

- C1. A gene pool is all of the genes present in a particular population. Each type of gene within a gene pool may exist in one or more alleles. The prevalence of an allele within the gene pool is described by its allele frequency. If a gene is monomorphic, the allele frequency is close to 100%. If it is polymorphic, each allele has a frequency that is between 1 and 99%. The sum of all the allele frequencies for a particular gene will add up to 100%.
- C2. A population is a group of interbreeding individuals. Let's consider a squirrel population in a forested area. Over the course of many generations, several things could happen to this population that may change its gene pool. A forest fire, for example, could dramatically decrease the number of individuals and thereby cause a bottleneck. This would decrease the genetic diversity of the population. A new predator may enter the region and natural selection may select for the survival of squirrels that are best able to evade the predator. Another possibility is that a group of squirrels within the population may migrate to a new region and found a new squirrel population.
- C3. The term *genetic polymorphism* refers to the phenomenon in which a gene is found in two or more alleles within a population. Mutation is the ultimate source of genetic variation.
- C4. A. Phenotype frequency and genotype frequency  
 B. Genotype frequency  
 C. Allele frequency
- C5. When a trait is polymorphic, this means that different individuals show phenotypic variation with regard to the trait. For example, petunias can have red or white flowers. Flower color is polymorphic in petunias. When a gene exists in two or more alleles, it is polymorphic. At the molecular level, alleles of a given gene have different DNA sequences. These differences could be very slight (e.g., a single-base change) or they could involve significant additions or deletions. Different alleles may cause differences in phenotype. For example, in Mendel's pea plants, the *T* allele resulted in tall plants while the *t* allele caused dwarf plants. However, alleles do not always cause differences in phenotype. A single-base substitution in a gene may not affect the amino acid sequence of the encoded polypeptide (e.g., the base change may affect the wobble base) or a single-base change might alter the amino acid sequence, but not in a way that alters the protein's function. Therefore, gene polymorphism does not always result in phenotypic polymorphism.
- C6. A. The genotype frequency for the *CF* homozygote is  $1/2,500$ , or  $0.004$ . This would equal  $q^2$ . The allele frequency is the square root of this value, which equals  $0.02$ . The frequency of the corresponding normal allele equals  $1 - 0.02 = 0.98$ .  
 B. *CF* homozygote is  $0.004$ . Normal homozygote is  $(0.98)^2 = 0.96$ . Heterozygote is  $2(0.98)(0.02)$ , which equals  $0.039$ .  
 C. If a person is known to be a heterozygous carrier, the chances that this particular person will happen to choose another as a mate is equal to the frequency of heterozygous carriers in the population, which equals  $0.039$ , or  $3.9\%$ . The chances that two randomly chosen individuals will choose each other as mates equals  $0.039 \times 0.039 = 0.0015$ , or  $0.15\%$ .
- C7. In the absence of other forces, inbreeding does not alter allele frequencies since it does not favor the transmission of one allele over another. It simply increases the likelihood of homozygosity (which is a genotype frequency). In human populations, inbreeding increases the frequency of individuals who are homozygous for rare recessive alleles that cause human disease.
- C8. For two alleles, the heterozygote is at a maximum when they are  $0.5$  each. For three alleles, the two heterozygotes are at a maximum when each allele is  $0.33$ .
- C9. If we apply the Hardy-Weinberg equation:

$$BB = (0.67)^2 = 0.45, \text{ or } 45\%$$

$$Bb = 2(0.67)(0.33) = 0.44, \text{ or } 44\%$$

$$bb = (0.33)^2 = 0.11, \text{ or } 11\%$$

The actual data show a higher percentage of homozygotes (compare  $45\%$  with  $50\%$  and  $11\%$  with  $13\%$ ) and a lower percentage of heterozygotes (compare  $44\%$  with  $37\%$ ). Therefore, these data would be consistent with inbreeding, which increases the percentage of homozygotes and decreases the percentage of heterozygotes.

- C10. Since this is a recessive trait, only the homozygotes for the rolling allele will be able to roll their tongues. If  $p$  equals the rolling allele and  $q$  equals the nonrolling allele, the Hardy-Weinberg equation predicts that the frequency of homozygotes who can roll their tongues would be  $p^2$ . In this case,  $p^2 = (0.6)^2 = 0.36$ , or  $36\%$ .
- C11. A. Yes.

