14 | DNA STRUCTURE AND FUNCTION

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

Solution The solution is (B). DNA was first isolated from white blood cells by Friedrich Miescher.

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.

Solution The solution is (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

Solution The solution is (C). Forensics looks at the nuclear genetic material.

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.

Solution The solution is (D). Radioactive phosphorous was found in the heavier particles that settled as pellets. The heavier bacterial cells settled down and formed pellets.

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

A 23%

B 27%

C 30%

D 54%

Solution The solution is (B). Because A binds to T, there is the same proportion of A and T in each DNA molecule.

6 If the sequence of the 5′ to 3′ strand is AATGCTAC, then the complementary sequence has which sequence?

A 3′-AATGCTAC-5′

B 3′-CATCGTAA-5′

C 3′-TTACGATG-5′

D 3′-GTAGCATT-5′

Solution The solution is (C). A binds to T and C binds to G in DNA molecules.

7 The DNA double helix does NOT have what?

A Antiparallel configuration

B Complementary base pairing

C Major and minor grooves

D Uracil

Solution The solution is (D). Uracil is a nucleotide base that is present in RNA and not in DNA.

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

Solution The solution is (A). A double-ring structure with a six-membered ring fused to a five-membered ring.

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

A Dideoxy chain termination

B Double helix determination

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C Polymerase chain reaction

D Polymer gel electrophoresis

Solution The solution is (A). The Dideoxy Chain Termination method was developed by Fred Sanger. It is a sequencing method based on the use of chain terminators.

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.

Solution The solution is (C). If a ddNTP is added to a growing a DNA strand, the chain is not extended any further because the free 3'OH group needed to add another nucleotide is not available.

11 In eukaryotes, what is DNA wrapped around?

A Histones

B Polymerase

C Single-stranded binding proteins

D Sliding clamp

Solution The solution is (A). In eukaryotes, the DNA is wrapped around proteins known as histones to form structures called nucleosomes.

12 Which enzyme is only found in prokaryotic organisms?

A DNA gyrase

B Helicase

C Ligase

D Telomerase

Solution The solution is (A). DNA gyrase helps to maintain the supercoiled structure in prokaryotes.

13 Where is uracil found?

A Chromosomal DNA

B Helicase

C Mitochondrial DNA

D mRNA

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Solution The solution is (D). Uracil is a nitrogenous base found in mRNA molecules. Its complementary base pair is adenine.

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

Solution The solution is (B). If a ddNTP is added to a growing DNA strand, the chain is not extended any further because the free 3'OH group needed to add another nucleotide is not available. ddNTP lack the 3'OH group on the five-carbon sugar.

15 What is NOT one of the proteins involved during the formation of the replication fork?

A Helicase

B Ligase

C Origin of replication

D Single-stranded binding proteins

Solution The solution is (C). The origin of replication is the point at which the DNA unwinds.

16 In which direction does DNA replication take place?

A 5' to 3'

B 3' to 5'

C 5'

D 3'

Solution The solution is (A). DNA polymerase adds nucleotides from 5' to 3' direction.

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

A Conservative

B Converse

C Dispersive

D Semiconservative

Solution The solution is (D). The semiconservative mode of replication suggested that each of the two parental DNA strands act as a template for new DNA to be synthesized. After replication, each double-stranded DNA includes one parental or "old" strand and one "new" strand.

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18 Which set of results was found in 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.

Solution The solution is (B). The semiconservative method suggested that each of the two parental DNA strands act as a template for new DNA to be synthesized. After replication, each double-stranded DNA includes one parental or "old" strand and one "new" strand. It was found in Meselson and Stahl's experiment.

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

A DNA gyrase

B Helicase

C Ligase

D Telomerase

Solution The solution is (B). Helicase opens the DNA helix by breaking hydrogen bonds between the nitrogenous bases ahead of the replication fork.

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

Solution The solution is (C). DNA polymerase III is the main enzyme in DNA replication that adds nucleotides in 5' to 3' direction.

21 Which portion of a chromosome contains Okazaki fragments?

A Helicase

B Lagging strand

C Leading strand

D Primer

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Solution The solution is (B). The replication of the strand that occurs in a direction away from the replication fork is known as lagging strand and contains Okazaki fragments.

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22 What does the enzyme primase synthesize?

