NCERT Solutions for Class 12 Biology
Chapter 6 Molecular Basis of Inheritance

Question 1.

Group the following as nitrogenous bases and nucleosides:
Adenine, cytidine, thymine, guanosine, uracil, and cytosine.

Solution:

Adenine, Guanosine, Thymine, Uracil, and Cytosine are nitrogenous bases. (Adenine and Guanosine → Purine, Thymine, Uracil and Cytosine → Pyrimidine) Cytidine is a nucleoside.

Question 2.

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

Solution:

According to Chargaff's rule, in a double-stranded DNA, the total number of cytosine molecules will be equal to the number of guanine molecules and the number of adenine molecules will be equal to the number of thymine molecules. Therefore, if a double-stranded DNA has 20 percent of cytosine then the guanine will also be 20 per cent. The remaining 60% will consist of adenine and thymine in equal amount. Thus adenine will be 30%.

Question 3.

If the sequence of one strand of DNA is written as follows:
5'-ATGCATGCATGCATGCATGCA
TGCATGC-3'
Write down the sequence of complementary strand in 5' -> 3' direction.

Solution:

5'-GCATGCATGCATGCATGCAT G C ATG CAT-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.

Solution:

If the sequence of coding strand is :
5' – ATGCATGCATGCATGCATGCATGCATGC – 3'
Then template strand is :
3' – TACGTACGTACGTACGTACGTACGTACG – 5'
The mRNA will be formed on the template strand in 5' —> 3' direction. Thus mRNA

sequence will be:
5'-AUGCAUGCAUGCAUGCAUGCAUGC-3'
Thymine in DNA is substituted by uracil in RNA.

Question 5.
Which property of DNA double helix led Watson and Crick to hypothesise a semi-conservative mode of DNA replication? Explain.
Solution:
The two strands of DNA show complementary base pairing. This property of DNA led Watson and Crick to suggest a semi-conservative mechanism of DNA replication in which one strand of a parent is conserved while the other complementary strand formed is new.

Question 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
Solution:
DNA dependent DNA polymerases and DNA dependent RNA polymerases.

Question 7.
How did Hershey and Chase differentiate between DNA and protein in their experiment while proving that DNA is the genetic material?
Solution:
They raised 2 types of bacteriophages

- On radioactive phosphorous (^{32}P)
- On radioactive sulphur (^{35}S).

^{35}S gets into protein and ^{32}P into DNA When both bacteriophages infected bacteria differently and by shaking them, the viral protein coat was separated

After raising these bacteria it was found that those infected with ^{32}P bacteriophage → radioactivity were found. But with ^{35}S → no radioactivity was found.

Question 8.
Differentiate between the following:

1. **Repetitive DNA and Satellite DNA**
2. **Template strand and Coding strand**
3. **mRNA and tRNA**

Solution:

1. Differences between repetitive DNA and satellite DNA are as follows:

	Repetitive DNA	Satellite DNA
(i)	It is that part of DNA which contains same sequences of bases repeated several times. In this repetitive DNA, the repeated sequences may be tandemly repetitive or interspersed repetitively.	It is that part of repetitive DNA that consists of repeated sequences in tandem, *i.e.*, it is tandemly repetitive DNA.
(ii)	The repeating units may be 'few base pairs long or hundred to thousands of base pairs long.	It has short sequence repeats (upto 60 bp long).
(iii)	It exists as light bands during CsCl density gradient analysis.	In CsCl density gradient analysis, it appears as small dark bands.
(iv)	Repetitive DNAs are separated from the bulk genome DNA as different peaks during density gradient centrifugation.	It gets separated from repetitive DNA as satellite. Satellite DNA are separated as small peaks.

2. Differences between template strand and coding strand are as follows:

	Template strand	Coding strand
(i)	It is also called antisense or (–) strand or master strand.	It is also called sense or (+) or non-template strand.
(ii)	It has 3′ → 5′ polarity.	It has 5′ → 3′ polarity.
(iii)	It is that strand upon which RNA is transcribed in 5′ → 3′ direction.	It has same sequence of bases found in *m*RNA except T at the place of U. It does not code for any information.

Example: 3′ ATGCATGCATGCATGC 5′
- Template strand of DNA
- Coding strand of DNA

5′ T A C G T A C G T A C G T A C G 3′
| | | | | | | | | | | | | | | | |
5′ U A C G U A C G U A C G U A C G 3′

5′UACGUACGUACGUACG3′-*m*RNA transcribed on template strand. It is complementary to the template strand and similar to the coding strand except that T is replaced by U.

3. Differences between mRNA and tRNA are as follows:

	*m*RNA	*t*RNA
(i)	It accounts for about 5% of total RNA in the cell.	It accounts for about 15% of total RNA in the cell.

