Molecular Basis Of Inheritance

1. You know that there are twenty different types of naturally occurring amino acids and four different types of bases in the DNA. A combination of 3 such bases code for a specific amino acid. If instead there are 96 different amino acids and 12 different bases in the DNA, then the minimum number of combination of bases required to form a codon is : (2024)

(A) 6

(B) 8

(C) 2

(D) 4

Ans. (C) 2

2. Restriction Endonuclease Hind II always cuts DNA molecules at a particular point by recognising a specific sequence of : (2024)

(A) Six base pairs

(B) Four base pairs

(C) Seven base pairs

(D) Three base pairs

Ans. (A) Six base pairs

3. Name and write two characteristics of the type of DNA that forms the basis of DNA fingerprinting technique. (2024)

Ans.

- Satellite DNA / Repetitive DNA / VNTR

- Do not code for any protein, form a large portion of human genome, show high degree of polymorphism

4. Mention any two applications of this technique. (2024)

Ans. useful in forensic applications, helps in determining population and genetic diversities, forms the basis of paternity testing, to study evolution, to trace path of hereditary diseases.

Previous Years' CBSE Board Questions

5.1 The DNA

MCQ

1. What would be the effect on histone proteins in the nucleus, on neutralisation of their positive charge?

(a) They would bind the DNA tighter.

(b) They would separate from DNA.

(c) They would no longer attract each other.

(d) They would cause supercoiling of DNA.

(Term I, 2021-22)

2. A DNA molecule is 160 base pairs long. It has 30% guanine. How many adenine bases are present in this DNA molecule?

(a) 48 (b) 64 (c) 96 (d) 192

(Term I, 2021-22)

3. In prokaryotes like E.coli the DNA in the nucleoid region is organised as

(a) negatively charged DNA wrapped around histone

(b) densely packed chromatin with NHC proteins

(c) large loops held by the proteins

(d) many repeating units of nucleosomes.

(Term I, 2021-22)

VSA (1 mark)

4. Name the transcriptionally active region of chromatin in a nucleus.

(Delhi 2015)

5. Name the negatively charged and positively charged components of a nucleosome.

(Delhi 2015C)

SA I (2 marks)

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

(2018)

7. Describe the structure of a nucleosome.

(Delhi 2017)

8. What is central dogma? Who proposed it?

(2/5, AI 2015C)

SA II (3 marks)

9. The length of DNA in any cell is far greater than the dimension of its nucleus. Explain how this enormous DNA is packaged in a eukaryotic cell.
(2023)

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

(b) Draw a diagrammatic sketch of a portion of DNA segment to support your answer. **(Delhi 2015)**

11. (a) A DNA segment has a total of 1,500 nucleotides, out of which 410 are guanine containing nucleotides. How many pyrimidine bases this segment possesses?

(b) Draw a diagrammatic sketch of a portion of DNA segment to support your answer. **(Delhi 2015)**

12. (a) ADNA segment has a total of 2,000 nucleotides, out of which 520 are adenine containing nucleotides. How many purine bases this DNA segment possesses?

(b) Draw a diagrammatic sketch of a portion of DNA segment to support your answer. **(Delhi 2015)**

13. Draw a labelled diagram of a nucleosome. Where is it found in a cell?
(Foreign 2014)

LA (5 marks)

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

(i) Histone octamer

(ii) Nucleosome

(iii) Chromatin

(b) Differentiate between euchromatin and heterochromatin.
(Delhi 2016)

5.2 The Search for Genetic Material

VSA (1 mark)

15. Why is RNA more reactive in comparison to DNA?
(Delhi 2015C)

SA II (3 marks)

16. Explain the discovery made by Hershey and Chase using radioactive sulphur and phosphorus in their experiment.
(2020)

17. Why is DNA a better genetic material when compared to RNA?
(Delhi 2015C)

LA (5 marks)

18. Describe the experiment carried out by Hershey and Chase. Write the conclusion they arrived at.

(2020)

19. (a) Explain Griffith's 'transforming principle' experiment.

(b) In the above experiment, "heat which killed one type of bacteria, did not destroy the properties of genetic material." Justify.
(2019 C)

20. (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.
(2018)

21. List the criteria a molecule that can act as genetic material must fulfil. Which one of the criteria are best fulfilled by DNA or by RNA thus making one of them a better genetic material than the other? Explain.
(Delhi 2016)

22. Answer the following questions based on Hershey and Chase experiments:

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

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

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

(d) State the conclusion drawn by them after the experiments.
(Delhi 2016)

23. (a) Describe the series of experiments of F. Griffith. Comment on the significance of the results obtained.

(b) State the contribution of MacLeod, McCarty and Avery.
(Al 2016)

24. How did Hershey and Chase established that DNA is transferred from virus to bacteria?

(Delhi 2015)

25. (a) Describe the experiment which demonstrated the existence of "transforming principle".

(b) How was the biochemical nature of this "transforming principle" determined by Avery, MacLeod and McCarty?
(Foreign 2015)

OR

(a) Describe the various steps of Griffith's experiments that led to the conclusion of the transforming principle.

(b) How did the chemical nature of the transforming principle get established?

(NCERT Exemplar, Al 2014)

26. How did Alfred Hershey and Martha Chase conclusively establish that DNA is the genetic material? Explain.
(Foreign 2015)

OR

Describe the Hershey and Chase experiment. Write the conclusion drawn by the scientist after their experiment.
(AI 2014)

27. How did Griffith prove transforming principle in genetics? Explain the procedure. **(Delhi 2015C)**

5.4 Replication

MCQ

28. Given below is a list of steps Meselson and Stahl carried out in their experiment to prove that DNA replication is semi-conservative. Select the option that gives the correct sequence of steps followed by them.

(i) Bacteria transferred to a N14 medium and sampled every 20 minutes.

(ii) All bacteria contain hybrid DNA (N14 DNA and N15 DNA).

(iii) Bacteria grown in N15 medium for many generations.

(iv) All bacteria contain N15 DNA.

(v) Bacteria contain either all N14 DNA or all hybrid DNA.

(a) (ii) → (iv) → (iii) → (i) → (v)

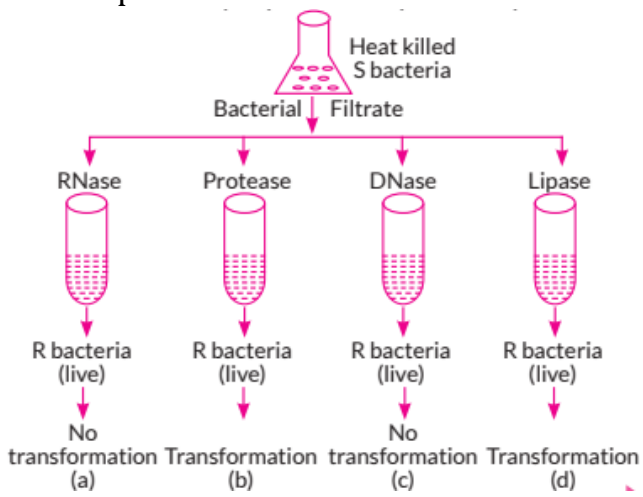
(b) (i) → (ii) → (v) → (iv) → (iii)

(c) (iii) → (iv) → (i) → (ii) → (v)

(d) (iv) → (iii) → (ii) → (v) → (i)

(2023)

29. Given below are the illustration of the different steps of experiments conducted by MacLeod, Mc Carty and Avery to find the chemical nature of the 'transforming principle' as DNA. Select the option that incorrectly depicts the step of the experiment.



(Term I, 2021-22)

30. Meselson and Stahl carried out centrifugation in $CsCl_2$ density gradient to separate:

(a) DNA from RNA

(b) DNA from protein

(c) the normal DNA from 15N-DNA

(d) DNA from tRNA.

(2020)

VSA (1 mark)

31. Write the dual purpose served by deoxyribo-nucleoside triphosphates in polymerisation. **(2018)**

32. Name the source of energy for the replication of DNA.
(1/3, Delhi 2015C)

33. Why is it not possible for an alien DNA to become part of chromosome anywhere along its length and replicate normally?
(AI 2014)

34. What will happen if DNA replication is not followed by cell division in a eukaryotic cell?

(AI 2014C)

SA I (2 marks)

35. Discuss the role, the enzyme DNA ligase plays during DNA replication.
(Delhi 2016)

36. Show DNA replication with the help of a diagram only.
(Delhi 2014C)

SA II (3 marks)

37. Describe the experiment where Matthew Meselson and Franklin Stahl used heavy isotope of nitrogen.
(2020)

38. Explain the mechanism of DNA replication with the help of a replication fork. What role does the enzyme DNA ligase play in a DNA replication fork?
(Delhi 2019)

39. Answer the following questions based on Meselson and Stahl's experiment on E.coli:

(a) Write the name of the chemical substance used as the only source of nitrogen in the experiment.

(b) Why did they allow the synthesis of the light and the heavy DNA molecules in the organism?

(c) How did they distinguish the heavy DNA molecules from the light DNA molecules? Explain.

(d) Write the conclusion the scientists arrived at, at the end of the experiment.
(AI 2019)

40. (a) Why does DNA replication occur within a replication fork and not in its entire length simultaneously?

(b) "DNA replication is continuous and discontinuous on the two strands within the replication fork." Give reasons.
(2019)

41. Describe the experiment that helped demonstrate the semi-conservative mode of DNA replication.
(Delhi 2016)

OR

How was a heavy isotope of nitrogen used to provide experimental evidence to semi-conservative mode of DNA-replication?
(Foreign 2015)

OR

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

(3/5, AI 2015C)

LA (5 marks)

42. (i) Draw a labelled diagram of a replication fork in a prokaryote indicating the process of DNA replication.

(ii) Differentiate between the two newly synthesised DNA strands within the fork.

(iii) Name the enzymes involved in the process of DNA replication.

(iv) Name the eukaryote where the semi-mode of replication was conservative experimentally proved.
(2023)

43. (a) Name the stage in cell cycle where DNA replication occur.

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

(c) Why is DNA replication said to be semi-conservative?
(AI 2016)

44. Describe Meselson and Stahl's experiment that was carried in 1958 on E. coli. Write the conclusion they arrived at after the experiment.
(AI 2016)

OR

Describe Meselson and Stahl's experiment and write the conclusion they arrived at. **(Foreign 2014)**

45. (a) Draw a labelled diagram of a "replicating fork" showing the polarity. Why does DNA replication occur within such 'forks?

(b) Name two enzymes involved in the process of DNA replication, along with their properties.

(AI 2015)

46. Explain the process of DNA replication with the help of a replicating fork.
(Delhi 2015C)

47. (a) Explain the process of DNA replication with the help of a schematic diagram.

(b) In which phase of the cell cycle does replication occur in eukaryotes? What would happen if cell division is not followed after DNA replication?
(Delhi 2014)

5.5 Transcription

MCQ

48. A region of coding strand of DNA has the following nucleotide sequence 5′-ATGCGGC-3′

The sequence of bases on mRNA transcribed by this would be

(a) 5'-AUGCGGC-3′ (b) 3′-AUGCGGC-3'

(c) 5'-TACGCCG-3′ (d) 3'-TACGCCG-5'
(Term I, 2021-22)

49. Which one of the following statement describe the function of the promoter in a transcription unit?

(a) Signals the termination of polypeptide chain.

(b) Serves a sequence where transcription will initiate.

(c) Serves as DNA template for transcription to take place.

(d) Determines the first nucleotide to be transcribed into RNA.
(Term 1, 2021-22)

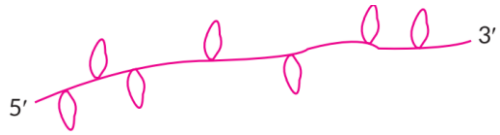
50. In a transcription unit in DNA the 'I' is located towards 3' end of the 'Il' strand and it usually defines the end of the process of transcription.

Choose the correct I and II from the options given below.

(a) Terminator, coding (b) Promoter, template

(c) rho factor, template (d) sigma factor, coding,
(Term 1, 2021-22)

51. Given below is a heterogeneous RNA formed during eukaryotic transcription.



How many introns and exons respectively are formed in this hnRNA?

(a) 7,7 (b) 8,7 (c) 8,8 (d) 7,8
(Term 1, 2021-22)

52. In a bacterium, when RNA polymerase binds to the promoter on a transcription unit during transcription, it

(a) terminates the process (b) helps remove introns

(c) initiates the process (d) inactivates the exons.
(2020)

VSA (1 mark)

53. What is a cistron?
(AI 2015)

54. Write the function of RNA polymerase II.
(Foreign 2015)

55. Name the enzyme that transcribes hnRNA in eukaryotes.
(Delhi 2015C)

56. Differentiate between exons and introns.
(1/3, AI 2015C)

SA I (2 marks)

57. Given below is one of the strands of a DNA segment:

$3' \xrightarrow{\text{TACGTACGTACGTACG}} 5'$

(a) Write its complementary strand.

(b) Write a possible RNA strand that can be transcribed from the above DNA molecule formed.

(2020)

58. Draw a schematic diagram of a transcription unit with the polarity of the DNA strands and label coding strand, template strand and terminator.
(2020 C)

59. Differentiate between a template strand and coding strand of DNA.
(2/3, Delhi 2015C)

60. State the difference between the structural genes in a transcription unit of prokaryotes and eukaryotes.
(AI 2014)

61. A template strand is given below. Write down the corresponding coding strand and the mRNA strand that can be formed, along with their polarity.

3 ATGCATGCATGCATGCATGCATGC 5'

(NCERT, Foreign 2014)

SA II (3 marks)

62. (i) How many types of RNA polymerases are there in a eukaryote cell? Mention which one of them transcribes hnRNA.

(ii) Write the changes that hnRNA undergoes before it leaves the nucleus as mRNA. **(2023)**

63. Construct and label a transcription unit from which the RNA segment given below has been transcribed. Write the complete name of the enzyme that transcribed this RNA.

(Delhi 2019)

64. With the help of a schematic diagram, explain the location and the role of the following in a transcription unit:

Promoter, Structural gene, Terminator.
(Delhi 2014C)

65. (a) What are the transcriptional products of RNA polymerase III?

(b) Differentiate between 'Capping' and 'Tailing.

(c) Expand hnRNA.
(AI 2014C)

LA (5 marks)

66. Name the different types of RNA polymerases in a eukaryotic cell. Write their roles in transcription.
(2020 C)

67. Name the type of cells and the process by which hnRNA is formed. Describe the processingmechanism it undergoes before it becomes functional.
(2020)

68. Compare the processes of DNA replication and transcription in prokaryotes.
(2019 C)

69. (a) Describe the process of transcription in bacteria.

(b) Explain the processing the hnRNA needs to undergo before becoming functional mRNA of eukaryotes.
(AI 2016)

70. Explain the process of transcription in prokaryotes. How is the process different in eukaryotes?

(AI 2015)

71. Explain the process of transcription in eukaryotes.
(Foreign 2015)

72. Describe the process of transcription in a bacterium. **(NCERT Exemplar, Al 2014C)**

5.6 Genetic Code

MCQ

73. Given below is a sequence of bases in mRNA of a bacterial cell. Identify the amino acid that would be incorporated at codon position 3 and codon position 5 during the process of its translation.

3' AUCAGGUUUGUGAUGGUACGA 5'

(a) Phenylalanine, Methionine (b) Cysteine, Glycine

(c) Alanine, Proline (d) Serine, Valine
(2023)

74. When an amino acid is coded by more than one codon, the genetic code is said to be

(a) universal (b) punctuate

(c) commaless (d) degenerate.
(Term I, 2021-22)

75. During elongation process of translation, the peptide

bond formation between amino acids is catalysed by

(a) ribosomal RNA (b) transfer RNA

(c) messenger RNA (d) small nuclear RNA.

(Term I, 2021-22)

VSA (1 mark)

76. Give an example of a codon having dual function.

(Delhi 2016)

77. How does a degenerate code differ from an unambiguous one?

(Foreign 2015)

SA I (2 marks)

78. State a functional difference between the following codons.

(a) AUG and UAA

(b) Specific and Degenerate

(2020)

79. Differentiate between the genetic codes given below:

(a) Unambiguous and Universal

(b) Degenerate and Initiator

(AI 2017)

80. Following are the features of genetic codes. What does each one indicate?

Stop codon; Unambiguous codon; Degenerate codon; Universal codon.

(AI 2016)

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

(b) Explain the basis on which he arrived at this conclusion.

(Delhi 2014)

82. 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 codes said to be degenerate?

(Foreign 2014)

SA II (3 marks)

83. (a) Name the scientist who postulated the presence of an adapter molecule that can assist in protein synthesis.

(b) Describe its structure with the help of a diagram. Mention its role in protein synthesis.

(Foreign 2014)

LA (5 marks)

84. (a) Write the contributions of the following scientists in deciphering the genetic code.

George Gamow, Hargobind Khorana; Marshall Nirenberg; Severo Ochoa

(b) State the importance of a genetic code in protein biosynthesis.
(Delhi 2019)

85. (a) Describe the structure and function of a tRNA molecule. Why is it referred to as an adapter molecule?

(b) Explain the process of splicing of hnRNA in a eukaryotic cell.

