Very Short Answer Questions (PY)

[1 Mark]

Q.1. How many base pairs would a DNA segment of length 1.36 mm have?

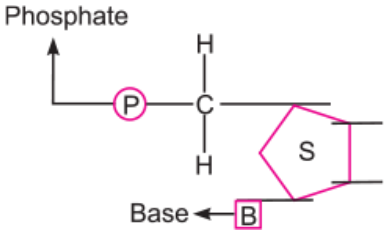
Ans. Distance between two base pairs = 0.34 mm or 0.34×10^{-6} mm
Number of base pairs in 1.36 mm DNA segment

$$= \frac{1}{0.34 \times 10^{-6}} \times 1.36$$
$$= 4 \times 10^{6} \text{ bp}$$

Q.2. Write the role of histone protein in packaging of DNA in eukaryotes.

Ans. Histones are positively charged basic proteins. The negatively charged DNA is wrapped around the positively charged histone octamer to form nucleosome.

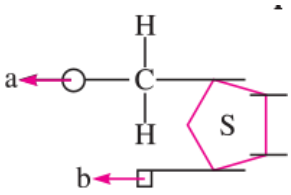
Q.3. Mention the carbon positions to which the nitrogenous base and the phosphate molecule are respectively linked in the nucleotide given below:



Ans.

Nitrogenous base is linked to first carbon.
Phosphate is linked to fifth carbon.

Q.4. What are '*a*' and '*b*' in the nucleotide with purine represented below?



Ans. '*a*' is phosphate group and '*b*' is purine (adenine/guanine).

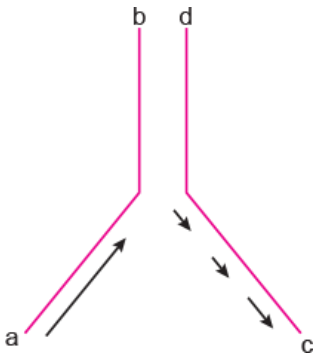
Q.5. How does the flow of genetic information in HIV deviate from the 'Central dogma' proposed by Francis Crick?

Ans. In HIV single stranded RNA is converted to double stranded DNA.

Q.6. Name the negatively charged and positively charged components of a nucleosome.

Ans. In a nucleosome, the negatively charged component is DNA and positively charged component is histone octamer.

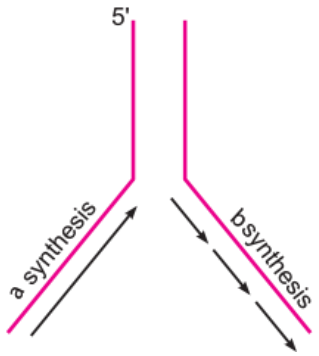
Q.7. Mention the polarity of the DNA strands *a–b* and *c–d* shown in the replicating fork given below.



***c–d* has polarity 5'–3'**

Ans. *a–b* has polarity 3'–5'

Q.8. Name the types of synthesis '*a*' and '*b*' occurring in the replication fork of DNA as shown below:



Ans.

a is continuous synthesis.
b is discontinuous synthesis.

Q.9. Name the enzyme involved in the continuous replication of DNA strand. Mention the polarity of the template strand.

Ans. DNA polymerase is involved in continuous replication of DNA strand. The polarity of template strand is 3′→5′.

Q.10. Name the enzyme and state its property that is responsible for continuous and discontinuous replication of the two strands of a DNA molecule.

Ans. DNA dependent DNA polymerase. It catalyses polymerisation in 5' → 3' direction only

Q.11. Name the transcriptionally active region of chromatin in a nucleus.

Ans. Euchromatin or exon.

Q.12. Mention the two additional processings which *hn*RNA needs to undergo after splicing so as to become functional.

Ans. Capping and tailing.

Q.13. When and at what end does the 'tailing' of *hn*RNA take place?

Ans. 'Tailing' of *hn*RNA takes place during conversion of *hn*RNA into functional *m*RNA after transcription. It takes place at the 3′-end.

Q.14. At which ends do 'capping' and 'tailing' of *hn*RNA occur, respectively?

Ans. Capping occurs at 5′-end and tailing occurs at 3′-end.

Q.15. What is cistron?

Ans. A cistron is a segment of DNA coding for a polypeptide.

Q.16. How does a degenerate code differ from an unambiguous one?

Ans. Degenerate code means that one amino acid can be coded by more than one codon. Unambiguous code means that one codon codes for only one amino acid.

Q.17. Mention two functions of the codon AUG.

Ans. Two functions of the codon AUG are:

i. It acts as a start codon during protein synthesis.
ii. It codes for the amino acid methionine.

Q.18. Mention the role of the codons AUG and UGA during protein synthesis.

Ans. The codon AUG initiates protein synthesis whereas the codon UGA stops protein synthesis.

Q.19. Write the function of RNA polymerase II.

Ans. RNA polymerase II transcribes precursor of *m*RNA or *hn*RNA.

Q.20. Give an example of a codon having dual function.

Ans. AUG acts as an initiation codon and also codes for methionine.

Q.21. Mention how does DNA polymorphism arise in a population.

Ans. DNA polymorphism in a population arise due to presence of inheritable mutations at high frequency.

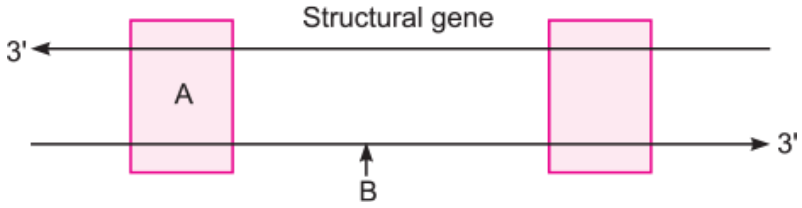
Q.22. Suggest a technique to a researcher who needs to separate fragments of DNA.

Ans. Gel electrophoresis is used to separate DNA fragments.

Q.23. Mention one difference to distinguish an exon from an intron.

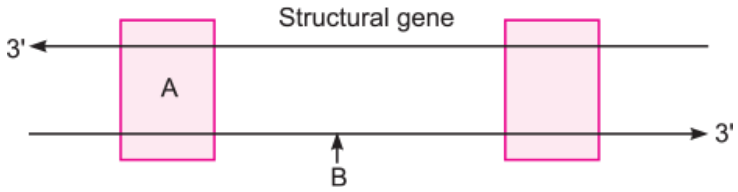
Ans. Exon is the coded or expressed sequence of nucleotides in *m*RNA.
Intron is the intervening sequence of nucleotides not appearing in processed *m*RNA.

Q.24. Name the parts 'A' and 'B' of the transcription unit given below.



Ans. 'A' is promoter sequence of DNA.
'B' is coding strand.

Q.25. What are a and b in the transcription unit represented below?



Ans.

a–Promoter
b–Terminator

Q.26. A region of a coding DNA strand has the following nucleotide sequence:

– A T G C –

What shall be the nucleotide sequence in

i. sister DNA segment it replicates, and
ii. m-RNA polynucleotide it transcribes?

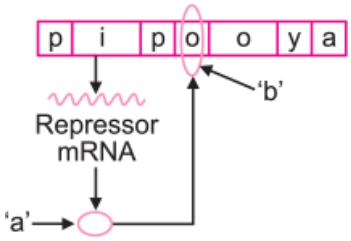
Ans.

i. – TACG –
ii. – UACG –

Q.27. Why *hn*RNA is required to undergo splicing?

Ans. *hn*RNA undergoes splicing in order to remove introns which are intervening or non-coding sequences and exons are joined to form functional *m*RNA.

Q.28. Given below is a schematic representation of a lac operon in the absence of an inducer. Identify '*a*' and '*b*' in it.



Ans. *a*–Repressor *b*–Repressor bound to the operator and prevents transcription of structural genes.

Q.29. State which human chromosome has

Q. the maximum number of genes and

Ans. Chromosome-1

Q. the one which has the least number of genes?

Ans. Y-Chromosome

Q.30. How is repetitive/satellite DNA separated from bulk genomic DNA for various genetic experiments?

Ans. By density gradient centrifugation.

Q.31. Mention the contribution of genetic maps in human genome project.

Ans. Genetic maps have played an important role in sequencing of genes, DNA fingerprinting, tracing human history, chromosomal location for disease associated sequences (*Any one*).

Very Short Answer Questions (OIQ)

[1 Mark]

Q.1. What are the two types of nucleic acids present in living system.

Ans. DNA and RNA.

Q.2. Who was the first to identify DNA and what was the name given to it by him?

Ans. DNA was first isolated by Friedrich Meischer in 1869 who named it as nuclein.

Q.3. Who proposed the famous double stranded helical structure of DNA?

Ans. James Watson and Francis Crick in 1953.

Q.4. How are the consecutive nucleotides linked together in a polynucleotide strands?

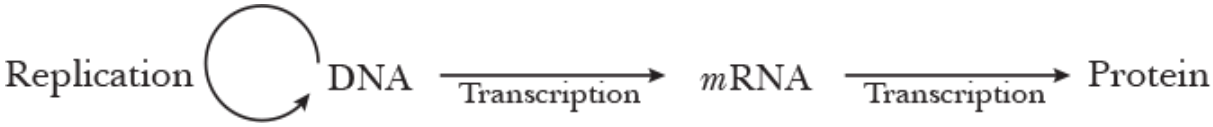
Ans. By phosphodiester bond.

Q.5. Who proposed central dogma of molecular biology?

Ans. Francis Crick.

Q.6. Write the central dogma of molecular biology.

Ans.



Q.7. What is the linkage between nitrogenous base and pentose sugar called?

Ans. N-glycosidic linkage.

Q.8. How many base pairs are present in one turn of DNA helix and what is the distance between consequent base pairs in a helix?

Ans. There are 10 base pairs in one turn and distance between consecutive bases is 0.34 nm.

Q.9. In an experiment, DNA is treated with a compound which tends to place itself amongst the stacks of nitrogenous base pairs. As a result of which the distance between two consecutive base increases, from 0.34 nm to 0.44 nm. Calculate the length of DNA double helix (which has 2 × 109 bp) in the presence of saturating amount of this compound.

Ans. $2 \times 10^9 \times 0.44$ nm.

Q.10. Calculate the length of the DNA of bacteriophage lambda that has 48502 base pairs.

Ans. Distance between two consecutive base pairs = 0.34×10^{-9} m

The length of DNA in bacteriophage lambda = $48502 \times 0.34 \times 10^{-9}$ m

$$= 16.49 \times 10^{-6} \text{ m}$$

Q.11. What do you mean by nucleoid?

