

CHAPTER 6

Small Populations and Genetic Drift



Land snail, Example 6.2

The race is not always to the swift, nor the battle to the strong, for time and chance happens to us all.

(**Ecclesiastes 9:11**)

. . . the conservationist is faced with the ultimate sampling problem—how to preserve genetic variability and evolutionary flexibility in the face of diminishing space and with very limited economic resources. Inevitably we are concerned with the genetics and evolution of small populations, and with establishing practical guidelines for the practicing conservation biologist.

(**Otto H. Frankel & Michael E. Soulé 1981, p. 31**)

Genetic change will not occur in populations if all the assumptions of the Hardy–Weinberg (HW) equilibrium are met (Section 5.1). However, these assumptions are not met in natural populations, and genetic changes result. In this and the next several chapters, we will see what happens when the assumptions of HW equilibrium are violated. In this chapter, we will examine what happens when we violate the assumption of infinite population size. That is, what is the effect on **allele** and **genotype** frequencies when population size (N) is finite?

All natural populations are finite so **genetic drift** will occur in all natural populations, even large ones. For example, consider a new mutation that increases fitness which occurs in an extremely large population of insects that numbers in the millions. Whether or not the single copy of this advantageous mutation is lost by chance from this population will be determined primarily by the sampling process that determines what alleles are transmitted to the next generation. For example, if the individual with the mutation does not reproduce, the new allele will

be lost immediately. And, even if the individual with the mutation produces two progeny, there is a 25% chance, based on **Mendelian segregation**, that the mutation will be lost. Thus, the fate of a rare allele in an extremely large population will be determined primarily by genetic drift.

Genetic drift is the primary force bringing about allele frequency changes throughout the genome over time. This has been confirmed by genomic approaches that now allow evaluating the relative importance of genetic drift in natural populations by examining allele frequency changes at thousands of **single nucleotide polymorphism (SNP)** loci over time. Chen et al. (2019) used pedigrees in a long-studied natural population of Florida scrub jay to test the relative roles of different evolutionary processes in shaping patterns of genetic change at over 15,000 SNP loci. They concluded that genetic drift is the predominant evolutionary force causing allele frequency change. Funk et al. (2016) and Perrier et al. (2017) came to a similar conclusion in their studies of the island fox and lake trout, respectively.

Understanding genetic drift and its effects is extremely important for conservation. Fragmentation and isolation due to habitat loss and modification have reduced the population size of many species of plants and animals throughout the world. We will see in future chapters how genetic drift is expected to affect genetic variation in these populations. More importantly, we will consider how genetic drift may reduce the fitness of individuals in these populations and limit the potential of these populations to evolve by natural selection.

6.1 Genetic drift

Genetic drift is random change in allele frequencies from generation to generation because of sampling error. That is, the finite number of genes transmitted to progeny will be an imperfect sample of the allele frequencies in the previous generation (Figure 6.1). The mathematical treatment of genetic drift began with R.A. Fisher (1930) and Sewall Wright (1931), who independently considered the effects of binomial sampling in small populations of constant size N in which the next generation is produced by drawing $2N$ genes at random from a large gamete pool to which all individuals contribute equally. This model is referred to as the **Wright–Fisher model** or Fisher–Wright model. However, Fisher and Wright strongly disagreed on the importance of drift in bringing about evolutionary change (Crow 2010). Genetic drift is sometimes called the “Sewall Wright effect” in recognition that the importance of drift in evolution was largely introduced by Wright’s papers.

It is often helpful to consider extreme situations in order to understand the expected effects of relaxing assumptions on models. Consider the example of a plant species capable of self-fertilization with a constant population size of $N = 1$, consisting of a single individual of genotype Aa ; the allele frequency in this generation is 0.5. We cannot predict what the allele frequency will be in the next generation because the genotype of the single individual in the next generation will depend upon which alleles are transmitted via the chance elements of Mendelian inheritance. However, we do know that the allele frequency in the next generation will be 0.0, 0.50,

or 1.0 because the only three possible genotypes are AA , Aa , or aa . Based upon Mendelian expectations, there is a 50% probability that the frequency of the A allele will be either zero or one in the next generation.

Genetic drift is an example of a **stochastic** process in which the actual outcome cannot be predicted because it is affected by random elements (chance). Tossing a coin is one example of a stochastic process. One-half of the time, we expect a head to result, and one-half of the time we expect a tail. However, we do not know what the outcome of any specific coin toss will be. We can mimic or simulate the effects of genetic drift by using a series of coin tosses. Consider a population initially consisting of two heterozygous (Aa) individuals, one male and one female. **Heterozygotes** are expected to transmit the A and a alleles with equal probability to each gamete. A coin is tossed to specify which allele is transmitted by heterozygotes; an outcome of a head (H) represents an A allele; and a tail (T) represents an a . No coin toss is needed for homozygous individuals since they will always transmit the same allele.

The results of one such simulation using these rules are shown in Table 6.1 and Figure 6.2. In the first generation, the female transmitted the A allele to both progeny because both coin tosses resulted in heads. The male transmitted an A to his daughter and an a to his son because the coin tosses resulted in a head and then a tail. Thus, the allele frequency (p) changed from 0.5 in the initial generation to 0.75 in the first generation, and the expected heterozygosity in the population changed as well. This process is continued until the seventh generation when both individuals become homozygous for the a allele, and, thus, no further gene frequency changes can occur.

Table 6.1 shows one of many possible outcomes of genetic drift in a population with two individuals. However, we are nearly certain to get a different result if we start over again. In addition, it would be helpful to simulate the effects of genetic drift in larger populations. In principle, this can be done by tossing a coin; however, it quickly becomes extremely time consuming.

A better way to simulate genetic drift is with computer simulations (Section A13). Computational

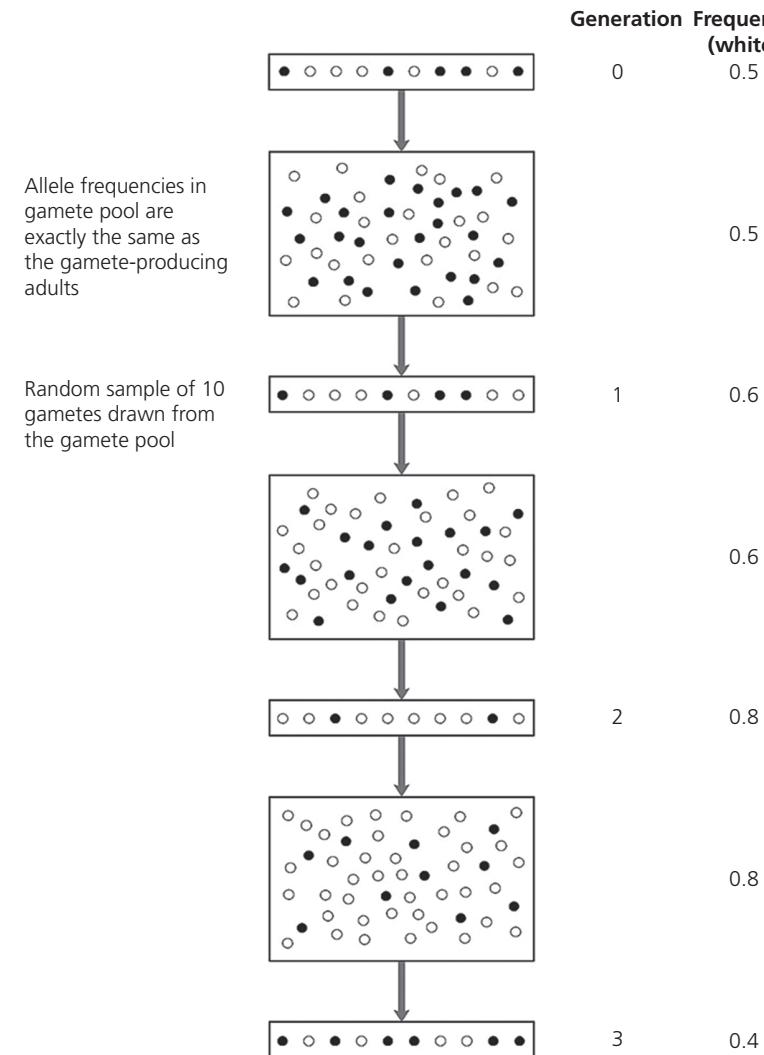


Figure 6.1 Random sampling of gametes resulting in genetic drift in a population. Allele frequencies in the gamete pools (large boxes) are assumed to reflect exactly the allele frequencies in the adults of the parental generation (small boxes). The allele frequencies fluctuate from generation to generation because the population size is finite ($N = 5$). Redrawn from Graur & Li (2000).

methods are available to produce a random number that is uniformly distributed between zero and one. This random number can be used to determine which allele is transmitted by a heterozygote. For example, if the random number is in the range of 0.0 to 0.5, we can specify that the *A* allele is transmitted; similarly, a random number in the range of 0.5 to 1.0 would specify an *a* allele. Models such as this are often referred to as Monte Carlo simulations in reference to the gambling tables in Monte Carlo. Figure 6.3 shows changes in allele frequencies in three populations of different sizes as simulated with a computer. The smaller the population size,

the greater are the changes in allele frequency due to drift (compare N of 10 with 200).

