another type of repair, nucleotide excision repair, the incorrect base is removed along with a few bases on the 5' and 3' end, and these are replaced by copying the template with the help of DNA polymerase. The ends of the newly synthesized fragment are attached to the rest of the DNA using DNA ligase, which creates a phosphodiester bond.

Most mistakes are corrected, and if they are not, they may result in a mutation defined as a permanent change in the DNA sequence. Mutations can be of many types, such as substitution, deletion, insertion, and translocation. Mutations can be induced or may occur spontaneously.

REVIEW QUESTIONS

1. Who was the first person to isolate the material that came to be known as nucleic acids?

a. Frederick Griffith
b. Friedrich Miescher
c. James Watson
d. Oswald Avery

2. What is bacterial transformation?

a. The transformation of a bacterium occurs during replication.
b. It is the transformation of a bacterium into a pathogenic form.
c. Transformation of bacteria involves changes in its chromosome.
d. Transformation is a process in which external DNA is taken up by a cell, thereby changing morphology and physiology.

3. What type of nucleic acid material is analyzed the most frequently in forensics cases?

a. cytoplasmic rRNA
b. mitochondrial DNA
c. nuclear chromosomal DNA
d. nuclear mRNA

4. The experiments by Hershey and Chase helped confirm that DNA was the hereditary material on the basis of the finding of what?

a. Radioactive phages were found in the pellet.
b. Radioactive cells were found in the supernatant.
c. Radioactive sulfur was found inside the cell.
d. Radioactive phosphorus was found in the cell.

5. If DNA of a particular species was analyzed and it was found that it contains 27% A, what would be the percentage of C?

a. 23%
b. 27%
c. 30%
d. 54%

6. If the sequence of the 5’ to 3’ strand is AATGCTAC, then the complementary sequence has the following sequence:

a. 3’-AATGCTAC-5’
b. 3’-CATCGTAA-5’
c. 3’-TTACGATG-5’
d. 3’-GTAGCATT-5’

7. The DNA double helix does not have which of the following?

a. antiparallel configuration
b. complementary base pairing
c. major and minor grooves
d. uracil

8. What is a purine?

a. a double ring structure with a six-membered ring fused to a five-membered ring
b. a single six-membered ring
c. a six-membered ring
d. three phosphates covalently bonded by phosphodiester bonds

9. What is the name of the method developed by Fred Sanger to sequence DNA?

a. Dideoxy Chain Termination method
b. Double Helix Determination
c. Polymerase Chain Reaction
d. Polymer Gel Electrophoresis

10. What happens when a dideoxynucleotide is added to a developing DNA strand?

a. The chain extends to the end of the DNA strand.
b. The DNA stand is duplicated.
c. The chain is not extended any further.
d. The last codon is repeated.

11. In eukaryotes, what is DNA wrapped around?

a. histones
b. polymerase
c. single-stranded binding proteins
d. sliding clamp

12. Which enzyme is only found in prokaryotic organisms?

a. DNA gyrase
b. helicase
c. ligase
d. telomerase

13. Uracil is found where?

a. chromosomal DNA
b. helicase
c. mitochondrial DNA
d. mRNA

14. What prevents the further development of a DNA strand in Sanger sequencing?

a. the addition of DNA reductase
b. the addition of dideoxynucleotides
c. the elimination of DNA polymerase
d. the addition of uracil

15. Which of the following is not one of the proteins involved during the formation of the replication fork?

a. helicase
b. ligase
c. origin of replication
d. single-strand binding proteins

16. In which direction does DNA replication take place?

a. 5’ to 3’
b. 3’ to 5’
c. 5’
d. 3’

17. Meselson and Stahl’s experiments proved that DNA replicates by which mode?

a. conservative
b. converse
c. dispersive
d. semi-conservative

18. Which set of results was found in the Meselson and Stahl’s experiments?

a. The original chromosome was kept intact and a duplicate was made.
b. The original chromosome was split and half went to each duplicate.
c. The original chromosome was mixed with new material and each duplicate strand contained both old and new.
d. The original chromosome was used as a template for two new chromosomes and discarded.

19. Which enzyme initiates the splitting of the double DNA strand during replication?

a. DNA gyrase
b. helicase
c. ligase
d. telomerase

20. Which enzyme is most directly responsible for the main process of producing a new DNA strand?

a. DNA pol I
b. DNA pol II
c. DNA pol III
d. DNA pol I, DNA pol II, and DNA pol III

21. Which portion of a chromosome contains Okazaki fragments?

a. helicase
b. lagging strand
c. leading strand
d. primer

22. Which of the following does the enzyme primase synthesize?

a. DNA primer
b. Okazaki fragments
c. phosphodiester linkage
d. RNA primer

23. The ends of the linear chromosomes are maintained by what?

a. DNA polymerase
b. helicase
c. primase
d. telomerase

24. What is the difference in the rate of replication of nucleotides between prokaryotes and eukaryotes?

a. Eukaryotes are 50 times slower.
b. Eukaryotes are 20 times faster.
c. Prokaryotes are 100 times slower.
d. Prokaryotes are 10 times faster.

25. What are Autonomously Replicating Sequences (ARS)?

a. areas of prokaryotic chromosomes that initiate copying
b. portions of prokaryotic chromosomes that can be transferred from one organism to another
c. areas of eukaryotic chromosomes that are equivalent to the origin of replication in *E. coli*
d. portions of eukaryotic chromosomes that replicate independent of the parent chromosome

26. What type of body cell does not exhibit telomerase activity?

a. adult stem cells
b. embryonic cells
c. germ cells
d. liver cells

27. During proofreading, which of the following enzymes reads the DNA?

a. DNA polymerase
b. helicase
c. topoisomerase
d. primase

28. If a prokaryotic cell is replicating nucleotides at a rate of 100 per second, how fast would a eukaryotic cell be replicating nucleotides?

a. 1000 per second
b. 100 per second
c. 10 per second
d. 1 per second

29. Which type of point mutation would have no effect on gene expression?

a. frameshift
b. missense
c. nonsense
d. silent

30. Which type of point mutation would result in the substitution of a stop codon for an amino acid?

a. frameshift
b. missense
c. nonsense
d. silent

31. You have developed skin cancer and you are pregnant. You are worried that your child will be born with the cancer you have while carrying the baby. Should you be worried?

a. Yes, the cancer can spread to the baby.
b. No, the mutations causing the cancer are in somatic cells, not reproductive germ cells.
c. Yes, the mutations can be passed on to the child through the placenta.
d. No, UV light only affects adult, somatic cells.