Ans. In prokaryotes, the DNA is organised in large loops held by positively charged proteins in a region called nucleoid.

Q.12. Name amino acid residues of histone proteins.

Ans. Lysine and arginine.

Q.13. How many base pairs are present in a nucleosome?

Ans. 200 bp.

Q.14. Name the causal organism of pneumonia.

Ans. *Streptococcus pneumoniae*.

Q.15. Write the conclusion Griffith arrived at the end of his experiment with *Streptococcus pneumoniae*.

Ans. Griffith concluded that the R-strain bacteria had somehow been transformed by heat-killed S-strain bacteria. This must be due to transfer of genetic material.

Q.16. Name the genetic material in TMV.

Ans. RNA.

Q.17. What type of transcription is found in retrovirus? Name the enzyme.

Ans. In retrovirus the genetic information flows from RNA to DNA and is called reverse transcription while the enzyme involved is called reverse transcriptase.

Q.18. Name the base triplets which code for amino acid as well as start signal for translation.

Ans. AUG and GUG.

Q.19. On which plant did Taylor and his colleagues performed their experiment?

Ans. *Vicia faba*.

Q.20. What do you understand by transformation?

Ans. It is a biological phenomenon by which the DNA from one type of cell, when introduced into another type, is able to bestow some of the properties of the former to the latter.

Q.21. When does DNA replicate in the cell cycle?

Ans. During S-phase.

Q.22. What is origin of replication or ori?

Ans. It is the specific point in DNA from where replication begins.

Q.23. In a nucleus, the number of RNA nucleoside triphosphates is 10 times more than the number of DNA nucleoside triphosphates, still only DNA nucleotides are added during the DNA replication, and not the RNA nucleotides. Why?

Ans. DNA polymerase is highly specific to recognise only deoxyribonucleoside triphosphates. Therefore it cannot hold RNA nucleotides.

Q.24. What is replication fork?

Ans. During DNA replication the two strands separate out to form a Y-shaped structure on either side of origin which is called replication fork.

Q.25. AUG codes for

a. glycine
b. alanine
c. leucine
d. methionine.

Ans. (*d*) methionine

Q.26. How many bases will be there in three codons? How many amino acids will this number of bases code for?

Ans. There will be nine bases in three codons. These bases will code for three amino acids.

Q.27. Name the RNA that carries amino acid sequence information.

Ans. *m*RNA.

Q.28. What is genetic code?

Ans. It is the sequence of base triplet in a DNA molecule which determines the sequence of amino acids in a polypeptide.

Q.29. Define a codon.

Ans. The triplet bases on *m*RNA that codes for a particular amino acid is called codon.

Q.30. Define an anticodon.

Ans. The triplet base present on the tRNA which is complementary to codon on *m*RNA is called anticodon.

Q.31. What is *hn*RNA?

Ans. The precursor RNA transcribed by RNA polymerase that contains both exons and introns.

Q.32. Define translation.

Ans. The polymerisation of amino acids to form polypeptide with the help of *m*RNA, ribosome, and *t*RNA is called translation.

Q.33. Name the organelles which help in translation.

Ans. Ribosomes

Q.34. Name the bond present between two amino acids in a polypeptide.

Ans. Peptide bond

Q.35. Name the amino acids having only one codon.

Ans. Methionine and tryptophan.

Q.36. Who proposed the operon concept?

Ans. Jacob and Monod (1961).

Q.37. What do you mean by nonsense codon?

Ans. The codon which do not code for any amino acid and leads to termination of translation process is called nonsense codon.

Q.38. Name the three nonsense codons.

Ans. UAA, UAG and UGA.

Q.39. What is the function of aminoacyl tRNA synthetase?

Ans. It catalyses the attachment of amino acid to *t*RNA.

Q.40. What are variable number tandem repeats (VNTRs)?

Ans. The short nucleotide repeat sequences in the DNA which vary in number from person to person and are inheritable are called variable number tandem reports.

Q.41. Sometimes cattle or even human beings give birth to their young ones that have extremely different sets of organs like limbs/position of eye(s), etc. Why?

Ans. This is due to a disturbance in coordinated regulation of expression of sets of genes associated with organ development or due to mutations.

Q.42. Why is lactose considered an inducer in lac operon?

Ans. Lactose binds to repressor and prevents it from binding with the operator, as a result RNA polymerase binds to promoter–operator region to transcribe the structural genes.

Q.43. Why are proteins either positively or negatively charged?

Ans. If the proteins are rich in basic amino acids, they are positively charged, and if the proteins are rich in acidic amino acids, they are negatively charged.

Q.44. In a double stranded DNA, which strand is transcribed and why?

Ans. The strand having the polarity 3′→5′ is transcribed because RNA polymerase polymerises nucleotides only in 5′→3′ direction.

Q.45. Answer the following questions:

Q. Who developed the technique for DNA fingerprinting?

Ans. Dr. Alec Jeffreys

Q. Who proposed central dogma?

Ans. Francis Crick

Q. Who proposed *lac* operon?

Ans. Jacob and Monod.

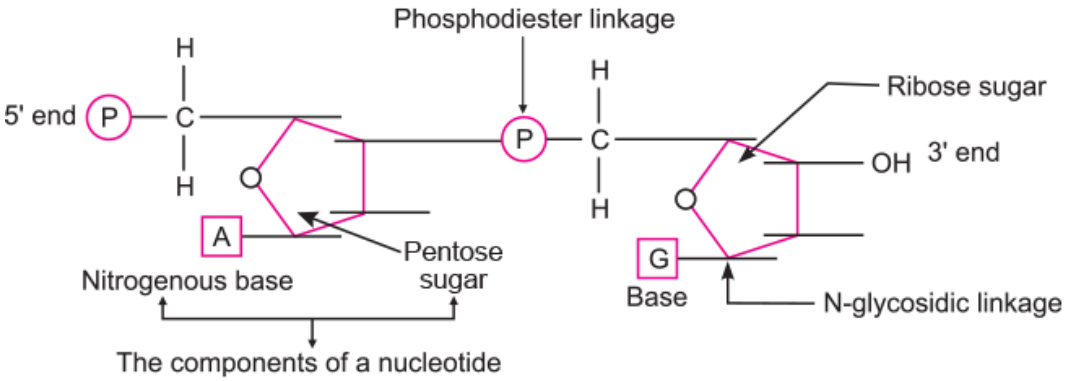
Short Answer Questions-I (PY)

[2 Marks]

Q.1. Draw a schematic representation of dinucleotide. Label the following:

i. The components of a nucleotide
ii. 5′ end
iii. N-glycosidic linkage
iv. Phosphodiester linkage.

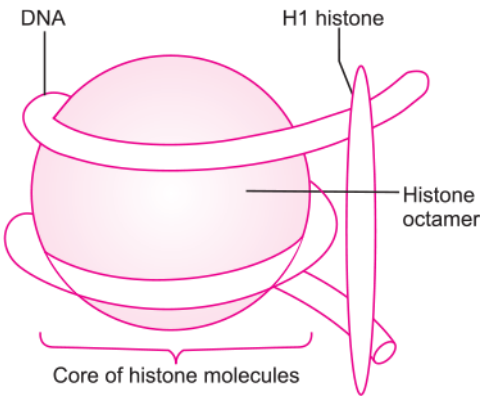
Ans. Nucleotide = Ribose sugar + Base + phosphate group.



Q.2. Describe the structure of a nucleosome.

Ans. Packaging of DNA in eukaryotes

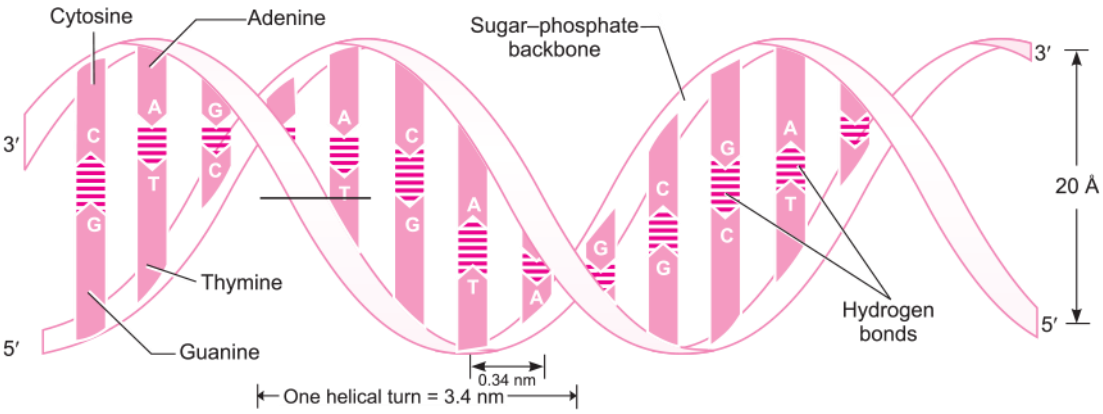
- The proteins associated with DNA are of two types—basic proteins (histone and protamine) and acidic non-histone chromosomal (NHC) proteins.
- The negatively charged DNA molecule wraps around the positively charged histone proteins to form a structure called nucleosome.
- The nucleosome core is made up of four types of histone proteins—H_2A, H_2B, H_3 and H_4— occurring in pairs.200 bp of DNA helix wrap around the nucleosome by 1¾ turns, plugged by H_1 histone protein.



Nucleosome

Q.3. Draw a schematic diagram of a part of double stranded dinucleotide DNA chain having all the four nitrogenous bases and showing the correct polarity.

Ans.



DNA double helix

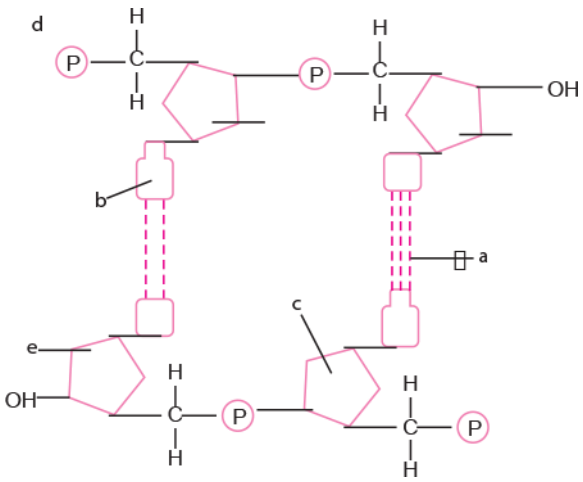
Q.4. Explain the role of ^{35}S and ^{32}P in the experiments conducted by Hershey and Chase.

