11

Short-term Changes in the Mean: Permanent versus Transient Response

The phenotypic gains from selecting for epistatic differences come from distorting the gametic array and soon disappear after selection is relaxed, as the gametic array returns to random. By contrast, the gains from changes in gene frequency are permanent. (Lush 1948)

Draft version 23 September 2007

While the basic breeders' equation is indeed the foundation for much of the theory of selection response in quantitative traits, its simple form $R = h^2 S$ arises because of certain simplifying assumptions. One interesting complication is that the response can have both transient and permanent components, and we examine common situations (additive epistasis, polyploidy, shared environmental effects, and maternal effects) where this occurs.

PERMANENT VERSUS TRANSIENT RESPONSE

As was discussed in LW Chapters 7 and 17, the slope of the parent-offspring regression can be inflated by epistasis, genotype $\times$ environment interactions and correlations, and environmental effects shared by parents and their offspring. Hence, even if the parent-offspring regression is linear, the slope can deviate significantly from $h^2/2$, altering the response from that predicted by the breeders' equation. For example, with epistasis and correlation between parental and offspring environmental values,

$$b_{op} = \frac{h^2}{2} + \frac{1}{\sigma_z^2}\left(\frac{\sigma_{AA}^2}{4} + \frac{\sigma_{AAA}^2}{8} + \frac{\sigma_{AAAA}^2}{16} + \cdots + \sigma(E_p, E_o)\right) \tag{11.1a}$$

Assuming a linear biparental regression, the response to a single generation of selection becomes

$$R = h^2\, S + \frac{S}{\sigma_z^2}\left(\frac{\sigma_{AA}^2}{2} + \frac{\sigma_{AAA}^2}{4} + \frac{\sigma_{AAAA}^2}{8} + \cdots + \sigma(E_{fa}, E_o) + \sigma(E_{mo}, E_o)\right) \tag{11.1b}$$

which can deviate significantly from $h^2\, S$. Why then do we pay so much attention to h^2?

The reason is that we are interested in the **permanent response** to selection. Recall that the main assumption throughout our treatment of short-term response is that changes in allele frequencies are negligible. Hence any changes in genetic variances are due to gametic-phase disequilibrium (discussed in Chapter 13) rather than changes in allele frequencies. Under this assumption, epistasis and/or shared environmental factors inflate the *transient* response to selection, but once selection stops, their contribution to response *decays away*. Changes in genotypic frequencies attributable to gametic-phase disequilibrium and environmental correlations are due to nonrandom associations built up by selection. Recombination and randomization of environmental effects causes these correlations to

decay. Conversely, under Hardy-Weinberg conditions, changes in allele frequencies are permanent. Once selection is stopped, Hardy-Weinberg implies the new allele frequencies are stable (assuming that our time scale for observing a population is such that drift and mutation have negligible effects). Hence, as will be shown shortly, the permanent response under the conditions leading to Equation 11.1b is $h^2\,S$. One exception, discussed in Chapter 19, is when significant inbreeding occurs. In this case, σ^2_{AA} and other non-additive variance components (σ^2_{DI}, σ_{ADI}) introduced in Chapter 5 can contribute to permanent response.

Response with Epistasis

Why might epistasis contribute to response, if only transiently? After all, allelic effects at a single locus can be passed from parent to offspring, but (in the absence of inbreeding) their interaction, namely dominance deviations, are not. What makes epistasis, itself interactions between alleles (A) and/or genotypes (D) at non-identical loci, any different? The reason that *additive* epistasis can contribute to response is that parents do indeed pass along single alleles (rather than genotypes) to their offspring. For k loci, the parent passes along k individual alleles, one from each locus. Additive (AA, AAA, etc.) interactions between alleles at different loci can thus be passed from a parent to its offspring. However, any epistatic term involving dominance (AD, DD, etc.) cannot be passed along (under random mating), as to transmit a D component, the parent must pass along *both* alleles at a given locus to its offspring.

The response when additive $\times$ additive epistatic variance is present was examined by Griffing (1960a,b) for the infinitesimal model (Chapter 24), although Lush (1948) and Kempthorne (1957) clearly grasped the central ideas of response with additive epistasis (as evidenced by our chapter quotation from Lush). Under the assumptions that phenotypes are normally distributed, that the effects at any particular locus are very small relative to the total phenotypic variation, and that no third (or higher) order additive epistasis is present, the response to one generation of selection is

$$R = S\left(h^2 + \frac{\sigma^2_{AA}}{2\,\sigma^2_z}\right) \tag{11.2}$$

One might expect that $R(t)$, the cumulative response after t generations of selection, is simply t times the result given by Equation 11.2. However, any increased response due to epistasis is only temporary, reflecting gametic-phase disequilibrium generated by selection. As disequilibrium decays under recombination, so does the component of response due to epistasis. This occurs because the contribution from epistasis is due to favorable *combinations* of alleles at different loci, above and beyond their individual contributions (which are accounted for by changes in the breeding values). Recombination breaks down these combinations, removing the epistatic contribution. Griffing showed that for two linked loci separated by recombination fraction c, the response when a generation of selection is followed by τ generations of no selection is

$$S\left(h^2 + (1-c)^\tau\,\frac{\sigma^2_{AA}}{2\,\sigma^2_z}\right) \tag{11.3}$$

which converges to $h^2\,S$. Equation 11.3 follows by noting that the probability a gamete containing specific alleles from both loci remains intact following one generation of recombination is $1-c$. Thus, after τ generations only $(1-c)^\tau$ of the favorable two-locus combinations selected at $\tau = 0$ remain unaltered by recombination.

Summing Equation 11.3 over t gives the cumulative response after t generations with constant selection differential S as

$$R(t) = t\,h^2\,S + R_{AA}(t) \tag{11.4a}$$

where

$$R_{AA}(t) = S\,\frac{\sigma^2_{AA}}{2\sigma^2_z}\,\left(\sum_{i=1}^{t}(1-c)^{i-1}\right) = S\,\left(\frac{1-(1-c)^t}{c}\right)\,\left(\frac{\sigma^2_{AA}}{2\,\sigma^2_z}\right) \tag{11.4b}$$

denotes the cumulative additive $\times$ additive epistatic contribution. The last equality follows using the partial sum of a geometric series,

$$\sum_{i=0}^{n} x^i = \frac{1-x^{n+1}}{1-x} \tag{11.5a}$$

We will also shortly make use of the related identity,

$$\sum_{i=1}^{n} x^i = \frac{1-x^{n+1}}{1-x} - 1 = \frac{x-x^{n+1}}{1-x} \tag{11.5b}$$

