	-9.84	-11.96	-12.45	-12.56	-12.59	-12.59
$\sigma_A^2(t)$	50.00	40.16	38.04	37.55	37.44	37.41	37.41
$h^2(t)$	0.50	0.45	0.43	0.43	0.43	0.43	0.43

Essentially all of the decline in additive variance occurs in the first three generations.

An important point to note is that the within-generation reduction in the variance is close to 80% ($\kappa = 0.787$), but the resulting decrease in the phenotypic variance (at equilibrium) is 100 -12.59 = 87.41, only a 13% decrease. As was found for the response in mean using the breeder's equation, only a fraction of the within-generation response is transmitted between generations. With the change in mean (Chapter 13), this arises because only a fraction of the variation is due to additive-genetic variance. This is a contributing factor with the change in variance as well, but a new complication is the additional variation generated by mendelian sampling each generation, partly mitigating the impact of selection in decreasing the variance.

We can also obtain the equilibrium additive variance directly from Equation 16.13a. Here $\widetilde{\sigma}_A^2 = \sigma_z^2\,\theta = 100\,\theta$, with

$$\theta = \frac{2 \cdot 0.5 - 1 + \sqrt{1 + 4 \cdot 0.5 \cdot (1 - 0.5) \cdot 0.787}}{2(1 + 0.787)} = 0.374$$

and hence $\widetilde{\sigma}_A^2 = 37.4$, as found by iteration. Likewise, Equation 16.13c gives the equilibrium heritability at

$$\widetilde{h}^2 = \frac{\theta}{1 + \theta - h^2} = \frac{0.374}{1 + 0.374 - 0.5} = 0.43$$

Again, this matches the value found by iteration.

How does this reduction in σ_A^2 influence the per-generation change in mean, $R(t)$? Since the selection $\overline{i}$ is unchanged (being entirely a function of the fraction p of adults saved), but h^2 and σ_z^2 change over time, substituting $\sigma_A(t) = h(t)\sigma_z(t)$ into Equation 13.6b gives the single-generation response in generation t as

$$R(t) = h^2(t)\,\overline{i}\,\sigma_z(t) = 1.402\,h^2(t)\,\sqrt{\sigma_z^2 + d(t)} = 1.402\,h^2(t)\,\sqrt{100 + d(t)}$$

Response declines from an initial value of $R = 1.4 \cdot 0.5 \cdot 10 = 7$ to an asympotic per-generation value of $\widetilde{R} = 1.4 \cdot 0.43 \cdot \sqrt{87.41} = 5.6$. Using the unadjusted breeder's equation to predict change in mean over several generations without accounting for the Bulmer effect overestimates the expected response by 25 percent.

Directional Truncation Selection: Experimental Results

How well do these predictions hold up for directional selection? Somewhat surprisingly, not many experiments have directly examined these issues. One reason is that the predicted change in h^2 under directional selection is usually expected to be small (Figure 16.4) and hence laborious to detect (requiring very large sample sizes). One indirect study is that of Atkins and Thompson (1986), who subjected Blackface sheep to selection for increased bone length. Following 18 years of selection, realized heritability was estimated to be 0.52 ± 0.02. Using the infinitesimal model, they predicted the expected base population heritability should be 0.57, in agreement with the estimated base population heritiability of 0.56 ± 0.04. Further, the infinitesimal model predicts a 10% decrease in phenotypic variance. The

observed values were a 9% decrease in the upwardly-selected line and an 11% decrease in the downwardly-selected line.

A more direct study is that of Sorensen and Hill (1982), who subjected two replicate lines of *Drosophila melanogaster* to directional truncation selection on abdominal bristle number for four generations and then relaxed selection (Table 16.2). They interpreted their data as being consistent with the presence of a major allele (or alleles) at low frequency in the base population. These alleles are lost by sampling accidents in some replicates (e.g., replicate 2 which shows no net increase in additive variance). If not lost, they are expected to increase rapidly in frequency due to selection, increasing additive variance (replicate 1), with this increase being partly masked by generation of negative disequilibrium with other loci. Once selection stops, disequilibrium breaks down, resulting in a further increase in additive variance (compare the additive variance in lines H3 and C7 in replicate 1). Hence, even when major alleles are present, generation of gametic-phase disequilibrium reduces the rate of selection response.