Ans. Viruses grown in the medium containing ^{32}P contained radioactive DNA but not radioactive protein because DNA contains phosphorus but proteins do not contain phosphorus. Similarly, viruses grown on radioactive sulphur contained radioactive protein but not radioactive DNA because DNA does not contain sulphur.

Q.5. How do histones acquire positive charge?

Ans. Histones are rich in the basic amino acid residues lysines and arginines, which carry positive charges in their side chains. Therefore, histones are positively charged.

Q.6. Study the given portion of double stranded polynucleotide chain carefully. Identify *a*, *b*, *c* and the 5′-end of the chain.



Ans.

a. Hydrogen bonds
b. Purines, *i.e.*, adenine or guanine.
c. Pentose sugar (deoxyribose sugar)
d. d is the 5′-end.

Q.7. Explain the two factors responsible for conferring stability to double helix structure of DNA.

Ans. Factors responsible for conferring stability to double helix structure are presence of hydrogenbonds, the plane of one base pair stacks over the other, complementary presence of thymine in place of uracil.

Q.8.

a. (A) — DNA $\xrightarrow{(B)}$ *m*RNA $\xrightarrow{(C)}$ Protein

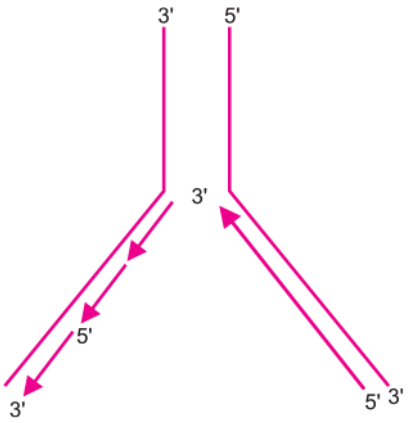
Look at the above sequence and mention the events (A), (B) and (C).

b. What does Central Dogma state in Molecular Biology? How does it differ in some viruses?

Ans.

a. A—DNA replication, B—Transcription, C—Translation
b. Central Dogma in Molecular Biology states that information flows in the order
DNA → RNA → Proteins
It differs in some viruses as the flow of information is in reverse direction, that is, from DNA to RNA.

Q.9.



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

Ans. The DNA-dependent DNA polymerase catalyses polymerisation only in one direction *i.e.*, 5′→3′. Therefore, in one strand with polarity 3′→5′ continuous replication takes place whereas the other strand with polarity 5′→3′ carries out discontinuous replication.
The strand with polarity 3′→5′ is called leading strand and the strand with polarity 5′→3′ is called lagging strand.

Q.10. State the dual role of deoxyribonucleoside triphosphates during DNA replication.

Ans.

i. Deoxyribonucleoside triphosphates act as substrates for polymerisation.
ii. These provide energy for polymerisation reaction.

Q.11. Discuss the role of enzyme DNA ligase plays during DNA replication.

Ans. DNA ligase joins or seals the discontinuous DNA fragments.

Q.12. A DNA segment has a total of 1500 nucleotides, out of which 410 are Guanine containing nucleotides. How many pyrimidine bases this DNA segment possesses?

Ans.

According to Chargaff 's rule

$$\frac{A}{G} = \frac{T}{G} = 1$$

G = C, G = 410, hence C = 410

G + C = 410 + 410 = 820

So, A + T = 1500 – 820 = 680

A = T, so $T = \frac{680}{2} = 340$

So, pyrimidines = C + T

= 410 + 340 = 750

Q.13. A DNA segment has a total of 2,000 nucleotides, out of which 520 are adenine containing nucleotides. How many purine bases this DNA segment possesses?

Ans.

[A] = [T]

A + T = 520 + 520 = 1040

Total number of nucleotides = 2000

∴ G + C = 2000 – 1040 = 960

$G = \frac{960}{2} = 480$

∴ Total number of purines (A + G) = 520 + 480 = 1000.

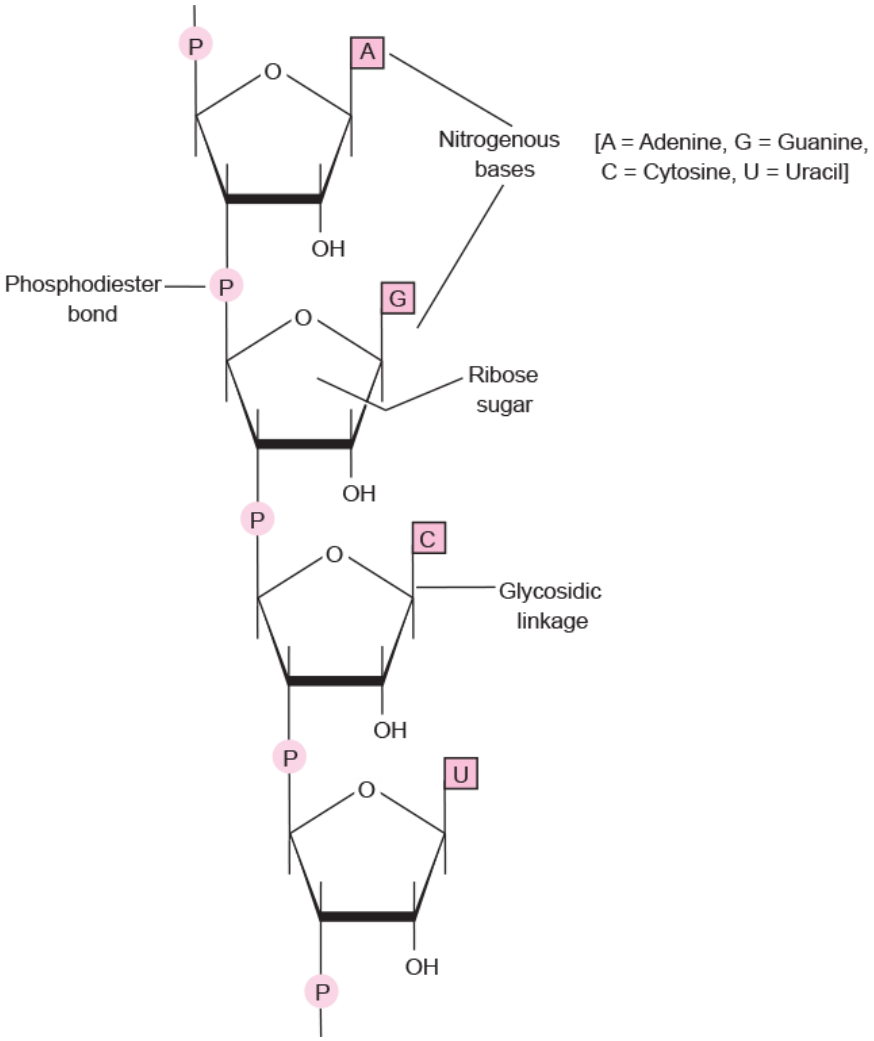
Q.14. A template strand is given below. Write down the corresponding coding strand and the *m*RNA strand that can be formed, along with their polarity.

3′ ATGCATGCATGCATGCATGCATGC 5′

Ans. Coding strand: 5′ TACGTACGTACGTACGTACGTACG 3′ ***m*RNA strand:** 5′ UACGUACGUACGUACGUACGUACG 3′

Q.15. Describe the structure of a RNA polynucleotide chain having four different types of nucleotides.

Ans.



Q.16. Differentiate between a template strand and a coding strand of DNA.

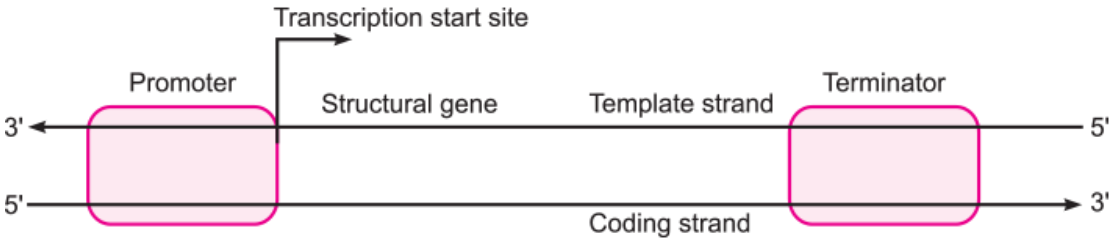
Ans.

S. No.	Template Strand	Coding Strand
(*i*)	The DNA strand that has the polarity and act as a template for transcription is known as template strand.	The strand which does not code anything and has polarity is called coding strand.
(*ii*)	Nucleotide sequence is complementary to the one present in *m*RNA.	The nucleotide sequence is the same to the one present in *m*RNA except for the

		presence of thymine instead of uracil.

Q.17. Draw a labelled schematic diagram of a transcription unit.

Ans.



Schematic structure of a transcription unit

Q.18. Explain the process of transcription in a bacterium.

Ans. Transcription in Prokaryotes

- In prokaryotes, the structural gene is polycistronic and continuous.
- In bacteria, the transcription of all the three types of RNA (*m*RNA, *t*RNA and *r*RNA) is catalysed by single DNA-dependent enzyme, called the **RNA polymerase**.
- In *E. coli* bacterium, the RNA polymerase has co-factors β, β′, α, α′ and ω along with σ (sigma) factor, to catalyse the process.
- The transcription is completed in three steps: initiation, elongation and termination.
- **Initiation:** σ (sigma) factor recognises the start signal and promotor region on DNA which then along with RNA polymerase binds to the promoter to initiate transcription.
- **Elongation:** The RNA polymerase after initiation of RNA transcription loses the σ factor but continues the polymerisation of ribonucleotides to form RNA.
- **Termination:** Once the RNA polymerase reaches the termination region of DNA, the RNA polymerase is separated from DNA–RNA hybrid, as a result nascent RNA separates. This process is called termination which is facilitated by a termination factor ρ (**rho**).
- In prokaryotes, *m*RNA does not require any processing, so both transcription and translation occur in the cytosol. It can be said that transcription and translation are coupled together.

Q.19.

i. **Name the scientist who suggested that the genetic code should be made of a combination of three nucleotides.**
ii. **Explain the basis on which he arrived at this conclusion.**

Ans.

i. George Gamow.
ii. He proposed that there are four bases and 20 amino acids So, there should be atleast 20 different genetic codes for these 20 amino acids.
The only possible combinations that would meet the requirement is combinations of 3 bases that will give 64 codons.

