What is DNA Replication?

Worksheet

DNA replication is the semiconservative copying of a DNA molecule, in which helicase unwinds the double helix and DNA polymerase synthesizes two new complementary strands, producing two identical DNA molecules from one.

Questions

1. DNA replication is described as semiconservative because:
A) both strands are new
B) both strands are original
C) each new molecule has one old and one new strand
D) no strands survive

2. Which enzyme unwinds the DNA double helix at the origin?
A) DNA polymerase
B) helicase
C) ligase
D) primase

3. Why is the lagging strand synthesized in fragments?
A) DNA polymerase is slow
B) polymerase only works 5'3'
C) there is no template
D) ligase is missing

4. What does DNA ligase do?
A) unwinds DNA
B) adds RNA primers
C) joins Okazaki fragments
D) removes primers

5. A DNA template strand reads 3'-TACGGCAT-5'. What is the sequence of the newly synthesized complementary strand?

6. Why is one new strand (leading) synthesized continuously while the other (lagging) is made in fragments?

7. A bacterial chromosome has 4.6 million base pairs and replicates from a single origin bidirectionally at about 1,000 bp/sec per fork. Roughly how long does replication take?

8. Define: What does 'semiconservative' mean for DNA replication?

9. Define: What does helicase do?

10. Define: What does DNA polymerase do?

Answer Key

1. C) each new molecule has one old and one new strand - Each daughter molecule retains one parental strand paired with one newly made strand.

2. B) helicase - Helicase breaks hydrogen bonds between strands, opening the replication fork.

3. B) polymerase only works 5'3' - Since polymerase adds nucleotides only 5'3', it must synthesize the lagging strand in short, discontinuous pieces.

4. C) joins Okazaki fragments - Ligase seals the gaps between Okazaki fragments to form a continuous strand.

5. DNA polymerase reads the template 3'5' and synthesizes the new strand 5'3'. Base pairing: A-T, T-A, C-G, G-C. Template 3'-TACGGCAT-5' New strand 5'-ATGCCGTA-3'

6. DNA polymerase only adds nucleotides in the 5'3' direction. The leading strand template runs 3'5' toward the fork, so synthesis is continuous, following the fork. The lagging strand template runs 5'3' toward the fork, so polymerase must work in short bursts (Okazaki fragments) away from the fork, later joined by ligase.

7. Bidirectional replication means two forks share the work, each copying half the genome. Bases per fork 4,600,000 / 2 = 2,300,000 bp Time = 2,300,000 bp 1,000 bp/sec 2,300 seconds 38 minutes

8. Each new DNA molecule has one original (parental) strand and one newly synthesized strand.

9. Unwinds the double helix at the origin, creating the replication fork.

10. Synthesizes new DNA by adding complementary nucleotides in the 5'3' direction.