

- C1. Quantitative traits are described numerically. Examples include height, weight, speed, and metabolic rate. In a population, a trait may be given a mean value, and the degree of variation may be described by the variance and standard deviation.
- C2. At the molecular level, quantitative traits often exhibit a continuum of phenotypic variation because they are usually influenced by multiple genes that exist as multiple alleles. A large amount of environmental variation will also increase the phenotypic overlaps among different genotypic categories.
- C3. A normal distribution varies in a symmetrical way around a mean value. When graphed, it exhibits a bell-shaped curve. It is common for quantitative traits in a population to have a normal distribution around a mean value. If a distribution is normal, the standard deviation can predict the percentage of individuals that will fall within certain limits. For example, approximately 68% of all individuals in a population will be within one (plus or minus) standard deviation unit from the mean.
- C4. A discontinuous trait is one that falls into discrete categories. Examples include brown eyes versus blue eyes in humans or purple versus white flowers in pea plants. A continuous trait is one that does not fall into discrete categories. Examples include height in humans and fruit weight in tomatoes. Most quantitative traits are continuous; the trait falls within a range of values. The reason why quantitative traits are continuous is because they are usually polygenic and greatly influenced by the environment. As shown in Figure 24.4*b*, this tends to create ambiguities between genotypes and a continuum of phenotypes.
- C5. With regard to genetics, a frequency distribution is a graph that compares the number of individuals and their phenotypes for a given trait. This is a common way to depict the distribution of a quantitative trait in a population. To make a frequency distribution for a continuous quantitative trait, it is necessary to divide individuals into arbitrary groups. For example, if the trait is weight, individuals could be divided into groups that are in multiples of 10 lb. Such a grouping would begin with individuals in the 0–10 lb range, 10–20 lb, 20–30 lb, etc. To make a frequency distribution, a population of individuals would be chosen, and then the number of individuals in each grouping would be determined. The groupings (weight categories) would be plotted on the x-axis, and the number of individuals in each group would be plotted on the y-axis.
- C6. To be in the top 2.5% is about two standard deviation units. If we take the square root of the variance, the standard deviation would be 20.6 lb. To be in the top 2.5% an animal would have to weigh 41.2 lb heavier than the mean, which equals 465.2 lb. To be in the bottom 0.13%, an animal would have to be three standard deviations lighter, which would be 61.8 lb lighter than the mean or 362.2 lb.
- C7. A. The differences in variance could be explained by variation in the way the potatoes are affected by environmental variation, or they could be explained by genetic differences. The strain with a higher variance may have more genetic variation.
- B. On the one hand, the strain with a higher variance may be better because the farmer may want to select for individuals who produce larger potatoes. On the other hand, if the farmer wants the size of his/her potatoes to be uniform, the population with a smaller variance would be better.
- C. You would use the strain with a higher variance, hoping that a significant proportion of the variance was due to genetic variation.
- C8. There is a positive correlation, but it could have occurred as a matter of chance alone. You would need to conduct more experimentation to determine if there is a significant correlation such as examining a greater number of pairs of individuals. If  $N = 500$ , the correlation would be statistically significant and you would conclude that the correlation did not occur as a matter of random chance. However, you could not conclude cause and effect.
- C9. A negative correlation means that two variables are related to each other in opposite ways. For example, a high amount of snowfall in the winter might be negatively correlated with the survival of wild species.
- C10. When a correlation coefficient is statistically significant, it means that the association is likely to have occurred for reasons other than random sampling error. It may indicate cause and effect but not necessarily. For example, large parents may have large offspring due to genetics (cause and effect). However, the correlation may be related to the sharing of similar environments rather than cause and effect.
- C11. Polygenic inheritance occurs when two or more different genes influence the outcome of a single trait. Such traits are difficult to study because there may be multiple genes with multiple alleles and environmental effects may be significant. Therefore, the discrete genotypes do not fall within discrete phenotypic categories. Instead, there tends to be overlap and this overlap confounds a genetic analysis. Molecular approaches, such as QTL mapping, can greatly help the situation.