If loci are unlinked ($c = 1/2$), $R_{AA}(t)$ rapidly converges to $S\,\sigma^2_{AA}/\sigma^2_z$, while if loci are completely linked ($c = 0$), $R_{AA}(t) = t\,S\,\sigma^2_{AA}/(2\sigma^2_z)$. More generally, the total epistatic contribution (for $c > 0$) approaches a limiting value of

$$\widetilde{R}_{AA} = \lim_{t\to\infty} R_{AA}(t) = \frac{1}{c}\left(S\,\frac{\sigma^2_{AA}}{2\,\sigma^2_z}\right) \tag{11.6a}$$

$\widetilde{R}_{AA}$ represents the balance between selection generating disequilibrium and recombination removing it. Equation 11.6a shows that the limiting contribution from epistatic loci is $1/c$ times the epistatic response in the first generation. For unlinked loci, this is just twice the initial response. With tight linkage, the total response can be significantly larger. Solving for t in $1-(1-c)^t = 1/2$ gives

$$t_{1/2} = \frac{-\ln(2)}{\ln(1-c)} \tag{11.6b}$$

as the time for half the total response to occur. For small c, this is approximately $\simeq 0.68/c$. Thus, as linkage becomes tigher, the total cumulative epistatic response increases, as does the time for half of this total response to occur.

Once selection stops, the epistatic contribution decays back to zero. With t generations of selection followed by τ generations of no selection, the cumulative response is

$$t\,h^2\,S + (1-c)^{\tau}\,R_{AA}(t) \tag{11.7}$$

which converges to $R = t\,h^2\,S$, the value predicted from the breeders' equation. The half-life for decay of R_{AA} is also given by Equation 11.6b.

The presence of epistasis can result in a curvilinear selection response if σ^2_{AA}/σ^2_z is sufficiently large. However, as Figure 11.1 shows, such curvilinearity is usually difficult to distinguish from a linear response. Further, much of the curvilinearity occurs in the first few generations (Equation 11.6b) unless there is tight linkage. With a constant selection

differential, the increment to response from epistasis decreases each generation as R_{AA} approaches its limiting value $\widetilde{R}_{AA}$, at which point the per-generation response is just h^2S and hence linear over future generations.

Once selection is relaxed, the total response decays back to that predicted from the breeders' equation. Interestingly, this situation mimics the effects of natural selection countering artificial selection, which also results in a decay of the cumulative response once artificial selection stops. Thus, in order to predict the *permanent* response correctly we must know h^2. If only the parent-offspring slope is estimated, this can overestimate the final amount of response due to the inclusion of σ^2_{AA} and higher-order (additive) epistatic variances, although the bias is generally likely to be small.

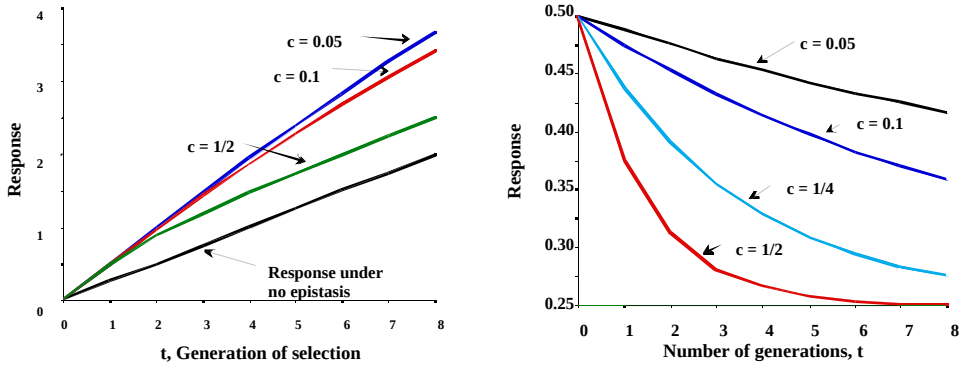

Figure 11.1. The permanent and transient response to selection assuming pairwise epistasis in a diploid, with $h^2 = 1/4$ and $\sigma^2_{AA}/\sigma^2_z = 1/2$. **Left**: The cumulative response (in units of S) assuming a constant amount of selection for various values of c. Note that even with this large amount of epistasis (σ^2_{AA} accounting for half the total variance), it is difficult to distinguish the curvilinear response with epistasis from a linear response. **Right**: The decay of the response to a single generation of selection due to the decay of the contribution from epistasis. With no epistasis, expected response here is 0.25. Provided $c > 0$, the cumulative response eventually decays to $h^2S = S/4$, the expectation under no epistasis.

Griffing's analysis is restricted to two loci, and hence limited to only pair-wise (additive $\times$ additive) epistasis. Equation 11.1 gives the single-generation response for arbitrary levels of additive epistasis, provided the biparental offspring regression is linear. Again assuming the infinitesimal model (and unlinked loci), Bulmer (1980) found the response due to a single generation of selection decays after one generation to

$$R = S\left(h^2 + \frac{1}{4}\frac{\sigma^2_{AA}}{\sigma^2_z} + \frac{1}{16}\frac{\sigma^2_{AAA}}{\sigma^2_z} + \frac{1}{64}\frac{\sigma^2_{AAAA}}{\sigma^2_z} + \cdots\right) \tag{11.8}$$

which again rapidly converges to $R = h^2\,S$ after several generations without selection. For n-locus additive epistasis (e.g., $\sigma^2_{A\cdots A}$, where there are n A's), the per-generation decay rate for unlinked loci is $(1/2)^{n-1}$, the probability that a parental gamete containing specific alleles at n unlinked loci is passed on to an offspring. The probability that such a gamete remains unchanged after t generations is $2^{-t(n-1)}$, which rapidly converges to zero. Example 11.2 (below) develops this point in detail. A final caveat is that these results apply to infinite populations. As we will see in Chapter 5, with finite populations some of the ad-

ditive epistatic contribution can be permanent due to some of the additive epistasis being transformed into simple additive variation by drift.

Selection on Autotetraploids

Polyploidy is very common in plants and can introduce complications in predicting the response to selection. For example, the dynamics of selection response for autotetraploids with dominance is very similar to diploids with epistasis. From LW Equation 7.22 and LW Table 7.5, the autotetraploid parent-offspring covariance when dominance (but no epistasis) is present is

$$\sigma(z_p, z_o) = \frac{\sigma_A^2}{2} + \frac{\sigma_D^2}{6}$$

This also assumes no shared environmental effects, genotype $\times$ environment interactions or correlations.