Table 16.2. Heritability and additive genetic variance in an experimental population undergoing directional selection on abdominal bristle number in *Drosophila melanogaster*. The base population is denoted by B. At the third generation of selection (H3) and following four generations of selection plus three generations of no selection (C7, in generation 7), h^2 was estimated from the response to divergent selection (Chapter 18) and σ_A^2 subsequently estimated by $\widehat{h}^2\sigma_z^2$. The standard error for $\widehat{h}^2$ in all cases was 0.04. After Sorensen and Hill (1982).

	$\widehat{h}^2(t)$			$\widehat{\sigma}_A^2(t)$		
	B	H3	C7	B	H3	C7
Replicate 1	0.42	0.45	0.59	3.63	5.83	7.66
Replicate 2	0.38	0.26	0.26	2.96	2.28	2.08

Effects of Epistasis: Does the Griffing Effect Overpower the Bulmer Effect?

As discussed in Chapter 15, Griffing (1960a,b) showed when additive epistasis is present, gametic-phase disequilibrium increases the response to directional selection, with the response augmented by $S\sigma_{AA}^2/2\sigma_z^2$. This (transient) increase in rate of response has been termed the **Griffing effect**. Thus, in the presence of additive epistasis, disequilibrium is on one hand expected to increase the rate of response, while it is also expected to decrease the rate of response by decreasing additive genetic variance (the Bulmer effect). Which change is more important? Based on a small simulation study, Mueller and James (1983) concluded that if epistatic variance is small relative to additive variance and the proportion of pairs showing epistasis is also small, the Bulmer effect dominates the Griffing effect, and disequilibrium reduces the response to selection. This is clearly an interesting area for more work.

Double Truncation Selection: Theory

Table 16.1 and Figure 16.2 show that $\kappa > 0$ under stabilizing double-truncation selection, so that selection reduces the within-generation phenotypic variance and generates negative disequilibrium. Conversely, $\kappa < 0$ for disruptive selection, with selection increasing the within-generation variance and generating positive disequilibrium. Hence, when the infinitesimal model assumptions hold, heritability is expected to decrease under stabilizing selection and increase under disruptive selection (Figure 16.3).

Consideration of Equation 16.13a shows that under stabilizing selection ($\kappa > 0$), the value $\theta = \widetilde{\sigma}_A^2/\sigma_z^2$ (which measures the fraction of the initial phenotypic variance that is additive genetic variance at equilibrium) satisfies $0 < \theta < h^2$. Similarly, under disruptive

selection $\theta > h^2$, with one twist. If disruptive selection is sufficiently strong ($\kappa < -[4h^2(1 - h^2)]^{-1}$) there is no positive real root for θ, and the variance increases without limit in the infinitesimal model (Bulmer 1976a). This is a consequence of the infinite number of loci in the infinitesimal limit. What happens under these conditions with a finite number of loci is suggested from simulation studies of Bulmer (1976a), who examined the behavior when disruptive selection generated sufficiently negative κ values to ensure no positive real root of Equation 16.13a. Bulmer assumed 12 identical additive diallelic loci (alternative alleles contributing 1 and 0, respectively, to the genotypic value). After a few generations, this population showed essentially complete disequilibrium, with most individuals having values 0, 12, and 24 (with frequencies $1/4$, $1/2$, $1/4$). At equilibrium, the population behaved like a single locus segregating two alleles (contributing 0 and 12), each with frequency $1/2$. Thus, the expectation when there is no positive real solution for $\widetilde{\sigma}_A^2$ is that the population approaches a state of essentially complete disequilibrium.

The approach to the equilibrium value $\widetilde{d}$ also behaves differently under disruptive selection. Under directional and stabilizing selection, the majority of reduction in the additive variance occurs in the first few generations. However, the increase in the variance to its equilibrium value under disruptive selection requires many more generations, as Example 16.3 illustrates.

Example 16.3. Consider a normally distributed character with $\sigma_z^2 = 100$ and $h^2 = 0.5$ in a random mating population. To compare the effects of stabilizing and disruptive selection, suppose in one replicate disruptive selection is practiced via double truncation with $p = 0.5$ (the upper and lower 25 percent of the population are saved), while stabilizing selection with $p = 0.5$ (the upper and lower 25 percent are culled) is practiced in the other. To obtain κ from Table 16.1, first note that for stabilizing selection, $x_{[1/2+p/2]} = x_{[0.75]}$, while for disruptive selection $x_{[1-p/2]} = x_{[0.75]}$. Using **R**, **`qnorm(0.75)`** returns 0.675, so that $x_{[0.75]}$ = 0.675. Likewise, φ(0.675) = 0.318, and Equations 16.11b/c yield

