CHAPTER

6 MOLECULAR BASIS OF INHERITANCE

Syllabus

➢ *Molecular Basis of Inheritance : Search for genetic material and DNA as genetic material; Structure of DNA and RNA; DNA packaging; DNA replication; Central dogma; transcription, genetic code, translation; gene expression and regulation—lac operon; genome and human and genome projects; DNA fingerprinting.*

Chapter Analysis

List of Topics		2016		2017		2018
		D	OD	D	OD	D/OD
The DNA-Search for genetic material	• Position of DNA in prokaryotic cell • Structure of nucleosome • Central Dogma • Biochemical characterization of Transforming Principal	1 Q (5 M)		1 Q (2 M)		1 Q (2 M) 1 Q (5 M)
Replication	• Semi-conservative mode of replication • Dual purpose of dNTPs • Mechanism of DNA replication	1Q (3 M)	1 Q (5 M)			1 Q (1 M)
Genetic Code	• Properties of Genetic code		1 Q (2 M)		1 Q (2 M)	
Transcription/ Translation/ Regulation of Gene Expression	• Process of transcription in bacteria • Splicing of hnRNA Structure and function of tRNA • Lac operon		1 Q (5 M)		1 Q (5 M)	
DNA Fingerprinting				1Q (3 M)		1Q (3 M)
Human Genome Project			1Q (3 M)		1Q (3 M)	

- *On the basis of above analysis, it can be concluded that this is also an important chapter from exam point of view. A long five mark question is always asked from topics like central dogma, Search for genetic material, Lac operon, process of splicing, mechanism of DNA replication, Process of transcription in bacteria. Other important topics are structure of DNA, packaging of DNA (nucleosome), DNA fingerprinting, Genetic code, function of mRNA, tRNA, rRNA, semi-conservative mode of replication and Human genome project. Overall, we can conclude that it is an important chapter.*

TOPIC-1
Nucleic Acid – DNA and RNA

Revision Notes

➢ **Nucleic Acids**
- DNA and RNA are the two types of nucleic acids.
- DNA is the genetic material in all the organisms except some viruses.
- RNA is the genetic material in some viruses.
- RNA mostly functions as messengers.

➢ **Structure of Polynucleotide Chain**
- Polynucleotides are the polymers of nucleotides.
- DNA and RNA are examples of polynucleotides.
- **A nucleotide has 3 components :**
  1. A nitrogenous base
  2. A pentose sugar (ribose in RNA and deoxyribose in DNA)
  3. A phosphate group
- Nitrogen bases are of 2 types :
  (a) Purines : It includes Adenine (A) and Guanine (G).
  (b) Pyrimidines : It includes Cytosine (C), Thymine (T) and Uracil (U). Thymine (5-methyl Uracil) present only in DNA) and Uracil only in RNA.
- A nitrogenous base is linked to the pentose sugar through a N-glycosidic linkage to form nucleoside.

Nucleosides in RNA	Nucleosides in DNA
Adenosine	*Deoxyadenosine*
Guanosine	*Deoxyguanosine*
Cytidine	*Deoxycytidine*
Uridine	*Deoxythymidine*

- Nitrogen base + sugar + phosphate group = Nucleotide (deoxyribonucleotide). In RNA, every nucleotide residue has an additional –OH group present at 2′-position in the ribose.
- 2 nucleotides are linked through **3′ – 5′ phosphodiester** bond to form dinucleotide.
- When series of nucleotides are linked together, it forms polynucleotide.

➢ **Structure of DNA**
- **Johann Friedrich Miescher (1869) :** Identified DNA and named it as 'Nuclein'.
- **James Watson & Francis Crick** proposed double helix model of DNA. It was based on the X-ray diffraction data produced by **Maurice Wilkins & Rosalind Franklin**.
- DNA is made of two polynucleotide chains coiled in a right handed fashion. Its backbone is formed of sugar and phosphates. The bases project inside.
- The two chains have anti-parallel polarity *i.e.* one chain has the polarity 5′ → 3′ and the other has 3′ → 5′.
- Nitrogen bases of opposite chains are held together by hydrogen bonds forming base pairs (bp).
- There are two hydrogen bonds between A and T (A = T) and three H-bonds between C and G (C ≡ G).
- Purine comes opposite to a pyrimidine. This generates uniform distance between the two strands.

➢ **Erwin Chargaff's Rule**
- Purines and pyrimidines are always in equal amounts *i.e.* A + G = T + C.
- In DNA, the proportion of A is equal to T and the proportion of G is equal to C *i.e.* A = T and G = C.
- The base ratio A + T/G + C may vary from species to species but constant for a given species.
- Length of DNA = number of base pairs × distance between two adjacent base pairs.
- Φ 174 (a bacteriophage) has 5386 nucleotides.
- Bacteriophage lambda has 48502 base pairs (bp).
- *E. coli* has 4.6×10^6 bp.
- Haploid content of human DNA = 3.3×10^9 bp.
- Number of base pairs in human = 6.6×10^9
- Length of DNA in humans = $6.6 \times 10^9 \times 0.34 \times 10^{-9} = 2.2$ m

- Length of DNA in *E. coli* =1.36 mm (1.36×10^{-3} m).
  $\therefore$ The number of base pairs = $1.36 \times 10^{-3}/0.34 \times 10^{-9} = 4 \times 10^{6}$ bp.

➢ **Packaging of DNA Helix**

- In prokaryotes (*e.g. E. coli*), the DNA molecule is held with some positively charged non-histone basic proteins like negatively charged polyamines and form 'nucleoid'.
- In eukaryotes, there is a set of positively charged basic proteins called histones.
- Histones proteins are rich in positively charged basic amino acid residues lysine and arginine.
- There are five types of histones proteins-H1, H2A, H2B, H3 and H4.
- Two molecules each of H2A, H2B, H3 and H4 organize to form a unit of eight molecules called as histone octamer.
- Negatively charged DNA is wrapped around positively charged histone octamer to form a structure called nucleosome.
- Nucleosomes are connected with one another with the help of linker DNA on which H1 Histone is present.

➢ **Nucleosome**

- A typical nucleosome contains 200 bp of DNA helix.
- Therefore, the total number of nucleosomes in human = 6.6×10^{9} bp/200 = 3.3×10^{7}.
- Nucleosomes constitute the repeated unit to form chromatin.
- Chromatin is the thread-like stained bodies.
- Nucleosomes in chromatin appears as "beads-on-string" when it is viewed under electron microscope..
- Chromatin is packaged to form a solenoid structure.
- Further supercoiling constitute looped structure called chromatin fibre.
  These chromatin fibers further coil and condense at metaphase stage of cell division to form chromosomes.
- Chromatin is packaged → solenoid → chromatin fibres → coiled and condensed at metaphase stage → chromosomes.
- Higher level packaging of chromatin requires non-histone chromosomal (NHC) proteins.
- Two types of chromatin are :
  (a) Euchromatin : Loosely packed and transcriptionally active chromatin and stains light.
  (b) Heterochromatin : Densely packed and inactive region of chromatin and stains dark.

➢ **The Search for Genetic Material**

Griffith's Experiment - Transforming Principle

- **Griffith** (1928) used mice and a bacterial strain, *Streptococcus pneumoniae*.
- *Streptococcus pneumoniae* has two strains :
  (a) Smooth (S) strain (Virulent) : Has polysaccharide mucous coat. Causes pneumonia.
  (b) Rough (R) strain (Non-virulent) : No mucous coat. Does not cause pneumonia.

➢ **Experiment**

- S-strain → Inject into mice → Mice die
- R-strain → Inject into mice → Mice live
- S-strain (Hk) → Inject into mice → Mice live
- S-strain (Hk) + R-strain (live) → Inject into mice → Mice die
- He concluded that there exists some 'transforming principle', that is transferred from heat-killed S-strain to R-strain. It enabled R-strain to synthesize smooth polysaccharide coat and become virulent. This must be due to the transfer of genetic material.

➢ **Biochemical Characterization of Transforming Principle**

- Oswald Avery, Colin MacLeod & Maclyn McCarty in 1944 worked to determine the biochemical nature of 'transforming principle' in Griffith's experiment.
- They purified biochemicals (proteins, DNA, RNA, etc.) from heat killed S cells using suitable enzymes.
- They discovered that —
  (a) Digestion of protein and RNA (using Proteases and RNases) did not affect transformation. So the transforming substance was not a protein or RNA.
  (b) Digestion of DNA with DNase inhibited transformation. It means that DNA caused transformation of R cells to S cells i.e. DNA was the transforming substance.

➢ **The Genetic Material is DNA**

- The fact that DNA is the genetic material also came from the experiments of **Alfred Hershey** and **Martha Chase (1952)**.
- They worked with viruses that infect bacteria and are called bacteriophages.

➢ **Hershey-Chase Experiment—Blender Experiment**
- Hershey and Chase made two preparations of bacteriophage - In one, proteins were labelled with ^{35}S by putting in medium containing radioactive sulphur (^{35}S). In the second, DNA was labelled with ^{32}P by putting in a medium containing radioactive Phosphorous (^{32}P).
- These preparations were used separately to infect *E. coli*.
- After infection, the *E. coli* cells were gently agitated in a blender to separate the phage particles from the bacteria.
- Then the culture was centrifuged. Heavier bacterial cells were formed as a pellet at the bottom. Lighter viral components outside the bacterial cells remained in the supernatant.
- They found that,
  (a) Supernatant contains viral protein labelled with ^{35}S, *i.e.* the viral protein had not entered the bacterial cells.
  (b) The bacterial pellet contains radioactive ^{32}P. This shows that viral DNA labelled with ^{32}P had entered the bacterial cells. This proves that DNA is the genetic material.

➢ **Properties of Genetic Material**
- A molecule that can act as a genetic material must fulfill the following criteria :
  (a) Be able to generate its replica by the process of Replication.
  (b) Chemically and structurally be stable.
  (c) Allows slow changes, the mutations that are required for evolution.
  (d) It should be able to store genetic information which can be inherited.
  (e) Be able to express itself as 'Mendelian Characters'.

➢ **DNA is a Better Genetic Material than RNA due to following reasons :**
- DNA is chemically less reactive and structurally more stable. It has the capacity to undergo repair.
- Due to unstable nature of RNA, RNA viruses (*e.g. Q.β bacteriophage, Tobacco Mosaic Virus, etc.*) mutate and evolve faster.
- For the storage of genetic information DNA is better due to its stability. But for the transmission of genetic information, RNA is better.
- RNA can directly code for the protein synthesis, hence can easily express the characters. DNA is dependent on RNA for protein synthesis.

Reasons for stability (less reactivity) of DNA	Reasons for mutability (high reactivity) of RNA
Double stranded	*Single stranded*
Presence of thymine	*Presence of Uracil*
Absence of 2′-OH	*Presence of 2′-OH*

- The two DNA strands are complementary. On heating, they separate. When appropriate conditions are provided they come together. (In Griffith's experiment, when the bacteria were heat killed, some properties of DNA did not destroy).

➢ **RNA World**
- RNA is a single stranded structure but it is often folded back upon itself forming helices. Nitrogenous bases are like those of DNA except that there is uracil in place of thymine.
- RNA was the first regulatory chemical and genetic material in early life forms.
- It acts as genetic material and bio catalyst.
- Essential life processes (metabolism, translation, splicing etc) evolved around RNA.
- DNA has evolved from RNA with chemical modifications that made it more stable.

➢ **Central Dogma of Molecular Biology**
- It was proposed by Francis Crick (1958). It states that the genetic information flows unidirectionally from DNA → RNA → Protein.

➢ **Teminism :** H. Temin and Baltimore in 1978 gave the concept of reverse flow of genetic information *i.e.* the formation of DNA from RNA. This is called as Reverse Central Dogma or Teminism or reverse transcription. This takes place in some of the viruses in the presence of an enzyme called reverse transcriptase.

➢ **Types of RNA**
- RNA is of 3 types –mRNA, tRNA and rRNA.
- mRNA constitutes 2–5% of the total cellular RNA, tRNA is about 15% and rRNA is about 70–80%.
- **mRNA (messenger RNA) :** Provides template for translation (protein synthesis) and is transcribed from DNA.
- **rRNA (ribosomal RNA) :** Structural and catalytic role during translation. *e.g.* ^{23}S rRNA in bacteria acts as ribozyme.
  It is the component of ribosome and is the most stable type of RNA.

- **tRNA (transfer RNA or sRNA or soluble RNA or adaptor RNA) :** Brings amino acids for protein synthesis and reads the genetic code.
- tRNA are smallest amongst all the RNA and is made up of 70–80 nucleotides only.

➢ **DNA Replication**
- Replication is the copying of DNA from parental DNA.
- **Watson** & **Crick** proposed Semi-conservative mode of replication.
- It suggests that the parental DNA strands act as template for the synthesis of new complementary strands. After the completion of replication, each DNA molecule would have one parental and one new strand.

➢ **Experimental Proof**
- **Mathew Meselson** & **Franklin Stahl (1958)** experimentally proved Semi-conservative mode.
- **Meselson & Stahl's Experiment :**
- They cultured *E. coli* in a medium containing $N^{15}H_4Cl$ (N^{15} : heavy isotope of N). N^{15} was incorporated into both strands of bacterial DNA and the DNA became heavier.
- Another preparation containing N salts labelled with N^{14} was also made. N^{14} was also incorporated in both strands of DNA and became lighter.
- These two types of DNA can be separated by centrifugation in a CsCl density gradient.
- They took *E. coli* cells from N^{15} medium and transferred to N^{14} medium.
- After one generation (*i.e.* after 20 minutes), they isolated and centrifuged the DNA. Its density was intermediate (hybrid) between ^{15}N DNA and ^{14}N DNA. This showed that in the newly formed DNA, one strand is old (N^{15} type) and one strand is new (N^{14} type). This confirms semi-conservative mode of replication.
- After II generations (*i.e.* after 40 minutes), there was an equal amounts of hybrid DNA and light DNA.
- **Taylor et. al (1958)** performed similar experiments on *Vicia faba* (faba beans) using radioactive thymidine to detect distribution of newly synthesized DNA in the chromosomes. It proved that the DNA in chromosomes also replicate semi-conservatively.

➢ **The Machinery and Enzymes for Replication**
- DNA replication starts at a point called *origin* (*ori*).
- A unit of replication with one origin is called a *replicon*.
- During replication, the two strands unwind and separate by breaking H-bonds in the presence of an enzyme, *Helicase*.
- Unwinding of the DNA molecule at a point forms a 'Y'-shaped structure called replication fork.
- The separated strands act as templates for the synthesis of new strands.
- DNA replicates in the 5′→3′ direction.
- *Deoxyribonucleoside triphosphates* (dATP, dGTP, dCTP & dTTP) act as substrate and also provide energy for polymerization.
- Firstly, a small RNA primer is synthesized in presence of an enzyme, *primase*.
- In the presence of an enzyme, DNA dependent *DNA polymerase*, many nucleotides join with one another to primer strand and form a polynucleotide chain (new strand).
- The DNA polymerase forms one new strand (leading strand) on a continuous stretch in the 3′→5′ direction (Continuous synthesis).
- The other new strand is formed in small stretches (Okazaki fragments) in 5′→3′ direction (Discontinuous synthesis).
- The Okazaki fragments are then joined together to form a new strand by an enzyme, *DNA ligase*. This new strand is called lagging strand.
- If a wrong base is introduced in the new strand, DNA polymerase can do proof reading.
- *E. coli* completes replication within 38 minutes *i.e.* 2000 bp per second.
- In eukaryotes, the replication of DNA takes place at S-phase of the cell cycle. Failure in cell division after DNA replication results in polyploidy.

➢ **Transcription**
- It is the process of copying genetic information from one strand of the DNA into RNA.
- Here, adenine pairs with uracil instead of thymine.
- Both strands are not copied during transcription, because
  - **(a)** The code for protein is different in both strands. This complicates the translation.
  - **(b)** If two RNA molecules are produced simultaneously they would be complimentary to each other, hence form a double stranded RNA. This prevents translation.

➢ **Transcription Unit**
- It is the segment of DNA between the sites of initiation and termination of transcription.
- It consists of 3 regions :
  - **(a) A promoter (Transcription start site) :** Binding site for RNA polymerase.

(b) Structural gene : The region between promoter and terminator where transcription takes place.

(c) A terminator : The site where transcription stops.

- The DNA- dependent RNA polymerase catalyzes the polymerization only in 5′→3′direction.
- 3′→5′ acts as template strand. 5′→3′ acts as coding strand.
- 3′–ATGCATGCATGCATGCATGCATGC–5′ template strand.
  5′–TACGTACGTACGTACGTACGTACG–3′ coding strand.

➢ **Transcription Unit and the Gene**

- **Gene :** Functional unit of inheritance. It is the DNA sequence coding for RNA molecule.
- **Cistron :** A segment of DNA coding for a polypeptide.
- Structural gene in a transcription unit is of two types :

(a) Monocistronic structural genes (split genes) : It is seen in eukaryotes. Here, the coding sequences (expressed sequences or exons) are interrupted by introns (intervening sequences).

(b) Polycistronic structural genes : It is seen in prokaryotes. Here, there are no split genes.

- **Exons and Introns :** In eukaryotes, the monocistronic structural genes have interrupted coding sequences *i.e.* the genes in eukaryotes are split. The coding sequences or expressed sequences are called as **exons**. Exons are said to be those sequences that appear in mature or processed RNA. The exons are interrupted by **introns**. Introns or intervening sequences do not appear in mature or processed RNA.

➢ **Steps of transcription in prokaryotes**

- **Initiation :** Here, the enzyme *RNA polymerase* binds at the promoter site of DNA. This causes the local unwinding of the DNA double helix. An initiation factor (σ factor) present in RNA polymerase initiates the RNA synthesis.
- **Elongation :** The RNA chain is synthesized in the 5′-3′ direction. In this process, activated ribonucleoside triphosphates (ATP, GTP, UTP & CTP) are added. This is complementary to the base sequence in the DNA template.
- **Termination :** A *termination factor* (ρ *factor*) binds to the RNA polymerase and terminates the transcription.
- In bacteria (Prokaryotes), transcription and translation can be coupled (Translation can begin before mRNA is fully transcribed) because mRNA requires no processing to become active.
- Transcription and translation take place in the same compartment (no separation of cytosol and nucleus).

➢ **In eukaryotes, there are 2 additional complexities :**

(a) There are three RNA polymerases :

- **RNA polymerase I :** Transcribes rRNAs (28S, 18S & 5.8S).
- **RNA polymerase II :** Transcribes the heterogeneous nuclear RNA (hnRNA). It is the precursor of mRNA.
- **RNA polymerase III :** Transcribes tRNA, 5S rRNA and snRNAs (small nuclear RNAs).

(b) The primary transcripts (hnRNA) : They contain both the exons and introns and are non-functional. Hence introns have to be removed. For this, it undergoes the following processes :

- **Splicing :** From hnRNA, introns are removed (by the spliceosome) and exons are spliced (joined) together.
- **Capping :** Here, a nucleotide methyl guanosine triphosphate (cap) is added to the 5′ end of hnRNA.
- **Tailing (Polyadenylation) :** Here, adenylate residues (200-300) are added at 3′-end. It is the fully processed hnRNA, now called mRNA.