The inflation in the parent-offspring covariance is due to dominance interactions between the two alleles per locus that each autotetraploid parent passes on to its offspring. Thus, like epistasis in diploids, favorable *combinations* of alleles can be passed down from parent to offspring in polyploids. With equal amounts of selection on both sexes (e.g., selection occurs before pollination), the resulting response (assuming linearity of the parent-offspring regression) is

$$R = S\left(h^2 + \frac{\sigma_D^2}{3\sigma_z^2}\right) \tag{11.9}$$

If selection occurs after pollination, S is replaced throughout the rest of our discussion by $S/2$. Gallais (1975) extended Griffing's (1960a) method (and hence assumed phenotypes are normally distributed with each gene having a very small effect on the character) to obtain the response after t generations of selection with constant differential S as

$$R(t) = th^2S + R_D(t) \tag{11.10a}$$

where

$$R_D(t) = S\,\frac{3}{2}\left[1 - \left(\frac{1}{3}\right)^t\right]\,\frac{\sigma_D^2}{3\sigma_z^2} \tag{11.10b}$$

which converges to a limiting value of

$$\widetilde{R}_D = S\,(\sigma_D^2/2\sigma_z^2) \tag{11.10c}$$

which is just a 50% increase over the first-generation response. Thus, as with the contribution from epistasis, the total contribution from dominance approaches a limiting value representing the balance between selection favoring specific combinations of alleles and reproduction re-shuffling those combinations. In particular, segregation reduces the departure from tetraploid Hardy-Weinberg proportions (LW Chapter 4) generated by the selection of favorable combinations of allelic pairs, reducing their contribution to response. The response for t generations of selection followed by τ generations of no selection is

$$t\,h^2\,S + (1/3)^\tau\,R_D(t)$$

which again rapidly converges to $t\,h^2\,S$. In LW Chapter 4, it was shown that in an autotetraploid the difference in the frequency of pairs of alleles from Hardy-Weinberg expectation decays by $1/3$ each generation in the absence of double reduction ($c = 0$), as would occur

for a locus completely linked to the centromere. More generally, if c is the per-generation probability of a double reduction, the decay rate of $(1/3)^t$ is replaced in the above equations by $(1-c)^t/3^t$. Swanson et al. (1974) found that if some double reductions occur ($c > 0$), the additive variance is slightly inflated over the value expected with no double reductions ($c = 0$), permanently increasing selection response. This results from the slight excess of homozygotes at equilibrium over the Hardy-Weinberg expectation (see LW Chapter 4). Wricke and Weber (1986) discuss additional topics on autotetraploid selection, while single-locus models have been examined by R. Hill (1971). By far the most complete treatment of selection with autopolypoids is the outstanding text by Gallais (2003).

ANCESTRAL REGRESSIONS

A general approach for examining which components of the response are transient is to consider the expected value of an offspring as a function of all its direct relatives that have been under selection (Bulmer 1971, 1980). If this **ancestral regression** is linear (as would occur if the joint distribution of the phenotypic values of all relatives is multivariate normal), response can be described by specifying the regression coefficients by an obvious extension of the biparental regression to now include all selected relatives back to the original unselected base population. For example, if selection starts in generation 0, the response in the first generation is $R(1) = 2\,\beta_{1,0}\,S_0$, where $\beta_{1,0}$ is the regression of offspring at generation one on a parent from generation zero (this assumes both parents have the same regression coefficients and selection differentials, an assumption that will be relaxed shortly). Likewise, the total response after two generations, $R(2) = 4\,\beta_{2,0}\,S_0 + 2\,\beta_{2,1}\,S_1$, depends on the nature of selection on the four grandparents (S_0) and both parents (S_1) as well as the transmission from grandparent to grandchild ($\beta_{2,0}$) and parent to offspring ($\beta_{2,1}$). Note that this formulation allows the parent-offspring regression to change through time (e.g., $\beta_{2,1}$ need not equal $\beta_{1,0}$), as might happen with inbreeding. Similarly, the response following three generations of selection depends upon the nature of selection on that individual's eight great-grandparents, four grandparents and two parents,

$$R(3) = 8\,\beta_{3,0}\,S_0 + 4\,\beta_{3,1}\,S_1 + 2\,\beta_{3,2}\,S_2$$

Proceeding in this fashion gives the response for generation T as

$$R(T) = \sum_{t=0}^{T-1} 2^{T-t}\,\beta_{T,t}\,S_t \tag{11.11a}$$

where $\beta_{T,t}$ is the partial regression coefficient for the phenotype of an individual in generation T on one (out of 2^{T-t}) of its relatives in generation $t < T$. With pure selfing each individual has only a single relative in each previous generation, giving the ancestral regression as

$$R(T) = \sum_{t=0}^{T-1} \beta_{T,t}\,S_t \tag{11.11b}$$

Recall from standard regression theory (LW Chapter 8) that the vector of partial regression coefficients $\boldsymbol{\beta} = \mathbf{V}^{-1}\,\boldsymbol{\sigma}$, where $\boldsymbol{\sigma}$ is a vector of covariances between the individuals in generation T with all relatives in previous generations and $\mathbf{V}$ is the phenotypic covariance

matrix for the entire collection of individuals. The key here is that the partial regression coefficients are entirely determined by the covariances between relatives. If we have independence so that the partial regression coefficients reduce to univariate regression coefficients (i.e., $\beta_i = \sigma(y, x_i)/\sigma^2_{x_i}$), then we have

$$R(T) = \sum_{t=0}^{T-1} 2^{T-t} \frac{\sigma_G(T,t)}{\sigma^2(z_t)} S_t \tag{11.11c}$$

where $\sigma_G(T,t) = \sigma(z_T, z_t)$ is the **cross-generation covariance**, the phenotypic covariance between an individual in generation t and its descendent in generation $T > t$. With selection under pure selfing, each individual has a single ancestor and the 2^{T-t} term in Equation 11.11c is absent. As we will see in Chapter 19, ancestral regression offers a very powerful approach for the analysis of selection under inbreeding, when the genetic variances change each generation.

If different relatives in the same generation experience different amounts of selection, with $S_{k,i}$ being the selection differential on relative i in generation k, then

$$R(T) = \sum_{t=0}^{T-1} \left[\beta_{T,t} \left(\sum_{i=1}^{n(t,T)} S_{t,i} \right) \right] \tag{11.12}$$

where $n(t,T)$ is the number of relatives in generation t that contribute to response in generation T. Note for the case of pure selfing $n(t,T) = 1$. Finally, we can also allow for different regression coefficients on each relative to completely generalize this approach,

$$R(T) = \sum_{t=0}^{T-1} \left(\sum_{i=1}^{n(t,T)} \beta_{T,t,i} S_{t,i} \right) \tag{11.13}$$

where $\beta_{T,t,i}$ is the regression coefficient of the phenotype of an individual in generation T on its i-th relative in generation t.

