

- C1. A. G→A, which is a transition.  
 B. T→G, which is a transversion.  
 C. A single-nucleotide deletion.  
 D. C→G, which is a transversion.
- C2. A gene mutation is a relatively small mutation that is localized to a particular gene. A chromosome mutation is a large enough change in the genetic material so that it can be seen with the light microscope. This would affect several genes. Genome mutations are changes in chromosome number.
- C3. It is a gene mutation, a point mutation, a base substitution, a transition mutation, a forward mutation, a deleterious mutation, a mutant allele, a nonsense mutation, a conditional mutation, and a temperature-sensitive lethal mutation.
- C4. A suppressor mutation suppresses the phenotypic effects of some other mutation. Intragenic suppressors are within the same gene as the first mutation. Intergenic suppressors are in some other gene.
- C5. A. It would probably inhibit protein function, particularly if it was not near the end of the coding sequence.  
 B. It may or may not affect protein function depending on the nature of the amino acid substitution and whether the substitution is in a critical region of the protein.  
 C. It would increase the amount of functional protein.  
 D. It may affect protein function if the alteration in splicing changes an exon in the mRNA that results in a protein with a perturbed structure.
- C6. The X rays did not produce a mutation because a mutation is a heritable change in the genetic material. In this case, the X rays have killed the cell, so changes in DNA structure cannot be passed from cell to cell or from parent to offspring.
- C7. A. Not appropriate, because the second mutation is at a different codon.  
 B. Appropriate.  
 C. Not appropriate, because the second mutation is in the same gene as the first mutation.  
 D. Appropriate.
- C8. An efficient nonsense suppressor would probably inhibit cell growth because all of the genes that have their stop codons in the correct location would make proteins that would be too long. This would waste cellular energy, and in some cases, the elongated protein may not function properly.
- C9. A. Silent, because the same amino acid (glycine) is encoded by GGA and GGT.  
 B. Missense, because a different amino acid is encoded by CGA compared to GGA.  
 C. Missense, because a different amino acid is encoded by GTT compared to GAT.  
 D. Frameshift, because an extra base is inserted into the sequence.
- C10. Here are two possible examples:  
 The consensus sequences for many bacterial promoters are  $-35: 5'-TTGACA-3'$  and  $-10: 5'-TATAAT-3'$ . Most mutations that alter the consensus sequence would be expected to decrease the rate of transcription. For example, a mutation that changed the  $-35$  region to  $5'-GAGACA-3'$  would decrease transcription.  
 The sequence  $5'-TGACGTCA-3'$  is recognized by the CREB transcription factor. If this sequence was changed to  $5'-TGAGGTCA-3'$  the CREB protein would not recognize it very well, and the adjacent gene would not be regulated properly in the presence of cAMP.
- C11. One possibility is that a translocation may move a gene next to a heterochromatic region of another chromosome and thereby diminish its expression; or it could be moved next to a euchromatic region and increase its expression. Another possibility is that the translocation breakpoint may move the gene next to a new promoter or regulatory sequences that may now influence the gene's expression.

C12. Random mutations are more likely to be harmful. The genes within each species have evolved to work properly. They have functional promoters, coding sequences, terminators, etc., that allow the genes to be expressed. Mutations are more likely to disrupt these sequences. For example, mutations within the coding sequence may produce early stop codons, frameshift mutations, and missense mutations that result in a nonfunctional polypeptide. On rare occasions, however, mutations are beneficial; they may produce a gene that is expressed better than the original gene or produce a polypeptide that functions better. As discussed in Chapter 25, beneficial mutations may be acted upon by natural selection over the course of many generations and eventually become the prevalent allele in the population.

C13. A. No, the position (i.e., chromosomal location) of a gene has not been altered.

