

CHAPTER 6

The Algebra of Evolution: Price's Theorem

The discussion of evolution in the previous chapters was framed almost exclusively in terms of allele-based theories. This is consistent with history, since up until the 1970s, nearly all rigorous evolutionary theory focused on changes in allele frequencies. Some researchers, including Wright, Kempthorne, Cockerham, and Robertson, laid the foundations of quantitative genetics by considering phenotypic traits controlled by large numbers of loci, but these were explicitly rooted in the allelic theory of population genetics.

One explanation for the focus on alleles has been that because there are fewer alleles than possible genotypes, and fewer genotypes than phenotypes (because of environmental effects), it should be much simpler to build models for change in allele frequencies than for changes in genotype or phenotype frequencies. In Chapter 1 we saw that this is not necessarily the case, in that models based on genotype frequencies turned out to be simpler and more general than models based on allele frequencies.

Phenotype-based theories actually subsume gene-based theories, since alleles and genotypes can be thought of as particular kinds of phenotypes. The central results derived in this chapter differ from everything we have seen so far not only in their focus on phenotypes rather than alleles, but also in their generality. These results apply to any measurable trait and encompass both selection and drift. Not only are the results of this chapter more general than those we have encountered so far, they involve a very different philosophy of how to build a scientific theory. In order to see this difference, we need to revisit how we began our analysis in each of the preceding chapters.

All of the results of classical population genetics can be thought of as intentionally simplified models of reality. In Chapters 1 to 5, we began the derivations by imposing some simplifying assumptions on the systems under study. These assumptions included random mating (see Chapters 1 and 5), infinite population size (see Chapters 1 and 2), frequency-independent selection (see Chapters 2 and 5), or no selection at all (see Chapters 3 and 4). None of these assumptions are likely to be completely true in most real systems of interest, and nobody thinks that they are. Rather, these assumptions serve to render highly complicated systems simple enough to allow us to build tractable mathematical models.

Such simplifying assumptions are the mainstay of applied mathematics and theory in most branches of science. Examples from other fields include ideal gasses in physics, optimal foragers in ecology, frictionless pulleys in engineering, pH (standing in for numerous interactions involving individual hydrogen ions) in chemistry, and rational consumers in economics. Some philosophers and scientists have gone so far as to suggest that any theory not based on simplifying assumptions will be so complicated that it will yield no useful insights.

In fact, though, there is another approach to constructing theories. Rather than immediately seek simplifying assumptions when faced with a complicated process, we can start with what we think is actually going on and ask what mathematical principles must follow from these basic properties of the system. When this approach works, it yields a body of results that define the appropriate mathematics to use when studying the system of interest. In this chapter, we will derive one example of this type of result for evolutionary theory.

Price's Theorem

Consider a trait ϕ , which can be any property we can assign a numerical value to. We will use the following symbols in our derivation:

N = Population size

ϕ_i = Phenotype of individual i ($0 < i \leq N$)

$\bar{\phi}$ = Mean phenotype in the population

$\delta_{i,j}$ = Difference between phenotype of the j^{th} descendant of individual i and i 's phenotype

$\bar{\delta}_i$ = Difference between the mean value of ϕ among i 's descendants and ϕ_i

W_i = Number of descendants of individual i

\bar{W} = Mean number of descendants per individual

Using this notation, the phenotypic value of descendant j of individual i in the current generation is $\phi_i + \delta_{i,j}$. The mean phenotype of the descendants, $\bar{\phi}'$, is then:

$$\bar{\phi}' = \frac{\sum_{i=1}^N \sum_{j=1}^{W_i} (\phi_i + \delta_{i,j})}{\sum_{i=1}^N W_i} \quad (6.1)$$

The numerator in Equation 6.1 adds up the phenotypic values of each of the descendants by looking in turn at each of the N individuals in the current generation, and then summing over the phenotypic values of each of their W_i descendants (Figure 6.1). The denominator is simply the total number of descendants.

Our next step is to interpret the summations in Equation 6.1. The following identities follow from the definition of the arithmetic mean:

$$\sum_{j=1}^{W_i} \phi_i = W_i \phi_i$$

$$\sum_{j=1}^{W_i} \delta_{i,j} = W_i \bar{\delta}_i$$

$$\sum_{i=1}^N W_i = N \bar{W}$$

These allow us to rewrite Equation 6.1 as:

$$\begin{aligned} \bar{\phi}' &= \frac{1}{N \bar{W}} \left[\sum_{i=1}^N W_i \phi_i + \sum_{i=1}^N W_i \bar{\delta}_i \right] \\ &= \frac{1}{\bar{W}} [E(W\phi) + E(W\bar{\delta})] \end{aligned} \quad (6.2)$$

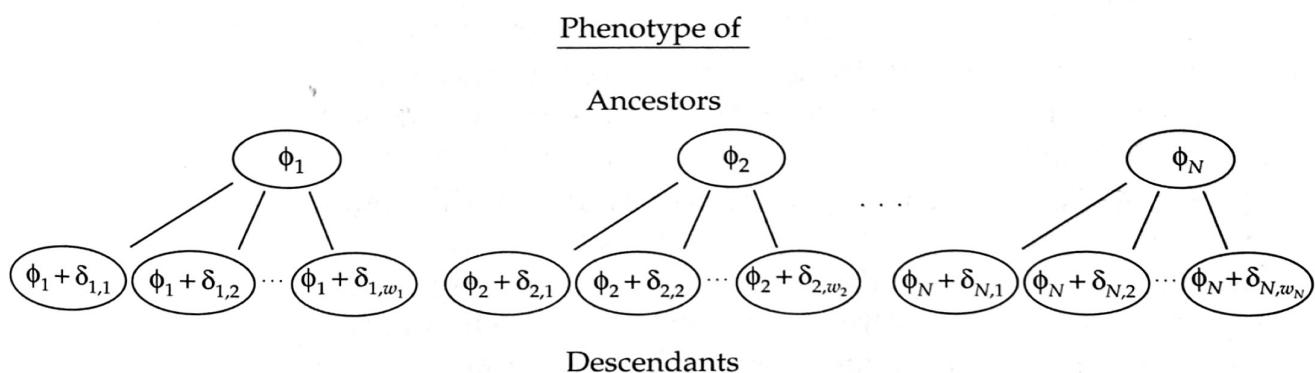


Figure 6.1 The basic setup for deriving Equation 6.4. Note that each individual in both the ancestor and descendant generations has a unique label.

Now, using the fact that $\text{cov}(x, y) = E(xy) - \bar{x} \cdot \bar{y}$, we can substitute for $E(W\phi)$ to get:

$$\begin{aligned}\bar{\phi}' &= \frac{1}{W} [\text{cov}(W, \phi) + \bar{W} \bar{\phi} + E(W\bar{\delta})] \\ &= \frac{1}{W} [\text{cov}(W, \phi) + E(W\bar{\delta})] + \bar{\phi}\end{aligned}\tag{6.3}$$

Subtracting $\bar{\phi}$ from both sides yields:

$$\Delta\bar{\phi} = \frac{1}{W} [\text{cov}(W, \phi) + E(W\bar{\delta})]\tag{6.4}$$

This is Price's theorem (Price 1970). It is a *theorem*, rather than a *theory*, because it is a purely mathematical result proven using only the definitions of mean and covariance and some general concepts, such as phenotype and descendant. Equation 6.4 does not involve biology, but it is clearly relevant to biology or any system in which there is a population of things that have descendants (which may be broadly defined to include the thing itself at some point in the future).

As we investigate how Equation 6.4 can be applied to different problems, it will become apparent that the two terms on the right-hand side can be assigned a number of different, but equally valid, biological interpretations. A useful way to start, though, is to recognize that the two terms on the right-hand side of Equation 6.4 can be thought of as encompassing the different kinds of processes that influence evolutionary dynamics:

- $\frac{1}{W} \text{cov}(W, \phi)$ The change due to differential survival and reproduction.
This encompasses both selection and drift.
- $\frac{1}{W} E(W\delta)$ The change resulting from processes involved in reproduction, such as recombination, regression towards the mean phenotype, or selection at a lower level of organization.

Nearly all discussions of Price's theorem treat it as a description of selection and transmission with no mention of drift. In fact, since we said nothing about what causes the covariance between fitness and phenotype, this term applies equally to drift and selection. In this chapter, we will first discuss Equation 6.4 in terms of selection, meaning that the value of the $\text{cov}(W, \phi)$ term is assumed to be partly a result of some causal effect of phenotype on fitness. We then turn our attention to drift, still using Equation 6.4 but considering the possibility that the covariance between actual fitness and phenotype results from random processes in a finite population.

