6. Molecular Basis of Inheritance

Question 1. Group the following as nitrogenous bases and nucleosides:

Adenine, Cytidine, Thymine, Guanosine, Uracil and Cytosine.

Answer: DNA is a polymer of nucleotides which are made up of sugar, a nitrogenous base and a phosphate moiety. DNA has four bases; two purines and two pyrimidines. The two purines are namely adenine and guanine and two pyrimidines are cytosine, thymine. A nucleotide unit without phosphate group is called nucleoside. Nitrogenous bases = Adenine, thymine, uracil and cytosine. Cytidine and Guanosine are the nucleosides.

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

Answer: In a DNA molecule, the number of cytosine molecules is equal to guanine molecules and the number of adenine molecules is equal to thymine molecules. Thus, if a double-stranded DNA has 20% cytosine, it has 20% guanine. Thus, C + G makes 40% of the total bases. The remaining 60% includes both adenine and thymine which are in equal amounts. So, the percentage of adenine is 30%.

Question 3. If the sequence of one strand of DNA is written as follows:

5′-ATGCATGCATGCATGCATGCATGCATGC-3′

Write down the sequence of complementary strand in 5'⟶3′ direction.

Answer: DNA is a two-stranded molecule. Each strand is a polynucleotide composed of A(adenosine), T (thymidine), C (cytidine), and G (guanosine) residues polymerized by "dehydration" synthesis in linear chains with specific sequences. Each strand has polarity which runs from 5′ to 3′.
In DNA, A pirs with T and G pairs with C.
Fo through the original 5′ to 3′ sequence pairing each A with T ad each C wth G.
While RNA is a single strand molecule. This Strand also consists polynucleotide composed A, C, G and U (uridine).
For a complementary strand replace A with U (because RNA does not consist T), T with A,

C with G, and G with C.
Therefore, if the sequence of one strand of DNA is written as:
5′-ATGCATGCATGCATGCATGCATGC-3′
The sequence of the complementary strand in 3′ -> 5′ is as follows:
3′ – TACGTACGTACGTACGTACGTACG – 5′
Subsequently, sequence of complementary strand in 5’⟶3′ direction is written as:
5′ – GCATGCATGCATGCATGCATGCAT – 3′

Question 4. If the sequence of the coding strand in a transcription unit is written as follows:

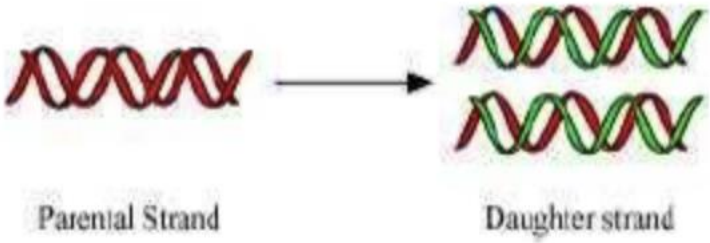
5′-ATGCATGCATGCATGCATGCATGC-3′

Write down the sequence of mRNA.

Answer:
If the coding strand in a transcription unit is 5'-ATGCATGCATGCATGCATGCATGC-3'
Then, the template strand in 3 ‘to 5’ direction would be
3'-TACGTACGTACGTACGTACGTACG-5'
It is known that the sequence of mRNA is same as the coding strand of DNA. However, in RNA, thymine is replaced by uracil.
Hence, the sequence of mRNA will be
5'-AUGCAUGCAUGCAUGCAUGCAUGC-3'

Question 5. Which property of DNA double helix led Watson and Crick to hypothesise semi-conservative mode of DNA replication? Explain.

Answer: Watson and Crick observed that the two strands of DNA are anti-parallel and complementary to each other with respect to their base sequences. This type of arrangement in DNA molecule led to the hypothesis that DNA replication is semiconservative. It means that the double-stranded DNA molecule separates and then, each of the separated strand acts as a template for the synthesis of a new complementary strand. As a result, each DNA molecule would have one parental strand and a newly synthesized daughter strand. Since only one parental strand is conserved in each daughter molecule, it is known as semi-conservative mode of replication.