The sampling process that we have examined here has two primary effects on the genetic composition of small populations:

1. Allele frequencies will change.
2. Genetic variation will be lost.

We can measure genetic changes in small populations either by changes in allele frequencies or increases in homozygosity caused by inbreeding. As allele frequencies change because of genetic drift, heterozygosity is expected to decrease (and

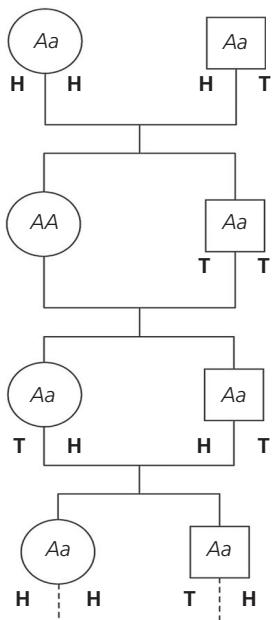


Figure 6.2 Simulation of genetic drift in a population consisting of a single female (circle) and male (square) each generation. A coin is tossed twice to simulate the two gametes produced by each heterozygote. A head (**H**) indicates that the *A* allele is transmitted and a tail (**T**) indicates the *a* allele. Homozygotes always transmit the allele for which they are homozygous.

homozygosity increase). For example, heterozygosity became zero in generation 16 with N of 10 because only one allele remained in the population. Once such a “fixation” of one allele or another occurs, it is permanent; only mutation (Chapter 12) or gene flow (Chapter 9) from another population can introduce new alleles. We will consider the effects of genetic drift on both allele frequencies and genetic variation in the next two sections.

6.2 Changes in allele frequency

We cannot predict the direction of change in allele frequencies from generation to generation because genetic drift is random. The frequency of any allele is equally likely to increase or decrease from one generation to the next because of genetic drift. Although we cannot predict the direction of change, we can describe the expected magnitude of the

Table 6.1 Simulation of genetic drift by coin tossing in a population of one female and one male over seven generations. A coin is tossed twice to specify which alleles are transmitted by heterozygotes; an outcome of a head (**H**) represents an *A* allele; and a tail (**T**) represents an *a*. The first toss represents the allele transmitted to the female in the next generation and the second toss the male (as shown in Figure 6.2). p is the frequency of the *A* allele. The observed and expected heterozygosities (assuming HW proportions) are also shown.

Generation	Mother	Father	p	H_o	H_e
0	<i>Aa</i> (HH)	<i>Aa</i> (HT)	0.50	1.000	0.500
1	<i>AA</i>	<i>Aa</i> (TT)	0.75	0.500	0.375
2	<i>Aa</i> (TH)	<i>Aa</i> (HT)	0.50	1.000	0.500
3	<i>aA</i> (HH)	<i>Aa</i> (TH)	0.50	1.000	0.500
4	<i>Aa</i> (TT)	<i>AA</i>	0.75	0.500	0.375
5	<i>aA</i> (HT)	<i>aA</i> (TT)	0.50	1.000	0.500
6	<i>Aa</i> (TT)	<i>aa</i>	0.25	0.500	0.375
7	<i>aa</i>	<i>aa</i>	0.00	0.000	0.000

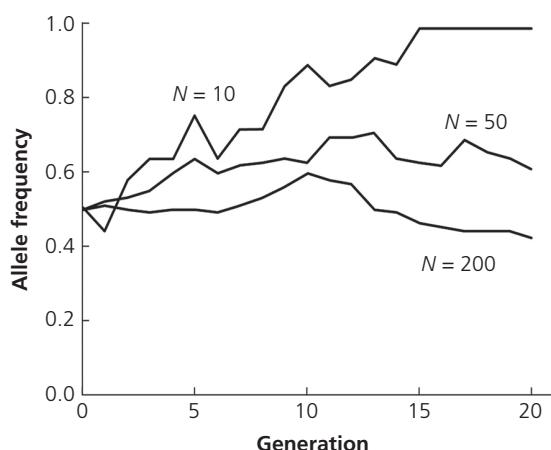


Figure 6.3 Results of computer simulations of changes in allele frequency by genetic drift for each of three population sizes (N) with an initial allele frequency of 0.5.

change in allele frequency. In general, the smaller the population, the greater the change in allele frequency that is expected (Figure 6.3).

The change in allele frequencies from one generation to the next because of genetic drift is a problem in sampling. A finite sample of gametes is drawn from the parental generation to produce the next generation. Both the sampling of gametes and the coin toss can be described by the binomial sampling distribution (Section A3.1). The variance of change in allele frequency from one generation to the next

is thus the binomial sampling variance:

$$V_q = \frac{pq}{2N}$$

Given that the current allele frequency is p with a population size of N , there is approximately a 95% probability that the allele frequency in the next generation will be within the interval:

$$p' = p \pm 2\sqrt{\frac{(pq)}{(2N)}} \quad (6.1)$$

For example, with an allele frequency of 0.50 and an N of 10, the allele frequency in the next generation will be in the interval 0.28 to 0.72 with 95% probability (Equation 6.1). In contrast, with a p of 0.5 and an N of 200, this interval is only 0.45 to 0.55.

6.3 The inbreeding effect of small populations

Genetic drift is expected to cause a loss of genetic variation from generation to generation. **Inbreeding** occurs when related individuals mate with one another. Inbreeding is one consequence of small population size; see Chapter 17 for a detailed consideration of inbreeding. For example, in an animal species with $N = 2$, the parents in each generation will be full sibs (i.e., brother and sister). Matings between relatives will cause an increase in homozygosity. The **inbreeding coefficient** (f) is the probability that the two alleles at a locus within an individual are identical by descent (i.e., identical because they are derived from a common ancestor in a previous generation). We will consider several different inbreeding coefficients that have specialized meaning (e.g., F_{IS} , F_{ST} , etc. in Chapter 9 and F in Chapter 17). We will use the general inbreeding coefficient f in this chapter as defined here, along with its counterpart heterozygosity (h), which is equal to $1 - f$.

In general, the increase in homozygosity due to genetic drift will occur at the following rate per generation:

$$\Delta f = \frac{1}{2N} \quad (6.2)$$

This effect was first discussed by Gregor Mendel, who pointed out that one-half of the progeny of

Table 6.2 This table appeared in Mendel's original paper in 1866. He was considering the expected genotypic ratios in subsequent generations from a single hybrid (i.e., heterozygous) individual that reproduced by self-fertilization. He assumed that each plant in each generation (Gen) had four offspring. The homozygosity (Homo) and heterozygosity (Het) columns did not appear in the original paper.

Gen	AA	Aa	aa	Ratio			Homo	Het
				AA :	Aa :	aa		
1	1	2	1	1	2	1	0.500	0.500
2	6	4	6	3	2	3	0.750	0.250
3	28	8	28	7	2	7	0.875	0.125
4	120	16	120	15	2	15	0.938	0.062
5	496	32	496	31	2	31	0.969	0.031
n				$2^n - 1$	2	$2^n - 1$	$1 - (1/2)^n$	$(1/2)^n$

a heterozygous self-fertilizing plant will be heterozygous; one-quarter will be homozygous for one allele; and the remaining one-quarter will be homozygous for the other allele (Table 6.2). This is as predicted by Equation 6.2 ($N = 1$, $\Delta f = 0.50$).

We have seen that the expected rate of loss of heterozygosity per generation is $\Delta f = 1/2N$; therefore, after t generations:

$$f_t = 1 - (1 - \frac{1}{2N})^t \quad (6.3)$$

f_t is the expected increase in homozygosity at generation t and is known by a variety of names (e.g., **autozygosity**, **fixation index**, or the inbreeding coefficient) depending upon the context in which it is used.