86. (a) What is a genetic code?
(AI 2017)

(b) Explain the following:

Degenerate code; Unambiguous code; Initiator code.
(Delhi 2014C)

5.7 Translation

MCQ

87. The different types of RNAs transcribed by RNA polymerase III in eukaryotes are

(a) tRNA, hnRNA, 28S rRNA

(b) 28S rRNA, 18S rRNA, 5.8S rRNA

(c) tRNA, 5S rRNA, snRNAs

(d) hnRNA, 18S rRNA, 28S rRNA.
(Term I, 2021-22)

VSA (1 mark)

88. Write the two specific codons that a translational unit of mRNA is flanked by one on either sides.

(AI 2015C)

SA I (2 marks)

89. What is aminoacylation? State its significance.
(AI 2016)

90. State the functions of ribozyme and release factor in protein synthesis respectively. **(AI 2015C)**

91. Where does peptide bond formation occur in a bacterial ribosome and how?
(Foreign 2014)

92. Explain aminoacylation of tRNA.
(Delhi 2014C)

LA (5 marks)

93. Explain the relationship of ribosomes, tRNA and mRNA during the process of translation in prokaryotes.

(2020)

OR

How do mRNA, tRNA and ribosomes help in the process of translation?

(AI 2015)

94. Name the major types of RNAs and explain their role in the process of protein synthesis in a prokaryote.

(Foreign 2014)

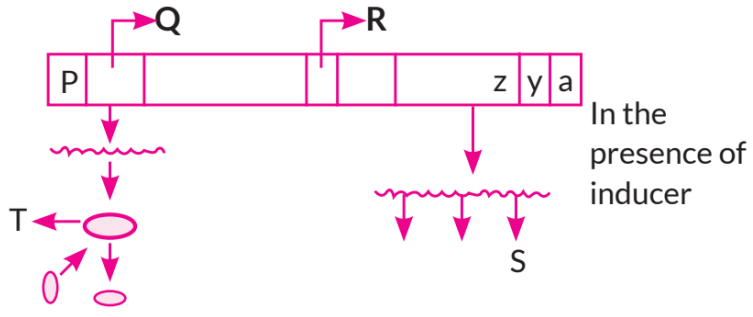
95. Explain the process of translation.

(Delhi 2014C)

5.8 Regulation of Gene Expression

MCQ

96. Identify the correct labelling for Q, R, S and T for the lac operon in E. coli as given below.



Choose the correct option from the given table.

	Q	R	S	T
(a)	Structural gene	Operator	β-Galacto-sidase	Inducer
(b)	Regulatory gene	Promoter	Transace-tylase	Repressor protein
(c)	Structural gene	Operator	Permease	Inducer
(d)	Regulatory gene	Promoter	β-Galacto-sidase	Repressor

(Term I, 2021-22)

SA I (2 marks)

97. How would lac operon operate in E. coli growing in a culture medium where lactose is present as source of sugar?
(AI 2014C)

LA (5 marks)

98. Explain the expression of lac operon genes in E. coli growing in lactose containing cultural medium.
(2020)

99. Explain the role of different genes in a lac operon when in a switched-on state.
(2020)

100. Study the schematic representation of the genes involved in the lac operon given below and answer the questions that follow:

(a) Identify and name the regulatory gene in this operon. Explain its role in 'switching off' the operon.

(b) Why is the lac operon's regulation referred to as negative regulation?

(c) Name the inducer molecule and the products of the genes 'z' and 'y' of the operon. Write the functions of these gene products.
(AI 2019)

101. Write the different components of a lac-operon in E. coli. Explain its expression while in an 'open' state.
(AI 2017)

102. Explain the role of lactose as an inducer in a lac operon.
(Delhi 2016)

OR

Describe how the lac operon operates, both in the presence and absence of an inducer in E. coli.

(AI 2014)

103. Sketch a schematic diagram of lac operon in switched on position. How is the operon switched off? Explain.
(AI 2015C)

5.9 Human Genome Project

MCQ

104. Choose the chromosome in a human that possesses least number of genes.

(a) 21st chromosome (b) Autosome

(c) X chromosome (d) Y chromosome
(2020)

VSA (1 mark)

105. Write the scientific importance of single nucleotide polymorphism identified in human genome.

(1/5, Foreign 2014)

SA I (2 marks)

106. State any four salient observations drawn from the Human Genome Project.
(2021 C)

107. Which human chromosome has (a) maximum number of genes, and which one has (b) fewest genes?
(2/5, Foreign 2014)

SA II (3 marks)

108. Human Genome Project (HGP) was a mega project launched in the year 1990 with some important goals.

(a) Enlist any four prime goals of HGP.

(b) Name any one common non-human animal model organism which has also been sequenced thereafter.
(2023)

109. What are 'SNPs'? Where are they located in a human cell? State any two ways the discovery of SNPs can be of importance to humans.
(2020)

110. (a) List the two methodologies which were involved in human genome project. Mention how they were used.

(b) Expand 'YAC' and mention what was it used for?
(AI 2017)

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

(b) 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.

(c) Expand 'SNPs' identified by scientists in HGP.
(AI 2016)

LA (5 marks)

112. (a) List any four major goals of human genome project.

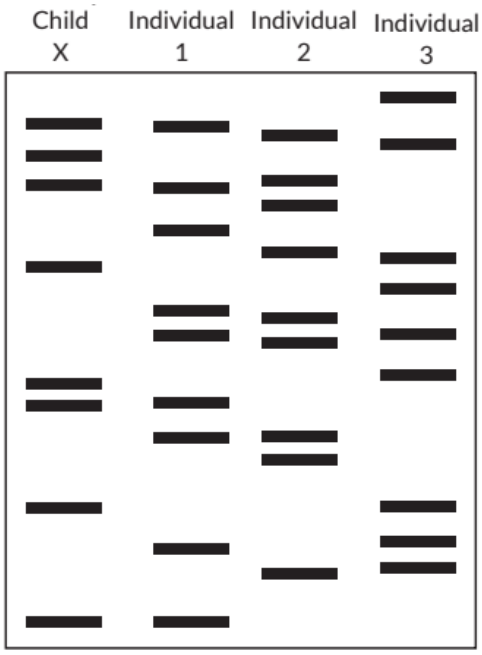
(b) Write any four ways the knowledge from HGP is of significance for humans.

(c) Expand BAC and mention its importance.
(2020)

5.10 DNA Fingerprinting

MCQ

113. DNA profiles of the child and three individuals 1, 2 and 3 who claim to be the parents of the child are given below. Select the option that shows the correct actual parent/parents of the child.



(a) Individual 1 and 3

(b) Individual 1 and 2

(c) Individual 2 and 3

(d) Individual 1 is the only parent of the child amongst 1, 2 and 3

(2023)

114. Which one of the following techniques is used in DNA fingerprinting for the detection of DNA?

(a) Northern blotting

(b) Western blotting

(c) Southern blotting

(d) In-situ hybridisation

(Term I, 2021-22)

VSA (1 mark)

115. How is repetitive/satellite DNA separated from bulk genomic DNA for various genetic experiments?
(Delhi 2014)

116. How does DNA polymorphism arise in a population? **(NCERT Exemplar, Delhi 2014)**

SA II (3 marks)

117. "A very small sample of tissue or even a drop of blood can help determine paternity". Provide a scientific explanation to substantiate how it is possible.
(AI 2019, 2015)

118. (a) Expand VNTR and describe its role in DNA fingerprinting.

(b) List any two applications of DNA fingerprinting technique.
(2018)

119. A number of passengers were severely burnt beyond recognition during a train accident. Name and describe a modern technique that can help in handing over the dead to their relatives.

(Delhi 2017)

OR

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.

(Delhi 2015)

120. Explain the significance of satellite DNA in DNA fingerprinting technique.
(AI 2015)

LA (5 marks)

121. Name and describe the steps involved in the technique widely used in forensics that serves as the basis of paternity testing in case of disputes.
(2023)

122. (a) Name and describe the technique which is an important tool of forensic science.

(b) Mention any two applications of this technique other than its use in forensic studies. **(2021 C)**

123. (a) Name the type of DNA that forms the basis of DNA fingerprinting and mention two features of this DNA.

(b) Write the steps carried out in the process of DNA fingerprinting technique and mention its applications.
(2020)

CBSE Sample Questions

5.1 The DNA

MCQ

1. Total number of nucleotide sequences of DNA that codes for a hormone is 1530. The proportion of different bases in the sequence is found to be adenine

= 34%, guanine = 19%, cytosine = 23%, thymine

= 19%.

Applying Chargaff's rule, what conclusion can be drawn?

(a) It is a double stranded circular DNA.

(b) It is a single stranded DNA.

(c) It is a double stranded linear DNA.

(d) It is a single stranded DNA coiled on histones.

(Term I, 2021-22)

2. A stretch of an euchromatin has 200 nucleosomes. How many base pairs will there be in the stretch and what would be the length of the typical euchromatin?

(a) 20,000 bp and 13,000 × 10-9 m

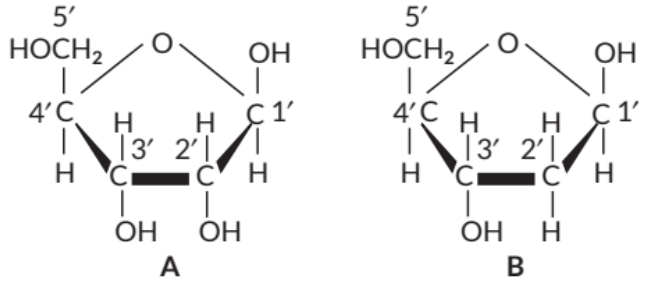
(b) 10,000 bp and 10,000 × 10-9 m

(c) 40,000 bp and 13,600 × 10-9 m

(d) 40,000 bp and 13,900 × 10-9 m

(Term I, 2021-22)

3. Observe structures A and B given below. Which of the following statements are correct?



(a) A is having 2'-OH group which makes it less reactive and structurally stable, whereas B is having 2'-H group which makes it more reactive and unstable.

(b) A is having 2'-OH group which makes it more reactive and structurally unstable, whereas B is having 2'-H group which makes it less reactive and structurally stable.

(c) A and B both have -OH groups which make it more reactive and structurally stable.

(d) A and B both are having -OH groups which make it less reactive and structurally stable.

(Term I, 2021-22)

5.2 The Search for Genetic Material

MCQ

4. Which of the following criteria must a molecule fulfil to act as a genetic material?

(i) It should not be able to generate its replica.

(ii) It should chemically and structurally be stable.

(iii) It should not allow slow mutation.

(iv) It should be able to express itself in the form of Mendelian characters.

(a) (i) and (ii) (b) (ii) and (iii)

(c) (iii) and (iv) (d) (ii) and (iv)

(Term I, 2021-22)

5. Oswald Avery, Colin MacLeod and Maclyn McCarty used enzymes to purify biochemicals such as proteins, DNA and RNA from the heat-killed S cells to see which ones could transform live R cells into S cells in Griffith's experiment. They observed that

(a) proteases and RNases affected transformation

(b) DNase inhibited transformation

(c) proteases and lipases affected transformation

(d) RNases inhibited transformation.

(Term I, 2021-22)

LA (5 marks)

6. Evaluate the suitability of DNA and RNA as genetic material and justify the suitability of the one that is preferred as an ideal genetic material.
(2020-21)

5.4 Replication

MCQ

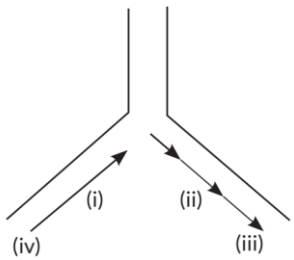
7. If Meselson and Stahl's experiment is continued for sixth generations in bacteria, the ratio of heavy strands 15N/15N :Hybrid15N/14N light 14N/14N containing DNA in the sixth generation would be

(a) 1:1:1 (b) 0:1:7

(c) 0:1:15 (d) 0:1:31.

(Term I, 2021-22)

8. Origin of replication of DNA in E. coli is shown below. Identify the labelled parts (i), (ii), (iii) and (iv).



(a) (i)- Discontinuous synthesis, (ii)- Continuous synthesis (iii) 3' end (iv) 5' end

(b) (i)- Continuous synthesis, (ii)- Discontinuous synthesis (iii) 5' end (iv) 3' end

(c) (i)- Discontinuous synthesis, (ii)- Continuous synthesis (iii) 5' end (iv) 3' end

(d) (i)- Continuous synthesis, (ii)- Discontinuous synthesis (iii) 3' end (iv) 5' end

(Term I, 2021-22)

LA (5 marks)

9. Explain the mechanism of DNA replication as suggested by Watson and Crick.

(2020-21)

5.5 Transcription

MCQ

10. The promoter site and the terminator site for transcription are located at

(a) 3' (downstream) end and 5′ (upstream) end, respectively of the transcription unit

(b) 5' (upstream) end and 3′ (downstream) end, respectively of the transcription unit

(c) the 5' (upstream) end of the transcription unit

(d) the 3' (downstream) end of the transcription unit. **(Term I, 2021-22)**

11. Which of the following is correct about mature RNA in eukaryotes?

(a) Exons and introns do not appear in the mature RNA.

(b) Exons appear, but introns do not appear in the mature RNA.

(c) Introns appear, but exons do not appear in the mature RNA.

(d) Both exons and introns appear in the mature RNA.

(Term I, 2021-22)

12. Two important RNA processing events lead to specialised end sequences in most human mRNAs:

(i) at the 5' end, and (ii) at the 3' end. At the 5' end the most distinctive specialised end nucleotide, (iii) is added and a sequence of about 200 (iv) is added to the 3' end.

(a) (i) initiator codon (ii) promotor (iii) terminator codon (iv) release factors

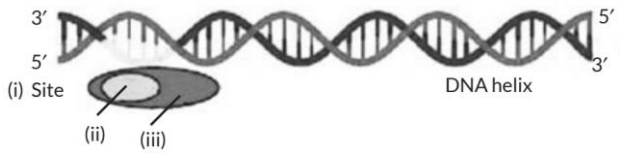
(b) (i) promotor (ii) elongation (iii) regulation (iv) termination

(c) (i) capping (ii) polyadenylation (iii) $^{m}G_{ppp}$ (iv) Poly A

(d) (i) repressor (ii) co-repressor (iii) operon (iv) release factors

(Term I, 2021-22)

13. Transcription unit is represented in the diagram given below.



Identify site (i), factor (ii) and enzyme (iii) responsible for carrying out the process.

(a) (i) Promoter site, (ii) Rho factor (iii) RNA polymerase

(b) (i) Terminator site, (ii) Sigma factor (iii) RNA polymerase

(c) (i) Promoter site, (ii) Sigma factor (iii) RNA polymerase

(d) (i) Promoter site, (ii) Sigma factor (iii) DNA polymerase

(Term I, 2021-22)

14. Assertion: Primary transcripts in eukaryotes are non-functional.

Reason: Methyl guanosine triphosphate is attached to 5' end of hnRNA.

(a) Both assertion and reason are true, and reason is the correct explanation of assertion.

(b) Both assertion and reason are true, but reason is not the correct explanation of assertion.

(c) Assertion is true but reason is false.

(d) Both assertion and reason are false.

(2020-21)

LA (5 marks)

15. Observe the segment of mRNA given below.

(a) Explain and illustrate the steps involved to make fully processed hnRNA.

(b) Gene encoding RNA Polymerase I and III have been affected by mutation in a cell. Explain its impact on the synthesis of polypeptide, stating reasons.
(2022-23)

5.6 Genetic Code

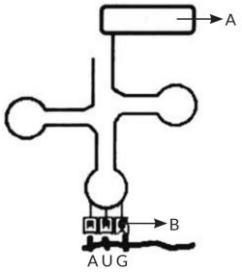
VSA (1 mark)

16. Predict the effect if, the codon UAU coding for an amino acid at the 25th position of a polypeptide of 50 amino acids, is mutated to UAA.
(2020-21)

5.7 Translation

MCQ

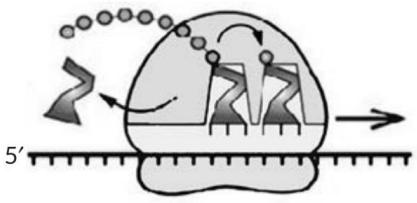
17. AUG on the mRNA will result in the activation of which of the following RNA having correct combination of amino acids?



	Site A	Site B
(a)	UAC	Methionine
(b)	Methionine	UAC
(c)	Methionine	AUG
(d)	AUG	Methionine

(Term I, 2021-22)

18. Which cellular process is shown below?



(a) DNA Replication

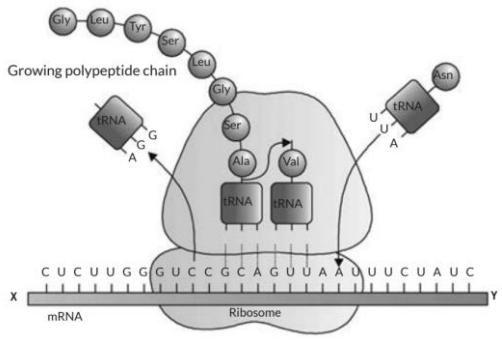
(b) Translation - Initiation

(c) Translation – Elongation

(d) Translation - Termination

(Term 1, 2021-22)

19. (a) Identify the polarity of X to Y in the diagram below and mention how many more amino acids are expected to be added to this polypeptide chain.



(b) Mention the codon and anticodon for alanine.