32. What is the initial mechanism for repairing nucleotide errors in DNA?

a. DNA polymerase proofreading
b. mismatch repair
c. nucleotide excision repair
d. thymine dimers

33. Nucleotide excision repair is often employed when UV exposure causes the formation of what?

a. phosphodiester bonds
b. purine conjugates
c. pyrimidine dimers
d. tetrad disassembly

CRITICAL THINKING QUESTIONS

34. Explain Griffith’s transformation experiments. What did he conclude from them?

a. Two strains of *S. pneumoniae* were used for the experiment. Griffith injected a mouse with heat-inactivated S strain (pathogenic) and R strain (non-pathogenic). The mouse died and S strain was recovered from the dead mouse. He concluded that external DNA is taken up by a cell that changed morphology and physiology.

b. Two strains of *Vibrio cholerae* were used for the experiment. Griffith injected a mouse with heat-inactivated S strain (pathogenic) and R strain (non-pathogenic). The mouse died and S strain was recovered from the dead mouse. He concluded that external DNA is taken up by a cell that changed morphology and physiology.

c. Two strains of *S. pneumoniae* were used for the experiment. Griffith injected a mouse with heat-inactivated S strain (pathogenic) and R strain (non-pathogenic). The mouse died and R strain was recovered from the dead mouse. He concluded that external DNA is taken up by a cell that changed morphology and physiology.

d. Two strains of *S. pneumoniae* were used for the experiment. Griffith injected a mouse with heat-inactivated S strain (pathogenic) and R strain (non-pathogenic). The mouse died and S strain was recovered from the dead mouse. He concluded that mutation occurred in the DNA of the cell that changed morphology and physiology.

35. Explain why radioactive sulfur and phosphorous were used to label bacteriophages in the Hershey and Chase experiments.

a. Protein was labeled with radioactive sulfur and DNA was labeled with radioactive phosphorous. Phosphorous is found in DNA, so it will be tagged by radioactive phosphorous.

b. Protein was labeled with radioactive phosphorous and DNA was labeled with radioactive sulfur. Phosphorous is found in DNA, so it will be tagged by radioactive phosphorous.

c. Protein was labeled with radioactive sulfur and DNA was labeled with radioactive phosphorous. Phosphorous is found in DNA, so DNA will be tagged by radioactive sulfur.

d. Protein was labeled with radioactive sulfur and DNA was labeled with radioactive phosphorous. Phosphorous is found in DNA, so DNA will be tagged by radioactive sulfur.

36. How can Chargaff's rules be used to identify different species?

a. The amount of adenine, thymine, guanine, and cytosine varies from species to species and are not found in equal quantities. They do not vary between individuals of the same species and can be used to identify different species.

b. The amount of adenine, thymine, guanine, and cytosine varies from species to species and is found in equal quantities. They do not vary between individuals of the same species and can be used to identify different species.

c. The amount of adenine and thymine is equal to guanine and cytosine and is found in equal quantities. They do not vary between individuals of the same species and can be used to identify different species.

d. The amount of adenine, thymine, guanine, and cytosine varies from species to species and they are not found in equal quantities. They vary between individuals of the same species and can be used to identify different species.

37. In the Avery, Macleod, and McCarty experiments, what conclusion would the scientists have drawn if the use of proteases prevented the transformation of R strain bacteria?

38. Describe the structure and complementary base pairing of DNA.

a. DNA is made up of two strands that are twisted around each other to form a helix. Adenine pairs up with thymine and cytosine pairs with guanine. The two strands are anti-parallel in nature; that is, the 3’ end of one strand faces the 5’ end of other strand. Sugar, phosphate and nitrogenous bases contribute to the DNA structure.

b. DNA is made up of two strands that are twisted around each other to form a helix. Adenine pairs up with cytosine and thymine pairs with guanine. The two strands are anti-parallel in nature; that is, the 3’ end of one strand faces the 5’ end of other strand. Sugar, phosphate and nitrogenous bases contribute to the DNA structure.

c. DNA is made up of two strands that are twisted around each other to form a helix. Adenine pairs up with thymine and cytosine pairs with guanine. The two strands are parallel in nature; that is, the 3’ end of one strand faces the 3’ end of other strand. Sugar, phosphate and nitrogenous bases contribute to the DNA structure.

d. DNA is made up of two strands that are twisted around each other to form a helix. Adenine pairs up with thymine and cytosine pairs with guanine. The two strands are anti-parallel in nature; that is, the 3’ end of one strand faces the 5’ end of other strand. Only sugar contributes to the DNA structure.

39. Provide a brief summary of the Sanger sequencing method.

a. Frederick Sanger’s sequencing is a chain termination method that is used to generate DNA fragments that terminate at different points using dye-labeled dideoxynucleotides. DNA is separated by electrophoresis on the basis of size. The DNA sequence can be read out on an electropherogram generated by a laser scanner.

b. Frederick Sanger’s sequencing is a chain elongation method that is used to generate DNA fragments that elongate at different points using dye-labeled dideoxynucleotides. DNA is separated by electrophoresis on the basis of size. The DNA sequence can be read out on an electropherogram generated by a laser scanner.

c. Frederick Sanger’s sequencing is a chain termination method that is used to generate DNA fragments that terminate at different points using dye-labeled dideoxynucleotides. DNA is joined together by electrophoresis on the basis of size. The DNA sequence can be read out on an electropherogram generated by a laser scanner.

d. Frederick Sanger’s sequencing is a chain termination method that is used to generate DNA fragments that terminate at different points using dye-labeled dideoxynucleotides. DNA is separated by electrophoresis on the basis of size. The DNA sequence can be read out on an electropherogram generated by a magnetic scanner.