Note that although we used absolute fitness values in our derivation of Equation 6.4, we could just as well use relative fitness, since any constant that

multiples all fitness values will appear in the numerator and the denominator of Equation 6.4 and will thus cancel out. In the rest of this chapter, we often use w for relative fitness. It is important to keep in mind, though, that we could always substitute W , which is the actual number of descendants.

Concepts Underlying Price's Theorem

The concepts required to interpret Equation 6.4 are very basic. Along with the mathematical operations of mean and covariance, we need only the concepts of (1) a population that changes over some time interval, (2) the relationship between ancestor and descendant, and (3) phenotype. All of these concepts may be defined much more broadly than their standard uses in biology, and this provides much of the power of Price's theorem.

Change over Time Though it is often convenient to use one generation as the time interval, this is not required by the derivation. We may use any time interval that is appropriate for the system under study. In cases of multilevel selection or situations in which the fitness effects are not expressed in the next generation (such as in Fisher's sex ratio theory), we may choose different time intervals. Note that the term W_i , the number of descendants of a particular individual, will change as we change the time interval.

Ancestor/Descendant Relations While we tend to assume that looking over a single generation, ancestors refer to individual parents and descendants refer to their individual offspring, we are not required to do so. All that is necessary is that the same kind of phenotype can be defined in both ancestor and descendant. This does not require that the ancestor and descendant be the same kind of unit. For example, in his original formulation, Price (1970) used diploid parents as the ancestors and successful gametes as the descendants. The character was the frequency of an allele within the unit, which can have the values 0 or 1 for a haploid gamete and 0, $\frac{1}{2}$, or 1 for a diploid parent. For morphological traits, it is sometimes useful to treat the ancestor as a mated pair of individuals and the descendants as their individual offspring. For a trait such as body size, the phenotype of the parents is the average of the value of the trait in the mother and father (called the midparent value in quantitative genetics) and the phenotype of the offspring is the value of the trait in each individual (which is the same as the average for that individual). It is also admissible to treat an individual as the ancestor and the same individual at a later point in time as the descendant. This would be appropriate when selection involves differential persistence, rather than differential reproduction.

Phenotype We define a phenotype as any property of an individual that can be represented as a number, and for which the range of possible values maps uniquely to some section of the real number line (meaning that no phenotype

state could be assigned more than one value). This includes such conventional things as body weight, the rate of expression of a gene product, and willingness to behave altruistically towards a stranger. Other phenotypes include things like the frequency of an allele within a genotype (used in Chapter 1) and fitness itself. As used here, phenotype also includes any mathematical function of traits, so ϕ can be defined as, (basal metabolic rate) \times (body weight) or (leaf area)², for example. This last fact will be very useful in our discussion of stabilizing selection.

Equation 6.4 is a foundational result in what we might call the algebra of evolution. It is an exact characterization of a relationship that must hold between phenotype, fitness, transmission, and evolution. We can gain further insight from Equation 6.4 by using it as a starting point to derive special case models. Furthermore, because any evolutionary process must satisfy Equation 6.4, we can use it as a link between the different branches of evolutionary theory.

A Note on Regressions and Covariances

The way in which regressions and covariances are used in this discussion is somewhat different from what many people are familiar with, so it is important to understand the differences between our use of these terms and the standard application in statistics. If you come across a linear regression almost anywhere else in science, it will be part of an attempt to estimate some underlying but not directly measurable relationship. Someone suspects that there is a complicated causal relationship between two things, such as exposure to a certain chemical and cancer, but does not know enough about the processes involved to derive an equation relating the two. They therefore use regression (usually linear) to stand in for the true but unknown function.

When regressions are used as estimates in this way, we of course need to assess their significance in any particular study. Statistical tests of regressions are based on assumptions about the underlying distributions, so statistics texts often contain a section with a title such as "Assumptions of the Linear Regression," which lists such assumptions as linearity and homoscedasticity. Such assumptions are not relevant to our analysis.

The regressions and covariances between fitness and phenotype used in this chapter are not estimates of some unmeasured latent factor; they are exactly what matters in determining the dynamics of evolution. As a consequence, Equation 6.4 and equations derived from it make no assumptions about the shape of the joint distribution of fitness and phenotype. In this chapter, when we talk about the linear regression of fitness on phenotype, we are not asserting that the actual causal relationship between fitness and phenotype is in any way linear. Rather, we are using the fact that the linear regression is precisely the thing that actually matters in determining the effects of selection on the mean phenotype.

Most of the applications of Price's theorem that have appeared in the literature of evolution have been concerned with behavioral evolution (Hamilton 1975, Queller 1992, Frank 1999) or multilevel selection (Price 1972, Wade 1985). These specific applications are considered in Chapter 10. For the remainder of this chapter, we examine what Equation 6.4 and some equivalent results tell us about the process of evolution and the specific models that we have considered in Chapters 1 to 5. In subsequent chapters (especially Chapters 7 and 10), we use the results of this chapter to derive models for the evolution of systems that are not amenable to classical population genetics.

Generalized Marginal Fitness

We can see the connection between Price's theorem and the results from classical population genetics by generalizing the concept of marginal fitness. Recall from Chapter 1 that the marginal fitness of an allele, w^* , is the average fitness of that allele over all of the genotypes in which it is found. This makes intuitive sense for an allele, which is a discrete element that can be thought of as leaving descendants itself. In fact, we can do the same thing to any phenotypic trait that yields a marginal fitness of the trait rather than an individual. In addition to linking our current results to classical population genetics, this will be particularly useful in understanding game theory (see Chapter 9).

We denote the marginal fitness of phenotypic trait ϕ by w_ϕ^* , defined by:

$$w_\phi^* = \frac{1}{N} \sum_{i=1}^N \left(W_i \frac{\phi_i}{\bar{\phi}} \right) \quad (6.5)$$

In words, w_ϕ^* is a weighted mean fitness; weighted by the ratio of each individual's phenotype to the mean phenotype (if there is only one phenotypic trait under consideration, we sometimes drop the subscript and write simply w^*). Equation 6.5 is a generalization of Equations 1.3 and 1.43. To clarify this connection, we define ϕ as the frequency of allele A_1 within a genotype (as discussed in Chapter 1) and the mean phenotype, $\bar{\phi}$, as the frequency of the allele in the population. Defining n_{11} and n_{12} as the numbers of individuals with genotypes A_1A_1 and A_1A_2 , respectively, and assigning genotypic fitnesses w_{11} and w_{12} to these, we can rewrite Equation 6.5 as:

$$\begin{aligned} w_\phi^* &= \frac{1}{N} \frac{w_{11}}{p} \sum_{i=1}^{n_{11}} 1 + \frac{1}{N} \frac{w_{12}}{p} \sum_{i=1}^{n_{12}} \frac{1}{2} \\ &= \frac{w_{11}}{p} \frac{n_{11}}{N} + \frac{w_{12}}{p} \frac{1}{2} \frac{n_{12}}{N} \end{aligned} \quad (6.6)$$

The terms n_{11}/N and n_{12}/N are the frequencies of A_1A_1 and A_1A_2 genotypes, respectively. Under Hardy-Weinberg assumptions, $n_{11}/N = p^2$ and

$n_{12}/N = 2p(1 - p)$. Substituting these values into Equation 6.6 yields the marginal fitness of the A_1 allele, as given in Equation 1.3.

Equation 6.5 represents the generalization of marginal fitness which allows us to rewrite Price's theorems in terms of the marginal fitness of traits. Recalling that by definition $\text{cov}(x, y) = E(xy) - \bar{x} \cdot \bar{y}$, we can write

$$\text{cov}(w, \phi) = \frac{1}{n} \sum_i w_i \phi_i - \bar{w} \bar{\phi} \quad (6.7)$$

or, substituting Equation 6.5 into Equation 6.7:

$$\bar{\phi}(w_\phi^* - \bar{w}) = \text{cov}(w, \phi) \quad (6.8)$$

This is a generalization of Equation 1.45 from Chapter 1, and it provides a link between gene-based models of evolution (which can be written in terms of the left-hand side of Equation 6.8) and phenotype-based models (which can be written in terms of the right-hand side of Equation 6.8).

Equation 6.8 also clarifies the relationship between two different concepts of "fitness." Depending on what is being studied and the preferences of the author, fitness has variously been described as a property of an individual organism, a phenotypic trait, or an allele. This is generally not a practical problem since people use the kind of fitness that is compatible with their modeling approach, but it can lead to confusion regarding exactly where selection is operating. As used in our discussion, individuals (at whatever level selection is acting; discussed in Chapter 10) have fitness values, while traits of those individuals have marginal fitness values. In Chapter 1, we were concerned with selection acting on individuals, but we followed the frequencies of alleles, and therefore assigned marginal fitnesses to alleles and used these to construct our models.