(c) Why are some untranslated sequences of bases seen in mRNA coding for a polypeptide? Where exactly are they present on mRNA?
(2022-23)

5.8 Regulation of Gene Expression

MCQ

20. In E.coli, the lac operon gets switched on when

(a) lactose is present and it binds to the repressor

(b) repressor binds to operator

(c) RNA polymerase binds to the operator

(d) lactose is present and it binds to RNA polymerase.
(Term I, 2021-22)

LA (5 marks)

21. Study the schematic representation of the genes involved in the lac operon given below and answer the questions that follow:

p	*i*	*p*	*o*	*z*	*y*	*a*

(a) The active site of enzyme permease present in the cell membrane of a bacterium has been blocked by an inhibitor, how will it affect the lac operon?

(b) The protein produced by the i gene has become abnormal due to unknown reasons. Explain its impact on lactose metabolism stating the reason.

(c) If the nutrient medium for the bacteria contains only galactose; will operon be expressed? Justify your answer.
(2022-23)

5.10 DNA Fingerprinting

MCQ

22. Short stretches of DNA used to identify complementary sequence in a sample are called

(a) probes

(b) markers

(c) VNTRS

(d) primers.

(Term I, 2021-22)

23. What are minisatellites?

(a) 10-40 bp sized small sequences within the genes.

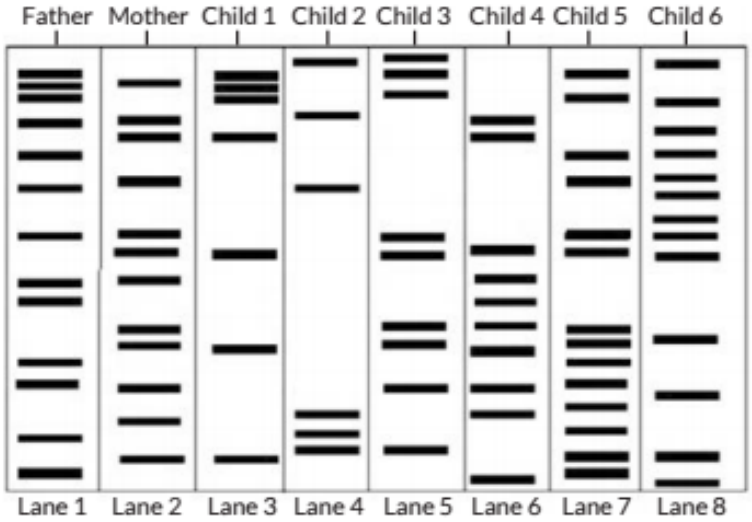
(b) Short coding repetitive region on the eukaryotic genome.

(c) Short non-coding repetitive sequence forming large portion of eukaryotic genome.

(d) Regions of coding strands of the DNA.

(Term I, 2021-22)

24. There was a mix-up at the hospital after a fire accident in the nursery division. Which of these children belong to the parents?



(a) All of the children

(b) Children 2, 3 and 6

(c) Children 1 and 3

(d) Children 2 and 4

(Term I, 2021-22)

Detailed SOLUTIONS

Previous Years' CBSE Board Questions

1. (b): Histone proteins in the nucleus would separate from DNA on neutralisation of the positive charge as the negatively charged DNA wrap around the positively charged histone octamer to form nucleosome.

2. (b): According to Chargaff's rule the amount of adenine is always equal to that of thymine and the amount of guanine is always equal to that of cytosine i.e., A = T and G = C. Also, the purines and pyrimidines are always in equal amounts, i.e., A+ G=T+ C. Now, given dsDNA has 30% guanine and hence cytosine will also be 30%.

So, A + T must be 40%. Therefore, percentage of adenine would be $40/2 = 20\%$.

The length of DNA molecule = 160 bp = 320 bases

Adenine bases present in DNA will be $= 320 \text{ x } \frac{20}{100} = 64$

3. (c): Prokaryotes does not have a well-defined nucleus. DNA being a negatively charged is held with some proteins (having positive charges) in the region termed as 'nucleoid'. The DNA in nucleoid is organised as large loops held by proteins.

4. Euchromatin is the transcriptionally active region of chromatin in a nucleus.

5. The negatively charged and positively charged components of a nucleosome are DNA and histones respectively.

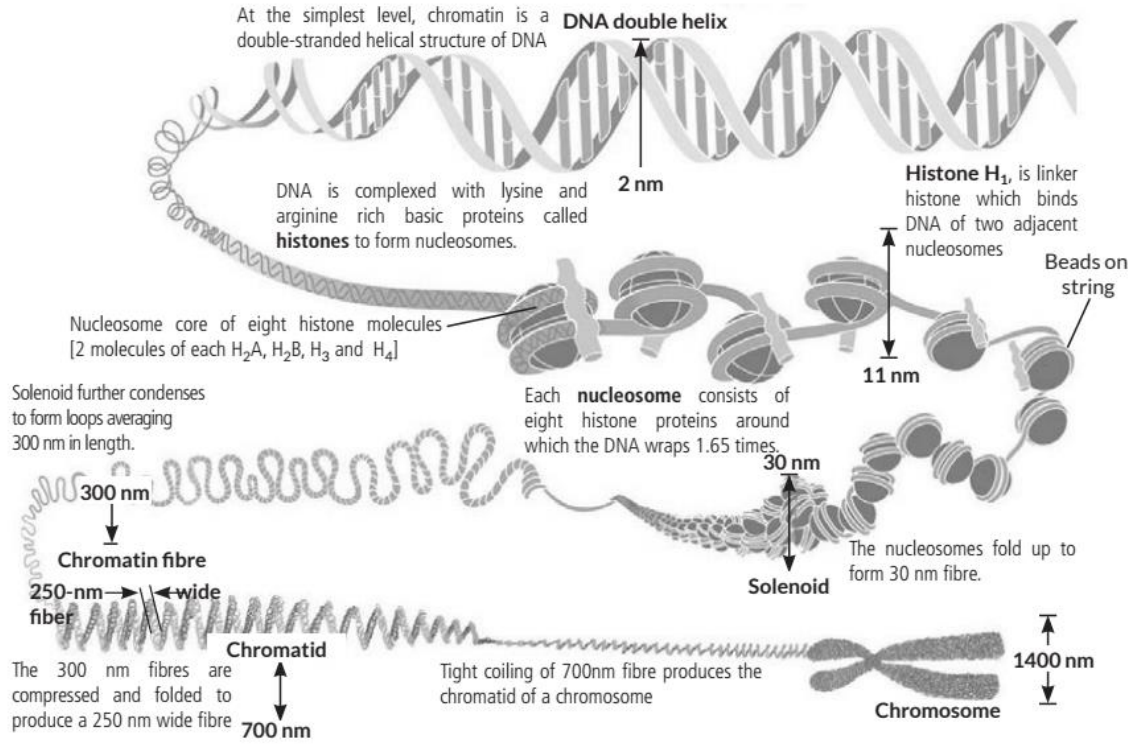
6. In prokaryotes, DNA lies in the cytoplasm which is supercoiled (coiled and recoiled) with the help of RNAs and non-histone basic proteins like polyamines. DNA being negatively charged is held in place with the help of these proteins that have positive charges in a region termed as nucleoid. The DNA in nucleoid is organised in large loops held by proteins.

7. DNA is wrapped around the positively charged histone octamer to form a structure called nucleosome. DNA packing in eukaryotes is carried out with help of lysine and arginine rich basic proteins called histones. The unit of compaction is nucleosome. There are five types of histone proteins – H_1, H_2A, H_2B, H_3 and H_4. Four of them (H_2A, H_2B, H_3 and H_4) occur in pairs to produce histone octamer, called nu-body or core of nucleosome. Their positively charged ends are towards the outside. They attract negatively charged strands of DNA. DNA over nu-body forms 1.75 left-handed turns to form nucleosome core. A typical nucleosome contains 200 bp of DNA helix. DNA connecting two adjacent nucleosomes is

called interbead or linker DNA. It bears H_1 histone protein. Nucleosome chain gives a beads-on-string appearance.

8. Central dogma refers to the flow of information from DNA to mRNA (transcription) and then decoding the information present in mRNA in the formation of polypeptide chain or protein (translation). It was proposed by Crick in 1958.

9. DNA packaging in eukaryotes is carried out with the help of basic amino acids residues lysine and arginine called histones. Histones are organised to form a unit of eight molecules called histone octamer. The negatively charged DNA is wrapped around the positively charged histone octamer to form nucleosome.



There are five types of histone proteins, i.e., H_1, H_2A, H_2B, H_3 and H_4. Four of them (H_2A, H_2B, H_3 and H_4,) occur in pairs to produce histone octamer or nu-body. A typical nucleosome contains 200 bp of DNA helix. Nucleosomes constitute the repeating unit of a structure in nucleus called chromatin (thread-like stained bodies seen in nucleus). The nucleosomes in chromatin appears as 'beads-on-string' under electron microscope (EM). The beads-on-string structure in chromatin is packaged to form chromatin fibers that are further coiled and condensed at metaphase stage of cell division to form chromosomes. In a typical nucleus, some regions of chromatin are loosely packed (and stains light) and are referred to as euchromatin. The chromatin that is more densely packed and stains dark are called as heterochromatin. Euchromatin is said to be transcriptionally active chromatin, whereas heterochromatin is inactive.

10. (a) According to Chargaff's rule,

$[A] + [G] = [C] + [T]$

Also, $[A] = [T]$ and $[C] = [G]$

As $[A] = [T]$, therefore $[T] = 240$

$[A] + [T] = 240 + 240 = 480$

As total number of nucleotides $= 1000$,

therefore $[G] + [C] = 1000 - 480 = 520$

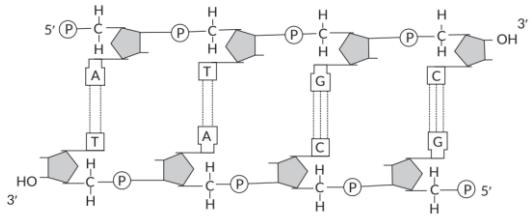
$[G] = [C]$

therefore, $[G] = [C] = \frac{520}{2} = 260$

Thus, total number of pyrimidines.

i.e. $[C] + [T] = 260 + 240 = 500$

(b) Diagrammatic representation of double stranded DNA chain having all four nitrogenous base and showing correct polarity is as follows:



11. (a) Cytosine and thymine are pyrimidines.

According to Chargaff's rule, purines and pyrimidine base pairs are in equal amount, therefore

Total nucleotides $= 1500$

$[A + G + C + T] = 1500$

$[A] = [T]$ and $[G] = [C]$

Guanine $= 410$

Therefore, $A + 410 + 410 + T = 1500$

$A + T + 820 = 1500$

$A + T = 1500 - 820$

$A + T = 680$

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

Therefore, total pyrimidine,

$C + T = [410 + 340] = 750$

(b) Refer to answer 10 (b).

12. (a) According to Chargaff's rule,

$[A] + [G] = [C] + [T]$

Also, $[A] = [T]$ and $[G] = [C]$

As $[A] = [T]$, therefore $[A] = [T] = 520$

$[A] + [T] = 520 + 520 = 1040$

As total number of nucleotides $= 2000$

therefore, $[G] + [C] = 2000 - 1040 = 960$

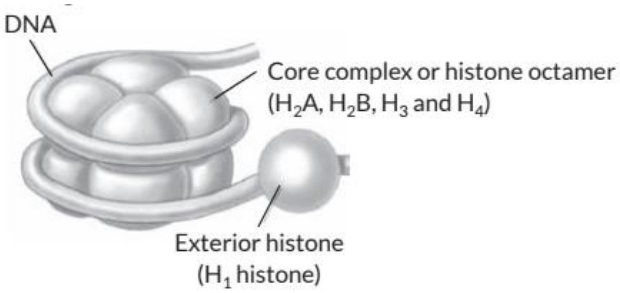
$[G] = [C] = \frac{960}{2} = 480$

Thus, total number of purines i.e.

$[A] + [G] = 520 + 480 = 1000$

(b) Refer to answer 10 (b).

13. Diagram of nucleosome is as follows:



A section of negatively charged DNA is wrapped around the positively charged histone octamer to form a structure called nucleosome. Nucleosome constitute the repeating unit of a structure in nucleus called chromatin, thread like stained bodies seen in nucleus. The nucleosomes in chromatin are seen as 'beads on string' structure when viewed under electron microscope.

14. (a) (i) Histone octamer: Histones are positively charged proteins, rich in basic amino acid residues lysines and arginines. These amino acids carry positive charges on their side chains. There are five types of histone proteins : H_1, H_2A, H_2B, H_3 and H_4. Four of them (H_2A, H_2B, H_3 and H_4) are organised in pairs to from a unit of eight molecules called histone octamer, nu-body or core of nucleosome. Negatively charged DNA wraps around this octamer to form nucleosome.

(ii) Nucleosome: It is the compaction unit. The positively charged ends of histone octamer attract the negatively charged strands of DNA. The DNA is thus wrapped around the positively charged histone octamer to form a structure called nucleosome. Around 200 bp of DNA is wrapped around the nu body or histone octamer for $1\frac{3}{4}$ turns. DNA connecting two adjacent nucleosomes is called linker DNA which bears H_1 histone protein. Nucleosome and linker DNA together constitute chromatosome. Nucleosome chain gives a 'bead on string' appearance under electron microscope.

(iii) Chromatin : The nucleosomal organisation has approximately 10 nm thickness, which further gets condensed and coiled to produce a solenoid (having 6 nucleosomes per turn) of 30 nm diameter. This solenoid structure further undergoes coiling to produce a chromatin fibre of 30-80 nm thickness. These chromatin fibres are further coiled and condensed to form chromatid which further forms chromosome at metaphase stage of cell division. The packaging can be summarised as follows:

DNA (2nm diameter) → Nucleosome (10 nm diameter) → Solenoid (30 nm diameter) → Chromatin fibre (30-80 nm diameter)

↓

Chromatid (700 nm diameter)

↓

Chromosome (1400 nm diameter)

(b) The differences between euchromatin and heterochromatin are as follows:

	Euchromatin	Heterochromatin
(i)	These are the regions, where chromatin is loosely packed.	These are the regions, where chromatin is densely packed.
(ii)	It stains lighter.	It stains darker.
(iii)	It is transcriptionally active.	It is transcriptionally inactive or late replicating.

15. RNA is more reactive in comparison to DNA because:

- 2'-OH group present in ribose sugar of every nucleotide of RNA is a reactive group. It makes RNA highly reactive, labile and easily degradable.

- RNA functions as an enzyme, therefore is reactive and unstable.

16. Hershey and Chase used to follow two types of culture media:

(i) Medium that contained radioactive phosphorus (^{32}P).

(ii) Medium that contained radioactive sulphur (^{35}S). They used two different kinds of culture media to detect whether the genetic material is DNA or protein.

Viruses grown in the medium with radioactive phosphorus contained radioactive DNA but not radioactive protein as DNA contains phosphorus but protein does not. Similarly, viruses grown on radioactive sulphur medium contained radioactive protein but not radioactive DNA because DNA does not contain sulphur. Hence, their experiment proved that DNA is the genetic material.

17. The criteria which makes DNA a better genetic material than RNA are as follows:

(i) DNA is chemically less reactive and structurally more stable than RNA as its nucleotides is not exposed except when they are to express their effect, whereas 2' -OH group in ribose sugar of every nucleotide of RNA makes it more reactive. RNA also functions as an enzyme and is therefore more reactive and unstable.

(ii) Presence of thymine in DNA instead of uracil in RNA provides stability to DNA.

(iii) Hydrogen bonding between purines and pyrimidines and their stacking make DNA more stable for storage of genetic information than RNA.

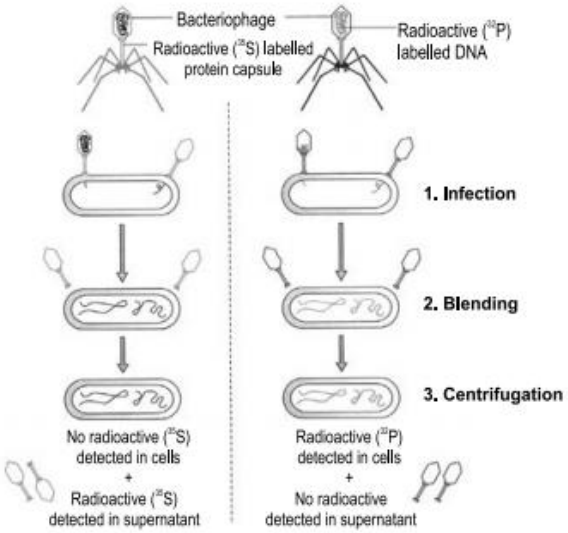
(iv) DNA has power of repairing and there is no such repairing mechanism in RNA.

18. Alfred D. Hershey and Martha Chase, choose T_2 bacteriophage as their experimental material. They decided to see which of the bacteriophage components-protein or DNA entered bacterial cells and directed reproduction of the virus. Hershey and Chase experiment is based on the fact that DNA but not the protein contains phosphorus, and similarly sulphur is present in proteins (cysteine and methionine) but not in DNA. They incorporated radioactive isotope of phosphorus (^{32}P) into phage DNA and that of sulphur (^{35}S) into proteins of separate phage cultures. These phage types were used independently to infect the bacterium Escherichia coli. After sometime, the cultures were agitated in a blender to separate the empty phage capsids from the surface of bacterial cells and the two were separated by centrifugation.