Q.20. Explain the dual function of AUG codon. Give the sequence of bases it is transcribed from and its anticodon.

Ans. The dual function of AUG codon:

a. It codes for amino acid methionine.
b. It is an initiation codon.

The sequence of bases from which it is transcribed is TAC. Its anticodon is UAC.

Q.21. Name the category of codons UGA belongs to. Mention another codon of the same category. Explain their role in protein synthesis.

Ans.

UGA is a stop or termination codon.
UAA, UAG are the other stop codons of the category.
They prevent the elongation of the polypeptide chain by terminating translation.

Q.22. Following are the features of genetic codes. What does each one indicate? Stop codon; Unambiguous codon; Degenerate codon; Universal codon.

Ans.

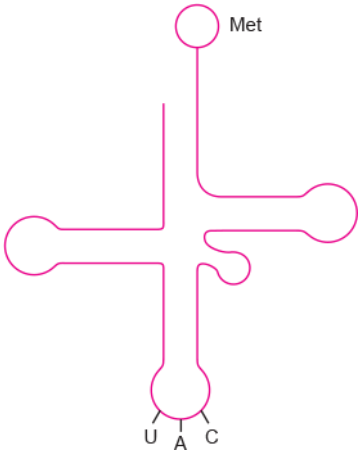
Stop codon does not code for any amino acid and terminates the synthesis of polypeptide chain.
Unambiguous codon: one codon codes for one amino acid only.
Degenerate codon: some amino acid are coded by more than one codon.
Universal codon: Genetic code is same for all organisms (bacteria to humans).

Q.23. Mention the role of ribosomes in peptide bond formation. How does ATP facilitate it?

Ans. There are two sites in the large subunit of the ribosome, for subsequent amino acids to bind to and thus, be close enough to each other for the formation of a peptide bond. The ribosome also acts as a catalyst for the formation of peptide bond 23S *r*RNA in bacteria is a ribozyme. Amino acids become activated by binding with its *t*RNA in the presence of aminoacyl *t*RNA synthetase and ATP.

Q.24. Draw the structure of a *t*RNA charged with methionine.

Ans.



Q.25. State the functions of the following in a prokaryote:

Q. *t*RNA

Ans. *t*RNA reads the genetic codes, carries amino acids to the site of protein synthesis and act as an adaptor molecule.

Q. *r*RNA

Ans. *r*RNA plays structural and catalytic role during translation.

Q.26. Where does peptide bond formation occur in a bacterial ribosome and how?

Ans. A peptide bond is formed between carboxyl group (—COOH) of amino acid at P-site and amino group (—NH) of amino acid at A-site by the enzyme **peptidyl transferase**.

Q.27. What is aminocylation? State its significance.

Ans. Aminoacylation of tRNA or charging of *t*RNA is the activation of amino acids in the presence of ATP and their linkage to their cognate *t*RNA.
If two such charged *t*RNAs are brought close enough, the formation of peptide bond between them would be favoured energetically.

Q.28. Mention two applications of DNA polymorphism.

Ans. DNA polymorphism is applicable in genetic mapping and DNA finger printing.

Q.29.

a. **Construct a complete transcription unit with promoter and terminator on the basis of the hypothetical template strand given below:**

b. Write the RNA strand transcribed from the above transcription unit along with its polarity.

Ans.

a.

b. Transcribed RNA

Q.30. Differentiate between the genetic codes given below:

a. Unambiguous and Universal.
b. Degenerate and Initiator

Ans.

(*a*) **Unambiguous:** One codon codes for only oneamino acid.	**Universal:** Codons are (nearly) same for all organisms (from bacteria to humans)
(*b*) **Degenerate:** More than one codon can code for the same amino acid.	**Initiator:** Start codon i.e., AUG is the imitation.

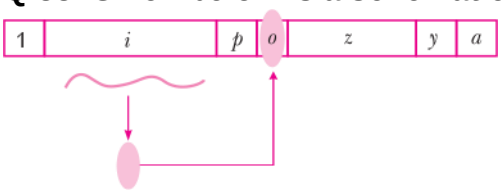
Q.31.

a. Name the enzyme responsible for the transcription of *t*RNA and the amino acid the initiator *t*RNA gets linked with.
b. Explain the role of initiator *t*RNA in initiation of protein synthesis.

Q.32. Three codons on *m*RNA are not recognised by *t*RNA, what are they? What is the general term used for them? What is their significance in protein synthesis?

Ans. UAA, UAG and UGA are the three codons that are not recognised by *t*RNA. They are also called nonsense or termination or stop codon. They terminate protein synthesis.

Q.33. Given below is a schematic representation of *lac* operon:



Q. Identify *i* and *p*.

Ans. i is the regulatory gene and *p* is the promoter gene.

Q. Name the 'inducer' for this operon and explain its role.

Ans. Lactose is the inducer. It is the substrate for the enzyme beta-galactosidase and it regulates switching on and off of the operon.

Q.34. How are the structural genes inactivated in *lac* operon in *E. coli*? Explain.

Ans. The regulator gene produces repressor which when free, binds to the operator region of the operon and prevents RNA polymerase from transcribing the structural genes.

Q.35. How are the structural genes activated in the lac operon in *E. coli*?

Ans. Lactose acts as the inducer that binds with repressor protein that cannot bind to operator and hence frees the operator gene. RNA polymerase freely moves over the structural genes, transcribing lac *m*RNA, which in turn produces the enzymes responsible for the digestion of lactose.

Q.36. State the difference between the structural genes in a transcription unit of prokaryotes and eukaryotes.

Ans.

S.No.	Prokaryotes	Eukaryotes
(*i*)	Polycistronic	Monocistronic
(*ii*)	No split genes present. The coding sequence is not interrupted.	Split genes present. The coding sequence is interrupted to form exon and intron.

Q.37. What are satellite DNA in a genome? Explain their role in DNA fingerprinting.

OR

Explain the significance of satellite DNA in DNA fingerprinting technique.

Ans. A small stretch of DNA sequence that repeats many a time, shows a high degree of polymorphism and forms a bulk of DNA in a genome called satellite DNA.

i. They do not code for any proteins.
ii. They form large part of the human genome.
iii. They show high degree of polymorphism and are specific to each individual.

Q.38. Where is an 'operator' located in a prokaryote DNA? How does an operator regulate gene expression at transcriptional level in a prokaryote? Explain.

Ans. The operator region is located adjacent to promoter elements or prior to structural gene. The operator regulates switching on and off the operon when the repressor binds to the operator region it is switched off and prevents transcription.

In the presence of inducer the repressor is inactivated and operator allows RNA polymerase to access the promoter. The operon is switched on and transcription proceeds.

Q.39. 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?

Ans. The genetic code is universal except in mitochondria and few protozoans.
Some codes are said to be degenerate because some amino acids are coded by more than one code.

Q.40. Answer the following questions:

Q. Name the enzyme that catalyses the transcription of *hn*RNA.

Ans. RNA polymerase II.

Q. Why does the *hn*RNA need to undergo changes? List the changes that *hn*RNA undergoes and where in the cell such changes take place.

Ans. *hn*RNA has non-functional introns in between the functional exons. To remove these, it undergoes changes. The changes that *hn*RNA undergoes include capping, *i.e.*, methyl guanosine triphosphate is added to 5′ end; tailing in which poly A tail is added at 3′ end; and splicing by which introns are removed and exons are joined.

Q.41. Answer the following questions:

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

Ans. The two methodologies involved in human genome project are:

i. Expressed Sequence Tags: Identifying all the genes that are expressed as RNA
ii. Sequence Annotation: Sequencing the whole set of genome coding or non coding sequences and later assigning different region with functions.

Q. Expand 'YAC' and mention what was it used for.

Ans. 'YAC' stands for Yeast Artificial Chromosome. It is used as a cloning vectors.

Short Answer Questions-I (OIQ)

[2 Mark]

Q.1. List the three major functions of a gene.

Ans. Three major functions of a gene are:

i. It should be able to store information and to express itself when required.
ii. It should be heritable from one generation to next.
iii. It should be autocatalytic, *i.e.*, should be able to produce its own replica.

Q.2. What are untranslated regions (UTRs)?

Ans. *m*RNA has some additional sequences that are not translated and are called untranslated regions (UTRs). The UTRs are present both at 3′-end (before the start codon) and at 5′-end (after the stop codon). They only help in efficient translation process.

Q.3. What are introns and exons? What process removes the unwanted RNA region and joins those that code for amino acids?

Ans. Introns: The non-coding region of DNA or gene are called introns.
Exons: The coding region of DNA or gene which translate polypeptide are called exons. RNA splicing is the process that removes the unwanted RNA region and joins those that code for amino acids.

Q.4. What are the functions of

i. methylated guanosine cap and
ii. poly-A tail in a mature *m*RNA?

Ans. Methylated guanosine cap helps in binding of *m*RNA to smaller ribosomal sub-unit during initiation of translation. Poly–A tail provides longevity to *m*RNA's life. Tail length and longevity of *m*RNA are positively correlated.

Q.5. Write the full form of SNPs, BAC and YAC.

Ans.

SNPs—Single nucleotide polymorphisms
BAC—Bacterial artificial chromosome
YAC—Yeast artificial chromosome

Q.6. What are the functions of DNA polymerase?

Ans. The functions of DNA polymerase are:

i. The DNA polymerase can catalyse the polymerisation of nucleotide to produce DNA strand by replication.
ii. The DNA polymerase has the ability of proofreading, i.e., to remove wrong base and to add correct bases over the wrong base.

Q.7. Explain what happens in frameshift mutation. Name one disease caused by the disorder.

Ans. The mutation in which addition/insertion or deletion of one or two bases changes the reading frame from the site of mutation is called frameshift mutation. It may result in polypeptide with different sequences of amino acid. A disease caused by frameshift mutation is muscular dystrophy

Q.8. What is meant by semi-conservative nature of DNA replication?

Ans. After DNA replication, the daughter DNA formed contains one parental strand and one newly synthesised strand. Such type of DNA replication is called semi-conservative DNA replication.

Q.9. Explain the process of charging of *t*RNA. Why is it essential in translation?

Ans. The amino acids are activated in the presence of ATP and linked to their cognate *t*RNA. This process is called charging of *t*RNA or amino-acylation of *t*RNA. When two such charged *t*RNAs are brought close enough, the formation of peptide bond between them would be favoured energetically. The presence of a catalyst would enhance the rate of peptide bond formation.

Q.10. Differentiate between codon and an anticodon.

Ans.