B. Yes, the expression of a gene has been altered because it has been moved to a new chromosomal location.

C. Yes, the expression of a gene has been altered because it has been moved to a new chromosomal location.

- C14. Yes, a person with cancer is a genetic mosaic. The cancerous tissue contains gene mutations that are not found in noncancerous cells of the body.
- C15. If a mutation within the germ line is passed to an offspring, all the cells of the offspring's body will carry the mutation. A somatic mutation affects only the somatic cell in which it originated and all of the daughter cells that the somatic cell produced. If a somatic mutation occurs early during embryonic development, it may affect a fairly large region of the organism. Since germ-line mutations affect the entire organism, they are potentially more harmful (or beneficial), but this is not always the case. Somatic mutations can cause quite harmful effects such as cancer. Germ-line mutations may be passed to offspring.
- C16. The drawing should show the attachment of a methyl or ethyl group to a base within the DNA. The presence of the alkyl group disrupts the proper base pairing between the alkylated base and the normal base in the opposite DNA strand.
- C17. A thymine dimer can interfere with DNA replication because DNA polymerase cannot slide past the dimer and add bases to the newly growing strand. Alkylating mutagens such as nitrous acid will cause DNA replication to make mistakes in the base pairing. For example, an alkylated cytosine will base pair with adenine during DNA replication, thereby creating a mutation in the newly made strand. A third example is bromouracil, which is a thymine analogue. It may pair with guanine during DNA replication.
- C18. A. Nitrous acid causes A→G and C→T mutations, which are transition mutations.  
B. 5-bromouracil causes G→A mutations, which are transitions.  
C. Proflavin causes small additions or deletions, which may result in frameshift mutations.
- C19. During TNRE, a trinucleotide repeat sequence gets longer. If someone was mildly affected with a TNRE disorder, he/she would be concerned that an expansion of the repeat might occur during gamete formation, yielding offspring more severely affected with the disorder.
- C20. A spontaneous mutation originates within a living cell. It may be due to spontaneous changes in nucleotide structure, errors in DNA replication, or products of normal metabolism that may alter the structure of DNA. The causes of induced mutations originate from outside the cell. They may be physical agents, such as UV light or X rays, or chemicals that act as mutagens. Both spontaneous and induced mutations may cause a harmful phenotype such as a cancer. In many cases, induced mutations are avoidable if the individual can prevent exposure to the environmental agent that acts as a mutagen.
- C21. Spontaneous mutations are random events in the sense that there is no outside force that is directing the mutation to a particular gene or a particular site within a gene. However, the structure of chromatin may cause certain regions of the DNA to be more susceptible to random mutations. For example, DNA in an open conformation may be more accessible to mutagens and more likely to incur mutations. Likewise, hot spots for mutation can occur within a single gene.
- C22. Nitrous acid can change a cytosine to uracil. Excision repair systems could remove the defect and replace it with the correct base.
- C23. Excision repair systems could fix this damage. Also, recombinational repair could fix the damage.
- C24. A. True  
B. False, the TNRE is not within the promoter, it is within the coding sequence.  
C. True, CAG is a codon for glutamine.  
D. False, CCG is a codon for proline.
- C25. A spontaneous mutation is a mutation that happens as a result of events that occur within a living cell. A spontaneous mutation is not caused by an environmental agent. An induced mutation is caused directly or indirectly by an environmental agent. An individual can avoid an induced mutation if he/she avoids the harmful environmental agent.
- C26. The mutation rate is the number of new mutations per gene per generation. The mutation frequency is the number of copies of a mutant gene within a population, divided by the total number of copies (mutant and nonmutant) of that gene. The mutation frequency may be much higher than the mutation rate if new mutations accumulate within a population over the course of many generations.
- C27. The mutation frequency is the total number of mutant alleles divided by the total number of alleles in the population. If there are 1,422,000 babies, there are 2,844,000 copies of this gene (because each baby has 2 copies). The mutation frequency is  $31/2,844,000$ , which equals  $1.09 \times 10^{-5}$ . The mutation rate is the number of new mutations per generation. There are 13 babies who did not have a parent with achondroplasia. Thirteen is the

number of new mutations. If we calculate the mutation rate as the number of new mutations in a given gene per generation, then we should divide 13 by 2,844,000. In this case, the mutation rate would be  $4.6 \times 10^{-6}$ .

C28.

A.

|  |
|--|
| TTGGHTGUTGG  |
| HHUUTHUGHUU  |
| ↓ First round of replication                       |
| TTGGHTGUTGG CCAAACACCAA                            |
| AACCCACAACC HHUUTHUGHUU                            |
| ↓ Second round of replication                      |
| B. TTGGHTGUTGG TTGGGTGTTGG CCAAACACCAA CCAAACACCAA |
| AACCCACAACC AACCCACAACC GGTTTGTGGTT HHUUTHUGHUU    |

C29. The effects of mutations are cumulative. If one mutation occurs in a cell, this mutation will be passed to the daughter cells. If a mutation occurs in the daughter cell, now there will be two mutations. These two mutations will be passed to the next generation of daughter cells, and so forth. The accumulation of many mutations eventually kills the cells. That is why mutagens are more effective at killing dividing cells compared to nondividing cells. It is because the number of mutations accumulates to a lethal level.