IMPORTANT DIAGRAMS:

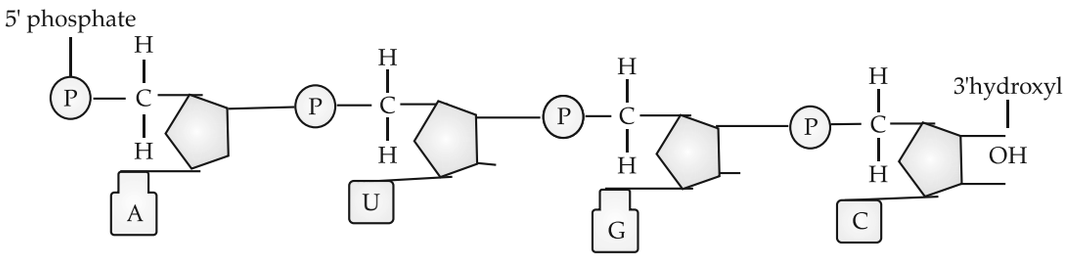


Fig 6.1: A polynucleotide Chain of RNA

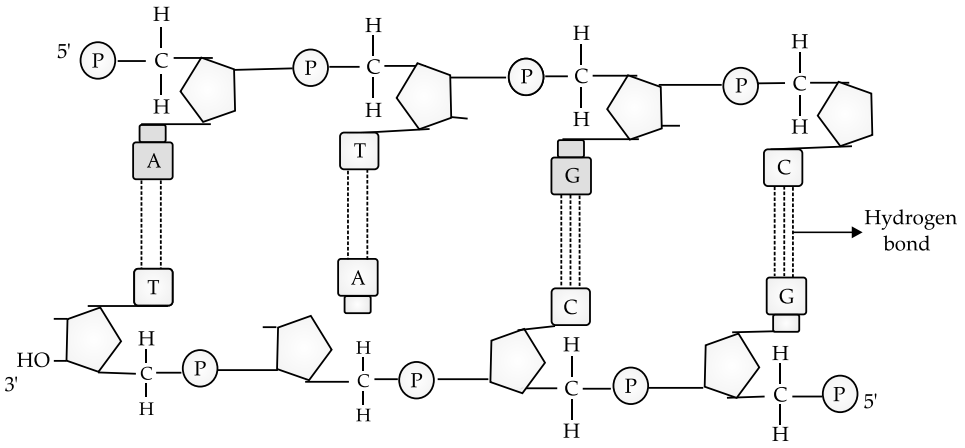


Fig 6.2: Double Stranded polynucleotide chain

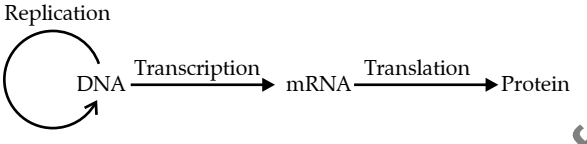


Fig 6.3: Central Dogma

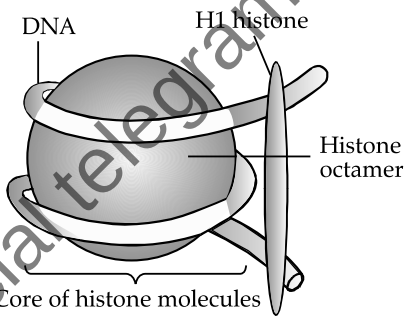


Fig 6.4: Nucleosome

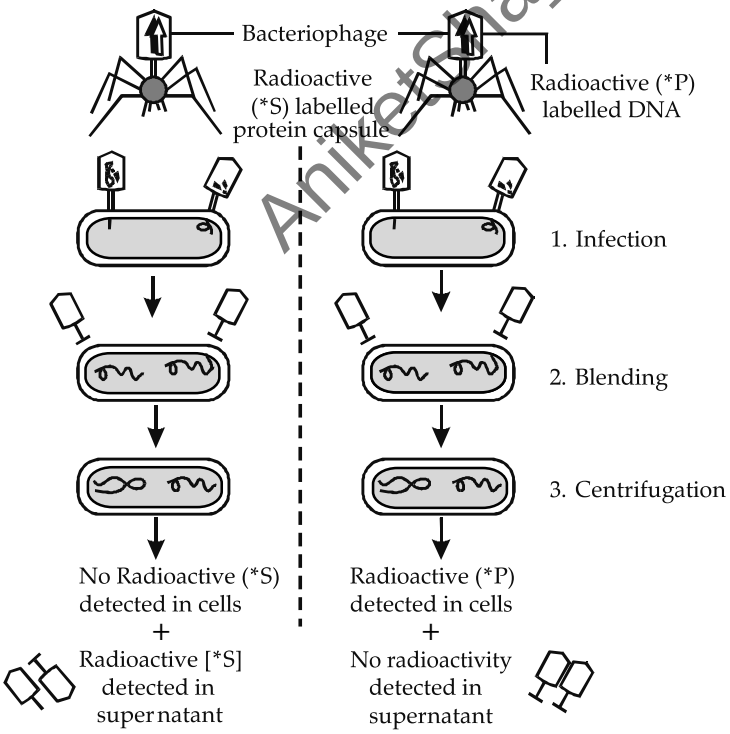


Fig 6.5: The Hershey and Chase Experiment

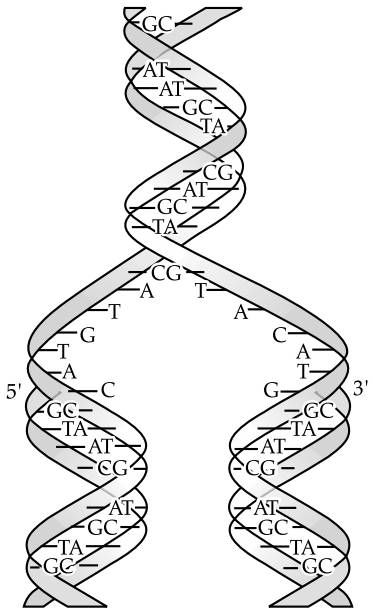


Fig 6.6: Watson Crick model of Semi-conservative DNA replication

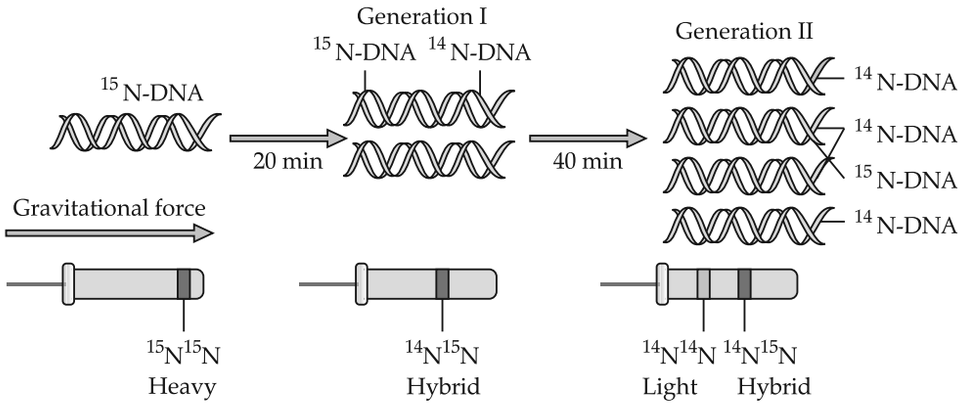


Fig 6.7: Meselson and Stahl's Experiment

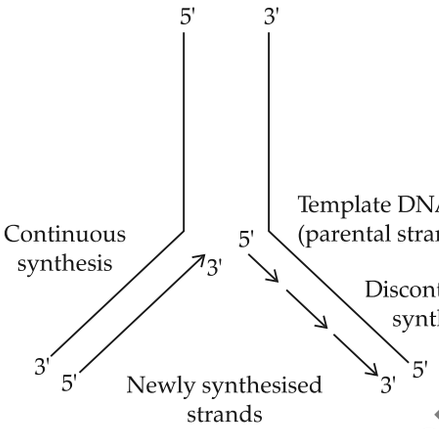


Fig 6.8: Replicating Fork

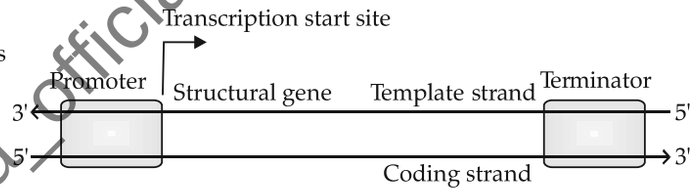


Fig 6.9: Schematic structure of a transcription unit

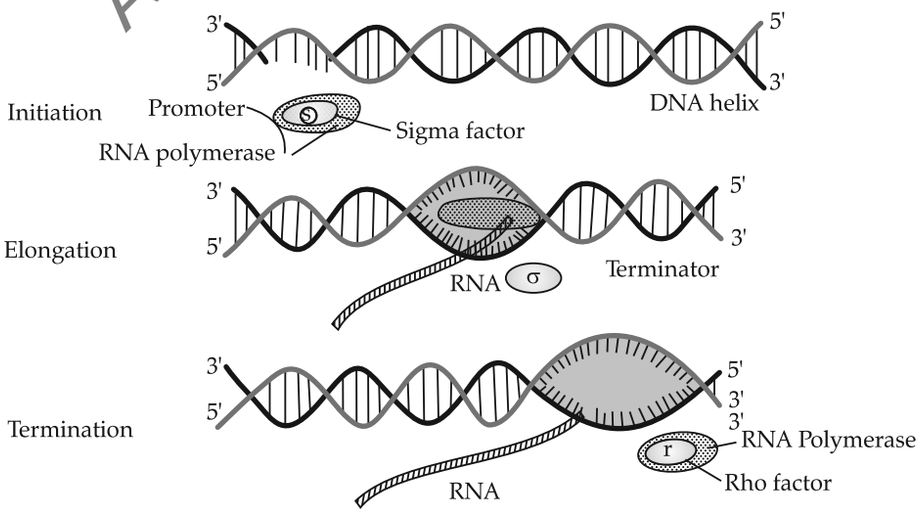


Fig 6.10: Process of Transcription in Bacteria

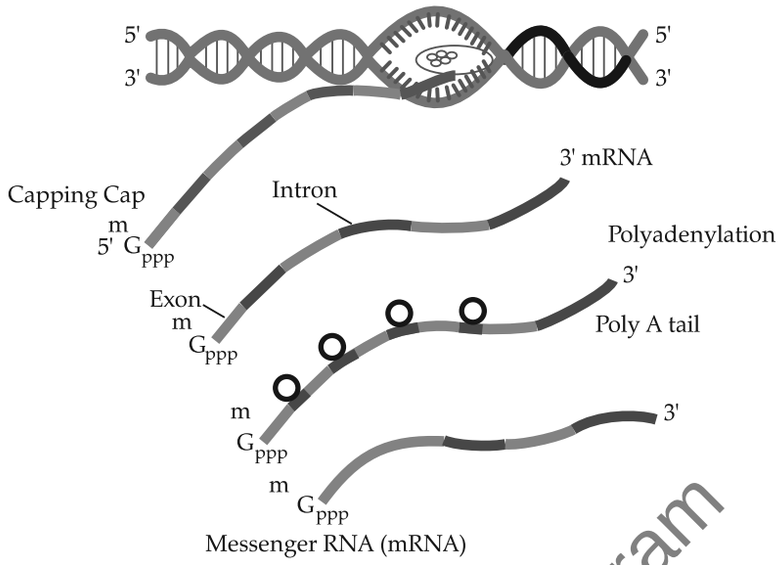


Fig 6.11: Process of Transcription in Eukaryotes

Very Short Answer Type Questions (1 mark each)

Q. 1.Give an example of a codon having dual function.
R **[Delhi Set-III, 2016]**

Ans. AUG. **[CBSE Marking Scheme, 2016] 1**

Commonly Made Error
- Some students write AUG in small letter and loose marks.

Q. 2. Write the dual purpose served by Deoxyribonucleoside triphosphates in polymerization.
R **[CBSE , Outside Delhi/Delhi, 2018]**

Ans. Acts as a substrate, provide energy (from the terminal two phosphates). ½ + ½
[CBSE Marking Scheme, 2018]

Q.3. Name one amino acid, which is coded by only one codon. R **CBSE, Comptt, Set-1, 2018**

Ans. Methionine / Tryptophan **1**
[CBSE Marking Scheme, 2018]

AI **Q. 4. Mention one difference to distinguish an exon from an intron.** U **[Foreign Set-I, 2016]**

Ans. **Exon :** Coded/expressed sequence of nucleotides in mRNA.
Intron : Intervening sequence of nucleotides not appearing in processed mRNA. **1**
[CBSE Marking Scheme, 2016]

Detailed Answer :

The exons are the coding segments or sequences of mRNA while the intron are the non-coding segments or intervening nucleotide sequences of mRNA which are removed during splicing through processing of mRNA.

Commonly Made Error
- Students get confused between technical terms like exon and intron. They often write opposite definitions and loose marks.

Q. 5. Retroviruses have no DNA. However the DNA of the infected host cell does possess viral DNA. How is it possible ?
A **[Outside Delhi Set-I, 2015]**

Ans. RNA is the genetic material in retrovirus. This RNA forms DNA by the process of reverse transcription with the help of the enzyme called reverse-transcriptase. **1**

Q. 6. Name the enzyme that transcribes hn-RNA in eukaryotes.
R **[Delhi Set-I, Comptt. 2015]**

Ans. RNA Polymerase II.
[CBSE Marking Scheme, 2015] 1

AI **Q. 7. Why is RNA more reactive in comparison to DNA?** U **[Delhi Set-I, Comptt. 2015]**

Ans. 2' – OH Present in RNA (in every nucleotide) make it reactive.
[CBSE Marking Scheme, 2015] 1

Detailed Answer :

RNA is more reactive than DNA because :

(i) It is single stranded.

(ii) 2' – OH group is present in every nucleotide.

(iii) It mutates faster. **(Any two)**

Q. 8. Name the negatively charged and positively charged components of a nucleosome.
R **[Delhi Set-I, Comptt. 2015]**

Ans. Negatively charged component is DNA, positively charged component is histone octamer. ½+½
[CBSE Marking Scheme, 2015]

Q. 9. Write the two specific codons that a translational unit of m-RNA is flanked by one on either sides.
R **[Outside Delhi Set-I, Comptt. 2015]**

Ans. Start codon - AUG
Stop codon - UAA/UGA/UAG ½+½
[CBSE Marking Scheme, 2015]

Answering Tip
- Students are advised to learn the initiation and termination codons. To make it interesting, they can learn it by mnemonics. For e.g. UAA- You Are Away, UAG- You Are Gone, UGA- You Go Away.

Q. 10. Name the transcriptionally active region of chromatin in a nucleus.
R **[Delhi Set-I, 2015]**

Ans. Euchromatin *i.e.* lightly stained transcriptionally active region. **[CBSE Marking Scheme, 2015] 1**

Commonly Made Error
- Students instead of euchromatin, they write heterochromatin. It seems they get confused between the terms.

Answering Tip
- Learn the differences between these two in tabular form for easy understanding and retention.

Q. 11. What is a cistron ? R **[Delhi Set-I, 2015]**

Ans. Cistron is a segment of gene which codes for a certain polypeptide or protein.
[CBSE Marking Scheme, 2015] 1

Answering Tip
- Practice writing all definitions emphasizing on operative terms.

Q. 12. Why is it not possible for an alien DNA to become a part of a chromosome anywhere along its length and replicate normally ?
U **[Outside, Delhi Set-I, 2014]**

Ans. This DNA must be linked to ori/origin of replication site to start replication.
[CBSE Marking Scheme, 2014] 1

Detailed Answer :
Alien DNA after becoming the part of chromosome anywhere will not be able to replicate normally because it requires a specific sequence of bases which constitute the ori (origin of replication), for starting replication within the host cell.

Q. 13. How is repetitive/satellite DNA separated from bulk genomic DNA for various genetic experiments ? A **[Delhi Set-III, 2014]**

Ans. Density gradient centrifugation. **1**
[CBSE Marking Scheme, 2014]

Q. 14. Name the specific components and the linkage between them that form deoxyadenosine.
R **[Delhi Set-I, Comptt. 2013]**

Ans. **Components :** Nitrogen base Adenine (a purine) + Deoxyribose sugar.
Linkage : N-Glycosidic linkage [C – N – C].
½ + ½

Q. 15. Which one out of Rho factor and Sigma factor acts as the initiation factor during transcription in a prokaryote ? R **[Delhi Set-I, Comptt. 2013]**

Ans. Sigma factor (σ). **1**

Q. 16. Which of the two subunits of ribosome encounters an mRNA ? R **[Delhi Set-II, Comptt. 2013]**

Ans. The small subunit of ribosome encounters an mRNA. **1**

Q. 17. Name the enzyme that joins the small fragments of DNA of a lagging strand during DNA replication.
R **[Delhi Set-III, Comptt. 2013]**

Ans. DNA ligase. **1**

Q. 18. Name the specific components and the linkages between them that form deoxyguanosine.
R **[Outside Delhi Set-I, Comptt. 2013]**

Ans. **Components :** Deoxyribose sugar and nitrogen base guanine.
Linkage : N-glycosidic linkage. ½ + ½ = **1**

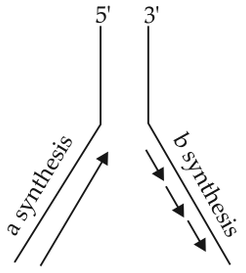
AI **Q. 19. Which one is tailed with adenylate residues between 3′ and 5′ end of hnRNA ?**
R **[Outside Delhi Set-II, Comptt. 2013]**

Ans. 3′ end is tailed with polyadenylate residues. **1**

Q. 20. Name the enzyme and state its property that is responsible for continuous and discontinuous replication of the two strands of a DNA molecule.
R **[Delhi Set-I, III, 2013]**

Ans. DNA polymerase.
Because it has exonuclease activity in 5′ □ 3′ direction. ½ + ½

Q. 21. Name the types of synthesis 'a' and 'b' occurring in the replication fork of DNA as shown below :
R **[Delhi & Outside Delhi Comptt. 2011]**



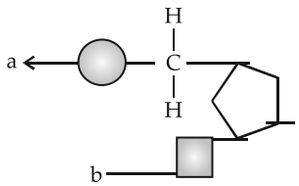
Ans. a— Leading strand (continuous)
b—Lagging strand (discontinuous) ½ + ½

Answering Tip
- Practice self-explanatory diagrams with proper labelling, arrows and headings.

Q. 22. Name the enzyme involved in the continuous replication of DNA strand. Mention the polarity of the template strand.
R **[Delhi & Outside Delhi 2010 (Imp.)]**

Ans. DNA polymerase is involved in the continuous replication of DNA strand.
Polarity of the strand is 3′ → 5′. ½ + ½

Q. 23. Name the component *a* and *b* in the nucleotide with a purine given below. R **[Delhi 2008]**



Ans. a— Phosphate group
b— Nitrogenous base ½ + ½ = **1**

AI **Q. 24. A region of a coding DNA strand has the following nucleotide sequence :**

– ATGC –

What shall be the nucleotide sequence in (i) sister DNA segment it replicates, and (ii) m-RNA polynucleotide it transcribes ?

E & A **[Foreign Set - I, II, III, 2017]**

Ans. (i) - TACG - **(ii)** - UACG- ½ + ½
[CBSE Marking Scheme, 2017]

Q. 25. Write the conclusion Griffith arrived at the end of his experiment with *Streptococcus pneumoniae.*

U **[Outside Delhi Comptt. - 2017, Set - I, II]**

Ans. He concluded that the R-strain bacteria somehow been transformed by heat - killed S-strain bacteria, this must be due to transfer of genetic material
½ + ½
[CBSE Marking Scheme, 2017]

Q. 26. Name the enzyme that helps to join DNA fragments.

U **[Outside Delhi Comptt. - Set-III, 2017]**

Ans. DNA ligase joins/seal or stick the DNA fragments. **1**

Commonly Made Error

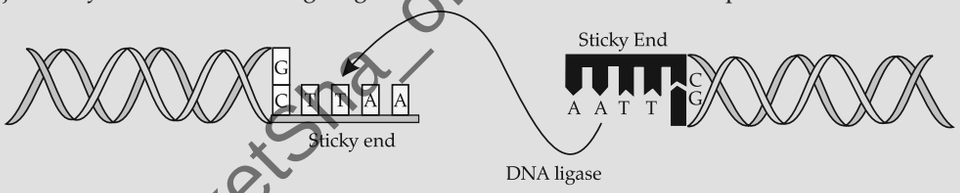
- Incorrect spelling of enzymes is commonly seen. Repeated tests will help the students to remember the names of the enzymes with correct spellings.

Short Answer Type Questions-I

(2 marks each)

Q. 1. Discuss the role the enzyme DNA ligase plays during DNA replication. U **[Delhi, Set-I, 2016]**

Ans. (Discontinuous) DNA fragments, are joined/sealed by them//sticky ends of vector and foreign DNA, joined by them. The following diagram can be considered in lieu of explanation.



1+1
[CBSE Marking Scheme, 2016]

Detailed Answer :

The DNA ligase enzyme joins or seals the discontinuous fragments of DNA. It helps in joining the DNA strands together by catalysing the formation of phosphodiester bond. It also plays an important role in repairing the single strand break in DNA duplex. It also plays an important role in joining the discontinuously synthesized fragments of lagging strand (okazaki fragments) of DNA.

Commonly Made Error

- Students write irrelevant stories. Be specific. Read question carefully and write only what is asked.

Q. 2. Why does hnRNA need to undergo splicing? Where does splicing occur in the cell ?

U **[CBSE, Delhi Set-I & III Comptt. 2016]**

Ans. hnRNA has both exons and introns, Introns are non-coding regions, which are removed by the process called splicing, splicing occurs in the nucleus. **[CBSE Marking Scheme, 2016] 2**

Detailed Answer :

hnRNA is the primary transcript. It is a non functional. It contains both the coding region-exons and non coding regions called introns in RNA. It is called as heterogenous nuclear RNA or hnRNA. It gets functional only after processing by splicing.

During splicing the introns are removed and exons are joined. hnRNA also undergoes two additional processes called capping and tailing. During capping, the unusual nucleotide methyl guanosine triphosphate (mGPPP) is added to the 5' end of hnRNA. In tailing, about 200-300 adenylate residues are added at 3' end of mRNA. Now, this is the fully processed hnRNA which is called as mRNA. It is now functional and is ready for translation. The splicing of hnRNA occurs in the nucleus. **2**

Answering Tip

- Ensure that the requirement for splicing is understood by explaining that the eukaryotic gene is interrupted and hence exons have to be excised for it to be functional.

Q. 3. State the functions of Ribozyme and release factor in protein synthesis respectively.

R **[Outside Delhi Set-I, Comptt. 2015]**

Ans. **Ribozyme**–helps in peptide bond formation. **1**
Release factor–terminates translation/release polypeptide from ribosome. ½+½
[CBSE Marking Scheme, 2015]

Q. 4. Protein synthesis machinery revolves around RNA but in the course of evolution it was replaced by DNA. Justify A **[CBSE SQP, 2015]**

Ans. Since RNA was unstable and prone to mutations, DNA evolved from RNA with chemical modifications that make it more stable.
DNA has double stranded nature and has complementary strands. This further resist changes by evolving a process of repair. **1+1=2**
[CBSE Marking Scheme, 2015]

Q. 5. State the difference between the structural genes in a Transcription Unit of Prokaryotes and Eukaryotes. U **[Outside Delhi Set-II, 2014]**

Ans.