A DNA primer

B Okazaki fragments

C Phosphodiester linkage

D RNA primer

Solution The solution is (D). Primase synthesizes RNA primers to initiate synthesis by DNA polymerase, which can add nucleotides only in the 5′ to 3′ direction.

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

A DNA polymerase

B Helicase

C Primase

D Telomerase

Solution The solution is (D). Telomerase maintains the linear end of the chromosomes. It consists of a catalytic part and a built-in RNA template.

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.

Solution The solution is (D). The advantage in prokaryotes is that RNA and protein synthesis occurs much more quickly than the eukaryotes. It is 10 times faster than eukaryotes.

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

Solution The solution is (C). Areas of eukaryotic chromosomes that are equivalent to the origin of replication in *E. coli.*

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26 What type of body cell does NOT exhibit telomerase activity?

A Adult stem cells

B Embryonic cells

C Germ cells

D Liver cells

Solution The solution is (D). Liver cells do not exhibit telomerase activity. Adult, embryonic, and germ cells do.

27 During proofreading, which enzyme reads the DNA?

A DNA polymerase

B Helicase

C Topoisomerase

D Primase

Solution The solution is (A). DNA polymerase edits DNA by proofreading every newly added base.

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 1,000 per second

B 100 per second

C 10 per second

D 1 per second

Solution The solution is (C). Rate of replication in prokaryotes is 10 times than eukaryotes. If replication in prokaryotes is 100 per second, then in eukaryotes it will be 10 per second.

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

A Frameshift

B Missense

C Nonsense

D Silent

Solution The solution is (D). Silent mutation is the one in which a nucleotide is substituted, but there is no effect on the protein sequence or gene expression.

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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

Solution The solution is (C). Nonsense mutation introduces a stop codon in place of an amino acid.

31 A woman has developed skin cancer and she is pregnant. She is worried that her child will be born with the cancer she has while carrying the baby.

Should she 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.

Solution The solution is (B). The mutation causing the cancer does not occur in the germ cells of the woman, but in the somatic cells. Therefore, it will not affect the baby.

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

Solution The solution is (A). DNA polymerase is an efficient enzyme, but can make mistakes while adding nucleotides during replication. It edits the DNA by proofreading every newly added base.

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

A Phosphodiester bonds

B Purine conjugates

C Pyrimidine dimers

D Tetrad disassembly

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Solution The solution is (C). Thymine and cytosine are pyrimidine dimers. On long exposure of UV rays, thymine dimers are formed, which puts people at higher risk of developing skin cancer. Nucleotide excision repair is a DNA repair mechanism that excises the thymine dimers in normal individuals.

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 (nonpathogenic). 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 (nonpathogenic). 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 (nonpathogenic). 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 (nonpathogenic). 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.

Solution The solution is (A). Two strains of *S. pneumoniae* were used in Griffith's transformation experiments. The R strain is nonpathogenic. The S strain is pathogenic and causes death. When Griffith injected a mouse with the heat-inactivated S strain and a live R strain, the mouse died. The S strain was recovered from the dead mouse. Thus, Griffith concluded that something had passed from the heat-killed S strain to the R strain, transforming the R strain into S strain in the process.

35 Which answer best explains why radioactive sulfur and phosphorus were used to label bacteriophages in the Hershey and Chase experiments?

A Protein was labeled with radioactive sulfur and DNA was labeled with radioactive phosphorus. Phosphorus is found in DNA, so it will be tagged by radioactive phosphorus.

B Protein was labeled with radioactive phosphorus and DNA was labeled with radioactive sulfur. Phosphorus is found in DNA, so it will be tagged by radioactive phosphorus.

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C Protein was labeled with radioactive sulfur and DNA was labeled with radioactive phosphorus. Phosphorus is found in DNA, so DNA will be tagged by radioactive sulfur.

D Protein was labeled with radioactive phosphorus and DNA was labeled with radioactive sulfur. Phosphorus is found in DNA, so DNA will be tagged by radioactive sulfur.

Solution The solution is (A). Hershey and Chase labeled one batch of phage with radioactive sulfur, 35S, to label the protein coat. Another batch of phage was labeled with radioactive phosphorus, 32P. Because phosphorus is found in DNA, but not protein, the DNA and not the protein would be tagged with radioactive phosphorus.

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 is 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 is not found in equal quantities. They vary between individuals of the same species and can be used to identify different species.