It is often more convenient to keep track of the amount of variation remaining in a population using h (heterozygosity), where:

$$f = 1 - h \quad (6.4)$$

Therefore, the expected decline in h per generation is:

$$\Delta h = -\frac{1}{2N} \quad (6.5)$$

so that after one generation:

$$h_{t+1} = (1 - \frac{1}{2N})h_t \quad (6.6)$$

Example 6.1 Bottleneck in the Mauritius kestrel

Kestrels on the Indian Ocean Island of Mauritius went through a bottleneck of one female and one male in 1974 (Nichols et al. 2001). The population had fewer than 10 birds throughout the 1970s, and there were fewer than 50 birds in this population for many years because of the widespread use of pesticides from 1940–1960. However, this population grew to nearly 500 birds by the mid-1990s. Nichols et al. (2001) examined the loss in genetic variation in this population at 10 microsatellite loci by comparing living birds to 26 ancestral birds from museum skins that were up to 170 years old. The heterozygosity of the restored population was 0.099 compared with heterozygosity in the ancestral birds of 0.231. Thus, 43% of the initial heterozygosity was retained.

The amount of heterozygosity expected to remain in Mauritius kestrels after one generation of a bottleneck of $N = 2$ can be estimated with Equation 6.6:

$$(1 - \frac{1}{2N})h_t = (1 - \frac{1}{4})(0.231) = 0.173$$

We can use Equation 6.7 to see that the amount of heterozygosity in the restored population of Mauritius kestrels is approximately the same as we would expect after a bottleneck of two individuals for three generations:

$$(1 - \frac{1}{2N})^t h_0 = (0.75)^3 (0.231) = 0.097$$

The actual bottleneck in Mauritius kestrels was almost certainly longer than three generations with more birds than two birds each generation. However, the equations in this chapter all assume **discrete generations** and cannot be applied directly to species such as the Mauritius kestrels that have **overlapping generations**.

The heterozygosity after t generations can be found by:

$$h_t = (1 - \frac{1}{2N})^t h_0 \quad (6.7)$$

where h_0 is the initial heterozygosity. Example 6.1 shows how these expressions can be used to predict the effects of population **bottlenecks**.

Figure 6.4 shows this effect at a locus with two alleles and an initial frequency of 0.5 in a series of computer simulations of eight populations that

consist of 20 individuals each. These 20 diploid individuals possess 40 gene copies at any given locus. Forty gametes must be drawn from these 40 parental gene copies to form the next generation. The genotype of any one selected gamete does not affect the probability of the next gamete that is drawn; this is similar to a coin toss where one outcome does not affect the probability of the next toss.

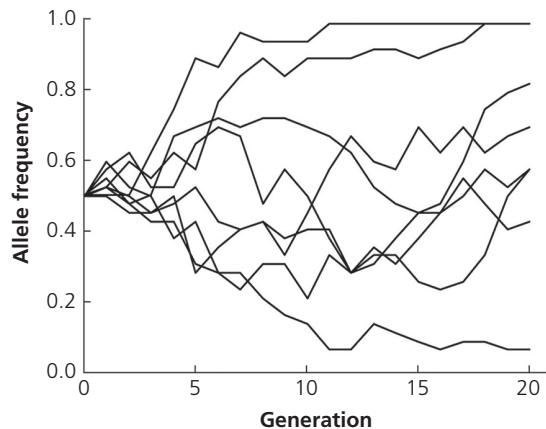


Figure 6.4 Computer simulations of genetic drift at a locus having two alleles with initial frequencies of 0.5 in eight populations of 20 individuals each.

Two of the eight populations simulated in Figure 6.4 became fixed for the *A* allele. Both of the alleles were retained by six of the populations after 20 generations. The heterozygosity in each of the populations is shown in Figure 6.5. There are large differences among populations in the decline in heterozygosity over time. Nevertheless, the mean decline in heterozygosity for all eight populations is very close to that predicted with Equation 6.6.

The heterozygosity at any single locus with two alleles is equally likely to increase or decrease from one generation to the next (except in the case of maximum heterozygosity when the allele frequencies are at 0.5). This may seem counterintuitive in view of Equation 6.6, which describes a monotonic decline in heterozygosity. Heterozygosity at a locus with two alleles is at a maximum when the two alleles are equally frequent ($p = q = 0.5$; Figure 6.6). The frequency of any particular allele is equally likely to increase or decrease due to genetic drift. Thus, heterozygosity will increase if the allele frequency

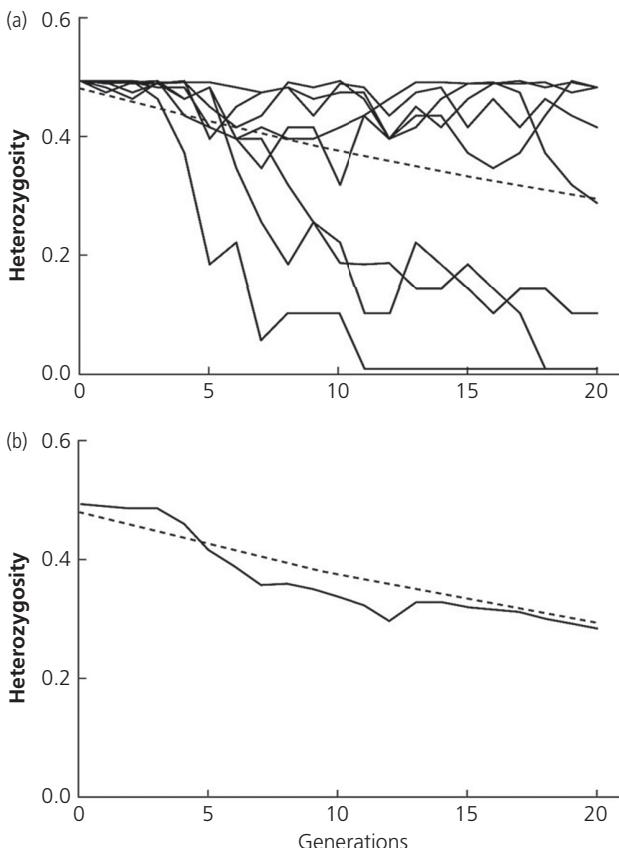


Figure 6.5 (a) Expected heterozygosities ($2pq$) in the eight populations ($N = 20$) undergoing genetic drift as shown in Figure 6.4. The dashed line shows the expected change in heterozygosity using Equation 6.6. (b) Mean heterozygosity for all loci (solid line) and the expected heterozygosity using Equation 6.6 (dashed line).

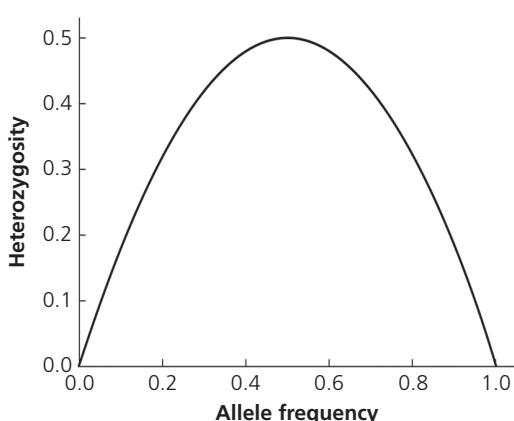


Figure 6.6 Expected heterozygosity ($2pq$) at a locus with two alleles as a function of allele frequency.

drifts toward 0.5, and it will decrease if the allele frequency drifts toward 0 or 1. However, the expected net loss is greater than the net gain in heterozygosity in each generation by $1/2N$.

6.4 Loss of allelic diversity

We have so far measured the loss of genetic variation caused by small population size by the expected reduction in heterozygosity (h). There are other ways to measure genetic variation and its loss. A second important measure of genetic variation is the number of alleles present at a locus (A). There are advantages and disadvantages to both of these measures.

Heterozygosity has been widely used because it is proportional to the amount of **genetic variance** at a locus, and it lends itself readily to theoretical

considerations of the effect of finite population size on genetic variation. In addition, the expected reduction in heterozygosity because of genetic drift is independent of the number of alleles present. Finally, estimates of heterozygosity from empirical data are relatively insensitive to sample size, whereas estimates of the number of alleles in a population are strongly dependent upon sample size. Therefore, comparisons of heterozygosities in different species or populations are generally more meaningful than comparisons of the number of alleles detected.