S. No.	Prokaryotes	Eukaryotes
(i)	Polycistronic	Monocistronic
(ii)	No split genes / Not interrupted coding sequence	Split genes / interrupted coding sequences / exon and intron

[CBSE Marking Scheme, 2014] 1 + 1 = 2

Detailed Answer :
In most eukaryotes, a structural gene codes for a single polypeptide *i.e.* it is monocistronic. Each gene in eukaryotes has exons and introns and is termed as split gene. Exons are coding sequences and introns are non coding which are removed by process of splicing while in most prokaryotes a structural gene codes for more than one polypeptide *i.e.* it is polycistronic. **1 + 1 = 2**

Q. 6. Explain the two factors responsible for conferring stability to double helix structure of DNA. U **[Outside Delhi Set-III, 2014]**

Ans. The two factors responsible for conferring stability to double helix structure of DNA are:
1. Stacking of one base over another
2. H-bonding between the nitrogenous base
(Any two) = 1 + 1
[CBSE Marking Scheme, 2014]

Detailed Answer :
Factors conferring stability to Double Helical Structure of DNA are :
(i) Complementarity of the two strands of DNA due to complementary nitrogenous bases which form strong hydrogen bonds with each other. Adenine forms two hydrogen bonds with thymine and cytosine form 3 hydrogen bonds with guanine.
(ii) The base pairs are stacked with their planes one over the other in the double helical structure which provides extra stability.
Also, DNA is less reactive due to absence of reactive —OH group at 2′ carbon. Evolution of a process of repairs which prevents their degradation and presence of thymine instead of uracil being more stable as nitrogenous base also provide stability to double helical structure of DNA. **1+1=2**

Q. 7. A template strand is given below. Write down the corresponding coding strand and the mRNA strand that can be formed along with their polarity. A **[CBSE Foreign 2014]**
3′ ATGCATGCATGCATGCATGCATGC 5′

Ans. Coding strand–
5' TACGTACGTACGTACGTACGTACG 3′
mRNA strand–
5' UACGUACGUACGUACGUACGUACG 3′
[CBSE Marking Scheme, 2014] 1 + 1

Answering Tip
- Practice writing the coding stand and mRNA strand with correct polarity. Writing polarity is must otherwise it may deduct your marks.

AI **Q. 8. Draw a neat labelled sketch of a replicating fork of DNA.** R **[CBSE Foreign 2014]**

Ans. **For diagram:** Refer Topic 1/Revision Notes/ Important diagrams/ Fig 6.8
Polarity of the two strands of the fork to be shown and polarity as well as arrow mark of the lagging and leading strands to be shown with correct labellings.
[CBSE Marking Scheme, 2014] ½ × 4=2

Answering Tip
- Carefully draw the diagram. Don't forget to show the polarity of the two strands of the fork as well as arrow mark of the lagging and leading strands with correct labellings. Each labeling carries a mark.

Q. 9. Draw a schematic diagram of a part of double stranded dinucleotide DNA chain having all the four nitrogenous bases and showing the correct polarity. R **[Delhi Set-II, 2012]**

Ans. **For Diagram:** Refer Topic 1/ Revision Notes/ Important diagrams/ Fig 6.2 **2**

Q. 10. Differentiate between a cistron and an exon. U **[Outside Delhi Set-I, Comptt. 2012]**

Ans. **Difference between cistron and an exon :**
Cistron : A segment of DNA coding for a polypeptide chain, the structural gene in a transcription unit could be monocistronic (mostly in eukaryotes) or polycistronic (mostly in bacteria or prokaryotes).
Exon : The coding sequences or expressed sequences are defined as exons. Exons are said to be those sequences that appear in mature or processed mRNA. **1 + 1**

AI **Q. 11. State the dual role of deoxyribonucleoside triphosphates during DNA replication.** R **[Delhi Set-I, II, III, 2011]**

Ans. The dual role of deoxyribonucleoside triphosphates are:
1. It serves are substrates for DNA synthesis
2. It provides energy for polymerisation reaction.
2

Q. 12. How do histones acquire positive charge ?

U **[Delhi Set-I, 2011]**

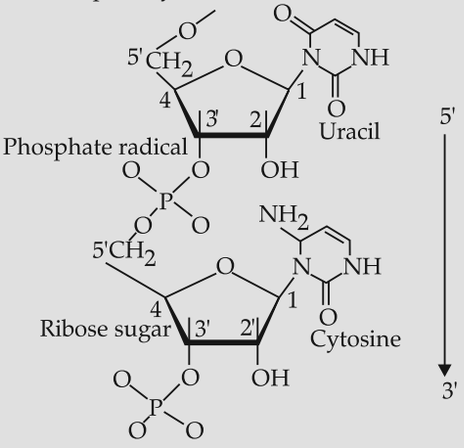
Ans. Histones are rich in basic amino acids Lysine, Arginine (present as residues in their side chains), which are positively charged. **½ × 4 = 2**

[CBSE Marking Scheme, 2011]

Q. 13. Make a labelled diagram of an RNA dinucleotide showing its 3′ –5′ polarity.

R **[Outside Delhi, Comptt. 2010]**

Ans. Labelled diagram of RNA dinucleotide showing its 3' – 5' polarity is as follows :



2

Answering Tip

- Polarity 5′ – 3′ should be Labelled properly.

Q. 14. Describe the structure of a nucleosome.

R **[Foreign, Set-II, 2017]**

Ans. A unit of eight molecules of positively charged histones, negatively charged DNA, wrapped around the histones octamer, contains 200 bp of DNA helix

OR

In lieu of the above explanation the following diagram along with the following statement can be considered

For Diagram: Refer Topic 1/ Revision Notes/ Important diagrams/ Fig 6.4

DNA is negatively charged, histone is positively charged, 200 bp of DNA helix **2**

[CBSE Marking Scheme, 2017]

Detailed Answer :

(i) A typical nucleosome contains 200 bp of DNA helix.

(ii) Negatively charged DNA is wrapped around positively charged histone octomer.

(iii) It constitute the repeating unit to form chromatin.

(iv) The chromatin appear as ''beads on string''.

(v) The chromatin is packed to form a solenoid structure and further supercoiling constitute looped structure called chromatin fibre.

(vi) Higher level packaging of chromatin requires non-histone chromosomal (NHC) proteins.

Q. 15. Although a prokaryotic cell has no defined nucleus, yet DNA is not scattered throughout the cell. Explain.

U **[CBSE, Outside Delhi/Delhi, 2018]**

Ans. DNA is negatively charged, positively charged protein, holds it in place, in large loops (in a region termed as nucleiod). **½ × 4**

[CBSE Marking Scheme, 2018]

Detailed Answer:

In prokaryotic cell, the DNA is not scattered throughout the cell but present in the form of a membrane less structure called nucleoid. The prokaryotic cells uses a specific mechanism to pack the genetic material tightly into this region.

The prokaryotic cell do take up a measure against this by folding the fibers and forming genophore.

Commonly Made Error

- Students make common mistake in understanding the nucleus of prokaryotic cell same as eukaryotic cell.

Short Answer Type Questions-II

(3 marks each)

Q. 1. Describe the experiment that helped demonstrate the semi-conservative mode of DNA Replication.

U **[Delhi Set-I, 2016]**

Ans. Grown *E.coli* in $^{15}NH_4Cl$ for many generations to get ^{15}N incorporated into DNA, then the cells were transferred into $^{14}NH_4Cl$, The extracted DNA was centrifuged in CsCl and measured to get their densities, DNA extracted from the culture after one generation (20 minutes), showed intermediate hybrid density, DNA extracted after two generations (40 minutes) showed light DNA and hybrid DNA.

For diagram: Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.7 **½ × 6 = 3**

A correctly labelled diagrammatic representation in lieu of the above explanation of experiment to be considered.

[CBSE Marking Scheme, 2016]

Detailed Answer :

Meselson and Stahl experiment :

(i) They used the bacterium *E. coli* with the technique of density gradient centrifugation, which separates molecules on the basis of their density.

(ii) They cultured *E. coli* in a medium containing heavy isotope of N^{15} as the sole nitrogen source. This led to the incorporation of N^{15} into the newly synthesized DNA, which ultimately made the DNA heavy.

(iii) This heavy DNA was separated from the normal DNA by density gradient centrifugation using cesium chloride as the gradient.

(iv) The cells were then transferred into the medium with N^{14} as the nitrogen source. Samples were taken from this medium and the DNA was extracted.

Observation : Since, *E.coli* divides every 20 minutes, the DNA extracted after 20 minutes *i.e.* after first generation in the experiment had a hybrid density *i.e.* it was intermediate between N^{14} and N^{15} type of DNA.

The DNA extracted after 40 minutes *i.e.* after second generation had equal amounts of hybrid and light densities.

Conclusion : This implies that in newly synthesized DNA one of its strands is old (N^{15} type) and the other strand is new (N^{14} type). Thus, replication is semi-conservative. **3**

Answering Tip

- Avoid writing answers which are simply repetition of the question. Instead be specific about the key word in that statement

Q. 2. (i) Why did Hershey and Chase use radioactive sulfur and radioactive phosphorus in their experiment ?

(ii) Write the conclusion they arrived at and how.

U **[Foreign Set-I, 2016]**

Ans. (i) Sulphur is a component of protein and thus would label the protein coat. Phosphorus is component of DNA. ½+½

(ii) Bacteria which were infected with viruses having radioactive DNA were found to contain radioactive DNA later on. ½

Bacteria which were infected with viruses having radioactive protein coat were not found to contain radioactivity. ½

Conclusion-DNA is the genetic material. **1**

[CBSE Marking Scheme, 2016]

Commonly Made Error

- Students often get confused about sulphur being in DNA and phosphorus in proteins. Also, they forget to write about the role of bacteriophage in the experiment.

AI **Q. 3. (i) A DNA segment has a total of 2,000 nucleotides, out of which 520 are adenine containing nucleotides. How many purine bases this DNA segment possesses ?**

(ii) Draw a diagrammatic sketch of a portion of DNA segment to support your answer.

A **[Delhi Set III-2015]**

Ans. (i) Number of Nucleotides = 2000

Number of Adenine (A-purine) containing nucleotides = 520

According to Chargaff's rule Purine pairs with pyrimidine, thus 'A' pairs with 'T' and 'G' pairs with 'C'.

∴ Number of Thymine (T-pyrimidine) nucleotides = 520

∴ Total number of A + T = 520+520 = 1040

∴ Number of G + C nucleotides = 2000 – 1040 = 960

∴ Number of guanine nucleotides = 960/2 = 480

∴ Number of purine bases (A + G) = 520 + 480 = 1000

(ii) For diagrammatic sketch of DNA segment, Refer: Topic 1/ Revision Notes/ Important diagrams/ Fig 6.6

Answering Tip

- Students gets confused in remembering bases that belongs to purine and pyrimdines: Remember it with help of mnemonics. **GAPU:** G & A belongs to purine

Q. 4. (i) Differentiate between a template strand and coding strand of DNA.

(ii) Name the source of energy for the replication of DNA.

U **[Delhi Set-I, Comptt. 2015]**

Ans. (i)

Role/Strand	Template strand	Coding strand
Function	Codes for the protein molecule	Does not code for anything
Polarity	3′ → 5′	5′ → 3′

1+1=2

(ii) Deoxynucleoside triphosphates. **1**

[CBSE Marking Scheme, 2015]

Commonly Made Error

- Students often write opposite answers for coding and template stand. It seems they get confused between the terms.

Answering Tip

- Always remember that coding strand is named because it has sequence that corresponds to the RNA generated from template or non coding.

AI **Q. 5. Why is DNA molecule considered as a better hereditary material than RNA molecule ?**

U **[CBSE, Comptt, Set 1, 2018]**

OR

Why is DNA a better genetic material when compared to RNA ?

[Delhi Set-I, Comptt. 2015], (DDE)

Ans. DNA molecule is a better hereditary material as:

(i) It is more stable (due to presence of thymine and not uracil as in RNA).

(ii) Less reactive than RNA (as RNA has 2′ - OH making it more reactive).

(iii) Being less reactive , DNA is not easily degradable (RNA being more reactive is easily degradable).

(iv) Rate of mutation is slow (Rate of mutation in RNA is faster). **(Any three) 1 × 3**

[CBSE Marking Scheme, 2018]

Q. 6. (i) A DNA segment has a total of 1000 nucleotides, out of which 240 of them are adenine containing nucleotides. How many pyrimidine bases this DNA segment possesses ?

(ii) Draw a diagrammatic sketch of a portion of DNA segment to support your answer.

A **[Delhi Set-I, 2015]**

Ans. (i) (a) A = T, A = 240 hence T = 240

A + T = 240 + 240 = 480

So, G + C = 1000 – 480 = 520

G = C, so C = $\frac{520}{2}$ = 260

So, pyrimidines = C + T

= 260 + 240 = 500

(b) Purine A and G always pair with T and C respectively

(c) $\frac{A}{G}=\frac{T}{C}=1$ (Chargaff rule)

(ii) For diagram: Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.2 or 6.6

Diagram showing polarity = ½

A – T = ½

G – C = ½

H-bond = ½ **1+2**

[CBSE Marking Scheme, 2015]

Detailed Answer :

(i) Adenine and guanine are purines. Cytosine and thymine are pyrimidines. According to Chargaff's complementarity rule, the amount of purines is always equal to amount of pyrimidines.

Thus, the numbers of adenine (A) will be equal to the number of thymine (T).

Number of Adenine (A) containing nucleotides = 240

Thus, A = T = 240

Therefore, A + T = 240 + 240 = 480

The number of cytosine (C) will be equal to number of guanine (G).

Thus, G + C = Total number of nucleotides. Nucleotides containing A and T nitrogenous bases= 1000 – 480 = 520

Therefore, G = 260, C = 260

Number of guanine will be equal to number of cytosine which will be 260.

Therefore, the number of pyrimidines that the segment possess = C + T = 260 + 240 = 500 **2**

(ii) For diagram: Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.2 or 6.6 **1**

Commonly Made Error

- Calculation error is commonly seen.

Q. 7. (i) Given below is a single stranded DNA molecule. Frame and label its sense and antisense RNA molecule.

5′ ATGGGGCTC 3′ sense

(ii) How the RNA molecules made from above DNA strand help in silencing of the specific RNA molecules ? A **[CBSE SQP 2015]**

Ans. (i) 5′ ATGGGGCTC 3′ sense

3′ TACCCCGAG 5′ antisense

RNA 5′ AUGGGGCUC 3′ sense

3′ UACCCCGAG 5′ antisense

(ii) The two strands of RNA (*i.e.* sense and antisense) being complementary will bind with each other and form double stranded RNA. As a result its translation and protein expression would be inhibited. **1+2**

[CBSE Marking Scheme, 2015]

Commonly Made Error

- Students often forget that in RNA, uracil is present in place of thymine.

Q. 8. (i) Write what DNA replication refers to.

(ii) State the properties of DNA replication model.

(iii) List any three enzymes involved in the process along with their functions.

R **[CBSE SQP, 2013, 2012]**

Ans. (i) DNA synthesis i.e. copying of DNA

(ii) (a) Semi-conservative.

(b) Semi-discontinuous.

(c) Unidirectional.

(iii) DNA polymerase III – adds nucleotides.

DNA polymerase I – fills the gaps.

RNA primase – brings primers.

Topoisomerase – causes unwinding.

DNA ligase – joins Okazaki fragments.

(Any 3 enzymes and their functions) 1 × 3 = 3

Q. 9. Describe the structure of an RNA polynucleotide chain having four different types of nucleotides.

U **[Delhi Set-I, 2013]**

Ans. (i) RNA is a single-chain poly-ribonucleotide that works as a carrier of coded genetic or hereditary information from DNA to cytoplasm by taking part in protein synthesis.

(ii) It contains 70–12000 four different types of ribonucleotides or ribotides joined end to end.

(iii) The axis or backbone is formed of alternate residues of phosphate and ribose sugars.

(iv) The phosphate combines with carbon 5′ of its sugar and carbon 3′ of the next sugar.

(v) Nitrogen bases are attached to sugars at carbon 1′ of the latter.

(vi) There are 4 bases : Adenine (A), Guanine (G), Uracil (U), Cytosine (C).

Figure representing polynuceotide chain of RNA: Refer to Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.1 ½ × 6 = 3

Q. 10. Draw a labelled diagram of nucleosome. Where is it found in a cell ?

R **[Outside Delhi Set-I, 2012]**

Ans. Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.4 **1**
Label any three parts ½ × 3 = 1½
Location : Chromatin of nucleus. ½
[CBSE Marking Scheme, 2012]

Commonly Made Error

- Students fail to draw a neat diagram. Make sure the lines are properly marked. Lines which are not properly marked will deduct your marks. Also, many of them forget to answer the 2nd part of the question.

Q. 11. List the salient features of double helix structure of DNA. U **[Outside Delhi Set-II, 2012]**

Ans. DNA helix is made up of two polynucleotide chains, each constituted by sugar-phosphate-bases, the chains are antiparallel in polarity (5′ → 3′ and 3′ → 5′), the bases are linked with H-bonds. Adenine pair with Thymine with two H-bonds while Guanine pair with Cytosine with three H-bonds, Coiling of the chain are in right handed fashion, pitch of the helix is 3.4 nm and there are 10 bp per turn, the plane of one base pair stack over the other in a double helix.

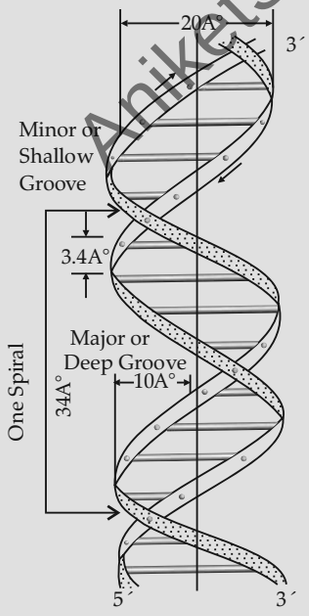


Fig. Coiling in double helix or duplex of DNA.
(Any six) ½ × 6=3
[CBSE Marking Scheme, 2012]

Q. 12. Describe the experiments that established the identity of 'transforming principles' of Griffith.
U **[Foreign Set – I, 2017]**

Ans. (i) Purification of biochemicals like Proteins, RNA & DNA from S cells (heat killed). ½

(ii) Presence of Protein & RNA in medium did not affect transformation. ½

(iii) DNA alone from S Bacteria caused R Bacteria to transform. ½

(iv) Digestion with DNAase inhibits transformation. ½

Conclusion : DNA is the transforming chemical / biochemical material as it was transferred from virus to bacteria. ½ + ½

[CBSE Marking Scheme, 2017]

Detailed Answer :

In 1944, Avery MacLeod and McCarty worked to determine the chemical nature of 'transforming principle'.

They purified biochemicals from heat killed S-cells.

(i) Proteins : Proteases–Transformation takes place So, protein is not a 'transforming principle'.

(ii) RNA : RNases–Transformation takes place. So, RNA is not a 'transforming Principle'.

(iii) DNA : DNases–Transformation inhibited. Therefore, DNA is the 'Transforming Principle'.

Commonly Made Error

- Many students, instead of describing Avery, McLeod and McCarty's experiment, describes Griffith's experiment or Meselson and Stahl's experiment. Some of them mention the use of DNAase, RNAase and protease but could not correlate it with the corresponding observations.

Answering Tips

- Explain the three experiments, Griffith's, Avery et al's, Hershey and Chase's experiments together and compare them to prove that DNA is the genetic material.
- Corelate the principles involved in these experiments with the procedures followed in each experiment.

Q. 13. (i) Construct a complete transcription unit with promotor and terminator on the basis of the hypothetical template strand given below :

A T G C A T G C A T A C

¬| | | | | | | | | | | |

(ii) Write the RNA strand transcribed from the above transcription unit along with its polarity.
E & A **[CBSE, SQP, 2018 Delhi Set-III, 2012]**

Ans. (i)

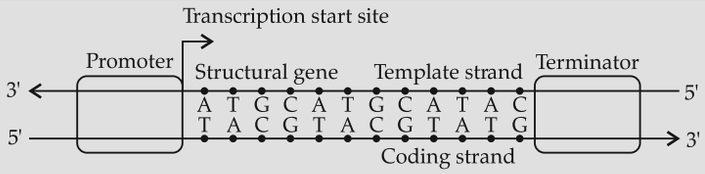


Fig. Complete structure of a transcription unit

(ii) Transcribed RNA

Schematic structure of a transcription unit **2+1**

[CBSE Marking Scheme, 2018]

Q. 14. Explain the role of DNA-dependent RNA polymerase in transcription.

U **[Delhi Set-III, 2012]**

Ans. RNA polymerase catalyzes RNA synthesis. To transcribe a gene, RNA polymerase proceeds through a series of well-defined steps, which are grouped into three phases : initiation, elongation and termination.

(i) Initiation : RNA polymerase binds with the promoter region of the DNA. The promoter – polymerase complex undergoes structural changes required for transcription.

(ii) Elongation : During elongation, RNA polymerase unwinds the DNA in front and re-anneals it behind, it dissociates the growing RNA chain from the template as it moves along. It also performs proof reading function.

(iii) Termination : Once the polymerase has transcribed the length of the gene, it stops and releases the RNA product. **1 × 3 = 3**

Q. 15. (i) Why did Meselson and Stahl used ^{14}N and ^{15}N isotopes as the sources of nitrogen present in the culture medium in their experiment ? Explain.