40. Compare and contrast the similarities and differences between eukaryotic and prokaryotic DNA.

a. Eukaryotes have a single, circular chromosome, while prokaryotes have multiple, linear chromosomes. Prokaryotes pack their chromosomes by super coiling, managed by DNA gyrase. Eukaryote chromosomes are wrapped around histone proteins that create heterochromatin and euchromatin, which is not present in prokaryotes.

b. Prokaryotes have a single, circular chromosome, while eukaryotes have multiple, linear chromosomes. Prokaryotes pack their chromosomes by super coiling, managed by DNA gyrase. Eukaryote chromosomes are wrapped around histone proteins that could form heterochromatin, which is not present in prokaryotes.

c. Prokaryotes have a single, circular chromosome, while eukaryotes have multiple, linear chromosomes. Eukaryotes pack their chromosomes by super coiling, managed by DNA gyrase. Prokaryotes chromosomes are wrapped around histone proteins that could form heterochromatin, which is not present in eukaryotes.

d. Prokaryotes have a single, circular chromosome, while eukaryotes have multiple, linear chromosomes. Prokaryotes pack their chromosomes by super coiling, managed by DNA gyrase. Eukaryote chromosomes are wrapped around histone proteins that could form heterochromatin, which is present in prokaryotes.

41. DNA replication is bidirectional and discontinuous; explain your understanding of those concepts.

a. DNA polymerase reads the template strand in the 3’ to 5’ direction and adds nucleotides only in the 5’ to 3’ direction. The leading strand is synthesized in the direction of the replication fork. Replication on the lagging strand occurs in the direction away from the replication fork in short stretches of DNA called Okazaki fragments.

b. DNA polymerase reads the template strand in the 5’ to 3’ direction and adds nucleotides only in the 5’ to 3’ direction. The leading strand is synthesized in the direction of the replication fork. Replication on the lagging strand occurs in the direction away from the replication fork in short stretches of DNA called Okazaki fragments.

c. DNA polymerase reads the template strand in the 3’ to 5’ direction and adds nucleotides only in the 5’ to 3’ direction. The leading strand is synthesized in the direction away from the replication fork. Replication on the lagging strand occurs in the direction of the replication fork in short stretches of DNA called Okazaki fragments.

d. DNA polymerase reads the template strand in the 5’ to 3’ direction and adds nucleotides only in the 3’ to 5’ direction. The leading strand is synthesized in the direction of the replication fork. Replication on the lagging strand occurs in the direction away from the replication fork in long stretches of DNA called Okazaki fragments.

42. Discuss how the scientific community learned that DNA replication takes place in a semiconservative fashion.

a. Meselson and Stahl experimented with *E. coli*. DNA grown in ^{15}N was heavier than DNA grown in ^{14}N. When DNA in ^{15}N was switched to ^{14}N media, DNA sedimented halfway between the ^{15}N and ^{14}N levels after one round of cell division, indicating fifty percent presence of ^{14}N. This supports the semi-conservative replication model.

b. Meselson and Stahl experimented with *S. pneumonia*. DNA grown in ^{15}N was heavier than DNA grown in ^{14}N. When DNA in ^{15}N was switched to ^{14}N media, DNA sedimented halfway between the ^{15}N and ^{14}N levels after one round of cell division, indicating fifty percent presence of ^{14}N. This supports the semi-conservative replication model.

c. Meselson and Stahl experimented with *E. coli*. DNA grown in ^{14}N was heavier than DNA grown in ^{15}N. When DNA in ^{15}N was switched to ^{14}N media, DNA sedimented halfway between the ^{15}N and ^{14}N levels after one round of cell division, indicating fifty percent presence of ^{14}N. This supports the semi-conservative replication model.

d. Meselson and Stahl experimented with *S. pneumonia*. DNA grown in ^{15}N was heavier than DNA grown in ^{14}N. When DNA in ^{15}N was switched to ^{14}N media, DNA sedimented halfway between the ^{15}N and ^{14}N levels after one round of cell division, indicating complete presence of ^{14}N. This supports the semi-conservative replication model.

43. Explain why half of DNA is replicated in a discontinuous fashion.

a. Replication of the lagging strand occurs in the direction away from the replication fork in short stretches of DNA, since access to the DNA is always from the 5’ end. This results in pieces of DNA being replicated in a discontinuous fashion.

b. Replication of the leading strand occurs in the direction away from the replication fork in short stretches of DNA, since access to the DNA is always from the 5’ end. This results in pieces of DNA being replicated in a discontinuous fashion.

c. Replication of the lagging strand occurs in the direction of the replication fork in short stretches of DNA, since access to the DNA is always from the 5’ end. This results in pieces of DNA being replicated in a discontinuous fashion.

d. Replication of the lagging strand occurs in the direction away from the replication fork in short stretches of DNA, since access to the DNA is always from the 3’ end. This results in pieces of DNA being replicated in a discontinuous fashion.

44. Explain the events taking place at the replication fork. If the gene for helicase is mutated, what part of replication will be affected?

a. Helicase separates the DNA strands at the origin of replication. Topoisomerase breaks and reforms DNA's phosphate backbone ahead of the replication fork, thereby relieving the pressure. Single-stranded binding proteins prevent reforming of DNA. Primase synthesizes RNA primer which is used by DNA polymerase to form a daughter strand. If helicase is mutated, the DNA strands will not be separated at the beginning of replication.

b. Helicase joins the DNA strands together at the origin of replication. Topoisomerase breaks and reforms DNA's phosphate backbone after the replication fork, thereby relieving the pressure. Single-stranded binding proteins prevent reforming of DNA. Primase synthesizes RNA primer which is used by DNA polymerase to form a daughter strand. If helicase is mutated, the DNA strands will not be joined together at the beginning of replication.

c. Helicase separates the DNA strands at the origin of replication. Topoisomerase breaks and reforms DNA's sugar backbone ahead of the replication fork, thereby increasing the pressure. Single-stranded binding proteins prevent reforming of DNA. Primase synthesizes DNA primer which is used by DNA polymerase to form a daughter strand. If helicase is mutated, the DNA strands will be separated at the beginning of replication.

d. Helicase separates the DNA strands at the origin of replication. Topoisomerase breaks and reforms DNA's sugar backbone ahead of the replication fork, thereby relieving the pressure. Single-stranded binding proteins prevent reforming of DNA. Primase synthesizes DNA primer which is used by RNA polymerase to form a parent strand. If helicase is mutated, the DNA strands will be separated at the beginning of replication.