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: There are two types of nucleic acid polymerases:
a. DNA-dependent DNA polymerase
b. DNA-dependent RNA polymerase
DNA-dependent DNA polymerase use a DNA template to synthesize a new DNA strand and DNA-dependent RNA polymerase use a DNA template to synthesize a new RNA 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 grew some bacteriophages on a medium containing radioactive phosphorus (32P) to identify DNA and some on a medium containing radioactive sulphur (35S) to identify protein. Then these radioactive-labelled phages were allowed to infect *E. coli* bacteria subjected to the process of centrifugation.
It gave an idea that DNA acted as hereditary material which was transmitted from bacteriophage to bacteria. Bacteria which were infected with bacteriophages had radioactive proteins.

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
Repetitive DNA are DNA sequences that contain small segments, which are repeated many times.	Satellite DNA are DNA sequences that contain highly repetitive DNA.

(b) mRNA and tRNA

mRNA	tRNA
mRNA or messenger RNA acts as a template for the process of transcription.	tRNA or transfer RNA acts as an adaptor molecule that carries a specific amino acid to mRNA for the synthesis of polypeptide.
It is a linear molecule.	It has clover leaf shape.

(c) Template strand and coding strand

Template strand	Coding strand
Template strand of DNA acts as a template for the synthesis of mRNA during transcription.	Coding strand is a sequence of DNA that has the same base sequence as that of mRNA (except thymine that is replaced by uracil in DNA).
It runs from 3' to 5'.	It runs from 5'to 3'.

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

Answer: The important functions of ribosome during translation are as follows.
Ribosome acts as the site where protein synthesis takes place from individual amino acids. It is made up of two subunits.
The smaller subunit comes in contact with mRNA and forms a protein synthesizing complex whereas the larger subunit acts as an amino acid binding site.
Ribosome acts as a catalyst for forming peptide bond. For example, 23s r-RNA in bacteria acts 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 some time after addition of lactose in the medium?

Answer: Inducer is a chemical (substrate, hormone or some other metabolite) which after coming in contact with the repressor, changes the latter into non-DNA binding state so as to free the operator gene. The inducer for lac-operon of Escherichia coli is lactose (actually allolactose, or metabolite of lactose). RNA polymerase is recognized by promoter gene. It passes over the freed operator gene and then catalyses transcription of mRNAs over the structural genes. The mRNA pass into the cytoplasm and form particular proteins or enzymes. Out of the three enzymes produced by lac-operon, permease is meant for bringing lactose inside the cell. galactosidase (= lactase) breaks lactose into two components, glucose and galactose. The enzyme like lactase or galactosidase which is formed in response to the presence of its substrate is often called inducible enzyme. Inducible operon systems generally occur in catabolic pathways. The lac-operon will not, however, remain operative indefinitely despite presence of lactose in the external environment. It will stop its activity with the accumulation of glucose and galactose in the cell beyond the capacity of the bacterium for their metabolism.

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

(a) Promoter

(b) tRNA

(c) Exons

Answer:
(a) Promoter
Promoter is a region of DNA that helps in initiating the process of transcription. It serves as the binding site for RNA polymerase.

(b) tRNA
tRNA or transfer RNA is a small RNA that reads the genetic code present on mRNA. It carries specific amino acid to mRNA on ribosome during translation of proteins.

(c) Exons
Exons are coding sequences of DNA in eukaryotes that transcribe for proteins.

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

Answer: Human genome project was considered to be a mega project because it had a specific goal to sequence every base pair present in the human genome. It took around 13 years for its completion and got accomplished in year 2006. It was a large scale project, which aimed at developing new technology and generating new information in the field of genomic studies. As a result of it, several new areas and avenues have opened up in the field of genetics, biotechnology, and medical sciences. It provided clues regarding the understanding of human biology.