B. The common ancestors are I-1 and I-2.

C.

$$F = \sum (1/2)^n (1 + F_A)$$

$$F = (1/2)^9 + (1/2)^9$$

$$F = 1/512 + 1/512 = 2/512 = 0.0039$$

D. Not that we can tell.

C12.A. The inbreeding coefficient is calculated using the formula

$$F = \sum (1/2)^n (1 + F_A)$$

In this case there is one common ancestor, I-2. Because we have no prior history on I-2, we assume she is not inbred, which makes  $F_A = 0$ . The inbreeding loop for IV-3 contains five people, III-4, II-2, I-2, II-5, and III-5. Therefore,  $n = 5$ .

$$F = (1/2)^5 (1 + 0) = 1/32 = 0.031$$

B. Based on the data shown in this pedigree, individual IV-4 is not inbred.

C13.A. The inbreeding coefficient is calculated using the formula

$$F = \sum (1/2)^n (1 + F_A)$$

In this case there are two common ancestors, I-1 and I-2. Since we have no prior history on I-1 or I-2, we assume they are not inbred, which makes  $F_A = 0$ . The two inbreeding loops for IV-2 contain five people, III-4, II-2, I-1, II-6, and III-5, and III-4, II-2, I-2, II-6, and III-5. Therefore,  $n = 5$  for both loops.

$$F = (1/2)^5 (1 + 0) + (1/2)^5 (1 + 0)$$

$$F = 0.031 + 0.031 = 0.062$$

B. Based on the data shown in this pedigree, individual III-4 is not inbred.

C14. Migration, genetic drift, and natural selection are the driving forces that alter allele frequencies within a population. Natural selection acts to eliminate harmful alleles and promote beneficial alleles. Genetic drift involves random changes in allele frequencies that may eventually lead to elimination or fixation of alleles. It is thought to be important in the establishment of neutral alleles in a population. Migration is important because it introduces new alleles into neighboring populations. According to the neutral theory, genetic drift is largely responsible for the variation seen in natural populations.

C15. In genetic drift, allele frequencies are drifting. It is an appropriate term because the word *drift* implies a random process. Nevertheless, drift can be directional. A boat may drift from one side of a lake to another. It would not drift in a straight path, but the drifting process will alter its location. Similarly, allele frequencies can drift up and down and eventually lead to the elimination or fixation of particular alleles within a population.

C16. A neutral force is one that alters allele frequencies without any regard to whether the changes are beneficial or not. Genetic drift and migration are the two main ways this can occur. An example is the founder effect, when a group of individuals migrate to a new location such as an island. Adaptive forces increase the reproductive success of a species. Natural selection is the adaptive force that tends to eliminate harmful alleles from a population and increase the frequency of beneficial alleles. An example would be the long neck of the giraffe, which enables it to feed in tall trees. At the molecular level, beneficial mutations may alter the coding sequence of a gene and change the structure and function of the protein in a way that is beneficial. For example, the sickle-cell anemia allele alters the structure of hemoglobin, and in the heterozygous condition, this inhibits the sensitivity of red blood cells to the malaria pathogen.

C17.

$$(1 - u)^t = \frac{P_t}{P_o}$$

$$(1 - 10^{-4})^t = 0.5/0.6 = 0.833$$

$$(0.9999)^t = 0.833$$

$$t = 1,827 \text{ generations}$$

C18. Genetic drift is due to sampling error, and the degree of sampling error depends on the population size. In small populations, the relative proportion of sampling error is much larger. If genetic drift is moving an allele toward fixation, it will take longer in a large population because the degree of sampling error is much smaller.

C19.A. Probability of fixation =  $1/2N = 1/2(4) = 1/8$ , or 0.125

B.  $\bar{t} \approx 4N = 4(4) = 16$  generations

C. The preceding calculations assume a constant population size. If the population grows after it has been founded by these four individuals, the probability of fixation will be lower and the time it takes to reach fixation will be longer.

C20. During the bottleneck effect, allele frequencies are dramatically altered due to genetic drift. In extreme cases, some alleles are lost while others may become fixed at 100%. The overall effect is to decrease the genetic diversity within the population. This may make it more difficult for the species to respond in a positive way to changes in the environment. Species that are approaching extinction are also facing a bottleneck as their numbers decrease. The loss of genetic diversity may make it even more difficult for the species to rebound.