45. What are Okazaki fragments and how they are formed?

a. Okazaki fragments are short stretches of DNA on the lagging strand, which is synthesized in the direction away from the replication fork.

b. Okazaki fragments are long stretches of DNA on the lagging strand, which is synthesized in the direction of the replication fork.

c. Okazaki fragments are long stretches of DNA on the leading strand, which is synthesized in the direction away from the replication fork.

d. Okazaki fragments are short stretches of DNA on the leading strand, which is synthesized in the direction of the replication fork.

46. Compare and contrast the roles of DNA polymerase I and DNA ligase in DNA replication.

a. DNA polymerase I removes the RNA primers from the developing copy of DNA. DNA ligase seals the ends of the new segment, especially the Okazaki fragments.

b. DNA polymerase I adds the RNA primers to the already developing copy of DNA. DNA ligase separates the ends of the new segment, especially the Okazaki fragments.

c. DNA polymerase I seals the ends of the new segment, especially the Okazaki fragments. DNA ligase removes the RNA primers from the developing copy of DNA.

d. DNA polymerase I removes the enzyme primase from the developing copy of DNA. DNA ligase seals the ends of the old segment, especially the Okazaki fragments.

47. If the rate of replication in a particular prokaryote is 900 nucleotides per second, how long would it take to make two copies of a 1.2 million base pair genome?

a. 22.2 minutes

b. 44.4 minutes

c. 45.4 minutes

d. 54.4 minutes

48. How do the linear chromosomes in eukaryotes ensure that their ends are replicated completely?

a. The ends of the linear chromosomes are maintained by the activity of the telomerase enzyme.

b. The ends of the linear chromosomes are maintained by the formation of a replication fork.

c. The ends of the linear chromosomes are maintained by the continuous joining of Okazaki fragments.

d. The ends of the linear chromosomes are maintained by the action of the polymerase enzyme.

49. Compare and contrast prokaryotic and eukaryotic DNA replication.

a. A prokaryotic organism's rate of replication is ten times faster than that of eukaryotes. Prokaryotes have a single origin of replication and use five types of polymerases, while eukaryotes have multiple sites of origin and use fourteen polymerases. Telomerase is absent in prokaryotes. DNA pol I is the primer remover in prokaryotes, while in eukaryotes it is RNase H. DNA pol III performs strand elongation in prokaryotes and pol δ and pol ε do the same in eukaryotes.

b. A prokaryotic organism's rate of replication is ten times slower than that of eukaryotes. Prokaryotes have a single origin of replication and use five types of polymerases, while eukaryotes have multiple sites of origin and use fourteen polymerases. Telomerase is absent in eukaryotes. DNA pol I is the primer remover in prokaryotes, while in eukaryotes it is RNase H. DNA pol III performs strand elongation in prokaryotes and pol δ and pol ε do the same in eukaryotes.

c. A prokaryotic organism's rate of replication is ten times faster than that of eukaryotes. Prokaryotes have five origins of replication and use a single type of polymerase, while eukaryotes have a single site of origin and use fourteen polymerases. Telomerase is absent in prokaryotes. DNA pol I is the primer remover in prokaryotes, while in eukaryotes it is RNase H. DNA pol III performs strand elongation in prokaryotes and pol δ and pol ε do the same in eukaryotes.

d. A prokaryotic organism's rate of replication is ten times slower than that of eukaryotes. Prokaryotes have a single origin of replication and use five types of polymerases, while eukaryotes have multiple sites of origin and use fourteen polymerases. Telomerase is absent in prokaryotes. DNA pol I is the primer remover in eukaryotes, while in prokaryotes it is RNase H. DNA pol III performs strand elongation in prokaryotes and pol δ and pol ε do the same in eukaryotes.

50. What would be the consequence of a mutation in a mismatch repair enzyme? How will this affect the function of a gene?

a. Mismatch repair corrects the errors after the replication is completed by excising the incorrectly added nucleotide and adding the correct base. Any mutation in a mismatch repair enzyme would lead to more permanent damage.

b. Mismatch repair corrects the errors during the replication by excising the incorrectly added nucleotide and adding the correct base. Any mutation in the mismatch repair enzyme would lead to more permanent damage.

c. Mismatch repair corrects the errors after the replication is completed by excising the added nucleotides and adding more bases. Any mutation in the mismatch repair enzyme would lead to more permanent damage.

d. Mismatch repair corrects the errors after the replication is completed by excising the incorrectly added nucleotide and adding the correct base. Any mutation in the mismatch repair enzyme would lead to more temporary damage.

51. A mutation has occurred in the DNA and in the mRNA for a gene. Discuss which would have a more significant effect on gene expression. Why?

a. Both will result in the production of defective proteins. The DNA mutation, if not corrected, is permanent, while the mRNA mutation will only affect proteins made from that mRNA strand. Production of defective protein ceases when the mRNA strand deteriorates.

b. Both will result in the production of defective proteins. The DNA mutation, if not corrected, is permanent, while the mRNA mutation will not affect proteins made from that mRNA strand. Production of defective protein continues when the mRNA strand deteriorates.

c. Only DNA will result in the production of defective proteins. The DNA mutation, if not corrected, is permanent. Production of defective protein ceases when the DNA strand deteriorates.

d. Only mRNA will result in the production of defective proteins. The mRNA mutation will only affect proteins made from that mRNA strand. Production of defective protein ceases when the mRNA strand deteriorates.