Hershey and Chase showed that in bacterial cells, infected with virus containing radioactive phosphorus (^{32}P), radioactivity was associated with bacterial cells and also, appeared in the progeny phage. However, in bacterial culture where radioactive sulphur (^{35}S) was used, all radioactive material was limited to phage 'ghosts' (empty viral protein coats). These results indicated that the DNA of the

bacteriophage and not the protein enters the host, where viral replication takes place. Therefore, DNA is the genetic material of T_2 bacteriophage. It directs protein coat synthesis and allows replication to occur.

Diagrammatic representation of Hershey and Chase experiment is as follows:



19. (a) Transformation is the phenomenon by which the DNA isolated from one type of cell, when introduced (artificially or naturally) into another type, is able to show some of the properties of the former to the latter. Griffith observed transformation in Streptococcus pneumoniae (bacterium responsible for causing pneumonia). He grew bacteria on a culture plate, some produced smooth shiny colonies (S) while others produced rough colonies (R). Mice infected with the S strain (virulent) die from pneumonia infection but mice infected with the R strain do not develop pneumonia.

S strain→ Injected into mice → Mice die

R strain → Injected into mice → Mice live

Griffith observed that heat-killed S strain bacteria, when injected into the mice, did not kill them.

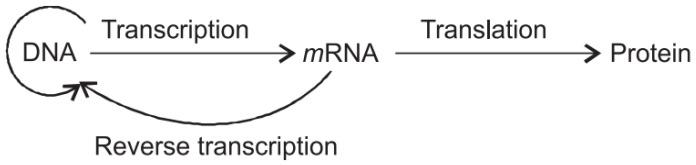
S strain (heat-killed) → Inject into mice → Mice live

When he injected a mixture of heat-killed S strain and live R bacteria, the mice died. Moreover, he recovered living S strain bacteria from the dead mice.

S strain (heat-killed) + R strain (live) → Injected into mice → Mice die

(b) In the above experiment performed by Griffith, heat killed S type of bacteria, but did not destroy the properties of genetic material as R strain bacteria had somehow been transformed to produce a smooth polysaccharide coat and become virulent.

20. (a) Francis Crick (1958) proposed 'Central dogma' in molecular biology which states that the flow of information first occurs from DNA to mRNA by the process of transcription and then the information present in mRNA is decoded for the formation of polypeptide chain by the process of translation. The central dogma suggests that DNA contains the information needed to make all of our proteins, and that RNA is a messenger that carries this information to ribosomes. The ribosomes serve as factories in the cell where the information is translated from a code into the functional product.



Yes, central dogma differs in retroviruses, e.g., HIV, etc., where it is called central dogma reverse (inverse flow of information) i.e., from RNA to DNA. RNA of these viruses first synthesises DNA through reverse transcription and DNA then transfers information to RNA which takes part in translation of coded information to form a polypeptide.

(b) In 1928, Frederick Griffith performed the transformation experiment using Streptococcus pneumoniae. When he injected heat killed, virulent S strain along with non-virulent, live R strain in mice, then the mice died. It showed that something from dead S strain transformed the non-virulent R strain into virulent one. During the course of his experiment, a living organism (bacteria) had changed in physical form. This phenomenon was called transformation by him. He concluded that the R strain bacteria had somehow been transformed by the heat-killed S strain bacteria. Some 'transforming principle', transferred from the heat-killed S strain, had enabled the R strain to synthesise a smooth polysaccharide coat and become virulent. This must be due to the transfer of the genetic material. However, the biochemical nature of genetic material was not defined from his experiments. Now, Avery, MacLeod and McCarty worked to determine the biochemical nature of transforming principle in Griffith's experiment. They later 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 DNA alone from S bacteria caused R bacteria to become transformed. They also discovered that protein-digesting enzymes (proteases) and RNA-digesting enzymes (RNases) did not affect transformation. Digestion with DNase did inhibit transformation, suggesting that the DNA caused the transformation and they concluded that DNA is the hereditary material.

21. A molecule that can act as genetic material must fulfill the following criteria:

(a) It should be able to generate its replica.

(b) It should be chemically and structurally stable.

(c) It should provide the scope for slow changes that are required for evolution.

(d) It should be able to express itself in the form of 'Mendelian characters!

The criteria which make DNA a better genetic material than RNA are as follows:

(i) DNA is chemically less reactive and structurally more stable than RNA as its nucleotides is not exposed except when they are to express their effect, whereas 2'-OH group in ribose sugar of every nucleotide of RNA makes it more reactive. RNA also functions as an enzyme and is therefore more reactive and unstable.

(ii) Presence of thymine in DNA instead of uracil in RNA provides stability to DNA.

(iii) Hydrogen bonding between purines and pyrimidines and their stacking make DNA more stable for storage of genetic information than RNA.

(iv) DNA has power of repairing and there is no such repairing mechanism in RNA.

22. (a) Hershey and Chase worked with virus T_2 bacteriophage. T_2 bacteriophage is a bacterial virus which has ability to infect Escherichia coli and it possess linear double stranded DNA (deoxyribose nucleic acid) as genetic material, therefore they used this bacteriophage or virus for their work.

(b) Hershey and Chase used to follow two types of culture media:

(i) Medium that contained radioactive phosphorus (^{32}P).

(ii) Medium that contained radioactive sulphur (^{35}S).

They used two different kinds of culture media to detect whether the genetic material is DNA or protein. Viruses grown in the presence of radioactive phosphorus contained radioactive DNA but not radioactive protein because DNA contains phosphorus but protein does not. Similarly, viruses grown on radioactive sulphur contained radioactive protein but not radioactive DNA because DNA does not contain sulphur.

(c) Blender was used in experiment to remove the empty phage capsids (or ghosts) sticking to the surface of bacteria. Centrifuge was used to separate virus particle from the bacteria. The bacterial cultures were centrifuged. Both the supernatant and the pellets were checked for radioactivity. In culture with radioactive ^{35}S it was found that phage with labelled protein did not make bacteria labelled. Instead, radioactivity was restricted to supernatant which was found to contain only capsid. On the other hand, in the second culture with ^{32}P it was found that supernatant containing capsid was not radioactive instead

bacteria become labelled proving that only DNA of the phage entered the bacteria.

(d) Hershey and Chase from this experiment concluded that genetic material is DNA and not the protein.

23. (a) Transformation is the phenomenon by which the DNA isolated from one type of cell, when introduced (artificially or naturally) into another type, is able to show some of the properties of the former to the latter.

Griffith observed transformation in Streptococcus pneumoniae (bacterium responsible for causing pneumonia). He grew bacteria on a culture plate, some produced smooth shiny colonies (S) while others produced rough colonies (R). Mice infected with the S strain (virulent) die from pneumonia infection but mice infected with the R strain do not develop pneumonia.

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Griffith observed that heat-killed S strain bacteria, when injected into the mice, did not kill them.

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

When he injected a mixture of heat-killed S strain and live R bacteria, the mice died. Moreover, he recovered living S strain bacteria from the dead mice.

S strain (heat - killed) + R strain (live) → Injected into mice → Mice die

From the experiment, Griffith concluded that the R strain bacteria had been transformed by the heat-killed S strain bacteria as some 'transforming principle' transferred from heat killed S strain enabled the R strain to become virulent.

(b) Avery, MacLeod and McCarty (1944) performed the biochemical characterisation of the 'transforming principle' of Griffith's experiment. They separated the extract of smooth, virulent bacteria into protein, DNA and carbohydrate fractions. Each fraction was separately added to a culture medium containing live rough bacteria. Only the culture that received the DNA fraction of the extract from virulent bacteria produced smooth bacteria.

This proved that DNA was the transforming agent. When DNA fraction was treated with deoxyribonuclease (an enzyme that digests DNA), it became inactive and incapable of transforming the rough strain into the smooth strain. This confirmed that DNA is the genetic material.

The following table represent the result of Avery's experiment.

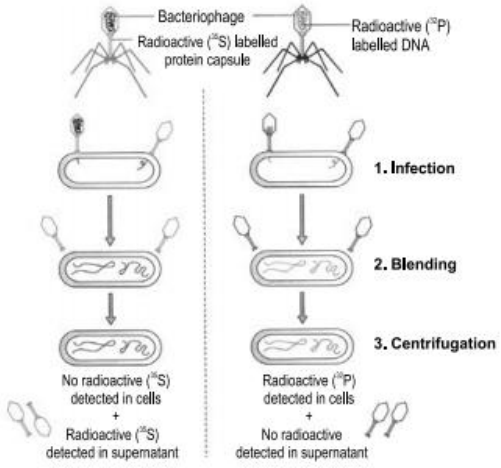
Mixture	Result
R-type bacteria + carbohydrates of S-type bacteria	R-type bacteria
R-type bacteria + protein of S-type bacteria	R-type bacteria
R-type bacteria + DNA of S-type bacteria	S-type bacteria
R-type bacteria + DNA of S-type bacteria + deoxy-ribonuclease	R-type bacteria

24. Refer to answer 18.

25. Refer to answer 23.

26. Alfred D. Hershey and Martha Chase, choose T_2 bacteriophage as their experimental material. They decided to see which of the bacteriophage components-protein or DNA-entered bacterial cells and directed reproduction of the virus. Hershey and Chase experiment is based on the fact that DNA but not the protein contains phosphorus, and similarly sulphur is present in proteins (cysteine and methionine) but not in DNA. They incorporated radioactive isotope of phosphorus (^{32}P) into phage DNA and that of sulphur (^{35}S) into proteins of separate phage cultures. These phage types were used independently to infect the bacterium Escherichia coli. After sometime, the cultures were agitated in a blender to separate the empty phage capsids from the surface of bacterial cells and the two were separated by centrifugation. Hershey and Chase showed that in bacterial cells, infected with virus containing radioactive phosphorus (^{32}P), radioactivity was associated with bacterial cells and also, appeared in the progeny phage. However, in bacterial culture where radioactive sulphur (35S) was used, all radioactive material was limited to phage 'ghosts' (empty viral protein coats). These results indicated that the DNA of the bacteriophage and not the protein enters the host, where viral replication takes place. Therefore, DNA is the genetic material of T_2 bacteriophage. It directs protein coat synthesis and allows replication to occur.

Diagrammatic representation of Hershey and Chase experiment is as follows:



27. Refer to answer 23 (a).

28. (c)

29. (a): Avery, Macleod and McCarty discovered that protease and RNases did not affect transformation but digestion with DNase did inhibit transformation. Lipases are involved in digestion of lipids, thus it will not affect transformation.

30. (c): Meselson and Stahl carried out centrifugation in $CsCl_2$ density gradient to separate the normal DNA from ^{15}N-DNA.

31. Deoxyribonucleoside triphosphates such as dATP, dCTP, dGTP and dTTP serve dual purpose during DNA replication. They act as substrates i.e., nucleotides for the replication process as well as provide energy for the polymerisation of nucleotides by cleavage of high energy terminal phosphate bonds.

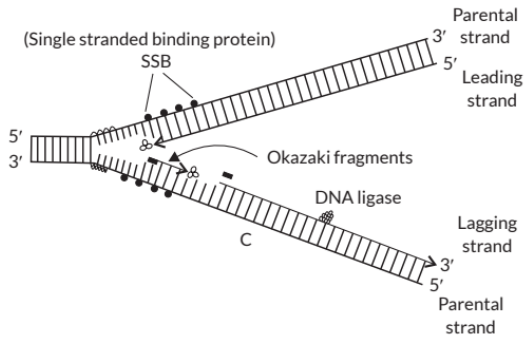
32. The sources of energy for the replication of DNA are phosphorylated nucleotides or deoxyribonucleoside triphosphates i.e., dATP, dCTP, dGTP and dTTP.

33. It is not possible for an alien DNA to become a part of the chromosome anywhere along the length and replicate normally because of absence of origin of replication (ori). It is the sequence where DNA replication starts. This site is also necessary for binding of DNA polymerase to start DNA replication. As this site may not present in all alien DNA molecules, hence they cannot replicate normally.

34. DNA replication doubles the amount of DNA in a cell and cell division again halves the amount of DNA i.e., maintains the normal amount of DNA in the daughter nuclei. Thus, if DNA replication is not followed by cell division in a eukaryotic cell, then amount of DNA will increase than normal, resulting in abnormal conditions such as polyploidy.

35. DNA ligase is an enzyme that catalyses the repair of a single strand break by formation of covalent phosphodiester bond between adjacent 3′ hydroxyl and 5' phosphoryl groups in double stranded DNA. During replication of DNA, short replicated fragments/ segments of DNA or Okazaki fragments are present on the lagging strand. These fragments are joined to form a continuous strand with the help of enzyme DNA ligase.

36. Diagrammatic representation of DNA replication is as follows:

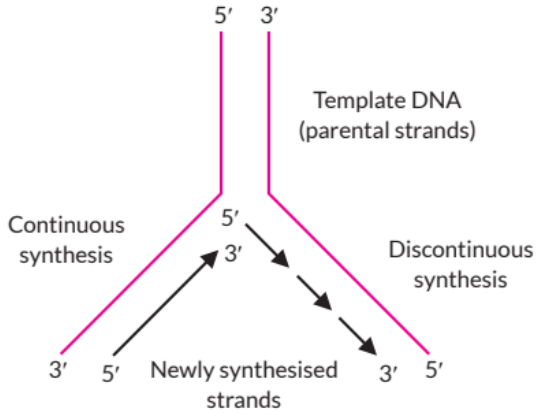


37. The work of Matthew Meselson and Franklin Stahl (1958) on E. coli proved semi-conservative replication of DNA. They first grew bacteria Escherichia coli in a medium containing heavy isotope ^{15}N for several generations. This led to the incorporation of heavy isotope in all nitrogen-containing compounds including bases. They were able to extract the bacterial DNA and centrifuge it in cesium chloride solution. Depending on the mass of the molecule, the DNA would settle out at a particular point in the tube. The ^{15}N bacteria were then transferred to a growth medium containing the normal, lighter isotope of nitrogen, ^{14}N, where they reproduced by cell division.

Meselson and Stahl found that DNA of the first generation was hybrid or intermediate (^{15N} and ^{14}N). It settled in cesium chloride solution at a level higher than the fully labelled DNA of parent bacteria ($^{15}N^{15}N$). The second generation of bacteria after 40 minutes, contained two types of DNA, 50% light ($^{14}N^{14}N$) and 50% intermediate ($^{15}N^{14}N$).

At succeeding generation times, the DNA extracts were found to have a lower proportion of ^{15}N as more ^{14}N was incorporated into the bacterial DNA. This observation is possible only if both strands separate during replication and one strand act as template for synthesis of new strand of DNA having ^{14}N. This was conclusive evidence for the semi-conservative method of DNA replication.

38. Diagrammatic representation of replicating fork is as follows:



The figure represents the mechanism of DNA replication, during which leading strand and lagging strand are formed on the two different template strands. DNA-polymerase can polymerise nucleotides only in 5'→ 3' direction. Since the two strands of DNA run in antiparallel directions, the two templates provide different ends for replication.

Replication, over the two templates, thus proceeds in opposite directions. One strand with polarity 3′ → 5′ replication is continuous because 3' end of the latter is always open for elongation. It is called leading strand.

Replication is discontinuous on the other template with polarity 5' 3' because only a short segment of DNA strand can be built in 5'→ 3' direction due to exposure of a small stretch of template at one time. Short segments of replicated DNA are called Okazaki fragments. Okazaki fragments are later joined together by means of enzyme, DNA ligase to form lagging strand.

DNA ligase is an enzyme that catalyses the repair of a single strand break by formation of covalent phosphodiester bond between adjacent 3′ hydroxyl and 5' phosphoryl groups in double stranded DNA.

During replication of DNA, short replicated fragments/segments of DNA or Okazaki fragments are present on the lagging strand. These fragments are joined to form a continuous strand with the help of enzyme DNA ligase.

39. (a) NH4Cl (Ammonium chloride) was used as a source of nitrogen by Meselson and Stahl in their experiment.

(b) They synthesised light and heavy DNA molecules in the organism (E. coli bacterium) so as to separate different generations on the basis of density gradient centrifugation.

(c) The DNA molecules from each generation, were tested through density gradient centrifugation using cesium chloride. The heavy DNA molecules settled at the bottom whereas successively light DNA molecules settled at the surface. In this way, the DNA molecules were distinguished.

(d) From the experiment scientists concluded that DNA replication is semi-conservative in nature.

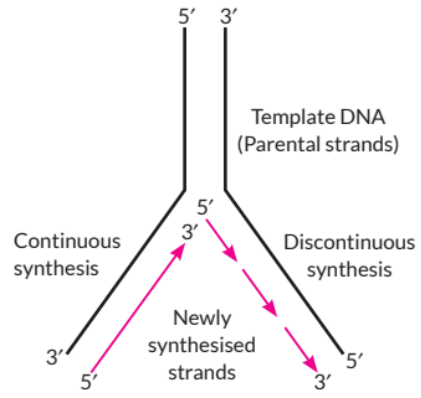
40. (a) The two strands of DNA cannot be separated in its entire length for long DNA molecules due to very high energy requirement, the replication occur within a small opening of the DNA helix known as replication fork.

