Chapter: Molecular Basis of Inheritance

Exercise questions

Question 1: Group the following as nitrogenous bases and nucleosides: Adenine, Cytidine, Thymine, Guanosine, Uracil, and Cytosine.

Answer: DNA is a nucleotide polymer composed of sugar, a nitrogenous base, and a phosphate component. Two purines and two pyrimidines make up DNA's four bases. Adenine and guanine are two purines, while cytosine and thymine are two pyrimidines. Nucleoside refers to a nucleotide unit that lacks a phosphate group. Adenine, thymine, uracil, and cytosine are the various nitrogenous bases. The nucleosides are cytidine and guanosine.

Question 2. If a double-stranded DNA has 20 percent of cytosine, calculate the percent of adenine in the DNA.

Answer: The DNA molecule should have an equal ratio of pyrimidine (cytosine and thymine) and purine (adenine and guanine) according to Chargaff's rule. It means the number of adenine molecules is the same as the number of thymine molecules, and the number of guanine molecules is the same as the number of cytosine molecules. Percentage A equals percent T, and percent G equals percent C.

If dsDNA has 20% cytosine, it must also have 20% guanine, according to the law. As a result, the ratio of G + C content is 40%. The remaining 60% is made up of both A and T molecules. The fraction of adenine molecules is 30% since adenine and guanine are always present in equal numbers.

Question 3. If the sequence of one strand of DNA is written as follows: 5'-ATGCATGCATGCATGCATGCATGCATGC-3' Write down the sequence of the complementary strand in 5'→3' direction.

Answer: In terms of base sequence, the DNA strands are complementary to one another. As a result, if one strand of DNA has the pattern 5'-- ATGCATGCATGCATGCATGCATGCATGC − 3’ The complementary strand's sequence will then be 3'-- TACGTACGTACGTACGTACGTACGTACG − 5’ As a result, the nucleotide sequence on DNA polypeptide in the 5' to 3' direction is 5'-- GCATGCATGCATGCATGCATGCATGCAT− 3’

Question 4. If the sequence of the coding strand in a transcription unit is written as follows: 5'-ATGCATGCATGCATGCATGCATGCATGC-3'. Write down the sequence of mRNA.

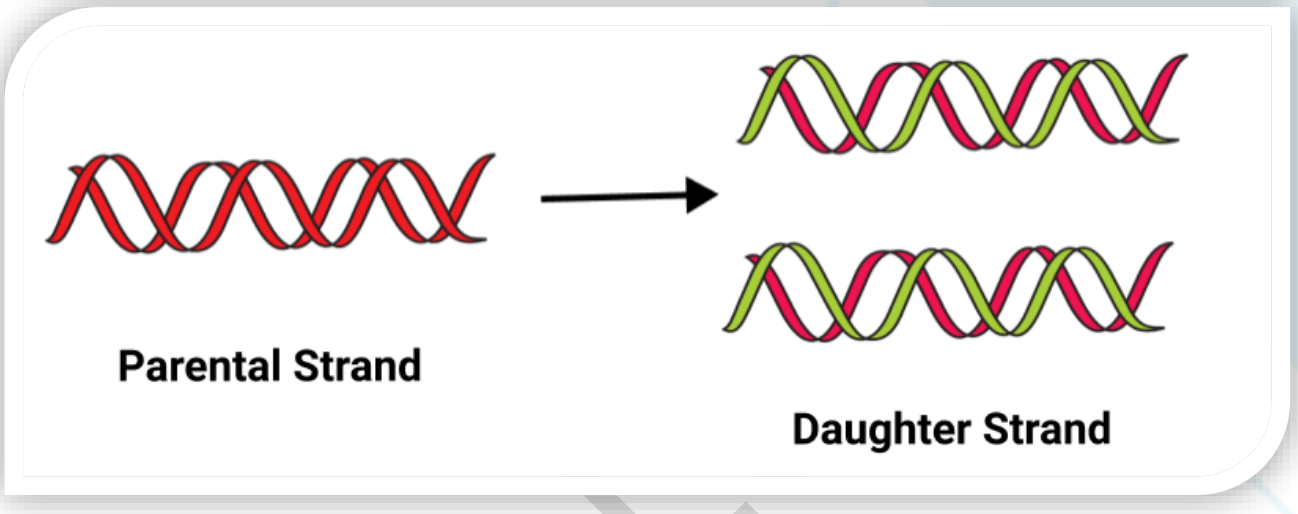
Answer: If the coding strand in a transcription unit is 5’− ATGCATGCATGCATGCATGCATGCATGC-3’The template strand would then be 3' − TACGTACGTACGTACGTACGTACGTACG-5’. The sequence of mRNA and the coding strand of DNA is known to be identical. Thymine, on the other hand, is replaced by uracil in RNA. As a result, the mRNA sequence will be 5'− AUGCAUGCAUGCAUGCAUGCAUGCAUGC-3’