Codon	Anticodon
The sequence of 3 nitrogen bases on *m*RNA that codes for a particular amino acid during translation is called codon.	The sequence of 3 nitrogenous bases on *t*RNA that are complementary to the codon on *m*RNA for a particular amino acid during translation is called anticodon.

Q.11. What is splicing? Why is splicing necessary in eukaryotic genes?

Ans. The process by which non-coding regions (intron) on *hn*RNA are removed and coding regions (exon) are joined to produce *m*RNA is called splicing. Splicing is necessary in eukaryotes to remove the non-coding introns from *hn*RNA to produce a meaningful functional *m*RNA. Prokaryotes do not have introns in the *m*RNA.

Q.12. A cistron consists of 20 codons. How many amino acids will it code in the polypeptide transcribed? Why?

Ans. It will code for 19 amino acids because, the last codon on *m*RNA will be a terminating codon, which will not code for any amino acid.

Q.13. In a nucleus, the number of RNA nucleoside triphosphates is 10 times more than the number of DNA nucleoside triphosphates, still only DNA nucleotides are added during the DNA replication and not the RNA nucleotides. Why?

Ans. DNA polymerase is highly specific to recognise only deoxyribonucleoside triphosphates. Therefore it cannot hold RNA nucleotides.

Q.14. What would happen if histones were to be mutated and made rich in amino acids aspartic acid and glutamic acid in place of basic amino acids such as lysine and arginine?

Ans. If histone proteins were rich in acidic amino acids instead of basic amino acids then they may not have any role in DNA packaging in eukaryotes as DNA is also negatively charged molecule. The packaging of DNA around the nucleosome would not happen. Consequently, the chromatin fibre would not be formed.

Q.15. Recall the experiment done by Frederick Griffith. If RNA, instead of DNA was the genetic material, would the heat killed strain of Streptococcus have transformed the R-strain into virulent strain? Explain your answer.

Ans. RNA is more labile and prone to degradation (owing to the presence of 2′–OH group in its ribose). Hence heat-killed S-strain may not have retained its ability to transform the R-strain.

Q.16. Retrovirus do not follow central dogma. Comment.

Ans. Genetic material of retrovirus is RNA. At the time of synthesis of protein, RNA is reverse transcribed to its complementary DNA first, then transcriped to RNA and proteins. Hence, retrovirus are not known to follow central dogma.

Q.17. An *m*RNA strand has a series of codon out of which three are given below:

(i) AUG (ii) UUU (iii) UAG

a. What will their DNA codon be translated into?
b. What are the DNA codon that would have transcribed these RNA codon?

Ans.

a.
   i. AUG—Methionine
   ii. UUU—Phenylalanine
   iii. UAG—No amino acid is coded as it is a stop codon.
b. TAC, AAA, ATC.

Q.18. Name indicating their functions, a few additional enzymes, other than DNA polymerase and ligase, that are involved in the replication of DNA with high degree of processivity and accuracy.

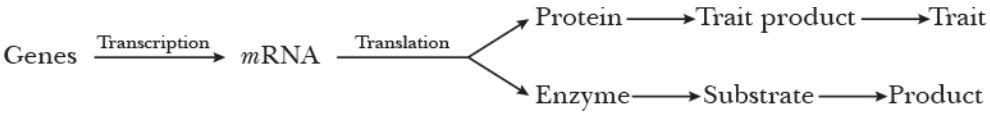
Ans.

i. **Helicase:** opens the helix
ii. **Topoisomerases:** removes the supercoiling of DNA relieves the tension due to unwinding
iii. **Primase:** synthesises RNA primer
iv. **Telomerase:** to synthesises the DNA of telomeric end of chromosomes.

Q.19. During *in vitro* synthesis of DNA, a researcher used 2′, 3′-dideoxycytidine triphosphate as raw nucleotide in place of 2′-deoxy cytidine triphosphate, other conditions remaining as standard. Will further polymerisation of DNA continue up to the end or not? Explain.

Q.20. "Genes contain the information that is required to express a particular trait." Explain.

Ans. The genes present in an organism show a particular trait by way of forming certain product. This is facilitated by the process of transcription and translation (according to central dogma of Biology)



Q.21. A low level of expression of *lac* operon occurs at all the time. Can you explain the logic behind this phenomena.

Ans. In the complete absence of expression of *lac* operon, permease will not be synthesised which is essential for transport of lactose from medium into the cells. And if lactose cannot be transported into the cell, then it cannot act as inducer. Hence, cannot relieve the *lac* operon from its repressed state. Therefore, *lac* operon is always expressed.

Q.22. A single base mutation in a gene may not 'always' result in loss or gain of function. Do you think the statement is correct? Defend your answer.

Ans. The statement is correct because of degeneracy of codons, mutations at third base of codon, usually doe not result into any change in phenotype. This is called silent mutations but at other times it can lead to loss or formation of malformed protein changing the phenotype.

Q.23. Protein synthesis machinery revolves around RNA but in the course of evolution it was replaced by DNA. Justify.

Ans. Since RNA was unstable and prone to mutations, DNA evolved from RNA with chemical modifications that makes it more stable.

DNA has double stranded nature and has complementary strands. These further resist changes by evolving a process of repair.

Q.24. What is a cistron? Why is the structural gene in a transcription unit of eukaryotes called monocistronic and that in prokaryotes/bacteria called polycistronic? Give reasons.

Ans. Cistron is a segment of DNA coding for a polypeptide. In eukaryotes the transcriptional unit have interrupted coding sequences - exons and introns. It codes for only one polypeptide, so it is called monocistronic.

In prokaryotes structural genes have many coding sequences, so it is called polycistronic.

Q.25. Would it be appropriate to use DNA probes such as VNTR in DNA fingerprinting of a bacteriophage?

Ans. Bacteriophage does not have repetitive sequence such as VNTR in its genome as its genome is very small and have all the codon sequenced. Therefore, DNA fingerprinting is not done for bacteriophages.

Q.26. Comment on the utility of variability in number of tandem repeats during DNA fingerprinting.

Ans. Tandemness in repeats provides many copies of the sequence for fingerprinting and variability in nitrogen base sequence in them. Being individual-specific, this proves to be useful in the process of DNA fingerprinting.

Q.27. Write the full form of VNTR. How is VNTR different from a probe?

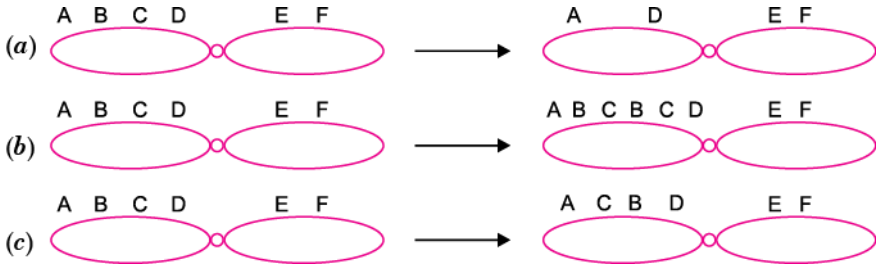
Ans. Full form of VNTR is Variable Number of Tandem Repeats

VNTR	Probe
The segment of DNA which shows very high no. of repetitive nucleotide sequences which vary from person to person are called variable number tandem repeats.	The small fragments of DNA strands which are highly selective and specific to be complementary to VNTR sequences are called probe.

Q.28. What is amplification with reference to DNA fingerprinting?

Ans. The process of multiplication of DNA by subjecting the desired DNA to polymerase chain reaction is called amplification.

Q.29. Mention the technical term in following diagram:



Ans.

a. Deletion
b. Duplication
c. Inversion.

Q.30. AUG GAC CUG AUA UUU UGA is the base sequence in a strand of mRNA.

i. Write the base sequence of the DNA strand from which it has been transcribed.
ii. Upon translation, how many amino acids will the resulting peptide have?

Ans.

i. TAC CTG GAC TAT AAA ACT
ii. Five amino acids.

Q.31. The base sequence of one strand of DNA is TACTAGGAT.

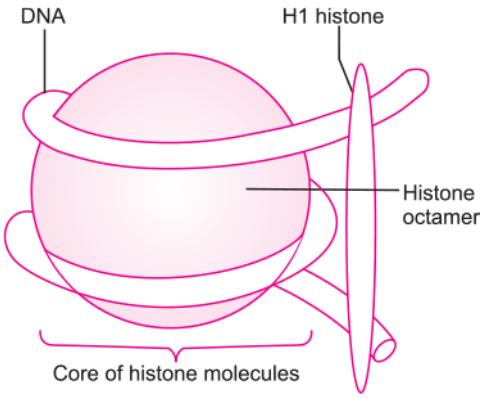
i. Write the base sequence of the RNA got after transcription of the given sequence.
ii. What is the distance maintained between the two consecutive pairs of bases in the DNA molecule?
iii. Who contributed the base complementary rule?

Short Answer Questions-II (PYQ)

[3 Marks]

Q.1. Draw a labelled diagram of a nucleosome. Where is it found in a cell?

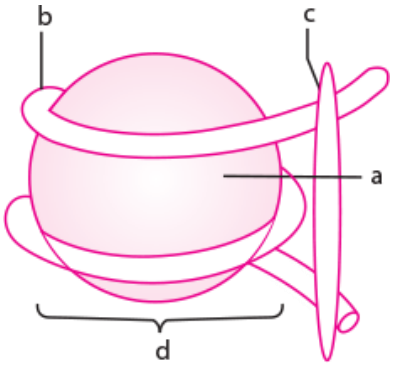
Ans.



Nucleosome
Nucleosome is found in the nucleus of the cell.

Q.2.

a. What is this diagram representing?
b. Name the parts *a*, *b* and *c*.
c. In the eukaryotes, the DNA molecules are organised within the nucleus. How is the DNA molecule organised in a bacterial cell in absence of a nucleus?

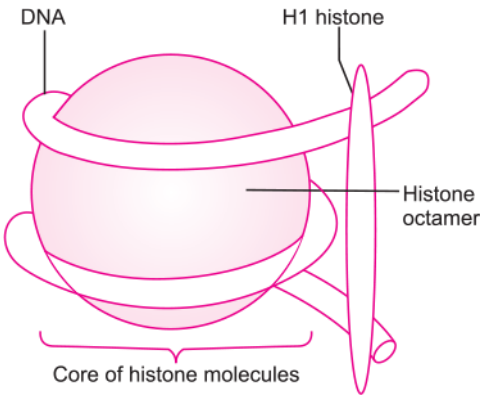


Q.3.

a. Draw a neat labelled diagram of a nucleosome.
b. Mention what enables histones to acquire a positive charge.