(ii) Write the conclusion drawn by them from the experiment. U **[Delhi Set-I, Comptt. 2012]**

Ans. (i) Meselson and Stahl used ^{14}N and ^{15}N isotopes as the sources of nitrogen present in the culture medium in their experiment as nitrogen is a major constituent of DNA. Moreover ^{15}N is by far the most abundant isotope of nitrogen and DNA with the heavier ^{15}N isotope is also functional. *E.coli* can be grown for several generations in a medium with ^{15}N easily. When DNA is extracted from these cells and centrifuged on a salt density gradient, the DNA separates out at the point at which its density equals that of the salt solution. **2**

(ii) The experiment proves the semi-conservative nature of replication of DNA. In this type of replication, one strand of daughter DNA is new and one strand is old. It means, one strand of daughter duplex is derived from the old DNA, while the other strand is formed new. It proves semi-conservative replication of DNA. **1**

Q. 16. (i) Draw a neat labelled diagram of a nucleosome.

(ii) Mention what enables histones to acquire a positive charge. R **[Outside Delhi Set-I, 2012]**

Ans. (i) Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.4

(ii) Basic amino acid residues of lysines, arginines. **3**

[CBSE Marking Scheme, 2012]

Detailed Answer :

(i) Histones acquire positive charge because they are rich in basic amino acid residues of arginine and lysine, which carry positive charges in their side chains.

Q. 17. (i) Name the enzyme that catalyses the transcription of hnRNA.

(ii) Why does the hnRNA need to undergo changes ? List the changes hnRNA undergoes and where in the cell such changes take place.

R **[Outside, Delhi Set-I, 2011]**

Ans. (i) RNA polymerase II. ½

(ii) Has (non-functional) introns. ½

(Methyl guanosine tri-phosphate is added to 5′ end) capping, tailing (Poly A tail at 3′ end added), splicing (introns are removed and exons are joined). **½ × 3 = 1½**

Nucleus. **[CBSE Marking Scheme, 2011]** ½

Detailed Answer :

(i) The enzyme RNA polymerase II catalyses the transcription of hnRNA.

(ii) The hnRNA in eukaryotes needs to undergo changes for converting it into functional RNA. The hnRNA contain both exons and introns. The exons are functional coding segments while introns are non functional and non coding sequences. This hnRNA undergo processing where the introns are removed and exons are joined by a process called splicing. Now this transcribed heterogenous nuclear RNA undergoes additional processing called capping and tailing. In capping methyl guanosine triose phosphate is added to 5' end and in tailing 200-300 adenylate residues are added at 3′ end of spliced RNA. This is completely processed hnRNA. This is now called a mRNA. Such changes of processing takes place in the nucleus of the cell.

Q. 18. The base sequence in one of the strands of DNA is TAGCATGAT.

(i) Give the base sequence of its complementary strand.

(ii) How are these base pairs held together in a DNA molecule ?

(iii) Explain the base complementarity rules. Name the scientist who framed this rule.

A **[Delhi Set-I, II, III, 2011]**

Ans. (i) ATCGTACTA **1**

(ii) Through Hydrogen bonds between A and T and C and G on the two strands. **½ + ½**

(iii) A = T and C → G, Watson and Crick / Chargaff. **1**

[CBSE Marking Scheme, 2011]

Detailed Answer :

(i) ATCGTACTA.

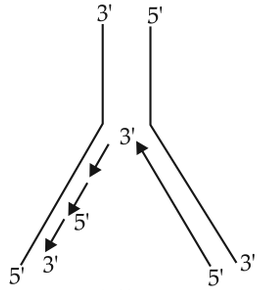
(ii) The base pairs are held together in a DNA molecule by hydrogen bond in such a way that Adenine (A) pairs with Thymine (T) by two Hydrogen bonds (A = T) and Guanine pairs with Cytosine (C) by three Hydrogen bonds (C → G).

(iii) The base complementarity rule is that the ratios between adenine-thymine and guanine-cytosine are constant and equal to one. The scientists who framed this rule were Erwin Chargaff and Watson and Crick.

Answering Tip

- All parts and sub parts of a question should be attempted together in the same sequence.

Q. 19.



Why do you see two different types of replicating strands in the given DNA replication fork ? Explain. Name these strands.

A **[Outside Delhi Set-I, II, III, 2011]**

Ans. (i) In long DNA molecules, since the two strands of DNA cannot be separated in its entire length, the replication occur within a small opening to the DNA helix, referred to as a replication fork.

(ii) The DNA-dependent DNA polymerases catalyse polymerization of the nucleotides only in 5′ → 3′ direction.

Note : For diagram: Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.8.

Consequently, on one of the template strands (with 3′ → 5′ polarity) the synthesis of DNA is continuous, while on the other template strand (with polarity 5′ → 3′), the synthesis of DNA is discontinuous *i.e.* short stretches of DNA are synthesized.

(iii) The discontinuously synthesized strands are later joined together by the enzyme DNA ligase. **1 + 1 + 1**

Q. 20. Identify A, B, C, D, E and F in the following table.

R **[Outside Delhi Comptt. – 2017, Set - I, III]**

S. No.	Component - I	Component - II	Chemical linkage bonding the two components	Product
I	A	B	C	Nucleoside
II	Nucleoside	D	E	Nucleotide
III	Nucleotide	Nucleotide	F	Dinucleotide

Ans. (I) A - Nitrogenous base / A - Pentose sugar.

B - Pentose Sugar / B - Nitrogenous base.

C - N-glycosidic linkage.

(II) D - phosphate group.

E - phospho ester linkage.

(III) F - (3' – 5') phosphodiester linkage. **3**

Q. 21. (i) Draw a labelled schematic diagram of a replication fork showing continuous and discontinuous replication of DNA strands.

(ii) State a reason why is the replication continuous and discontinuous in the diagram drawn.

R **[Foreign - Set - II, 2017]**

Ans. (i) For Diagram: Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.8 **2**

(ii) 2 strands are antiparallel, DNA polymerase acts only in one direction i.e. 5' → 3'

½ + ½ = 1

[CBSE Marking Scheme, 2017]

Q. 22. In a typical nucleus, some regions of chromatin are stained light and others dark. Explain why is it so and what is its significance ?

A **[Outside Delhi Set-I. Comptt. 2016]**

Ans. Light stained-loosely packed-Euchromatin.
Dark stained-densely packed-Heterochromatin.
Euchromatin-transcriptionally active.
Heterochromatin-transcriptionally inactive.

[CBSE Marking Scheme, 2016] 3

Detailed Answer :

Euchromatin is lightly stained, diffused but narrow fibrous part of chromatin. It is normal chromatin which possesses active genes. It is transcriptionally active. During nuclear division it replicates normally. It is formed through loose spiralization of nucleosome strands.

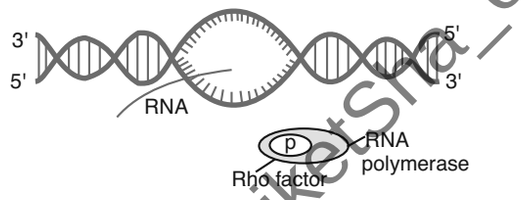
Heterochromatin is darkly stained granular part of chromatin and is formed by solenoid type of coiling of nucleosomes. Transcription does not occur in these regions. Active genes are also absent in it.

Q. 23. Describe the termination process of transcription in bacteria.

U **[Outside Delhi Set-III, 2010]**

Ans. **(i)** RNA polymerase binds to the promotor and initiates transcription. It uses nucleotide triphosphates as substrates and polymerises in a template dependent fashion following the rule of complementary. It somehow also facilitates opening of the helix structure and continues elongation. Only a short stretch of RNA remains bound to the enzyme. Once the polymerase reaches the terminator region, the nascent RNA falls off, also the RNA polymerase. This results into termination of the transcription.

(ii) RNA polymerase associates transiently with termination factor (rho) to terminate the transcription. Association of this factor alters the specificity of the RNA polymerase to terminate.



1½ + 1½ = 3

Q. 24. Name the specific enzyme responsible for nucleotide polymerisation in DNA replication. Write two characteristic features of this enzyme. Name the region on *E. coli* DNA where this enzyme can initiate replication.

U **[Delhi Comptt - 2017, Set - II]**

Ans. **(i)** DNA - dependent DNA polymerase. ½
(ii) The enzyme uses DNA template to catalyse the polymerisation of deoxyribonucleotides. **1**
(iii) Have to catalyse the reaction with high accuracy. **1**
(iv) Origin of replication / Ori. ½
[CBSE Marking Scheme, 2017]

Answering Tip

- Students should make tablular chart mentioning all the enzymes associated with replication, transcription and translation to remember the roles of all the enzymes and understand the difference amongst them.

Q. 25. (a) Mention two events in which DNA is unzipped.
(b) Predict the consequences when both the template and the coding strands of a DNA segment participate in transcription process?

A **[CBSE, SQP, 2018]**

Ans. **(a)** Replication and Transcription. ½ + ½
(b) If both the stands take part in transcription,
(i) One segment of DNA would be coding for two different proteins which will complicate the genetic information machinery
(ii) Two RNA molecules will be produced, complementary to each other, hence form a double stranded RNA, translation would not be possible. **1+1**
[CBSE Marking Scheme, 2018]

Answering Tip

- Replication, transcription and translation should be taught together. This will help students to understand these processes clearly.

Q. 26. Name the three RNA polymerases found in eukaryotic cells and mention their functions.

R **[CBSE, Comptt,Set -1, 2018]**

Ans. RNA polymerase - I, transcribes rRNAs (28S -18S and 5.8S). ½ × 2
RNA polymerase - II, transcribes precursor of mRNA / hnRNA / heterogeneous RNA. ½ × 2
RNA polymerase - III, transcribes tRNA / 5Sr RNA / snRNA. ½ × 2
[CBSE Marking Scheme, 2018]

AI **Q. 27. Explain the post transcriptional modifications the hn-RNA undergoes in eukaryotic cell.**

R **[Outside Delhi, Set-1-2016]**

Ans.
- Splicing , Introns are removed and exons are joined. ½ × 2
- Capping, Methyl guanosine triphosphate / mGPPP is added to the 5′ end of hnRNA. ½ × 2
- Tailing, Polyadenylate residues are added to 3′-end in a template independent manner. ½ × 2

[CBSE Marking Scheme, 2018]

Q. 28. A DNA segment has a total of 1500 nucleotides out of which 410 are guanine containing nucleotides. How many Pyrimidine bases this DNA segment possesses. A **[Delhi Set-II, 2015]**

Ans. ∴ G = 410 ∴C= 410 (because C = G)

$\therefore \quad G + C = 410 + 410 = 820$

$\therefore \quad A + T = 1500 - 820 = 680$

$\therefore \quad T = \frac{680}{2} = 340$

Thus the pyrimidine bases C + T
= 410 + 340
= 750 **3**

Q. 29. If the base adenine constitute 30% of an isolated DNA fragment, then what is the expected percentage of the base cytosine in it.

E & A **[Delhi Comptt. 2011]**

Ans. As A = 30%

T = 30% (as A = T)

A + T = 60%

G + C = 100 – 60 = 40%

∴ C (Cytosine) =20% (as C = G) **3**

Q. 30. Name two basic amino acids that provide positive charges to histone proteins.

R **[Delhi Set-1-Comptt. 2012]**

Ans. Histone proteins have a positively charged surface because of the presence and abundance of two basic amino acids : (i) Lysine and (ii) Arginine as compared to other amino acids. **3**

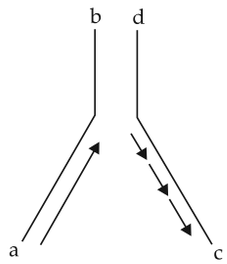
Q. 31. (i) If the sequence of the coding strand in transcription unit is written as follows :

5'—ATGCATGCATGCATGCATGCATGCATGCAT G—3′

write down the sequence of mRNA.

(ii) How is repetitive/satellite DNA separated from bulk genomic DNA for various genetic experiments.

(iii) Mention the polarity of DNA strands a-b & c-d shown in the replicating fork given below :



E & A **[Delhi Set. III-2014]**

Ans. (i) 5'—AUGCAUGCAUGCAUGCAUGCAUG —3'

(ii) By density gradient centrifugation.

(iii) Polarity of DNA strand a–b is 3'→5' & c–d has polarity 5'→3'. **1 × 3 = 3**

Commonly Made Error

- Students often write incorrect sequence of mRNA. It seems they are unaware of this concept of writing the sequence with polarity. Practice writing the sequence of mRNA. Don't forget to mention the polarity of strand.

AI **Q. 32. Which one of these an intron and an exon is reminiscent of antiquity ?**

R **[Outside Delhi Set-I Comptt. 2013]**

Ans. The primary transcript in eukaryotes contain both exons & introns (the non coding sequences). The introns are removed during processing by splicing & the exons are joined. The presence of introns in primary transcript is the reminiscent of antiquity. **3**

Long Answer Type Questions

(5 marks each)

AI **Q. 1. Describe Meselson and Stahl's experiment that was carried in 1958 on *E.coli.* Write the conclusion they arrived at after the experiment.**

U **[Outside Delhi Set-I, 2016]**

OR

Describe Meselson and Stahl's experiment and write the conclusion they arrived at.

[Delhi Set-II, 2014]

Ans. See Q. No. 1 (S.A.T.Q.-II) **5**

Q. 2. (i) Describe the series of experiments of F. Griffith. Comment on the significance of the results obtained.

(ii) State the contribution of Macleod, McCarty and Avery. U **[Outside Delhi Set-II, 2016]**

OR

(i) Explain with the help of Griffith's experiment how the search for genetic material was conducted and what was the conclusion drawn ?

(ii) How did Macleod, McCarty and Avery establish the biochemical nature of the so called "genetic material" identified by Griffith in his experiment.

[Delhi Set-II, Comptt. 2016]

OR

(i) Describe the various steps of Griffith's experiment that led to the conclusion of the 'Transforming principle'.

(ii) How did the chemical nature of the 'Transforming principle' get established ?

[Delhi Set-III, 2014; Delhi Set-II, Comptt. 2015]

OR

Describe Frederick Griffith's experiment on *Streptococcus pneumoniae.* Discuss the conclusion he arrived at. **[Outside Delhi Set-II, 2014]**

Ans. (i) *Streptococcus pneumoniae* :

S – Strain (virulent) injected into mice → mice die. ½

R – strain injected into mice → mice alive. ½

S – strain (heat killed) injected into mice → mice alive. ½

R – strain (alive) + S (heat killed) strain inject into mice → mice die. ½

R strain (non-virulent) picked up genetic material from S strain (virulent) and get transformed. **1**

(ii) They (worked on the bio-chemical nature of transforming principle in Griffith's experiment) purified proteins, DNA and RNA from heat killed S cells, they discovered protein digesting enzyme (protease), RNA digesting enzyme (RNAase) did not affect transformation, Digestion with DNase inhibited transformation, concluded DNA is the heredity material.**[CBSE Marking Scheme, 2016] 2**

Detailed Answer :

(i) Griffith's experiment : Griffith used mice and *Streptococcus pneumoniae* for his experiment.

Streptococcus pneumoniae has two strains :

(a) Smooth (S) strain (virulent) : It has polysaccharide mucus coat and can cause pneumonia.

(b) Rough (R) strain (Non-virulent) : It has no mucous coat and therefore do not cause pneumonia.

To test for the trait of pathogenicity, Griffith injected mice with mixes of the two strains :

(c) S-strain → Inject into mice → Mice die

(d) R-strain → Inject into mice → Mice live

(e) S-strain (Heat killed) → Inject into mice → Mice live

(f) S-strain (Heat killed) + R-strain (live) → Inject into mice → Mice die

He concluded that some 'transforming principle', transferred from heat-killed S-strain to R-strain. It enabled R-strain to synthesize smooth polysaccharide coat and become virulent. This must be due to the transfer of some genetic material. **2½**

(ii) Oswald Avery, Colin Macleod and McCarty worked to determine the biochemical nature of 'transforming principle' in Griffith's experiment. They purified biochemicals (proteins, DNA, RNA etc.) from the heat killed S cells to see which ones could transform live R cells into S cells.

They discovered that :

(i) Digestion of protein and RNA (using Proteases and RNases) did not affect transformation. So the transforming substance was not a protein or RNA.

(ii) Digestion of DNA with DNase inhibited transformation. It means that DNA caused transformation of R cells to S cells *i.e.* DNA was the transforming substance. Therefore they concluded that DNA is the hereditary material. **2½**

Commonly Made Error

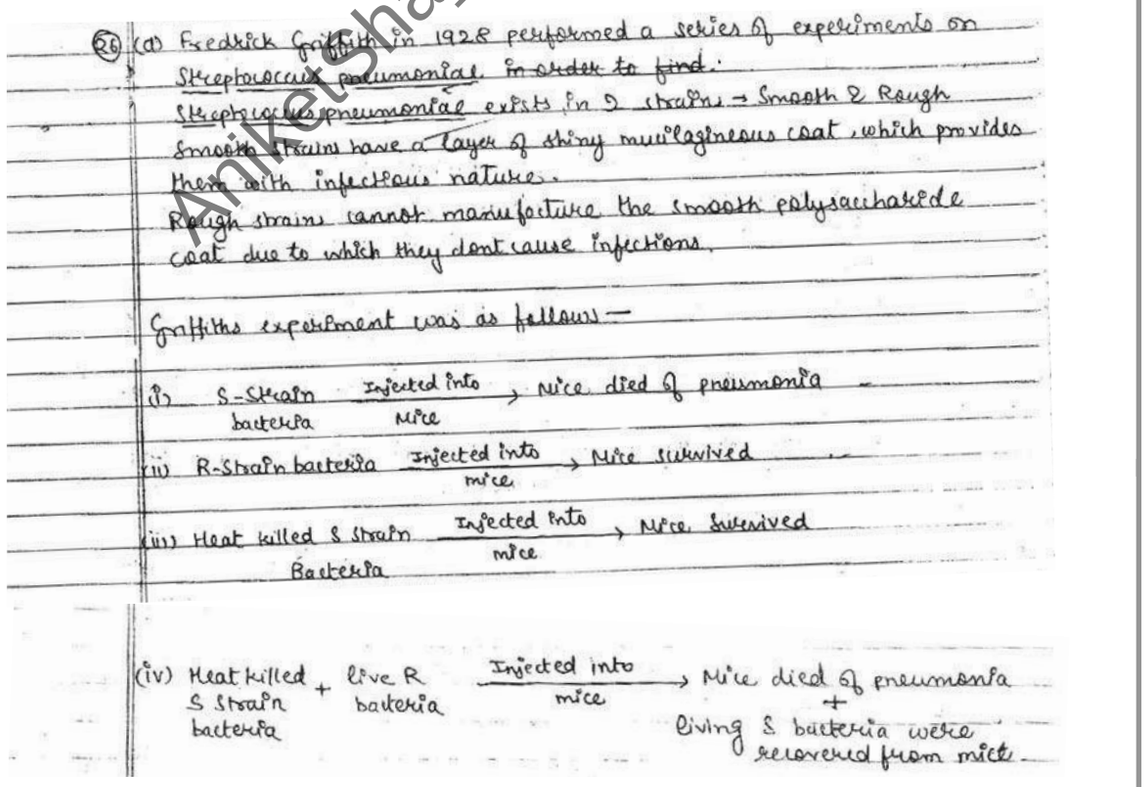
- Students often get confused between 'R strain' and 'S strain'. Also, they forget to mention about 'avirulent' and 'virulent'.
- Many students forget to write the conclusion of the experiment.

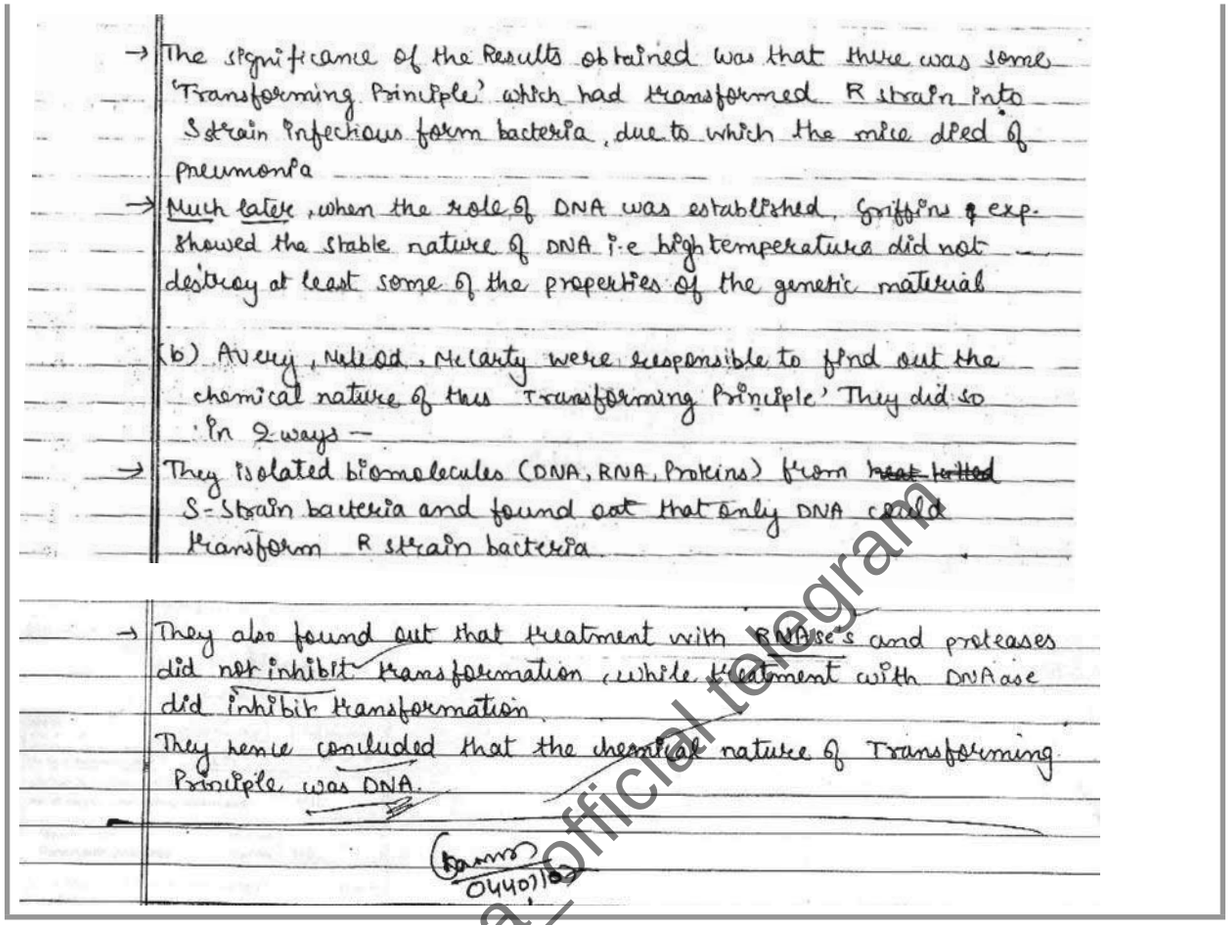
Answering Tip

- Discuss specific steps in detail and correlate each step with the previous step and the next step.