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

Answer: DNA fingerprinting is a very easy and quick way to compare the DNA sequence of any two individuals. It includes identifying differences in some specific regions in DNA sequence called as repetitive DNA sequences. In these regions, a small stretch of DNA is repeated many times and they are specific for every individual. The technique of fingerprinting was initially developed by Alec Jeffrey.

Applications of DNA fingerprinting

1. It is used in forensic science in order to identify individuals.
2. It can be used to establish paternity or maternity related disputes.
3. DNA fingerprinting is used to establish evolutionary relationships between organisms.

Question 14. Briefly describe the following:

(a) Transcription

(b) Polymorphism

(c) Translation

(d) Bioinformatics

Answer: (a) Transcription

Transcription is the process of synthesis of RNA from DNA template. A segment of DNA gets copied into mRNA during the process. The process of transcription starts at the promoter region of the template DNA and terminates at the terminator region. The segment of DNA between these two regions is known as transcription unit. The transcription requires RNA polymerase enzyme, a DNA template, four types of ribonucleotides, and certain cofactors such as Mg2+.

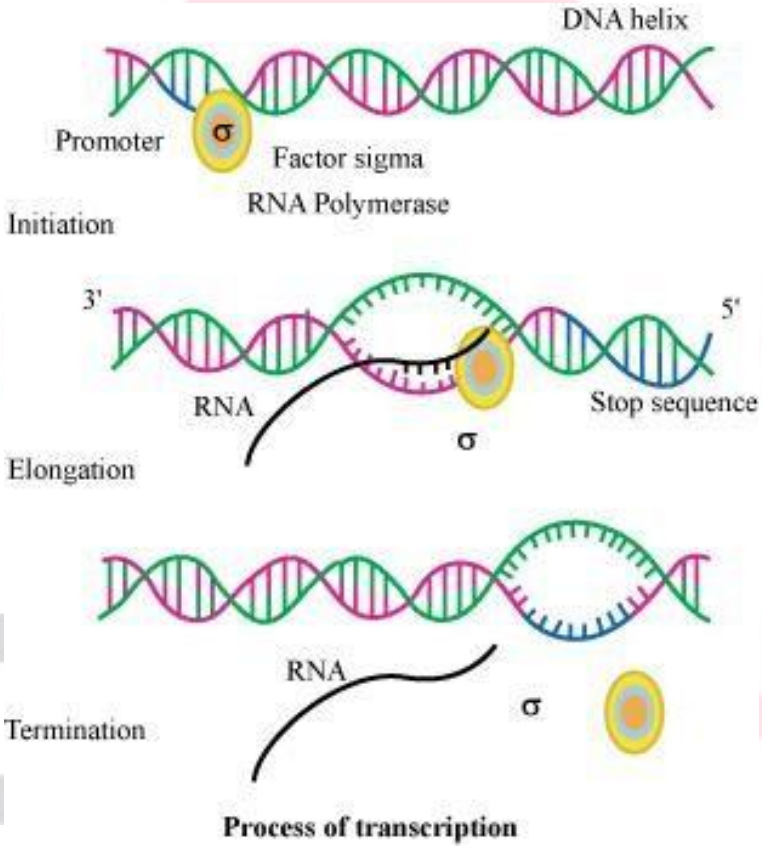
The three important events that occur during the process of transcription are as follows.

(i) Initiation

(ii) Elongation

(iii) Termination

The DNA-dependent RNA polymerase and certain initiation factors (σ)bind at the double stranded DNA at the promoter region of the template strand and initiate the process of transcription. RNA polymerase moves along the DNA and leads to the unwinding of DNA duplex into two separate strands. Then, one of the strands, called sense strand, acts as template for mRNA synthesis. The enzyme, RNA polymerase, utilizes nucleoside triphosphates (dNTPs) as raw material and polymerizes them to form mRNA according to the complementary bases present on the template DNA. This process of opening of helix and elongation of polynucleotide chain continues until the enzyme reaches the terminator region. As RNA polymerase reaches the terminator region, the newly synthesized mRNA transcripted along with enzyme is released. Another factor called terminator factor (ρ)is required for the termination of the transcription.