Beyond clarifying what we mean by fitness, Equation 6.8 allows us to rewrite Price's theorem in a way that makes clear the connection between classical population genetics and Equation 6.4. Substituting Equation 6.8 into Equation 6.4 yields:

$$\Delta\bar{\phi} = \frac{1}{\bar{w}} [\bar{\phi}(w_\phi^* - \bar{w}) + E(w\bar{\delta})] \quad (6.9)$$

The form of Equation 6.9 should look immediately familiar. In our discussion of two-locus models in Chapter 2, we defined x_{ij} as the frequency of the A_iB_j haplotype and found the change in this frequency over a generation to be:

$$\Delta x_{ij} = \frac{1}{\bar{w}} [x_{ij}(w_{ij}^* - \bar{w}) \pm rDw_{1122}] \quad (6.10)$$

Here the marginal fitness, as defined in Equation 2.7, is another special case of Equation 6.5. The rDw_{1122} term measures the rate at which a particular haplotype is created or destroyed by recombination and thus takes the place of $E(w\bar{\delta})$ in Equation 6.9 (the \pm operator results from the fact that some haplotypes are created by recombination, while others are broken up; we insert + when $i \neq j$, and - when $i = j$).

Equation 6.9 also illuminates the case of fertility selection discussed in Chapter 1. Recall that with fertility selection we could not assume Hardy-Weinberg frequencies, so we had to follow the frequencies of genotypes across generations. Genotype frequencies changed as a result of selection and as a result of the reshuffling of alleles when individuals mate. This reshuffling of alleles ought to be captured by the $E(w\bar{\delta})$ term in Equation 6.9.

Considering just the A_1A_1 genotype, with frequency γ_{11} , this genotype is created in $\frac{1}{4}$ of all offspring from matings in which both parents are A_1A_2 and is destroyed whenever an A_1A_1 individual mates with an A_2A_2 individual (since all of their offspring will be heterozygous). Denoting the fertility of $A_iA_j \times A_kA_m$ matings as w_{ijkm} , and assuming that individuals mate at random and it does not matter which sex has which genotype, we conclude that the change due to the process of reproduction rather than selection is given by:

$$E(w\bar{\delta}) = \frac{1}{4} \gamma_{12}^2 w_{1212} - \gamma_{11} \gamma_{22} w_{1122} \quad (6.11)$$

Thus, the equation for change in the frequency of the A_1A_1 genotype can be written in the form of Equation 6.9 to yield:

$$\Delta\gamma_{11} = \frac{1}{\bar{w}} \left[\gamma_{11} (w_{11}^* - \bar{w}) + \frac{1}{4} \gamma_{12}^2 w_{1212} - \gamma_{11} \gamma_{22} w_{1122} \right] \quad (6.12)$$

The marginal fitness, w_{11}^* , is given by Equation 1.41. With a little bit of algebra you can confirm that Equation 6.12 is equivalent to Equation 1.40 in Chapter 1.

The examples of fertility selection and selection on two loci show that the $E(w\bar{\delta})$ term in Equations 6.4 and 6.9 is just as important as the covariance term. Whenever we are modeling the evolution of something over a generation, we need to consider both parts of Equations 6.4 and 6.9. However, it is sometimes enlightening to focus only on the covariance term, since this clarifies the evolutionary role played by differential survival and differential reproduction.

The Selection Differential

As the previous section shows, the second term on the right-hand side of Equation 6.4 (Price's theorem) plays an important role and cannot be ignored when we are interested in studying the complete process of evolution. It is informative, though, to briefly consider the covariance term from Equation

6.4 by itself, since this provides insight into the workings of selection and drift. In this section, we consider just the effects of selection by focusing on the selection differential, denoted S , which measures the change in mean phenotype due only to selection, prior to reproduction. We thus temporarily ignore the $E(w\delta)$ term in Equation 6.4. (Alternately, if the average phenotype of offspring is the same as that of their parents, then $E(w\delta) = 0$ and the selection differential gives the change over a generation.)

Robertson (1966) first presented the covariance formula for the selection differential. It is sometimes useful to rewrite the result in terms of the regression of fitness on phenotype, since this corresponds more closely to our intuitive notion of the strength of selection than the covariance does. Setting $E(w\delta) = 0$ in Equation 6.4, and recalling that $\text{cov}(x, y) = \beta_{y,x} \cdot \text{var}(x)$, we define the selection differential, S_ϕ , as:

$$S_\phi = \frac{1}{\bar{w}} \text{cov}(w, \phi) = \frac{1}{\bar{w}} \beta_{w,\phi} \text{var}(\phi) \quad (6.13)$$

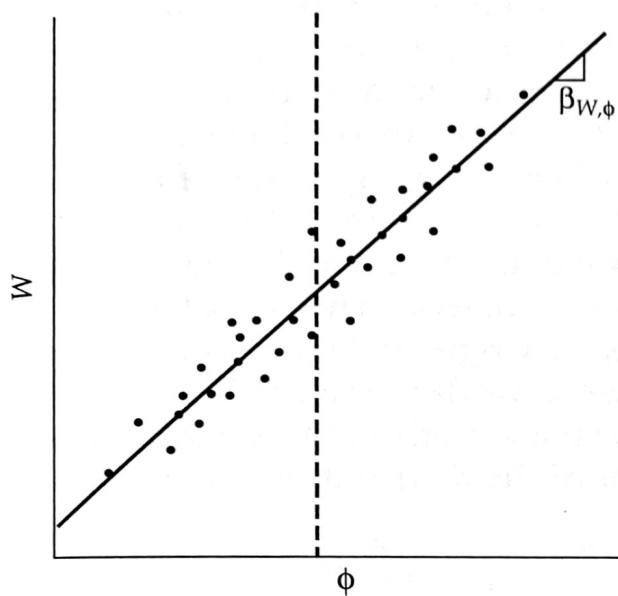
The far right formula in Equation 6.13 illustrates an important, and initially surprising, result. The regression term, $\beta_{w\phi}$, measures the linear relationship between fitness and phenotype, which leaves out quite a bit of information. The fact that the change in mean phenotype, resulting from selection, is determined completely by the variance in phenotype and the linear relationship between fitness and phenotype seems surprising because very different distributions could have the same phenotypic variance and regression slope (Figure 6.2).

The key to understanding this is to note that the regression of fitness on phenotype determines only the change in mean phenotype, not the change in the variance or any other moment of the distribution. Finding the changes in other moments is straightforward, though, because any mathematical function of a phenotypic trait can be thought of as just another trait. For example, we can substitute the function $(\phi - \bar{\phi})^2$ for ϕ in Equations 6.4 and 6.8. Doing so yields the change in the mean value of $(\phi - \bar{\phi})^2$. Recall that $\text{var}(\phi)$ is, by definition, the mean value of $(\phi - \bar{\phi})^2$. Thus we have just calculated the change in the variance of the phenotype distribution:

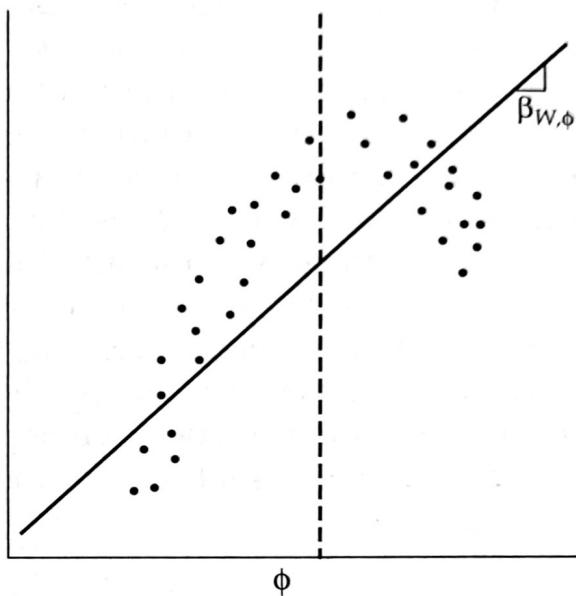
$$\Delta \text{var}(\phi) = \frac{1}{\bar{w}} \left\{ \text{cov} \left[w, (\phi - \bar{\phi})^2 \right] + E \left[w \bar{\delta} (\phi - \bar{\phi})^2 \right] \right\} \quad (6.14)$$

Figure 6.2 Regressions of fitness on phenotype and on the squared deviation from mean phenotype, and the corresponding changes in the distribution of phenotypes, for two different cases. (C) and (E) correspond to the same joint distribution of fitness and phenotype shown in (A). (D) and (F) correspond to the distribution shown in (B).