Nevertheless, heterozygosity has the disadvantage of being relatively insensitive to the effects of bottlenecks (Allendorf 1986). The difference between heterozygosity and A is greatest with extremely small bottlenecks (Figure 6.7). For example, a population with two individuals is expected to lose only 25% ($1/2N = 25\%$) of its heterozygosity. Thus, 75% of the heterozygosity in a population will be retained even through such an extreme bottleneck. However, two individuals can possess a maximum of four different alleles. Thus, considerably more of the allelic variation may be lost during a bottleneck if there are many alleles present at a locus.

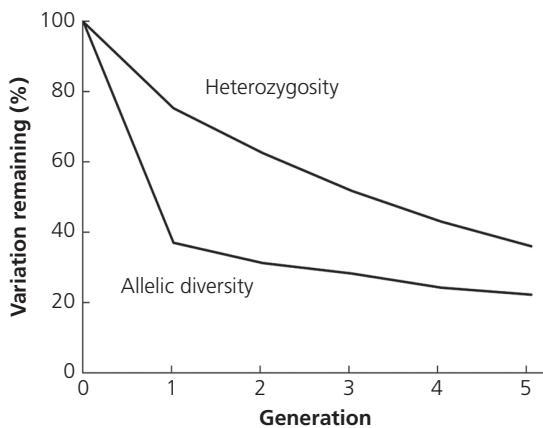


Figure 6.7 Simulated loss of heterozygosity and allelic diversity at eight microsatellite loci during a bottleneck of two individuals for five generations. The initial allele frequencies are from a population of brown bears from the Western Brooks Range of Alaska. Redrawn from Luikart & Cornuet (1998).

The effect of a bottleneck on the number of alleles present is more complicated than the effect on

heterozygosity because it is dependent on both the number and frequencies of alleles present (Allendorf 1986). The probability of an allele being lost during a bottleneck of size N is:

$$(1 - p)^{2N} \quad (6.8)$$

where p is the frequency of the allele. This is the probability of sampling all of the gametes to create the next generation ($2N$) without selecting at least one copy of the allele in question. Rare alleles (say $p < 0.10$) are especially susceptible to loss during a bottleneck. However, the loss of rare, potentially important, alleles will have little effect on heterozygosity. For example, an allele at a frequency of 0.01 has a 60% chance of being lost following a bottleneck of 25 individuals (Equation 6.8). Figure 6.8 shows the probability of the loss of rare alleles during a bottleneck of N individuals. Greenbaum et al. (2014) provide a method to estimate the expected effects of a bottleneck on allelic diversity.

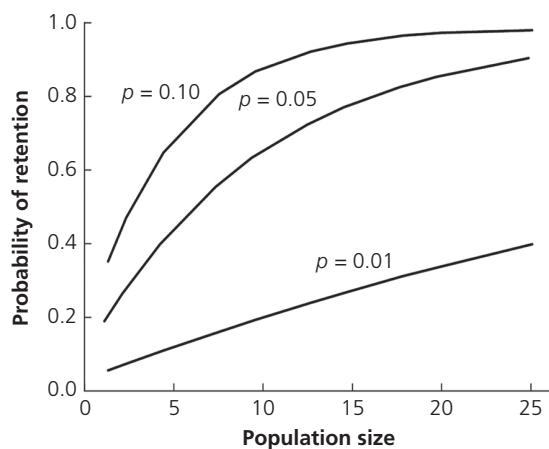


Figure 6.8 Probability of retaining a rare allele ($p = 0.01, 0.05$, or 0.10) after a bottleneck of size N for a single generation (Equation 6.8).

In general, if a population is reduced to N individuals for one generation then the expected total number of alleles (A') remaining is:

$$E(A') = A - \sum_{j=1}^A (1 - p_j)^{2N} \quad (6.9)$$

where A is the initial number of alleles and p_j is the frequency of the j th allele. For example, consider a

locus with two alleles at frequencies of 0.9 and 0.1 and a bottleneck of just two individuals. In this case:

$$E(A') = 2 - (1 - 0.9)^4 - (1 - 0.1)^4 = 1.34$$

Thus, on the average, we expect to lose one of these two alleles nearly two-thirds of the time. In contrast, there is a much greater expected probability of retaining both alleles at a locus with two alleles if the two alleles are equally frequent:

$$E(A') = 2 - (1 - 0.5)^4 - (1 - 0.5)^4 = 1.88$$

Thus, the expected loss of alleles during a bottleneck depends upon the number and frequencies of the alleles present. This is in contrast to heterozygosity, which is lost at a rate of $1/2N$, regardless of the current heterozygosity.

The loss of alleles during a bottleneck will have a drastic effect on the overall genotypic diversity of a population. As we saw in Section 5.2, the number of genotypes grows very quickly as the number of alleles increases. For example, the number of possible genotypes at a locus with two, five, and 10 alleles is three, 15, and 55, respectively. Thus, the loss of alleles during a bottleneck will greatly reduce the genotypic diversity in a population.

6.5 Founder effect

The founding of a new population by a small number of individuals will cause abrupt changes in allele frequency and loss of genetic variation (Example 6.2). Such severe bottlenecks in population size are a special case of genetic drift. Perhaps surprisingly, however, even extremely small bottlenecks have relatively little effect on heterozygosity. For example, with sexual species the smallest possible bottleneck is $N = 2$. Even in this extreme case, the population will only lose 25% of its heterozygosity in one generation (Equation 6.5). Stated in another way, just two individuals randomly selected from any population, regardless of size, will contain 75% of the total heterozygosity in the original population. We can also use Equation 6.5 to estimate the size of the founding population if we know how much heterozygosity has been lost through the founding bottleneck.

Table 6.3 Allele frequencies (p) and heterozygosities (h) at two loci in 16 subpopulations of guppies four generations after being founded by a single female and a single male. H_e is the mean heterozygosity at the two loci. Data from Nakajima et al. (1991).

Subpopulation	AAT-1		PGM-1		H_e
	p	h	p	h	
1	0.521	0.499	0.677	0.437	0.468
2	0.738	0.387	0.600	0.480	0.433
3	0.377	0.470	0.131	0.227	0.349
4	0.915	0.156	0.939	0.114	0.135
5	0.645	0.458	0.638	0.461	0.460
6	0.571	0.490	0.548	0.495	0.492
7	0.946	0.102	0.833	0.278	0.190
8	0.174	0.287	0.341	0.449	0.368
9	0.617	0.473	0.500	0.500	0.486
10	0.820	0.295	0.640	0.461	0.378
11	0.667	0.444	0.917	0.152	0.298
12	0.219	0.342	0.531	0.498	0.420
13	1.000	0.000	0.838	0.272	0.136
14	0.250	0.375	0.853	0.251	0.313
15	0.375	0.469	0.740	0.385	0.427
16	0.152	0.258	0.582	0.486	0.372
—	—	—	—	—	—
Average	0.562	0.344	0.644	0.372	0.358
Original Colony	0.581	0.487	0.605	0.478	0.482

A laboratory experiment with guppies clearly demonstrates the effect of reduced heterozygosity as a function of the size of the bottleneck (Nakajima et al. 1991). Sixteen separate **subpopulations** were derived from a large random mating laboratory colony of guppies by mating a female with a single male. After four generations, each of these subpopulations contained more than 500 individuals. Approximately 45 fish were then sampled from each subpopulation and genotyped at two allozyme loci that were polymorphic in the original colony (Table 6.3).

The mean heterozygosity at both loci in these 16 subpopulations was 0.358, in comparison with heterozygosity in the original colony of 0.482. Thus, the mean heterozygosity in the subpopulations, following a bottleneck of two individuals, was 26% lower than in the population from which the subpopulations were founded. This agrees very closely with Equation 6.5, which predicts a 25% reduction following a bottleneck of two individuals. Nevertheless, there are large differences in the amount of heterozygosity lost among subpopulations. For example, subpopulations 4 and 13 lost over 70%

Example 6.2 Effects of founding events on allelic diversity in a snail

The land snail *Theba pisana* was introduced from Europe into Western Australia in the 1890s. A colony was founded in 1925 on Rottnest Island with animals taken from the mainland population near Perth. Johnson (1988) reported the allele frequencies at 25 allozyme loci. Figure 6.9 shows the loss of rare alleles caused by the bottleneck associated with the founding of a population in Perth on the mainland and in the second bottleneck associated with the founding of a population on nearby Rottnest Island. The height of each bar represents the number of alleles in that sample that had the frequency specified on the x-axis. For example, there were seven alleles that had a frequency of less than 0.05 in the founding French population. However, there were no alleles in either of the two Australian populations at a frequency of less than 0.05.

