

NCERT Solutions for Class 12 Biology

Chapter 5 – Molecular Basis of Inheritance

5.1

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

Ans:

Nitrogenous Bases:

Adenine, thymine, uracil, and cytosine.

Nucleosides:

Cytidine and guanosine

5.2

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

Ans: The pair of adenine & thymine molecules has the same proportion in the double helix model of DNA with 2 strands, while guanine and cytosine molecules have a comparable proportion. Whenever the percentage of cytosine has a 100% DNA has turned out to be 20%, the percentage of guanine would likewise have turned out to be 20%. The other 60% of DNA is created based on adenine & thymine, with cytosine & guanine making up the rest, which is 40%. As a result, 30% of DNA is adenine & 30% comprises thymine. Therefore, 30% of DNA possesses the availability of adenine compounds in its structure.

5.3

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

5' -ATGCATGCATGCATGCATGCATGC-3'

**Write down the sequence of complementary strand in 5'→3'
direction.**

Ans: Each base combination with other base pairs, such as adenine and thymine or cytosine and guanine, generates mutually beneficial DNA double strands. Every strand's provided pattern has

emerged as 5'- ATGCATGCATGCATGCATGCATGC – 3'

In the 3' to 5' direction, the order of events will develop as follows,

3'- TACGTACGTACGTACGTACGTACG – 5'

Hence, in a 5' to 3' pathway, the complementary strands are going to create an ordered model that resembles close to 5'- GCATGCATGCATGCATGCATGCAT – 3'

5.4

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

5' -ATGCATGCATGCATGCATGCATGC-3'

Write down the sequence of mRNA.

Ans: The coding segment in the transcription block is not responsible for anything since the pattern stays the same, whereas uracil replaces thymine.

When the offered string consists of 5'- ATGCATGCATGCATGCATGCATGC-3'

Therefore, the mRNA structure's pattern will be replicated as,

5' – AUGCAUGCAUGCAUGCAUGCAUGCAUGC-3'

5.5

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

Explain.

Ans: The work of Watson and Crick's semi-conservative theory of DNA replication was based on the subsequent characteristics of the DNA double helix formation:

1. The DNA double-strand's complementary & antiparallel properties with regard to nucleotide order. As a result, each single strand serves as a trigger point for building additional strands.
2. The overall existence of a single parental segment alongside a single newly synthesized strand contributes to the semi-conservative features of DNA.
3. Because DNA is complementary, the starting position of the strand serving as the template determines the daughter strand's pattern.

5.6

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

Ans: There are primarily four distinct types of nucleic acid polymeric enzymes, including

- **DNA-dependent DNA polymerases:** These polymerase-type enzymes are the primary ones that assist in the replication process of the parent sequences (Template DNA), which is how a new set of DNA strands is created.
- **DNA-dependent RNA polymerase:** It's the primary polymerase enzyme that depends on the transcription mechanism, which builds RNA after duplicating a single DNA strand.
- It includes RNA-dependent DNA polymerase & RNA-dependent RNA polymerase.

5.7

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

Ans: The method that follows was used by Alfred Hershey and Martha Chase in 1952 to determine the genetic code between DNA and protein using bacteriophage & strains of E. Coli.

- They cultivated certain types of viruses within radioactive phosphorus along with others in radioactive sulfur compounds, to determine the genetic material between DNA and protein.
- The virus found in radioactive phosphorus contains radioactive DNA, although it doesn't contain any protein, while the virus from radioactive sulfur contains radioactive protein without any DNA.
- The disease spreads as a result of the radioactive viruses and radioactive phages being introduced into E. Coli.
- The infectious virus fragment can be separated from the bacterium within a centrifuge after the viral envelope is removed by stirring the phages in the pulverizer.
- While the virus-carrying protein might not be capable of transferring the disease to bacteria, the virus-carrying DNA must accomplish this process.

Hence, it depends on the DNA that solely represents the genetic compound linking DNA & proteins.