Solution The solution is (A). The content of DNA is different indifferent species and the amounts of adenine, thymine, guanine, and cytosine are found in different quantities. Therefore, the amounts of adenine, thymine, guanine, and cytosine are consistent for a species and can be used to identify that 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?

Solution The conclusion would be that proteins are the heritable material in cells instead of nucleic acids.

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 antiparallel in nature; that is, the 3' end of one strand faces the 5' end of the other strand. Sugar, phosphate, and nitrogenous bases contribute to the DNA structure.

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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 antiparallel in nature; that is, the 3′ end of one strand faces the 5′ end of the 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 the 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 antiparallel in nature; that is, the 3′ end of one strand faces the 5′ end of the other strand. Only sugar contributes to the DNA structure.

Solution The solution is (A). DNA is made up of two strands that are twisted around each other to form a right-handed helix. Base pairing takes place between a purine and pyrimidine; namely, A pairs with T and G pairs with C. Adenine and thymine are complementary base pairs, and cytosine and guanine are also complementary base pairs. The base pairs are stabilized by hydrogen bonds; adenine and thymine form two hydrogen bonds and cytosine and guanine form three hydrogen bonds. The two strands are anti-parallel in nature; that is, the 3′ end of one strand faces the 5′ end of the other strand. The sugar and phosphate of the nucleotides form the backbone of the structure, whereas the nitrogenous bases are stacked inside.

39 Which answer provides 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.

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Solution The solution is (A). In Frederick Sanger's dideoxy chain termination method, dye-labeled dideoxynucleotides are used to generate DNA fragments that terminate at different points. The DNA is separated by capillary electrophoresis on the basis of size, and from the order of fragments formed, the DNA sequence can be read. The DNA sequence readout is shown on an electropherogram that is generated by a laser 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 create heterochromatin and euchromatin, 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. Prokaryote chromosomes are wrapped around histone proteins that create heterochromatin and euchromatin, 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 create heterochromatin and euchromatin, which is present in prokaryotes.

Solution The solution is (B). Prokaryotes have a single, circular chromosome, while eukaryotes have multiple, linear chromosomes. Prokaryotes pack their chromosomes into the cell using super coiling, managed DNA gyrase. Eukaryote chromosomes are wrapped around histone proteins that create heterochromatin and euchromatin that is not found in prokaryotic cells.

41 DNA replication is bidirectional and discontinuous. How can you 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

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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.

Solution The solution is (A). DNA polymerase can add nucleotides only in the 5′ to 3′ direction. DNA polymerase recognizes the 3′OH end as its landing site; thus, polymerase "reads" the template strand in the 3′ to 5′ direction and builds the new DNA complementary DNA polymer in the 5′ to 3′ direction. One strand—called the leading strand—is synthesized continuously in the direction of the replication fork (the direction in which helicase is separating the two strands), with polymerase adding new nucleotides one-by-one. However, replication of the other strand—called the lagging strand—occurs in a direction away from the replication fork, in short stretches of DNA known as Okazaki fragments.

42 How did the scientific community learn 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 50 percent presence of 14N. This supports the semiconservative 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 50 percent presence of ^{14}N. This supports the semiconservative 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 50 percent presence of ^{14}N. This supports the semiconservative 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 semiconservative replication model.

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Solution The solution is (A). Meselson and Stahl experimented with *E. coli* grown first in heavy nitrogen (^{15}N) then in ^{14}N. DNA grown in ^{15}N is heavier than DNA grown in ^{14}N, and sediments to a lower level in cesium chloride solution in an ultracentrifuge. When DNA grown in ^{15}N is switched to media containing ^{14}N, after one round of cell division the DNA sediments halfway between the ^{15}N and ^{14}N levels, indicating that it now contains 50 percent ^{14}N. In subsequent cell divisions, an increasing amount of DNA contains ^{14}N only. These data support the semiconservative replication model.

43 Why is half of DNA 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 '' end. This results in pieces of DNA being replicated in a discontinuous fashion.

Solution The solution is (A). Since access to the DNA strand is always from the 5′ end, the replication of one strand, called the lagging strand, occurs in a direction away from the replication fork, in short stretches of DNA. This results in pieces of DNA being replicated in a discontinuous fashion. These pieces will be joined into a single strand of DNA.

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

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strand. If helicase is mutated, the DNA strands will not be joined together at the beginning of replication.