Ans.

(a)



(b) Basic amino acid residues of lysines and arginines.

Q.4. List the salient features of double helix structure of DNA.

Ans. Following are some features of DNA:

- **i.** DNA is made up of two polynucleotide chains, where the backbone is made up of sugar and phosphate groups and the nitrogenous bases project towards the centre.
- **ii.** There is complementary base pairing between the two strands of DNA.
- **iii.** The two strands are coiled in right-handed fashion and are anti-parallel in orientation. One chain has a 5′→3′ polarity while the other has 3′→5′ polarity.
- **iv.** The diameter of the strand is always constant due to pairing of purine and pyrimidine, *i.e.*, adenine is complementary to thymine while guanine is complementary to cytosine.
- **v.** The distance between two base pairs in a helix is 0.34 nm and a complete turn contains approximately ten base pairs. The pitch of the helix is 3.4 nm and the two strands are right-handed coiled.

Q.5. It is established that RNA is the first genetic material. Explain giving three reasons.

Ans. The reasons in support are:

- **i.** Processes like metabolism, translation and splicing evolved around RNA.
- **ii.** RNA is reactive and catalyses reactions.
- **iii.** In some viruses, RNA is the hereditary material.
- **iv.** RNA is unstable and can be easily mutated leading to evolution. (*Any three*)

Q.6. Why is DNA considered a better hereditary material than RNA?

Ans. DNA is considered a better hereditary material than RNA because of the following reasons:

- **i.** It is able to generate its replica (replication).

ii. It is chemically and structurally stable.
iii. It provides the scope for slow changes (mutation) that are required for evolution.
iv. It expresses itself in the form of Mendelian characters through RNA.

Q.7. A typical mammalian cell has 22 metres long DNA molecule whereas the nucleus in which it is packed measures about 10^{-6} m. Explain how such a long DNA molecule is packed within a tiny nucleus in the cell.

Ans. Packaging of DNA in eukaryotes

- The proteins associated with DNA are of two types—basic proteins (histone and protamine) and acidic non-histone chromosomal (NHC) proteins.
- The negatively charged DNA molecule wraps around the positively charged histone proteins to form a structure called **nucleosome**.
- The nucleosome core is made up of four types of histone proteins—H_2A, H_2B, H_3 and H_4— occurring in pairs.
- 200 bp of DNA helix wrap around the nucleosome by 1¾ turns, plugged by H_1 histone protein.

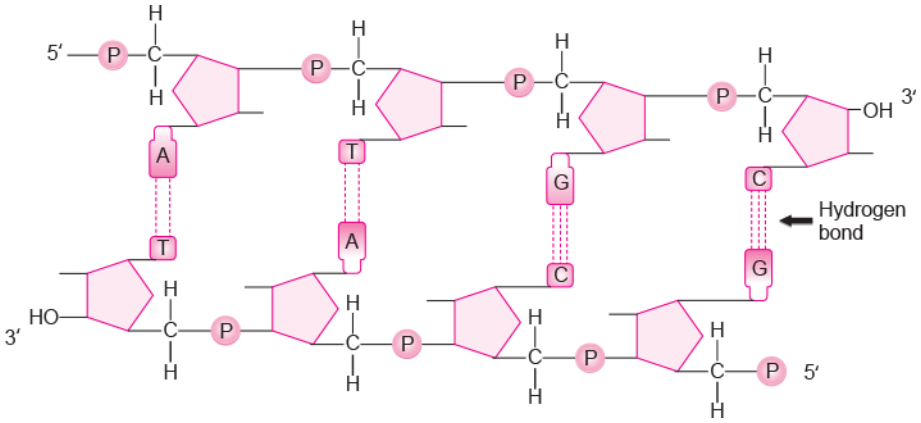
Q.8.

a. A DNA segment has a total of 1000 nucleotides, out of which 240 of them are adenine containing nucleotides. How many pyrimidine bases this DNA segment possesses?
b. Draw a diagrammatic sketch of a portion of DNA segment to support your answer.

Ans.

a. A = T, A = 240, hence T = 240
A + T = 240 + 240 = 480
So, G + C = 1000 – 480 = 520
G = C, so C = 52025202 =260
So, pyrimidines = C + T
= 260 + 240 = 500

b.



Q.9.

a. Why did Hershey and Chase use radioactive sulphur and radioactive phosphorus in their experiment?
b. Write the conclusion they arrived at and how.

Ans.

- **Procedure:**
  - **i.** Some bacteriophage virus were grown on a medium that contained radioactive phosphorus (^{32}P) and some in another medium with radioactive sulphur (^{35}S).
  - **ii.** Viruses grown in the presence of radioactive phosphorus (^{32}P) contained radioactive DNA.
  - **iii.** Similar viruses grown in presence of radioactive sulphur (^{35}S) contained radioactive protein.
  - **iv.** Both the radioactive virus types were allowed to infect *E. coli* separately.
  - **v.** Soon after infection, the bacterial cells were gently agitated in blender to remove viral coats from the bacteria.
  - **vi.** The culture was also centrifuged to separate the viral particle from the bacterial cell.
- **Observations and Conclusions:**
  - **i.** Only radioactive ^{32}P was found to be associated with the bacterial cell, whereas radioactive ^{35}S was only found in surrounding medium and not in the bacterial cell.
  - **ii.** This indicates that only DNA and not protein coat entered the bacterial cell.
  - **iii.** This proves that DNA is the genetic material which is passed from virus to bacteria and not protein.

Q.10. Describe Frederick Griffith's experiment on Streptococcus pneumoniae. Discuss the conclusion he arrived at.

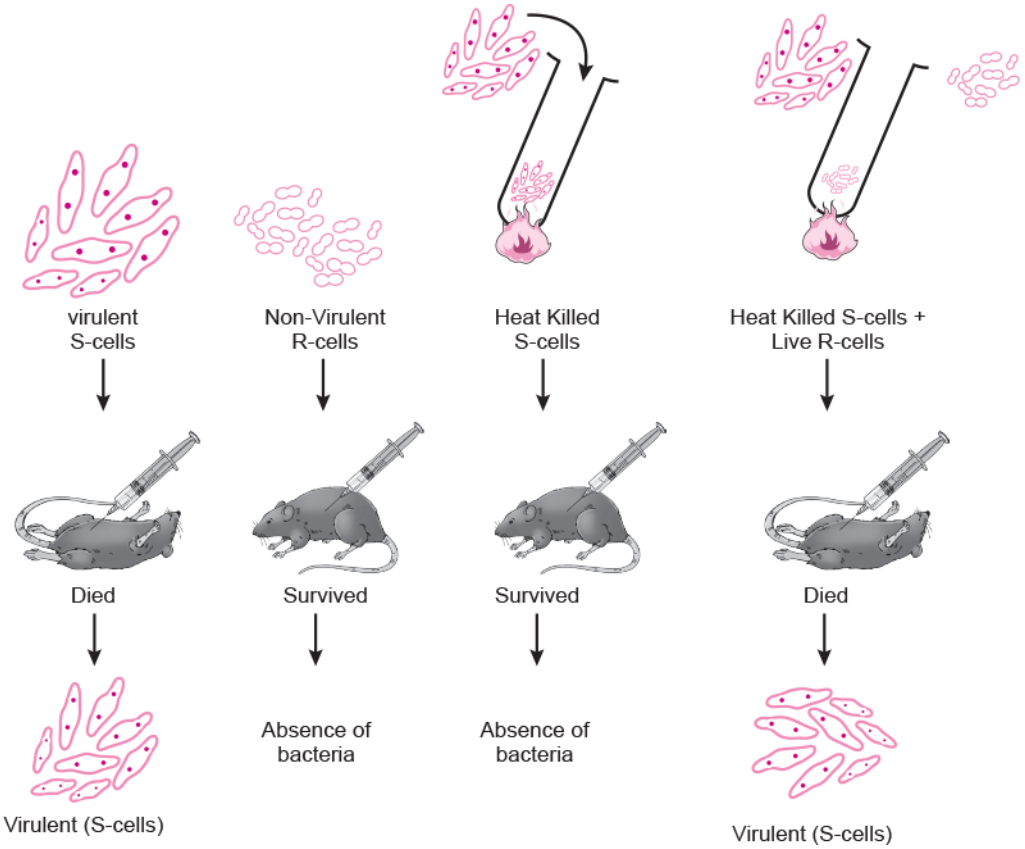
OR

Describe the experiment with Streptococcus pneumoniae that demonst`rated the existence of some "transforming principle".

Ans.

Transforming Principle

- **Frederick Griffith** (1928) conducted experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
- He observed two strains of this bacterium—one forming smooth shiny colonies (S-type) with capsule, while other forming rough colonies (R-type) without capsule.
- When live S-type cells were injected into mice, they died due to pneumonia.
- When live R-type cells were injected into mice, they survived.
- When heat-killed S-type cells were injected into mice, they survived and there were no symptoms of pnuemonia.
- When heat-killed S-type cells were mixed with live R-type cells and injected into mice, they died due to unexpected symptoms of pneumonia and live S-type cells were obtained from mice.
- He concluded that heat-killed S-type bacteria caused a transformation of the R-type bacteria into S-type bacteria but he was not able to understand the cause of this bacterial transformation.



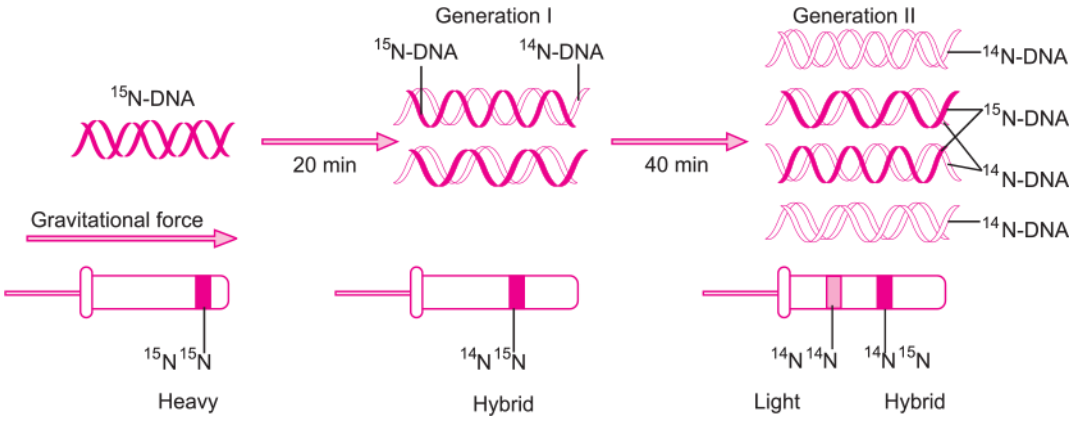
- Griffith's experiment on transformation

Q.11. Describe the experiments that established the identity of 'transforming principles' of Griffith.