OR

Ans.




→ The significance of the Results obtained was that there was some 'Transforming Principle' which had transformed R strain into S strain infectious form bacteria, due to which the mice died of pneumonia

→ Much later, when the role of DNA was established, Griffin's exp. showed the stable nature of DNA i.e high temperature did not destroy at least some of the properties of the genetic material

(b) Avery, McLeod, McCarty were responsible to find out the chemical nature of this 'Transforming Principle' They did so in 2 ways –

→ They isolated biomolecules (DNA, RNA, Proteins) from ~~heat killed~~ S-Strain bacteria and found out that only DNA could transform R strain bacteria

→ They also found out that treatment with RNAse's and proteases did not inhibit transformation, while treatment with DNAase did inhibit transformation.
They hence concluded that the chemical nature of Transforming Principle was DNA.

04/07/22

AI Q. 3. Answer the following questions based on Hershey and Chase experiments :

(i) Name the kind of virus they worked with and why ?

(ii) Why did they use two types of culture media to grow viruses in ? Explain.

(iii) What was the need for using a blender and later a centrifuge during their experiments ?

(iv) State the conclusion drawn by them after the experiments. U **[Delhi Set-III, 2016]**

Ans. (i) Bacteriophage, they infect bacteria. ½ + ½

(ii) Two types of culture media were used in order to make protein of viruses (with the help of S^{35}) radioactive in one case, and DNA molecule in virus (with the help of P^{32} radioactive in other case. ½ × 2 = 2

so as to identify which one of the two had entered into the bacteria during viral infection.

(iii) Blender : To separate the viral protein coats that are still attached to the surface of bacteria. ½

Centrifuge : To separate lighter supernatant (containing viral protein coats) from denser residue (containing bacteria). ½

(iv) DNA is the genetic material *i.e.* passed from virus to bacteria. **[CBSE Marking Scheme, 2016] 1**

Detailed Answer :

(i) Hershey & Chase carried out experiments with viruses which infect bacteria. Such viruses are called **bacteriophage**. While infecting bacteria the protein capsid or coat remains outside on the bacterial wall and its genetic material (DNA) enters the bacterial cell which treats the bacterial DNA as its own to synthesize the viral particle inside the bacterial cell.

(ii) They used two separate culture media for growing these bacteriophages, one culture medium containing radioactive phosphorus (P^{32}) and the other containing radioactive sulphur (S^{35}). The bacteriophages were then cultured on these two types of media separately.

The viruses cultured in a medium enriched with radioactive phosphorus, was found to contain radioactive DNA but not radioactive protein because phosphorus is a component of DNA and not of protein. Similarly, the bacteriophages grown in the medium enriched with radioactive sulphur contained radioactive protein and not radioactive DNA because sulphur is a component of some amino acids forming proteins of capsids of viruses.

(iii) The blender was used to remove the proteinaceous capsids of virus which were attached with the bacterial cell wall. The bacteria infected with virus (bacteriophages) were agitated in the blender for separating viral coats from bacteria. Centrifugation later was done which resulted in the formation

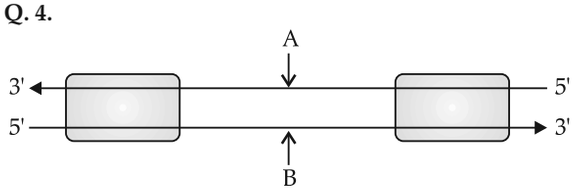
of a supernatant containing viral capsids and the bacteria got sedimented at the bottom.

(iv) Hershey & Chase concluded after the experiment that the genetic material that is passed from virus to the bacteria is not the protein coat but DNA. It proves the DNA is the genetic material and not the protein.

Answering Tips

- Understand the three experiments, Griffith's, Avery et al's, Hershey and Chase's experiments together and compare them to prove that DNA is the genetic material.
- Corelate the principles involved in these experiments with the procedures followed in each experiment.

Q. 4.



(i) Identify strands 'A' and 'B' in the diagram of transcription unit given above and write the basis on which you identified them.

(ii) State the functions of Sigma factor and Rho factor in the transcription process in a bacterium.

(iii) Write the functions of RNA polymerase-I and RNA polymerase-III in eukaryotes.

A **[Foreign Set-I, 2016]**

Ans. (i) A-Template strand **1**

B-Coding strand **1**

Template strand has polarity 3′-5′

Coding strand has polarity 5′-3′

On the basis of polarity with respect to promoter. ½ + ½

(ii) Sigma factor associates with RNA polymerase to initiate transcription, Rho factor gets associated to RNA polymerase to terminate transcription. ½ + ½

(iii) RNA polymerase I - Transcribes -RNAs ½

RNA polymerase III - Transcribes tRNA / 5srRNA / 5nRNA ½

[CBSE Marking Scheme, 2016]

Detailed Answer :

(i) Strand **A** is the **template strand** because it has 3′→5′ polarity. It acts as a template and is therefore so called.

Strand **B** is called as the **coding strand** because it has 5′→3′ polarity. It does not get transcribed.

Template and coding strands are identified on the basis of polarity with respect to promoter.

(ii) In bacterium, the sigma (σ) factor initiates transcription. This σ factor recognizes the start signal and promotor region of the transcription unit which then along with RNA polymerase enzyme gets associated to the promotor to initiate transcription. Rho is the termination factor. It facilitate in terminating the process of transcription. When the RNA polymerase reaches the terminator region the RNA polymerase is separated from DNA-RNA hybrid and as a result transcription terminates.

(iii) In eukaryotes, the RNA-Polymerase-I transcribes rRNAs (28S, 18S & 5S) & RNA-polymerase III transcribes tRNA, 5S rRNA & SnRNAs (Small nuclear RNAs).

In bacteria, a single DNA dependent RNA-polymerase transcribes all the three types of RNAs *i.e.* mRNA, tRNA & rRNA).

Q. 5 Describe the packaging of DNA helix in a prokaryotic cell and an eukaryotic nucleus.

R **[Foreign Set-I, 2016]**

Ans. Prokaryotes : Negatively charged DNA is held with positively charged proteins in nucleoid, DNA in nucleoid is organised in large loops held by protein. ½ × 4 = **2**

Eukaryotes : In nucleus, the negatively charged DNA is wrapped around positively charged histone octomer to form nucleosome, nucleosomes are repeated to constitute chromatin at higher level, additional set of non-histone chromosomal protein gets associated with chromatin. ½ × 6 = **3**

[CBSE Marking Scheme, 2016]

Detailed Answer:

Packaging of DNA helix in prokaryotes : In prokaryotes, there is no true nucleus. The DNA is present in a region called nucleoid. The DNA which is negatively charged is held with some positively charged non-histones basic proteins. DNA in nucleoid is organized in large loops held by protein.

DNA Packaging in eukaryotes : In eukaryotes, there is true nucleus. Chromosomes are made up of DNA and histone proteins. The negatively charged DNA is wrapped around positively charged histone octamer (2 molecules each of H_2A, H_2B, H_3 & H_4) to form nucleosome which form the repeating units of chromatin. Nucleosomes are further coiled and packed to form **solenoids.** Further, super coiling forms chromatin fibers and then chromatids. They further coils and condenses at metaphase stage of cell division to form chromosomes.

AI **Q. 6. (i) Name the stage in the cell cycle where DNA replication occurs.**

(ii) Explain the mechanism of DNA replication. Highlight the role of enzymes in the process.

(iii) Why is DNA replication said to be semi-conservative ? U **[Delhi Set-I, II, III, 2015]**

Ans. (i) S-phase (synthesis phase) is the part of the cell cycle in which DNA replication takes place. **1**

(ii) Process of DNA replication :

(a) The process of DNA replication begins at a point called the origin of replication (ori), to form a replication fork.

(b) The separated strands act as templates for the synthesis of new strands.

(c) DNA replicates in the 5′ → 3′ direction.

(d) dNTPs (Deoxyribonucleoside-tri phosphate) act as substrate and also provide energy for polymerization of nucleotides.

(e) DNA polymerase is an enzyme that assembles a new DNA strand that is complementary to the template strand.

(f) DNA polymerase continues to move along the template strand and add new nucleotides to the growing or complementary strand until the entire genome is replicated.

(g) The DNA polymerase forms one new strand (leading strand) in a continuous stretch in the 5′ → 3′ direction (Continuous synthesis).

(h) The other new strand is formed in small stretches (Okazaki fragments) in 5′ → 3′ direction (discontinuous synthesis).

(i) The Okazaki fragments are then joined together to form a new strand by an enzyme DNA ligase. This new strand is called lagging strand.

For Diagram: Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.8 **2**

(iii) DNA replication is said to be semi-conservative and discontinuous. Semi-conservative replication means that double stranded DNA molecule would produce two copies that each contained one of the original strands and one new strand. **2**

Q. 7. (a) Why does DNA replication occur in small replication forks and not in its entire length ?

(b) Why is DNA replication continuous and discontinuous in a replication fork ?

(c) State the importance of origin of replication in a replication fork.

R **[CBSE, Comptt, Set-1, 2018]**

Ans.(a) DNA being very long , requires high energy for opening along its entire length.

(b) DNA dependent DNA polymerase catalyse polymerisation only in one direction i.e. 5′ 3′. Two strands of DNA are anti parallel and have opposite polarity.

(c) Site where replication originates. **2 + 2 + 1**

[CBSE Marking Scheme, 2018]

Q. 8. (i) How are the following formed and involved in DNA packaging in a nucleus of a cell ?

(a) Histone Octamer,

(b) Nucleosome,

(c) Chromatin.

(ii) Differentiate between Euchromatin and Heterochromatin. U **[Delhi Set-I, 2016], (NCERT)**

Ans. (i) (a) Eight molecules of positively charged basic proteins called histones are organised to form histone octamer.

(b) Negatively charged DNA wrapped around positively charged histone octamer to give rise to nucleosome.

(c) Nucleosome constitute the repeating unit of a structure called chromatin. **3**

(ii)

S. No.	Euchromatin	Heterochromatin
(i)	Loosely packed.	Densely packed.
(ii)	Stains light.	Stains dark.
(iii)	Transcriptionally active.	Transcriptionally inactive.

(Any two differences) 1 + 1 = 2

(CBSE Marking Scheme, 2016)

Detailed Answer :

(i) (a) Histone Octamer : It is a unit comprising two molecules each of four histones namely H_2A, H_2B, H_3 and H_4. These histone molecules are positively charged and interacts with negatively charged DNA to keep it associated with itself.

(b) Nucleosome : The negatively charged DNA wrapped around the histone octamer (positively charged) to form a nucleosome. Oudit (1975) called it as the nu-body. It consists of 200 base pairs and a histone octamer. Nucleosome act as building block for packaging the DNA into chromatin.

(c) Chromatin : It is thread like and a complex of DNA and histone protein. It helps in packing of DNA into the nucleus. The nucleosomes in chromatin look like beads on a string. The nucleosomes are the repeating units of chromatin and separated from one-another by the region of DNA which is coiled as linker DNA which is composed of 60 base pairs and one histone molecule H1. The nucleosomes are further coiled and packed into a structure of higher organization which is known as solenoid. Each solenoid is formed by six nucleosomes per turn. Further supercoiling tends to form chromatin fiber and then chromatid. They further coils condense at metaphase stage to form chromosomes. **3+2=5**

Q. 9. (i) What is Central dogma ? Who proposed it ?

(ii) Describe Meselson and Stahl's experiment to prove that the DNA replication is semi-conservative.

U **[Outside Delhi Set-I, Comptt. 2015]**

Ans. (i) Central dogma : Refer Topic 1/ Revision Notes/ Important diagrams/ Fig 6.3

Given by Francis Crick. **1**

(ii) Meselson and Stahl experiment : For diagram: Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.7

(Same value points to be awarded in an explanation) **½ × 6 = 3**

[CBSE Marking Scheme, 2015]

Detailed Answer :

(i) Central Dogma : The principle of central dogma of molecular biology was proposed by Francis Crick. This states that the genetic information always flows unidirectionally from DNA to mRNA (Transcription) and then from mRNA to protein or (polypeptide translation).

(ii) Meselson & Stahl's experiment :

Refer to SATQ-II Q. No. 1 **5**

Commonly Made Error

- While explaining Central Dogma, students often write 'DNA to RNA' but they forget to mention about protein.

Answering Tip

- Learn Central dogma with the help of flow chart.

Q. 10. (i) Explain the process of DNA replication with the help of schematic diagram. [Delhi Comptt. Set-I, 2015]

(ii) In which phase of the cell cycle does replication occur in Eukaryotes ? What would happen if cell - division is not followed after DNA replication ? A **[Outside Delhi Set-II, 2014]**

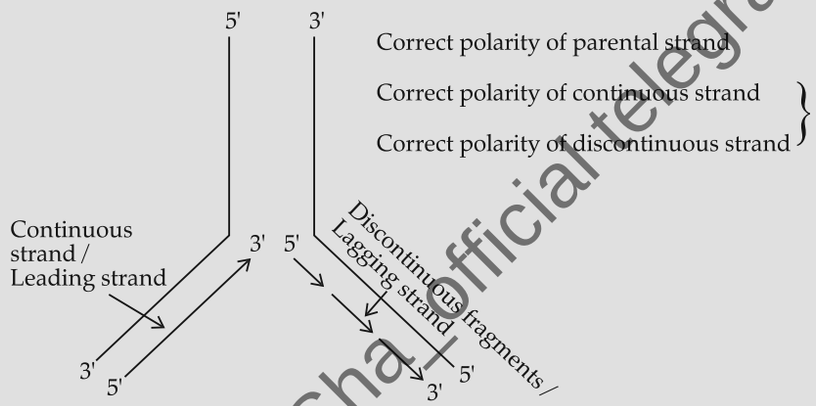
OR

Explain the process of DNA replication with the help of a replicating fork. [Delhi Set-I, Comptt. 2015]

Ans. (i) –Replication of DNA begins at ori site to form a replication fork. ½

– DNA dependant DNA polymerase forms a new strand in 5′ □ 3′ direction. ½

– Role of DNA ligase is to join discontinuously synthesised fragments. ½



2½

(iii) S-phase. ½

Polyploidy **[CBSE Marking Scheme, 2014]** ½

Detailed Answer :

(i) Refer LAQ/Q. No. 6 (ii)

(ii) DNA replication takes place in S-phase (Synthetic phase) of cell cycle in eukaryotes. If this replication of DNA is not followed by cell division the DNA contents of the cell will get doubled *i.e.* duplicate set of DNA will be formed. This will result in autopolyploidy.

Q. 11. (i) Hershey and Chase carried their experiment in three steps : infection, blending, centrifugation. Explain each step.

(ii) Write the conclusion and interpretation of the result they obtained.

U **[Outside Delhi Comptt. 2017, Set - I]**

OR

Describe the Hershey and Chase experiment. Write the conclusion drawn by the scientists after their experiment.

[Delhi Set-I, 2015; Outside Delhi Set-II, 2014]

OR

How did Alfred Hershey and Martha Chase arrive at the conclusion that DNA is the genetic material ? [Outside Delhi Set-I, 2010]

Ans. (i) Infection : Radioactive phosphorus / phosphorus labelled bacteriophages were allowed to infect *E.coli* - growing in a culture medium, simultaneously radioactive sulphur / Sulphur labelled bacteriophage was allowed to infect *E.coli* growing in another culture medium.

1 + 1 = 2

(a) Blending : As infection proceeds – the viral coats are removed from the bacteria by agitating in a blender. ½

(b) Centrifugation : virus particles were separated from bacteria by spinning them in a centrifuge. ½

(ii) Conclusion : DNA is the genetic material. **1**

Interpretation : Sulphur labelled viral protein did not enter the bacteria during infection, whereas phosphorus labelled viral DNA entered into the bacteria to cause infection.

½ + ½

[CBSE Marking Scheme, 2017]

Detailed Answer :

Infection :

(i) Hershey and Chase made two preparation of bacteriophage - In one, proteins were labeled with

S^{35} by putting in medium containing radioactive sulphur (S^{35}). In the second, DNA was labeled with P^{32} by putting in a medium containing radioactive phosphorus (P^{32}).

(ii) These preparations were used separately to infect *E.coli.*

Blending :

(i) After infection, the *E.coli* cells were gently agitated in a blender to separate the phage particles from the bacteria.

Centrifugation :

(i) Then the culture was centrifuged. Heavier bacterial cells were formed as a pellet at the bottom. Lighter viral components outside the bacterial cells remained in the supernatant.

(ii) They found that,

(a) Supernatant contains viral protein labelled with S^{35} *i.e.* the viral protein had not entered the bacterial cells.

(b) The bacterial pellet contains radioactive P. This showed that viral DNA labelled with P^{32} had entered the bacterial cells. This proves that DNA is the genetic material.

For diagram: Refer Topic 1/ Revision Notes/ Important Diagrams/ Fig 6.5

AI **Q. 12. (i) Describe the process of transcription in bacteria.**

(ii) Explain the processing the hnRNA needs to undergo before becoming functional mRNA in eukaryotes. U **[Outside Delhi Set-I, 2016]**

OR

Explain the process of transcription in a prokaryote. [Outside Delhi Comptt. 2017, Set - II]

Ans. (i) Bacteria transcription is the process in which messenger RNA transcripts of genetic material in bacteria are produced to be translated for the production of proteins. Bacterial transcription occurs in the cytoplasm alongside translation.

The process of transcription is completed in three steps : Initiation, elongation and termination.

(a) Initiation : The enzyme binds at the promoter site of DNA and initiates the process of transcription. It causes the local unwinding of the DNA double helix. An initiation sigma factor (σ) present in RNA polymerase initiates the RNA synthesis.

(b) Elongation : The RNA chain is synthesized in the 5′-3′ direction. RNA polymerase uses nucleoside triphosphate as substrate and polymerisation occurs according to complementarity.

(c) Termination : Termination occurs when termination factor (rho) alters the specificity of RNA polymerase to terminate the transcription. As the RNA polymerase proceeds to perform elongation, a short stretch of RNA remains bound to the enzyme. As the enzyme reaches the termination region, this nascent RNA falls off and transcription is terminated. **3**

(ii) The precursor of mRNA i.e. hnRNA contains both introns and exons. Introns are removed and exons are joined by a process called splicing. The remaining mRNA is processed in two ways :

(a) Capping : Here, an unusual nucleotide called methyl guanosine triphosphate (cap) is added to the 5′ end of hnRNA.

(b) Tailing : Here, adenylate residues (200-300) are added at 3′ end of hnRNA in a template independent manner.

When hnRNA is fully processed, it is known as mRNA, which is transported out of the nucleus to get translated. **2**

Commonly Made Error

- Students often write *replication* instead of *transcription*.
- They also get confused between *sense strand* and *anti-sense strand*. They forget to mention about 3′- 5′ or 5′- 3′
- Many students while explaining *capping* and *tailing*, forget to mention about *5-end* or *3-end*. Some students, when writing on *splicing*, mention only *removal of intron* without mentioning *followed by joining of exons*.

Q. 13. (a) State the 'Central dogma' as proposed by Francis Crick. Are there any exceptions to it ? Support your answer with a reason and an example.

(b) Explain how the biochemical characterisation (nature) of "Transforming Principle" was determined, which was not defined from Griffith's experiments. R **[Outside Delhi/Delhi, 2018]**

Ans. (b) Protein, DNA and RNA were purified from heat killed S strain / smooth *Streptococcus pneumonia* = ½

Protein + Protease → transformation occurred (R cell to S type) = ½

RNA + RNA ase → transformation occurred (R cell to S type) = ½

DNA + DNA ase → transformation inhibited = ½

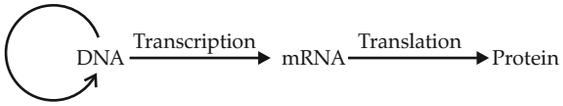
Hence DNA alone is the transforming material = ½

[2 + 3 = 5 marks]

[CBSE Marking Scheme, 2018]

Detailed Answer:

(a) Central dogma proposed by Francis Crick states that the genetic information flows from DNA to RNA through transcription and from RNA to proteins through translation.



Yes, there are some exceptions to this process. In some viruses, the genetic material is in the form of RNA. In such cases, the direction of genetic information flow is reversed. The RNA is first converted into DNA through the process of reverse transcription. The DNA thus formed follows the usual path of central dogma i.e. it is first transcribed into RNA, which is then translated into proteins.

An example of organism exhibiting reverse transcription is *Influenza* A virus.

(b) Biochemical characterization of transforming principle was discovered by Oswald Avery, Colin MacLeod and Maclyn McCarty

- They worked to determine the biochemical nature of 'transforming principle' in Griffith's experiment.
- They purified biochemicals (proteins, DNA, RNA etc.) from the heat killed S cells to see which one could transform live R cell into S cells.