To apply ancestral regression for predicting response, we require that the regression remains linear and that selection-induced changes in the variances and covariances are negligible. Thus, while we allow changes in $\beta_{T,t}$ due to the particular genetic system being considered (e.g., selfing wherein the additive genetic variance decreases by a predictable amount each generation in the absence of selection) we assume that selection does not confound these changes. Bulmer (1980) shows that under the infinitesimal model the joint distribution of an offspring and all its direct ancestors is multivariate normal and hence the ancestral regression is linear. Since selection does not change allele frequencies under the infinitesimal model, this might suggest that the regression coefficients $\beta_{T,t}$ are unaffected by selection. The problem, however, is that selection generates gametic-phase disequilibrium that can significantly alter the genotypic moments (Chapters 13, 24). For now, we assume that these changes (over short time scales) are small enough to be neglected.

Example 11.1: As an application of ancestral regressions, consider additive by additive epistasis. In this case, Cockerham (1984) found (under the infinitesimal model) that for two linked loci, the cross-generation covariance is

$$\sigma_G(\tau + t, \tau) = \frac{\sigma^2_A(\tau)}{2^t} + \frac{\sigma^2_{AA}(\tau)}{2} \left(\frac{1-c}{2} \right)^t$$

giving

$$2^t\,\sigma_G(\tau+t,\tau) = \sigma_A^2(\tau) + (1-c)^t\,\frac{\sigma_{AA}^2(\tau)}{2}$$

Provided the genetic variances remain constant, applying Equation 11.11a we recover Equation 11.3.

The behavior of the regression coefficients over time thus informs us as to the permanency of response. Note from Equation 11.11a that unless $2^t\,\beta_{\tau+t,\tau}$ remains constant as t increases, the contribution to cumulative response from selection on adults in generation τ changes over time. For example, when loci are strictly additive (no dominance or epistasis), $\sigma_G(\tau+t,\tau) = 2^{-t}\,\sigma_A^2(\tau)$ and thus $2^t\,\beta_{\tau+t,\tau} = h_\tau^2$, the standard result from the breeders' equation. However, unless $2^t\,\sigma_G(\tau+t,\tau)$ remains constant, any response contributed decays. Hence any term of $\sigma_G(\tau+t,\tau)$ that decreases by more than $1/2$ each generation contributes only to the transient response. An exception is with pure selfing where the total contribution in generation $t+\tau$ from an ancestor in generation τ is proportional to $\sigma_G(\tau+t,\tau)$, so that any components that decline as τ increases will contribute to the transient response.

Example 11.2: As an example of the power of ancestral regressions, we develop the expected response under arbitary levels of additive epistasis (under the infinitesimal model with unlinked loci). First, considering only additive terms, LW Equation 7.12 gives the genetic covariance between x and y as

$$\begin{aligned}\sigma_G^2(x,y) &= (2\Theta_{x,y})\,\sigma_A^2 + (2\Theta_{x,y})^2\,\sigma_{AA}^2 + (2\Theta_{x,y})^3\,\sigma_{AAA}^2 + \cdots + (2\Theta_{x,y})^i\,\sigma_{A^i}^2 \\ &= \sum_{i=1}^{n} (2\Theta_{x,y})^i\,\sigma_{A^i}^2\end{aligned}$$

The coefficient of coancestry $\Theta_{t,t+\tau}$ between a parent in generation t and its direct great-offspring in generation $t+\tau$ under random mating is

$$\Theta_{t,t+\tau} = \left(\frac{1}{2}\right)^{\tau+1}$$

Now let's compute the contribution $\sigma_{G,i}(t+\tau,t)$ to the total genetic covariance due to i-th order additive epistasis. Substituting the above results gives

$$\frac{\sigma_{G,i}(t+\tau,t)}{\sigma_{A^i}^2} = (2\Theta_{t+\tau,t})^i = 2^i\left(\frac{1}{2}\right)^{(\tau+1)i} = \left(\frac{1}{2}\right)^{\tau i}$$

Hence, the ancestral regression term is

$$2^\tau\,\frac{\sigma_{G,i}(t+\tau,t)}{\sigma_{A^i}^2} = 2^\tau 2^{-\tau i} = \left(\frac{1}{2}\right)^{\tau(i-1)} = \left(\frac{1}{2^{i-1}}\right)^\tau$$

Hence, with constant selection S, the contribution to total response from i-th order additive epistasis is just

$$R_{A^i}(t) = S\frac{\sigma^2(A^i)}{\sigma^2(z)}\sum_{\tau=1}^{t}\left(\frac{1}{2^{i-1}}\right)^\tau$$

Recalling Equation 11.5b,

$$\sum_{\tau=1}^{t}\left(\frac{1}{2^{i-1}}\right)^{\tau}=\frac{x-x^{t+1}}{1-x}\quad\text{where}\quad x=(1/2)^{i-1}$$

The limit of this sum is

$$\frac{x}{1-x}=\frac{(1/2)^{i-1}}{1-(1/2)^{i-1}}=\frac{1}{2^{i-1}-1}$$

Since the initial contribution ($t=1$) is $(1/2)^{i-1}$, the extra increment to response beyond that seen in the first generation is

$$\widetilde{R}_{A^i}-R_{A^i}(1)=\frac{1}{2^{i-1}-1}-\frac{1}{2^{i-1}}=\frac{1}{(2^{i-1}-1)2^{i-1}}$$

The response in generation one and at the limit (both in units of of $S\sigma^2(A^i)/\sigma_z^2$, and the fraction of total response occuring in the first generation for second- through fifth-order additive epistasis, are as follows:

	AA	AAA	AAAA	AAAAA
$R(1)$	0.500	0.250	0.125	0.063
Limit	1.000	0.333	0.143	0.067
% $R(1)$/limit	50.0	75.0	87.5	93.8

Thus, all else being equal, the limiting contribution decreases dramatically with the order of the epistasis and essentially all of the response occurs in the first generation.

RESPONSE DUE TO ENVIRONMENTAL CORRELATION

As Equation 11.1 indicates, shared parent-offspring environmental effects (e.g., $\sigma(E_p,E_o)\neq 0$) can influence response. We show here that this contribution is also transient. Consider a character whose variation is entirely environmental, in which case the phenotypic value can be decomposed as

$$z=\mu+E=\mu+e_{fa}+e_{mo}+e$$

where μ is the mean value of the character when environmental effects are randomly distributed, and the environmental value E has been decomposed into the maternal and paternal contributions to the offspring due to shared environmental effects (e_{mo} and e_{fa}) and a residual due to special environmental effects (e). In order to predict the shared environmental contribution from a parent, we assume the simplest model, that a fraction b of the total environmental value of a parent is passed on to its offspring. This model serves as a useful introduction to some of the dynamics that can occur with maternal effects (which are examined in the next section). Thus, the expected contribution from a father to his offspring is $e_{fa}=bE_{fa}=b(z_{fa}-\mu)$ where E_{fa} is the father's total environmental value. To simplify matters further, we assume that this regression coefficient is independent of the sexes of the parent and offspring, although this can easily be relaxed. If we assume that parents and offspring have the same phenotypic variance, then $b=\rho/2$, where ρ is the slope

of the midparent-offspring regression. Note that ρ can be negative. For example, suppose parents and offspring compete for a limited amount of common resource. Larger parents may gather a disproportionate share of resources, resulting in smaller offspring.