Question 5. Which property of DNA double helix led Watson and Crick to hypothesize semiconservative mode of DNA replication? Explain.

Answer: In terms of base sequences, Watson and Crick discovered that the two strands of DNA are antiparallel and complementary to each other. The theory that DNA replication is semiconservative

was based on this type of arrangement in the DNA molecule. It means that the double-stranded DNA molecule splits into two strands, each of which serves as a template for the creation of a new complementary strand. As a result, each DNA molecule would have one parental strand and a daughter strand that had just been created.

The semi-conservative method of replication is named after the fact that only one parental strand is conserved in each daughter molecule.



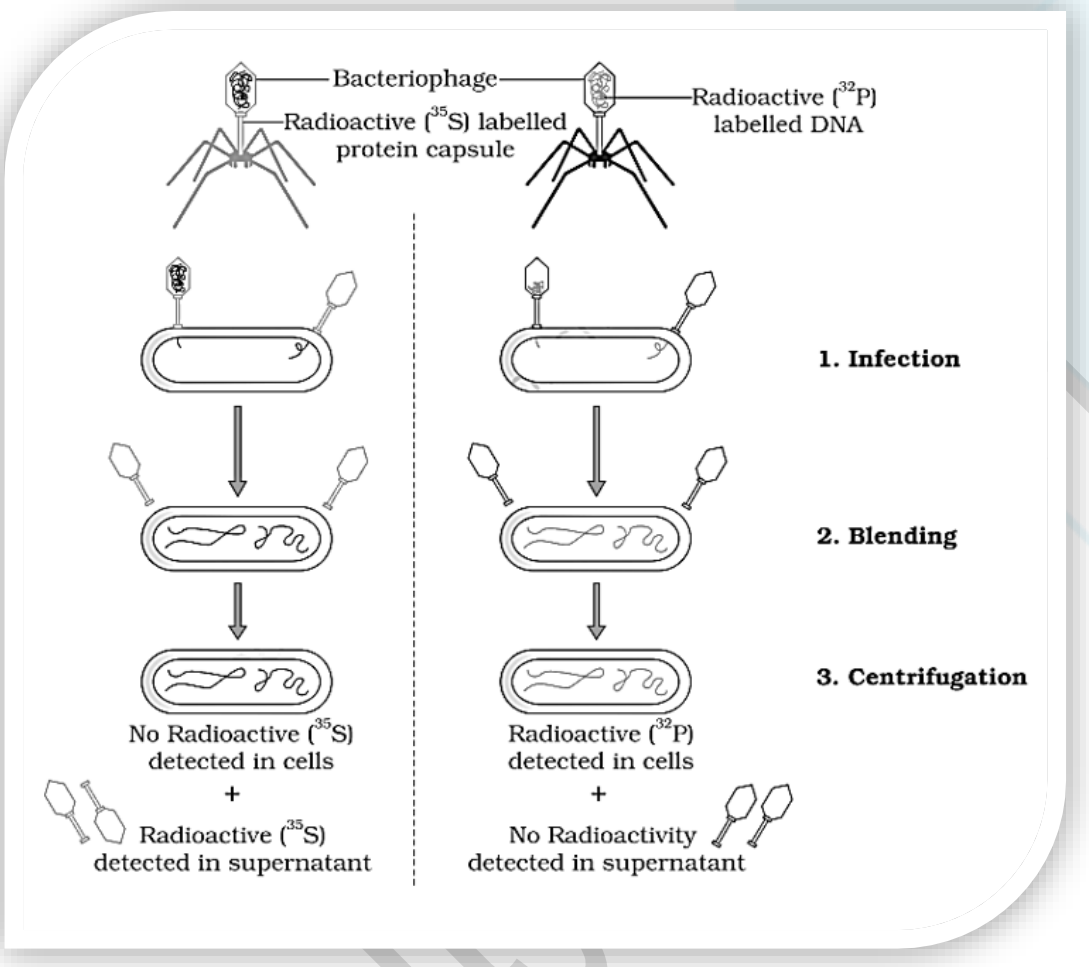
Question 6. Depending upon the chemical nature of the template (DNA or RNA) and the nature of nucleic acids synthesized from it (DNA or RNA), list the types of nucleic acid polymerases.