Heat-killed S strain + Live R strain $\xrightarrow[\text{Digest RNA and proteins}]{\text{RNase, Proteases}}$

Transformation occurs Heat-killed S strain + Live R strain $\xrightarrow[\text{Digest RNA}]{\text{DNase}}$

Transformation does not occur and mouse survives.

They discovered that :

- DNA alone is transformed.
- Proteases and RNases did not affect transformation.
- Digestion with DNase inhibited transformation, suggesting that the DNA caused the transformation.

Thus, they concluded that DNA is the hereditary material. **2+3**

Q. 14. How does the flow of information in HIV deviate from the Central Dogma proposed by Francis Crick. E & A **[CBSE Foreign, 2013]**

Ans. According to Central Dogma of molecular biology, there is unidirectional flow of genetic information from DNA to m RNA and from here to protein.

$$\text{DNA} \xrightarrow[\text{Transcription}]{} \text{mRNA} \xrightarrow[\text{Translation}]{} \text{Proteins}$$

But in HIV (Human immuno-deficiency virus) there is central dogma reverse *i.e.* the flow of genetic information is in reverse direction. It is because the virus contains the genetic RNA and produces an enzyme **reverse transcriptase.** This enzyme helps to synthesize DNA from genetic RNA of HIV by a process called as **reverse** transcription or **Teminism**. This newly synthesized DNA functions as master copy producing mRNA through transcription & RNAs controlling translation to synthesize protein.

$$\text{RNA} \xrightarrow[\text{Transcription}]{\text{Reverse}} \text{DNA} \xrightarrow{\text{Transcription}} \text{mRNA} \xrightarrow{\text{Translation}} \text{Protein}$$

The phenomenon of reverse transcription was discovered by Temin & Baltimore (1970) in Retrovirus. **5**

TOPIC-2
Genetic Code, Translation, Lac Operon, Human Genome Project and DNA Fingerprinting

Revision Notes

- **Genetic Code** : It is the sequence of nucleotides in mRNA that contains information for protein synthesis (translation).
- There are 20 amino acids that are involved in translation.
  - **George Gamow :** Suggested that for coding 20 amino acids, the code should be made up of 3 consecutive nucleotides.
  - **Har Gobind Khorana :** Developed the chemical method in synthesizing RNA molecules with defined combinations of bases (homopolymers and co-polymers).
  - **Marshall Nirenberg :** Developed cell-free system for protein synthesis.
  - *Severo Ochoa* (polynucleotide phosphorylase) enzyme is used to polymerize RNA with defined sequences in a template independent manner.
- **Salient Features of Genetic Code**
  - The genetic code is a triplet code (three-letter code) where three adjacent nitrogen bases code for a single amino acid.
  - 61 codons code for amino acids. 3 codons (UAA, UAG and UGA) do not code for any amino acids. They function as stop codons (Termination codons or non-sense codons).
  - Genetic code is universal *e.g.* From bacteria to human UUU codes for Phenylalanine. Some exceptions are found in mitochondrial codons and in some protozoans.
  - No punctuations between adjacent codons (comma less code). The codon is read in mRNA in a continuous fashion.
  - Genetic code is non-overlapping.
  - A single amino acid is represented by many codons (except AUG for methionine and UGG for tryptophan). Such codons are called degenerate codons.
  - Genetic code is unambiguous and specific. *i.e.* one codon specifies only one amino acid.
  - The codon is read in 5' $\rightarrow$ 3' direction.
  - AUG has dual functions. It codes for Methionine (met) and also acts as initiator codon. In eukaryotes, *methionine* is the first amino acid and *formyl methionine* in prokaryotes.

- **Mutations and Genetic Code**
  - The relationships between genes and DNA are best understood by mutation studies.
  - Effects of large deletions and rearrangements in a segment of DNA may result in loss or gain of a gene and so a function.
  - A classical example of point mutation is a change of single base pair in the gene for beta globin chain of haemoglobin that results in the change of amino acid residue glutamate to valine. It results into a diseased condition called as sickle cell anaemia.
  - Insertion or deletion of one or two bases changes the reading frame from the point of insertion or deletion.
  - When there is shifting of the reading frame due to insertion or deletion of the nucleotide, such mutation is known as frame shift mutation.
  - This forms the genetic basis of proof that codon is a triplet and it is read in a contiguous manner.
- **The Adaptor Molecule – tRNA**
  - The tRNA is a molecule has about 60% of its part double stranded and the rest remains single stranded which has unpaired bases.
  - The tRNA has
    (a) An anticodon (NODOC) loop that has bases complementary to the CODON with which it gets attached in mRNA.
    (b) An amino acid acceptor end to which amino acid binds. This end or site lies at the 3' end & CCA–OH group. The 5' end bears G.
    (c) T Ψ C loop : This is the site for attaching with ribosome. This has some unusual bases like Ψ (pseudouridine) and ribothymidine.
    (d) DHU-Loop : It is the binding site for the enzyme aminoacyl synthetase. It is the largest loop and has Dihydrouridine.
    (e) Extra arm : It is a variable side arm lying between T Ψ C and anticodon loop.
  - tRNA is called adaptor molecule because it picks up amino acids from cytoplasm and transfers them to ribosomes during protein synthesis.
  - For initiation, there is another tRNA called initiator tRNA.
  - There are no tRNAs for stop codons.
  - 2-D structure of tRNA looks like a clover-leaf according to Robert Holly (1965). 3-D structure looks like inverted 'L' according to Klug (1974).
- **Translation – Protein Synthesis**

  It takes place in ribosomes. It includes 4 steps :

  1. **Charging of tRNA (aminoacylation of tRNA)**
     - Formation of peptide bond requires energy obtained from ATP.
     - For this, amino acids are activated (amino acid + ATP) and linked to their cognate tRNA in the presence of *aminoacyl tRNA synthetase*. So, the tRNA becomes charged.
  2. **Initiation**
     - It begins at the 5'-end of mRNA in the presence of an *initiation factor*.
     - The mRNA binds to the small subunit of ribosome. Now the large subunit binds to the small subunit to complete the initiation complex.
     - Large subunit has 2 binding sites for tRNA- aminoacyl tRNA binding site (A site) and peptidyl site (P site).
     - Initiation codon for methionine is AUG. So,methionyl tRNAcomplex would have UAC at the Anticodon site.
  3. **Elongation**
     - At the P-site the first codon of mRNA binds with anticodon of methionyl tRNA complex.
     - Another aminoacyl tRNA complex with an appropriate amino acid enters the ribosome and attaches to A site.
     - Its anticodon binds to the second codon on the mRNA and a peptide bond is formed between first and second amino acids in presence of an enzyme, *peptidyl transferase*.
     - The uncharged tRNA moves from P site to E site and the peptidyl-tRNA moves to the P site. This is called translocation.
     - Then 3rd codon comes into A site and a suitable tRNA with 3rd amino acid binds at the A site. This process is repeated.
     - A group of ribosomes associated with a single mRNA for translation is called a polyribosome (polysomes).
     - A ribozyme is a ribonucleic acid (RNA) enzyme that entalyses a chemical reaction. The ribozyme catalyses specific reactions in a similar way to that of *protein synthesis*. Also called catalytic RNA, ribozyme are found in ribosome where they join amino acids together to form *protein* chains.

4. Termination

- When aminoacyl tRNA reaches the termination codon like UAA, UAG & UGA, the termination of translation occurs. The polypeptide and tRNA are released from the ribosomes.
- The ribosome dissociates into large and small subunits at the end of protein synthesis.

A mRNA has additional sequences that are not translated (untranslated regions or UTR). UTRs are present at both 5′-end (before start codon) and 3′-end (after stop codon). They are required for efficient translation process.

➢ **Regulation of Gene Expression**

Gene expression results in the formation of a polypeptide. In eukaryotes, the regulation includes the following levels:

- Transcriptional level (formation of primary transcript).
- Processing level (regulation of splicing).
- Transport of mRNA from nucleus to the cytoplasm.
- Translational level.

➢ **Importance of regulation of gene expression:**

- Gene regulation is the process to switch off or switch on the genes as per the requirement of the organism.
- Gene regulation is required so that there is no waste of energy in expressing the genes not required at the time.
- However, there are housekeeping genes which are always expressed in the cell.

The metabolic, physiological and environmental conditions regulate expression of genes. *E.g*.

- In *E. coli*, the enzyme *beta-galactosidase* hydrolyses lactose into galactose and glucose. In the absence of lactose, the synthesis of beta-galactosidase stops.
- The development and differentiation of embryo into adult are result of the regulation of several set of genes.

➢ **Operon Concept :** This is a regulatory system that is observed in bacteria.

- "Each metabolic reaction is controlled by a set of genes" .
- All the genes regulating a metabolic reaction constitute an *Operon E.g. lac* operon, *trp* operon, *ara* operon, *his* operon, *val* operon etc.
- When a substrate is added to growth medium of bacteria, a set of genes is switched on to metabolize it. This is called induction.
- When a metabolite (product) is added, the genes to produce it are turned off. This is called repression.

➢ **The Lac Operon**

- **Lac operon in *E. coli* :** The operon controlling lactose metabolism. It consists of a regulator gene, 3-structural genes, an operator gene, promoter gene, a repressor and an inducer.

  (a) A regulatory or inhibitor (i) gene : Codes for the repressor.

  (b) 3 structural genes :

  (i) z gene : Codes for β-*galactosidase* (hydrolyze lactose to galactose and glucose).

  (ii) y gene : Codes for *permease* (increase permeability of the cell to lactose).

  (iii) a gene : Codes for a *transacetylase*.
- The genes present in the operon function together in the same or related metabolic pathway. There is an **operator** region for each operon.
- If there is no lactose (inducer), lac operon remains switched off. In the absence of inducer, repressor gene is active. The regulator gene synthesizes mRNA to produce the **repressor protein**, this protein binds to the operator genes and blocks RNA polymerase movement. So the structural genes are not expressed.
- In the absence of glucose, If lactose is provided in the growth medium, the lactose is transported into the *E. coli* cells by the action of permease. Lactose (inducer) binds with repressor protein.
- So, repressor protein cannot bind to **operator gene**. The operator gene becomes free and induces the RNA polymerase to bind with **promoter gene** then transcription starts. Regulation of lac operon by repressor is called negative regulation.

➢ **Human Genome Project (HGP)**

- The entire DNA in the haploid set of chromosome of an organism is called a Genome.
- In Human genome, DNA is packed in 23 chromosomes.
- Human Genome Project (1990-2003) is the first effort in identifying the sequence of nucleotides and mapping of all the genes in human genome.
- Human genome contains about 3×10^9 bp.

- **Goals of HGP**
  - **(a)** To identify all the estimated genes in human DNA.
  - **(b)** To determine the sequences of the 3 billion chemical base pairs that make up human DNA.
  - **(c)** To store this information in databases.
  - **(d)** To improve tools for data analysis.
  - **(e)** To transfer related technologies developed during the project of society to other sectors of society.
  - **(f)** To address the ethical, legal and social issues (ELSI) that may arise from the project.
- **HGP was Closely Associated with Bioinformatics**
  Application of computer science and information technology to the field of biology and medicine helps in analyzing DNA sequence data.
- **Methodologies of HGP**
  There are two major approaches namely, ESTs and sequence annotation.
  - **Expressed Sequence Tags (ESTs) :** Focused on identifying all the genes that are expressed as RNA and sequencing the same.
  - **Sequence annotation :** Sequencing whole set of genome containing all the coding & non-coding regions and later assigning functions to different regions.
- **Procedure :**
  Isolate total DNA from a cell → Convert into random fragments of smaller size → Clone in suitable host (*e.g.* BAC – bacterial artificial chromosomes & YAC – yeast artificial chromosomes) for amplification through PCR (polymerase chain reaction) → Fragments are sequenced using Automated DNA sequencers (using Frederick Sanger method) → Sequences are arranged based on the overlapping regions → Alignment of sequences using computer based programs → Genetic and physical maps on the genome were generated using information on polymorphism of restriction endonuclease recognition sites and some repetitive DNA sequences (micro-satellites).
- **Salient Features of Human Genome**
  - **(a)** Human genome contains 3164.7 million nucleotide bases pairs.
  - **(b)** Total number of genes = about 25,000.
  - **(c)** Average gene consists of 3000 bases, but sizes vary. Largest known human gene (dystrophin on X-chromosome) contains 2.4 million bases.
  - **(d)** 99.9% nucleotide bases are identical in all people. It is 0.1% what makes each of us unique.
  - **(e)** Functions of over 50% of discovered genes are unknown.
  - **(f)** Chromosome I has most genes (2968) and Y has the fewest (231).
  - **(g)** Less than 2% of the genome codes for proteins.
  - **(h)** Repeated sequences make up very large portion of human genome. Repetitive sequences are stretches of DNA sequences that are repeated many times. They have no direct coding functions but they shed light on chromosome structure, dynamics and evolution.
  - **(i)** About 1.4 million locations where single-base DNA differences (SNPs- Single nucleotide polymorphism or 'snips') occur in humans.
- **DNA Fingerprinting (DNA profiling)**
  - It is the technique to compare the DNA fragments of two individuals.
  - Developed by **Alec Jeffreys (1985)**. He is considered as the father of DNA finger printing. Lalji Singh is the Father of Indian DNA finger printing.
- **Basis of DNA Fingerprinting**
  - DNA carries some non-coding sequences called repetitive sequence [Variable Number Tandem Repeats (VNTR)].
  - Number of repeats is specific. It varies from person to person and is specific to a person.
  - The size of VNTR varies from 0.1 to 20 kb.
  - Repetitive DNA are separated from bulk genomic DNA as different peaks during density gradient centrifugation.
  - The bulk DNA forms a major peak and the other small peaks are called as satellite DNA.
  - Satellite DNA is classified into many categories (micro-satellites, mini-satellites etc) based on base composition (A : T rich or G : C rich), length of segment and number of repetitive units.
  - An inheritable mutation observed in a population at high frequency is called DNA polymorphism (variation at genetic level).
  - Polymorphism is higher in non-coding DNA sequence. This is because mutations in these sequences may not have any immediate effect in an individual's reproductive ability.
  - These mutations accumulate generation after generation and cause polymorphism. For evolution & speciation, polymorphisms play important role.
- **Steps of DNA Fingerprinting (Southern Blotting Technique)**
  - **(a)** Isolate DNA (from any cells like blood stains, semen stains or hair roots).
  - **(b)** Make copies (amplification) of DNA by Polymerase Chain Reaction (PCR) if the amount of isolated DNA is small.

(c) Digest DNA by restriction endonucleases.
(d) Separate DNA fragments by gel electrophoresis over agarose polymer gel.
(e) Treat with alkali solution (NaOH) to denature DNA bonds so as to split them into single stranded DNAs in the gel.
(f) Transfer (blotting) single stranded DNA fragments to synthetic membranes such as nitrocellulose or nylon, and then baked in a vacuum oven at 80°C for 3-5 hours (to fix the DNA fragment on the membrane).
(g) Nitrocellulose filter membrane is placed in a solution containing radioactive labelled single stranded DNA probe. The DNA probes are small radio active synthetic DNA segments of known sequences of nitrogen bases. These DNA probe binds with the complimentary sequences of the DNA fragment on the membrane to form a hybridized DNA.
(h) The filter paper is washed to remove unbound probe.
(i) The hybridized DNA is photographed on to an X-ray film by autoradiography. The image (in the form of dark & light bands) obtained is called DNA fingerprint. This gives the characteristic pattern of an individual's DNA.

➢ **Applications of DNA Fingerprinting are:**
- Forensic tool to solve paternity, rape, murder, etc.
- For the diagnosis of genetic diseases.
- To determine phylogenetic status of animals.

IMPORTANT DIAGRAMS:

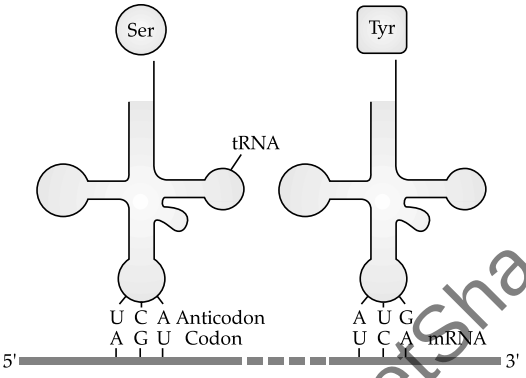


Fig 6.1: tRNA- the adaptor molecule

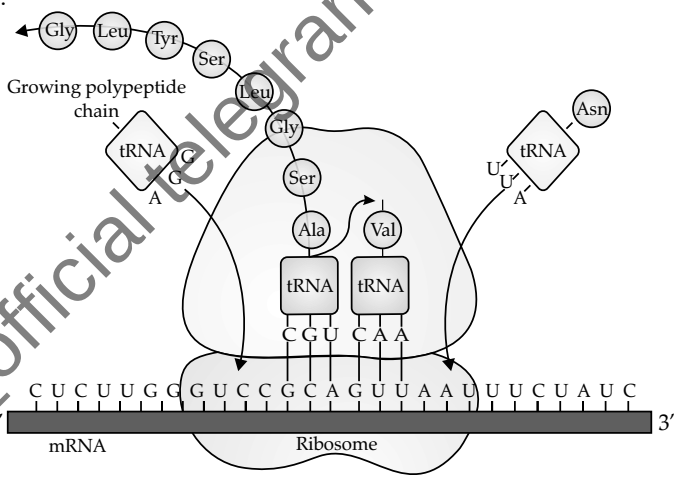


Fig 6.2: Translation

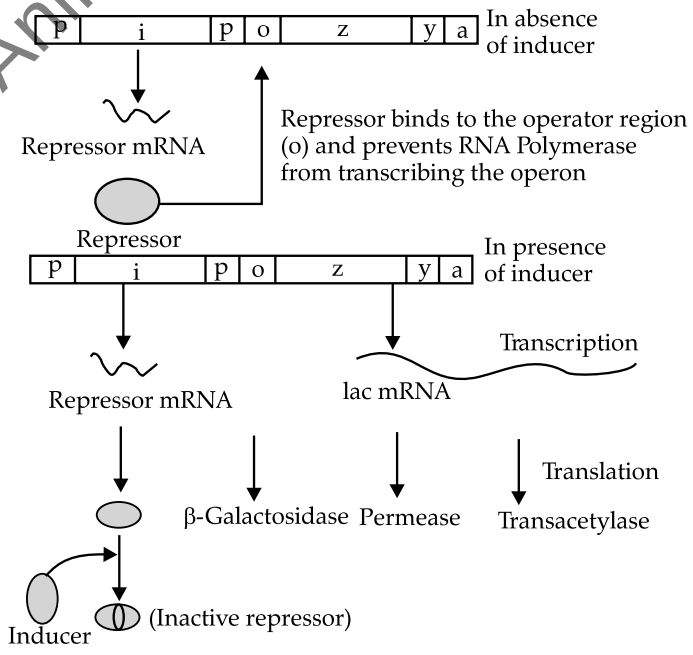


Fig 6.3: The Lac Operon

Very Short Answer Type Questions (1 mark each)

Q. 1. Mention two applications of DNA-polymorphism.
A [Foreign Set-I-2016]

Ans. Genetic mapping & DNA-finger printing. **1**

Q. 2. Mention the contribution of genetic maps in human genome project. **A [Delhi Set-I, 2011]**

Ans. Sequencing of genes, DNA finger printing, tracing human history, chromosomal location for disease associated sequences. **(Any one) 1**
[CBSE Marking Scheme, 2011]

Q. 3. State which human chromosome has
(i) The maximum number of genes and
(ii) The one which has the least number of genes.
A [Foreign 2011]

Ans. **(i)** Chromosome no. 1 : 2968 genes
(ii) Y chromosomes : 231 genes **1**

AI Q. 4. Mention the role of the codons AUG and UGA during protein synthesis.
[Outside Delhi Set-I, 2011]

Ans. AUG – codes for methionine / initiation codon.
UGA – termination codon / stop codon. ½ + ½
[CBSE Marking Scheme, 2011]

Answering Tip
- Role of codons during protein synthesis should be properly learnt.

Short Answer Type Questions-I (2 marks each)

Q. 1. Following are the features of genetic codes. What does each one indicate ? Stop codon, Unambiguous codon, Degenerate codon, Universal codon.
U [Outside Delhi Set-I, 2016]

Ans. The features of genetic code are :
(i) Stop codon : does not code for any amino acid / terminates the synthesis of polypeptide chain.
(ii) Unambiguous codon : one codon codes for one amino acid only.
(iii) Degenerate codon : some amino acid are coded by more than one codon.
(iv) Universal codon : genetic code is same for all organisms (bacteria to humans). **½ × 4 = 2**
[CBSE Marking Scheme, 2016]

Detailed Answer :

The features of genetic codes are :

(i) Stop codon : Termination codons or stop codons are UAA, UAG and UGA. They do not code for any amino acids. They represent termination of translation.

(ii) Unambiguous codon : The genetic code is specific and non-ambiguous *i.e.* one codon specifies only one amino acid.

(iii) Degenerate codon : This indicates that a single amino acid is represented by more than one codons.

(iv) Universal codon : This indicates that one codon codes for the same amino acid in all species. From bacteria to human, UUU codes for phenyl alanine. **½ × 4 = 2**

Commonly Made Error
- Students often get confused between terms like unambiguous, degenerate, universal etc.