Ans.

i. **Experimental proof for semi-conservative mode of DNA replication**

- **Matthew Meselson** and **Franklin Stahl** in 1958 performed experiments on *E. coli* to prove that DNA replication is semi-conservative.
- They grew *E. coli* in a medium containing $^{15}NH_4Cl$ (in which ^{15}N is the heavy isotope of nitrogen) for many generations.
- As a result, ^{15}N got incorporated into newly synthesised DNA.
- This heavy DNA can be differentiated from normal DNA by centrifugation in caesium chloride (CsCl) density gradient.
- Then they transferred the cells into a medium with normal $^{14}NH_4Cl$ and took the samples at various definite time intervals as the cells multiplied.
- The extracted DNAs were centrifuged and measured to get their densities.
- The DNA extracted from the culture after one generation of transfer from the ^{15}N medium to ^{14}N medium (*i.e.*, after 20 minutes; *E. coli* divides every 20 minutes) showed an intermediate hybrid density.
- The DNA extracted from culture after two generations (*i.e.*, after 40 minutes) showed equal amounts of light DNA and hybrid DNA.
- Similar experiment was performed by Taylor and colleagues in 1958, on *Vicia faba* to prove that the DNA in chromosome also replicate semi-conservatively.



Q.12. Describe the experiment that proved that DNA is the genetic material.

Ans. Proof for DNA as the Genetic Material

- **Hershey** and **Chase** conducted experiments on bacteriophage to prove that DNA is the genetic material.
- **Procedure:**
  i. Some bacteriophage virus were grown on a medium that contained radioactive phosphorus (^{32}P) and some in another medium with radioactive sulphur (^{35}S).
  ii. Viruses grown in the presence of radioactive phosphorus (^{32}P) contained radioactive DNA.

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  ii. This indicates that only DNA and not protein coat entered the bacterial cell.
  iii. This proves that DNA is the genetic material which is passed from virus to bacteria and not protein.

Q.13. In a series of experiments with *Streptococcus* and mice, F. Griffith concluded that R-strain bacteria had been transformed. Explain.

Ans. Transforming Principle

- **Frederick Griffith** (1928) conducted experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
- He observed two strains of this bacterium—one forming smooth shiny colonies (S-type) with capsule, while other forming rough colonies (R-type) without capsule.
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- He concluded that heat-killed S-type bacteria caused a transformation of the R-type bacteria into S-type bacteria but he was not able to understand the cause of this bacterial transformation.

Q.14. How was a heavy isotope of nitrogen used to provide experimental evidence to semiconservative mode of DNA-replication?

OR

Describe the experiment that helped to demonstrate the semi-conservative mode of DNA replication.

Ans. Experimental proof for semi-conservative mode of DNA replication

- Matthew Meselson and Franklin Stahl in 1958 performed experiments on E. coli to prove that DNA replication is semi-conservative.

- They grew E. coli in a medium containing $^{15}NH_4Cl$ (in which ^{15}N is the heavy isotope of nitrogen) for many generations.
- As a result, ^{15}N got incorporated into newly synthesised DNA.
- This heavy DNA can be differentiated from normal DNA by centrifugation in caesium chloride (CsCl) density gradient.
- Then they transferred the cells into a medium with normal $^{14}NH_4Cl$ and took the samples at various definite time intervals as the cells multiplied.
- The extracted DNAs were centrifuged and measured to get their densities.
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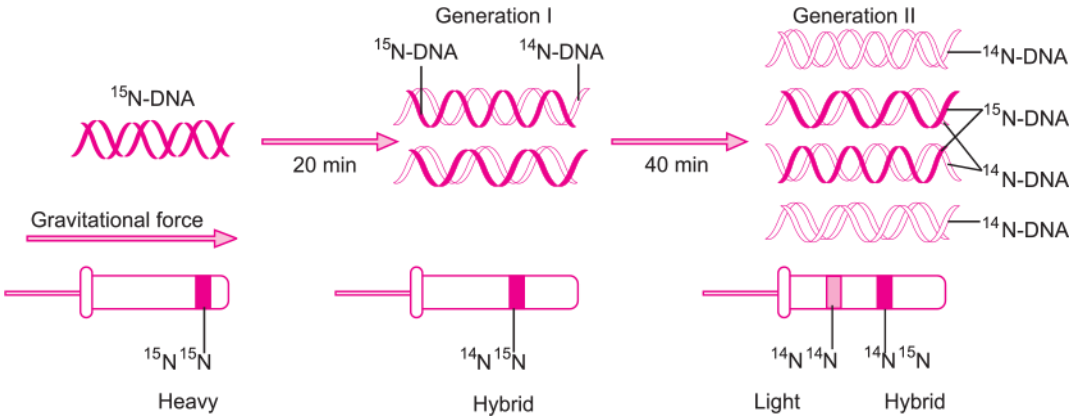
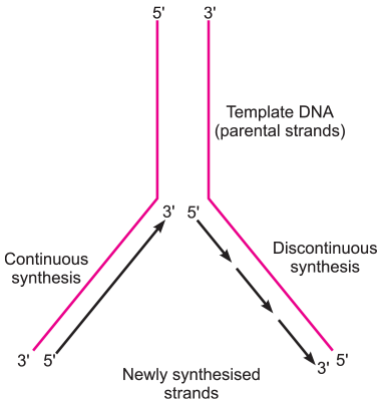
- The DNA extracted from culture after two generations (*i.e.*, after 40 minutes) showed equal amounts of light DNA and hybrid DNA.
- Similar experiment was performed by Taylor and colleagues in 1958, on Vicia faba to prove that the DNA in chromosome also replicate semi-conservatively.



Meselson and Stahl's experiment

Q.15. Draw a labelled schematic sketch of replication fork of DNA. Explain the role of the enzymes involved in DNA replication.

Ans.



Replication fork
Enzymes involved in DNA replication are:

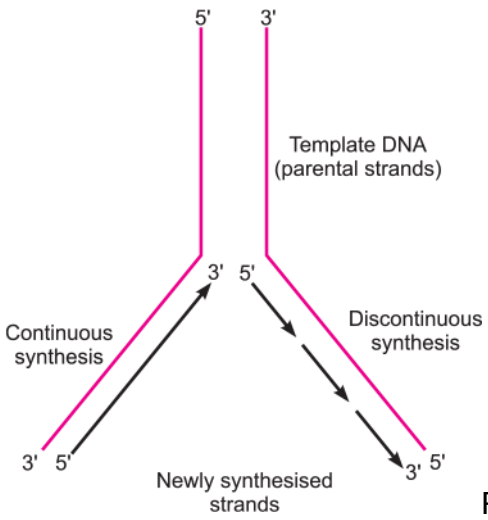
i. DNA-dependent DNA polymerase, which catalyses the polymerisation of polynucleotides in a very short time only in 5′→3′ direction with accuracy.
ii. DNA ligase, which joins the discontinuously synthesised short segments called Okazaki fragments formed on one of the template strands.

Q.16.

a. Draw a labelled schematic diagram of a replication fork showing continuous and discontinuous replication of DNA strands.
b. State a reason why is the replication continuous and discontinuous in the diagram drawn.

Ans.

a.



Replication fork

b. The two strands of DNA are anti parallel, *i.e.*, one strand runs in the direction 5' to 3' and the other runs in the direction 3' to 5'. DNA polymerase adds deoxyribonucleotides only in one direction, *i.e.*, 5' to 3'. Thus, producing Okazaki fragments in the other strands.

Q17.

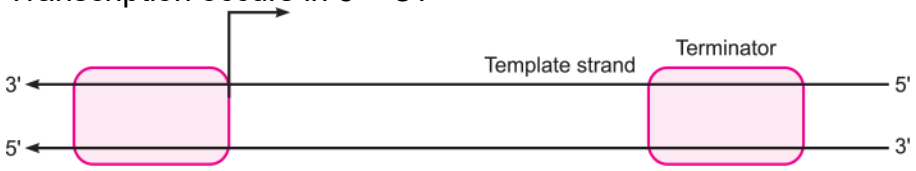
a. Draw a schematic representation of the structure of a transcription unit and show the following in it:
   i. Direction in which the transcription occurs
   ii. Polarity of the two strands involved
   iii. Template strand
   iv. Terminator gene

b. Mention the function of promoter gene in transcription.

Ans.

a.

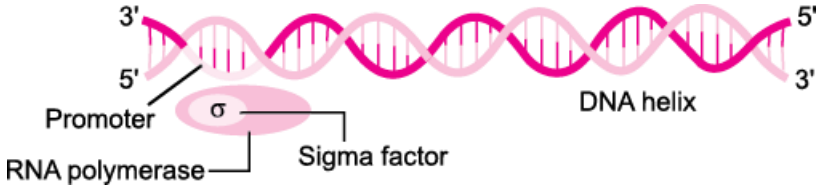
i. Transcription occurs in 5′→3′.



b. Promotor gene has DNA sequence that provide binding site for RNA polymerase.

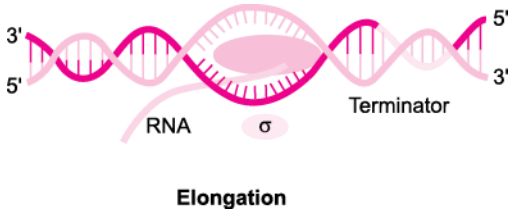
Q.18. Describe the initiation process of transcription in bacteria.

Ans. In bacteria, the transcription of all the three types of RNA (*m*RNA, *t*RNA, *r*RNA) is catalysed by single DNA-dependent enzyme called the RNA polymerase. The RNA polymerase has cofactors that catalyse the process. During initiation, σ (sigma) factor recognises the start signal and promotor region on DNA which then along with RNA polymerase binds to the promoter to initiate transcription.



Q.19. Describe the elongation process of transcription in bacteria.