$$\kappa = \pm(2 \cdot 0.318 \cdot 0.675)/0.5 = \pm 0.858$$

where the plus is used for stabilizing selection, the minus for disruptive selection. Equation 16.12d becomes

$$d(t+1) = \frac{d(t)}{2} \mp 0.429 \frac{[\,50 + d(t)\,]^2}{100 + d(t)}$$

where (since the equation is in terms of $-\kappa$) the minus corresponds to stabilizing selection, the plus for disruptive selection. Starting selection on a base population with $d = 0$,

Disruptive selection

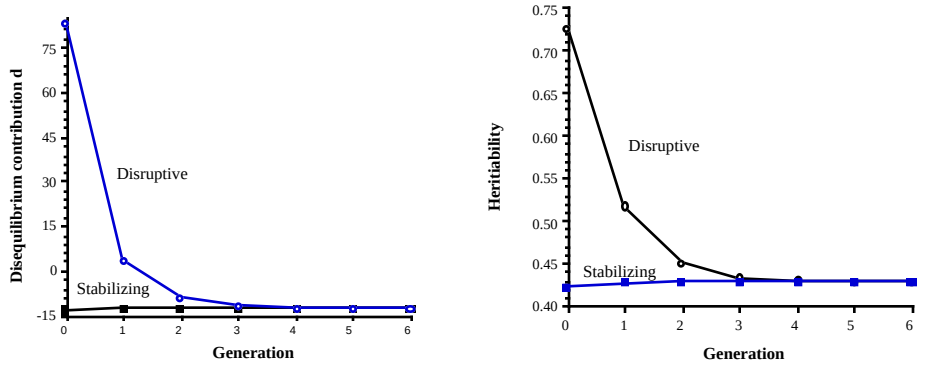
Generation	0	1	2	3	4	5	20	∞
$d(t)$	0.00	10.73	19.65	27.22	33.72	39.34	74.83	82.69
$\sigma_A^2(t)$	50.00	60.37	69.65	77.22	83.72	89.34	124.83	132.69
$h^2(t)$	0.50	0.55	0.58	0.61	0.63	0.64	0.71	0.73

Stablizing selection

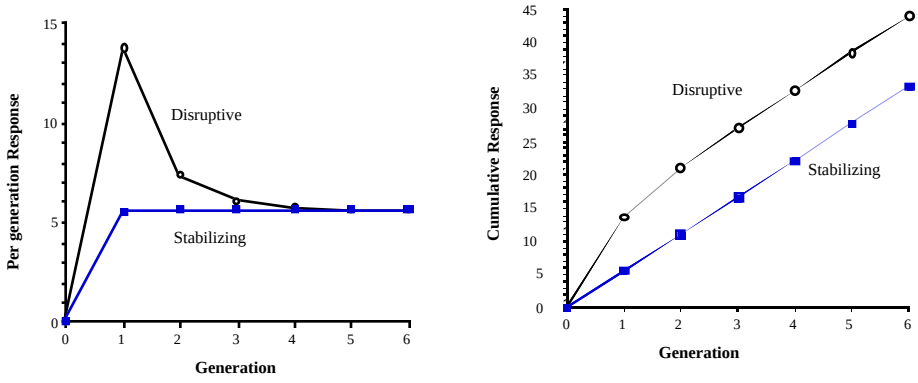
Generation	0	1	2	3	4	5	∞
$d(t)$	0.00	−10.73	−12.77	−13.20	−13.29	−13.31	−13.32
$\sigma_A^2(t)$	50.00	39.27	37.23	36.80	36.71	36.69	36.68
$h^2(t)$	0.50	0.44	0.43	0.42	0.42	0.42	0.42

Note that with disruptive selection, the absolute change in d is much greater and the time to approach equilibrium considerably longer than with stabilizing selection.

Now suppose that after the equilibrium value of d has been reached, both of the two above populations are then subjected to directional selection. In particular, assume directional truncation selection with the upper 20 percent of the population being saved. The recursion equation for the disequilibrium contribution is given in Example 16.2, but now the initial disequilibrium values are $d(0) = -13.32$ for the population with a previous history of stabilizing selection and $d(0) = 82.69$ for the population with a previous history of disruptive selection. If stabilizing/disruptive selection is stopped for k generations before truncation selection, $d(0)$ is replaced by $d(0)/2^k$. From Example 16.2, the per-generation response is $R(t) = h^2(t)\,1.4\,\sigma_z(t)$, which is plotted below for both populations. The resulting changes in d and the heritability under these two treatments are plotted below.