(ii)	It consists of 75-6000 bases.	It consists of 73-93 bases.
(iii)	Its mol. wt. ranges from 25000-2000000 daltons.	Its mol. wt. is about 25000 daltons.
(iv)	Its sedimentation coefficient is 6-30S.	Its sedimentation coefficient is 4S.
(v)	It is longest RNA with maximum molecular weight but is least abundant.	It is smallest RNA and is coiled like a clover leaf.
(vi)	It carries the codes which form proteins.	It carries code complementary to the RNA code.
(vii)	It is synthesised by RNA polymerase II in nucleus.	It is synthesised by RNA polymerase III in nucleus.
(viii)	It has no modification of bases in coding region.	About 5% bases are modified.

(ix)	It is of various types depending upon number of genes.	It is of about 100 types.
(x)	It is short lived (3 seconds to few days) and generally degrades after protein synthesis.	It is quite stable, is used again and again, and degrades very slowly.
(xi)	It is called template/ nuclear/ messenger or informational RNA as it carries genetic information provided by DNA.	It is called soluble or adapter RNA and carries amino acids to *m*RNA during protein synthesis.

Question 9.

List two essential roles of ribosome during translation

Solution:

Two essential roles of the ribosome during translation are:

1. One of the RNA acts as a peptidyl transferase ribozyme for the formation of peptide bonds.
2. The ribosome provides sites for attachment of mRNA and charged tRNA for polypeptide synthesis.

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?

Solution:

The lac operon is regulated by the amount of lactose in the medium where the bacteria are grown. When the amount of lactose is exhausted in the medium, the lac operon shuts down.

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

1. **Promoter**
2. **tRNA**
3. **Exons**

Solution:

1. Promoter: It is located at the 5' end of the transcription unit and provides site for attachment of transcription factors (TATA Box) and RNA polymerase.
2. tRNA: It takes part in the transfer of activated amino acids from cellular pool to ribosome so that they can take part in protein formation.
3. Exons: In eukaryotes, DNA is mosaic of exons and introns. Exons are coding sequences of DNA which are both transcribed and translated.

Question 12.
Why is the Human Genome Project called a mega project?
Solution:
The human genome was a megaproject that aimed to sequence every base in the human genome. The estimated cost of the project would be a billion (1 billion = 100 crores) US dollars.

Question 13.
What is DNA fingerprinting? Mention its application.
Solution:
DNA fingerprinting is the identification of differences in specific regions of DNA sequences based on DNA polymorphism, repetitive DNA, and satellite DNA.
Application of DNA fingerprinting: Settling, paternity disputes and identity of criminal by different DNA profiles in forensic laboratories.

Question 14.
Briefly describe the following:

1. **Transcription**
2. **Polymorphism**
3. **Translation**
4. **Bioinformatics**

Solution:
1. Transcription – It is the process of copying genetic information from the anti-sense or template strand of the DNA into RNA. It is meant for taking the coded information from DNA in nucleus to the site where it is required for protein synthesis. Principle of complementarity is used even in transcription. The exception is that uracil is incorporated instead of thymine opposite adenine of template. The segment

of DNA that takes part in transcription is called transcription unit. It has three components

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- a promoter,
- the structural gene and
- a terminator.

2. Polymorphism – It is the variation at genetic level, arisen due to mutations. Such variations are unique at particular site of
DNA. They occur approximately once in every 500 nucleotides or about 107 times per genome. These are due to deletions, insertions, and single-base substitutions. These alterations in healthy people, occur in non-coding regions of DNA and do not code for any protein but are heritable. The polymorphism in DNA sequences is the basis of genetic mapping of human genome as well as DNA fingerprinting.

3. Translation – It is the mechanism by which the triplet base sequence of mRNA guides the linking of a specific sequence of amino acids to form a polypeptide chain (protein) on ribosomes in the cell cytoplasm. All the protein that a cell needs are synthesised by the cell within itself.
The raw materials required in protein synthesis are ribosomes, amino acids, mRNA, tRNAs and amino acyl tRNA synthetase. Mechanism of protein synthesis involves following steps:

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- Activation of amino acids
- Charging or aminoacylation of tRNA
- Initiation
- Elongation (Polypeptide chain formation)
- Termination

The ribosomes move along the mRNA 'reading' each codon in turn. Molecules of transfer RNA (tRNA), each bearing a particular amino acid, are brought to their correct positions along the mRNA, molecule base pairing occurs between the bases of the codons and the complementary base triplets of tRNA. In this way, amino acids are assembled in the correct sequence to form the polypeptide chain.

5. Bioinformatics – Bioinformatics is the combination of biology, information technology and computer science. Basically, bioinformatics is a recently developed science which uses information technology to understand biological phenomenon. It broadly involves the computational tools and methods used to manage, analyse and manipulate volumes of biological data.