There are two main side effects to this treatment. First, some normal (noncancerous) cells of the body, particularly skin cells and intestinal cells, are actively dividing. These cells are also killed by chemotherapy and radiation therapy. Secondly, it is possible that the therapy may produce mutations that will cause noncancerous cells to become cancerous. For these reasons, there is some maximal dose of chemotherapy or radiation therapy that is recommended.

C30. The answer is 5-bromouracil. If this chemical is incorporated into DNA, it can change an AT base pair into a CG base pair. A lysine codon, AAG, could be changed into a glutamic acid codon, CAG, with this chemical. By comparison, UV light is expected to produce thymine dimers, which would not lead to a mutation creating a glutamic acid codon, and proflavin is expected to cause frameshift mutations.

C31. A. Yes.

- B. No, the albino trait affects the entire individual.
- C. No, the early apple-producing trait affects the entire tree.
- D. Yes.

C32. A. If UvrA was missing, the repair system would not be able to identify a damaged DNA segment.

- B. If UvrC was missing, the repair system could identify the damaged segment, but it would be unable to make cuts in the damaged DNA strand.
- C. If UvrD was missing, the repair system could identify the damaged segment and make cuts in the damaged strand, but it could not unwind the damaged and undamaged strands and thereby remove the damaged segment.
- D. If DNA polymerase was missing, the repair system could identify the damaged segment, make cuts in the damaged strand, and unwind the damaged and undamaged strands to remove the damaged segment, but it could not synthesize a complementary DNA strand using the undamaged strands as a template.

C33. Methyl-directed mismatch repair is aimed at eliminating mismatches that may have occurred during DNA replication. In this case, the wrong base is in the newly made strand. The binding of MutH, which occurs on a hemimethylated sequence, provides a sensing mechanism to distinguish between the unmethylated and methylated strands. In other words, MutH binds to the hemimethylated DNA in a way that allows the mismatch repair system to know which strand is methylated and which is not.

C34. Recombinational repair occurs when the DNA is being replicated. If DNA damage occurred in exactly the same location in both replicated helices, recombinational repair could not work because it relies on the use of a strand in one replicated helix to act as a template to repair the complementary strand of the other replicated helix.

C35. The DNA-N-glycosylase would first make a cut between the base and the sugar. This would release the thymine base from the nucleotide to which it was directly attached, but the thymine would still be connected to the adjacent (3') thymine. AP endonuclease would then make a nick in this DNA strand and the thymine dimer would be removed and repaired by nick translation. Finally, the strand would be sealed by DNA ligase.

- C36. In *E. coli*, the TRCF recognizes when RNA polymerase is stalled on the DNA. This stalling may be due to DNA damage such as a thymine dimer. The TRCF removes RNA polymerase and recruits the excision DNA repair system to the region, thereby promoting the repair of the template strand of DNA. It is beneficial to preferentially repair transcribed DNA because it is functionally important. It is a DNA region that encodes a gene.
- C37. A. Nucleotide excision repair.  
B. Mismatch repair.  
C. Recombinational repair and nucleotide excision repair.
- C38. The underlying genetic defect that causes xeroderma pigmentosum is a defect in one of the genes that encode a polypeptide involved with nucleotide excision repair. These individuals are defective in repairing DNA abnormalities such as thymine dimers, abnormal bases, etc. Therefore, they are very sensitive to environmental agents such as UV light. Since they are defective at repair, UV light is more likely to cause mutations in these people, compared to unaffected individuals. For this reason, people with XP develop pigmentation abnormalities and premalignant lesions and have a high predisposition to skin cancer.
- C39. The mismatch repair system, which detects mistakes made by DNA polymerase, would not function properly. As described in Figure 16.21, the MutH protein recognizes the sequence GATC when it is hemimethylated. If an *E. coli* strain was missing the dam methylase, this sequence would not be methylated, and MutH could not bind there. Therefore, mistakes, involving base pair mismatches caused by DNA polymerase, would not be repaired. This would increase the spontaneous mutation rate in this strain.
- C40. Both types of repair systems recognize an abnormality in the DNA and excise the abnormal strand. The normal strand is then used as a template to synthesize a complementary strand of DNA. The systems differ in the types of abnormalities they detect. The mismatch repair system detects base pair mismatches, while the excision repair system recognizes thymine dimers, chemically modified bases, missing bases, and certain types of cross-links. The mismatch repair system operates immediately after DNA replication, allowing it to distinguish between the daughter strand (which contains the wrong base) and the parental strand. The excision repair system can operate at any time in the cell cycle.