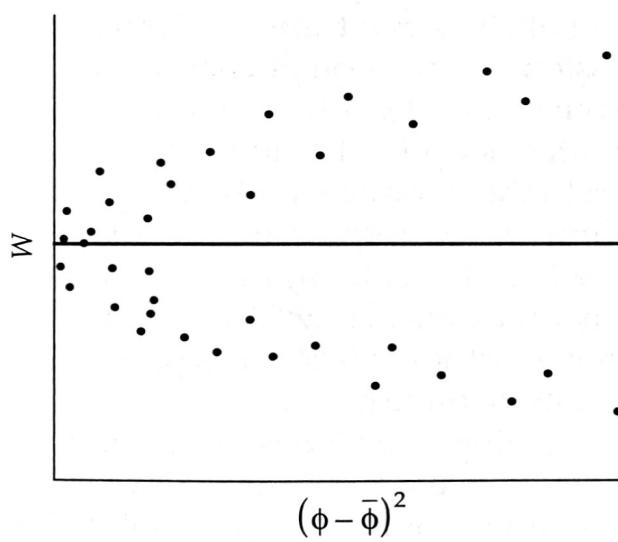
(A)



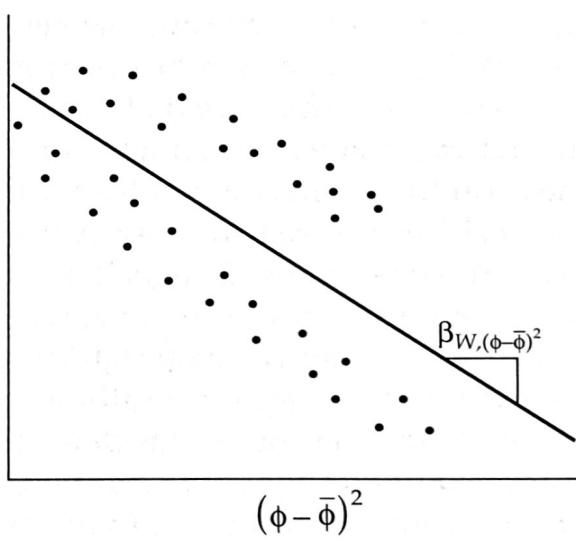
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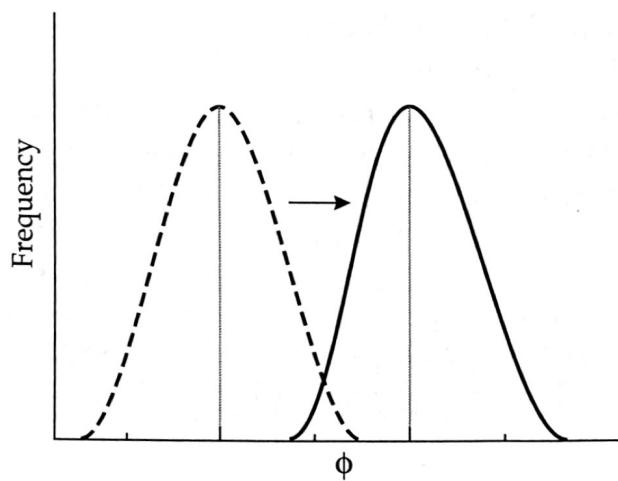
(C)



(D)



(E)



(F)

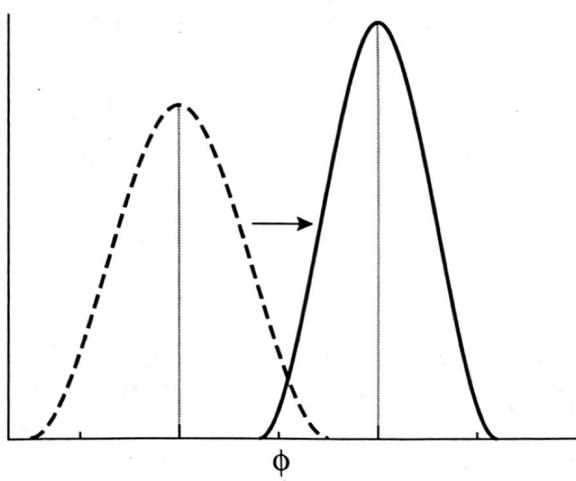


Figure 6.2 illustrates how the relationship between fitness and phenotype influences the change in different moments of the phenotype distribution (see the discussion of moments in Appendix B). In Figure 6.2A, the slope of the regression of fitness on phenotype is positive, so the mean of the phenotype distribution changes, but the regression of fitness on $(\phi - \bar{\phi})^2$ has zero slope, so there is no change in the variance. The slope of the regression of fitness on phenotype in Figure 6.2B is the same as that in Figure 6.2A, so the mean changes by the same amount. But because of the shape of the joint distribution of w and ϕ , the regression of fitness on $(\phi - \bar{\phi})^2$ is also nonzero. Figure 6.2D shows that the variance as well as the mean changes. In Figure 6.2E and F, the descendant distribution is slightly skewed towards the right. This is because in each case, there is a positive slope to the regression of fitness on $(\phi - \bar{\phi})^3$ (not shown), meaning that the third moment of the distribution increases, producing the *skewness*.

Directional and Stabilizing Selection

Figure 6.2 illustrates another important point, that it is possible to have both directional and stabilizing selection acting at the same time. By **directional selection**, we mean a nonzero linear regression of fitness on phenotype, which (all else held equal) leads to a change in the mean phenotype in the population. **Stabilizing selection** refers to a negative slope of the regression of fitness on $(\phi - \bar{\phi})^2$. This results in a reduction in the variance in phenotypic values within the population. A positive slope of the regression of fitness on $(\phi - \bar{\phi})^2$ constitutes **disruptive selection**, which leads to an increase in phenotypic variance. (As always, when we say that a particular kind of selection is acting, we tacitly mean that the regression of fitness on phenotype is a consequence of some causal influence of phenotype on fitness.)

Note that although this definition of stabilizing selection is widely used in evolutionary genetics (Lande and Arnold 1983, Rice 1998), it is somewhat different from the definition found in most textbooks, which defines stabilizing selection as selection favoring phenotypes near the population mean and often treats it as being incompatible with directional selection. In fact, not only can stabilizing selection coexist with directional selection, its strength is largely independent of the strength of directional selection.

In Figure 6.2B, the phenotype with the highest fitness is intermediate, so we can still think of stabilizing selection in this case as being selection against extreme phenotypes. However, this interpretation breaks down in the examples shown in Figure 6.3A, where the most fit individuals are those with the highest phenotypic value. When we plot fitness against $(\phi - \bar{\phi})^2$ (see Figure 6.3C), we find a negative regression slope, meaning that selection is also reducing the phenotypic variance of the population. Figure 6.3B and D show the corresponding case of disruptive selection. Here, the strength of direc-