Provided E_{fa} and E_{mo} are uncorrelated, the expected value of an offspring from parents with phenotypic values z_{fa} and z_{mo} is

$$E(\, z_o \,|\, z_{mo}, z_{fa}\,) = \mu + \frac{\rho}{2}\,(\, z_{fa} - \mu\,) + \frac{\rho}{2}\,(\, z_{mo} - \mu\,) \tag{11.14}$$

Denoting the mean of adults selected in generation t by μ_t^*, the mean at generation $t+1$ is given by

$$\mu_{t+1} = \mu + \rho\,(\,\mu_t^* - \mu\,)$$

where $(\,\mu_t^* - \mu\,)$ is the environmental deviation in selected parents at generation t, ρ of which is passed on to their offspring. Rewriting the mean after selection as $\mu_t^* = \mu_t + S_t$,

$$\mu_{t+1} = \mu + \rho\,(\,\mu_t + S_t - \mu\,) \tag{11.15}$$

The change in mean in generation t, $\Delta\mu_t = \mu_{t+1} - \mu_t$, is

$$\begin{aligned}\Delta\mu_t &= [\,\mu + \rho\,(\,\mu_t + S_t - \mu)\,] - [\,\mu + \rho\,(\mu_{t-1} + S_{t-1} - \mu\,)\,] \\ &= \rho\,[\,(\,\mu_t - \mu_{t-1}) + (S_t - S_{t-1}\,)\,] \\ &= \rho\,[\,\Delta\mu_{t-1} + (S_t - S_{t-1})\,]\end{aligned} \tag{11.16a}$$

Suppose that constant selection (with differential S) is applied starting at generation 1. Here, $\Delta\mu_0 = 0$, $S_0 = 0$, and $S_t = S$ for $t \geq 1$. Equation 11.16a gives $\Delta\mu_1 = \rho\, S$. Further iterations yield

$$\Delta\mu_t = \rho^t\, S \tag{11.16b}$$

which decreases each generation, approaching zero for large t. Hence, even under continued selection, the response to selection eventually stops. The reason for this decline in the per generation rate of response can be seen from Equation 11.16b. Change in the character mean due to previous selection decays, countering gain from selection in the current generation. Only a fraction ρ of the change from generation $t-1$ is passed on, and, in general, only ρ^k of the response from generation $t-k$ persists by generation t. Summing over Equation 11.16b, the total response to selection after t generations is

$$R(t) = \mu_{t+1} - \mu_0 = \sum_{i=1}^{t} \Delta\mu_i = S \sum_{i=1}^{t} \rho^i \tag{11.16c}$$

Recalling the partial sum of a geometric series (Equation 11.5b), this reduces to

$$R(t) = S\,\frac{\rho}{1-\rho}\,(\,1 - \rho^t\,) \tag{11.17a}$$

As was the case for epistasis, the total cumulative response reaches an equilibrium value representing the balance between selection generating correlations and reproduction removing them, with

$$\widetilde{R} = \lim_{t\to\infty} R(t) = S\frac{\rho}{1-\rho} \tag{11.17b}$$

Thus, no matter how long selection is applied, the mean can never change by more than $S\rho/(1-\rho)$. Further, none of this response is permanent. Suppose selection is stopped after t

generations, giving $S_t = S$, $S_{t+\tau} = 0$ for $\tau \geq 1$. Substituting into Equation 11.16a and using Equation 11.16b, the expected change in generation $t + \tau$ is

$$\Delta\mu_{t+\tau} = \rho^\tau \left(\Delta\mu_t - S \right) = -S\,\rho^\tau \left(1 - \rho^t \right) \tag{11.18}$$

By generation $t + \tau$ the cumulative response is

$$R(t+\tau) = R(t) + \sum_{i=1}^{\tau} \Delta\mu_{t+i} = R(t) - S\left(1 - \rho^t \right) \sum_{i=1}^{\tau} \rho^i = \rho^\tau\, R(t) \tag{11.19}$$

which converges to zero, with the rate of decay being set by ρ (Figure 11.2). Hence, while there can be some selection response when the resemblance between relatives is entirely environmental, any response is transient, decaying away once selection stops. Further, no matter how long selection proceeds, the response reachs a limit beyond which no further response is possible (Equation 11.17b).

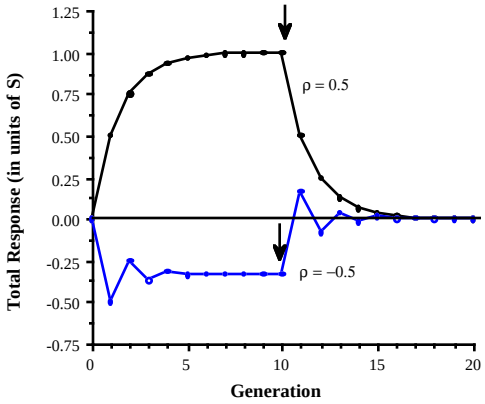

Figure 11.2. Response when resemblance between relatives is due entirely to correlation between environmental values in parents and offspring. Selection with constant differential S starts at $t = 0$ and continues until generation 10 (indicated by the arrow), at which point selection is stopped. Note the interesting dynamics that occur if environmental values are negatively correlated. The response to selection is **reversed** with respect to the selection differential. In this case, selection for *increased* character value results in a *decreased* mean value, with the total response eventually converging to $-S/3$ (for $\rho = -0.5$). Once selection is relaxed there is an initial positive response (generation 11), although response quickly decays to zero.

MATERNAL EFFECTS

Any influence that the mother's phenotype has on the phenotype of her offspring (beyond being a predictor of breeding value) is considered a **maternal effect** (LW Chapter 23). Body size, amount of care invested in offspring, and endosperm production are examples of **maternal performance characters** that potentially influence a variety of characters in the progeny. **Paternal effects** are also possible, especially in situations where the father plays some role in caring for the offspring. While paternal effects are not considered here, they can be treated in exactly the same fashion as maternal effects.