Answer: DNA-dependent DNA polymerases and DNA-dependent RNA polymerases are the two types of nucleic acid polymerases. DNA-dependent DNA polymerases synthesize a new strand of DNA using a DNA template, whereas DNA-dependent RNA polymerases synthesize RNA using a DNA template strand.

Question 7. How did Hershey and Chase differentiate between DNA and protein in their experiment while proving that DNA is the genetic material?

Answer: Hershey and Chase employed bacteriophage and E.coli to demonstrate that DNA is the genetic material. They used various radioactive isotopes to mark the bacteriophage's DNA and protein coat. They grew some bacteriophages in radioactive phosphorus (32P) media to identify DNA and others in radioactive sulfur (35S) medium to detect protein. The phages were then given radioactive labels and allowed to infect E.coli bacteria. The bacteriophage's protein coat was removed from the bacterial cell after infection by mixing, followed by centrifugation. Because the protein coat was

lighter than the infected bacterium, it was spotted in the supernatant.



Question 8. Differentiate between the following:

(a) Repetitive DNA and Satellite DNA

(b) mRNA and tRNA

(c) Template strand and Coding strand

Answer:

(a) Repetitive DNA and Satellite DNA

	Repetitive DNA	Satellite DNA
1	DNA sequences that are repeated are known as repetitive DNA. It is made up of small portions repeated several times.	The term "satellite DNA" refers to DNA that is in sequences containing DNA that is extremely repetitive.

(b) mRNA and tRNA

	mRNA	tRNA
1	The messenger RNA, or mRNA, serves as a template for the transcription process.	tRNA, or transfer RNA, is an adapter molecule that transports a specific amino acid to mRNA for polypeptide synthesis.
2	It is a linear molecule.	It has a cloverleaf shape.

(c) Template strand and coding strand

	Template strand	coding strand
1	During transcription, the template strand of DNA serves as a template for the creation of mRNA.	The coding strand is a DNA sequence that has the identical nucleotide sequence as mRNA (except that in RNA, thymine is substituted by uracil).
2	It measures 3' to 5' in length.	It measures 3' to 5' in length.

Question 9. List two essential roles of ribosomes during translation.