52. Discuss the effects of point mutations on a DNA strand.

a. Mutations can cause a single change in an amino acid. A nonsense mutation can stop the replication or reading of that strand. Insertion or deletion mutations can cause a frame shift. This can result in non-functional proteins.

b. Mutations can cause a single change in amino acid. A missense mutation can stop the replication or reading of that strand. Insertion or deletion mutations can cause a frame shift. This can result in non-functional proteins.

c. Mutations can cause a single change in amino acid. A nonsense mutation can stop the replication or reading of that strand. Substitution mutations can cause a frame shift. This can result in non-functional proteins.

d. Mutations can cause a single change in amino acid. A nonsense mutation can stop the replication or reading of that strand. Insertion or deletion mutations can cause a frame shift. This can result in functional proteins.

53. Discuss the significance of mutations in tRNA and rRNA.

a. Mutations in tRNA and rRNA would lead to the production of defective proteins or no protein production.

b. Mutations in tRNA and rRNA would lead to changes in the semi-conservative mode of replication of DNA.

c. Mutations in tRNA and rRNA would lead to production of a DNA strand with a mutated single strand and normal other strand.

d. Mutations in tRNA and rRNA would lead to skin cancer in patients of xeroderma pigmentosa.

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54. What would Chase and Hershey have concluded if the supernatant contained radioactive labeled-phosphorus?

a. DNA was the primary source of heritable information.

b. RNA was the primary source of heritable information.

c. Protein was the primary source of heritable information.

d. Phages were the primary source of heritable information.

55. Which piece of evidence supports that the material Miescher discovered was DNA?

a. The precipitate contained sulfur.

b. The precipitate contained oxygen.

c. The precipitate contained phosphorus.

d. The precipitate contained protein.

56. Explain how forensic scientists are able to use DNA analysis to identify individuals.

a. Comparison of DNA from a known source or individual with analysis of the sequence of an unknown sample of DNA allows scientists to find out if both of them are similar or not.

b. DNA from the unknown sample is sequenced and analyzed. The result of the analysis is then matched with any random population. The matching individual then helps in forensics.

c. Comparison of DNA from a known source or individual with analysis of the sequence of bases in strands of an unknown sample of RNA allows scientists to find out if both of them are similar or not.

d. Comparison of DNA from a known source or individual with analysis of the sugars and phosphates in strands of an unknown sample of DNA allows scientists to find out if both of them are similar or not.

57. Discuss the contributions of Francis Crick, James Watson, and Rosalind Franklin to the discovery of the structure of DNA.

a. Rosalind Franklin used X-ray diffraction methods to demonstrate the helical nature of DNA, while Watson and Crick formulated the double stranded structural model of DNA.

b. Rosalind Franklin, Watson and Crick first employed the technique of X-ray diffraction to understand the storage of DNA. Since it did not work out, Watson and Crick then ran experiments to ascertain the DNA structure.

c. Rosalind Franklin, Watson and Crick used X-ray diffraction methods to demonstrate the helical nature of DNA, while Rosalind Franklin formulated the double stranded structural model of DNA.

d. Watson and Crick used X-ray diffraction methods to demonstrate the helical nature of DNA, while Rosalind Franklin formulated the double stranded structural model of DNA.

58. What do RNA and DNA have in common?

a. Both contain four different nucleotides.

b. Both are usually double-stranded molecules.

c. Both contain adenine and uracil.

d. Both contain ribose.

59. Which of the following would be a good application of plasmid transformation?

a. to make copies of DNA

b. to isolate a change in a single nucleotide

c. to separate DNA fragments

d. to sequence DNA

60. Explain how the components of DNA fit together.

a. DNA is composed of nucleotides, consisting of a 5 carbon sugar, a phosphate, and a nitrogenous base. DNA is a double helical structure in which complementary base pairing occurs. Adenine pairs with thymine and guanine pairs with cytosine. Adenine and thymine form two hydrogen bonds and cytosine and guanine form three hydrogen bonds. The two individual strands of DNA are held together by covalent bonds between the phosphate of one nucleotide and sugar of the next. The two strands run antiparallel to each other.

b. DNA is composed of nucleotides, consisting of a 5 carbon sugar, a phosphate, and a nitrogenous base. DNA is a double helical structure in which complementary base pairing occurs. Adenine pairs with cytosine and guanine pairs with thymine. Adenine and cytosine form two hydrogen bonds and guanine and thymine form three hydrogen bonds. The two individual strands of DNA are held together by covalent bonds between the phosphate of one nucleotide and sugar of the next. The two strands run antiparallel to each other.

c. DNA is composed of nucleotides, consisting of a 5 carbon sugar, a phosphate, and a nitrogenous base. DNA is a double helical structure in which complementary base pairing occurs. Adenine pairs with cytosine and guanine pairs with thymine. Adenine and cytosine form three hydrogen bonds and guanine and thymine form two hydrogen bonds. The two individual strands of DNA are held together by covalent bonds between the phosphate of one nucleotide and sugar of the next. The two strands run antiparallel to each other.

d. DNA is composed of nucleotides, consisting of a 5 carbon sugar, a phosphate, and a nitrogenous base. DNA is a double helical structure in which complementary base pairing occurs. Adenine pairs with cytosine and guanine pairs with thymine. Adenine and cytosine form three hydrogen bonds and guanine and thymine form two hydrogen bonds. The two individual strands of DNA are held together by covalent bonds between the phosphate of one nucleotide and sugar of the next. The two strands run parallel to each other.