Assuming a maternal effect, the phenotype of a character can be decomposed as $z = G + M + e$, the sum of a genotypic value G plus a maternal component M plus an environmental deviation e (this assumes no interactions between G, M, and e). There are a number of subtle (and important) features with this apparently simple model. First, how many characters are we really considering? The maternal effect may be regarded as either a direct function of the character being considered, or it may be due to a character (or suite of characters) correlated with the one being considered. For example, weight may be correlated with the amount of lactation, in which case maternal weight can influence offspring weight indirectly because larger females tend to have increased lactation. In the latter case, if there is a genetic basis to the maternal effect, selection on the direct character (e.g., body weight) is expected to give a correlated response in the maternal performance characters (e.g., lactation), and vice versa (Kirkpatrick and Lande 1989). We return to these points when we discuss evolution of correlated characters in Chapters 30 - 36. For now attention is restricted to single-character models.

Response under Falconer's Model

The simplest model of maternal effects (motivated by the inheritance of litter size in mice) is that of Falconer (1965), which deals with a single maternal character: the only character that has a maternal influence on z is z itself (reviewed in LW Chapter 23). Falconer assumes the maternal contribution is a linear function of the maternal phenotype z_{mo}, so that $M = m z_{mo}$ and the phenotypic decomposition becomes

$$z = G + m\, z_{mo} + e \tag{11.20}$$

Conceivably, M could be a nonlinear function of z_{mo}, but linearity is assumed for tractability. We refer to Equation 11.20 as the **dilution model**, as the effect of the maternal phenotype is diluted over several generations. The parameter m can be regarded as the partial regression coefficient (holding genotypic value constant) of offspring phenotype on maternal phenotype and and can be estimated as the difference between the mother- and father-offspring regression slopes (LW Equation 23.13). Negative estimates of m have been reported. Falconer (1965) estimated $m = -0.15$ for litter size in mice and Janssen et al. (1988) estimated m values of -0.58 and -0.40 for age of maturity in two replicate lines of springtails (insects in the order Collembola). Maternal effects can result in unusual dynamics such as time lags. This is not surprising considering the dynamics of selection response when variation in the character is entirely environmental (Figure 11.2).

Assume that the joint distribution of phenotypes and breeding values in parents and offspring is multivariate normal. Further assuming no epistasis, the expected phenotypic value of an offspring whose mother has phenotypic value z_{mo} is

$$E(z_o \mid A_{mo}, A_{fa}, z_{mo}) = \frac{A_{mo}}{2} + \frac{A_{fa}}{2} + m\, z_{mo} \tag{11.21a}$$

where A_{mo} and A_{fa} are the maternal and paternal breeding values (see Example 7 in LW Chapter 8). Averaging over the selected parents, the mean in generation $t+1$ is

$$\mu_z(t+1) = \frac{A^*_{fa}(t) + A^*_{mo}(t)}{2} + m\, \mu^*_{mo}(t) \tag{11.21b}$$

where $A^*_{fa}(t)$ and $A^*_{mo}(t)$ are the mean breeding values of the selected parents and $\mu^*_{mo}(t)$ the mean phenotypic value of selected mothers in generation t. Using the regression of breeding value on phenotype,

$$A = \mu_A + b_{Az}\,(\,z - \mu_z\,) + e$$

allows us to predict the breeding value A of an individual from its phenotypic value z. Thus we can rewrite $A^*_{mo}(t)$ as

$$\begin{aligned} E_s\,(\,A_{mo}\,) &= E_s\left(\,\mu_A(t) + b_{Az}\,[\,z_{mo} - \mu_z(t)\,] + e\,\right) \\ &= \mu_A(t) + b_{Az} S_{mo}(t) \end{aligned} \tag{11.22}$$

where $E_s(\ )$ denotes the expected value over the selected parents. A similar expression holds for $A^*_{fa}(t)$. In the absence of maternal effects, $b_{Az} = h^2$. However, the dilution model generates a covariance between M and A, specifically $\sigma_{A,M} = m\,\sigma^2_A\,/\,(\,2-m\,)$, which in turn alters the covariance between z and A (Falconer 1965, Kirkpatrick and Lande 1989, LW Chapter 23). The resulting regression slope (at equilibrium) is

$$b_{Az} = h^2 \frac{2}{2-m} \tag{11.23}$$

(Falconer 1965, Van der Steen 1985, Kirkpatrick and Lande 1989). If there is a negative maternal effect ($m < 0$), $b_{Az} < h^2$, reducing the correlation between breeding value and phenotype. Conversely, $m > 0$ increases the correlation between breeding value and phenotype above h^2. Applying Equations 11.21–11.23 and using $\mu^*_{mo}(t) = \mu_z(t) + S_{mo}(t)$, gives

$$\mu_z(t+1) = \mu_A(t) + \frac{h^2}{2-m}\Big(S_{mo}(t) + S_{fa}(t)\Big) + m\Big(\mu_z(t) + S_{mo}(t)\Big) \tag{11.24}$$

(Van der Steen 1985, Kirkpatrick and Lande 1989). The change in population mean over one generation, $\Delta\mu_z(t)$, is thus

$$\Delta\mu_z(t) = \mu_z(t+1) - \mu_z(t) =$$

$$\begin{aligned} &\left[\,\mu_A(t) + \frac{h^2}{2-m}\Big(S_{mo}(t) + S_{fa}(t)\Big) + m\Big(\mu_z(t) + S_{mo}(t)\Big)\right] \\ &\quad - \left[\,\mu_A(t-1) + \frac{h^2}{2-m}\Big(S_{mo}(t-1) + S_{fa}(t-1)\Big) + m\Big(\mu_z(t-1) + S_{mo}(t-1)\Big)\right] \end{aligned}$$

$$= \frac{h^2}{2-m}\Big(S_{mo}(t) + S_{fa}(t)\Big) + m\,S_{mo}(t) + m\Big(\Delta\mu_z(t-1) - S_{mo}(t-1)\Big) \tag{11.25}$$

The last simplification follows from the regression of breeding value on phenotype, with

$$\mu_A(t) = \mu_A(t-1) + \frac{h^2}{2-m}\Big(S_{mo}(t-1) + S_{fa}(t-1)\Big)$$

Equation 11.25 can be interpreted as follows: the first two terms are the change in character value resulting from selection in generation t due to genetic ($h^2\,/\,[\,2-m\,]$) and maternal (m) contributions. The final term, which can also be expressed as $m\,[\,\mu_z(t) - \mu^*_z(t-1)\,]$, represents the decay in the maternal contribution from the previous generation.

Starting with an unselected base population, the response to a single generation of selection is

$$\Delta\mu_z(1) = S_{mo}(1)\left(\frac{h^2}{2-m} + m\right) + S_{fa}(1)\,\frac{h^2}{2-m} \tag{11.26}$$

An interesting consequence of Equation 11.26 is that if $m < 0$, there is some possibility of a **reversed response**, where $\Delta\mu_z$ has opposite sign of S. If $S_{fa} = S_{mo} = S$, a reversed response is expected if

$$m < 1 - \sqrt{1 + 2h^2} \tag{11.27a}$$

If selection is only occuring on females, this condition is

$$m < 1 - \sqrt{1 + h^2} \tag{11.27b}$$

An example of an apparent maternally-induced reversed response was seen by Falconer (1960, 1965) in his selection experiments on litter size in mice. This character shows a negative maternal effect, with m and h^2 estimated to be -0.13 and 0.11, respectively. Since selection for litter size occurs only in females, Equation 11.27b implies that a reversed response in the first generation is expected (as $1 - \sqrt{1 + 0.11} \simeq -0.05 > m$). As Figure 11.3 shows, a reversed response was indeed observed.