Initially there is a large difference between the replicates, but after three generations both have essentially the same rate of response, converging to $\widetilde{d} = -12.59$ and hence a per-generation response of $\widetilde{R} = 5.6$, the equilibrium value under directional truncation selection (see Example 16.2). As plotted below, the replicate originally subjected to disruptive selection shows a higher cumulative response, due to larger responses resulting from higher heritabilities in the first few generations. This difference in cumulative response is permanent — it does not decay away once selection stops.



Hence, we expect that if an unselected base population is divided into three replicates, one first subjected to disruptive selection, another to stabilizing selection, and the third to no selection, that when directional selection is applied on these replicates, the largest response should occur in the disruptively-selected replicate and the smallest in the replicate that first underwent stabilizing selection. This pattern is indeed seen in artifical selection experiments on *Drosophila* sternopleural bristles (Thoday 1959) and wing length (Tantawy and Tayel 1970).

Double Truncation Selection: Experimental Results

Experiments examining the effects of selection on variance are reviewed by Prout (1962), Thoday (1972), Soliman (1982), and Hohenboken (1985). One complication with many of the experimental results is that only phenotypic variances are examined, so that care must be taken to distinquish between changes in genetic, versus environmental, variances.

As expected under the infinitesimal model, several experiments using stabilizing artificial selection (typically by double-truncation) show a reduction in the phenotypic variance that is largely due to reduction in the additive variance, relative to control populations. Examples include sternopleural bristle number (Gibson and Bradley 1974), developmental time (Prout 1962), wing venation (Scharloo 1964, Scharloo et al. 1967), and wing length (Tantawy and Tayel 1970) in *Drosophila melangaster*, and developmental time in *Tribolium castaneum* (Soliman 1982). Gibson and Bradley (1974) found that some of the decrease in the phenotypic variance was due to a decrease in the environmental variance. Other experiments observed different results. For example, selection on sternopleural bristle number by Gibson and Thoday (1963) resulted in no change in the phenotypic variance because the decrease in additive variance was apparently countered by an increase in the environmental variance (strictly speaking, the increase was in the residual variance, which could include nonadditive genetic variances as well as environmental effects). Likewise, 95 generations of stabilizing selection on pupa weight in *T. castaneum* by Kaufman et al. (1977) resulted in a decrease in the additive variance, but only a slight decrease in the heritability, reflecting a corresponding decrease in the residual variance as well. Bos and Scharloo (1973a,b) observed no decrease in the phenotypic variance following stabilizing selection on *Drosophila* body size. Grant and Mettler (1969) observed a significant increase in variance in one replicate and a significant decrease in the other for two replicate lines subjected to stabilizing selection for a *Drosophila* behavioral trait (escape behavior). Falconer (1957) reported no decrease in additive variance when abdominal bristle number in *Drosophila melanogaster* was subjected to stabilizing selection. However, a re-analysis by Bulmer (1976a) suggested that indeed a reduction in variance occurred, close to the value predicted from the infinitesimal model. Hence, the conclusion is that while reductions in the environmental variance itself sometimes occur, the reduction in the additive variance is often the main source for the observed decrease in phenotypic variance. We will return the expected response in the environmental variation in Chapter 17.

Disruptive selection experiments generally show rather large increases in the phenotypic variance. Increases in the heritability and/or additive variance were observed in *Drosophila* for sternopleural bristle number (Thoday 1959, Millicient and Thoday 1961, Barker and Cummins 1969) and wing venation traits (Scharloo 1964, Scharloo et al. 1967), and for pupal weight in *Tribolium* (Halliburton and Gall 1981). Increases in the residual variance were also seen in many of these studies, reflecting changes in either the environmental and/or nonadditive genetic variances. On the other hand, for *Drosophila* development time, Prout (1962) observed that the heritability actually decreased relative to the base population, indicating that the large increase observed in phenotypic variance was due to changes in the residual variance. Robertson (1970) observed an increase in the phenotypic variance following disruptive selection on sternopleural bristles, but no corresponding (significant) increase in heritability.