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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.

Solution The solution is (A). A replication fork is formed when helicase separates the DNA strands at the origin of replication. The DNA tends to become more highly coiled ahead of the replication fork. Topoisomerase breaks and reforms DNA's phosphate backbone ahead of the replication fork, thereby relieving the pressure that results from this supercoiling. Single-strand binding proteins bind to the single-stranded DNA to prevent the helix from re-forming. Primase synthesizes an RNA primer. DNA polymerase III uses this primer to synthesize the daughter DNA strand.

If helicase is mutated and cannot function, the DNA strands will not 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.

Solution The solution is (A). Replication of the lagging strand in DNA replication occurs in a direction away from the replication fork in short stretches of DNA known as Okazaki fragments.

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.

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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.

Solution The solution is (A). DNA polymerase I has exonuclease activity that removes RNA primers from the developing copy while DNA ligase seals the ends of the new 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 min

B 44.4 min

C 45.4 min

D 54.4 min

Solution The solution is (B). The rate of replication equals 900 nucleotides per second. For 1.2 million base pairs, the time taken for replication would be $1.2 \text{ million} \div 900 = 22.2 \text{ min}$ (1,333.3 s). To make two copies, the time taken will be $22.2 \times 2 = 44.4$ min.

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.

Solution The solution is (A). Telomerase enzyme replicates the ends of chromosomes by attaching to the 3′ chromosomal end of the DNA strand. When the 3′ end is elongated, then DNA polymerase adds complementary nucleotides to the end of chromosomes.

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49 What is the best way to compare and contrast prokaryotic and eukaryotic DNA replication?

A A prokaryotic organism's rate of replication is 10 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 14 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 10 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 14 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 10 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 14 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 10 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 14 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.

Solution The solution is (A). Prokaryotic organisms have a single origin of replication, while eukaryotic ones have multiple sites. The rate of replication of prokaryotic cells is approximately 10 times that of eukaryotes. There are five types of DNA polymerases used by prokaryotes and 14 in eukaryotes. Telomerase functions in eukaryotic cells, but not prokaryotic one. The RNA primer remover in prokaryotic organisms is DNA pol I, but RNase H in eukaryotic cells. Strand elongation is performed by DNA pol III in prokaryotes and by Pol δ, pol ε in eukaryotic organisms.

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50 What would be the consequence of a mutation in a mismatch repair enzyme? How would 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.

Solution The solution is (A). Some errors are not corrected during replication, but instead are corrected after replication is completed; this type of repair is known as mismatch repair. The enzymes recognize the incorrectly added nucleotide and excise it; this then is replaced by the correct base. If this remains uncorrected, it may lead to more permanent damage.

51 A mutation has occurred in the DNA and in the mRNA for a gene. Which one 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 affect only 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 affect only proteins made from that mRNA strand. Production of defective protein ceases when the mRNA strand deteriorates.

Solution The solution is (A). Both will result in a defective protein produced from the gene information. The DNA mutation, if not corrected, is permanent; the mRNA mutation will affect only proteins made from that RNA strand. When the mRNA strand deteriorates, the production of the defective protein ceases.

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52 What are 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 nonfunctional 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 nonfunctional 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 nonfunctional 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.

Solution The solution is (A). If one base is replaced by another base, but the coding for an amino acid is not changed, there is no effect on the DNA strand and a silent mutation has occurred. A missense mutation happens when a point mutation causes a change in a single amino acid. A nonsense mutation causes a stop message to be read, and the replication or reading of that strand is stopped at that point. Insertion or deletion mutations cause a frame shift from that point on and a non-functional protein will result.

53 What is 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 semiconservative 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*.

Solution The solution is (A). A mutation in a single type of tRNA will affect the transfer of one amino acid. The result of this will be a decrease in proteins that require this amino acid, as it will not be brought to the assembly points of proteins in adequate amounts. A mutation in rRNA will affect the assembly of all proteins and lead to significant deficiencies in these molecules.

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TEST PREP FOR AP® COURSES

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.

Solution The solution is (C). Protein would have been identified as 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.

Solution The solution is (C). The precipitate contained phosphorus, which is abundant in DNA.

56 How are forensic scientists 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 then is 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.

Solution The solution is (A). Analysis of the sequence of bases in strands of DNA and their comparison to DNA from a known source or individual allows scientists to state that they are the same, or very similar, thus identifying the unknown source of the sample of DNA.

