19/MHS03/014

ASSIGNMENT.

1. STEPS OF DNA REPLICATION.

REPLICATION: Before DNA can be responsible, the double stranded molecule must be unzipped into two single strands, DNA has four bases called ADENINE (A), THYMINE (T), CYTOSINE (C), and GUANINE (G) that forms pairs between the two strands. Adenine only pairs with thymine and cytosine only binds with Guanine. In order to unwind DNA, these interactions between base pairs must be broken. This is performed by an enzyme known as DNA helicase. DNA helicase disrupts the hydrogen bonding between base pairs to separate the strands into a Y shape as the REPLICATION FORK. This area will be the template for replication to begin.

DNA is directional in both strands, signified by a 5' and 3' end. This notation signifies which side group is attached to the DNA backbone. The 5' end has a phosphate (P) group attached, while the 3' end has a hydroxyl (OH) group attached. This directionality is important for replication as it only progresses in the 5' to 3' direction. However, the replication fork is bi-directional; one strand is oriented in the 3' to 5' direction (leading strand) while the other is oriented 5' to 3' (lagging strand). The two sides are therefore replicated with two different processes to accommodate the directional differences.

REPLICATION BEGINS.

STEP 2. PRIMER BINDING:
The leading strand is the simplest to replicate. Once the DNA strands have been separated, a short piece of RNA called a PRIMER binds to the 3' end of the strand. The primer always binds at the starting point for replication. Primers are generated by the enzyme DNA primase.

STEP 3. ELONGATION: Enzymes known as DNA Polymerases are responsible for creating the new strand by a process called ELONGATION. There are 5 different known types of DNA polymerase in bacteria and human cells. While polymerase I, II, IV and V are responsible for error checking and repair. DNA polymerase III binds to the strand at the site of the primer and begins adding new base pairs complementary to the strand during replication. In eukaryotic cells, polymerases alpha, delta, and epsilon are the primary polymerases involved in DNA replication. Because replication proceeds in the 5' to 3' direction on the leading strand, the newly formed strand is continuous.

The lagging strand replication by binding with multiple primers. Each primer is only several bases apart. DNA polymerase then adds pieces of DNA, called the OKAZAKI FRAGMENTS, to the strand between primers. This process of replication is discontinuous as the newly created fragments are disjointed.

STEP 4. TERMINATION: Once both the continuous and discontinuous strands are formed, an enzyme called EXONUCLEUS removes all RNA primers from the original strands. These primers are then replaced with appropriate bases. Another exonucleus proofreads the newly formed DNA to check, remove and replace any errors. Another enzyme called DNA ligase joins okazaki fragments together forming a single unified strand. The ends of the linear DNA present a problem as DNA polymerase can only add nucleotides in the 5' to 3' direction. The ends of the parent strands consists of repeated DNA called telomeres. Telomeres act as protective caps at the end of the chromosomes

to prevent nearby chromosomes from fusing. A special type of DNA polymerase enzyme called TELOMERASE catalyzes the synthesis of telomere sequences at the ends of the DNA. Once completed, the parent strand and its complementary DNA strand coils into the familiar double helix shape. In the end, replication produces two DNA molecules, each with one strand from the parent molecule and one new strand.

2. ENZYMES IN DNA REPLICATION AND ITS FUNCTIONS.

TOPOISOMERASE: It relaxes the super-coiled DNA.

DNA HELIASE: Unwinds the double helix at the replication fork.

PRIMASE: Provides the starting point for DNA polymerase to begin synthesis of the new strand.

DNA POLYMERASE: Provides the new DNA strand and also proofreads and corrects some errors.

DNA LIGASE: Re-joins the two DNA strands into a double helix and joins okazaki fragments of the lagging strand.