DNA STRUCTURE AND REPLICATION - 7.1

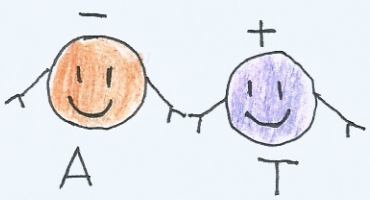
▷ Watson and crick model suggested semi-conservative replication

Franklin's x-ray diffraction studies showed that the DNA helix was tightly packed.

- Watson and Crick had to build the model in such a way that the strands were close and the model required bases to fit together.

For this – pyrimidine had to be paired with a purine
– the bases had to be upside down in relation to one another.

Adenine had a surplus negative charge whereas Thymine had a surplus positive charge so they were paired togther as they were compatible.



Cytosine bonds with guanine as 3 hydrogen bonds are formed-this gives the structure stability.

Complementary base paining suggested a mechanism of DNA replication.

∴ Watson and crick's model led to the hypothesis of semi-conservative replication.

LEADING AND LAGGING STRAND

DNA replication is **continuous** on the **leading** strand (5'3'). It is **discontinuous** on the **lagging strand**.

- The lagging strand is made in fragments moving away from the replication fork.

The fragments are called okazaki fragments.

PROTEINS INVOLVED IN REPLICATION

Helicase: It unwinds the DNA at the replication fork

Topoisomerase: Releases the strain that develops in front of helicase.

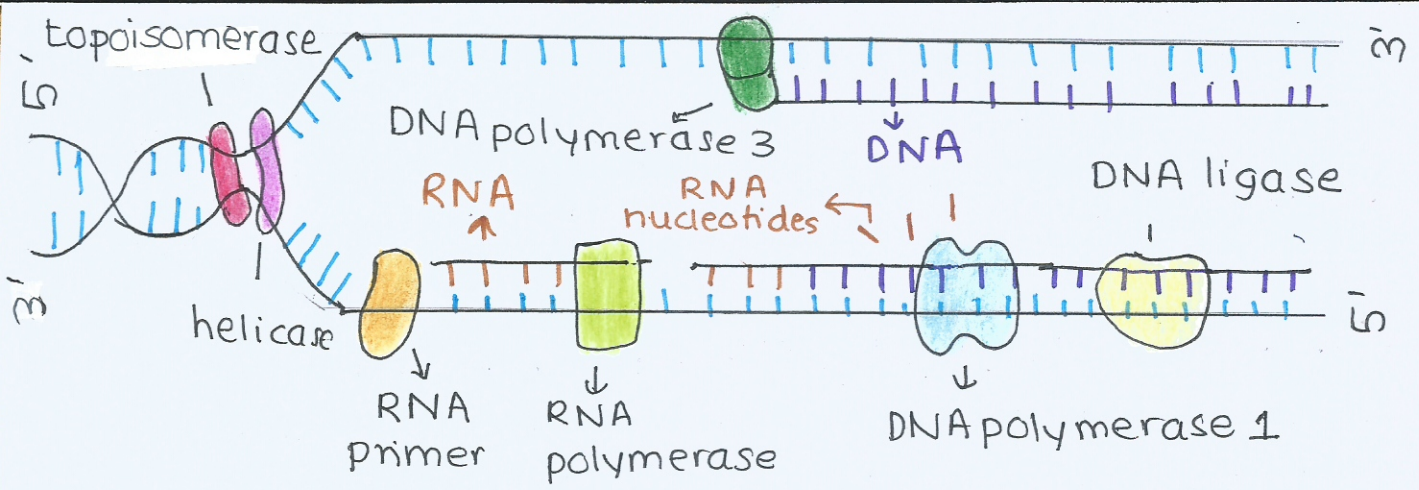
RNA primer: It is necessary to initiate the replication and the activity of DNA polymerase.

DNA primase: It creates one RNA primer on the leading strand and multiple on the lagging strand.

DNA polymerase 3: It attaches to the 3'end of the strands and links the bases covalently in a 5'3' direction. On the lagging strand, it moves away from the replication fork and synthesises in fragments.

DNA polymerase 1: It removes the RNA primers from the lagging strand and replaces them with DNA nucleotides.

DNA ligase: It connects the gaps between the okazaki fragments on the lagging strand.



DIRECTION OF REPLICATION

- DNA polymerase can only add nucleotides to the 3' end of a primer.

There are many replication sites in eukaryotes whereas prokaryotes have one site.

- The phosphate group of the new nucleotides is added to the 3' carbon of the pentose sugar.

∴ Replication occurs in 5'3' direction.

NON-CODING REGIONS OF DNA

- Only some DNA sequences code are responsible for the production of proteins. - These are called **coding sequences.**

A lot of non-coding sequences are found in genomes.

used as a guide to produce tRNA and rRNA

NON-CODING SEQUENCES

play a role in regulation of gene expression (enhancers and silencers)

gene expression

Most of the eukaryotic genome is non-coding.

▷ They have repetitive sequences of two types.

moderately repetitive sequences	highly repetitive sequences

In humans 60% of the DNA consists of repetitive sequences.

Example: These sequences are found on the ends of eukaryotic chromosomes called telomeres.

telomeres serve as a protective function.

- During interphase, the enzymes cannot continue replication all the way to the end of the chromosome.
- If telomeres were absent, the genes will be lost at the end of chromosomes.
- sacrificing the repetitive sequences found in telomeres serves as a protective function.

DNA PROFILING

Tandem repeats are used in DNA profiling.

- A variable number tandem repeat VNTR is a short nucleotide sequence that shows variations between individuals in terms of the number of times the sequence is repeated.
- Each variety can be inherited as an allele.

Analysis of these combinations in individuals is the basis behind DNA profiling.

Use: genealogical investigations.