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57 What were the contributions of Francis Crick, James Watson, and Rosalind Franklin to the discovery of the structure of DNA?

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

Solution The solution is (A). Franklin was using X-ray diffraction methods to understand the structure of DNA. Watson and Crick were able to piece together the puzzle of the DNA molecule on the basis of Franklin's data.

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.

Solution The solution is (A). Both contain four different nucleotides.

59 What 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

Solution The solution is (C). DNA fragments move through gel based on their negative charge.

60 How do the components of DNA fit together?

A DNA is composed of nucleotides, consisting of a five-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.

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B DNA is composed of nucleotides, consisting of a five-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 five-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 five-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.

Solution The solution is (A). DNA is made up of two strands that are twisted around each other to form a right-handed helix. Base pairing takes place between a purine and pyrimidine; namely, A pairs with T and G pairs with C. Adenine and thymine are complementary base pairs, and cytosine and guanine are also complementary base pairs. The base pairs are stabilized by hydrogen bonds; adenine and thymine form two hydrogen bonds, and cytosine and guanine form three hydrogen bonds. The two strands are anti-parallel in nature; that is, the 3′ end of one strand faces the 5′ end of the other strand. The sugar and phosphate of the nucleotides form the backbone of the structure, whereas the nitrogenous bases are stacked inside.

61 What is the best way to 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.

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

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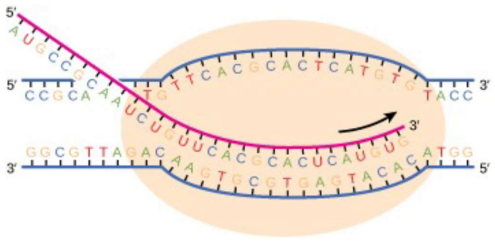
dideoxynucleotides (ddNTPs) are added to each tube respectively. Each one of them carries a specific fluorescent label. Chain elongation continues until a fluorescent ddNTP is added to the growing chain, after which chain termination occurs. Gel electrophoresis is performed and the length of each base is detected by laser scanners with wavelengths specific to the four different ddNTPs.

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.

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.

Solution The solution is (B). The DNA sample to be sequenced is denatured or separated into two strands by heating it to high temperatures. The DNA is divided into four tubes in which a primer, DNA polymerase, and all four nucleotides (A, T, G, and C) are added. In addition to each of the four tubes, limited quantities of one of the four dideoxynucleotides are added to each tube respectively. The tubes are labeled as A, T, G, and C according to the ddNTP added. For detection purposes, each of the four dideoxynucleotides carries a different fluorescent label. Chain elongation continues until a fluorescent dideoxy nucleotide is incorporated, after which no further elongation takes place. After the reaction is over, electrophoresis is performed. Even a difference in length of a single base can be detected. The sequence is read from a laser scanner.

62 What process is illustrated in the figure?



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A Transcription

B Mutation

C Excision

D Translation

Solution The solution is (A). RNA is being made from DNA.

63 How does the model of DNA replication illustrate 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.

Solution The solution is (A). The DNA tends to become more highly coiled ahead of the replication fork. Topoisomerase breaks and reforms DNA's phosphate backbone ahead of the replication fork, thereby relieving the pressure that results from this supercoiling.

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

Solution The solution is (A). Weather variations would affect the entire isolated population.

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 sunburn

Solution The solution is (B). UV light exposure can cause melanoma.

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

A Substitution

B Translocation

C Missense

D Transversion

Solution The solution is (B). Sometimes a piece of DNA from one chromosome may get translocated to another chromosome or to another region of the same chromosome; this chromosomal mutation is known as translocation.

67 Why are patients with *Xeroderma pigmentosa* 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 nonformation of dimers distorts the structure of DNA and they have high risk of contracting skin cancer.

Solution The solution is (D). Affected individuals have skin that is highly sensitive to UV rays from the sun. When individuals are exposed to UV, pyrimidine dimers are formed; people with *Xeroderma pigmentosa* are not able to repair the damage. These are not repaired because of a defect in the nucleotide excision repair enzymes, whereas in normal individuals, the thymine dimers are excised and the defect is corrected. The thymine dimers distort the structure of the DNA double helix, and this may cause problems during DNA replication. People with *Xeroderma pigmentosa* may have a higher risk of contracting skin cancer than those who do not have the condition.