(b) The DNA-dependent DNA polymerases catalyse polymerisation only in 5'-3' due to which some additional complications are created at the replicating fork. On one strand, the replication is continuous on the template with polarity 3' 5', while on the other, the replication is discontinuous on the template with polarity 5'-3'. The short stretches of DNA, each primed by RNA are called Okazaki fragments.

41. The work of Matthew Meselson and Franklin Stahl (1958) on E. coli proved semi-conservative replication of DNA. They first grew bacteria Escherichia coli in a medium containing heavy isotope ^{15}N for several generations. This led to the

incorporation of heavy isotope in all nitrogen-containing compounds including bases. They were able to extract the bacterial DNA and centrifuge it in cesium chloride solution. Depending on the mass of the molecule, the DNA would settle out at a particular point in the tube. The ^{15}N bacteria were then transferred to a growth medium containing the normal, lighter isotope of nitrogen, ^{14}N, where they reproduced by cell division. Meselson and Stahl found that DNA of the first generation was hybrid or intermediate (^{15}N and ^{14}N). It settled in cesium chloride solution at a level higher than the fully labelled DNA of parent bacteria ($^{15}N^{15}N$). The second generation of bacteria after 40 minutes, contained two types of DNA, 50% light ($^{14}N^{14}N$) and 50% intermediate ($^{15}N^{14}N$). At succeeding generation times, the DNA extracts were found to have a lower proportion of ^{15}N as more ^{14}N was incorporated into the bacterial DNA. This observation is possible only if both strands separate during replication and one strand act as template for synthesis of new strand of DNA having ^{14}N. This was conclusive evidence for the semi-conservative method of DNA replication.

42. (i): Replication fork in a prokaryote indicating the process of DNA replication is as follows:



(ii) DNA is made differently on the two strands at a replication fork. One new strand, the leading strand, runs 5' to 3' towards the fork and is made continuously. The other, the lagging strand, runs 5' to 3' away from the fork and is made in small pieces called Okazaki fragments.

(iii) Enzymes involved in the process of DNA replication are: DNA polymerase, DNA ligase, helicase, topoisomerase, phosphorylase and primase.

(iv) In Vicia faba, the semi-conservative mode of replication of DNA was experimentally proved.

43. (a) DNA replication occurs during S-phase of the cell cycle.

(b) DNA replication is a multistep complex process, which requires a dozen enzymes and protein factors. It begins at a particular spot called origin of replication or ori.

Separating the two strands of DNA is accomplished by the helicase enzymes that travel along the helix, opening the double helix as they move. Unwinding also creates a coiling tension in front of the moving replication fork, a structure that will be formed when DNA replication begins. This tension is reduced by topoisomerases.

The very important DNA synthesising enzyme is DNA polymerase III. It along with other DNA polymerases (I and II) has the ability to elongate an existing DNA strand but cannot initiate the synthesis.

All the three DNA polymerases function in 5' → 3' direction only for DNA polymerisation and have 3' → 5' exonuclease activity.

To initiate DNA synthesis, a small segment of RNA (10 to 60 nucleotides) called an RNA primer complementary to the template DNA is synthesised by a unique RNA polymerase known as primase.

While on the one strand the DNA synthesis is continuous in 5' 3’ direction, on the other strand, DNA is synthesised in small stretches resulting in discontinuous DNA synthesis. This happens in the opposite direction to the first strand but maintains the overall 5' → 3' direction as required. Such a process is also referred to as semi-discontinuous replication. The short stretches of DNA, each primed by RNA are called Okazaki fragments.

RNA primer is then removed, and the gap is filled by DNA polymerase. The enzyme ligase then seals these fragments.

The strand which supports the continuous DNA synthesis is the leading strand and the one, which is replicated in short stretches is called the lagging strand.

(c) DNA replication is said to be semi-conservative since daughter DNA duplex comprise of one parental and one newly synthesised strand.

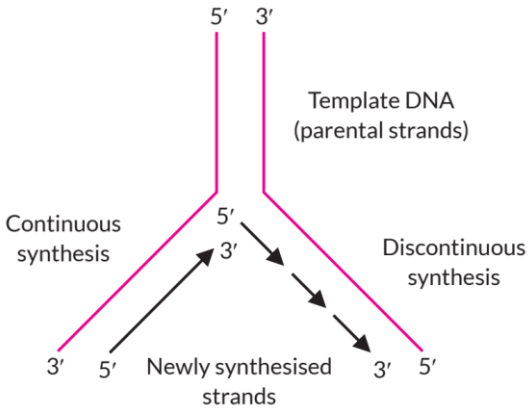
44. The work of Matthew Meselson and Franklin Stahl (1958) on E.coli proved semi-conservative replication of DNA. They first grew Escherichia coli bacteria in a medium containing heavy isotope of nitrogen (^{15}N) for several generations. This led to the incorporation of heavy isotope in all nitrogen-containing compounds including bases. They were able to extract the bacterial DNA and centrifuge it in cesium chloride solution. Depending on the mass of the molecule, the DNA would settle out at a particular point in the tube (heavy DNA molecule can be distinguished from normal DNA by centrifugation in cesium chloride density gradient).

The ^{15}N bacteria were then transferred to a growth medium containing the normal, lighter isotope of nitrogen, ^{14}N, where they reproduced by cell division. Extracts of DNA from the first-generation offspring were shown to have a lower density, since half the DNA was made up of the original strand containing ^{15}N and

the other half was made up of the new strand containing ^{14}N. At succeeding generation times, the DNA extracts were found to have a lower proportion of ^{15}N as more ^{14}N was incorporated into the bacterial DNA. This was conclusive evidence for the semi-conservative method of DNA replication.

The conclusion they arrived at after the experiment is that the DNA replication is semi-conservative. Semiconservative means that when the double stranded DNA helix was replicated, each of the two double stranded DNA helices of newly synthesised strands consisted of one strand coming from the original helix and one newly synthesised. So, in this way at each replication, one strand of parent DNA is conserved in the daughter while the second is freshly synthesised.

45. (a) Diagrammatic representation of replicating fork is as follows:



Due to high energy requirement whole of DNA does not open in one stretch. The point of separation proceeds slowly towards both directions. It gives the appearance of Y-shaped structure called replication fork.

(b) Two enzymes involved in the process of DNA replication are:

(i) Helicase - causes the unwinding of DNA strand.

(ii) Topoisomerase - releases the tension of DNA strand.

46. DNA replication occurs during S-phase of cell cycle. It is a multistep complex process which requires over a dozen enzymes and protein factors. It begins at a particular spot called origin of replication or Ori. Replication of DNA is energetically highly expensive. The main enzyme of DNA replication is DNA dependent DNA polymerase.

Deoxyribonucleoside monophosphates occur freely inside the nucleoplasm. They are first phosphorylated and changed to active forms. The phosphorylated nucleotides are dATP (deoxyadenosine triphosphate), dGTP (deoxyguanosine triphosphate), dCTP (deoxycytidine triphosphate) and dTTP (deoxythymidine triphosphate).

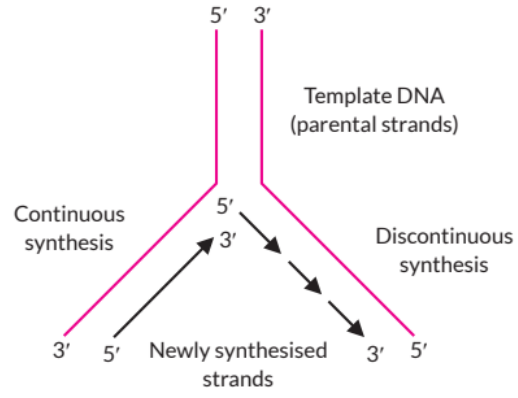
Enzyme helicase (unwindase) acts over the Ori site and unzips (unwinds) the two strands of DNA by destroying hydrogen bonds. Unwinding creates tension in the uncoiled part by forming more supercoils. Tension is released by enzymes topoisomerases. With the help of various enzymes both the strands of DNA become open for replication.

However, whole of DNA does not open in one stretch due to very high energy requirement. The point of separation proceeds slowly towards both the directions. In each direction, it gives the appearance of Y-shaped structure called replication fork. RNA primer is a small strand of RNA which is synthesised at the 5' end of new DNA strand with the help of DNA specific RNA polymerase enzyme called primase.

Prokaryotes have three major types of DNA synthesising enzymes called DNA polymerases III, II and I. In eukaryotes five types of DNA polymerases are found - α, B, y, 8 and ε, but the major three being a, 8 and ε. The two separated DNA strands in the replication fork function as templates.

As replication proceeds, new areas of parent DNA duplex unwind and separate so that replication proceeds rapidly from the place of origin towards the other end. RNA primer is removed and the gap filled with complementary nucleotides by means of DNA polymerase I. DNA polymerase can polymerise nucleotides only in 5' → 3' direction on 3' → 5′ strand because it adds them at the 3' end. Since the two strands of DNA run in antiparallel directions, the two templates provide different ends for replication. Replication over the two templates thus proceeds in opposite directions. One strand with polarity 3'→ 5' forms its complementary strand continuously because 3' end of the latter is always open for elongation. It is called leading strand.

Replication is dicontinuous on the other template with polarity 5′→ 3' because only a short segment of DNA strand can be built in 5' →→ 3' direction due to exposure of a small stretch of template at one time. Short segments of replicated DNA are called Okazaki fragments. Okazaki fragments are joined together by means of enzyme, DNA ligase. DNA strand built up of Okazaki fragments is called lagging strand.



47. (a) Refer to answer 46.

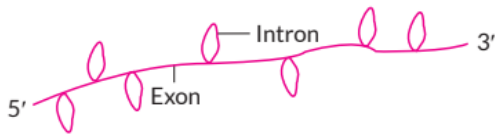
(b) In eukaryotes, the replication of DNA takes place during S-phase of the cell cycle. The replication of DNA and cell division cycle should be highly coordinated. A failure in cell division after DNA replication results into polyploidy (a chromosomal anomaly).

48. (a): The sequence of bases on mRNA transcribed is same as coding strand except, the base thymine is replaced by uracil, i.e., 5'-AUGCGGC-3'.

49. (b): Promoter is a DNA sequence that provides binding site for RNA polymerase and initiates transcription.

50. (a): In transcription unit, the terminator is located towards 3'-end (downstream) of the coding strand and it usually defines the end of the process of transcription.

51. (d): In the given figure, exons are coding regions and introns are non-coding regions. Introns are removed by cutting and joining of exons in a defined order by splicing mechanism. Thus, there are 7 introns and 8 exons in the given heterogenous RNA.



52. (c)

53. Cistron is a segment of DNA consisting of a stretch of base sequences that codes for one polypeptide chain, one transfer RNA (tRNA), ribosomal RNA (rRNA) molecule or performs any other specific function in connection with transcription, including controlling the functioning of other cistrons.

54. In eukaryotes, RNA polymerase II transcribes precursor of mRNA, the heterogeneous nuclear RNA (hnRNA).

55. RNA polymerase II

56. Exons are the segments in genes which contain coding nucleotide sequences. These sequences are ultimately translated into polypeptide. Thus, exons carry genetic information. Introns are the segments in genes which contain non-coding nucleotide sequences. These do not form part of mRNA and are removed during the processing of hnRNA (splicing).

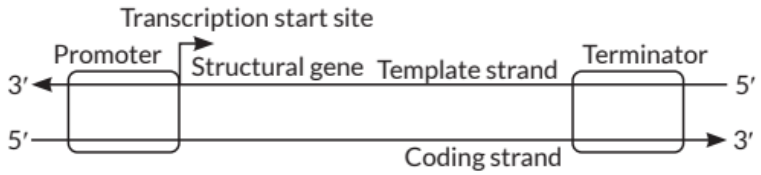
57. (a) The complementary strand for the given strand of DNA segment is

5′ - ATGCATGCATGCATGC – 3

(b) In RNA, the thymine is replaced by uracil. So, the RNA strand transcribed from the above molecule could be

5'-AUGCAUGCAUGCAUGC - 3'

58. The schematic diagram of a transcription unit is shown as follows:



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

	Template strand	Coding strand
(i)	Strand of DNA having 3′ → 5′ polarity.	Strand of DNA having 5′→ 3′ polarity.
(ii)	Participates in transcription.	Do not take part in transcription.

60. Differences between structural gene in prokaryotes and structural gene in eukaryotes are as follows:

	Structural gene in prokaryotes	Structural gene in eukaryotes
(i)	Consists of functional coding sequences.	Consists of both exons and introns.
(ii)	Information is continuous as only exons are present.	Information is split due to presence of introns in between exons.
(iii)	Splicing does not take place.	Splicing occur to make functional mRNA.

61. The corresponding coding strand is :

5' TACGTACGTACGTACGTACGTACG 3'

The corresponding mRNA strand is

5' UACGUACGUACGUACGUACGUACG 3'

62. (i) Three types of RNA polymerase is there in a eukaryotic cell - RNA polymerase I, RNA polymerase II and RNA polymerase III. RNA polymerase II transcribes hnRNA.

(ii) hnRNA undergoes splicing, capping and tailing before it leaves the nucleus as mRNA.

- Splicing: Eukaryotic transcripts contain both the exons (functional coding sequence) and the introns (non-functional coding sequence). Splicing is removal of introns and fusion of exons to form functional RNAs.

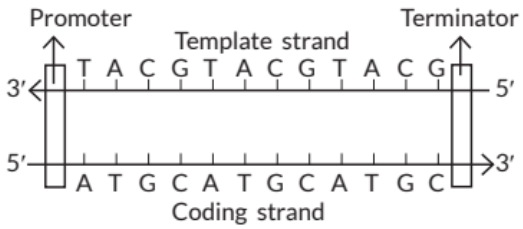
- Capping: In capping, methyl guanosine triphosphate is added to the 5'-end of hnRNA.

- Tailing: In tailing, adenylate residues (200-300) are added at 3'-end in a template independent manner.

It is the fully processed hnRNA, now called mRNA, that is transported out of the nucleus for translation.

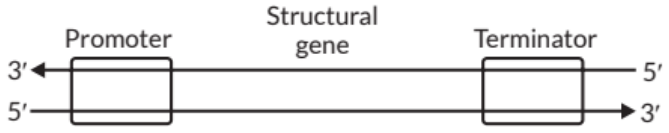
63. RNA segment that has been transcribed from a transcription unit which has the polarity (5' → 3') have uracil at the place of thymine. Given RNA strand:

For the given RNA, the transcription unit is given as:



DNA dependent RNA polymerase is an enzyme that transcribed this RNA segment.

64. Schematic representation of transcription unit is as follows:



(i) Promoter - The promoter is located towards 5'-end of the coding strand. It is a DNA sequence that provides binding site for RNA polymerase, and it is the presence of a promoter in a transcription unit that defines the template and coding strands.

(ii) Structural gene - The structural genes code for the enzymes and proteins. It transcribes the mRNA for the same.

(iii) Terminator - The terminator is located towards 3'-end of the coding strand and it defines the end of the process of transcription.

65. (a) The transcriptional products of RNA polymerase III are tRNA, 5SrRNA and snRNA.

(b) In capping, additional nucleotides (methyl guanosine triphosphate) are added to the 5'-end of hnRNA. In tailing, adenylate residues (200 - 300) are added at the 3′-end in a template independent manner.

(c) Heterogeneous nuclear RNA.

66. There are atleast three RNA polymerases in the nucleus (in addition to the RNA polymerase found in the organelles) i.e., RNA polymerase I, RNA polymerase II and RNA polymerase III.

(i) The RNA polymerase I is involved in transcription of rRNAs (28S, 18S, and 5.8S).

(ii) The RNA polymerase II is involved in transcription of the heterogeneous nuclear RNA (hnRNA) which is the precursor of mRNA.

(iii) The RNA polymerase III is involved in transcription of tRNA, 5SrRNA, and snRNAs (small nuclear RNAs).

67. In eukaryotic cells, the primary transcript is often larger than the functional mRNA and is known as heterogeneous RNA or hnRNA. It undergoes modification termed as post-transcriptional processing to become functional m-RNA. It has four steps.

(i) Cleavage: Larger RNA precursors are cleaved to form smaller RNAs.

(ii) Splicing Eukaryotic transcripts possess extra segments called introns or intervening sequences or non-coding sequences. They do not appear in mature or processed RNA. The functional coding sequences are called exons. Splicing is removal of introns and fusion of exons to form functional RNAs.

(iii) Terminal additions (capping and tailing): Additional nucleotides are added to the ends of RNAs for specific functions, e.g., CCA segment in tRNA, cap nucleotides at 5'-end of mRNA or poly-A segments (200-300 residues) at 3'-end of mRNA. Cap is formed by modification of GTP into 7-methyl guanosine or 7-mG.

(iv) Nucleotide modifications : They are most common in tRNA-methylation (e.g., methyl cytosine, methyl guanosine), deamination (e.g., inosine from adenine), dihydrouracil, pseudouracil, etc.

68. The comparison between processes of prokaryotic DNA replication and transcription are as follows:

S. No.	Replication	Transcription
1.	It is the process of synthesis of DNA from DNA.	It is the process of synthesis of RNA from DNA.
2.	Both the strands take part in replication.	Only one strand functions as template.
3.	It is catalysed by DNA polymerase.	It is catalysed by RNA polymerase.
4.	It occurs during S phase of cell cycle.	It occurs throughout during G_1 and G_2 phases of cell cycle.
5.	RNA primer is essential for initiation.	A primer is not required.

