C1. The first principle is that there is genetic variation within natural populations. Therefore, offspring can inherit different alleles, which may affect their phenotype. The second principle is natural selection. This process selects for individuals that have phenotypes that make them reproductively superior. Reproductive superiority may be related to survival because certain alleles may be favored under particular environmental conditions. In addition, natural selection may be a sexual selection process whereby phenotypes that are more likely to mate and produce offspring are at a reproductive advantage.

C2. Evolution is unifying because all living organisms on this planet evolved from the same primordial organism. At the molecular level, all organisms have a great deal in common. With the exception of a few viruses, they all use DNA as their genetic material. This DNA is found within chromosomes, and the sequence of the DNA is organized into units called genes. Most genes are structural genes that encode the amino acid sequence of polypeptides. Polypeptides fold to form functional units called proteins. At the cellular level, all living organisms also share many similarities. For example, living cells share many of the same basic features including a plasma membrane, ribosomes, enzymatic pathways, etc. In addition, as discussed in Chapter 7, the mitochondria and chloroplasts of eukaryotic cells are evolutionarily derived from bacterial cells.

C3. Reproductive isolation occurs when two species are unable to mate and produce viable offspring. As discussed in Table 26.1, several prezygotic and postzygotic mechanisms can prevent interspecies matings. According to the biological species concept, reproductive isolation is the underlying cause of speciation. Speciation occurs when a group becomes reproductively isolated from another group. The recognition species concept is similar except that it places a greater emphasis on the forces of natural selection in promoting reproductive isolation. According to the species recognition concept, natural selection promotes reproductive isolation by selecting for groups of individuals who are reproductively compatible.

C4. Sexual selection is a form of natural selection that favors traits that make it more likely for an organism to reproduce. In many species of animals, natural selection selects for male traits that make it more likely to find a mate and successfully produce offspring. For example, the bright plumage of male birds makes it easier for the female to identify the males of their own species. Many species of deer have antlers so that males may spar with each other as a way to achieve reproductive superiority.

C5. A. Postzygotic

B. Prezygotic

C. Prezygotic

D. Postzygotic

C6. Anagenesis is the evolution of one species into another, while cladogenesis is the divergence of one species into two or more species. Cladogenesis is more prevalent. There may be many reasons why. It is common for an abrupt genetic change such as alloploidy to produce a new species from a preexisting one. Also, migrations of a few members of species into a new region may lead to the formation of a new species in the new region (i.e., allopatric speciation).

C7. Sometimes a single mutation or a few mutations will dramatically alter the phenotypic characteristics of an individual. If the phenotypic changes are beneficial, natural selection may lead to a rapid change in the gene pool. Similarly, when a small group of individuals migrate to a new area that has a different environment, natural selection may quickly lead to a change in the gene pool by favoring adaptations that are beneficial. A third mechanism that does not rely on natural selection is allotetraploidy. When this occurs, the allotetraploid is reproductively isolated from the corresponding diploid species because a cross between the allotetraploid and the diploid will produce infertile offspring.

C8. A. Allopatric

B. Sympatric

C. At first, it may involve parapatric speciation with a low level of intermixing. Eventually, when smaller lakes are formed, allopatric speciation will occur.

C9. Allotetraploids are usually reproductively isolated from the two original species due to hybrid sterility. The hybrid may survive, but it will not have an even number of sets of chromosomes. Therefore, when it undergoes meiosis, each chromosome will not have a homologue to pair with. Therefore, the cells that are produced will be highly aneuploid and lead to inviable offspring. Allotetraploids tend to be fertile because they have an even number of chromosomes that can pair during meiosis and do not form aneuploid cells.

C10. The main evidence in favor of punctuated equilibrium is the fossil record. Paleontologists rarely find a gradual transition of fossil forms. The transition period in which environment pressure and genetic changes cause a previous species to evolve into a new species is thought to be so short that few, if any, of the transitional members would be preserved as fossils. Therefore, the fossil record primarily contains representatives from the long equilibrium periods. Also, rapid evolutionary change is consistent with known genetic phenomena, including single-gene mutations that have dramatic effects on phenotypic characteristics, the founder effect, and genetic events such as changes in chromosome structure (e.g., inversions and translocations) or chromosome number, which may abruptly create individuals with new phenotypic traits. In some cases, however, gradual changes are observed in certain species over long periods of time. In addition, the gradual accumulation of mutations is known to occur from the molecular analyses of DNA.