Q. 2. What is aminoacylation ? State its significance.
R [Outside Delhi Set-II, 2016]

Ans. Amino acids are activated in the presence of ATP and linked to (cognate) t-RNA.
Carries amino acid to the site of synthesis/reaches amino acids to the respective codon.
[CBSE Marking Scheme, 2016] 1 + 1

Detailed Answer :

Aminoacylation is the process of adding an activated amino acid to the acceptor arm of a transfer RNA.

It is an essential step for the synthesis of protein as it activates the amino acids (amino acid + ATP) and helps in linking them to their cognate tRNA in the presence of an enzyme aminoacyl tRNA synthetase.
1+1=2

AI Q. 3. Differentiate between the features of genetic code given below :

(a) Unambiguous and Universal

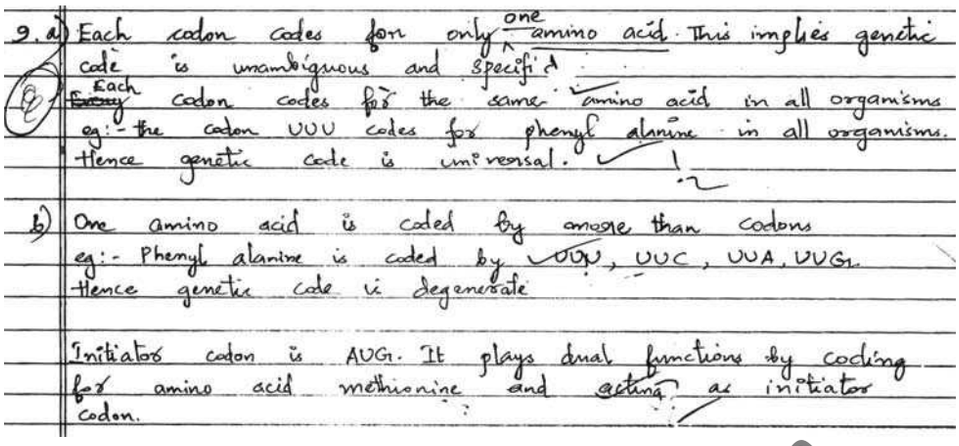
(b) Degenerate and Initiator

A [Outside Delhi, 2017, Set - I, II, III]

Ans.

(a)	Unambiguous :	Universal :
	One codon codes for only one amino acid	Genetic code or codons are (nearly) same for all organisms or from bacteria to human
(b)	**Degenerate :**	**Initiator :**
	More than one codon code for the same amino acid.	Start codon or AUG

OR



[Topper's Answer, 2017]

Q. 4. State the roles of AUG codon at 5' end and UAG at 3' end of a certain m-RNA during translation.

R **[Delhi Comptt. - 2017, Set-I, II, III]**

Ans. AUG codon at 5' end = Start codon (for translation)/codes for methionine. **1**
UAG codon at 3' end = Stop codon (for translation)/terminate polypeptide chain. **1**
[CBSE Marking Scheme, 2017]

Detailed Answer :

AUG has dual functions. It codes for Methionine (met) and it also act as initiator codon.

UAG codon functions as stop codon.

Answering Tip

- Students are advised to learn the initiation and termination codons in tabular form for easy understanding and retention.

Q. 5. 'Degenerate' and 'Universal' are salient features of a genetic code. Explain.

A **[Delhi Comptt. 2017, Set-I, II, III]**

Ans. **Degenerate :** Same amino acids are coded by more than one codon. **1**
Universal : One codon shall code for the same amino acid in all organisms (UUU would code for phenylalanine from bacteria to human beings). **1**
[CBSE Marking Scheme, 2017]

Commonly Made Error

- Students often get confused between the technical terms of genetic code. For 'degenerate' instead of writing 'same amino acids coded by more than one codon', they write 'one codon specifies only one amino acid'.

Answering Tip

- Carefully learn all the features of genetic code with the help of suitable examples.

Q. 6. One of the salient features of the genetic code is that it is nearly universal from bacteria to humans. Mention two exceptions to this rule. Why are some codons said to be degenerate ?

A **[Foreign Set-III, 2014]**

Ans. **(i)** Mitochondrial codons. ½
(ii) Some protozoans. ½
Since some amino acids are coded by more than one codon hence it is called as degenerate. **1**
[CBSE Marking Scheme, 2014]

Detailed Answer :

(i) The genetic code is universal except in mitochondria and some protozoans. For example, codon UAA and UGA are termination codons. They do not code for any amino acid but in *Paramaecium* and a few other ciliates, these codons code for glutamine. Similarly, in yeast mitochondria the codon UGA codes for tryptophan instead of its general terminating character in nuclear genes. The codon AUA codes for isoleucine in nuclear gene but it codes for methionine in mammalian mitochondria.

(ii) When more than one codon code for a single amino acid, it is said to be degenerate codon *e.g.* UUU and UUC code for amino acid phenyl alanine.

Q. 7. Where does peptide bond formation occur in a bacterial ribosome and how ? R **[Foreign 2014]**

Ans. Between the two amino acids (found on charged tRNA), bound to the two sites of the large sub units of bacterial ribosomes, when two charged tRNAs are brought close enough, peptide bond is formed with the help of ribozyme. **½ × 4 =2**
[CBSE Marking Scheme, 2014]

Detailed Answer :

A peptide bond (–CO–NH–) is formed between carboxyl group (–COOH) of amino acid attached to tRNA at P site and amino group ($–NH_2$) attached to tRNA at A-site in presence of enzyme peptidyl transferase, in large subunit of ribosome. The aminoacyl tRNA complex reach the A site and attaches to mRNA codon with the help of its anticodon and then the peptide bond is formed between amino acids found on charged tRNA.

Q. 8. (i) Name the scientist who suggested that the genetic code should be made of a combination of three nucleotides.

(ii) Explain the basis on which he arrived at this conclusion. R **[Delhi Set-I, 2014]**

Ans. (i) George Gamow. ½

(ii) There are four bases and 20 amino acids. ½

(There should be atleast 20 different genetic codes for these 20 amino acids).

Only possible combinations that would meet the requirement in combinations of 3 bases that will give 64 codons. **[CBSE Marking Scheme, 2014]** 1

Detailed Answer :

(i) George Gamow suggested that the genetic code should be made of a combination of three nucleotides.

(ii) There are four types of nitrogenous bases in DNA while the number of amino acids used in protein synthesis is 20. If the code is singlet *i.e.* consisting of only one nucleotide, this will provide only 4 codons, *viz.* A, C, G and U/T which are insufficient to code for 20 amino acids. Similarly a combination of two nitrogen bases (doublet codon) will provide $4 \times 4 = 16$ codons which are still insufficient for 20 amino acids. Gamow (1954) suggested that the code should be a triplet *i.e.* made up of different combination of three nucleotides. This will give $4 \times 4 \times 4 = 64$ codons which are more than enough to code 20 amino acids.

Q. 9. Write the full form of VNTR. How is VNTR different from 'Probe' ? U **[Delhi Set-I, 2011]**

Ans. VNTR – Variable Number Tandem Repeats. **1**

Probe – is labelled / radio active (single stranded hybridised DNA fragments). **1**

[CBSE Marking Scheme, 2011]

Detailed Answer :

(i) Full form of VNTR is Variable Number of Tandem Repeats.

(ii) VNTR are short nucleotide repeats in DNA which vary in number in different individuals but specific to each individual. while DNA probes are radioactive, labelled, DNA fragments having repeated base sequence complementary to VNTRs.

Q. 10. Why does the lac operon shut down some time after the addition of lactose in the medium where *E.coli* was growing? Why low level expression of lac operon is always required?

U **[CBSE, SQP, 2018]**

Ans. After addition of lactose, complete breakdown of lactose to glucose and galactose takes place. Therefore, there is no more lactose to bind to the repressor protein and the lac operon shuts down. **1**

A very low level of expression of *lac* operon has to be present in the cell all the time, otherwise lactose cannot enter the cells. **1**

[CBSE Marking Scheme, 2018]

Short Answer Type Questions-II

(3 marks each)

AI **Q. 1. Where is an 'operator' located in a prokaryote DNA ? How does an operator regulate gene expression at transcriptional level in a prokaryote ? Explain.** A **[Foreign Set-III, 2016]**

Ans. The operator region is located adjacent to promoter elements / prior to structural gene.

In regulation of gene expression :

switch off - the repressor binds to the operator region and prevents transcription.

switch on - In the presence of inducer the repressor is inactivated (by the interaction with the inducer), operator allows RNA polymerase access to the promoter and transcription proceeds. **1+2**

[CBSE Marking Scheme, 2016]

Commonly Made Error

- Students write function instead of location. Carefully read the question.

Answering Tips

- Comprehend what is being asked before beginning to write your answers.
- Instead be specific about the key word in that statement.

Q. 2. (i) How many codons code for amino acids and how many are unable to do so ?

(ii) Why are codes said to be (i) degenerate and (ii) unambiguous ? A **[Delhi Set I & II, Comptt. 2016]**

Ans. (i) Sixty one, Three.

(ii) (a) Degenerate—One amino acid may be coded by several codons.

(b) Unambiguous or specific—Each codon codes for a specific amino acid. **3**

[CBSE Marking Scheme, 2016]

Detailed Answer :

(i) There are on the whole 64 codons which are of triplet nature. Out of which 61 codons code for amino acids and 3 codons (UAA, UGA & UAG) do not code for any amino acid. They act as stop codons or terminating codons.

(ii) The code is said to be degenerate because some of the amino acids are coded by more than one codons. The code is said to be ambiguous because it is specific *i.e.* one codon codes for only one particular amino acid.

Q. 3. Write any three goals of Human Genome Project.

R **[Outside Delhi Set I & II Comptt. 2016]**

Ans. The three main goals of HGP are :

(i) To determine the sequences of 3 billion base pairs that make up the human DNA.

(ii) To identify all the estimated genes in human DNA.

(iii) To store this information in databases. **3**

Q. 4. (i) What do 'Y' and 'B' stand for in 'YAC' and 'BAC' used in Human Genome Project (HGP). Mention their role in the project.

(ii) Write the percentage of the total human genome that codes for proteins and the percentage of discovered genes whose functions are known as observed during HGP.

(iii) Expand 'SNPs' identified by scientists in HGP.

R **[Outside Delhi Set-I, 2016]**

Ans. (i) Y = Yeast ½

B = Bacterial ½

Used as vector for cloning foreign DNA ½

(ii) (<) 2% , (<) 50%. ½ + ½ = **1**

(iii) Single Nucleotide Polymorphism ½

[CBSE Marking Scheme, 2016]

Detailed Answer :

(i) YAC (Yeast Artificial Chromosomes) and BAC (Bacterial Artificial chromosomes) are cloning vectors. They are used in Human genome project for cloning or amplification of human DNA fragments.

(ii) Total number of genes (coding for protein) in the human genome is 30,000 which is less than 2% of the total genome and almost 50% of the discovered genes have unknown functions.

(iii) SNPs stand for Single Nucleotide Polymorphism.

1+1+1=3

Commonly Made Error

- While writing full form of BAC, instead of 'Bacterial', students write Bacteria. Similarly, they write incorrect expansion for SNPs.

Answering Tip

- Expansion of abbreviations should be practiced carefully.

AI **Q. 5. Following the collision of two trains a large number of passengers are killed. A majority of them are beyond recognition. Authorities want to hand over the dead to their relatives. Name a modern scientific method and write the procedure that would help in the identification of kinship.**

C **[Outside Delhi Set-I, 2015]**

Ans. DNA fingerprinting is used for identification of kinship.

Procedure :

(i) Variable number of tandem repeats (VNTR's) are satellite DNA's that show high degree of polymorphism. They are used as probes in DNA fingerprinting.

(ii) Fragments of DNA from an individual are isolated and cut with restriction endonucleases.

(iii) Fragments are separated according to their size and molecular weight through gel electrophoresis.

(iv) Fragments separated through electrophoresis gel are blotted (immobilised) on a synthetic membrane such as nylon or nitrocellulose.

(v) Immobilised fragments are hybridised with a VNTR probe.

(vi) Hybridised DNA fragments can be detected by autoradiography.

(vii) VNTRs are different in size, ranging from 0.1 to 20 kb. Hence, in the autoradiogram, a band of different sizes will be obtained.

(viii) These bands are the characteristic feature of an individual. They are different in each and every individual except identical twins.

[CBSE Marking Scheme, 2015] 3

Commonly Made Error

- Students forget to write certain keywords like VNTR and RFLP.
- They are aware of the applications of DNA fingerprinting but not of its technique.

Q. 6. Given below are the sequence of nucleotides in a particular mRNA and amino acids coded by it :

UUU AUG UUC GAG UUA GUG UAA

Phe –Met –Phe –Glu –Leu –Val

Write the properties of the genetic code that can be and that cannot be correlated from the above given data. E & A **[Delhi Set-I, Comptt. 2013]**

Ans. Properties of genetic code that can be correlated are:

(i) The codon is a triplet *e.g.* UUU, AUG etc. They form triplets.

(ii) One codon codes for only one amino acid and not other hence it is unambiguous and specific.

(iii) AUG has a dual function as it codes for methionine and also acts as the initiator codon.

(iv) UAA is the stop codon. It codes for valine.

(v) Code is commaless, continuous and does not have pauses.

(vi) The sequence of triple N-bases in mRNA corresponds to the sequence of amino-acids in a polypeptide.

Property that cannot be correlated is that mostly AUG work as an initiating codon. **3**

Q. 7.

i	p	o	z	y	a

Given above is the schematic representation of lac operon of *E. coli.* Explain the functioning of this operon when lactose is provided in the growth medium of the bacteria.

A **[Delhi Set-I, Comptt. 2013]**

OR

A considerable amount of lactose is added to the growth medium of *E.coli.* How is the lac operon switched on in the bacteria ? Mention the state of the operon when lactose is digested.

[Outside Delhi Comptt. 2010]

Ans. An operon is a part of genetic material (or DNA), which acts as a single regulated unit of one or more

structural genes, an operator gene, a promotor gene, a regulator gene, a repressor and an inducer or compressor.

For Diagram: Refer Topic 2/ Revision Notes/ Important Diagrams/ Fig 6.3

In lac operon, when lactose is added, it enters the cell with the help of permease, a small amount of which is already present in the cell. Lactose binds itself to active repressor and changes its structure. The repressor now fails to bind to the operator. Then RNA polymerase starts transcription of operon by binding to the promoter site P. All the three enzymes for lactose metabolism are synthesized. Finally all the lactose molecules are used up in the whole process of induction. It can be understood by the above mentioned figure.

After sometime, when the whole lactose is consumed, there is no inducer present to bind to the repressor. Then the repressor becomes active again, attaches itself to the operator and finally switches off the operon. **1½ + ½= 3**

Answering Tip

- While learning Lac- operon, discuss its each component individually with the function. Also, discuss the working of Lac-operon in the presence of lactose and in its absence.

Q. 8. How are the structural genes activated in the lac operon in *E. coli* ?

U **[Outside Delhi Set-II, 2012]**

Ans. Lactose acts as the inducer, binds with repressor protein, frees operator gene, RNA polymerase freely moves over the structural genes, transcribing lac mRNA, which in turn produces the enzymes responsible for the digestion of lactose.

A complete labelled diagram depicting the concept can be evaluated in lieu of explanation. **3**

[CBSE Marking Scheme, 2012]

Detailed Answer: Refer LAQ/ Q. 10

Q. 9. Unambiguous, universal and degenerate are some of the terms used for the genetic code. Explain the salient features of each one of them.

U **[Delhi Set-I, 2011]**

Ans. **Unambiguous** – One codon codes for one amino acid = *e.g.* AUG (methionine). **½ + ½**

Universal – Codon and its corresponding amino acid are the same in all organisms. **½**

Example : Bacteria to human UUU codes for phenylalanine (phe). **½**

Degenerate – Some amino acids are coded by more than one codon. **½**

Example : UUU and UUC code for phenylalanine(phe). **½**

[CBSE Marking Scheme, 2011]

Detailed Answer :

Unambiguous code means that one codon codes for only one amino acid *e.g.* AUG codes for only methionine.

Universal code means that codon and its corresponding amino acid are the same in all organisms *e.g.* from bacteria to human, UUU codes for phenylalanine.

Degenerate code means that some amino acids are coded by more than one codon *e.g.* UUU and UUC code for phenylalanine. **3**

AI **Q. 10. Differentiate between the following :**

(i) Promoter and terminator in a transcription unit.

(ii) Exon and intron in an unprocessed eukaryotic mRNA.

(iii) Inducer and repressor in lac operon.

U **[Delhi Set-I, II, III, Comptt. 2011]**

Ans. **(i) Promotor and terminator in a transcription unit :** Promoter is located towards 5′ end while terminator is located towards 3′ end.

(ii) Exon and intron in an unprocessed eukaryotic mRNA :

Exon : The coding sequences or expressed sequences are defined as exons. Exons are said to be those sequences that appear in mature or processed RNA.

Introns : The exons are interrupted by introns. Introns or intervening sequences that do not appear in mature or processed RNA.

(iii) Inducer and repressor in lac operon :

Inducer : Lactose is the substrate for the enzyme beta-galactosidase and it regulates switching on and off of the operon. It is termed as Inducer.

Repressor : The repressor of the operon is synthesized (all the time constitutively) from the gene. The repressor protein binds to the operator region of the operon and prevents RNA polymerase from transcribing the operon. **1 × 3 = 3**

Answering Tips

- Differences when asked should be compatible.
- Answers should be specific and precise. Answers like present and not present are not acceptable.
- Emphasize on precise answer using correct keywords.

Q. 11. (i) Name the scientist who called tRNA an adapter molecule.

(ii) Draw a clover leaf structure of tRNA showing the following :

(a) tyrosine attached to its amino-acid site

(b) anticodon for this amino acid in its correct site (codon for tyrosine is UCA)

(iii) What does the actual structure of tRNA look like ?

R **[Outside Delhi Set-I, II, III, 2011; Outside Delhi Comptt. 2010]**

Ans. **(i)** Francis Crick called t-RNA an adapter molecule.

(ii) For diagram: Refer Topic 2/ Revision Notes/ Important diagrams/ Fig 6.1

(iii) t-RNA—The actual structure of tRNA looks like a clover leaf having four arms/loops viz: the acceptor arm, ribosomal binding arm, anticodon loop and

DHU arm. This clover leaf model of tRNA was proposed by Robert Holley in 1968.

According to Kim (1973), the adapter molecule looks like an L-shaped structure. This is 3-dimensional and is known as the L-shaped model of tRNA.

1 × 3 = 3

Answering Tips

- Learn names of scientists with correct spelling.
- Importance must be given to drawing accurate, neat and labelled diagrams.

Q. 12. (i) List the structural genes involved in the digestion of lactose in *E.coli.* Highlight the function of any one.

(ii) What triggers the transcription of these genes ?

R **[Outside Delhi Set-II, Comptt. 2010]**

Ans. **(i)** There are three structural genes (z, y, a) which transcribes a polycistronic mRNA.

(a) Gene z codes β-galactosidase (β-gal), which catalyses the hydrolysis of lactose into galactose and glucose.

(b) Gene y codes for permease, which increases the permeability of the cell to β-galactosidase (lactose).

(c) Gene a codes for transacetylase, which catalyses the transacetylation of lactose into its active form.

(ii) RNA polymerase triggers the transcription of these genes. **2 + 1 = 3**

Q. 13. A criminal blew himself up in a local market when he was chased by cops. His face was beyond recognition. Suggest and describe a modern technique that can help establish his identity.

C **[Delhi, 2017, Set-II]**

OR

A number of passengers were severely burnt beyond recognition during a train accident. Name and describe a modern technique that can help establish their identity.

[Delhi, 2017, Set-I]

OR

During a fire in an auditorium a large number of assembled guests got burnt beyond recognition. Suggest and describe a modern technique that can help hand over the dead to their relatives.

[Delhi, 2017, Set-III]

Ans. DNA finger printing **1**

Isolation of DNA and digestion of DNA by restriction endonucleases, separation of DNA fragments by gel electrophoresis and transferring (blotting) of separated DNA fragments to synthetic membrane or nitrocellulose or nylon, hybridization using VNTR probe and detection of hybridised DNA fragments by autoradiography, matching the banding pattern so obtained with that of relative. **½ × 4**

[CBSE Marking Scheme, 2017]

Detailed Answer :

DNA fingerprinting is the technique of determination of nucleotide sequence of certain areas of DNA, which are unique to each individual.

Step/Procedure in DNA Fingerprinting :

(i) Extraction of DNA — using high speed refrigerated centrifuge.

(ii) Amplification — many copies are made using PCR.

(iii) Restriction Digestion → using restriction enzymes DNA is cut into fragments.

(iv) Separation of DNA fragments → using electrophoresis agarose polymer gel.

(v) Southern Blotting → Separated DNA sequences are transferred to nitrocellulose or nylon membranes.

(vi) Hybridization → The nylon membranes exposed to radioactive probes.

(vii) Autoradiography → The dark bands develop at the probe site.

(viii) Matching the banding pattern so obtained with that of relative.

Commonly Made Error

- Students get confused and write procedure in incorrect sequence.

Answering Tip

- Use chart to learn the procedure of DNA fingerprinting in correct sequence.

Q. 14. (i) List the two methodologies which were involved in human genome project. Mention how they were used.

(ii) Expand 'YAC' and mention what was it used for.