69. (a) Transcription is the process of copying genetic information from one strands of DNA into RNA. A transcription unit of a DNA has three regions a promoter, a structural gene and a terminator.

Bacterial structural gene in a transcription unit is polycistronic. Transcription requires a DNA dependent RNA polymerase. Prokaryotes have only one DNA dependent RNA polymerase which synthesises all types of RNA.

Three major types of RNAs in bacteria are mRNA (messenger RNA), tRNA (transfer RNA), and rRNA (ribosomal RNA). All three RNAs are needed to synthesise a protein in a cell. The mRNA provides the template, tRNA brings amino acids and reads the genetic code, and rRNAs play structural and catalytic role during translation. In bacteria/prokaryotes, transcription occurs in contact with cytoplasm as their DNA lies in the cytoplasm.

RNA polymerase binds to promoter and initiates transcription (Initiation). It uses nucleoside triphosphates as substrate and polymerises the mRNA strand in a template depended fashion following the rule of complementarity. It also facilitates opening of the helix and continues elongation. Only a short stretch of RNA remains bound to the enzyme. Once the polymerases reaches the terminator region, the nascent RNA falls off, so also the RNA polymerase. This results in termination of transcription.

(b) Refer to answer 67.

70. Mechanism of transcription in prokaryotes:

In bacteria/prokaryotes, transcription occurs in contact with cytoplasm as their DNA lies in the cytoplasm.

(i) Activation of ribonucleotides - The four types of ribonucleotides are adenosine monophosphate (AMP), guanosine monophosphate (GMP), uridine monophosphate (UMP) and cytidine monophosphate (CMP). They occur freely in the nucleoplasm. Prior to transcription the nucleotides are activated through phosphorylation. Enzyme phosphorylase is required along with energy. The activated or phosphorylated ribonucleotides are adenosine triphosphate (ATP), guanosine triphosphate (GTP), uridine triphosphate (UTP) and cytidine triphosphate (CTP).

(ii) Binding of RNA polymerase to DNA duplex - On a signal from the cytoplasm, DNA segment become ready to transcribe. The RNA polymerase enzyme binds to a specific site, called promoter, in the DNA double helix. Prokaryotes have only one RNA polymerase that synthesise all types of RNA. The promoter also determines which DNA strand is to be transcribed. Thus, a promotor region has RNA polymerase recognition site and RNA polymerase binding site.

(iii) Base pairing-Ribonucleoside triphosphates present in the surrounding medium come to lie opposite the nitrogen bases of the DNA template (anti-sense strand). They form complementary pairs; U opposite A, A opposite T, C opposite G and G opposite C. A pyrophosphate is released from each ribonucleoside triphosphate to produce ribonucleotide.

(iv) Formation of RNA chain - With the help of RNA polymerase the adjacent ribonucleotides held over DNA template join to form RNA chain. A single RNA polymerase recognise promoter and initiation region in prokaryotes. As the RNA chain formation initiates, the sigma (α) factor of the RNA polymerase separates. RNA polymerase (core enzyme) moves along the DNA template causing elongation of RNA chain at the rate of some 30 nucleotides per second. RNA synthesis stops as soon as polymerase reaches the terminator region. Rho factor (ρ) has ATPase activity and also possesses 4-8 adenine ribonucleotides.

(v) Separation of RNA chain - With the help of rho factor, the fully formed RNA chain is now released. One gene forms several molecules of RNA, which are released from the DNA template one after the other on completion. The released RNA is called primary transcript.

(vi) Duplex formation - As the RNA chain is released, the transcribed region of the DNA molecule gets hydrogen bonded to the sense strand and the two are spirally coiled to assume the original double helical form. The protective protein coat is added again to the DNA duplex. Gyrases, helicases and helix stabilizing proteins are released.

Differences between prokaryotic and eukaryotic transcription are:

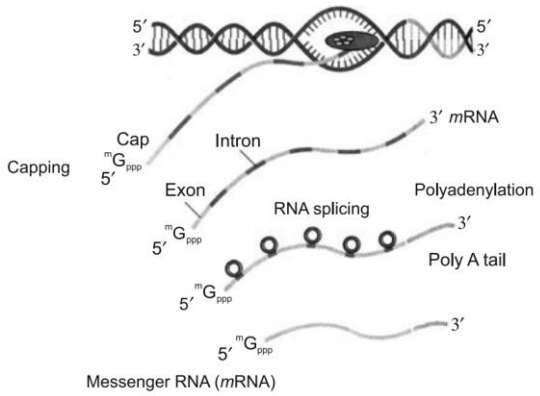
	Prokaryotic transcription	Eukaryotic transcription
(i)	It occurs in contact with cytoplasm.	It occurs inside the nucleus.
(ii)	There is no specific period for its occurrence.	Major part of transcription occurs in G_1 and G_2 phases.
(iii)	It is coupled to translation.	Transcription and translation are spacially separated.
(iv)	There is only one RNA polymerase.	There are three types of RNA polymerases.
(v)	RNA polymerase does not have separate transcription factors.	Transcription factors are involved in recognition of promotor site.
(vi)	*m*RNA is generally polycistronic.	*m*RNA is generally monocistronic.
(vii)	Splicing is generally not required.	In most of the cases, splicing is required for removing intervening sequences.

71. In eukaryotes, transcription occurs throughout I-phase in differentiated cells but more so in G_1 and G_2 phases of cell cycle inside the nucleus. Depending upon the requirement, a structural gene may transcribe one to numerous RNA molecules. The transcription products move out into cytoplasm for translation. Transcription requires a DNA dependent RNA polymerase. Eukaryotes have three RNA polymerase, Pol I (Pol A) (for ribosomal or rRNAs except 5S rRNA). Pol II (for mRNA, hnRNAs) and Pol III (for transfer or tRNA, 5S rRNA., and some snRNAs). Eukaryotic RNA polymerases also require transcription factors for initiation.

Prior to transcription, the nucleotides are activated through phosphorylation. Enzyme phosphorylase is required along with energy. Each DNA transcription segment has a promoter region, initiation site, coding region and a terminator region. RNA polymerase (common in prokaryotes and specific in eukaryotes) binds itself to the promoter region. The two strands of DNA uncoil progressively from the site of polymerase binding. One of the two strands of DNA (3'→ 5') functions as a template for transcription of RNA. Transcript formation occurs in 5' → 3' direction.

Ribonucleoside triphosphate present in the surrounding medium form complementary pairs. With the help of RNA polymerase, the adjacent ribonucleotides held over DNA template join to form RNA chain. In eukaryotes, there are separate transcription factor and RNA polymerase for activation of transcription. RNA polymerase (core enzyme) moves along the DNA template causing elongation of RNA chain at the rate of some 30 nucleotides per second.

RNA synthesis stops as soon as polymerase reaches the terminator region. In eukaryotes, the transcription unit yields a monocistronic mRNA. Diagrammatic representation of transcription in eukaryotes is as follows:



72. Mechanism of transcription in prokaryotes:

In bacteria/prokaryotes, transcription occurs in contact with cytoplasm as their DNA lies in the cytoplasm.

(i) Activation of ribonucleotides - The four types of ribonucleotides are adenosine monophosphate (AMP), guanosine monophosphate (GMP), uridine monophosphate (UMP) and cytidine monophosphate (CMP). They occur freely in the nucleoplasm. Prior to transcription the nucleotides are activated through phosphorylation. Enzyme phosphorylase is required along with energy. The activated or phosphorylated ribonucleotides are adenosine triphosphate (ATP), guanosine triphosphate (GTP), uridine triphosphate (UTP) and cytidine triphosphate (CTP).

(ii) Binding of RNA polymerase to DNA duplex - On a signal from the cytoplasm, DNA segment become ready to transcribe. The RNA polymerase enzyme binds to a specific site, called promoter, in the DNA double helix. Prokaryotes have only one RNA polymerase that synthesise all types of RNA. The promoter also determines which DNA strand is to be transcribed. Thus, a promotor region has RNA polymerase recognition site and RNA polymerase binding site.

(iii) Base pairing - Ribonucleoside triphosphates present in the surrounding medium come to lie opposite the nitrogen bases of the DNA template (anti-sense strand). They form complementary pairs; U opposite A, A opposite T, C opposite G and G opposite C. A pyrophosphate is released from each ribonucleoside triphosphate to produce ribonucleotide.

(iv) Formation of RNA chain - With the help of RNA polymerase the adjacent ribonucleotides held over DNA template join to form RNA chain. A single RNA polymerase recognise promoter and initiation region in prokaryotes. As the RNA chain formation initiates, the sigma (α) factor of the RNA polymerase separates.

RNA polymerase (core enzyme) moves along the DNA template causing elongation of RNA chain at the rate of some 30 nucleotides per second. RNA synthesis stops as soon as polymerase reaches the terminator region. Rho factor (ρ) has ATPase activity and also possesses 4-8 adenine ribonucleotides.

(v) Separation of RNA chain - With the help of rho factor, the fully formed RNA chain is now released. One gene forms several molecules of RNA, which are released from the DNA template one after the other on completion. The released RNA is called primary transcript.

(vi) Duplex formation - As the RNA chain is released, the transcribed region of the DNA molecule gets hydrogen bonded to the sense strand and the two are spirally coiled to assume the original double helical form. The protective protein coat is added again to the DNA duplex. Gyrases, helicases and helix stabilising proteins are released.

73. (a): In the given sequence of bases in mRNA, at the 3rd position UUU codes for phenylalanine and at the 5th position AUG codes for methionine during the process of translation.

74. (d): When an amino acid is coded by more than one codon, the genetic code is said to be degenerate.

75. (a): During elongation process of translation, peptide bond formation between amino acids is catalysed by peptidyl transferase (23S rRNA in bacteria).

76. AUG codon has dual functions. It codes for methionine (met) and also acts as an initiation codon for polypeptide synthesis.

77. The difference between unambiguous and degenerate codons is:

Unambiguous codons	Degenerate codons
They specify only one amino acid.	More than one codons that code for a single amino acids.

78. (a) AUG or methionine is an initiation codon as polypeptide synthesis is signalled by it whereas UAA (ochre) is termination codon as polypeptide chain termination is signalled by it.

(b) Genetic code is non-ambiguous, i.e., one codon specifies only one amino acid which implies that codons are specific. Degeneracy of code implies that some amino acids can be influenced by more than one codon. e.g., Phenylalanine is specified by two codons UUU and UUC.

79. (a) Differences between unambiguous and universal genetic codes are:

	Unambiguous code	Universal code
(i)	A codon specifies only one amino acid.	The codons specifies the same amino acids from a virus to a tree or human being.
(ii)	*E.g.*, AUG codes for methionine.	*E.g.*, from bacteria to human UUU would code for phenylalanine.

(b) Difference between the degenerate and initiator code is:

Degenerate code	Initiator code
More than one codon code for a single amino acid.	Signal polypeptide synthesis. It has dual functions.

80. (i) Stop codon : Codons that do not code for any amino acids and signal polypeptide chain termination. E.g., UAA, UAG, UGA.

(ii) Unambiguous codon : Codons that specify only one amino acid and not any other. E.g., AUG codes for methionine.

(iii) Degenerate codon : More than one codons codes for a single amino acid. In degenerate codons, generally the first two nitrogen bases are similar while the third one is different. E.g., UUU and UUC codes for phenylalanine.

(iv) Universal codon: A codon that is applicable universally i.e., specifies the same amino acid from a virus to a tree or human being.

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

(b) He proposed that since there are only 4 bases and if they have to code for 20 amino acids, the code should constitute a combination of bases made up of three nucleotides. Combination of 4^3 (4 x 4 x 4) would generate 64 codons; generating many more codons than required.

82. Exceptions to the universality of genetic code are:

(i) UAA and UGA are termination codons and do not code for any amino acid. But in Paramecium and some other ciliates, these codons code for glutamine.

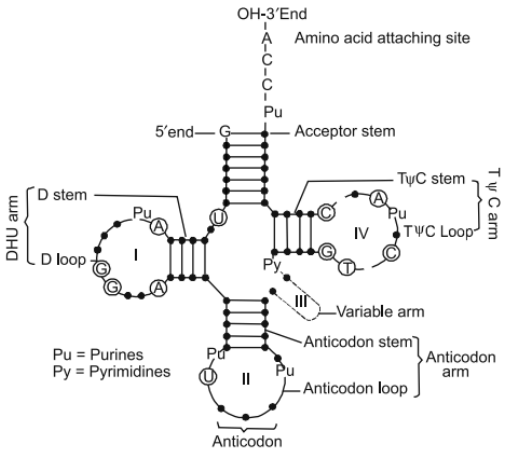
(ii) Genetic code is non-overlapping in most organisms. But, $\Phi \times 174$ has 5375 nucleotides that code for 10 proteins which require more than 6000 bases. Three of its genes E, B and K overlap other genes. Nucleotide sequence at the beginning

of E gene is contained within gene D. Likewise gene K overlaps with genes A and C. A similar condition is found in SV-40.

More than one codons code for a single amino acid, thus are called degenerate codons. In degenerate codes, the first two nitrogen bases are similar while the third one is different, e.g., UUU and UUC are the degenerate codes that code for amino acid phenylalanine.

83. (a) Crick postulated the presence of tRNA as an adapter molecule.

(b) Following is the clover leaf model of tRNA.



Role of tRNA in protein synthesis:

(i) tRNA is an adapter molecule meant for transferring amino acids during protein synthesis. tRNA binds to a particular amino acid at 3′ end. The charged tRNA take

the same amino acid to mRNA over particular codons corresponding to their anticodons.

(ii) tRNA holds peptidyl chains over the mRNAs.

(iii) The initiator tRNA has the dual function of initiation of protein synthesis as well as bringing in of the first amino acid.

84. (a) George Gamow suggested triplet code i.e., the genetic code should be made up of three nucleotides. He proposed that since there are only 4 bases and if they have to code for 20 amino acids, the code should constitute a combination of bases made up of three nucleotides. A combination of 4^3 (4 x 4 × 4) would generate 64 codons; generating many more codons than required. Hargobind Khorana developed the technique of synthesising RNA molecules with well-defined combination of bases (homopolymers and copolymers). He observed that these bases stimulated the formation of polypeptides having alternately similar amino acids such as cysteine-valine-cysteine. Marshall Nirenberg found out the

method of protein synthesis in cell free systems. Severo Ochoa discovered polynucleotide phosphorylase which could polymerise ribonucleotides to produce RNA without any template.

(b) The genetic code consists of 64 triplets or codons. With three exceptions (UAA, UAG and UGA), each codon encodes for one of the 20 amino acids used in the biosynthesis of proteins. The ribosome, the "protein synthesis machinery", deciphers codons aligned along mRNA to synthesise a specific polypeptide, which then folds into a defined structure or conformation.

85. (a) Structure of tRNA can be explained by means of L-form model (given by Klug 1974) and by means of clover leaf model (given by Holley 1965). In tRNA molecule, about half of the nucleotides are base paired to produce paired stems. Five regions are unpaired or single stranded - AA-binding site, TψC loop, DHU loop, extra arm and anticodon loop.

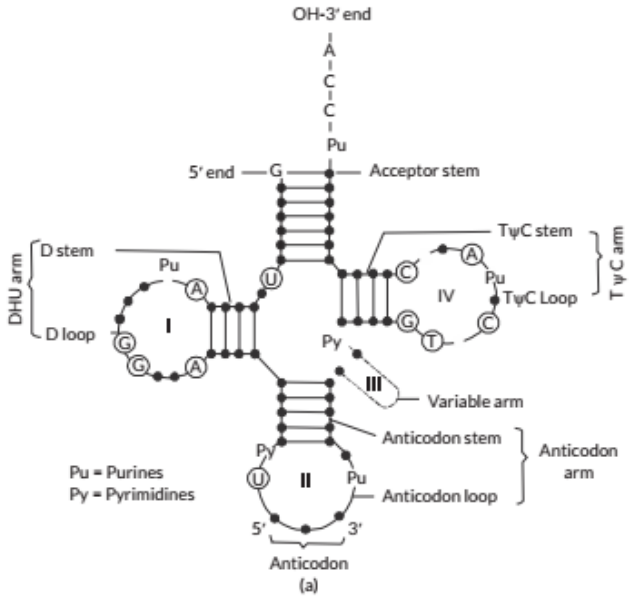
(i) Anticodon Loop - It has 7 bases out of which three bases form anticodon (nodoc) for recognising and attaching to the codon of mRNA.

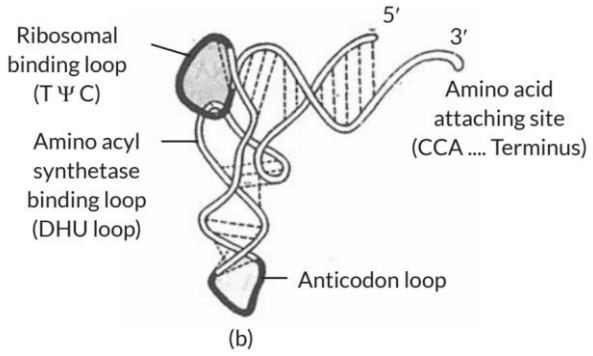
(ii) AA-Binding Site - It is amino acid binding site. The site lies at the 3' end opposite the anticodon and has CCA - OH group. The 5' end bears G. Amino acid or AA binding site and anticodon are the two recognition sites of tRNA.