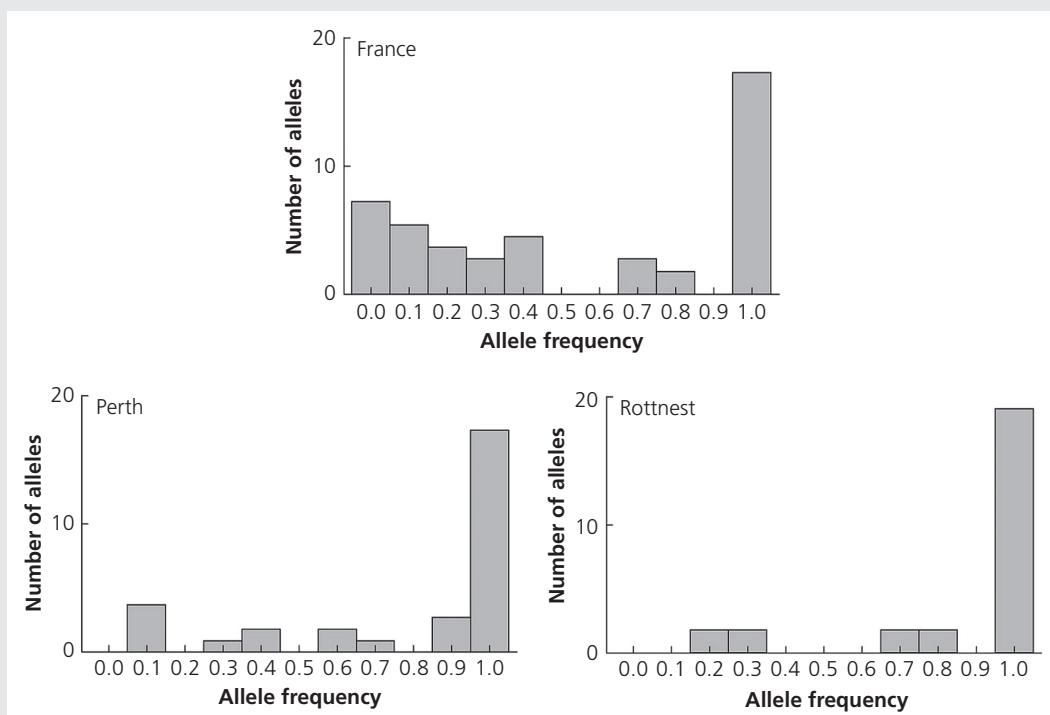


Figure 6.9 Effects of bottlenecks on the number of rare alleles at 25 allozyme loci in the land snail *Theba pisana* that was introduced from Europe into Western Australia in the 1890s. Data from Johnson (1988).

The distribution of allele frequencies, such as plotted in Figure 6.9, can be used to detect bottlenecks even when data are not available from the pre-bottlenecked population (Luikart et al. 1998). Rare alleles ($\text{frequency} < 0.05$) are expected to be common in samples from populations that have not been bottlenecked in their recent history, such as observed in the French sample of these snails. The complete absence of such rare alleles in Australia would have suggested that these samples came from recently bottlenecked populations even if the French sample was not available for comparison.

of their heterozygosity, while subpopulations 6 and 9 actually had increased heterozygosity!

The total amount of heterozygosity lost during a bottleneck depends upon how long it takes the population to return to a “large” size. That is, species such as guppies, in which individual females may produce 50 or so progeny, may quickly attain large enough population sizes following a bottleneck so that little further variation is lost following the initial bottleneck. However, species with lower population growth rates may persist at small population sizes for many generations during which heterozygosity is further eroded.

The growth rate of a population following a bottleneck can be modeled using the so-called logistic growth equation, which describes the size of a population after t generations based upon the initial population size (N_0), the intrinsic growth rate (r), and the equilibrium size of the population (K):

$$N(t) = \frac{K}{1 + be^{-rt}} \quad (6.10)$$

The constant e is the base of the natural logarithm (~2.72), and b is a constant equal to $(K - N_0)/N_0$.

We can estimate the total expected loss in heterozygosity in the guppy example depending upon the rate of population growth of the subpopulations. The initial size of the subpopulations (N_0) was 2, and we assume the carrying capacity (K) was 500. We can then examine three different intrinsic growth rates (r): 1.0, 0.5, and 0.2. An r of 1.0 indicates that population size is increasing by a factor of 2.72 (e) each generation when population size is far below K . Similarly, r values of 0.5 and 0.2 indicate growth rates of 1.65 and 1.22 at small population sizes, respectively.

Equation 6.10 can be used to predict the expected population size each generation following the bottleneck. We expect heterozygosity to be eroded at a rate of $1/2N$ in each of these generations. Figure 6.10 shows the expected loss in heterozygosity in our guppy example for 10 generations following the bottleneck. As expected, populations having a relatively high growth rate ($r = 1.0$) will lose little heterozygosity following the initial bottleneck. However, heterozygosity is expected to continue

to erode even 10 generations following the bottleneck in populations with the slowest growth rate. In general, bottlenecks will have a greater and more long lasting effect on the loss of genetic variation in species with smaller intrinsic growth rates (e.g., large mammals) than species with high intrinsic growth rates (e.g., insects).

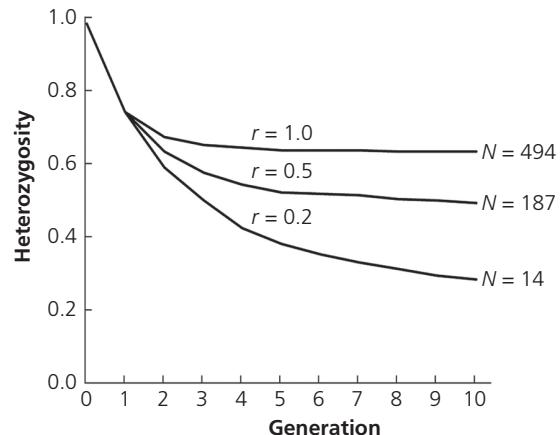


Figure 6.10 Expected heterozygosities in three subpopulations of guppies going through a bottleneck of two individuals and growing at different rates (r) according to the logistic growth equation (Equation 6.10). N is the expected population size for each subpopulation in the 10th generation.

Founder events and population bottlenecks will have a greater effect on the number of alleles in a population than on heterozygosity (Figure 6.7). Loci that are part of the major histocompatibility (MHC) system in vertebrates have been found to have many nearly equally frequent alleles. For example, Knafler et al. (2012) described allelic variation in 50 breeding pairs of the Magellanic penguins at the MHC $DR\beta 1$ gene. They discovered 45 alleles in this sample of 200 gene copies. As we have seen, two birds chosen at random from this population are expected to retain 75% of the heterozygosity. However, two birds can at best possess four of the 45 different MHC alleles. Thus, at least 41 of the 45 alleles (91%) will be lost in a bottleneck of two individuals compared with the loss of 25% of the heterozygosity. Thus, bottlenecks of short duration may have little effect on heterozygosity but will severely reduce the number of alleles present at some loci (Example 6.3).

Example 6.3 Founding events in the Laysan finch

The Laysan finch is an endangered Hawaiian honeycreeper found on several islands in the Pacific Ocean (Tarr et al. 1998, Figure 6.11). The species underwent a bottleneck of ~100 birds on Laysan Island after the introduction of rabbits in the early 1900s. The population recovered rapidly after eradication of the rabbits and has fluctuated around a mean of 10,000 birds since 1968. In 1967, the US Fish and Wildlife Service translocated 108 finches to Southeast Island, one of several small islets ~300 km northwest of Laysan that comprise Pearl and Hermes Reef (PHR). The translocated population declined to 30–50 birds and then rapidly increased to some 500 birds on Southeast Island. Several smaller populations have since become established in other islets within PHR. Two birds colonized Grass Island in 1968 and six more finches were moved to this islet in 1970. The population of birds on Grass Island has fluctuated between 20 and 50 birds. In 1973, a pair of finches founded a population on North Island. The population of birds on North Island has fluctuated between 30 and 350 birds.



Figure 6.11 Laysan finch. Photo courtesy of C.R. Kohley.

Tarr et al. (1998) assayed variation at nine microsatellite loci to examine the effects of the founder events and small population sizes in these four populations (Table 6.4). Their empirical results are in close agreement with theoretical expectations. The average heterozygosity on Southeast Island is ~8% less than on Laysan Island; the heterozygosities on the two other islands are ~30% less than the original founding population on Laysan. All three newly founded populations have fewer alleles than the founding population on Laysan. In all cases, the proportion of alleles retained is less than the proportion of heterozygotes retained. The extreme case is Grass Island, where 75% of the heterozygosity was retained, but only 53% of the allelic variation was retained.