A **[Outside Delhi - 2017, Set - I]**

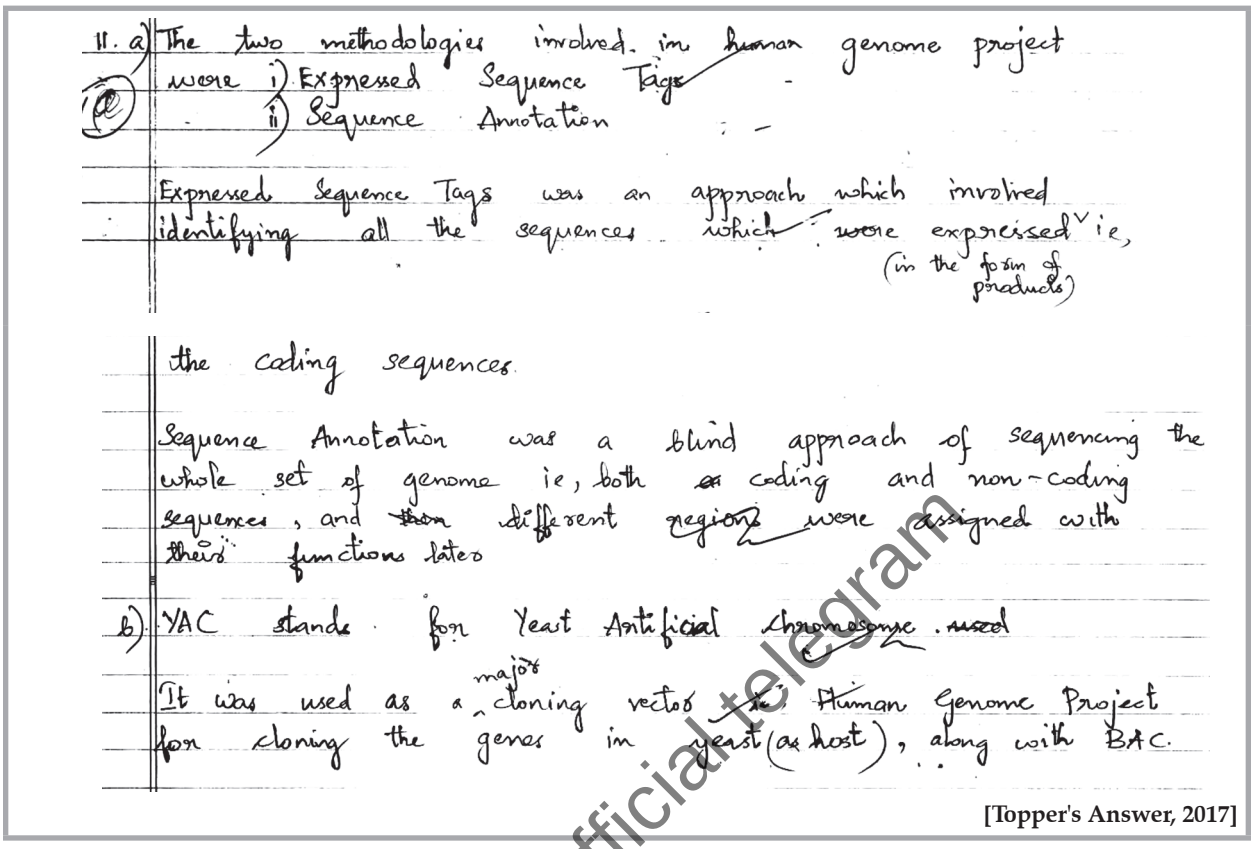
Ans. **(i)** Expressed Sequence Tags, Identifying the genes that are expressed as RNA. **½ + ½**

Sequence Annotation, sequencing the whole set of genome coding or non coding sequences and later assigning different region with functions. **½ + ½**

(ii) Yeast Artificial Chromosome, used as cloning vectors (cloning / amplification). **½ + ½**

[CBSE Marking Scheme, 2017]

OR


11. a) The two methodologies involved in human genome project were i) Expressed Sequence Tags
ii) Sequence Annotation

Expressed Sequence Tags was an approach which involved identifying all the sequences which were expressed ie, (in the form of products) the coding sequences.

Sequence Annotation was a blind approach of sequencing the whole set of genome ie, both coding and non-coding sequences, and different regions were assigned with their functions later.

b) YAC stands for Yeast Artificial Chromosome. used

It was used as a major cloning vector in Human Genome Project for cloning the genes in yeast (as host), along with BAC.

[Topper's Answer, 2017]

Q. 15. (a) Explain VNTR and describe its role in DNA fingerprinting.

(b) List any two applications of DNA fingerprinting technique.

A **[Outside Delhi/Delhi, 2018]**

Ans. (a) VNTR-(i) Variable Number of Tandem Repeats. ½

(ii) used as a probe (because of its high degree of polymorphism). ½

(b) Forensic science / criminal investigation (any point related to forensic science) / determine population and genetic diversities / paternity testing / maternity testing / study of evolutionary biology.

(Any two) 1+1

[CBSE Marking Scheme, 2018]

Long Answer Type Questions

(5 marks each)

AI **Q. 1. (i) Explain the role of regulatory gene, operator, promoter and structural genes in lac operon when *E. coli* is growing in a culture medium with the source of energy as lactose.**

(ii) Mention what would happen if lactose is withdrawn from the culture medium.

U **[Delhi Set-III, Comptt. 2016]**

Ans. (i) Regulatory gene : codes for repressor of lac operon. **1**

Operator : Provides site for binding of repressor protein to prevent transcription. **1**

Promoter : Provides site for binding of RNA polymerase. **1**

Structural Genes : codes for enzymes/gene products required for metabolism of lactose. **1**

(ii) If lactose is withdrawn from the culture medium the operon is not induced or expressed. 1

[CBSE Marking Scheme, 2016]

Detailed Answer :

An operon is a part of DNA that functions as a gene regulatory unit in transcription.

(i) Regulatory gene : This gene controls the operator gene. This produces a protein substance known as repressor which combines with the operator gene to stop its function.

(ii) Operator : It controls the functioning of structural genes which are expressed when operator gene is turned on by inducer and not expressed when operator is turned off by repressor.

(iii) Promoter : It is the site at which the RNA polymerase binds and reaches the structural genes for the transcription of mRNA to start.

(iv) Structural genes : These genes produce mRNA which synthesize the specific proteins such as enzyme required for metabolism of Lactose.

(v) If lactose is withdrawn from the culture medium the structural gene is not expressed. The repressor units binds with the operator gene and turns it off. As a result the structural genes are inactivated and therefore the transcription and protein (enzyme) synthesis stops.

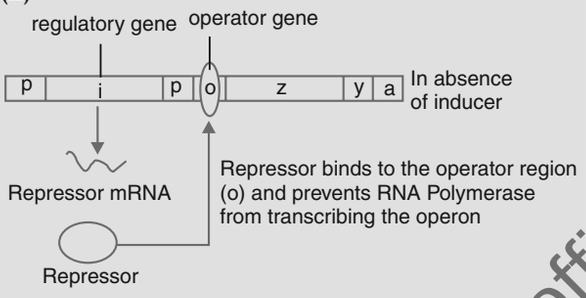
Q. 2. (i) Write any two different levels at which regulation of Gene Expression could be exerted in Eukaryotes.

(ii) Give a labelled schematic representation of ''lac operon'' in its ''Switched Off'' position.

U **[Outside Delhi Set I, Comptt. 2016]**

Ans. (i) Transcriptional level (formation of primary transcript).
- Processing level (regulation of splicing).
- Transport of *m*RNA from nucleus to cytoplasm.
- Translational level. **(Any two) 2**

(ii)



[CBSE Marking Scheme, 2016] 6×½=3

Q. 3. Explain sequentially the process of 'Translation' in a prokaryote. Name the cellular factory where this process occurs.

U **[Outside Delhi Set I, Comptt. 2016]**

Ans. (i) Small subunit of ribosome encounters mRNA and protein synthesis process begins. There are two sites in the large subunit for subsequent amino acids to bind to and thus be close enough to each other for the formation of the peptide bond.

(ii) The order and sequence of the amino acid are defined by the bases in m-RNA.

(iii) In the first phase the amino acid are activated in the presence of ATP and linked to t-RNA(aminoacylation of t-RNA).

(iv) Ribozyme/Ribosome acts as a catalyst for formation of peptide bond.

(v) A translational unit has a sequence of RNA that is flanked by start codon (AUG) at 5' end and stop codon at 3' end (UAA, UAG, UGA).

(vi) Initiation–ribosome binds to m-RNA at start codon (recognized by tRNA).

(vii) Elongation phase: Amino acids linked to tRNA bind to appropriate codon of mRNA by complementary base pairing.

(viii) Ribosome moves codon to codon along mRNA, polypeptide sequence formed as dictated by DNA and represented by mRNA.

(ix) At the end, termination occurs by a release factor which binds to stop codon releasing the polypeptide. **½×9=4½**
Ribosome is the cellular factory. **½**

[CBSE Marking Scheme, 2016]

AI **Q. 4. (i) How is DNA fingerprinting done ? Name any two types of human samples which can be used for DNA fingerprinting. Explain the process sequentially.**

(ii) Mention any two situations when the technique is useful. A **[Outside Delhi Set-II Comptt. 2016]**

Ans. (i) High degree of polymorphism forms the basis of DNA fingerprinting. It involves isolation of DNA, digestion of DNA by restriction endonucleases, separation of DNA fragments by electrophoresis, transferring/blotting of separated DNA fragments to synthetic membranes (nylon or nitrocellulose), Hybridisation using labelled VNTR probes, detection of hybridised DNA fragments by autoradiography. **6×½=3**
DNA from blood/hair follicle/skin/bone/saliva/sperm **(Any two).** **½+½=1**

(ii) Helps as identification tool in forensic applications, in determining population and genetic diversity and helps in paternity testing. **(Any two)**
½ + ½ = 1

[CBSE Marking Scheme, 2016]

Answering Tips
- Express main concepts pointwise wherever it is possible.
- Use correct spelling of technical terms.

Q. 5. (i) Absence of lactose in the culture medium affects the expression of a Lac-operon in *E. coli*. Why and how ? Explain.

(ii) Write any two ways in which the gene expression is regulated in eukaryotes.

U **[Outside Delhi Set - III, 2017]**

Ans. (i) (a) Lactose acts as inducer as lactose switches on the operon.

(b) Repressor protein produced by regulatory gene (i-gene) is free (in the absence of inducer).

(c) Repressor protein binds with the operator gene (o-gene).

(d) Preventing RNA polymerase to transcribe the structural gene and operon is switched off
1 + 1 + 1 + 1=5

OR

Schematic diagram should be used to explain the above points - For diagram: refer: LAQ/ Q. 2.

(ii) (a) Transcriptional level (formation of primary transcripts).

(b) Processing level (formation of primary transcripts).

(c) Transport of messenger RNA from nucleus to the cytoplasm.

(d) Translational level **(Any two).** **½ + ½**

[CBSE Marking Scheme, 2017] 5

Q. 6.(i) Describe the structure and function of a t-RNA molecule. Why is it referred to as an adapter molecule ?

(ii) Explain the process of splicing of hn-RNA in a eukaryotic cell. U **[Outside Delhi – 2017, Set-I]**

Ans. (i) Clover-leaf shaped or inverted L shaped molecules has an anti codon loop with bases complementary to specific codon, has an amino acid acceptor end. **1 + 1**

As it reads the code on one hand binds with the specific amino acid on the other hand. **1**

(ii) Introns are removed, exons are joined in a definite order. **1 + 1**

OR

Process of splicing shown diagrammatically.

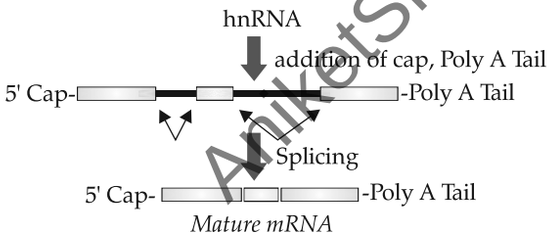
[CBSE Marking Scheme, 2017]

Detailed Answer :

tRNA is a small RNA containing about 80 nucleotides folded over itself in such a way that about 60% of it becomes a double stranded while the rest remains single stranded. This folding of tRNA gives it a clover leaf like structure. tRNA has recognition sites : the anticodon site and the amino acid binding site at 3' end. Besides this it has two lateral arms, the Ribosomal binding arm and the DHU arm.

(i) Intiator t-RNA recognise start codon (AUG) so it act as adapter molecule that reads the genetic code.

(ii) During the process of splicing of hnRNA, introns are removed (by the spliceosome) and exons spliced (joined) together.



Q. 7. Explain the process of protein synthesis from processed m-RNA. U **[CBSE, SQP, 2017]**

Ans. For initiation, the ribosome binds to the mature m-RNA at the start codon (AUG) that is recongnized by the initiator t-RNA. During elongation, charged t-RNA sequentially binds to the appropriate codon in m-RNA with the aniticodon present on tRNA. The ribosome moves from one codon to another adding amino acids one after the other to form polypeptide *i.e.* translation. During termination, the release factor binds to stop codon (UAA, UAG, UGA), terminating translation and releasing the polypeptide chain. **½ × 10 = 5**

Q. 8. Which methodology is used while sequencing the total DNA from a cell ? Explain it in detail.

U **[CBSE, SQP, 2017]**

Ans. Methodology used : Sequence Annotation :

(i) total DNA from a cell is isolated. **½ × 2 = 1**

(ii) converted into random fragments of relatively smaller sizes **½**

(iii) and cloned in suitable host using specialized vectors. **½**

(iv) The cloning results in amplification of each piece of DNA fragment. **½**

(v) The fragments are sequenced using automated DNA sequencers, **½**

(vi) these sequences are then arranged based on some overlapping regions present in them. **½**

(vii) This requires generation of overlapping fragments for sequencing. **½**

(viii) Specialized computer based programmes are developed and **½**

(ix) these sequences are subsequently annotated and assigned to each chromosome. **½**

Q. 9. Describe the interaction of t-RNA, m-RNA and ribosomes during the events of translation.

U **[Foreign Set - I, 2017 - II]**

Ans. (i) For initiation, the ribosome binds to the mRNA at the start codon / AUG. **1**

(ii) Charged tRNA binds to the appropriate codon on mRNA forming complementary base pairs on tRNA as anti codon in the ribosome. **2**

(iii) Ribosomes moves from codon to codon along mRNA, aminoacids are added one by one brought by tRNA, form the polypeptide chain. **2**

[CBSE Marking Scheme, 2017]

Detailed Answer :

(i) During initiation, the ribosome binds to m-RNA at start codon.

(ii) Charged tRNA bind to the appropriate codon on mRNA and forms complementary base pairs on tRNA as anticodon in the ribosome.

(iii) Ribosome move codon to codon along mRNA, polypeptide sequence formed as dictated by DNA and represented by mRNA.

Q. 10. Write the different components of a lac-operon in *E. coli.*, Explain its expression while in an 'open' state. U **[CBSE, Comptt, Set-1, 2018, Outside Delhi, 2017, Set-I]**

OR

Explain the role of lactose as an inducer in a lac operon. [Delhi Set-I, 2016]

Ans. The arrangement where a (Polycistronic) structural gene is regulated by a common promoter and regulatory genes.

Lactose acts as inducer, binds with repressor protein, RNA polymerase freely moves over the structural genes , transcribes lac mRNA , which in turn produce enzymes - transacetylase, permease, ß-galactosidase (by lac z), responsible for digestion of lactose.

// In lieu of above explanation the following diagram can be considered.

For Diagram: Refer Topic 2/ Revision Notes/ Important Diagrams/ Fig 6.3 (In presence of Inducer). **[CBSE Marking Scheme, 2018] 1+ 4**

Q. 11. Explain the structure of t-RNA with the help of a diagram. Describe its role in the process of translation.

U **[Outside Delhi Set-III, Comptt. 2015]**

Ans. (i) Structure of tRNA :

tRNA (Transfer RNA), also called as soluble RNA (sRNA) is a small RNA containing about 80 nucleotides folded over itself in such a way that about 60% of it becomes a double stranded structure while the rest remains single stranded. This folding of tRNA gives it a clover leaf like structure (R Holley 1966), but it looks like an L-shaped structure (Kim 1971). tRNA has two recognition sites : the anticodon site (Complementary to the codon of mRNA) and the amino acid binding site–CCA–OH at 3' end. Besides this it has two lateral arms, the Ribosomal binding arm and the DHU arm. The former helps in ribosomal binding and the latter is related with formation of polypeptide bonds between amino acids. In between anticodon loop and ribosomal binding arm there is present a small lump or mini loop. Initiator t-RNA recognises start codon (AUG)/ t-RNA act as the adapter molecule that reads the genetic code.

Two such charged t-RNA are brought close enough to favour peptide bond formation. **1**

For diagram- Refer to Topic 2/ Revision Notes/ Important Diagrams/ Fig 6.1 **1+½+½=2**

t-RNA has an anticodon loop that has bases complementary to the code and it also has an amino acid acceptor end to which it binds to amino acid. **1**

Amino acid are activated in the presence of ATP and linked to their cognate t-RNA, called as charging/amino-acylation of t-RNA.

(ii) Role of tRNA in translation :

The tRNA is meant for transferring amino acid to ribosomes for the synthesis of polypeptide chain. The tRNA pick up the specific amino acids at their CCA or 3' end & the charged tRNA take the same to mRNA over particular codon corresponding to their anticodons. The tRNA hold the peptidal chain over mRNA. **[CBSE Marking Scheme, 2015] 1**

Answering Tip

- Understand the structure of tRNA with proper diagram for easy retention. Lay emphasis on its role during translation (protein synthesis).

AI **Q. 12. (i) Name the scientist who postulated the presence of an adapter molecule that can assist in protein synthesis.**

(ii) Describe its structure with the help of a diagram. Mention its role in protein synthesis.

U **[Delhi Set-III, 2014]**

Ans. (i) Francis Crick ½

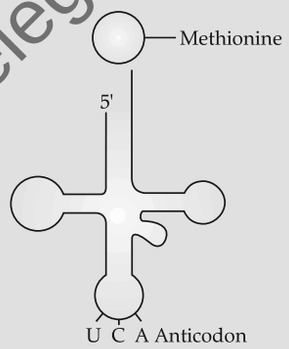
(ii) Clover leaf / inverted L,

Anticodon loop (complementary to codon of mRNA), acceptor end to bind amino acid.

½ × 3 = 1½

It reads the codons on mRNA with the help of anticodon loop, brings the corresponding amino acid for the formation of polypeptide chain.

½ + ½



[CBSE Marking Scheme, 2014] 2

Answering Tip

- Name of the scientist should be learnt thoroughly with correct spelling.

Q. 13. Describe how the lac operon operates, both in the presence and absence of an inducer in *E.coli*.

A **[Delhi Set-III, 2014; Outside Delhi Set-II, Comptt. 2015]**

Ans. For diagram- Refer to Topic 2/ Revision Notes/ Important Diagrams/ Fig 6.3

(i) structural gene z, y, a.
(ii) operator
(iii) i
(iv) repressor
(v) binding
(vi) Operon shut
(vii) inducer
(viii) inducer + binding
(ix) operator free
(x) enzymes / operator **½ × 10 = 5**

[CBSE Marking Scheme, 2014]

Q. 14. Name the major types of RNAs and explain their role in the process of protein synthesis in prokaryote.

R **[Delhi Set-II, 2014]**

Ans. Three types of RNAs : (i) mRNA (ii) tRNA (iii) rRNA. ½ × 3 = 1½

Role :

mRNA – Provides the template for protein synthesis by bringing the genetic information from DNA to the site of protein synthesis / ribosome, also provides site to initiate and terminate the process of protein synthesis. 1½

tRNA – Its anti codon loop read the genetic code on mRNA, brings the corresponding amino acid and bound its amino acid binding end on to the mRNA. ½ + ½

rRNA – Forms a structural component of ribosome, (23SRNA) acts as a catalyst / ribozyme for the formation of peptide bond.

[CBSE Marking Scheme, 2014] ½ + ½

Answering Tip

- Write answers in points using correct keywords. Don't waste time in elaborating the answer.

Know the Terms

- **Anticodon :** A sequence of three nitrogeneous bases on tRNA which is complementary to the codon on mRNA.
- **BAC :** Bacterial Artificial Chromosome.
- **Capping :** Addition of methyl guanosine triphosphate to the 5′ end of hnRNA.
- **DNA Polymorphism :** The variations at genetic level, where an inheritable mutation is observed.
- **Euchromatin :** The region of chromatin which is loosely packed and genetically active.
- **Exons :** The regions of a gene which become part of mRNA and code for different regions of proteins.
- **Heterochromatin :** The chromatin that is more densely packed, stains dark and is genetically inactive.
- **HGP :** Human Genome Project.
- **hnRNA :** Heterogeneous nuclear RNA. It is precursor of mRNA.
- **Introns :** The regions of a gene which are removed during the processing of mRNA.
- **IRGSP :** International Rice Genome sequencing Project.
- **Nucleosome :** The structure formed when negatively charged DNA is wrapped around positively charged histone octamer.
- **Operon :** A group of genes which control a metabolic pathway.
- **Replication fork :** The Y shaped structure formed when double stranded DNA is unwound upto a point during its replication.
- **Satellite DNA :** The repetitive DNA sequences which form a large portion of genome and have high degree of polymorphism but do not code for any proteins.
- **SNPs :** Single Nucleotide Polymorphism.
- **Splicing :** The process in eukaryotic genes in which introns are removed and the exons are joined together to form mRNA.
- **Transcription :** The process of copying genetic information from one strand of DNA into RNA.
- **Transformation :** The phenomenon by which the DNA isolated from one type of a cell, when introduced into another type is able to express some of the properties of the former into the latter.
- **Translation :** The process of polymerisation of amino-acids to form a polypeptide as dictated by mRNA.
- **VNTR :** Variable Number of Tandem Repeats.
- **YAC :** Yeast Artificial Chromosome.

❐❐❐