C21. When two populations intermix, both populations tend to have more genetic variation because each population introduces new alleles into the other population. In addition, the two populations tend to have similar allele frequencies, particularly when a large proportion migrates.

- C22. Directional selection favors the phenotype at one phenotypic extreme. Over time, natural selection is expected to favor the fixation of alleles that cause these phenotypic characteristics. Disruptive selection favors two or more phenotypic categories. It will lead to a population with a balanced polymorphism for the trait. Stabilizing selection favors individuals with intermediate phenotypes. It will also tend to promote polymorphism, since the favored individuals may be heterozygous for particular alleles.
- C23. Darwinian fitness is the relative reproductive potential of an individual in a population. The most successful individuals are given a value of 1.0. Characteristics that promote survival, ability to attract a mate, or an enhanced fertility would be expected to promote Darwinian fitness. Examples are the thick fur of a polar bear, which helps it to survive in a cold climate; the bright plumage of male birds, which helps them to attract a mate; and the high number of gametes released by certain species of fish, which helps their fertility.
- C24. The intuitive meaning of the mean fitness of a population is the relative likelihood that members of a population will reproduce. If the mean fitness is high, it is likely that an average member will survive and produce offspring. Natural selection increases the mean fitness of a population.
- C25. The genetic load refers to all the genetic variation within a population that has the potential to be deleterious. It is a common consequence of genetic variation since genetic balances can arise. For example, heterozygote advantage can lead to the prevalence of alleles that are deleterious in the homozygous condition. In general, it happens that alleles, or combinations of alleles, that are advantageous in one circumstance are not advantageous in another. Since populations shuffle their genes from one generation to the next, and may move to new environments, genetic load may occur.
- C26. A. Random mutation is the source of genetic variation that may lead to antibiotic resistance. A random mutation may create an antibiotic-resistance allele. This could occur in different ways. Two possibilities are:
1. Many antibiotics exert their effects by binding to an essential cellular protein within the microorganism and inhibiting its function. A random mutation could occur in the gene that encodes such an essential cellular protein; this could alter the structure of the protein in a way that would prevent the antibiotic from binding to the protein or inhibiting its function.
  2. As another possibility, microorganisms, which are killed by antibiotics, possess many enzymes, which degrade related compounds. A random mutation could occur in a gene that encodes a degradative enzyme so that the enzyme now recognizes the antibiotic and degrades it.
- B. When random mutations occur, they may be lost due to genetic drift. This is particularly likely when the frequency of the mutation is very low in a large population. Alternatively (and much less likely), a random mutation that confers antibiotic resistance could become fixed in a population.
- C. If a random mutation occurs that confers antibiotic resistance, and if the mutation is not lost by genetic drift, natural selection will favor the growth of microorganisms that carry the antibiotic-resistance allele if the organisms are exposed to the antibiotic. Therefore, if antibiotics are widely used, this will kill microorganisms that are sensitive and favor the proliferation of ones that happen to carry antibiotic-resistance alleles.
- C27. A. True.  
 B. True.  
 C. False; it causes allele loss or fixation, which results in less diversity.  
 D. True.
- C28. A. Migration will increase the genetic diversity in both populations. A random mutation could occur in one population to create a new allele. This new allele could be introduced into the other population via migration.  
 B. The allele frequencies between the two populations will tend to be similar to each other, due to the intermixing of their alleles.  
 C. Genetic drift depends on population size. When two populations intermix, this has the effect of increasing the overall population size. In a sense, the two smaller populations behave somewhat like one big population. Therefore, the effects of genetic drift are lessened when the individuals in two populations can migrate. The net effect is that allele loss and allele fixation are less likely to occur due to genetic drift.
- C29. A. Disruptive. There are multiple environments that favor different phenotypes.  
 B. Directional. The thicker the fur, the more likely that survival will occur.  
 C. Stabilizing. Low birth weight is selected against because it results in low survival. Also, very high birth weight is selected against because it could cause problems in delivery, which also could decrease the survival rate.  
 D. Directional. Sturdy stems and leaves will promote survival in windy climates.