It is worth noting that heterozygosities at four of the nine loci are actually greater in the post-bottleneck population on Southeast Island than on Laysan; see the discussion in Section 6.3 and Figure 6.5. This demonstrates that it is important to examine many loci in order to detect and quantify the effects of bottlenecks in populations on heterozygosity.

Continued

Example 6.3 Continued

Table 6.4 Numbers of alleles (A) and observed heterozygosities (Het) at nine microsatellite loci in Laysan finches in four island populations. The number in parentheses after the name of the island is the sample size. The populations on the other three islands were all founded from birds from Laysan. The bottom row shows the average allelic diversity and heterozygosity in the sample. The value at the bottom of the A column is $(A' - 1)/(A - 1)$, where A' is the number of alleles in the sampled population, and A is the number of alleles in the Laysan sample (Allendorf 1986). This value ranges from 100%, when all alleles are retained, to zero when all alleles except one are lost. Data from Tarr et al. (1998).

Locus	Laysan (44)		Southeast (43)		North (43)		Grass (36)	
	A	Het	A	Het	A	Het	A	Het
Tc.3A2C	2	0.558	2	0.535	2	0.535	2	0.528
Tc.4A4E	2	0.386	2	0.605	2	0.209	2	0.556
Tc.5A1B	3	0.372	3	0.233	1	0	2	0.583
Tc.5A5A	3	0.409	2	0.071	2	0.372	2	0.278
Tc.1A4D	3	0.659	3	0.744	3	0.698	2	0.528
Tc.11B1C	3	0.636	3	0.674	3	0.628	3	0.194
Tc.11B2E	3	0.614	3	0.488	1	0	2	0.500
Tc.11B4E	4	0.614	4	0.628	2	0.256	3	0.444
Tc.12B5E	5	0.568	4	0.442	3	0.372	1	0
All loci	3.11	0.535	2.89	0.491	2.11	0.341	2.11	0.401
	100%	100%	90%	92%	53%	64%	53%	75%

6.6 Genotypic proportions in small populations

We saw in the guppy example (Table 6.3) that the separation of a large random mating population into a number of subpopulations can cause a reduction in heterozygosity, and a corresponding increase in homozygosity. However, genotypes within each subpopulation will be in HW proportions as long as random mating occurs within the subpopulations. It may seem paradoxical that heterozygosity is decreased in small populations, but the subpopulations themselves remain in HW proportions. The explanation is that the reduction in heterozygosity is caused by changes in allele frequency from one generation to the next, while HW genotypic proportions will occur in any one generation as long as mating is random (Section 5.3).

In fact, there actually is a tendency for an excess of heterozygotes in small populations of animals and plants with separate sexes (Example 6.4). Different allele frequencies in the two sexes will cause an excess in heterozygotes relative to HW proportions

(Robertson 1965; Kirby 1975). An extreme example of this is hybrids produced by males from one strain (or species) and females from another so that all progeny are heterozygous at any loci where the two strains differ. In this case, however, genotypic proportions will return to HW proportions in the next generation.

In small populations, allele frequencies are likely to differ between the sexes just due to chance. On average, the frequency of heterozygotes in the progeny population will exceed HW expectations by a proportion of:

$$\frac{1}{8N_m} + \frac{1}{8N_f} \quad (6.11)$$

where N_m and N_f are the numbers of male and female parents (Robertson 1965). This result holds regardless of the number of alleles at the locus concerned. This reduces to $1/2N$ if there is an equal number of males and females.

Let us consider the extreme case of a population with one female and one male ($N = 2$) and two alleles (Table 6.5). There are six possible types of matings.

Mating between identical **homozygotes** (either *AA* or *aa*) will produce monomorphic progeny. Progeny produced by matings between two heterozygotes will result in the expected HW proportions. However, the other three matings will result in an excess of heterozygotes. The extreme case is a mating between opposite homozygotes, which will produce all heterozygous progeny. On average, there will be a 25% excess of heterozygotes in populations produced by a single male and a single female (Equation 6.11).

With more than two alleles, there will be a deficit of each homozygote and an overall excess of heterozygotes. However, some heterozygous genotypes may be less frequent than expected by HW proportions, despite the overall excess of heterozygotes.

Table 6.5 Expected Mendelian genotypic proportions for all possible matings at a locus with two alleles in a population with a single female and a single male. F_{IS} is a measure of the deficit of heterozygotes observed relative to the expected HW proportions (Section 9.1). A negative F_{IS} indicates an excess of heterozygotes.

Mating	AA	Aa	aa	Freq(A)	F_{IS}
AA × AA	1.00	0	0	1.00	—
AA × Aa	0.50	0.50	0	0.75	-0.33
AA × aa	0	1.00	0	0.50	-1.00
Aa × Aa	0.25	0.50	0.25	0.50	0.00
Aa × aa	0	0.50	0.50	0.25	-0.33
aa × aa	0	0	1.00	0.00	—

Let's revisit the Channel Island fox study (Funk et al. 2016) that we looked at in Section 5.3.4. In

Example 6.4 An island population of little spotted kiwi

The population of little spotted kiwi on Long Island, New Zealand, was founded by the introduction of one female in 1982 and one male in 1989 (Taylor et al. 2017a). This population was sampled in 2011–2013 when it comprised the founding pair (alive and still reproductively active), first-generation offspring (27 samples), and later descendants (14 samples).

Table 6.6 shows tests for HW proportions at five of the 15 polymorphic microsatellite loci in this population. The two founders were homozygous for different alleles (11 and 22) at the *Aptowe31* locus. All F_1 individuals were heterozygous (12) at this locus. A 25% excess of heterozygotes is expected if all of the progeny came from just the two founding individuals (Equation 6.11). On average, there was a 37% excess of heterozygotes at these five polymorphic loci, just slightly greater than the expected value of 25%.

Table 6.6 Observed (and expected) genotypic proportions at five microsatellite loci in little spotted kiwi sampled from Long Island, New Zealand. $\hat{p}(1)$ and $\hat{p}(2)$ are the estimated frequencies of the 1 and 2 allele. F_{IS} equals $[1 - (H_o/H_e)]$ and is a measure of the departure from HW proportions (see Section 9.1). A negative F_{IS} indicates an excess of heterozygotes. From Taylor et al. (2017a) and personal communication. * $P < 0.05$, *** $P < 0.001$.

Locus	Genotype						$\hat{p}(1)$	$\hat{p}(2)$	F_{IS}
	11	12	22	13	23	33			
<i>Aptowe1</i>	27 (28.5)	16 (13.0)	0 (1.5)	—	—	—	0.814	0.186	-0.23
<i>Aptowe29</i>	6 (11.6)	16 (9.9)	0 (2.1)	14 (8.8)	2 (3.8)	0 (1.7)	0.553	0.237	-0.42*
<i>Aptowe31</i>	6 (11.3)	31 (20.4)	4 (9.3)	—	—	—	0.524	0.476	-0.52***
<i>Aptowe35</i>	3 (2.9)	14 (10.5)	3 (9.5)	2 (5.8)	20 (10.5)	0 (2.9)	0.261	0.476	-0.35*
<i>Apt59</i>	18 (20.9)	24 (18.1)	1 (3.9)	—	—	—	0.696	0.304	-0.32*
Mean									-0.37

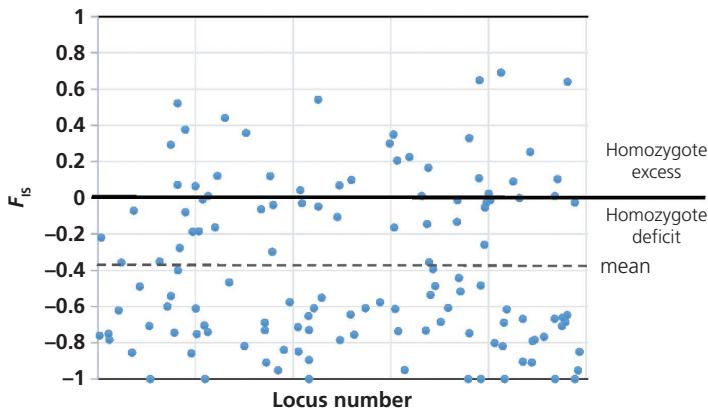


Figure 6.12 Distribution of F_{IS} values at 131 SNP loci in a sample of 46 Channel Island foxes from San Nicolas Island (data from Funk et al. 2016). F_{IS} is the proportional excess (positive values) or deficit (negative values) of homozygotes (Section 9.1).