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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.

Solution The solution is (A). Nucleotide excision repairs thymine dimers. When exposed to UV, thymines lying adjacent to each other can form thymine dimers. In normal cells, they are excised and replaced.

69 How can mutations 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.

Solution The solution is (A). Substitution mutations can cause a different amino acid to be placed at a specific location in a protein that could alter its characteristics and

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change the population over time. It might result in more resistance to bacterial infections or even to direct sunlight. Frameshift mutations could, conceivably, make an entirely different protein, giving the resulting offspring a new characteristic not possessed previously.

SCIENCE PRACTICE CHALLENGE QUESTIONS

14.1 Historical Basis of Modern Understanding

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.

Mouse injected with heat-killed virulent S strain lives.

Mouse injected with both heat-killed S strain and live non-virulent R strain dies.

A. As described in the figure, 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.

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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:

1. Transferring DNA among different species
2. Transferring free DNA across the cell membrane without energy expenditure
3. Transferring DNA between different strains of the same species of bacteria
4. Phagocytosis of bacteriophages

The evolution of antibiotic resistance via HGT poses a challenge to medical technology. On the other hand, transformation often is 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.

Solution Sample answer:

A. (3)

B. (4)

C. (1)

D. The factor is identified. It might be any environmental factor, such as temperature, salinity, or pH. The method of control could be specified, such as heat bath or buffer, but the target of assessment would be the identification of the factor and the need to vary it measurably while fixing values of other factors. One of these fixed values should be population density which, based on lab experiences, the

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student should be able to identify as optical density. Assay could be fluorescent if the student had prior experience with this method or the use of antibiotic resistance. Cells that had been transformed would then be counted in terms of the number of viable or fluorescent colonies. A test of the assumption that uptake is proportional to extracellular DNA should be included in the design with variation in DNA concentration at fixed values of other parameters.

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."

Solution Sample answer: Although the number of amino acids and the 3-D shape increases the complexity of proteins, a very long, linear sequence of four bases stores sufficient information.

The pairing is the AT and CG forms that are supported by the structure with a pair of strands, each with corresponding bases. The authors glibly point to the creation of a whole field, genomics, based on the weakness of the hydrogen bonding between the complementary strands.

14.2 DNA Structure and Sequencing

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 (see figure) has been foundational to the rapid development of more modern, rapid, and inexpensive 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.

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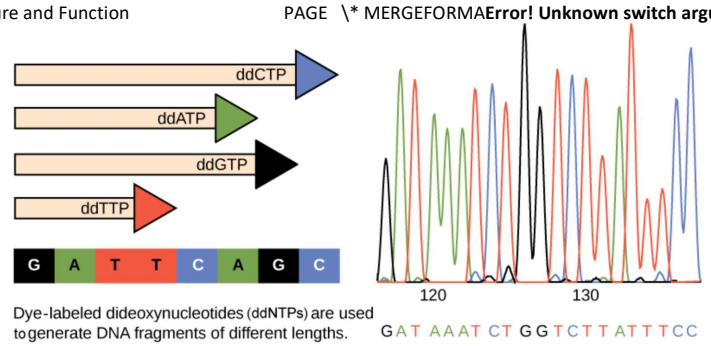
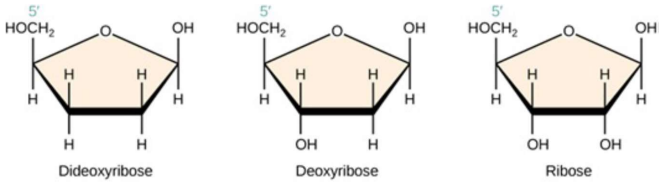


Dye-labeled dideoxynucleotides (ddNTPs) are used to generate DNA fragments of different lengths.

A. Using the diagrams 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 United States 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.

Solution Sample answer:

A. Without the OH at the 3′ position a Pi group cannot bond and extend the sugar backbone.

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B. Chain termination would occur at each G leading to the fragments 3'CTCATDC5', 3'CATGC5', and 3'C5'.