(iii) TψC Loop - It has 7 bases out of which ψ (pseudouridine) and rT (ribothymidine) are unusual bases. The loop is the site for attaching to ribosome.

(iv) DHU Loop - The loop contains 8-12 bases. It is largest loop and has dihydrouridine. It is binding site for aminoacyl synthetase enzyme.

(v) Extra Arm - It is a variable side arm or loop which lies between T ψ C loop and anticodon. It is not present in all tRNAs. Following is the (a) clover leaf model and (b) L-form model of tRNA.





Functions of tRNA are:

(i) tRNA is meant for transferring amino acids during protein synthesis. tRNA binds to a particular amino acid at 3' end. The charged tRNA take the same amino acid to mRNA over particular codons corresponding to their anticodons.

(ii) tRNA holds peptidyl chains over the mRNAs.

(iii) The initiator tRNA has the dual function of initiation of protein synthesis as well as bringing in of the first amino acid. tRNA is known as an adapter molecule because it transfers amino acids to ribosomes during protein synthesis for synthesis of polypeptides.

(b) Eukaryotic transcripts possess extra segments called introns or intervening sequences or non-coding sequences. RNA contains both the exons and introns. The functional coding sequences are called exons. Splicing is removal of introns and fusion of exons to form functional hnRNAs. Each intron starts with dinucleotide GU and ends with dinucleotide AG (GU-AG rule). They are recognised by components of splicing apparatus of sn-RNPs or small nuclear ribonucleoproteins (viz, U1, U2, U4, U5, U6). A complex called spliceosome is formed between 5' end (GU) and 3' end (AG) of intron. Energy is obtained from ATP. It removes the intron. The adjacent exons are brought together. The ends are then sealed by RNA ligase.

86. (a) The relationship between the sequence of amino acids in a polypeptide and nucleotide sequence of DNA or mRNA is called genetic code.

(b) (i) Degenerate codon : More than one codons codes for a single amino acid. In degenerate codons, generally the first two nitrogen bases are similar while the third one is different. E.g., UUU and UUC codes for phenylalanine.

(ii) Unambiguous codon: Codons that specify only one amino acid and not any other. E.g., AUG codes for methionine.

(iii) Initiator code: Initiator codons are AUG and rarely GUG, which code respectively for methionine and valine. They initiate the process of translation.

87. (c): The different types of RNAs transcribed by RNA polymerase III in eukaryotes are tRNA, 5srRNA and snRNAs.

88. The two specific codons are initiation codon on one side (AUG or GUG) and termination codon (UAA, UAG or UGA) on the other side of mRNA.

89. Aminoacylation or charging of the tRNA is the process during which the amino-acyl-adenylate-enzyme complex reacts with tRNA specific for the amino acid to form aminoacyl-tRNA complex. Enzyme and AMP are released. tRNA complexed with amino acid is sometimes called charged tRNA. The amino acid is linked to 3-OH-end of tRNA through its -COOH group,

$AA \sim AMP - E + tRNA \rightarrow AA - tRNA + AMP + E$

Aminoacyl adenylate enzyme

The aminoacyl-tRNA complex specific for the initiation codon reaches the P-site to initiate the process of protein synthesis.

90. Ribozyme (catalytic RNA) is present in ribosome and joins the amino acids together by peptide bond formation to form protein chains. Release factor (RF) is GTP dependent. It binds to the stop codon, terminates translation and release the complete polypeptide from the ribosome.

91. Peptide bond formation occurs in the peptidyl transferase centre present in the larger subunit of ribosome. Peptide bond formation occurs between the nascent polypeptide chain and the new amino acid resulting in the elongation of polypeptide chain. An aminoacyl tRNA complex reaches the A-site and attaches to mRNA codon next to initiation codon with the help of its anticodon. The step requires GTP and an elongation factor.

A peptide bond (-CO-NH-) is established between the carboxyl group (-COOH) of amino acid attached to tRNA at P-site and amino group ($-NH_2$) of amino acid attached to tRNA at A-site. The reaction is catalysed by enzyme peptidyl transferase which is an RNA-enzyme. A lot of energy is consumed in protein synthesis. For every single amino acid incorporated in the peptide chain one ATP and two GTP molecules are used.

92. Aminoacylation or charging of the tRNA is the process during which the amino-acyl-adenylate-enzyme complex reacts with tRNA specific for the amino acid to form aminoacyl-tRNA complex. Enzyme and AMP are released. tRNA complexed with amino acid is sometimes called charged tRNA. The amino acid is linked to 3-OH-end of tRNA through its -COOH group,

$AA \sim AMP - E + tRNA \rightarrow AA - tRNA + AMP + E$

Aminoacyl adenylate enzyme

The aminoacyl-tRNA complex specific for the initiation codon reaches the P-site to initiate the process of protein synthesis.

93. (i) mRNA-Messenger RNA bring coded information from DNA and takes part in its translation by bringing amino acids in a particular sequence during the synthesis of polypeptide. However, the codons of mRNA are not recognised by amino acids but by anticodons of their adapter molecules (tRNAs → aa-tRNAs). Translation occurs over the ribosomes. The same mRNA may be reused over and again. In the form of polysome, it can help synthesise a number of copies simultaneously.

(ii) tRNAs -They are transfer or soluble RNAs which pick up particular amino acids (at CCA or 3' end) in the process called charging. The charged tRNAs take the same to mRNA over particular codons corresponding to their anticodons. A tRNA can pickup only a specific amino acid though an amino acid can be specified by 2-6 tRNAs. Each tRNA has an area for coming in contact with ribosome (T ψ C) and the enzyme amino-acyl tRNA synthetase (DHU).

(iii) Ribosomes - Protein synthesis occurs over the ribosomes. Ribosomes are, therefore, also called protein factories. Each ribosome has two unequal parts, small and large. The larger subunit of ribosome has a groove for pushing out newly formed polypeptide and protecting the same from cellular enzymes. The smaller subunit fits over the larger one like a cap but leaves a tunnel for mRNA. The two subunits come together only at the time of protein formation. Mg^{2+} is essential for it. Soon after the completion of protein synthesis, the subunits separate.

94. The three types of RNA are ribosomal RNA, messenger RNA and transfer RNA. Their roles are:

(i) rRNA - It binds protein molecules and give rise to ribosomes. 55 rRNA and surrounding protein complex provide binding site for tRNA. rRNA get associated with specific proteins to form ribosome subunits.

(ii) mRNA - Messenger RNA bring coded information from DNA and takes part in its translation by bringing amino acids in a particular sequence during the synthesis of polypeptide. However, the codons of mRNA are not recognised by amino acids but by anticodons of their adapter molecules (tRNAs → aa-tRNAs). Translation occurs over the ribosomes. The same mRNA may be reused. In the form of polysome, it can help synthesise a number of copies simultaneously.

(iii) tRNAs -They are transfer or soluble RNAs which pick up particular amino acids (at CCA or 3' end) in the process called charging. The charged tRNAs take the same to mRNA over particular codons corresponding to their anticodons. A tRNA can pickup only a specific amino acid though an amino acid can be specified

by 2-6 tRNAs. Each tRNA has an area for coming in contact with ribosome (T ψ C) and the enzyme amino-acyl tRNA synthetase (DHU).

95. The process of decoding of the message from mRNA to protein with the help of tRNA, ribosome and enzyme is called translation (protein synthesis). Protein synthesis occurs over ribosomes.

The 4 main steps in protein synthesis (translation) are: activation, initiation, elongation and termination of polypeptide chain.

The newly synthesised mRNA joins the smaller subunit of ribosome at 5' end. mRNAs carry the codon and tRNAs carry the anticodon for the same codon. Activation of amino acid is catalysed by the enzyme aminoacyl tRNA synthetase in the presence of ATP. In presence of ATP an amino acid combines with its specific amino acyl-tRNA synthetase to produce aminoacyl adenylate enzyme complex. This reacts with tRNA to form aminoacyl-tRNA complex. Activated tRNA is taken to ribosome mRNA complex for initiation of protein synthesis.

Initiation of protein synthesis is accomplished with the help of initiation factor which are 3 (IF3, IF2, IF1) in prokaryotes and 9 in eukaryotes (elF2, eIF3, elF1, eIF4A, elF4B, eIF4C, eIF4D, eIF5, elF6). The ribosome binds to the mRNA at the start codon (AUG) that is recognised only by the initiator tRNA. A polypeptide chain forms as tRNAs deliver amino acids to the ribosome. Large ribosomal subunit binds the initiation complex forming two (A and P) binding site for tRNA molecules. The first site is P site or peptidyl site which is occupied by $tRNA^{met}$. The second site is A or amino acyl site and is positioned over the second codon.

The ribosome proceeds to the elongation phase of protein synthesis. During this stage, complexes composed of an amino acid linked to tRNA, sequentially bind to the appropriate codon in mRNA by forming complementary base pairs with the tRNA anticodon. The ribosome moves from codon to codon along the mRNA. Amino acids are added one by one, translated into polypeptide sequences dictated by DNA and represented by mRNA. The enzyme peptidyl synthetase catalyses the formation of peptide bond between the carboxylic group of amino acid at P site and amino group of amino acid at A site. Enzyme translocase brings about the movement of mRNA by one codon.

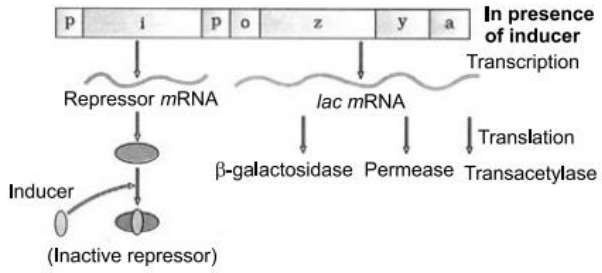
The termination of protein synthesis occur when a non-sense codon reaches at A site of ribosome. The chain detaches from the ribosome. A release factor binds to the stop codon, terminating translation and releasing the complete polypeptide from the ribosome. Two subunits of ribosomes dissociate with the help of dissociation factor.

96. (b): In the given figure, Q stands for regulatory genes, R is operator gene, S is enzyme transacetylase and T is repressor protein.

97. When lactose is present in the culture medium, then the lac operon in E. coli is switched on. It is because the inducer (lactose) binds to the repressor protein thereby inactivating it. It prevents binding of repressor to the operator. Consequently, RNA polymerase gets access to the promoter and transcription of structural genes proceeds.

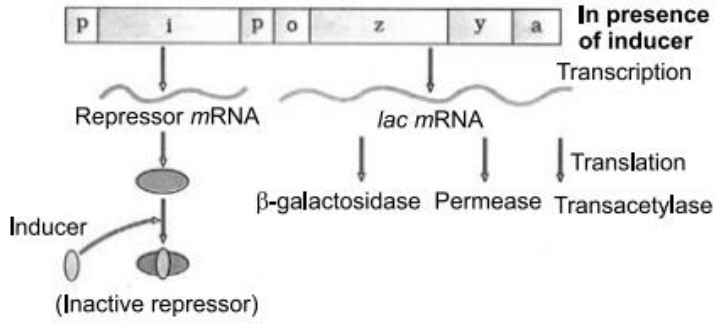
98. Lac operon is the operon of E. coli associated with lactose metabolism. It is an inducible operon that consists of a regulator, a promoter, an operator and three structural genes z, y and a. The structural genes are activated in presence of lactose that acts as an inducer. The structural genes are normally inactivated, as a repressor molecule binds to an operator gene preventing transcription. These genes get activated when lactose binds to the repressor disabling it from binding with operator. Now operator gene becomes free, permitting transcription thus expression of structural genes.

Its expression can be explained with the schematic diagram of lac operon in open state as follows:



99. In lac operon, the regulatory gene is called i gene because it produces an inhibitor or repressor. Inducer for the lac operon is lactose. Its role is to bind with repressor, change the latter into non-DNA binding state so as to free the operator gene and switch on lac operon. The products of gene z and y of the lac operon are β-galactosidase and premease respectively. β-galactosidase brings about hydrolysis of lactose to form glucose and galactose. Galactoside permease is required for entry of lactose into the bacterium. The a gene encodes a transcetylase.

Schematic diagram of lac operon in 'switched on' position is as follows:



The operon gets switched ‘off’ in the absence of lactose (inducer). The repressor molecule binds with the operator region of the operon and prevents RNA polymerase from transcribing the operon.

100. (a) The given schematic representation is of lac operon. In lac operon, the regulatory gene is called i-gene because it produces an inhibitor or repressor. The repressor binds to operator gene and stops the operator from working. In the absence of an inducer (i.e., lactose), the repressor binds to the operator gene making it non-functional. RNA polymerase enzyme cannot move over it to reach the structural genes. Thus, structural genes are inactivated and transcription cannot take place.

(b) As regulatory gene exerts a negative control over the working of structural genes, therefore regulation of lac operon is called negative regulation.

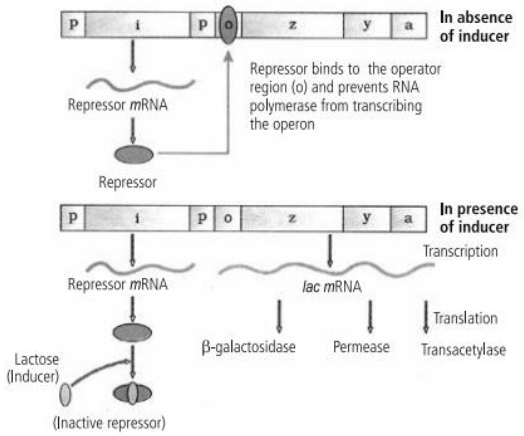
(c) 'Inducer' for the given operon is 'lactose. Its role is to bind with repressor, change the latter into non-DNA binding state so as to free the operator gene and switch on the lac operon. The products of the genes 'z' and 'y' of the lac operon are β-galactosidase and premease respectively. β-galactosidase brings about hydrolysis of lactose to form glucose and galactose. Galactoside permease is required for entry of lactose into the bacterium.

101. Refer to Answer 98.

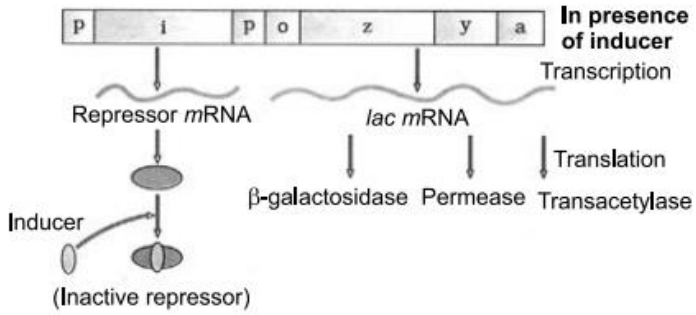
102. Lactose is the substrate for the enzyme beta-galactosidase and it regulates switching on and off of the operon. Hence, it acts as an inducer in lac operon. If lactose is provided in the growth medium of the bacteria, the lactose is transported into the cells through the action of permease and induces the operon.

In the presence of an inducer (lactose), repressor is inactivated by interaction with the inducer. This allows RNA polymerase access to the promoter and transcription proceeds. The operon gets switched 'off' in the absence of lactose as the repressor molecule binds with the operator region of the operon and prevents RNA polymerase from transcribing the operon.

Diagrammatic representation of lac operon is as follows:



103. Schematic diagram of lac operon in 'switched on' position is as follows:



The operon gets switched 'off' in the absence of lactose (inducer). The repressor molecule binds with the operator region of the operon and prevents RNA polymerase from transcribing the operon.

104. (d): Y-chromosome possesses least number of genes.

105. Single nucleotide polymorphism (SNPs or snips) help in finding chromosomal locations for disease associated sequences and tracing human history.

106. Some of the salient observations drawn from human genome project are as follows:

(i) The human genome consists of 3164.7 million bp.

(ii) The average gene consists of 3000 bases, though sizes vary greatly, with the largest known human gene dystrophin having 2.4 million bases.

(iii) Proteins are coded by less than 2 per cent of the genome.

(iv) Scientists have identified about 1.4 million locations where single base DNA differences called SNPs - single nucleotide polymorphism occur in humans. These locations would help to identify chromosomal locations for disease associated sequences and tracing human history.

107. (a) Chromosome 1 has most genes (2968).

(b) Chromosome Y has fewest (231).

108. (a) Four prime goals of the human genome project are as follows:

(i) The determination of the sequences of base pairs of human DNA.

(ii) The identification of all the genes (approximately 20,000-25,000) in human DNA.

(iiii) Storage of the genetic information in databases.

(iv) Improvement in tools for data analysis.

(b) Drosophila melanogaster is a common non-human model organism which has been sequenced after human genome.

109. 'SNP's, stands for single nucleotide polymorphism. About 1.4 million single base DNA differences or SNPs have been identified in humans. SNPs occur normally throughout a person's DNA almost once in every 1000 nucleotides on average.

Their number may be more than 10 million. They are helpful in finding chromosomal locations with disease associated sequences and tracing human history.

110. (a) The two methodologies involved in human genome project (HGP) are:

(i) Expressed sequence tags or ESTs, i.e., identification of all the genes that are expressed as RNA and sequencing the same.

(ii) Sequence annotation, i.e., sequencing whole set of genome and then assigning the functions to different regions.

HGP followed the second methodology which involves the following steps:

(i) The whole DNA of the cell is isolated and broken randomly into fragments.