C11. Reproductive isolation does not really apply to bacteria. Two different bacteria of the same species do not produce gametes that have to fuse to produce an offspring, although bacteria can exchange genetic material (as described in Chapter 6). For this reason, it becomes more difficult to distinguish different species of bacteria. A geneticist would probably divide bacteria into different species based on the sequences of their DNAs. When the sequence differences had reached some arbitrary level, two populations of bacteria would be considered separate species. Historically, bacteria were first categorized as different species based on morphological and physiological differences. Later, when genetic tools such as DNA sequencing became available, the previously identified species could be categorized based on genetic sequences. One issue that makes categorization rather difficult is that a species of bacteria can exist as closely related strains that may have a small number of genetic differences.

C12. A. Yes, it may help the females identify the males of this species.

B. Yes, it helps the males to reproduce.

C. No, it may help the females survive, but it probably does not help the males to identify the females.

D. Yes, it may help the females identify the males of this species.

C13. Allopatric speciation involves a physical separation of a species into two or more separate populations. Over time, each population accumulates mutations that alter the characteristics of each population. Since the populations are separated, each will evolve different characteristics and eventually become distinct species. Sympatric speciation is just the opposite. Members of a population are not physically separated, but something happens (e.g., polyploidy) that abruptly results in reproductive isolation between members of the population. For example, a species could be diploid and a member of the population could become tetraploid. The tetraploid member would be reproductively isolated from the diploid members because hybrid offspring would be triploid and sterile. Therefore, the tetraploid individual has become a separate species. Parapatric speciation is a mixture of allopatric and sympatric. There is some physical separation of two or more populations, but the separation is not absolute. On occasion, members of different populations can interbreed. Even so, the (somewhat) separated populations will tend to accumulate different genetic changes (e.g., inversions) that will ultimately lead to reproductive isolation among the different populations.

C14. One of the major goals in the field of molecular evolution is to understand, at the molecular level, how changes in the genetic material have led to the formation of present-day species. Along these same lines, molecular biologists would like to understand why genetic variation is prevalent within a single species, and also to examine the degree of differences in genetic variation among different species. Comparisons of the genetic material at the molecular level can help to elucidate evolutionary relationships. The field of molecular evolution also is aimed at understanding how genes change at the molecular level. Geneticists would like to know the rate of genetic change and whether changes are neutral or adaptive.

C15. Line up the sequences where the two Gs are underlined.

TTGCATAGGCATACCGTATGATATCGAAAACTAGAAAAATAGGGCGATAGCTA

GTATGTTATCGAAAAGTAGCAAAATAGGGCGATAGCTACCCAGACTACCGGAT

C16. The rate at which a gene evolves depends on whether mutations in the gene will affect the function of the encoded RNA or protein. If a gene can tolerate many mutations without inhibiting the function of the encoded RNA or protein, it will evolve rapidly. Some genes, however, are unable to tolerate many mutations because most mutations inhibit function. When examining evolutionary relationships between species, it is helpful to have a moderate number of differences between the species, but not too many and not too few. Rapidly evolving genes are useful to examine relationships between closely related species because they will probably have a significant number of differences. More distantly related species can be compared by analyzing slowly evolving genes.

C17. A gene sequence can evolve more rapidly. The purpose of structural genes is to encode a polypeptide with a defined amino acid sequence. Many nucleotide changes will have no effect on the amino acid sequence of the polypeptide. For example, mutations in introns and mutations at the wobble base may not affect the amino acid sequence of the encoded polypeptide. These neutral mutations will happen rather rapidly on an evolutionary timescale because natural selection will not remove them from the population. In contrast, changes in the amino acid sequence may alter the structure and function of the polypeptide. Most random mutations that affect the polypeptide sequence are more likely to be detrimental than beneficial, and detrimental mutations will be eliminated by natural selection. This makes it more difficult for the amino acid sequence of the polypeptide to evolve. Only neutral changes and beneficial changes will happen rapidly, and these are less likely to occur in the amino acid sequence compared to the gene sequence.

C18. Some regions of a polypeptide are particularly important for the structure or function of a protein. For example, a region of a polypeptide may form the active site of an enzyme. The amino acids that are found within the active site are likely to be exquisitely located for the binding of the enzyme's substrate and/or for catalysis. Changes in the amino acid sequence of the active site usually have a detrimental effect on the enzyme's functions. Therefore, these types of polypeptide sequences (like those found in active sites) are not likely to change. If they did change, natural selection would prevent the change from being transmitted to future generations. In contrast, other regions of a polypeptide are less important. These other regions would be more tolerant of changes in amino acid sequence and therefore would evolve more rapidly. When comparing related protein sequences, regions that are important for function can often be identified based on less sequence variation.