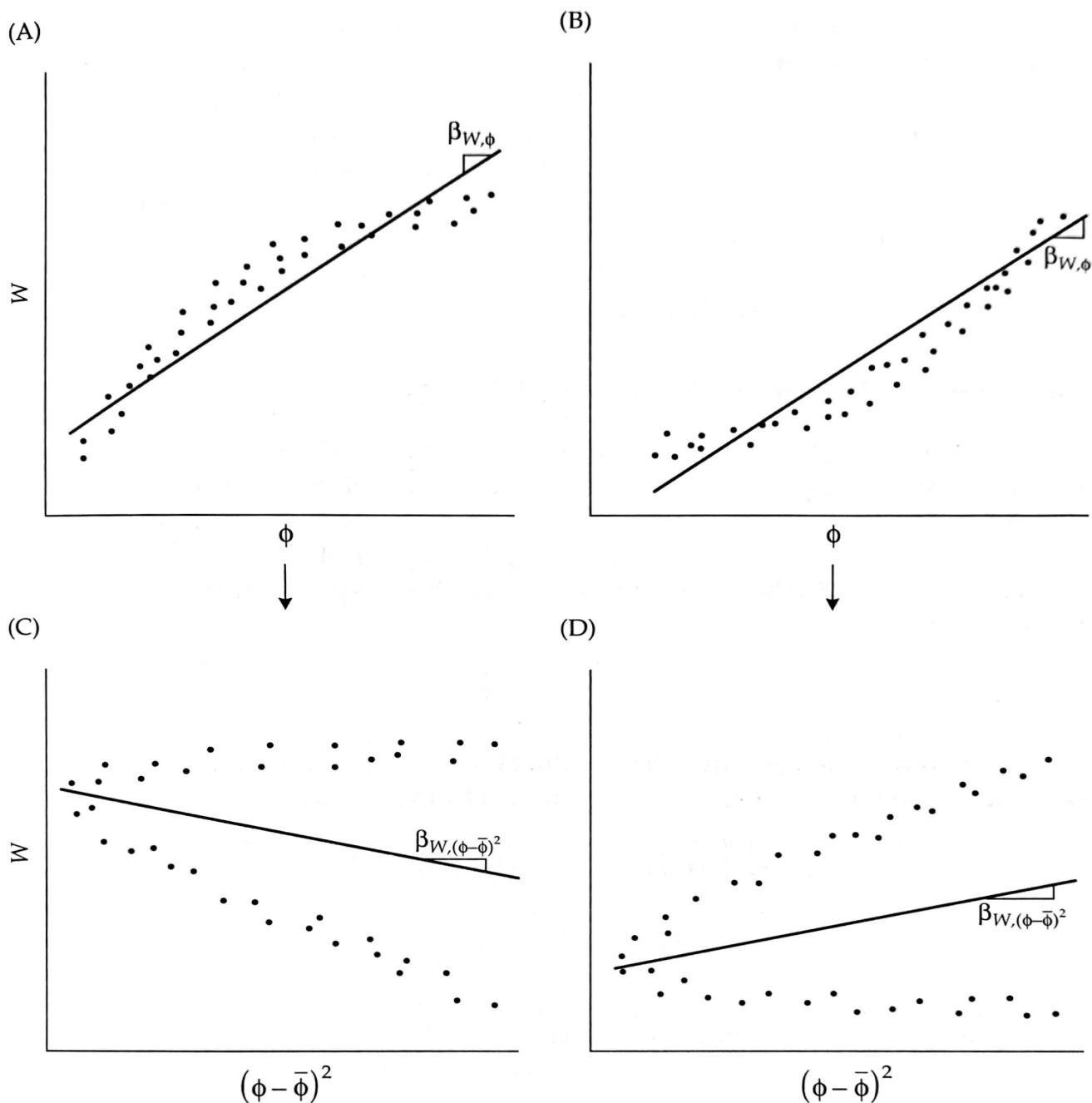


Figure 6.3 (A) The regression of fitness on phenotype for a case in which there is simultaneous directional and stabilizing selection. Stabilizing selection can be seen in (C), which plots fitness against $(\phi - \bar{\phi})^2$ for the same data as shown in (A). (B) and (D) show corresponding graphs for a case of disruptive selection.

tional selection is the same as in Figure 6.3A, but selection in this case also tends to increase the phenotypic variance.

The mean and variance represent the first two moments of a univariate distribution (see Appendix B). Thus, we can think of directional selection as acting to change the first moment of the phenotype distribution and stabiliz-

ing or disruptive selection as acting to change the second moment. Though we do not have names for other possible cases, it is easy to see that selection could act to change any moment of the phenotype distribution. For example, the third moment, which is one measure of the asymmetry of the distribution (skewness) will change if the regression of fitness on $(\phi - \bar{\phi})^3$ is nonzero. Though this is rarely discussed, it will generally be the case whenever there is also directional selection. Higher moments of the phenotype distribution will become particularly important when we study the evolution of developmental interactions in Chapter 8.

Relationship between Parents and Offspring

We now turn to the second term on the right-hand side of Equation 6.4. Because the term $E(w\bar{\delta})$ captures the evolutionary effects of processes acting during reproduction, we can approach it by specifying the relationship between mean offspring phenotype and parent phenotype. For the most general case, ϕ_i^o denotes the mean phenotype of the offspring of parent i (Figure 6.4A), thus:

$$\phi_i^o = \phi_i + \bar{\delta}_i \quad (6.15)$$

We can expand the second term on the right-hand side of Equation 6.4 and rewrite it as a covariance, using the fact that $E(xy) = \text{cov}(x, y) + E(x)E(y)$:

$$\begin{aligned} \Delta\bar{\phi} &= \frac{1}{W} [\text{cov}(W, \phi) + \text{cov}(W, \bar{\delta}) + E(W)E(\bar{\delta})] \\ &= \frac{1}{W} \text{cov}(W, \phi + \bar{\delta}) + E(\bar{\delta}) \end{aligned} \quad (6.16)$$

Substituting from Equation 6.9 yields:

$$\Delta\bar{\phi} = \frac{1}{W} \text{cov}(W, \phi^o) + \bar{\delta}_T \quad (6.17)$$

where:

$$\bar{\delta}_T = \bar{\phi}^o - \bar{\phi} \quad (6.18)$$

Thus, what ultimately matters in evolution is the covariance between the fitness of parents and the phenotype of their offspring. This combines the effects of selection, drift, and transmission, though a population-wide bias in transmission is captured by the $\bar{\delta}_T$ term. Note that $\bar{\delta}_T$ is the change in the mean population phenotype that would result from the process of reproduction alone. Unlike the analogous term in Equation 6.4, $\bar{\delta}_T$ is not an

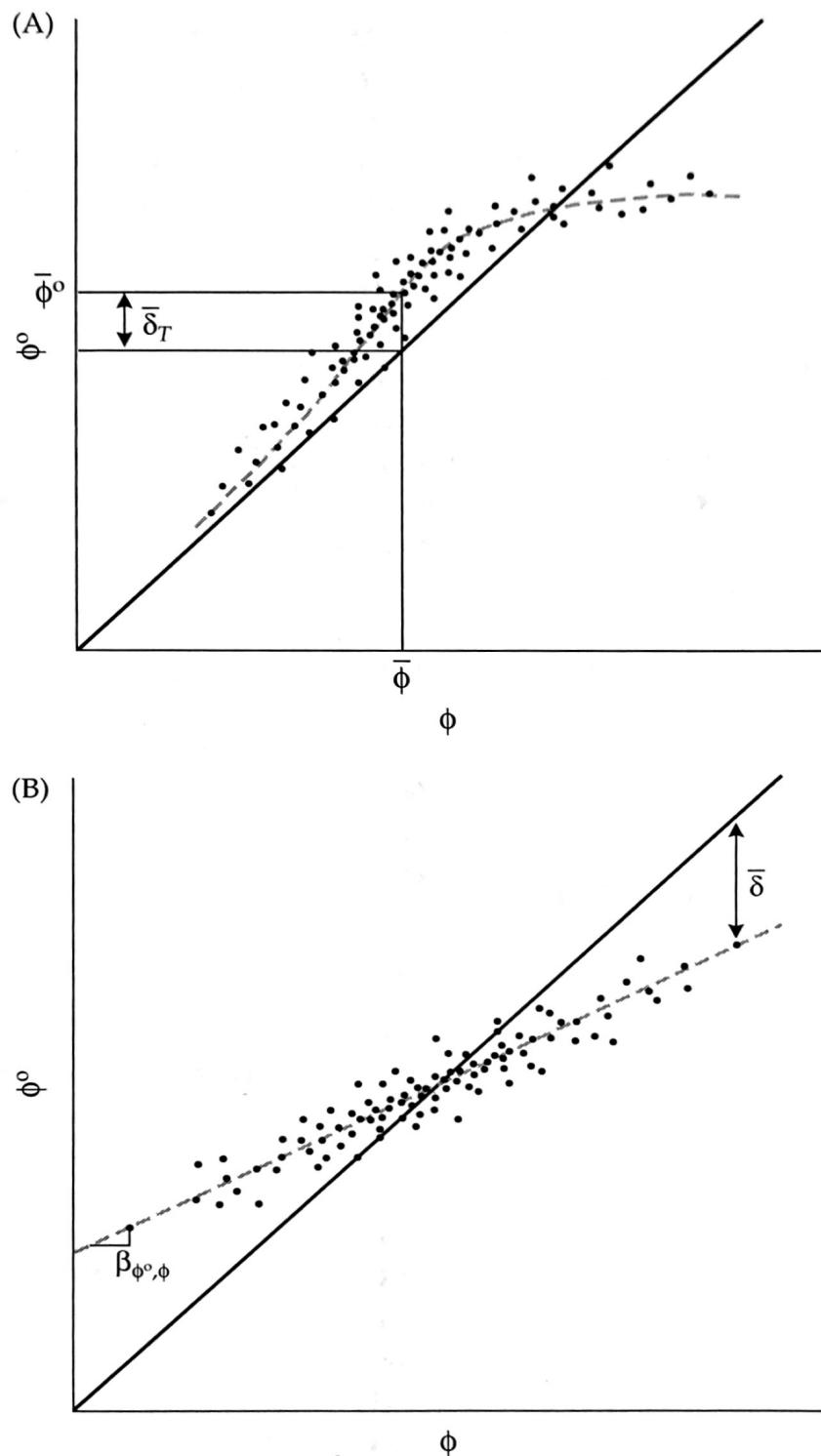


Figure 6.4 Plots of offspring phenotype against parent phenotype. (A) A general, nonlinear case illustrating the terminology used in Equation 6.17. (B) A linear relationship between offspring and parents, corresponding to Equation 6.22.

average value weighted by fitness, it is simply the difference that we would see between the mean phenotype of all individuals in the parent generation and the mean phenotype in the offspring generation in the absence of selection or drift (Figure 6.4).