While a change in variance is one prediction from the infinitesimal model, a more striking prediction is what happens to the variance upon relaxation of selection. Here any gametic-phase disequilibrium generated by selection quickly decays (for unlinked loci). Thus, more solid support would come from experiments that also follow the variance upon relaxation

of selection. This was done by Sorensen (1980) and Sorensen and Hill (1982), who selected on abdominal bristle number in *Drosophila melanogaster*. They observed large changes in the phenotypic variance, with realized heritability increasing from 0.37 to 0.69 in two generations of selection. Following four generations of no selection, heritability decreased to 0.44 (the standard error for all heritability estimates was 0.04). This pattern is expected given the decay of gametic-phase disequilibrium (which here is positive, inflating σ_A^2).

RESPONSE UNDER NORMALIZING SELECTION

While double-truncation is the common mode of artificial stabilizing selection, one standard model assumed for stabilizing selection in natural populations is **normalizing** (or **nor-optimal**) selection (Weldon 1895, Haldane 1954),

$$W(z) = \exp\left(-\frac{(z-\theta)^2}{2\omega^2} \right) \tag{16.17}$$

The optimal value is $z = \theta$, and the strength of selection is given by ω^2, which corresponds to the variance term in a normal. When ω^2 is large (corresponding to a large variance in the fitness function), selection is weak as the fitness function falls off slowly around θ. Conversely, a small value of ω^2 corresponds to a small variance in the fitness function and strong selection, with fitness quickly declining away from θ. Formally, ω^2 is compared to the phenotypic variance, with $\omega^2 \gg \sigma_z^2$ corresponding to weak selection and $\omega^2 \ll \sigma_z^2$ to strong selection. If phenotypes are normally distributed before selection with mean μ and variance σ_z^2, after selection phenotypes remain normally distributed with new mean and variance

$$\mu^* = \mu + \frac{\sigma_z^2}{\sigma_z^2 + \omega^2}(\,\theta - \mu\,) \quad \text{and} \quad \sigma_{z*}^2 = \sigma_z^2 - \frac{\sigma_z^4}{\sigma_z^2 + \omega^2} \tag{16.18a}$$

Note that we cannot write $\sigma_{z^*}^2 = (1-\kappa)\,\sigma_z^2$, as here κ is no longer a constant, but rather a function of the changing variance σ_z^2. However, under this model the distribution of genotypes remains normal after selection and hence parent-offspring regressions remain linear throughout. Thus, we can apply the breeder's equation to predict changes in the mean and Equation 16.7a to predict changes in the variance (under the infinitesimal model). Here,

$$S = \frac{\sigma_z^2}{\sigma_z^2 + \omega^2}(\,\theta - \mu\,) \quad \text{and} \quad \delta\left(\sigma_{z^*}^2\right) = -\frac{\sigma_z^4}{\sigma_z^2 + \omega^2} \tag{16.18b}$$

The change in mean is thus given by

$$R(t) = h^2(t)\,S(t) = h^2(t)\,\frac{\sigma_z^2(t)\;[\,\theta - \mu(t)\,]}{\sigma_z^2(t) + \omega^2} \tag{16.19}$$

implying that the mean converges to θ, as the sign of R is given by the sign of $\theta - \mu(t)$, which in positive when $\mu(t)$ is below θ and negative when above. From Equation 16.7a, the change in the disequilibrium contribution is given by

$$d(t+1) = \frac{d(t)}{2} - \frac{h^4(t)}{2}\,\frac{\sigma_z^4(t)}{\sigma_z^2(t) + \omega^2} = \frac{d(t)}{2} - \frac{1}{2}\,\frac{[\,\sigma_a^2 + d(t)\,]^2}{\sigma_z^2 + d(t) + \omega^2} \tag{16.20a}$$

Note that both directional and stabilizing selection can simultaneously occur with normalizing selection — if $\mu \neq \theta$, the mean changes under selection. However, observe from both

Equations 16.18a and 16.20a that the change in variance is independent of the current mean value μ. The equilibrium value $\widetilde{d}$ satisfies

$$\widetilde{d} = \frac{\widetilde{d}}{2} - \frac{1}{2}\frac{[\sigma_a^2 + \widetilde{d}]^2}{\sigma_z^2 + \widetilde{d} + \omega^2} \tag{16.20b}$$

which rearranges to the quadratic equation

$$2\widetilde{d}^2 + \left(\sigma_z^2 + \omega^2 + 2\sigma_a^2\right)\widetilde{d} + \sigma_a^4 = 0 \tag{16.20c}$$