C19. You would expect the sequences of plant storage proteins to evolve rapidly. The polypeptide sequence is not particularly important for the structure or function of the protein. The purpose of the protein is to provide nutrients to the developing embryo. Changing the sequence would be tolerated. However, major changes in the amino acid composition (not the sequence) may be selected against. For example, the storage protein would have to contain some cysteines in its amino acid sequence because the embryo would need some cysteine to grow. However, the location of cysteines within the amino acid sequence would not be important; it would only be important that the gene sequence have some cysteine codons.

C20. There are lots of possibilities. A few are listed here.

1. DNA is used as the genetic material.
2. The semiconservative mechanism of DNA replication is the same.
3. The genetic code is fairly universal.
4. Certain genes are found in all forms of life (such as 16S rRNA genes).
5. Gene structure and organization is pretty similar among all forms of life.
6. RNA is transcribed from genes.
7. mRNA is used as a messenger to synthesize polypeptides.

C21. The α–globin sequences in humans and horses are more similar to each other, compared to the α–globin in humans and the ß-globin in humans. This suggests that the gene duplication that produced the α– and ß-globin gene occurred first. After this gene duplication occurred, each gene accumulated several different mutations that caused the sequences of the two genes to diverge. At a much later time, during the evolution of mammals, a split occurred that produced different branches in the evolutionary tree of mammals. One branch led to the formation of horses and a different branch led to the formation of humans. During the formation of these mammalian branches (which has been more recent), some additional mutations could occur in the α– and ß-globin genes. This would explain why the α–globin gene in humans and horses is not exactly the same. However, it is more similar than the α– and ß-globin genes within humans because the divergence of humans and horses occurred much more recently that than the gene duplication that produced the α– and ß-globin genes. In other words, there has been much less time for the α–globin gene in humans to diverge from the α–globin gene in horses.

C22. Both theories propose that random mutations occur in populations. The primary difference between the neutral theory and the selectionist theory is the relative contributions of neutral mutations and nonneutral mutations for explaining present-day variation. Are most forms of genetic variation neutral or brought about by natural selection? Both sides agree that natural selection has been an important force in shaping the phenotypes of all species. It is natural selection that favors the traits that allow organisms to survive in their environments. Within each species, however, there is still a great deal of variation (i.e., not all members of the same species are genetically identical). The neutral theory would argue that most of this variation is neutral. Random mutations occur, which have no effect on the phenotype of the individual, and genetic drift causes the allele frequency to rise to significant levels. The neutral theory suggests that most (but certainly not all) variation can be explained in this manner. In contrast, the selectionist theory suggests that most of the variation seen in natural populations is due to natural selection. The neutral theory of evolution is sometimes called non-Darwinian evolution because it isn't based on natural selection, which was a central tenet in Darwin's theory.

C23. A. This is an example of neutral mutation. Mutations in the wobble base are neutral when they do not affect the amino acid sequence.

B. This is an example of natural selection. *Carbonaria* moths can avoid predation in polluted woods while *typical* moths can avoid predation in unpolluted woods.

C. This is an example of natural selection. Random mutations that occur in vital regions of a polypeptide sequence are likely to inhibit function. Therefore, these types of mutations are eliminated by natural selection. That is why they are relatively rare.

D. This is a combination of neutral mutation and natural selection. The prevalence of mutations in introns is due to the accumulation of neutral mutations. Most mutations within introns do not have any effect on the expression of the exons, which contain the polypeptide sequence. In contrast, mutations within the exons are more likely to be affected by natural selection. As mentioned in the answer to part C, mutations in vital regions are likely to inhibit function. Natural selection tends to eliminate these mutations. Therefore, mutations within exons are less likely than mutations within introns.

C24. Natural selection plays a dominant role in the elimination of deleterious mutations and the fixation of beneficial mutations. Genetic drift also would affect the frequencies of deleterious and beneficial alleles, particularly in small populations. Neutral alleles are probably much more frequent than beneficial alleles. Neutral alleles are not acted upon by natural selection. Nevertheless, they can become prevalent within a population due to genetic drift. The neutral theory suggests that most of the genetic variation in natural populations is due to the accumulation of neutral mutations. A large amount of data supports this theory, although some geneticists still oppose it.

C25. Generally, one would expect a similar number of chromosomes with very similar banding patterns. However, there may be a few notable differences. An occasional translocation could change the size or chromosomal number between two different species. Also, an occasional inversion may alter the banding pattern between two species.

C26. The rate of deleterious and beneficial mutations would probably not be a good molecular clock. Their rate of formation might be relatively constant, but their rate of elimination or fixation would probably be quite variable. These alleles are acted upon by natural selection. As environmental conditions change, the degree to which natural selection would favor beneficial alleles and eliminate deleterious alleles would also change. For example, natural selection favors the sickle-cell allele in regions where malaria is prevalent but not in other regions. Therefore, the prevalence of this allele does not depend solely on its rate of formation and random genetic drift.