Equations 6.4, 6.9, and 6.17 are mathematically equivalent; they are different ways of writing the same thing. These different formulations are useful for different applications, though. We saw earlier that Equation 6.9 is the natural form to use when discussing population genetics. In Chapter 7, Equation 6.17 will emerge as the most useful form for deriving models in quantitative genetics.

Breeder's Equation

As a preview of the application of these equations to quantitative genetics, consider the simple case in which the relationship between offspring phenotype and parental phenotype is described by a linear regression with random noise (see Figure 6.4B). In this case, we can write the mean phenotype of the offspring of parent i as:

$$\phi_i^o = \bar{\phi} + \beta_{\phi^o, \phi} (\phi_i - \bar{\phi}) \quad (6.19)$$

Substituting Equation 6.19 into Equation 6.17, setting $\bar{\delta}_T = 0$, and noting that for any constant, c , $\text{cov}(x, c) = 0$, we find

$$\begin{aligned} \Delta(\bar{\phi}) &= \frac{1}{w} \text{cov}(w, \beta_{\phi^o, \phi} \phi) \\ &= \frac{1}{w} \beta_{\phi^o, \phi} \text{cov}(w, \phi) \end{aligned} \quad (6.20)$$

Now we can apply the fact that $\text{cov}(x, y) = \beta_{y,x} \text{var}(x)$ and take apart the covariance term in Equation 6.20:

$$\Delta(\bar{\phi}) = \frac{1}{w} \beta_{\phi^o, \phi} \beta_{w, \phi} \text{var}(\phi) \quad (6.21)$$

The regression of mean offspring phenotype on parent phenotype can now be combined with the variance in parental phenotype into a new covariance term:

$$\Delta(\bar{\phi}) = \frac{1}{w} \beta_{w, \phi} \text{cov}(\phi^o, \phi) \quad (6.22)$$

We will see in Chapter 7 that the covariance between a trait in parents and the mean value of that trait in their offspring is the same as the additive genetic variance for that trait. (More precisely, additive genetic variance is an estimator of this covariance, but it is only meaningful in an evolutionary sense to the extent that it accurately predicts the parent–offspring covariance.) We can see that Equation 6.22 is one form of the **breeder's equation** from quantitative genetics. In Chapter 7, we derive the multivariate equivalent of Equa-

tion 6.22, which includes multiple phenotypic traits and is a powerful tool for studying phenotypic evolution.

Fisher's Fundamental Theorem

As mentioned in the discussion of the concept of phenotype earlier in this chapter, a phenotype can be any measurable attribute of an individual. Since fitness is such an attribute, we can substitute the fitness of offspring for ϕ^o in Equation 6.17 to derive the change in mean fitness over a generation:

$$\Delta \bar{W} = \frac{\text{cov}(W, W^o)}{\bar{W}} + \bar{\delta}_T(W) \quad (6.23)$$

Recalling the equivalence of parent–offspring covariance and additive genetic variance mentioned in the previous section, we see that Equation 6.23 is a statement of Fisher's fundamental theorem of natural selection (Frank 1995).

As discussed in Chapter 1, Fisher felt that this equation held great significance for the understanding of evolution. The fact that we can derive it from Price's theorem with no further assumptions means that whatever its significance, Fisher's fundamental theorem is in fact a general theorem that applies to any evolving system.

Generalized Drift

Equations 6.4 and 6.17 tell us exactly what the evolutionary consequences of covariation between fitness and phenotype will be, but they say nothing about why such a covariance would exist in the first place. In our discussion so far, we have assumed that covariance between fitness and phenotype is a consequence of some causal effect of phenotype on fitness (i.e., selection), but this need not be the case. As we discussed briefly in Chapter 3, in a finite population, a nonzero covariance between fitness and phenotype could result simply from random variation in survivorship or reproductive success.

Most models of genetic drift assume that the only source of variation is in the sampling of alleles during reproduction (see Chapter 3). In this section, we use Equation 6.4 to derive more general results that allow us to incorporate different sources of random variation.

When we say that there is selection acting on some phenotypic trait, ϕ , we mean that the value of that trait has some causal influence on fitness. It will almost always be the case, though, that other factors independent of ϕ also influence fitness. As a result, there will be a distribution of fitness values associated with each value of ϕ (Figure 6.5). In an infinitely large population we expect that the effect of ϕ on fitness will manifest as a nonzero regression of fitness on some function of ϕ . In a finite population, though, we do not see the

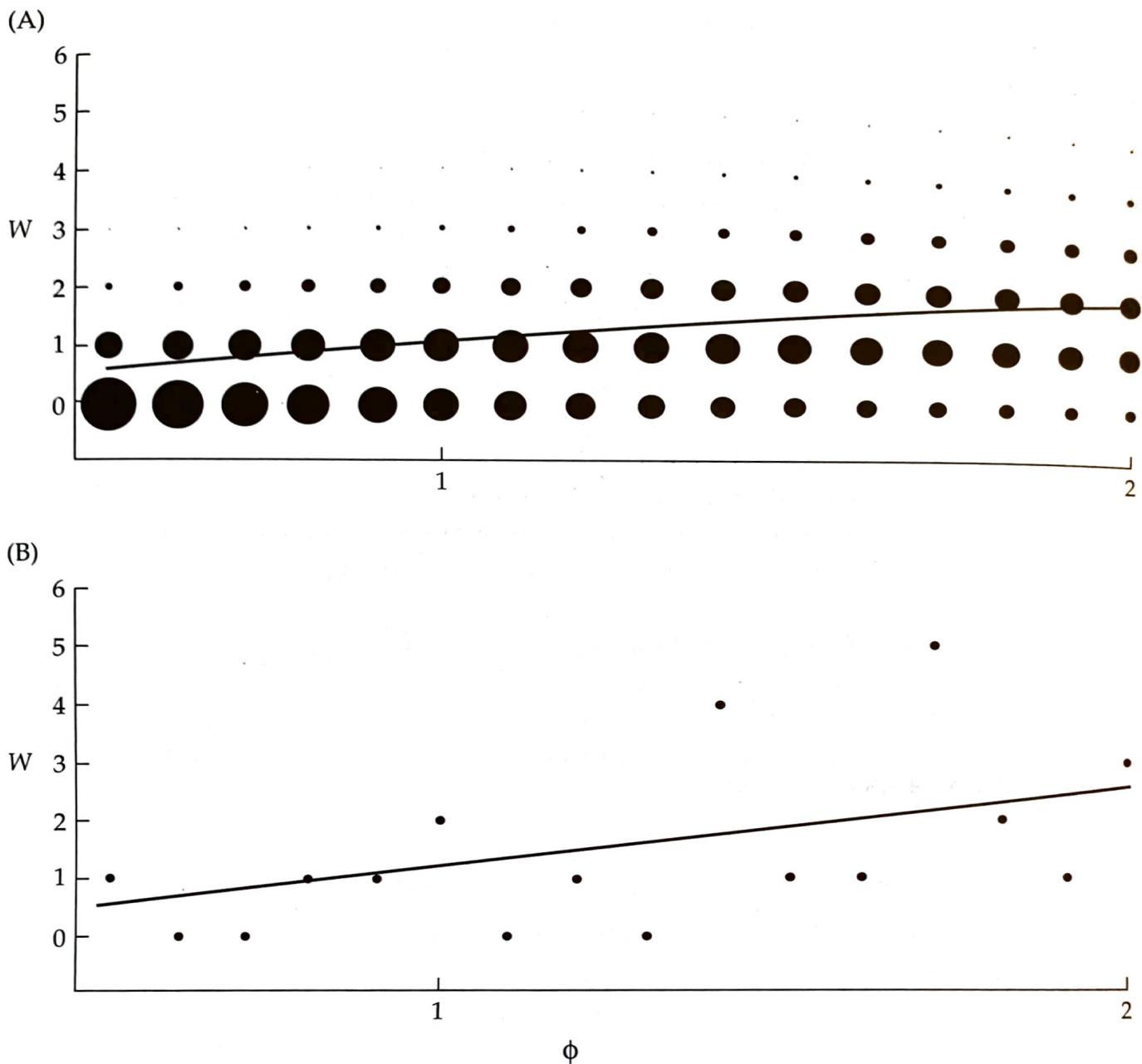


Figure 6.5 (A) The distributions of potential fitness values for different phenotypes in a case of directional selection on the phenotype. (B) A sample of points, drawn from the distribution in (A), corresponding to the actual fitnesses of a finite number of individuals.

entire distribution of fitness values associated with each phenotype present in the population, but rather see a sample of a finite number of points from each distribution.