Example 16.4. Suppose normalizing selection occurs on a normally distributed character with $\sigma_z^2 = 100$, $h^2 = 0.5$, and $\omega^2 = 200$. The dynamics of the disequilibrium contribution are given by

$$d(t+1) = \frac{d(t)}{2} - \frac{1}{2}\frac{[50 + d(t)]^2}{300 + d(t)}$$

Solving Equation 16.20c, gives $\widetilde{d} = -6.46$ and $\widetilde{h}^2 = (50 - 6.46)/(100 - 6.46) = 0.47$. Most of the reduction in heritability occurs in the first few generations,

Generation	0	1	2	3	4	5	∞
d_t	0	-4.17	-5.64	-6.16	-6.35	-6.42	-6.46
$\sigma_A^2(t)$	50.00	45.83	44.37	43.84	43.65	43.58	43.54
$h^2(t)$	0.50	0.48	0.47	0.47	0.47	0.47	0.47

Thus, under the infinitesimal model, the distribution reaches equilibrium with the phenotypes (before selection) normally distributed with mean θ and variance $\widetilde{\sigma}_z^2 = 100 - 6.46 = 93.54$.

SELECTION WITH ASSORTATIVE MATING

Recall (LW Chapter 7) that assortative mating changes the additive genetic variance relative to a random mating population, mainly by generating gametic-phase disequilibrium. Assortative mating results in some inbreeding (measured by a slight increase in homozygosity), but if the number of loci is large, the deviation of genotypes from Hardy-Weinberg frequencies is expected to be small. In the limiting infinitesimal model, no changes in genotypic frequencies occur at single loci, although large changes in variance can occur due to gametic-phase disequilibrium. Positive assortative mating (where ρ, the phenotypic correlation between mates, is positive) generates positive gametic-phase disequilibrium, increasing σ_A^2, while negative assortative mating ($\rho < 0$, also referred to as **disassortative mating**) generates negative d, decreasing σ_A^2. As with selection, these changes in the variance are temporary, with values returning to those in the base population after a few generations of random mating.

Results Using the Infinitesimal Model

Assortative mating is easily incorporated into the infinitesimal model (Fisher 1918, Bulmer 1980). We assume assortative mating follows selection, so that the selected parental phenotypic values z_f^* and z_m^* are correlated. Returning to Equation 16.5a, the variance in the offspring is given by

$$\sigma^2(z_o) = \frac{h^4}{4}\sigma^2\left(z_m^* + z_f^*\right) + \sigma_e^2 \tag{16.21a}$$

Writing the variance of a sum as $\sigma^2(x+y) = \sigma_x^2 + \sigma_y^2 + 2\rho_{xy}\sigma_x\sigma_y$, this becomes

$$\sigma^2(z_o) = \frac{h^4}{4}\left(\sigma^2(z_m^*) + \sigma^2(z_f^*) + 2\rho\,\sigma(z_f^*)\,\sigma(z_m^*)\right) + \sigma_e^2 \qquad (16.21b)$$

Assuming selection is such that $\sigma^2(z_x^*) = (1-\kappa_x)\sigma_z^2$ for $x = f$ or m, Equation 16.21b becomes

$$\sigma^2(z_o) = \frac{h^4}{2}\,\sigma_z^2\left(1 - \frac{\kappa_f + \kappa_m}{2} + \rho\sqrt{(1-\kappa_f)\,(1-\kappa_m)}\right) + \sigma_e^2 \qquad (16.21c)$$

Comparing this with Equation 16.12a and 16.12d, we see that under assortative mating, Equation 16.12 holds with

$$\kappa = \frac{\kappa_f + \kappa_m}{2} - \rho\sqrt{(1-\kappa_f)\,(1-\kappa_m)} \qquad (16.21d)$$

Likewise, Equations 16.13a-13d hold with κ replaced by Equation 16.21d. This generalization is due to Tallis (1987, Tallis and Leppard 1988a), and has been extended to multiple traits by Tallis and Leppard (1988b). If there is no selection ($\kappa_f = \kappa_m = 0$), $\kappa = -\rho$ and previous results for assortative mating (LW Equations 7.18-7.20) follow immediately from Equations 16.12, 16.7c, and 16.13 (respectively). More generally, when the amount of selection and assortative mating change each generation,

$$d(t+1) = \frac{d(t)}{2} - \frac{\kappa(t)}{2}\,h^2(t)\,\sigma_A^2(t) \qquad (16.22)$$

where $\kappa(t)$ is given by Equation 16.21d with κ_f, κ_m and ρ taking on values for generation t.