Figure 5.2, we saw the distribution of F_{IS} values in a sample of 46 foxes from Santa Catalina Island. There was a slight excess of homozygotes in this sample. Very different results were found in an examination of the same loci in 46 foxes from nearby San Nicolas Island. There is a substantial deficit of homozygotes in this sample ($F_{IS} = -0.386$; Figure 6.12). This almost certainly results from the small population size of foxes on this island. An estimate of the genetically effective population size (Chapter 7) of foxes on this island is approximately two. Supporting this observation, only 131 of these SNP loci were polymorphic compared with 3,940 loci in the Santa Catalina sample.

6.7 Effects of genetic drift

We have considered in some detail how genetic drift is expected to affect allele frequencies and reduce the amount of genetic variation in small populations. We will now preview the effects that this loss of genetic variation is expected to have on the population itself (Box 6.1). That is, how will the loss of genetic variation expected in small populations affect the capability of a population to persist and evolve? We will take a more in-depth look at these effects in later chapters.

6.7.1 Changes in allele frequency

Large changes in allele frequency from one generation to the next are likely in small populations due to chance. This effect may cause an increase in frequency of alleles that have harmful

effects. Such **deleterious** alleles are continually introduced by mutation but are kept at low frequencies by natural selection. Moreover, most of these harmful alleles are recessive so that their harmful effects on the phenotype are only expressed in homozygotes.

Let us consider the possible effect of a population bottleneck of two individuals. As we have seen, most rare alleles will be lost in such a small bottleneck. However, any allele for which one of the two founders is heterozygous will be found in the new population at a frequency of 25%. Thus, rare deleterious alleles present in the founders will jump in frequency to 25%. Of course, at most loci the two founders will not carry a harmful allele. However, every individual carries harmful alleles at some loci. Therefore, we cannot predict which particular harmful alleles will increase in frequency following a bottleneck, but we can predict that several harmful alleles that were rare in the original population will be found at much higher frequencies. And if the bottleneck persists for several generations, these harmful alleles may become more frequent in the new population.

This effect is commonly seen in domestic animals such as dogs in which breeds often originated from a small number of founders. Different dog breeds usually have some characteristic genetic abnormality that is much more common within the breed than in the species as a whole (Hutt 1979). For example, dalmatians were originally developed from a few founders that were selected for their running ability and distinctive spotting pattern. Dalmatians are susceptible to kidney stones because they excrete

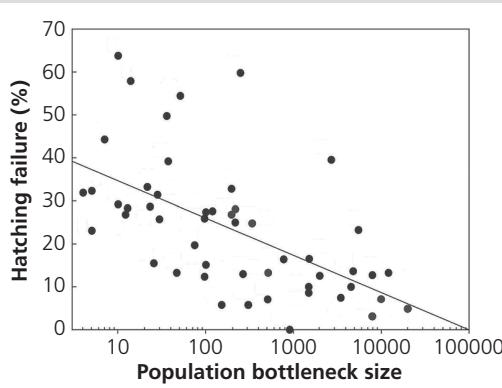
Box 6.1 Population bottlenecks and decreased hatching success in endangered birds


Figure 6.13 Effect of bottleneck size (smallest number of individuals recorded in the population) and percent hatching failure in threatened birds. Hatching failure is plotted on a linear scale and bottleneck size is plotted on a logarithmic scale, although both were log transformed in analyses. Redrawn from Heber & Briskie (2010).

Many populations have undergone severe bottlenecks because of reduced population size and increased fragmentation caused by habitat loss. As we have seen in this chapter, small populations are vulnerable to genetic drift and the inbreeding effect of small populations. Increased hatching failure is a common result of inbreeding in

birds. Heber & Briskie (2010) have shown that bottlenecks in endangered birds have a major effect on hatching success.

Hatching failure is generally less than 10% in noninbred bird populations. Hatching failure is sometimes more than 50% in some inbred populations. Given the increase of inbreeding in smaller populations, Heber and Briskie tested if hatching success decreases in bird populations that have gone through a population bottleneck.

They summarized rates of hatching failure in 51 threatened bird species from 31 families. The size of introductions ranged from 4 to 20,000 individuals. They estimated hatching failure as the proportion of eggs incubated to term that failed to hatch, excluding failure due to desertion, predation, or adverse weather. Under this definition, eggs that failed to hatch were either infertile or died during embryonic development, both of which are thought to increase as inbreeding increases (Jamieson & Ryan 2000).

Heber and Briskie found a substantial increase in hatching failure associated with bottlenecks with smaller population sizes ($P < 0.001$; Figure 6.13). The exact threshold of population size below which inbreeding depression is likely to cause a problem varies among species and traits. Nevertheless, hatching failure was greater than 10% in all species that went through a bottleneck of fewer than 150 individuals.

exceptionally high amounts of uric acid in their urine. This difference is due to a recessive allele at a single locus (Trimble & Keeler 1938). Apparently, one of the principal founders of this breed carried this recessive allele, and it subsequently drifted to high frequency in this breed.

Similar effects occur in small wild populations of conservation concern. For example, the Scottish population of red-billed choughs currently has fewer than 60 breeding pairs (Trask et al. 2016). Some of the nestlings in this population are affected by lethal blindness, which is inherited as a Mendelian autosomal recessive allele. The estimated frequency of the blindness allele is 0.126. As we will see in Chapter 8 and Example 21.3, reducing the frequency of such harmful recessive alleles is very

difficult because almost all of the copies are present in phenotypically normal heterozygotes rather than in affected homozygotes.

6.7.2 Loss of allelic diversity

We have seen in Section 6.4 that genetic drift will have a much greater effect on the allelic diversity of a population than on heterozygosity if there are many alleles present at a locus. Evidence from many species indicates that loci associated with disease resistance often have many alleles. The best example of this is the MHC in vertebrates (Edwards & Hedrick 1998). MHC in humans consists of five major tightly linked genes on chromosome 6 (Pierini & Lenz 2018). Many alleles occur at all of these

loci; for example, there are 10 or more nearly equally frequent alleles at the *HLA-A* locus and 15 or more at the *HLA-B* locus.

MHC molecules assist in the triggering of the immune response to disease-causing organisms. Individuals heterozygous at MHC loci are relatively more resistant to a wider array of pathogens than are homozygotes (Hedrick 2002). Most vertebrate species that have been studied have been found to harbor many MHC alleles. Thus, the loss of allelic diversity at MHC loci is likely to render small populations of vertebrates much more susceptible to disease epidemics (e.g., Ujvari & Belov 2011; Quigley et al. 2020).

A similar situation holds in Resistance genes (R-genes) that are found in many plants. These genes are involved in pathogen recognition, and they often have many alleles at individual loci (Bergelson et al. 2001). Marden et al. (2017) found that tropical species with smaller local population sizes had lower R-gene allelic diversity and lower recognition-dependent immune responses. This resulted in greater susceptibility to species-specific pathogens that may facilitate disease transmission in species with smaller local populations.

6.7.3 Inbreeding depression

The harmful effects of inbreeding have been known for a long time. Experiments with plants by Darwin and others demonstrated that loss of vigor generally accompanied continued selfing and that crossing different lines maintained by selfing restored the lost vigor. Livestock breeders also generally accepted that continued inbreeding within a herd or flock could lead to a general deterioration that could be restored by outcrossing. The first published experimental report of the effects of inbreeding in animals was with rats (Crampe 1883; Ritzema-Bos 1894).

The implication of these results for wild populations did not go unnoticed by Darwin. It occurred to him that fallow deer kept in British parks might be affected by isolation and “long-continued close interbreeding.” He was especially concerned because he was aware that the effects of inbreeding

may go unnoticed because they accumulate slowly. Darwin (1896, p. 99) inquired about this effect and received the following response from an experienced gamekeeper:

... the constant breeding in-and-in is sure to tell to the disadvantage of the whole herd, though it may take a long time to prove it; moreover, when we find, as is very constantly the case, that the introduction of fresh blood has been of the greatest use to deer, both by improving their size and appearance, and particularly by being of service in removing the taint of “rickback” if not other diseases, to which deer are sometimes subject when the blood has not been changed, there can, I think, be no doubt but that a judicious cross with a good stock is of the greatest consequence, and is indeed essential, sooner or later, to the prosperity of every well-ordered park.

Despite Darwin’s concern and warning, these early lessons from agriculture were largely ignored by those responsible for the management of wild populations of game and by captive breeding programs of zoos for nearly 100 years (see Voipio 1950 for an exception).