To make this clear, in Figure 6.5A, individuals with a phenotypic value of $\phi = 1$ have an expected fitness of 1, but this is just the mean value of a distribution of possible fitness values, which in Figure 6.5A is a Poisson distribution (see Chapter 4). If there are actually only two individuals in the population with phenotype $\phi = 1$, then their fitness values will be two points randomly chosen from the fitness distribution associated with their phenotype.

The actual joint distribution of fitness and phenotype in a population of size N is a set of N points with coordinates (ϕ, w) . The ϕ values of these points are just the phenotypic values of all of the parents, and the w values are chosen at random from the fitness distribution associated with the corresponding ϕ value. Random variation in the w values produce random variation in the covariance between fitness and phenotype, and this will manifest as drift.

There are actually two potential sources of random variation that could influence evolution: variation in the covariance between parental fitness and parental phenotype, and variation in the relation between offspring phenotype and parent phenotype. We first consider variation in the covariance between parental fitness and parental phenotype, then generalize this to include both sources of variation.

As in Chapter 3, we are not concerned with the expected covariance between fitness and phenotype, but rather with the variance in this covariance since this gives us the variance in phenotypic change over a generation. Using the definition of covariance we can write this as:

$$\text{var}\left[\frac{\text{cov}(w, \phi)}{\bar{w}}\right] = \text{var}\left[\frac{1}{\bar{w}N} \sum_{i=1}^N (w_i - \bar{w})(\phi_i - \bar{\phi})\right] \quad (6.24)$$

Using the fact that $\text{var}(x) = E(x^2) - [E(x)]^2$, we can rewrite the right-hand side of Equation 6.24 as:

$$\begin{aligned} & E\left[\frac{1}{\bar{w}^2 N^2} \sum_i \sum_j (w_i - \bar{w})(w_j - \bar{w})(\phi_i - \bar{\phi})(\phi_j - \bar{\phi})\right] \\ & - \left\{ E\left[\frac{1}{\bar{w}N} \sum_i (w_i - \bar{w})(\phi_i - \bar{\phi})\right] \right\}^2 \end{aligned} \quad (6.25)$$

In dealing with Equation 6.25, it is important to understand exactly what we are taking the expected values of. The phenotypes of the parents are fixed, so the random variables that we need to find the expected values for are the w_i terms. As in our derivation of variance effective population size in Chapter 4, it is important here to be careful about when we take the expected values, since $E(w_i w_j)$ may not be the same as $E(w_i)E(w_j)$. We thus need to first multiply out the terms in Equation 6.25 that contain w_i , then take the expected values to get:

$$\begin{aligned} & \frac{1}{N^2} \sum_i \sum_j [E(w_i w_j) - E(w_i)\bar{w} - E(w_j)\bar{w} + \bar{w}^2](\phi_i - \bar{\phi})(\phi_j - \bar{\phi}) \\ & - \left\{ \frac{1}{N} \sum_i [E(w_i) - \bar{w}] (\phi_i - \bar{\phi}) \right\}^2 \end{aligned} \quad (6.26)$$

We define $\hat{w}_i = E(w_i)$ as the expected fitness, prior to actual reproduction, of individual i . Noting that $E(w_i w_j) = \text{cov}(w_i, w_j) + \hat{w}_i \hat{w}_j$, we can rewrite Equation 6.26 as:

$$(1) \quad \text{var}\left[\frac{\text{cov}(w, \phi)}{\bar{w}}\right] = \frac{1}{\bar{w}^2 N^2} \sum_i \sum_j \left\{ [\text{cov}(w_i, w_j) + \hat{w}_i \hat{w}_j - \hat{w}_i \bar{w} - \hat{w}_j \bar{w} + \bar{w}^2] (\phi_i - \bar{\phi})(\phi_j - \bar{\phi}) \right\}$$

$$(2) \quad - \left\{ \frac{1}{\bar{w}N} \sum_i (\hat{w}_i - \bar{w})(\phi_i - \bar{\phi}) \right\}^2 \quad (6.27)$$

The two parts of Equation 6.27 are numbered for reference in the following discussion.

We can divide part (1) of Equation 6.27 into two parts by separating the cases in which $i = j$, which will be a single summation because there are only N such cases, from the cases in which $i \neq j$. Recalling that $\text{cov}(x, x) = \text{var}(x)$, we rewrite part (1) of Equation 6.27 as:

$$\begin{aligned} & \frac{1}{\bar{w}^2 N^2} \sum_i \left\{ [\text{var}(w_i) + (\hat{w}_i - \bar{w})^2] (\phi_i - \bar{\phi})^2 \right\} \\ & + \frac{1}{\bar{w}^2 N^2} \sum_i \sum_{j \neq i} \left\{ [\text{cov}(w_i, w_{j \neq i}) + (\hat{w}_i - \bar{w})(\hat{w}_j - \bar{w})] (\phi_i - \bar{\phi})(\phi_j - \bar{\phi}) \right\} \end{aligned} \quad (6.28)$$

As for part (2) of Equation 6.27, squaring the summation and then partitioning the resulting double summation as we did in Equation 6.28 yields:

$$\begin{aligned} & \frac{1}{\bar{w}^2 N^2} \sum_i [(\hat{w}_i - \bar{w})^2 (\phi_i - \bar{\phi})^2] \\ & + \frac{1}{\bar{w}^2 N^2} \sum_i \sum_{j \neq i} [(\hat{w}_i - \bar{w})(\hat{w}_j - \bar{w})(\phi_i - \bar{\phi})(\phi_j - \bar{\phi})] \end{aligned} \quad (6.29)$$

If we were to fix the size of the population in the next generation, then the covariance between the fitness of one individual and the fitness of another would be negative. It is more biologically reasonable, though, to assume that while the fitness of an individual is influenced by the distribution of parent phenotypes and the overall population size, the actual fitness of one individual is independent of the actual fitness of others. This allows for the possibility that in any given generation many individuals might get lucky (or unlucky) and the population size would change accordingly. (Note that this does not preclude density dependence, since the increased population size would influence the mean fitness in the next generation.) We thus can set $\text{cov}(w_i, w_j) = 0$ for $j \neq i$ in Equation 6.28.

Subtracting Equation 6.29 from Equation 6.28 according to Equation 6.27 now yields:

$$\text{var}\left[\frac{\text{cov}(w, \phi)}{\bar{w}}\right] = \frac{1}{\bar{w}^2 N^2} \sum_{i=1}^N \left[\text{var}(w_i) (\phi_i - \bar{\phi})^2 \right] \quad (6.30)$$

Or, denoting $\text{cov}(w, \phi)/\bar{w}$ by S_ϕ and defining $\text{var}_i(w)$ as the variance in the fitness distribution of an individual (as opposed to the variance in fitness for the entire population), we have:

$$\text{var}(S_\phi) = \frac{1}{N \bar{w}^2} E \left[\text{var}_i(w) (\phi - \bar{\phi})^2 \right] \quad (6.31)$$

If the variance in potential fitness of individuals, $\text{var}_i(w)$, is a constant, then Equation 6.31 becomes:

$$\text{var}(S_\phi) = \frac{\text{var}_i(w) \text{var}(\phi)}{N \bar{w}^2} \quad (6.32)$$