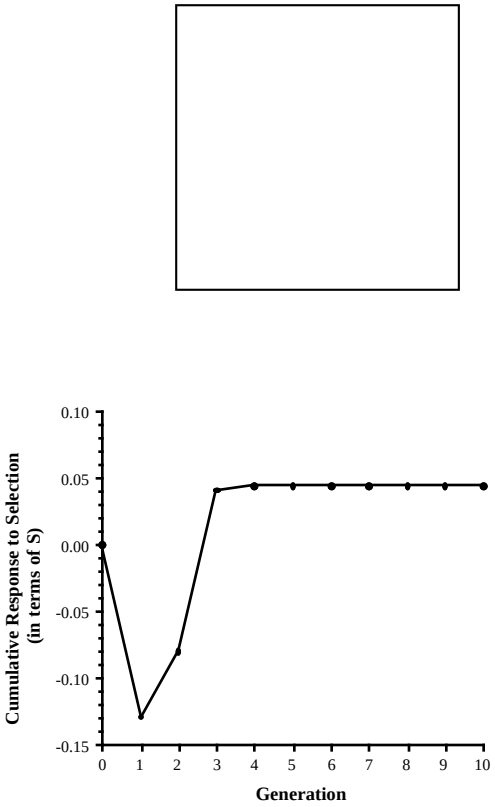

Figure 11.3. **Top:** Falconer's (1960, 1965) experiments on selection response for litter size in mice. The dashed line is the response to selection for small litters, the thick line selection for large litters, and the thin line the control. Note the reversed response in the first generation in both the up- and down-selected lines. **Bottom:** Prediction from the model, using Falconer's estimated values of $h^2 = 0.11$ and $m = -0.13$. The predicted change in population mean following a single generation of selection on females with $S_{mo} > 0$ is plotted. There is a reversed response in the first generation, even though the net genetic change is to increase the

character. By generation 3, the nongenetic change in phenotypic mean has largely decayed away, revealing the net genetic change of $S_{mo}\, h^2/[(1-m)(2-m)] = 0.044 S_{mo}$.

An observed reversed response is misleading because the *permanent* response is expected to have the same sign as S, while the initial observed response also includes a transient component that (in this case) is of opposite sign and of larger magnitude than the permanent response component. It may take several generations for this transient component to decay and reveal the actual genetic changes (Figure 11.3), which is (for a single generation of selection) $S\, h^2\, [\, 2\, /\, (2-m)(1-m)\,]$, as shown by Equation 11.33 (below).

The possibility of reversed response hints at some of the complicated dynamics that can appear when maternal effects are present. To examine these dynamics in more detail, consider the dilution model with constant directional selection occuring equally on both sexes. i.e., $S_{fa}(t) = S_{mo}(t) = S$ for $t \geq 1$. Iteration of Equation 11.25 gives

$$\Delta\mu_z(t) = S\left[\frac{2h^2}{(1-m)(2-m)}\left(1-m^t\right)+m^t\right] \tag{11.28a}$$

which converges (for $|m| < 1$) to

$$\Delta\mu_z = S\,\frac{2h^2}{(1-m)(2-m)} \tag{11.28b}$$

Thus after a sufficient number of generations, the per generation change is constant. If $|m|$ is near zero, the per generation response rapidly converges to the asymptotic value, while if $|m|$ is near one, the rate of convergence is considerably slower. Summing over the single-generation changes (Equation 11.28a) the cumulative response to t generations of selection is

$$R(t) = \frac{S}{1-m}\left[t\,\frac{2h^2}{2-m} + m\,(1-m^t)\left(1-\frac{2h^2}{(1-m)(2-m)}\right)\right] \tag{11.29a}$$

which converges (for $|m| < 1$) to

$$\frac{S}{1-m}\left[\frac{2h^2}{2-m}\left(t-\frac{m}{1-m}\right)+m\right] \tag{11.29b}$$

How much of this response is permanent? Suppose selection ends at generation t, and denote by τ the number of generations since selection was stopped. Iterating Equation 11.25 with $S(t) = S$, $S(t+\tau) = 0$ for $\tau \geq 1$ yields

$$\Delta\mu_z(t+\tau) = m^\tau(\Delta\mu_z(t) - S\,) \tag{11.30}$$

where $\Delta\mu_z(t)$ is given by Equation 11.28a. Thus, *response continues even after the cessation of selection*. Using Equation 11.5b to sum Equation 11.30 over τ yields the cumulative response *following* the last generation of selection,

$$R^*(\tau) = \frac{m(1-m^\tau)}{1-m}\,(\,\Delta\mu_z(t) - S\,) \tag{11.31}$$

which converges as $\tau \to \infty$ to

$$R^* = S\,\frac{m\,(1-m^t)}{1-m}\left[\frac{2h^2}{(1-m)(2-m)} - 1\right] \tag{11.32}$$

Summing Equations 11.29a and 11.32, the permanent response to t generations of selection is

$$R(t) + R^* = t\,h^2\,S\,\frac{2}{(1-m)(2-m)} \tag{11.33}$$

If R^* is opposite in sign to S, there is some erosion of the cumulative response upon relaxation of selection (we have already seen a special case of this with reversed response). For $|m| < 1$, erosion in response occurs if

$$0 < m < \frac{3 - \sqrt{1 + 8h^2}}{2} \tag{11.34a}$$

On the other hand, if maternal effects are either negative ($m < 0$) or sufficiently large

$$m > \frac{3 - \sqrt{1 + 8h^2}}{2} \tag{11.34b}$$

the response continues for a few generations following the relaxation of selection. This occurs by the transient component of response decaying away to reveal the actual permanent response due to changes in breeding values. Figure 11.4 plots some sample trajectories.