5.8

Differentiate between the followings:

(a) Repetitive DNA and Satellite DNA

(b) mRNA and tRNA

(c) Template strand and Coding strand

Ans: (a)

| Repetitive DNA | Satellite DNA |
|------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------|
| 1) This kind of DNA pattern is composed of smaller & repeating categories. | 1) One kind of redundant sequence in DNA is composed of extremely repetitive DNA. |
| 2) They may be isolated from bulk DNA using density gradient centrifugation, and whenever this configuration occurs, they show up as bright streaks. | 2) They are capable of being isolated from bulk DNA using density centrifugation, where they show up as tiny spikes and dark stripes. |
| 3) It can be either big or small. Base pairs could extend from a few to hundreds or thousands. | 3) They can reach an average length of one hundred base pair combinations, and are usually smaller. |

(b)

| mRNA | tRNA |
|----------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1) It can additionally be referred to as messenger RNA since it aids in delivering the template during the procedure of transcription. | 1) It is sometimes referred by the term transfer RNA because it serves as an adapter during transcription, bringing amino acids & reading the genetic information. |
| 2) Its shape remains linear in structure. | 2) It resembles a cloverleaf structure and possesses an inverted L form. |
| 3) It displays ribosome binding alone. | 3) It exhibits ribosome & amino acid interaction. It has a ribosome connected to one end, while amino acids are linked to the opposing side. |

(c)

| Template helix | Coding helix |
|-----------------------|---------------------|
|-----------------------|---------------------|

| | |
|-------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|
| 1) Template segments serve as the starting point for the creation of mRNA throughout the course of transcription. | 1) The coding segment functions as a complementary helix of the template strand during transcription and cannot be coded for anything at all. |
| 2) It consists of a sequence that is complementary to the mRNA. | 2) Its overall formation is identical to that of mRNA, except that uracil present in mRNA substitutes for thymine in DNA. |
| 3) The movement happens in the direction from 3' to 5' | 3) The movement occurs in the direction from 5' to 3'. |

5.9

List two essential roles of ribosome during translation.

Ans: The two primary functions of ribosomes in the translation process are outlined below:

1. The ribosome functions as a cellular manufacturing operation center, facilitating the creation of proteins. During its inactive form, it breaks down into 2 distinct subunits: A massive subunit & a small subunit. Amino acids are bound in large subunits & protein synthesis starts whenever mRNA reaches the tiny subunits.
2. Ribosomes are additionally utilized as ribozymes, which are catalysts for the creation of peptide bonds throughout the translation process.

5.10

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?

Ans:

- Lactose functions as a stimulant for the lac operon, controlling when the operon switches on & off. In addition, the lac operon has 3 structurally related genes (z, y, and a) together with one regulatory gene.
- The structural gene's z code with beta-galactosidase, y code with permease, and a sequence that stands for transacetylase, whereas the regulatory genetic material I codes for repressor. Lactose was metabolized by each of the three structural genes.
- When lactose has been added to the E. Coli substrate, permease transports it into the cell's membrane and binds the transcription repressor. This causes RNA polymerase to come into

contact with the area of the promoter, which starts with the production of structural gene products, alongside causes glucose and galactose to undergo metabolism.

- The amount of lactose decreases as a result of its metabolic processes, and a repressor begins to develop. RNA polymerase replication is stopped when the repressor binds to the operator. Due to the transcription activity being stopped, this is known as negative governance.

5.11

Why is the Human Genome project called a mega project?

Ans: The Human Genome Project is considered a megaproject for the following reasons:

- The human genome contains around 3×10^9 base pairs. If each base pair costs 3 US dollars, the estimated cost is 9 billion US dollars.
- If this sequence were typed into a book, each page would include 1000 letters, and each book would contain around 1000 pages, resulting in the production of 3300 volumes from a single human cell.

For all of this, high-performance computing machines are necessary for data storage, retrieval, and analysis.

5.12

Why is the Human Genome project called a mega project?

Ans: Many factors make the Human Genome Project a megaproject:

1. The human genome is roughly 3×10^9 base pairs in size. Therefore, if 3 US dollars is needed for each base combination, the projected cost would be around 9 billion dollars (US).
2. There would be 3300 books made from just one human cell if its logical arrangement were written out and put in a work of literature. A book would have about 1000 pages, with 1000 letters appearing on every single page.