To see how Equation 6.32 relates to our discussion of genetic drift in Chapter 3, consider the case shown in Figure 3.3B, where phenotype corresponds to allele type, and can be quantified by designating $\phi = 1$ for allele A_1 and $\phi = 0$ for allele A_2 . In the absence of mutation, the descendants of an allele are exact copies of their parent, so $E(w\bar{\delta}) = 0$ and Equation 6.32 will give us the actual change over a generation. If the alleles are selectively neutral and the population is not growing or shrinking, then the expected fitness of each allelic type is 1, so $\bar{w} = 1$. If, as we expect for neutral alleles, the distribution of family sizes is a Poisson distribution (see Chapter 4), then the variance is equal to the mean, so $\text{var}_i(w) = 1$. Equation 6.32 therefore yields:

$$\text{var}(\Delta\bar{\phi}) = \frac{\text{var}(\phi)}{N} \quad (6.33)$$

To put this result in the language of Chapter 3, we define p as the frequency of the A_1 allele. The phenotype will now be 1 with probability p and 0 with probability $(1-p)$, and the mean phenotypic value will be p . Given this, the phenotypic variance is:

$$\begin{aligned} \text{var}(\phi) &= p(1-p)^2 + (1-p)(0-p)^2 \\ &= p - 2p^2 + p^3 + p^2 - p^3 \\ &= p(1-p) \end{aligned} \quad (6.34)$$

Finally, note that the value of N in Equation 6.33 is the total number of alleles. In Chapter 3 we defined N as the number of diploid individuals, so under

that notation the total number of alleles is $2N$. Thus, under the standard notation for genetic drift (see Chapter 3), Equation 6.33 becomes:

$$\text{var}(\Delta p) = \frac{p(1-p)}{2N} \quad (6.35)$$

This is identical to Equations 3.3 and 5.25, though here we derived it without making any appeal to the binomial distribution. If the distribution of family sizes is not a Poisson distribution, then we need only multiply the right-hand side of Equation 6.35 by $\text{var}_i(w)$.

Equation 6.31 gives us a very general result that we can use to study drift in a wide variety of systems. It also illustrates some general principles of stochastic evolution. As the discussion in Chapter 3 leads us to expect, the variance in phenotypic change is inversely proportional to population size. It is also inversely proportional to the square of mean population fitness, which we saw in Chapter 1 is a measure of population growth rate. (This term was tacitly assumed to be equal to 1 in Chapter 3, since we assumed fixed population size.)

The critical new term in Equation 6.31 is $\text{var}_i(w)$, the variance in fitness associated with an individual's phenotype. This never came up in Chapter 3 because we were tacitly assuming that it was the same as the mean fitness (due to the implicit Poisson assumption; see Chapter 4). The classical population genetic theory of drift is based on a very specific model of reproduction, with the values of terms like $\text{var}_i(w)$ determined almost before we begin, so we often fail to see that we are making assumptions about them.

Finally, note that the $\text{var}_i(w)$ term in Equation 6.31 is multiplied by the corresponding value of $(\phi - \bar{\phi})^2$. This means that the variance in fitness associated with phenotypes that lie far from the mean have a particularly large impact on stochastic evolution.

The derivation that we just followed considered only random variation in fitness. There is also, of course, random variation in the phenotype of an individual's offspring. This is not a serious issue when the units that we are studying are alleles, since mutation is the main source of variation between parent alleles and their descendants, and allelic mutation rates are generally small. When we are interested in an arbitrary phenotypic trait, though, there is often substantial variation introduced by the process of reproduction. In order to study this, we need to find the variance of Equation 6.17, which involves the covariance between the fitness of parents and the mean phenotype of their offspring.

Recalling that ϕ_i^0 is the expected phenotype of the offspring of parent i , and $\delta_{i,j}$ is the difference between the phenotype of offspring j from parent i and the phenotype of i , we can follow the approach that we used to solve Equation 6.24, only substituting $\phi_i + \delta_{i,j}$ for ϕ_i . Doing this and being careful to take the expected value with respect to $\delta_{i,j}$ as well as with respect to w_i yields:

$$\text{var}(\Delta\bar{\phi}) = \frac{1}{\bar{w}^2 N^2} \left[\sum_i \text{var}(w_i) \text{var}(\delta_i) + \text{var}(w_i) (\phi^o - \bar{\phi}^o)^2 + \text{var}(\delta_i) (\hat{w}_i - \bar{w})^2 \right] + \text{var}(\bar{\delta}_T) \quad (6.36)$$

Converting the summations into expected values by bringing $1/N$ inside the brackets in Equation 6.36 yields:

$$\text{var}(\Delta\bar{\phi}) = \frac{E[\text{var}_i(w)\text{var}_i(\delta)] + E[\text{var}_i(w)(\phi^o - \bar{\phi}^o)^2] + E[\text{var}_i(\phi^o)(\hat{w} - \bar{w})^2]}{N\bar{w}^2} + \text{var}(\bar{\delta}_T) \quad (6.37)$$

The new term, $\text{var}_i(\delta)$, is the variance in the distribution of offspring phenotypes associated with parent i , analogous to $\text{var}_i(w)$. Equation 6.37 includes all sources of variation that could influence evolution.

If $\text{var}_i(w)$ and $\text{var}_i(\delta)$ are constants, meaning that all individuals have the same variance in fitness and offspring phenotype, then Equation 6.37 simplifies to:

$$\text{var}(\Delta\bar{\phi}) = \frac{\text{var}_i(w)[\text{var}_i(\delta) + \text{var}(\phi^o)] + \text{var}_i(\delta)\text{var}(\hat{w})}{N\bar{w}^2} \quad (6.38)$$

We can further simplify this, with no added assumptions, by noting that if $\text{var}_i(\delta)$ is a constant, then it is independent of ϕ^o , so we can write:

$$\text{var}(\Delta\phi) = \frac{\text{var}_i(w)\text{var}(\phi^o + \delta) + \text{var}_i(\delta)\text{var}(\hat{w})}{N\bar{w}^2} \quad (6.39)$$

Here, $\text{var}(\phi^o + \delta)$ is the total variance in the expected offspring distribution.

Putting It All Together

We have seen in this chapter that a single mathematical principle, represented variously but equivalently by Equations 6.4, 6.9, and 6.17, unites most of the material we covered in the first five chapters of this book. This includes selection models that focused on alleles (see Equation 1.7), genotypes (see Equations 1.40 and 6.12), and haplotypes (see Equation 6.10), as well as the drift equation (see Equation 3.3) that was the foundation of our treatment of drift in Chapter 5.

Historically, all of these results were arrived at separately, roughly as we derived them in earlier chapters. Being able to derive central results concerning both selection and drift from the same basic principles is particularly interesting, since the traditional approaches to these subjects look very different. Why was the fundamental unity of these processes not apparent until fairly recently?

The answer to this question takes us back to the distinction between different kinds of theories discussed at the start of this chapter. In the model-building approach to theory, the first step in constructing a model is to decide on a set of simplifying assumptions that will hopefully make the resulting model tractable while still describing the processes of interest. Though this is a powerful and successful approach, it can sometimes hide underlying unity. Classical models of selection and drift provide a good illustration of this fact.

Since selection involves a deterministic effect of phenotype on fitness, it seems reasonable that a good place to start building selection models is to use deterministic equations that assign a single fitness value to each phenotype (which includes genotype). To avoid having to deal with stochastic variation (which is not what we are currently trying to model), we make the assumption of effectively infinite population size, hoping that this will be a reasonably good approximation. As good model builders, we thus make assumptions at the outset that lead us, down the line, to using mathematical techniques that are incompatible with drift.

The same thing happens when we set out to model drift. There are so many sources of reproductive variation that we cannot hope to understand the details of all of them. As good model builders, we thus pick one source of variation that is fairly well characterized, the random sampling of alleles during reproduction. This immediately suggests a set of mathematical techniques, based on sampling theory, that form the basis of our future research. If these methods preclude the study of selection, this is okay since we are not currently modeling selection.

This should not be taken as a criticism of model building; the track record of discoveries made by these methods, in evolutionary biology and elsewhere, is the only recommendation that they need. However, it does suggest the value of sometimes also following a different approach. In deriving Equation 6.4, Price started with only a basic description of the kinds of quantities involved in evolution: phenotypes of parents, phenotypes of their offspring, and numbers of offspring. He then asked what basic mathematical relations must hold between these basic pieces, without imposing any further restrictions.

The resulting equation initially seems so simple that it is hard to see how it relates to actual evolutionary questions. When we look closely at this result, though, we see that it shows an underlying unity that was obscured by our special case models. It also provides a foundation on which to build new models, a fact that we will use in the following chapters of this book.

Not all fields of science have the kind of foundational analytical results that we have used in this chapter. In many subjects, building special case models is the only approach to theory. It is hardly surprising, though, that evolutionary biology has such foundational theories. Since the initial work of Darwin and Wallace, it has seemed to many people that at its core evolution has simple and universal principles. What we have seen in this chapter is that phrasing these universal principles mathematically need not narrow them, but rather allows us to see their full significance.