- C12. Quantitative trait loci are sites within chromosomes that contain genes that affect a quantitative trait. It is possible for a QTL to contain one gene, or it may contain two or more closely linked genes. QTL mapping, which involves linkage to known molecular markers, is commonly used to determine the locations of QTLs.
- C13. A. The probability of inheriting two light alleles from a parent would be  $0.5 \times 0.5 = 0.25$ . The probability of inheriting two light alleles from both parents would be  $0.25 \times 0.25 = 0.0625$ , or 6.25%.
- B. The probability of inheriting three light alleles from a parent would be  $0.5 \times 0.5 \times 0.5 = 0.125$ . The probability of inheriting three light alleles from both parents would be  $0.125 \times 0.125 = 0.0156$ , or 1.56%.
- C. The probability of inheriting four light alleles from a parent would be  $0.5 \times 0.5 \times 0.5 \times 0.5 = 0.0625$ . The probability of inheriting four light alleles from both parents would be  $0.0625 \times 0.0625 = 0.0039$ , or 0.39%.
- C14. If the broad sense heritability equals 1.0, it means that all of the variation in the population is due to genetic variation rather than environmental variation. It does not mean that the environment is unimportant in the outcome of the trait. Under another set of environmental conditions the trait may have turned out quite differently.
- C15. The dominance hypothesis proposes that the inbred strains are homozygous for harmful recessive alleles whereas the hybrid is not. The overdominance hypothesis suggests that certain combinations of alleles are particularly beneficial in the heterozygote. Overall, it is difficult to judge which hypothesis is correct, although geneticists rarely observe overdominance in single genes. An exception is the sickle-cell allele, which we have discussed throughout this textbook. On the other hand, the formation of recessive alleles that are harmful is a widespread phenomenon. These observations tend to support the dominance hypothesis, but the situation is by no means resolved.
- C16. Hybrid vigor is the phenomenon in which an offspring produced from two inbred strains is more vigorous than the corresponding parents. Tomatoes and corn are often the products of hybrids.
- C17. The primary advantage of selective breeding in agriculture is that it improves the magnitude of quantitative traits. For example, selective breeding can increase fruit size, fruit number, etc. A disadvantage is that selective breeding will diminish the overall genetic diversity in the population, and this may result accidentally in the prevalence of traits that are not desirable. For example, as a tomato breeder selects for bigger and juicier tomatoes, he/she may unwittingly obtain a variety that has bigger and juicier tomatoes, but the plants may be more susceptible to pathogens, compared to the original (nonselected) parental strain.
- Undesirable traits, like pathogen sensitivity, are often inherited in a recessive manner. These are due to rare recessive alleles that happen to become monomorphic, as a random result of selective breeding. The creation of hybrids may overcome the adverse effects of such rare recessive alleles. Two different varieties that have been independently subjected to selective breeding are not likely to be monomorphic for the same recessive alleles. Therefore, when two varieties are crossed, the hybrids become heterozygous and carry one copy of the normal allele at each gene and one copy of a detrimental recessive allele. If the allele is recessive, it will not have an adverse effect on the phenotype of the organism.
- C18. When a species is subjected to selective breeding, the breeder is focusing his/her attention on improving one particular trait. In this case, the rose breeder is focused on the size and quality of the flowers. Since the breeder usually selects a small number of individuals (e.g., the ones with best flowers) as the breeding stock for the next generation, this may lead to a decrease in the allelic diversity at other genes. For example, several genes affect flower fragrance. In an unselected population, these genes may exist as “fragrant alleles” and “nonfragrant alleles.” After many generations of breeding for large flowers, the fragrant alleles may be lost from the population, just as a matter of random chance. This is a common problem of selective breeding. As you select for an improvement in one trait, you may inadvertently diminish the quality of an unselected trait.
- Other people have suggested that the lack of fragrance may be related to flower structure and function. Perhaps the amount of energy that a flower uses to make beautiful petals somehow diminishes its capacity to make fragrance.
- C19. When you examine a trait in a population, it often varies among different members. Sometimes the variation is large and sometimes it is small. The variation can be caused by genetic differences among the members of the population, and it can be caused by the fact that each member of the population is exposed to a slightly or greatly different environment. The proportion of the variation that is caused by genetic differences among the members of the population is the heritability of the trait. It is applicable only to a particular population raised in a particular environment because each population has its own unique amount of genetic variation (based on the genetic heritage of its members), and the members of each population are exposed to their own unique environmental conditions.

- C20. Broad sense heritability takes into account all genetic factors that affect the phenotypic variation in a trait. Narrow sense heritability considers only alleles that behave in an additive fashion. In many cases, the alleles affecting quantitative traits appear to behave additively. More importantly, if a breeder assumes that the heritability of a trait is due to the additive effects of alleles, it is possible to predict the outcome of selective breeding. This is also termed the *realized heritability*.
- C21. A. False. The environment has very little impact on the amount of variation in the trait. However, environment always contributes greatly to the outcome of every trait. You could not have a living organism without an environment.  
 B. True.  
 C. Probably true, but we cannot say for sure. Quantitative traits are usually polygenic.  
 D. False. You cannot say anything about the heritability of egg weight in Montana chickens. It depends on the amount of genetic variation in the population and on the type of environment in which they are raised.
- C22. A. Because of their good nutrition, you may speculate that they would grow to be taller.  
 B. If the environment is rather homogeneous, then heritability values tend to be higher because the environment contributes less to the amount of variation in the trait. Therefore, in the commune, the heritability might be higher, because they uniformly practice good nutrition. On the other hand, since the commune is a smaller population, the amount of genetic variation might be less, so this would make the heritability lower. However, since the problem states that the commune population is large, we would probably assume that the amount of genetic variation is similar to the general population. Overall, the best guess would be that the heritability in the commune population is higher because of the uniform nutrition standards.  
 C. As stated in part B, the amount of variation would probably be similar, since the commune population is large. As a general answer, larger populations tend to have more genetic variation. Therefore, the general population probably has a bit more variation, but it may not be much more than the commune population.
- C23. Eventually, the alleles that are being selected will become monomorphic in the population, and further selection will have no effect.
- C24. A natural population of animals is more likely to have a higher genetic diversity compared to a domesticated population. This is because domesticated populations have been subjected to many generations of selective breeding, which decreases the genetic diversity. Therefore,  $V_G$  is likely to be higher for the natural population. The other issue is environment. It is difficult to say which group would have a more homogeneous environment. In general, natural populations tend to have a more heterogeneous environment, but not always. If the environment is more heterogeneous, this tends to cause more phenotypic variation, which makes  $V_E$  higher.

$$\begin{aligned}\text{Heritability} &= V_G/V_T \\ &= V_G/(V_G + V_E)\end{aligned}$$

When  $V_G$  is high, this increases heritability. When  $V_E$  is high, this decreases heritability. In the natural wolf population, we would expect that  $V_G$  would be high. In addition, we would guess that  $V_E$  might be high as well (but that is less certain). Nevertheless, if this were the case, the heritability of the wolf population might be similar to the domestic population. This is because the high  $V_G$  in the wolf population is balanced by its high  $V_E$ . On the other hand, if  $V_E$  is not that high in the wolf population, or if it is fairly high in the domestic population, then the wolf population would have a higher heritability for this trait.

- C25. A. Dominance hypothesis  
 B. Both hypotheses  
 C. Overdominance hypothesis