61. Describe the Sanger DNA sequencing method used for the human genome sequencing project.

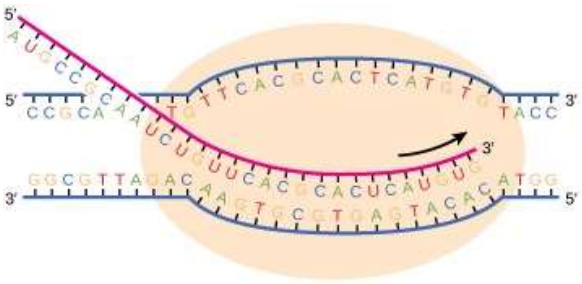
a. A DNA sample is denatured by heating and then put into four tubes. A primer, DNA polymerase and all four nucleotides are added. Limited quantities of one of the four dideoxynucleotides (ddNTPs) are added to each tube respectively. Each one of them carries a specific fluorescent label. Chain elongation continues until a fluorescent ddNTP is added to the growing chain, after which chain termination occurs. Gel electrophoresis is performed and the length of each base is detected by laser scanners with wavelengths specific to the four different ddNTPS's.

b. A DNA sample is denatured by heating and then put into four tubes. A primer, RNA polymerase and all four nucleotides are added. Limited quantities of one of the four dideoxynucleotides (ddNTPs) are added to each tube respectively. Each one of them carries a specific fluorescent label. Chain elongation continues until a fluorescent ddNTP is added to the growing chain, after which chain termination occurs. Gel electrophoresis is performed and the length of each base is detected by laser scanners with wavelengths specific to the four different ddNTPS's.

c. A DNA sample is denatured by heating and then put into four tubes. A primer, DNA polymerase and all four nucleotides are added. Limited quantities of one of the four dideoxynucleotides (ddNTPs) are added to each tube respectively. Each one of them carries a specific fluorescent label. Chain elongation continues until a fluorescent ddNTP is removed from the growing chain, after which chain termination occurs. Gel electrophoresis is performed and the length of each base is detected by laser scanners with wavelengths specific to the four different ddNTPS's.

d. A DNA sample is denatured by heating and then put into four tubes. A primer, DNA polymerase and all four nucleotides are added. Limited quantities of one of the four deoxynucleotides (dNTPs) are added to each tube respectively. Each one of them carries a specific fluorescent label. Chain elongation continues until a fluorescent dNTP is added the growing chain, after which chain termination occurs. Gel electrophoresis is performed and the length of each base is detected by laser scanners with wavelengths specific to the four different dNTPS's.

62.



What process is illustrated in the figure?

a. transcription

b. mutation

c. excision

d. translation

63. Describe how the model of DNA replication illustrates the function of topoisomerase.

a. Topoisomerase relieves the pressure that results from supercoiling by breaking and reforming DNA's phosphate backbone ahead of the replication fork.

b. Topoisomerase increases the pressure to increase supercoiling by breaking and reforming DNA's phosphate backbone ahead of the replication fork.

c. Topoisomerase relieves the pressure that results from supercoiling by breaking and reforming DNA's nucleotide base pairs ahead of the replication fork.

d. Topoisomerase relieves the pressure that results from separation of DNA strands by breaking and reforming DNA's phosphate backbone ahead of the replication fork.

64. Flamingos have genotypes for white feathers yet often appear with pink feathers within the same population. What is most likely affecting the phenotype of some flamingos, causing their feathers to turn pink in an isolated population?

a. weather variations

b. dietary changes

c. DNA mutations

d. translation failure

65. What can be the result of DNA failing to undergo repair after too much UV exposure?

a. second degree burns

b. a malignant melanoma

c. a breakdown of deep layers of the skin

d. a sun burn

66. Identify the type of change that can occur in the DNA of a chromosome that is termed a chromosomal mutation.

a. substitution
b. translocation
c. missense
d. transversion

67. Explain why patients with Xeroderma Pigmentosa are more prone to cancer than the rest of the population.

a. Xeroderma Pigmentosa patients cannot employ the nucleotide excision repair mechanism. When these patients are exposed to UV light, thymine dimers are formed and they are not able to repair this defect. These dimers distort the structure of DNA and cause them to have a high risk of contracting skin cancer.
b. Xeroderma Pigmentosa patients can employ the nucleotide excision repair mechanism. When these patients are exposed to UV light, the thymine dimers are formed and they are able to repair this defect. These dimers do not distort the structure of DNA and they have moderate risk of contracting skin cancer.
c. Xeroderma Pigmentosa patients cannot employ the nucleotide excision repair mechanism. When these patients are exposed to UV light, the adjacent adenine forms dimers and they are not able to repair this defect. These dimers distort the structure of DNA and they have high risk of contracting skin cancer.
d. Xeroderma Pigmentosa patients cannot employ the nucleotide excision repair mechanism. When these patients are exposed to UV light, the adjacent thymine cannot form thymine dimers and they are not able to repair this defect. The non-formation of dimers distorts the structure of DNA and they have high risk of contracting skin cancer.

68. You are looking at two fragments of DNA. Both have the sequence CATTCTG on one strand and GTAAGAC on the other. One of the fragments is exposed to UV light, the other is not. What will happen to the fragments and how might these mutations be repaired?

a. The fragment exposed to UV light contains thymine dimers. Thymines lying adjacent to each other can form thymine dimers when exposed to UV light. They can be repaired by nucleotide excision.
b. The fragment exposed to UV light contains adenine dimers. Adenines lying adjacent to each other can form dimers when exposed to UV light. They can be repaired by nucleotide excision.
c. The fragment exposed to UV light contains thymine dimers. Thymines lying parallel to each other can form thymine dimers when exposed to UV light. They can be repaired by nucleotide excision.
d. The fragment exposed to UV light contains thymine dimers. Thymines lying adjacent to each other can form thymine dimers when exposed to UV light. They can be synthesized by nucleotide excision.

69. Discuss how mutations can increase variation within a population.

a. Substitution mutations may cause a different amino acid to be placed at a specific location, causing small changes in the protein. Frameshift mutations usually cause multiple amino acid changes, increasing chances that a new protein will form, leading to radically different characteristics in the offspring.
b. Substitution mutations may cause multiple amino acid changes, increasing chances that a new protein will form, leading to radically different characteristics in the offspring. Frameshift mutations may cause a different amino acid to be placed at a specific location, causing small changes in a protein.
c. Substitution mutations may cause a different amino acid to be placed at a specific location, resulting in major changes to the protein and leading to radically different characteristics in the offspring. Frameshift mutations cause multiple amino acid differences in a protein, leading to small changes in the protein.
d. Substitution mutations result in a different amino acid being placed at a specific position in a protein, causing small changes. Silent mutations could result in new characteristics possessed by an offspring when a stop codon is substituted for an amino acid.