Process of transcription

(b) Polymorphism

Polymorphism is a form of genetic variation in which distinct nucleotide sequence can exist at a particular site in a DNA molecule. This heritable mutation is observed at a high frequency in a population. It arises due to mutation either in somatic cell or in the germ cells. The germ cell mutation can be transmitted from parents to their offsprings. This results in accumulation of various mutations in a population, leading to variation and polymorphism in the population. This plays a very important role

in the process of evolution and speciation.

(c) Translation

Translation is the process of polymerizing amino acid to form a polypeptide chain. The triplet sequence of base pairs in mRNA defines the order and sequence of amino acids in a polypeptide chain.

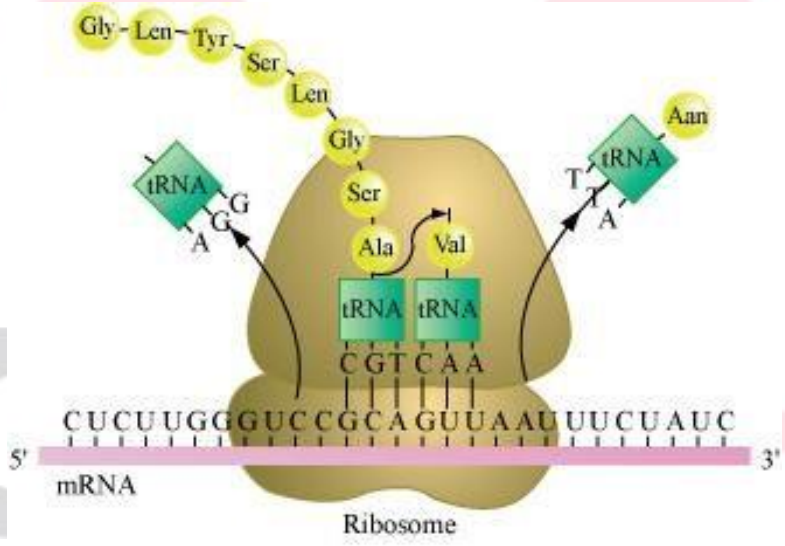
The process of translation involves three steps.

(i) Initiation

(ii) Elongation

(iii) Termination

During the initiation of the translation, tRNA gets charged when the amino acid binds to it using ATP. The start (initiation) codon (AUG)present on mRNA is recognized only by the charged tRNA. The ribosome acts as an actual site for the process of translation and contains two separate sites in a large subunit for the attachment of subsequent amino acids. The small subunit of ribosome binds to mRNA at the initiation codon (AUG) followed by the large subunit. Then, it initiates the process of translation. During the elongation process, the ribosome moves one codon downstream along with mRNA so as to leave the space for binding of another charged tRNA. The amino acid brought by tRNA gets linked with the previous amino acid through a peptide bond and this process continues resulting in the formation of a polypeptide chain. When the ribosome reaches one or more STOP codon(VAA, UAG, and UGA), the process of translation gets terminated. The polypeptide chain is released and the ribosomes get detached from mRNA.



Translation of proteins

(d) Bioinformatics

Bioinformatics is the application of computational and statistical techniques to the field of molecular biology. It solves the practical problems arising from the management and analysis of biological data. The field of bioinformatics developed after the completion of human genome project(HGP). This is

because enormous amount of data has been generated during the process of HGP that has to be managed and stored for easy access and interpretation for future use by various scientists. Hence, bioinformatics involves the creation of biological databases that store the vast information of biology. It develops certain tools for easy and efficient access to the information and its utilization. Bioinformatics has developed new algorithms and statistical methods to find out the relationship between the data, to predict protein structure and their functions, and to cluster the protein sequences into their related families.