(ii) They are inserted into specialised vectors like BAC (bacterial artificial chromosomes) and YAC (yeast artificial chromosome).

(iii) The fragments are cloned in suitable hosts like bacteria and yeast. PCR (polymerase chain reaction) can also be used for cloning or making copies of DNA fragments.

(iv) The fragments are sequenced as annotated DNA sequences.

(v) The sequences were then arranged on the basis of some overlapping regions. It necessitated the generation of overlapping fragments for sequencing.

(vi) Computer based programmes were used to align the sequences.

(vii) The sequences were then annotated and assigned to different chromosomes. All the human chromosomes have been sequenced, 22 autosomes, X and Y.

(viii) With the help of polymorphism in microsatellites and restriction endonuclease recognition sites, the genetic and physical maps of the genome have also been prepared.

(b) YAC is a vector and is expanded as yeast artificial chromosome. This vector is used to clone DNA fragments of more than 1 Mb in size; therefore, they have been

exploited extensively in mapping the large genome i.e., human genome project. They also contain restriction enzyme sites and genes which act as selectable markers in yeast.

111. (a) In human genome project, 'Y' stands for yeast in YAC (yeast artificial chromosomes) and 'B' stands for bacterial in BAC (bacterial artificial chromosomes). These are specialised vectors used during sequencing in human genome project.

(b) In human genome, less than 2 percent of the genome codes for proteins and functions of only 50% of discovered genes are known.

(c) Human genome has SNPs at 1.4 million locations. Expanded form of SNPs is Single Nucleotide Polymorphism.

112. (a) Four major goals of human genome project is:

(i) Identification of all the approximately 20,000-25,000 genes in human DNA.

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

(iii) To store this information in databases.

(iv) To improve tools for data analysis.

(b) Four ways in which knowledge of HGP is of significant for humans are:

(i) SNPs will be helpful in finding chromosomal locations with disease associated sequences and tracing human history.

(ii) Satellite DNA viz., minisatellite sequences called VNTRs are used in DNA fingerprinting.

(iii) Repetitive sequences called junk DNA provide information about chromosome structure, dynamics and evolution.

(iv) It will be possible to study how various genes and proteins work together.

(c) BAC Bacterial Artificial Chromosome. BAC is the vector into which DNA fragments are inserted to form rDNA (recombinant DNA) using recombinant DNA technology and are then multiplied in suitable host.

113. (d)

114. (c): In DNA fingerprinting, DNA is detected using Southern blotting where the separated DNA sequences are transferred from gel onto a nitrocellulose or nylon membrane.

115. Repetitive/satellite DNA can be separated from bulk genomic DNA by using density gradient centrifugation.

116. DNA polymorphism in a population arise due to mutations.

117. DNA fingerprinting helps in determining the paternity from a small sample of tissue or a drop of blood. DNA fingerprinting is a technique for identifying individuals, generally using repeated sequences in the human genome that produce a pattern of bands which is unique for every individual. Important for DNA fingerprinting are short nucleotide repeats that vary in number from person to person, but are inherited. These are the Variable Number of Tandem Repeats or VNTRs. The VNTRs of two persons may be of the same length and sequence at certain sites, but vary at others. DNA fingerprints can be prepared from extremely minute amounts of blood, semen, hair bulb or any other cells of the body.

118. (a) VNTR stands for Variable Number of Tandem Repeats that are short nucleotide repeats in DNA which are specific to each individual and vary in number from person to person but are inherited. The number of repeats in VNTRs are important for DNA fingerprinting technique and are also referred as "minisatellites". Each individual inherits these repeats from his/her parents which are used as genetic markers in a personal identity test. As a result, the size of VNTR varies from 0.1 to 20 kb. Consequently, after hybridisation with VNTR probe, the autoradiogram gives many bands of differing sizes. These bands give characteristic pattern for an individual DNA which is used to identify individuals.

(b) Applications of DNA fingerprinting are as follows:

(i) Paternity or maternity disputes can be solved by DNA fingerprinting as it can identify the real genetic mother, father and the offspring.

(ii) This technique is being used to identify genes connected with hereditary diseases.

(iii) It is useful in detection of crime and legal pursuits.

(iv) It can identify racial groups, their origin, historical migrations and invasions. **(Any two)**

119. DNA fingerprinting technology can help to identify the dead individuals. It is a technique of determining nucleotide sequences of certain portion of DNA which are unique to each individual. DNA fingerprints can be prepared from extremely minute amounts of blood, semen, hair bulb or certain other cells of the body. The major steps are as follows:

(i) DNA is extracted from the cells. It is cut into fragments with restriction enzymes. The fragments of DNA also contain VNTRS (Variable Number Tandem Repeats) which vary in number from person to person.

(ii) DNA fragments are passed through gel electrophoresis. Fragments of particular size having VNTRs are multiplied using PCR. Alkaline chemical is used to split dsDNA to ssDNA.

(iii) Separated DNA sequences are transferred from gel onto a nitrocellulose or nylon membrane.

(iv) Radioactive DNA probes complementary to VNTRS are poured over the nylon membrane. Some of them bind with VNTRS (Southern Blotting).

(v) X-ray film is exposed to the nylon sheet which gives dark bands at the probe sites. Thus, hybridised fragments are detected by autoradiography. The dark bands on X-ray film represent the DNA fingerprints (DNA profiles).

120. Satellite DNA are short, non-coding sequences of DNA. Satellite DNA are very specific in each individual, vary in number from person to person and are inherited. They do not code for any protein. They form large part of human genome. These sequences show high degree of polymorphism. Each individual inherits the satellite DNA from, his/her parents which are used as genetic markers in DNA fingerprinting.

121. The DNA fingerprinting technique is widely used in forensic that serves as the basis of paternity testing in case of disputes.

The major steps involved in DNA fingerprinting are as follows:

(i) DNA is extracted from the cells. It is cut into fragments with restriction enzymes. The fragments of DNA also contain VNTRS (Variable Number Tandem Repeats) which vary in number from person to person.

(ii) DNA fragments are passed through gel electrophoresis. Fragments of particular size having VNTRs are multiplied using PCR. Alkaline chemical is used to split dsDNA to ssDNA.

(iii) Separated DNA sequences are transferred from gel onto a nitrocellulose or nylon membrane.

(iv) Radioactive DNA probes complementary to VNTRS are poured over the nylon membrane. Some of them bind with VNTRS (Southern Blotting).

(v) X-ray film is exposed to the nylon sheet which gives dark bands at the probe sites. Thus, hybridised fragments are detected by autoradiography. The dark bands on X-ray film represent the DNA fingerprints (DNA profiles).

122. (a) DNA fingerprinting is an important tool of forensic science.

The major steps involved in DNA fingerprinting are as follows:

(i) DNA is extracted from the cells. It is cut into fragments with restriction enzymes. The fragments of DNA also contain VNTRS (Variable Number Tandem Repeats) which vary in number from person to person.

(ii) DNA fragments are passed through gel electrophoresis. Fragments of particular size having VNTRs are multiplied using PCR. Alkaline chemical is used to split dsDNA to ssDNA.

(iii) Separated DNA sequences are transferred from gel onto a nitrocellulose or nylon membrane.

(iv) Radioactive DNA probes complementary to VNTRS are poured over the nylon membrane. Some of them bind with VNTRS (Southern Blotting).

(v) X-ray film is exposed to the nylon sheet which gives dark bands at the probe sites. Thus, hybridised fragments are detected by autoradiography. The dark bands on X-ray film represent the DNA fingerprints (DNA profiles).

(b) Applications of DNA fingerprinting are as follows:

(i) Paternity or maternity disputes can be solved by DNA fingerprinting as it can identify the real genetic mother, father and the offspring.

(ii) This technique is being used to identify genes connected with hereditary diseases.

123. (a) Satellite DNA or repetitive DNA forms the basis of DNA fingerprinting. Two features of satellite DNA are:

(i) They do not code for any protein.

(ii) These sequences show high degree of polymorphism.

(b) The major steps involved in DNA fingerprinting are as follows:

(i) DNA is extracted from the cells. It is cut into fragments with restriction enzymes. The fragments of DNA also contain VNTRS (Variable Number Tandem Repeats) which vary in number from person to person.

(ii) DNA fragments are passed through gel electrophoresis. Fragments of particular size having VNTRs are multiplied using PCR. Alkaline chemical is used to split dsDNA to ssDNA.

(iii) Separated DNA sequences are transferred from gel onto a nitrocellulose or nylon membrane.

(iv) Radioactive DNA probes complementary to VNTRS are poured over the nylon membrane. Some of them bind with VNTRS (Southern Blotting).

(v) X-ray film is exposed to the nylon sheet which gives dark bands at the probe sites. Thus, hybridised fragments are detected by autoradiography. The dark bands on X-ray film represent the DNA fingerprints (DNA profiles).

Applications of DNA fingerprinting are as follows:

(i) Paternity or maternity disputes can be solved by DNA fingerprinting as it can identify the real genetic mother, father and the offspring.

(ii) This technique is being used to identify genes connected with hereditary diseases.

(iii) It is useful in detection of crime and legal pursuits.

(iv) It can identify racial groups, their origin, historical migrations and invasions.

CBSE Sample Questions

1. (b)

2. (c): A typical nucleosome contains 200 bp of DNA helix. So, number of base pairs in euchromatin containing 200 nucleosomes will be $= 200 \times 200 = 40{,}000$ bp

The length of euchromatin = total no. of base pairs x distance between two consecutive bp

$= 40{,}000 \text{ bp} \times 0.34 \times 10\text{-}9 \text{ m/bp}$

$= 13600 \times 10\text{-}9\text{m}$

3. (b): A is a structure of ribose sugar and B is a structure of deoxyribose sugar. Ribose sugar is present in RNA in which an additional OH group is present at 2'-carbon which makes it more reactive and structurally unstable, whereas deoxyribose sugar is present in DNA having 2'-H group which makes it less reactive and structurally more stable.

4. (d): The criteria for being a genetic material are:

(i) It should be able to generate its replica.

(ii) It should be chemically and structurally stable.

(iii) It should allow slow mutation.

(iv) It should be able to express itself in the form of Mendelian characters.

5. (b): Avery, MacLeod and McCarty observed that protein digesting enzymes (proteases) and RNA digesting enzymes (RNases) did not affect transformation so the transforming substance in Griffith experiment was not a protein or RNA,

but digestion with DNase did inhibit transformation. Thus, they concluded that DNA caused the transformation and is the genetic material.

6. Evaluation of DNA and RNA on the basis of the properties of the genetic material:

(i) Genetic material should be able to generate its replica (Replication). As per the rule of base pairing and complementarity, both the nucleic acids (DNA and RNA) have the ability to direct their duplications.

(ii) The genetic material should be chemically and structurally stable enough not to change with different stages of life cycle, age or with change in physiology of the organism. Presence of 2'-OH group and uracil make RNA more reactive and structurally less stable than DNA. Therefore, DNA is a better genetic material than RNA.

(iii) It should provide the scope for slow changes (mutation) that are required for evolution. Both DNA and RNA are able to mutate. In fact, RNA being unstable, mutates at a faster rate. Consequently, viruses having RNA genome and having shorter life span mutate and evolve faster.

(iv) It should be able to express itself in the form of 'Mendelian Characters: RNA can directly code for the synthesis of proteins, hence can easily express the characters. DNA, however, is dependent on RNA for synthesis of proteins. The protein synthesising machinery has evolved around RNA. Thus, both RNA and DNA can function as genetic material, but DNA being more stable is preferred for storage of genetic information.

7. (d): The sixth generation after 120 minutes contained 3.125% $^{15}N^{14}N$ and 96.875% $^{14}N^{14}N$ DNA in ratio of 1:31. At each replication, one strand of parent DNA is conserved in the daughter strand while the second strand is freshly synthesised.

8. (d): (i) - Continuous synthesis, (ii) - Discontinuous synthesis, (iii) - 3' end, (iv) - 5' end

9. Mechanism of replication of DNA suggested by Watson and Crick are as follows -

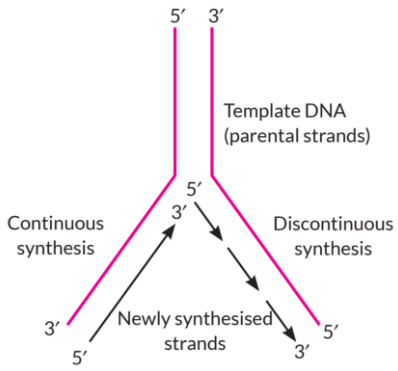
The two strands of DNA would separate and act as a template for the synthesis of new complementary strands. After the completion of replication, each DNA molecule would have one parental and one newly synthesised strand. This scheme was termed as semi-conservative replication of DNA.

In E. coli, the process of replication requires a set of catalysts or enzymes and the main enzyme is referred to as DNA-dependent DNA polymerase, since it uses a DNA template to catalyse the polymerisation of deoxynucleotides.

In addition to DNA polymerases, many additional enzymes are required to complete the process of replication with high degree of accuracy. Energetically replication is a very expensive process. Deoxyribonucleoside triphosphates serve dual purposes. In addition to acting as substrates, they provide energy for polymerisation reaction. For long DNA molecules, since the two strands of DNA cannot be separated in its entire length (due to very high energy requirement), the replication occurs within a small opening of the DNA helix, referred to as replication fork. The DNA-dependent DNA polymerases catalyse polymerisation only in one direction, i.e., 5'-3'.

Consequently, on one strand (the template with polarity 3'→ 5'), the replication is continuous, while on the other (the template with polarity 5′ 3′), it is discontinuous. The discontinuously synthesised fragments are later joined by the enzyme DNA ligase. The DNA polymerases on their own cannot initiate the process of replication. There is a definite region in E. coli DNA where the replication originates, such regions are termed as origin of replication. In eukaryotes, the replication of DNA takes place at S-phase of the cell-cycle. The replication of DNA and cell-division cycle should be highly coordinated. A failure in cell division after DNA replication results into polyploidy.

The figure representing replication fork is as follows:



10. (b): Promoter site for transcription is located at 5'-end (upstream) of the coding strand while terminator site is located towards 3'-end (downstream) of the coding strand.

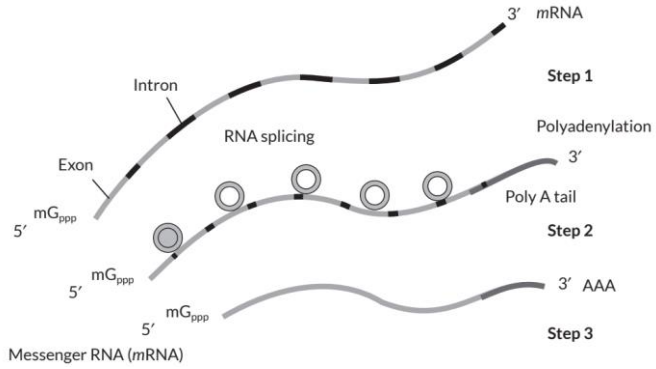
11. (b): In eukaryotes, mature RNA consists of exons (coding sequences) only and introns (non-coding sequences) are removed from the hnRNA by the process of RNA splicing.

12. (c)

13. (c): (i) Promoter site, (ii) Sigma factor and (iii) RNA polymerase.

14. (b)

15. (a) The hnRNA undergoes processes called capping and tailing followed by splicing. In capping, an unusual nucleotide (methyl guanosine triphosphate) is added to the 5'-end of hnRNA. In tailing, adenylate residues (about 200-300) are added at 3'-end in a template independent manner. Now the hnRNA undergoes a process where the introns are removed and exons are joined to form mRNA called splicing.



(b) Due to mutation in gene encoding RNA polymerase I and III, the process of translation will not happen, thus the polypeptide synthesis is stopped or hampered.

The reason for the above is:

RNA polymerase I transcribes rRNAs which is the cellular factory for protein synthesis.

RNA polymerase III helps in transcription of tRNA which is the adaptor molecule, that transfers amino acids to the site of protein synthesis.

16. A polypeptide of 24 amino acids will be formed as UAA is a stop codon which will prevent further translation.

17. (b): A-Methionine, B-UAC

18. (c)

19. (a) X to Y is 5'→3'

No more amino acids will be added after stop codon UAA.

(b) Codon-GCA; Anticodon-CGU

(c) The untranslated regions are required for an efficient translation process. They are present before the initiation codon at the 5'-end and after the stop/termination codon, at the 3'-end.

20. (a): Lactose is the substrate for the enzyme beta galactosidase and it regulates switching on and off of the operon. If lactose is present, it inactivates the repressor by binding to it thus, allowing transcription of genes. If lactose is

absent, repressor binds to the operator region and prevents RNA polymerase from transcribing the operon.

21. (a) When the active site of enzyme permease present in the cell membrane of a bacterium has been blocked by an inhibitor, the lactose is not transported into the cell. As lactose is the inducer, the lac operon will not be switched on.

(b) Since the repressor protein synthesized by the i gene is abnormal, it will not bind to the operator region of the operon, resulting in a continuous state of transcription process.

(c) No, because galactose is not an inducer. It is a product of lactose metabolism.

22. (a)

23. (c): Minisatellites are short non-coding but inheritable sequence of bases which are repeated many times and vary in number from person to person.

24. (c): Children 1 and 3 belong to the parents as their VNTR bands are matching with the parents.