SCIENCE PRACTICE CHALLENGE QUESTIONS

70. The proof that DNA, not protein, is the carrier of genetic information involved a number of historical experiments, including transformation or horizontal gene transfer (HGT), which is the uptake and expression of extracellular DNA.

A. As described in Figure 14.3, transformation or HGT

was first reported by Griffith in 1928 in an experiment in which the following occurred:

1. heat-treated, pathogenic bacteria recovered their pathogenicity when incubated with nonpathogenic bacteria
2. plasmids were transferred to nonpathogenic bacteria from pathogenic bacteria through conjugation
3. nonpathogenic bacteria acquired pathogenicity when incubated in a broth containing heat-treated, pathogenic bacteria
4. polysaccharide cell capsules from pathogenic bacteria were transferred to nonpathogenic bacteria

B. Griffith's experiment, however, left undetermined the identity of the cellular component that encoded genetic information. The identity of DNA as the carrier of genetic information was resolved through the experiments by Martha Chase and Alfred Hershey because they observed the following:

1. injections with a serum containing chemically isolated polysaccharides and nonpathogenic bacteria were not lethal
2. pathogenic bacterial DNA that was radioactively labeled using a phosphorus isotope was not present in mice that died
3. bacteriophages from a bacterial culture grown in a nutrient-containing medium and radioactively labeled using a sulfur isotope transferred the label to bacteria incubated in an unlabeled nutrient-containing medium
4. bacteriophages from a bacterial culture grown in a nutrient-containing medium and radioactively labeled using a sulfur isotope did not transfer the label to bacteria incubated in an unlabeled nutrient-containing medium

C. Transformation and transduction increase variation within populations of bacteria and archaebacteria by the following:

a. transferring DNA among different species
b. transferring free DNA across the cell membrane without energy expenditure
c. transferring DNA between different strains of the same species of bacteria
d. phagocytosis of bacteriophages

The evolution of antibiotic resistance via HGT poses a challenge to medical technology. On the other hand, transformation is often assayed by incorporating an antibiotic-resistance gene in the plasmid to be transferred into the host organism. In natural environments, bacterial and archaebacterial cells become competent (able to transport DNA through the cytoplasmic membrane) in response to stress such as UV radiation, high population density, or heat shock. Such conditions are often difficult to model in the laboratory, where competence can be induced by high concentrations of divalent cations, Ca^{+2} or Mg^{+2}, or electrical shock. In either setting, extracellular DNA can be transported into the cell, and (to a good approximation) uptake is proportional to the concentration of extracellular DNA.

D. **Identify** a factor that might affect transformation or HGT. Then, **design a plan** to evaluate the dependence of transformational efficiency (defined as the number of transformations per gram of extracellular DNA) of plasmids that transfer antibiotic resistance to a particular strain of *Escherichia coli* that is not resistant on that factor.

71. Prior to the work of Hershey and Chase, scientists thought that inheritance involved "nucleoproteins." The amount of information to be transmitted between generations did not seem consistent with the chemical simplicity of the few nucleotides found in polymers of deoxyribonucleic acids in comparison to the diversity of protein polymers. Briefly **explain**:

- the relationship between the structure of polymeric DNA and the information stored
- the relationship between the interactions between base pairs on complementary strands of the double helix and Chargaff's observation on the relative abundance of nucleotides in DNA
- the meaning of the statement from the *Nature* publication on the structure of DNA by Watson and Crick: "It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material."

72. In 1977, Fred Sanger developed a method to determine the order of nucleotides in a strand of DNA. Sanger won a Nobel Prize for his work, and his method of sequencing based on dideoxy chain termination (Figure 14.8) has been foundational to the rapid development of more modern, rapid, and cheap methods of sequencing. The challenge of the $1,000 in one-day sequencing of the human genome was achieved in 2016 by next-generation sequencing (NGS), a "catch-all" term describing several sequencing methods.

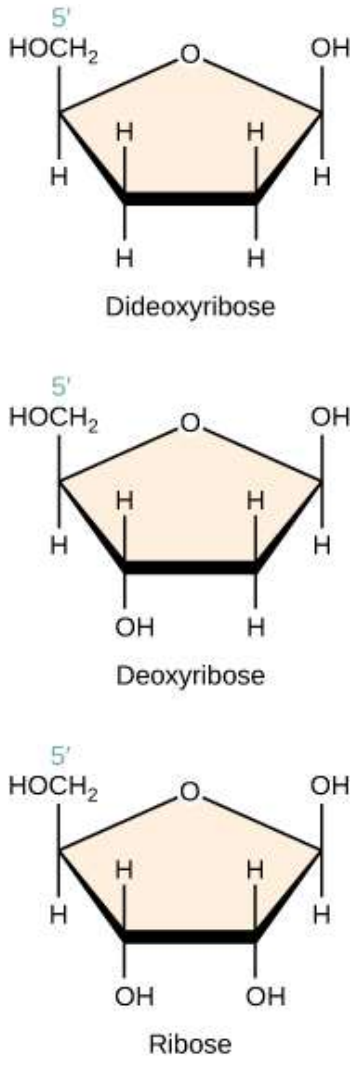


Figure 14.23

A. Using the diagrams shown above for reference, **explain** the effect of the addition of dideoxynucleotides on chain growth of the DNA strand that is copied during sequencing in terms of the structures of dideoxyribose and deoxyribose.

B. Suppose that a single strand to be sequenced is 5'CGAGTACG3'. In the presence of each of the four deoxynucleotides and the dideoxynucleotide ddCTP, **describe** the strands that would be formed from this template. Include in your description an annotation indicating the 3' and 5' ends of the fragments resulting from the procedure.

C. Next-generation sequencing makes termination technology very rapid and relatively inexpensive. All babies born in the U.S. are currently screened by state-mandated tests for several genetic conditions. The number of conditions tested ranges from 29 (GA and KS) to 59 (IL and MS). It is proposed that whole-genome sequencing should be mandatory for all newborns. The Genetic Information Nondiscrimination Act (2008) prevents health insurers from denying coverage or increasing costs of premiums based on genetic information. It also prohibits employers from making use of these data for hiring, firing, or promotion. The act passed in the House with a vote of 420 to 3, although it was lobbied against by organizations representing business (human resources, health insurance, and manufacturers), including the U.S. Chamber of Commerce. The act does not cover life, long-term care, or disability insurance. **Pose** three **questions** that are relevant to the use of whole-genome data.