High-end computing machines are needed for all of this to store, retrieve, and monitor information.

5.13

What is DNA fingerprinting? Mention its application.

Ans: DNA fingerprinting is the process employed to determine and examine each person's unique DNA variations. The following are some of the numerous uses for DNA fingerprinting:

1. The technique is employed in forensic medicine to identify possible suspects in criminal activity.
2. The method is employed to determine family ties and parenthood.
3. This process is employed to identify and safeguard livestock & commercial types of crops.
4. The process is employed to determine the evolutionary connections & relationships among the different creatures.

5.14

Briefly describe the following:

(a) Transcription

(b) Polymorphism

(c) Translation

(d) Bioinformatics

Ans: (a)

Ans: Transcription has become the mechanism by which mRNA is created from a DNA template. One DNA strand gets translated into mRNA throughout this entire procedure. The promoter section within the template DNA is where it begins, and the end of the domain is where it finishes or ends. There exists a transcribing block among each of these areas. DNA-dependent RNA polymerase catalyzes the transcription pathway.

- The 3 primary transcriptional activities are beginning, extension, and closure.
- The procedure of transcription begins when the initiation factor-like (σ) and DNA-dependent RNA polymerase connect to the promoter area of the template helix.
- The sense segment, also known for being the template strand, initiates mRNA production once the DNA double helix unravels as a result of the enzyme. Transcription continues unless it reaches the terminator area.
- Both the enzymatic process & the freshly synthesized mRNA get released when the transcription enzymes that exist come to the terminator domain. The termination ratio (ρ) causes the end of the contract.

(b)

Ans: A type of genetic diversity known as polymorphism occurs when different nucleotide chains can be present at a certain location in a population's DNA strand. In a group of people, this transmissible trait is found frequently. It develops as a result of an alteration in germination cells or somatic cells of the body. Parents are capable of passing on the germinal cell mutation to their children. A group of individuals experiences diversity and polymorphism as a consequence of a compilation of different genes. This aspect is crucial to the processes of diversification &

development. DNA fingerprinting & genetic mapping are based on polymorphism within the sequence of DNA.

(c)

Ans: The polymerization of amino acids to create a polypeptide chain is known as translation. The order and arrangement of amino acids within a polypeptide chain are determined by the triplet arrangement of base pairings in mRNA. Three stages are involved in the translation procedure: beginning, progression, and conclusion.

Once the amino acid attaches itself to tRNA with ATP, tRNA gets electrically charged around the start of translation. Because the positively charged tRNA can detect the start (initiation) codon (AUG) found on mRNA. The ribosome is a protein that has two distinct locations in a large component for the binding of successive amino acids, which also serves as a real venue for the translation mechanism. The start codon (AUG) is where the small and large ribosome subunits bind with mRNA, respectively.

After that, it starts the translation operation. To make room for the attachment of a different charged tRNA, the ribosome transfers one codon downstream alongside the mRNA throughout the lengthening phase. A polypeptide chain is a structure that is created when the amino acid carried by tRNA forms a peptide bond that links the preceding amino acid. This procedure is repeated. The procedure for translation ends once the protein ribosome hits several STOP codons (UAA, UAG, and UGA). These ribosomes separate themselves from the mRNA & the polypeptide chain that follows becomes detached.

(d)

Ans: Applying mathematical and statistical techniques towards the study of molecular biology is known as bioinformatics. It resolves the real-world issues that come up when biological data is managed & analyzed. Following the conclusion of the Human Genome Project (HGP), the discipline of bioinformatics emerged.

The reason is due to the massive volume of data created throughout the HGP procedure, which needs to be organized and preserved for later utilization by different scientists, enabling convenient access and analysis.

Therefore, building biological information systems to house the large amount of biological data is a component of bioinformatics. It creates particular gadgets for quick and simple accessibility and the consequent use of data. To determine the connections among the data, forecast the composition and functions of proteins, and group gene sequences into families that are related, bioinformatics is developing innovative mathematical methods & techniques.