A seminal paper in 1979 by Kathy Ralls and her colleagues had a dramatic effect on the application of genetics to the management of wild and captive populations of animals. They used zoo pedigrees of 12 species of mammals to show that individuals from matings between related individuals tended to show reduced survival relative to progeny produced by matings between unrelated parents. The pedigree inbreeding coefficient (F_P) is the expected increase in homozygosity for inbred individuals; it is also the expected decrease in heterozygosity throughout the genome of inbred individuals (Section 17.1.1). One of us (FWA) can clearly remember being excitedly questioned in the hallway by our departmental mammalogist who had just received his weekly issue of *Science* and could not believe the data of Ralls and her colleagues. Subsequent studies (Ralls & Ballou 1983; Ballou 1997) have supported their original conclusions (Figure 6.14).

Inbreeding depression results from both increased homozygosity and reduced heterozygosity (Section 17.4). That is, a greater number of deleterious recessive alleles will be expressed in inbred individuals because of their increased homozygosity. In addition, fitness of inbred

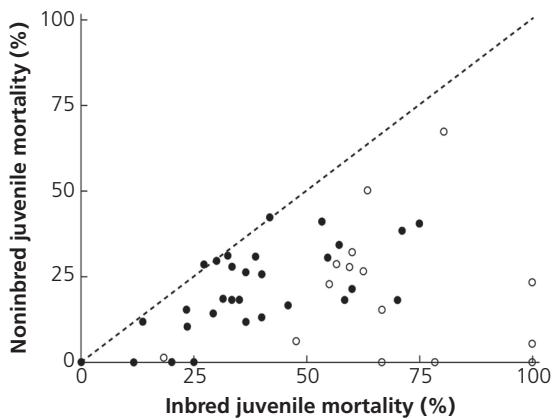


Figure 6.14 Effects of inbreeding on juvenile mortality in 44 captive populations of mammals (16 ungulates, 16 primates, and 12 small mammals). The line shows equal mortality in inbred and noninbred progeny. The preponderance of points below the line (42 of 44, 95%) indicates that inbreeding generally increased juvenile mortality. The open circles indicate populations in which juvenile mortality of inbred and noninbred individuals were significantly different ($P < 0.05$; exact test). Data from Ralls & Ballou (1983).

individuals will be reduced at loci at which the heterozygotes have a selective advantage over all homozygous types (**heterozygous advantage** or overdominance). Both of these mechanisms are likely to contribute to inbreeding depression, but it

is thought that increased expression of deleterious recessive alleles is the more important mechanism (Charlesworth & Charlesworth 1987; Hedrick & Kalinowski 2000). Inbreeding depression is considered in detail in Chapter 17.

Guest Box 6 Detecting bottlenecks in the critically endangered kākāpō

Yasmin Foster, Nicolas Dussex, and Bruce C. Robertson

Reducing the impact of bottlenecks and genetic drift by maintaining or increasing genetic diversity (via genetic rescue) is paramount to species recovery (Bell et al. 2019). Bottlenecks and the subsequent inbreeding and loss of heterozygosity have implications for population persistence and adaptive potential. To understand the role genetics plays in conservation outcomes, whole genome sequencing approaches can be used to detect bottlenecks and resulting losses of genetic diversity, and study the associated impacts of inbreeding depression.

The New Zealand kākāpō is a unique parrot, being flightless, nocturnal, and displaying a polygynous **lek** breeding system where certain males dominate breeding (Figure 6.15). The extant population consists of 211 individuals (June 2020) founded by a small insular population from Stewart Island discovered in the 1970s (61 birds) and one surviving male from the mainland of New Zealand (Powlesland et al. 2006). Kākāpō are unusually long-lived and individuals from the founding population still contribute their genetic potential. Understanding the genetic diversity of these founding individuals, including the differences between the two descendant groups, is crucial for long-term species management. Since the late 1990s, genetic management of kākāpō has aimed to increase genetic diversity by favoring the mating of the mainland lineage, and reducing consanguineous matings via placement of breeders on various offshore islands (Robertson 2006).



Figure 6.15 Male kākāpō, Jamieson, named after the late Professor Ian Jamieson (see Section 18.8). Photo courtesy of Jake Osborne.

Kākāpō genetic management has employed microsatellites, mitochondrial, and immunity-associated DNA-based approaches to assess differences in heterozygosity, allelic diversity, and relatedness between the founding island and mainland kākāpō, to construct their demographic history and to detect bottlenecks (Robertson et al. 2009; Grueter et al. 2015a).

Genetic analyses have informed relatedness and assigned relationships of the founding population, ultimately to maintain diversity by choosing unrelated individuals for mating and artificial insemination (Clout & Merton 1998; Bergner et al. 2014). Significant loss of immunity-associated MHC allelic diversity has been identified between the two descendant groups (Knafler et al. 2014), and **heterozygosity-fitness correlations (HFCs)** were detected for both clutch size and hatching success in female kākāpō (White et al. 2015). Temporal comparisons between historical and modern data reveal the genetic consequences of bottlenecks (Díez-del-Molino et al. 2018); using microsatellite and mitochondrial DNA of museum and modern kākāpō samples indicated severe reduction in genetic diversity (Bergner et al. 2016; Dussex et al. 2018b), consistent with a near-extinction of the species.

Genome-wide SNPs and a chromosome-level genome assembly are currently used in kākāpō management. Genomic relatedness matrices using reduced-representation sequencing now aid in choosing the most unrelated kākāpō for artificial insemination and breeding management. Inbreeding events lead to the accumulation of runs of homozygosity (ROH) across the genome (Section 17.1.2). Historical and modern kākāpō genomes indicate differences in inbreeding and mutational load between extinct and extant populations (Figure 6.16, Dussex et al. 2021). Despite having lower genetic diversity than mainland descendants, the highly inbred Stewart Island population (isolated from the mainland for some 10,000 years) shows reduced mutational load consistent with purging of harmful mutations (via purifying selection). Additionally, individual inbreeding is not associated with the survival of chicks, despite significant differences between descendant groups, further supporting purging of deleterious alleles (Foster et al. 2021).

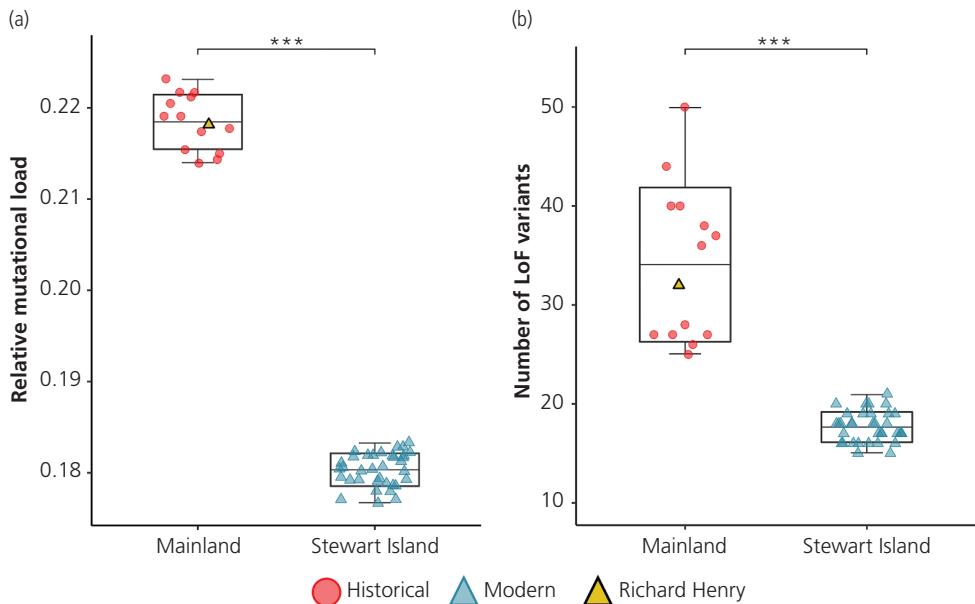
Guest Box 6 Continued

Figure 6.16 Estimates of mutational load in kākāpō (Dussex et al. 2021). (a) Individual relative mutational load measured as the sum of all homozygous and heterozygous derived alleles multiplied by their conservation score over the total number of derived alleles. (b) Number of loss of function (LoF) variants. Modern birds include Stewart Island birds and Richard Henry. Middle thick lines within boxplots and whiskers extending from it represent mean and standard deviation, respectively ($P < 0.001$).