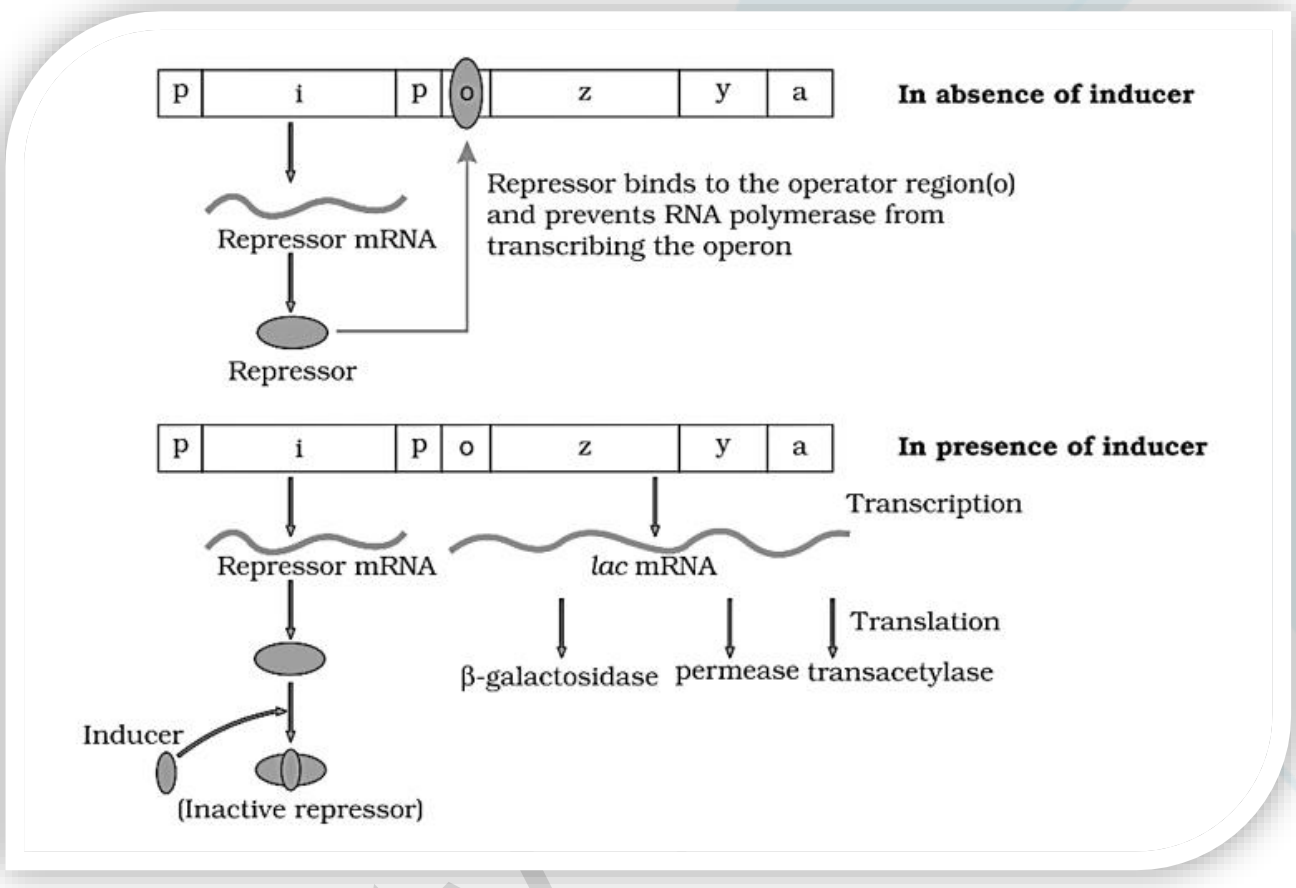
Answer: The following are some of the most important functions of the ribosomes during translation.

- The ribosome is the spot where individual amino acids are combined to form proteins. It consists of two components. The smaller subunit interacts with mRNA to form a protein-synthesis complex, whereas the bigger subunit serves as an amino acid binding site.
- The ribosome serves as a catalyst in the formation of peptide bonds. In bacteria, for example, 23s rRNA functions as a ribozyme.

Question 10. In the medium where E. coli was growing, lactose was added, which induced the lac operon. Then, why does lac operon shut down sometime after the addition of lactose in the medium?