C. Questions could address ownership (ownership is a difficult question—is the DNA on a licked postage stamp still owned?—similar to questions of permissible searches), the relative benefits to society and perhaps to the individual of genomic information could include reduced cost of insurance, reduced cost of medical treatment, increased efficiency and effectiveness of medical treatment, the possible creation of caste systems. A really good scientific question might be the extent to which possibly identifiable, distinct phenotypes such as intelligence, athleticism, beauty, artistic talent, etc., can be associated with a gene or an array of genes, as opposed to environmental factors or behaviors. A search will show that the omission of life insurance from GINA has led to some discussion and some possible concerns. The student might question the reason that life insurance or disability insurance was omitted. Questions might address whether or not courts have heard claims based on GINA—there have been some and they are easily found. Questions about data security will be asked.

14.3 Basics of DNA Replication

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 from their 1958 paper summarizes their findings. **Describe** how this representation illustrates the manner in which DNA is copied for transmission between generations.

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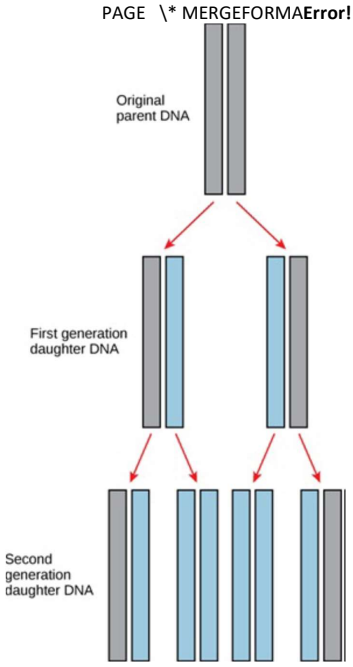
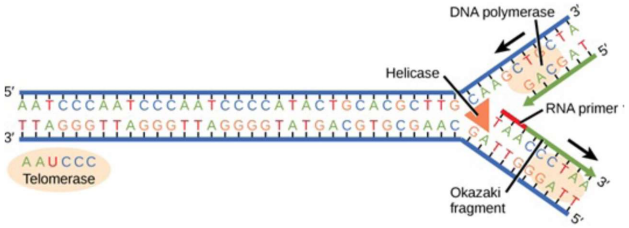


B. During the synthesis of new strands of DNA from the parent strands, DNA polymerase can only add nucleotides at the terminal 3′ of a growing strand. Using the diagram, **describe** the similarities and differences between the DNA replication of both strands.



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.

Solution Sample answer:

A. The semiconservative nature of replication is illustrated by this very effective representation in which the newly synthesized strands are unshaded. The student

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might be expected to describe the use of centrifugation to separate light and heavy isotopes of nitrogen.

B. The description should include the breaking of hydrogen bonds by helicase, the attachment of DNA polymerase to the leading strand, the creation of a template for synthesis on the lagging strand with RNA primer and the synthesis of fragments as required by the 3' to 5' direction of addition. Names of specific enzymes are not expected to be memorized and this item illustrates how they would be provided but that the information provided can be used.

C. Telomerase as assessable content is out of scope although it is described in the text. What would be appropriate for assessment on the AP Biology Exam would be the recognition that the RNA primer might not have a sufficient number of bases remaining on the lagging strand as DNA pol approaches the telomere. This results in a segment of the lagging side not being copied. Without telomerase to repair the lost telomeric sequence, the number of repeats is reduced until eventually the cell cannot divide, leading to cell death. Cancer cells activate telomerase and so avoid cell death.

14.4 DNA Replication in Prokaryotes

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

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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.

Solution Sample answer:

A. Multiple copies of mtDNA allow expression even though some copies code for proteins that do not function.

B. As mutations accumulate the cell become less efficient. When a cell line has less than a threshold number of functional mitochondrial, the cell dies and that cell line is deleted. This applies to both somatic cells and to gametes.

C. The mtDNA evidence indicates that the Sima people are more closely related to the Denosivans. However, the DNA evidence indicates the opposite conclusion.

D. The recovery of both mtDNA and nuclear DNA was a major feat. However, suppose that the mtDNA reveals a maternal ancestor of different lineage. Because of the very high mutation rate of mtDNA large variations between family lines occur while an ancestral line within a family remains very similar. mtDNA from other bones at Sima might reveal other maternal lines and this would be consistent with the DNA result, implying a common maternal ancestor related to Denosivans. Evidence that would confirm this would be provided by a third, as yet undiscovered or unstudied, population whose mtDNA could be sequenced.

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