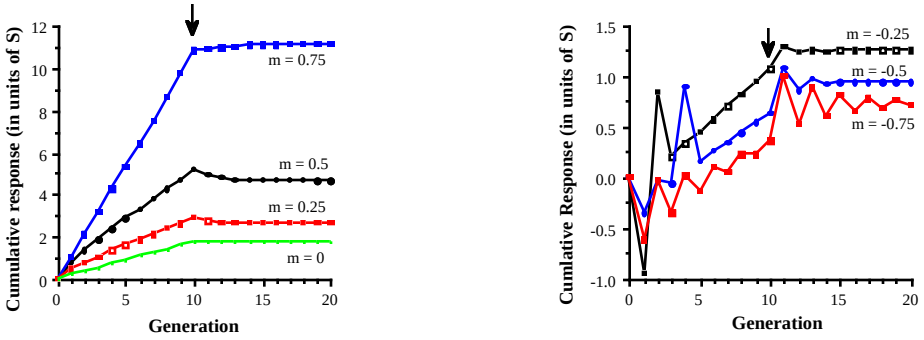

Figure 11.4. Examples of the predicted selection response with maternal effects under Falconer's dilution model. Selection starts at generation zero, with $S_{fa} = S_{mo} = S$ until generation 10 (arrow), at which point selection stops. We assume $h^2 = 0.35$, with the different curves corresponding to different maternal effect values, m. **Left:** Positive maternal effects ($m > 0$). For this value of h^2, Equations 11.34a gives the critical m value as 0.52, so that for $m = 0.75$ response continues (for a few generations) after selection is relaxed, while response decays for $m = 0.5$ and 0.25. **Right:** Negative maternal effects ($m < 0$). The dynamics here are considerably more interesting. For this h^2 value, Equation 11.34b implies that response continues once selection stops for all values of $m < 0$.

In summary, the presence of maternal effects introduces several complications. First, predicting the response to selection requires not only of the inheritance parameters (m, h^2) and current selection differential, but also requires knowledge of previous selection ($\Delta\mu_z(t-1)$, $S_{mo}(t-1)$). Second, after selection is stopped, the mean is likely to continue to change due to lag effects (e.g., Figure 11.4). If $m < 0$, the response will continue, while if $m > 0$ the response can either continue or decay. This clearly causes problems if we

are trying to estimate the nature of selection acting on a character by comparing changes in means between generations. For example, an observed cross-generation decrease in a character could be due to four very different causes: (i) $S < 0$, (ii) $S > 0$ and a reversed response due to maternal effects, (iii) no selection in the observed generation but a previous history of $S > 0$, with the decrease in mean due to a positive maternal effect (reflecting a decay in response), or (iv) no current selection but a previous history of $S < 0$, with the decrease in mean due to a negative (or sufficiently large positive) maternal effect (reflecting a continuation of response).

Other Models of Maternal Effects

Willham (1963, 1972), expanding on the early results of Dickerson (1947), obtained covariances between relatives under a more general model that assumes the maternal effect can be further decomposed as $M = G_M + e_M$. G_M is the contribution to z resulting from the mother's genotypic value for the maternal performance character, while e_M is the contribution resulting from the environmental value of the maternal performance character (reviewed in LW Chapter 23). Hence, even though from the offspring's standpoint, M is treated as an environmental effect, it can have both a genetic and environmental basis in the mother. As Kirkpatrick and Lande (1989) have pointed out, this model is really a two-character model: the character directly being followed z (e.g., body weight) and some other character z_M (e.g., lactation) that has a maternal effect on z. Generalizations of the Dickerson-Willham model have been proposed by Riska et al. (1985) and Kirkpatrick and Lande (1989), but we will defer further discussion of these multiple character models until we discuss the evolution of correlated characters in Chapters 31-36. Mueller and James (1985) examine selection on maternal characters with overlapping generations.

Literature Cited

Bulmer, M. G. 1971. The effect of selection on genetic variability. *Amer. Natl.* 105: 201–211. [11]

Bulmer, M. G. 1980. *The mathematical theory of quantitative genetics.* Oxford Univ. Press, NY. [11]

Cockerham, C. C. 1984. Additive by additve variance with inbreeding and linkage. *Genetics* 108: 487–500. [11]

Dickerson, G. E. 1947. Composition of hog carcasses as influenced by heritable differences in rate and economy of gain. *Iowa Agr. Exp. Stat. Res. Bull.* 354: 492–524. [11]

Falconer, D. S. 1960. The genetics of litter size in mice. *J. Cell and Comp. Physiol.* 56 (Suppl 1): 153–167. [11]

Falconer, D. S. 1965. Maternal effects and selection response. *In* S. J. Geerts (ed.) *Genetics today, proceedings of the XI international congress on genetics, Vol 3* pp. 763–774. Pergamon, Oxford. [11]

Gallais, A. 1975. Selection with truncation in autotetraploids: Comparison with diploids. *Theor. Appl. Genet.* 46: 386–394. [11]

Gallais, A. 2003. *Quantitative Genetics and Breeding Methods in Autopolyploid Plants.* INRA, Paris. [11]

Griffing, B. 1960a. Theoretical consequences of truncation selection based on the individual phenotype. *Aust. J. Biol. Sci.* 13: 307–343. [11]

Griffing, B. 1960b. Accommodation of linkage in mass selection theory. *Aust. J. Biol. Sci.* 13: 501–526. [11]

Hill, R. R. Jr. 1971. Selection in autotetraploids. *Theor. Appl. Genet.* 41: 181–186. [11]

Janssen, G. M., D. DeJong, E. N. G. Joose, and W. Scharloo. 1988. A negative maternal effect in springtails. *Evolution* 42: 828–834. [11]

Kempthorne, O. 1957. *An introduction to genetic statistics.* WIley and Sons, New York.

Kirkpatrick, M. and R. Lande. 1989. The evolution of maternal characters. *Evolution* 43: 485–503. [11]

Lush, J. L. 1948. *The Genetics of Populations.* Animal Husbandry Department, Iowa State University, Ames. [11]

Mueller, J. P. and J. W. James. 1983. Effect on linkage disequilibrium of selection for a quantitative character with epistasis. *Theor. Appl. Genet.* 65: 25–30. [11]

Riska, B., J. J. Rutledge, and W. R. Atchley. 1985. Covariance between direct and maternal genetic effects in mice with a model of persistent environmental influences. *Genet. Res.* 45: 287–297. [11]

Swanson, M. R., J. W. Dudley, and S. G. Carmer. 1974. Simulated selection in autotetraploid populations. II: Effects of double reduction, population size, and selection intensity. *Crop. Sci.* 14: 630–636. [11]

Van der Steen, H. A. M. 1985. The implication of maternal effects for genetic improvement of litter size in pigs. *Livestock Prod. Sci.* 13: 159–168. [11]

Willham, R. L. 1963. The covariance between relatives for characters composed of components contributed by related individuals. *Biometrics* 19: 18–27. [11]

Willham, R. L. 1972. The role of maternal effects in animal breeding. II. biometrical aspects of maternal effects in animals. *J. Anim. Sci.* 35: 1288–1293. [11]

Wricke, G., and W. E. Weber. 1986. *Quantitative genetics and selection in plant breeding.* Walter de Gruyter and Co., New York. [11]