Answer: An operator gene, a promoter gene, and a regulator gene make up the Lac operon, which is a DNA tract made up of three contiguous structural genes. It breaks down lactose into glucose and galactose in a coordinated manner. Lactose works as an inducer in the lac operon. It attaches to the repressor and makes it inactive. RNA polymerase interacts withfollowingter region after lactose binds to the repressor. As a result, three structural genes create their products and the corresponding enzymes. Lactose is converted into glucose and galactose by these enzymes, which operate on lactose.

When the level of the inducer drops due to enzyme metabolization, it triggers the manufacture of the repressor from the regulator gene. The repressor attaches to the operator gene and inhibits the operon from being transcribable by RNA polymerase. As a result, the transcribing is halted. Negative regulation is the term for this form of regulation.



Question 11. Explain (in one or two lines) the function of the followings:

(a) Promoter

(b) tRNA

(c) Exons

Answer:

- (a) Promoter - A promoter is a DNA region that aids in the initiation of transcription. It acts as an RNA polymerase binding site.
- (b) tRNA- The transfer RNA, often known as tRNA, is a tiny RNA that reads the genetic code on mRNA. During protein translation, it transports specific amino acids to mRNA on the ribosome.
- (c) Exons - Exons are DNA coding sequences that transcribe proteins in eukaryotes.

Question 12. Why is the Human Genome project called a megaproject?

Answer: The Human Genome Project was regarded as a megaproject because its goal was to sequence every single base pair in the human genome. It took around 13 years to complete and was completed in 2006. It was a large-scale effort with the goal of developing new technology and gathering fresh data in the field of genomic research. As a result, various new fields and pathways in genetics,

biotechnology, and medical sciences have opened up. It gave us hints on how to better comprehend human biology.

Question 13. What is DNA fingerprinting? Mention its application.

Answer: DNA fingerprinting is a technique for identifying and analyzing differences in DNA between individuals. It is based on DNA sequence variability and polymorphism.

Applications:

- In forensic science, it is used to identify prospective criminal suspects.
- It's utilized to prove paternity and establish familial ties.
- It is used to identify and protect the commercial crop and livestock types.
- It's utilized to figure out an organism's evolutionary history and the relationships between different groupings of organisms.

Question 14. Briefly describe the following:

(a)Transcription

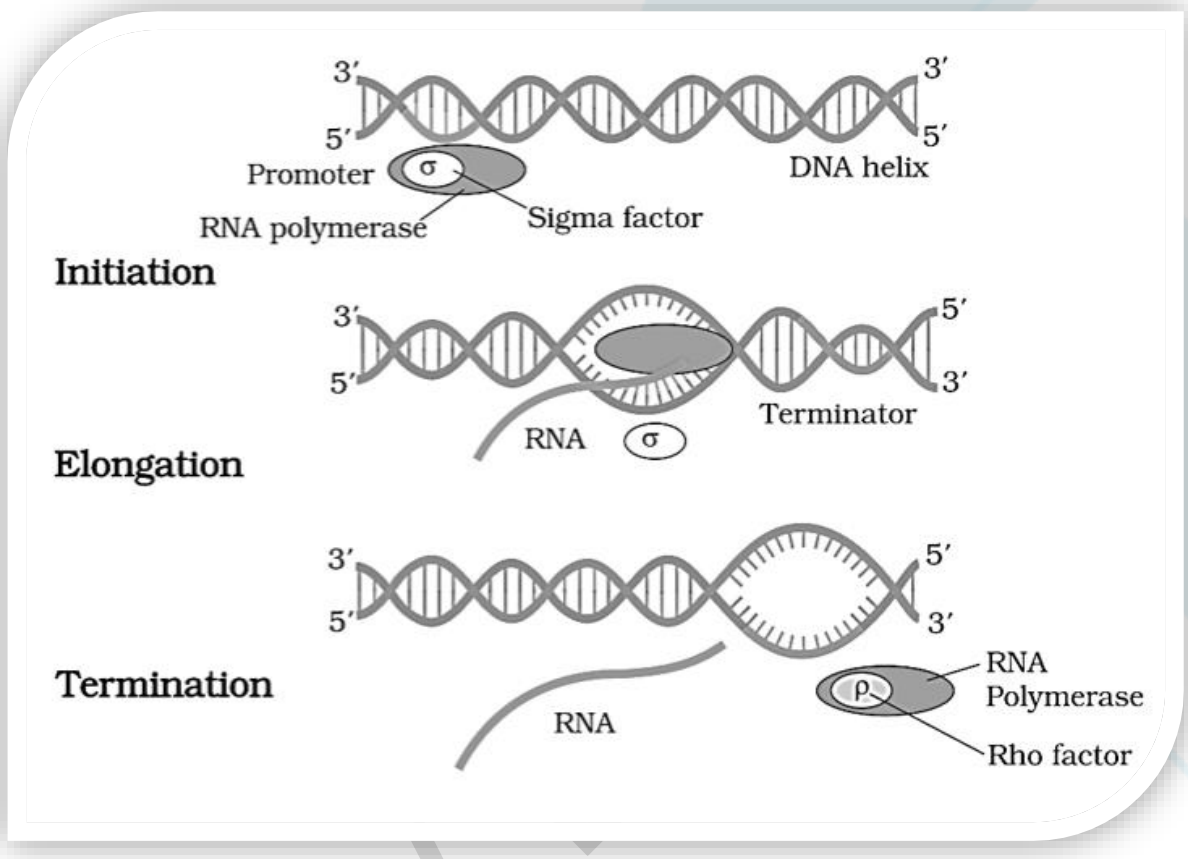
(b)Polymorphism

(c) Translation

(d)Bioinformatics

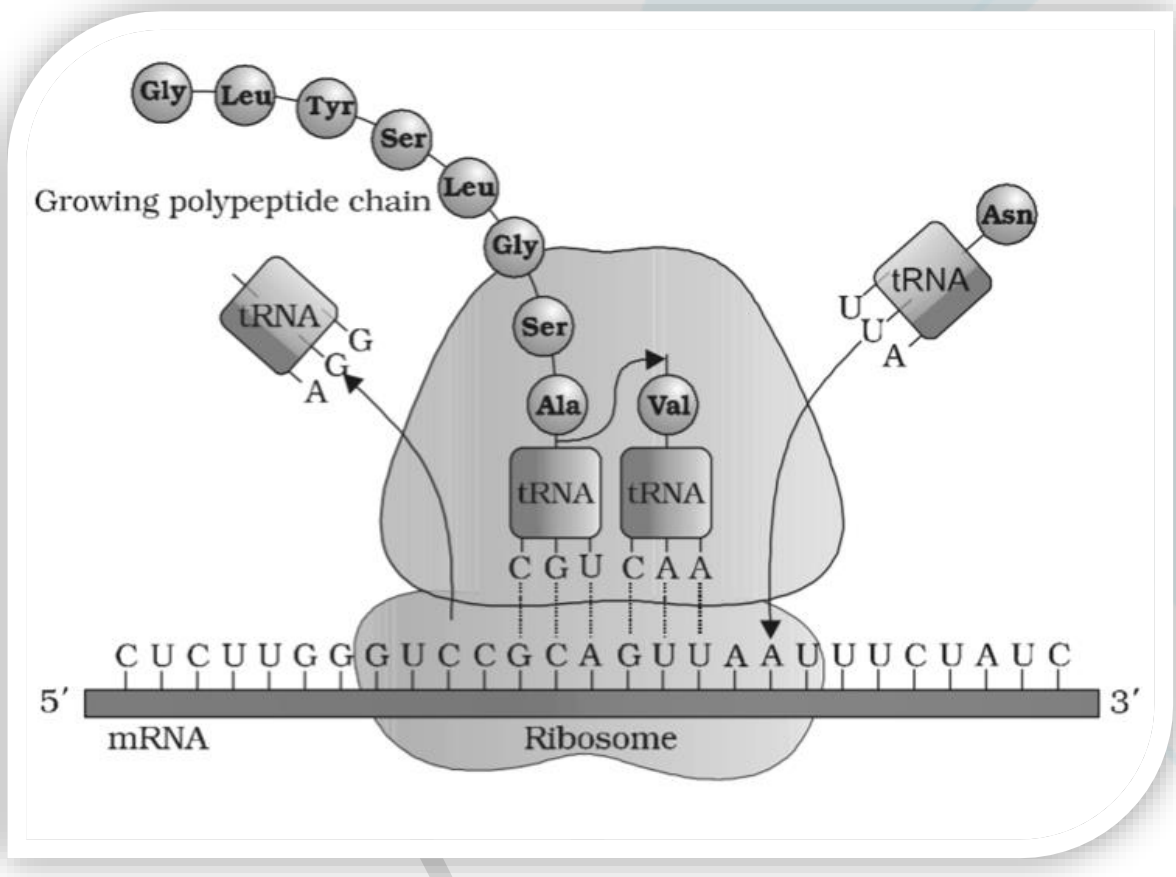
Answer:

(a) Transcription - The process of synthesizing RNA from a DNA template is known as transcription. During the process, a piece of DNA is replicated into mRNA. The transcription process begins at the template DNA's promoter region and ends at the terminator region. The transcription unit is the DNA segment that connects these two areas. The RNA polymerase enzyme, a DNA template, four types of ribonucleotides, and certain cofactors like Mg2+ are all required for transcription. The following are the three major events that occur throughout the transcription process - Initiation, Elongation, Termination. The DNA-dependent RNA polymerase and certain initiation factors () bind to the double-stranded DNA in the template strand's promoter region and start the transcription process. The unwinding of the DNA duplex into two distinct strands is caused by RNA polymerase as it proceeds along with the DNA. The sense strand, one of the strands, then serves as a template for mRNA production. RNA polymerase takes nucleoside triphosphates (dNTPs) as a starting material and polymerizes them to produce mRNA based on the corresponding bases on the template DNA. This helix opening and polynucleotide chain elongation process proceeds until the enzyme reaches the terminator region.



(b) Polymorphism - Polymorphism is a type of genetic diversity in which a DNA molecule can have many nucleotide sequences at the same time. This heritable mutation is found in a large number of people in a population. It develops as a result of a mutation in either the somatic or germ cells. The germ cell mutation can be passed down from one generation to the next. This leads to the accumulation of diverse mutations in a population, resulting in population variety and polymorphism. This is extremely significant in the evolution and speciation processes.

(c) Translation - The process of polymerizing amino acids to form a polypeptide chain is known as translation. The order and sequence of amino acids in a polypeptide chain are determined by the triplet sequence of base pairs in mRNA. When the amino acid binds to it with ATP during the start of translation, tRNA becomes charged. Only the charged tRNA recognises the start (initiation) codon (AUG) found on mRNA. The ribosome serves as the actual site of translation and comprises two distinct sites for the attachment of the following amino acids in a big subunit. At the start codon (AUG), the small subunit of the ribosome attaches to mRNA, followed by the big subunit. The translation procedure is then started. During the elongation step, the ribosome moves one codon downstream with the mRNA to make room for another charged tRNA to bind. The amino acid carried by tRNA forms a peptide bond with the previous amino acid, and this process repeats again, resulting in the development of a polypeptide chain. The translation process is stopped when the ribosome reaches one or more STOP codons (VAA, UAG, and UGA). Ribosomes separate from mRNA as the polypeptide chain is released.



(d) Bioinformatics - The use of computer and statistical approaches to the science of molecular biology is known as bioinformatics. It answers the practical issues that arise from biological data administration and analysis. Following the conclusion of the human genome project, the field of bioinformatics grew (HGP). This is due to the massive volume of data created throughout the HGP process, which must be managed and preserved for simple access and interpretation by numerous scientists in the future. As a result, bioinformatics entails the establishment of biological databases that store a tremendous amount of biological data. It creates technologies that make access to and use of information simple and efficient.