73. Our understanding of the mechanisms of DNA replication is important to research on cancer and aging. Additionally, the molecular basis of Mendelian genetics was established.

A. The mechanism of DNA replication was investigated by Meselson and Stahl. The diagram below from their 1958 paper summarizes their findings. **Describe** how this representation illustrates the manner in which DNA is copied for transmission between generations.

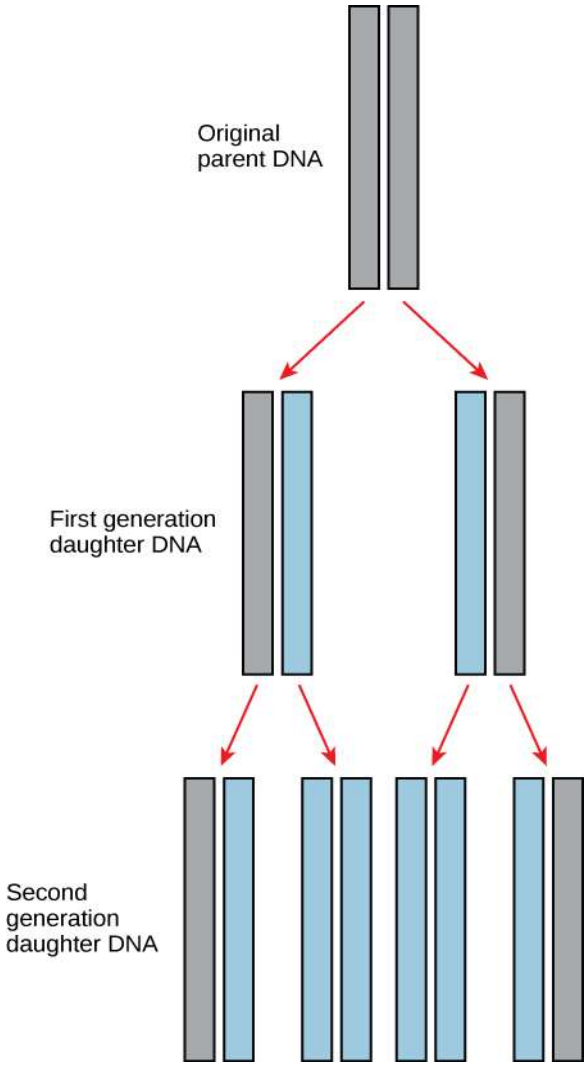


Figure 14.24

B. During the synthesis of new strands of DNA from the

parent strands, DNA polymerase can only add nucleotides at the terminal 3’ of a growing strand. Using the diagram below, **describe** the similarities and differences between the DNA replication of both strands.

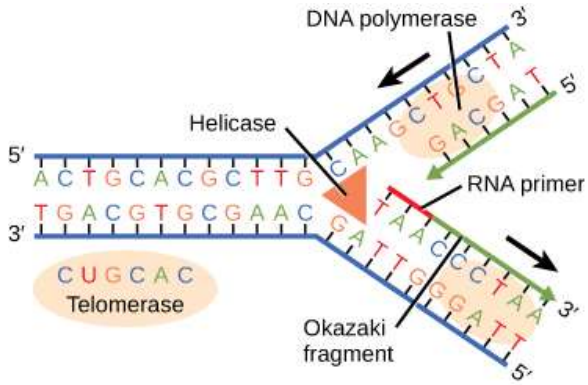


Figure 14.25

C. Shown at the left end of the upper parent strand is the six-base repeat sequence TTAGGG. In humans, this is the repeated, telomeric sequence that is attached to the telomere. The RNA primer in humans spans 10 base pairs, unlike in the drawing where it spans only three. In somatic cells, an enzyme called telomerase no longer functions. **Explain** the function of telomerase in the development of stem cells and cancer cells, and the inhibition of telomerase in programmed cell death or apoptosis.

74. The mitochondria of eukaryote cells contain their own circular DNA (mtDNA), consistent with their origin according to the theory of endosymbiosis. The mitochondrial genome is highly conserved in Eukarya. In humans, the 50 to 100 mitochondria in each of the cells in most tissues have 5 to 10 copies of the genome. Each has 37 genes that primarily encode proteins of the electron transport chain. Point mutations in which a single nucleotide is incorrectly placed is not repaired because the error-checking provided by DNA polymerase is not present in the mitochondria. The mutation rate for mtDNA is approximately 100 times higher than the mutation rate for nuclear DNA. The simultaneous existence of multiple alleles in each cell is likely, a condition called heteroplasmy. In mammals, sperm mitochondria are destroyed prior to fertilization.

A. **Explain** how point mutations in mtDNA can result in a loss of function in critical cellular components such as cytochrome c yet not be lethal to the cell.

B. Oocyte mitochondria are randomly segregated during meiosis, resulting in variation in the frequency of mtDNA mutations in offspring relative to the parent. **Explain** how a loss of function does not accumulate, lowering the metabolic performance from generation to generation.

As described in the Evolution Connection in this chapter of the text, a fossil fingertip found in a Siberian cave revealed an evolutionary link between Neanderthals and Denisovans. Fossils from 28 individuals were located in the “pit of bones,” Sima de los Huesos, in Spain, thousands of miles from the Siberian cave. In 2013, mtDNA from a femur of one of these individuals was compared with mtDNA of Denisovans, Neanderthals, and modern humans. It was found that the Sima fossil shared many more alleles with Denisovans than with either Neanderthals or modern humans. In 2016, the same group of scientists who sequenced the mtDNA from the femur of one of the Sima fossils partially sequenced the DNA from that fossil, showing a clear connection to Neanderthals.

C. **Analyze** these data to draw alternative conclusions regarding the relatedness of the three fossils and support each with evidence.

D. **Design** a plan to differentiate or resolve these alternative conclusions.