Under the infinitesimal model, analyzing the joint effects of assortative mating and selection is straightfoward. When selection is the same in both sexes, the effect of assortative mating is to change κ to $\kappa - \rho(1-\kappa)$. Negative gametic-phase disequilibrium is generated when this quantity is positive (indicating a reduction in variance), while positive disequilibrium is generated when it is negative. Note that if $\kappa > 0.5$, $\kappa - \rho(1-\kappa) > 0$ and no amount of positive assortative mating can generate positive disequilibrium. However, for all values of κ, there is some amount of negative assortative mating such that $\kappa - \rho(1-\kappa) > 0$. Even if selection generates positive disequilibrium ($\kappa < 0$ such as with disruptive selection), sufficiently strong negative assortative mating ($\rho < \kappa/[\,1-\kappa\,]$) generates negative disequilibrium, reducing the additive genetic variance.

Assortative Mating and Enhanced Response

Since positive assortative mating increases the additive genetic variance, Breese (1956) and James and McBride (1958) suggested that response to selection could be increased by employing assortative mating. Since the response to selection depends on the additive variance of the parents, at least one generation of assortative mating is required in order for the response to differ from random mating. Experimental support from an increase in response with assortative mating is mixed. Studies in both *Drosophila melanogaster* (McBride and Robertson 1963) and *Trobolium castaneum* (Wilson et al. 1965; Campo and Garcia Gil 1993, 1994) observed slight (but not statistically significant) increases in response when parents were assortatively mated. Conversely, Sutherland et al. (1968) and Garcia and Sanchez (1992) found no effect of assortative mating when selecting on body weight in mice and *Drosophila* pupal weight (respectively).

Jorjani (1995) suggested that the combination of both a small expected increase coupled with **unconscious assortative mating** in the presumed random-mating controls accounts for

this lack of consistency. Wright (1921) first noticed that random mating in small populations can still generate correlations between mates, creating what he termed unconscious assortative mating. Simulation studies by Jorjani et al (1997a,b,c) showed that this effect is common in small populations, and rather large population sizes (N_e over 400-800) are required to avoid it.

The efficiency of assortative mating under truncation selection has been examined in detail by Baker (1973), DeLange (1974), Fernando and Gianola (1986), Smith and Hammond (1987), Tallis and Leppard (1988a), and Shepherd and Kinghorn (1994). The general conclusion is that the relative increase in response is greatest when h^2 is large and selection is weak. However, unless the population is subjected to multiple generations of assortative mating before selection, the increase (for individual selection under the infinitesimal model) is at most six percent, consistent with the very small increases seen in experiments. However, if there are a small number of loci, Fernando and Gianola found a larger effect, which appears to have arisen from faster allele frequency change under assortative mating (as opposed to generation of positive disequilibrium). Likewise, Shepherd and Kinghorn (1994) found a much larger effect gain with assortative mating when selection (and mating) are based on estimating breeding values (BLUP Selection) as opposed to simple individual selection. As Example 16.5 demonstrates, under the infinitesimal model the per-generation increase in response of a population subjected to multiple rounds of assortative mating prior to selection rapidly decays to zero once selection starts.

Example 16.5. Starting with a base population initially in gametic-phase equilibrium with $h^2 = 0.5$, $\sigma_z^2 = 100$, individuals are positively assortatively mated (with $\rho = 0.5$) for k generations before being subjected to directional truncation selection with $p = 0.20$. What is the difference in response to one generation of selection in these assortatively mated populations relative to a random mating base population? From Example 16.2, the response in generation t is given by $R(t) = 1.4\, h^2(t)\, \sigma_z(t)$. The expected disequilibrium contribution following k generations of assortative mating (here, $\kappa = -\rho = -0.5$) is given by iterating Equation 16.22,

$$d(t+1) = \frac{d(t)}{2} + 0.25\, h^2(t)\sigma_A^2(t)$$

where $d(0) = 0$, $h^2(0) = 0.5$ and $\sigma_A^2(0) = 50$. Iteration gives the following values for a single generation of response following k generations of assortative mating:

k	0	1	2	3	5	10	∞
$d(t)$	0.00	6.25	10.57	13.58	17.17	20.09	20.71
$h^2(t)$	0.50	0.53	0.55	0.56	0.57	0.58	0.59
$R(t)$	7.00	7.64	8.06	8.35	8.69	8.95	9.01
$R(t)/R_{rm}$	1.00	1.09	1.15	1.19	1.24	1.28	1.29

where $R_{rm} = 7.00$ is the response under random mating. While there can be up to a 29% increase in the rate of response to a single generation of selection, it is extremely inefficient to assortatively mate a population for several generations before applying selection. For example, with a single generation of assortative mating followed by a single generation of selection, the total response is 7.64. If instead one just selected both generations, the responses are 7.0 in the first generation and (from Example 16.2) 5.29 in the second, for a total response almost twice as large. Further, once selection starts, d decays very rapidly, greatly reducing R/R_{rm}. Assuming $d(0) = 20.71$, after a single generation of selection, $d(1) = -3.84$, $h^2 = 0.48$, and the response in the next generation drops to 6.59 (compared to a response of 5.98 under random mating).

Example 16.6. Consider the same population and selection parameters as in the previous example, but now selection and assortative mating occur simultaneously starting at generation 0. What is the difference in response if random mating occurs in one replicate and assortative mating with $\rho = 0.5$ in the other? From Example 16.2, $\kappa_f = \kappa_m = 0.787$, giving

$$\kappa - \rho(1 - \kappa) = 0.787 - 0.5(1 - 0.787) = 0.6805$$

and (from Equation 16.22), the change in d in the assortatively mated population becomes

$$d(t+1) = \frac{d(t)}{2} - \frac{0.6805}{2} h^2(t)\, \sigma_A^2(t)$$

Assuming the initial population is in gametic phase disequilibrium ($d(0) = 0$), iteration yields

Generation	0	1	2	3	4	5	∞
$d(t)$	0.00	−8.51	−10.66	−11.22	−11.37	−11.42	−11.43
$h^2(t)$	0.50	0.45	0.44	0.44	0.44	0.44	0.44
$R(t)$	7.00	6.07	5.82	5.76	5.74	5.74	5.74
$R_{rm}(t)$	7.00	5.92	5.66	5.62	5.61	5.60	5.60
$R(t)/R_{rm}(t)$	1.00	1.03	1.03	1.02	1.02	1.02	1.02

where $R_{rm}(t)$, the response in generation t of random mating, comes from Example 16.2. Thus, there is at most a 3% increase in the rate of response. Note that the response in the first generation (generation 0) is the same in both populations — the response to selection depends on the variance of the parents, and in the first generation both populations have the same variance (as $d(0) = 0$ in each). Even with perfect positive assortative mating $\rho = 1$, $\kappa - \rho(1 - \kappa) = 2\kappa - 1 = 0.574$, with a maximum value of $R(t)/R_{rm}(t)$ just under 1.05.

Disruptive Selection, Assortative Mating, and Reproductive Isolation

We would be remiss if we did not mention a historical interest between disruptive selection and assortative mating as a mechanism for reproductive isolation. In the early 1960's the general view was that speciation (reproductive isolation between populations) required geographic (or other) isolation, a view strongly championed by Mayr (1963). However, the idea that **sympatric speciation** (Maynard-Smith 1962, 1966) could develop without the need for such isolation was bolstered by an experimental observation by Gibson and Thoday (1962). They observed that disruptive selection on sternopleutral bristle in *D. melanogaster* seemed to generate two distinct groups (high vs. low files) which appeared to assortatively mate (individuals with intermediate phenotype were absent from the population, where they would be expected if random mating occurred). Their explanation was that crosses between high and low parents generate less fit offspring (having intermediate values) and that natural selection occurred to generate preferential mating over the short time course of this experiment. It appeared that only 12 generations of disruptive selection had generated partial reproductive isolation. However, this striking observations was not repeatable (Scharloo et al. 1967, Charbora 1968, Baker and Cumming 1968, Thoday and Gibson 1970). Indeed, Scharloo (1971) suggested that the base population for selection used by Thoday and Gibson might have been composed of flies from different geographic origins, and hence already possessing partial isolation that was uncovered, rather than evolved, by their experiment. While Today and Gibson's interpretation of their experiments is now largely discounted, the notion of **reinforcement** (the evolution of mating preferences to reduce the production of less fit hybrids when diverged populations come back into contact), remains an important concept (Noor 1999, Servedio and Noor 2003, Ortiz-Barrientos et al. 2009).

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