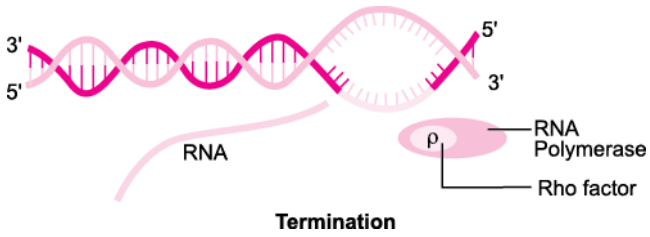
Ans. After initiation, RNA polymerase loses the σ factor but continues the polymerisation of ribonucleotides to form RNA. It uses nucleoside triphosphates as substrate and polymerises in a template-dependent fashion, following the rule of complementarity.



Elongation

Q.20. Describe the termination process of transcription in bacteria.

Ans. Once the RNA polymerase reaches the termination region of DNA, the RNA polymerase is separated from DNA–RNA hybrid, as a result nascent RNA separates. This process is facilitated by a termination factor r (rho). In prokaryotes, *m*RNA does not require any processing, so transcription and translation both occur in the cytosol.



Termination

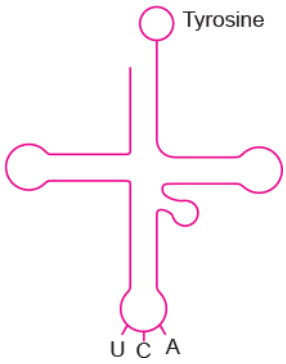
Q.21.

a. Name the scientist who called *t*RNA an adaptor molecule.
b. Draw a clover leaf structure of *t*RNA showing the following:
  i. Tyrosine attached to its amino acid site.
  ii. Anticodon for this amino acid in its correct site (codon for tyrosine is UCA).
c. What does the actual structure of *t*RNA look like?

Ans.

(a) Francis Crick

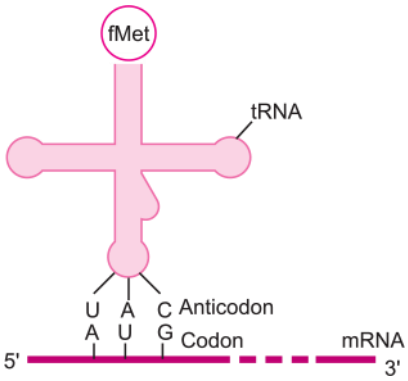
(b)



(c) The actual structure of *t*RNA looks like inverted L.

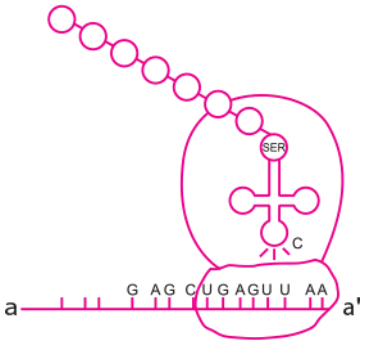
Q.22. One of the codons on *m*RNA is AUG. Draw the structure of *t*RNA adapter molecule for this codon. Explain the uniqueness of this *t*RNA.

Ans. This *t*RNA is specific for amino acid Methionine and it also acts as initiator codon (initiator *t*RNA)



Q.23.

a. Identify the polarity from *a* to *a′* in the given diagram and mention how many more amino acids are expected to be added to this polypeptide chain.
b. Mention the DNA sequence coding for serine and the anticodon of *t*RNA for the same amino acid.
c. Why are some untranslated sequence of bases seen in *m*RNA coding for a polypeptide? Where exactly are they present on *m*RNA?



Ans.

a. Polarity from a to a' is 5'→ 3'.
No more amino acid will be added to this polypeptide chain.
b. TCA; anticodon is UCA.
c. The untranslated sequence of bases are required for efficient translation process. They are present before the start codon at the 5'-end and after the stop codon at 3'-end.

Q.24. Explain the process of charging of tRNA. Why is it essential in translation?

Ans. Charging of *t*RNA: The amino acids are activated in the presence of ATP and linked to their cognate tRNA. This process is called charging of *t*RNA or amino-acylation of *t*RNA. When two such charged *t*RNAs are brought close enough, the formation of peptide bond between the corresponding amino acids would be favoured energetically. The presence of a catalyst would enhance the rate of peptide bond formation.

Q.25. Explain the process of translation in a bacterium.

Ans. Translation

- Translation is the process of synthesis of protein from *m*RNA with the help of ribosome.
- A translational unit in *m*RNA from 5' → 3' comprises of a start codon, region coding for a polypeptide, a stop codon and untranslated regions (UTRs) at both 5'-end and 3'-end for efficient process.
- There are three stages of protein synthesis:
  - **i. Initiation**
    - Assembly of ribosome on *m*RNA.
    - Activation of amino acids and its delivery to *t*RNA
  - **ii. Elongation**
    - Repeated cycle of amino acid delivery.
    - Peptide bond formation and movement along the *m*RNA called **translocation**.
  - **iii. Termination**
    - The release of a polypeptide chain.

Q.26. How is the translation of *m*RNA terminated? Explain.

Ans. Termination of polypeptide

- When the A-site of ribosome reaches a termination codon which does not code for any amino acid, no charged tRNA binds to the A-site.
- Dissociation of polypeptide from ribosome takes place, which is catalysed by a '**release factor**'.
- There are three termination codons namely UGA, UAG and UAA.

Q.27. Unambiguous, universal and degenerate are some of the terms used for the genetic code. Explain the salient features of each one of them.

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

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

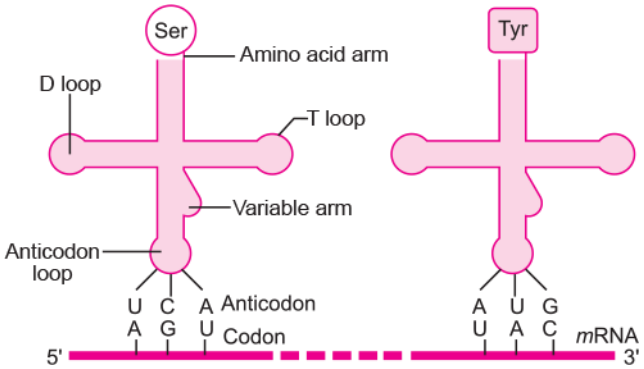
Degenerate code means that same amino acids are coded by more than one codon, *e.g.*, UUU and UUC code for phenylalanine.

Q.28.

a. Draw the structure of the initiator *t*RNA adaptor molecule.
b. Why is *t*RNA called an adaptor molecule?

Ans.

a.



b. *t*RNA is called an adaptor molecule because on one end it reads the code on *m*RNA and on other end it would bind to the amino acid corresponding to the anticodon.

Q.29. Identify giving reasons, the salient features of genetic code by studying the following nucleotide sequence of mRNA strand and the polypeptide translated from it.

AUG UUU UCU UUU UUU UCU UAG

Met – Phe – Ser – Phe – Phe – Ser

Ans.

S. No.	Salient features of genetic code	Reason
(*i*)	The codon is a triplet.	*e.g., AUG, UUU, etc, are triplets*
(*ii*)	One codon codes for only one amino acid,hence it is unambiguous and specific.	*e.g., UUU codes for serine, AUG for methionine, etc.*
(*iii*)	AUG has dual function as it codes for methionine and it also acts as initiator codon.	*AUG is seen at the beginning of the polypeptide chain.*
(*iv*)	UAG does not code for any amino acid hence iscalled stop codon and leads to end of translation.	No amino acid is coded by UAG in the polypeptide chain given.

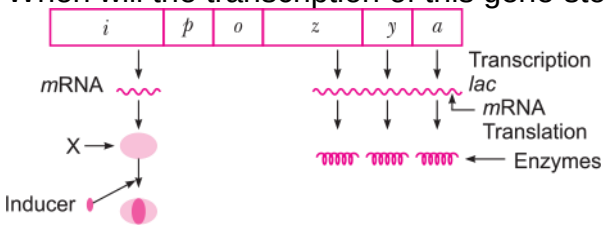
Q.30. How is *hn*RNA processed to form mRNA?

Ans. The hnRNA undergoes the following processes to form mRNA:

i. **Capping:** Addition of methyl guanosine triphosphate at 5'-end.
ii. **Tailing:** Addition of 200-300 adenylate residues at 3'-end.
iii. **Splicing:** Removal of introns and rejoining of exons.

Q.31.

a. Name the molecule 'X' synthesised by 'i' gene. How does this molecule get inactivated?
b. Which one of the structural genes codes for β-galactosidase?
c. When will the transcription of this gene stop?

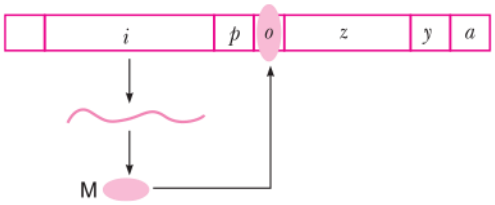


Ans.

a. The molecule 'X' is repressor. It gets inactivated when lactose (inducer) binds with the repressor molecule.
b. z gene codes for β-galactosidase.
c. Transcription of the gene stops when lactose is absent and thus repressor is free to bind with the operator.

Q.32.

a. Name the molecule 'M' that binds with the operator.
b. Mention the consequences of such binding.
c. What will prevent the binding of the molecule 'M' with the operator gene? Mention the event that follows.



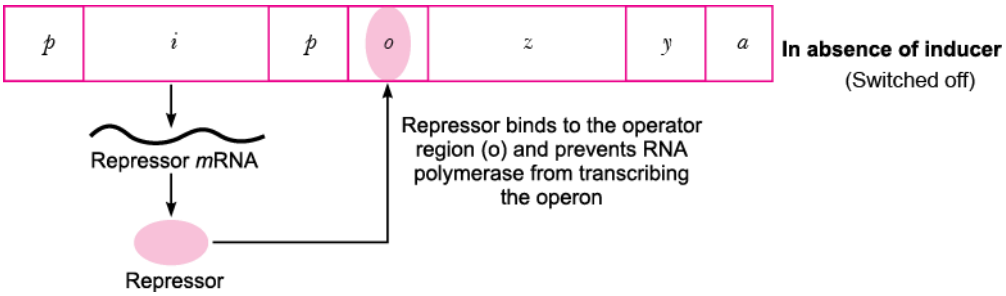
Ans.

a. M is the repressor.
b. When repressor binds with the operator, transcription stops.
c. An inducer prevents the binding of repressor to operator and starts transcription *i.e.*, lactose here.

Q.33. Draw a schematic diagram of *lac* operon in its 'switched off' position. Label the following:

i. The structural genes
ii. Repressor bound to its correct position
iii. Promoter gene
iv. Regulatory gene.

Ans.



The *lac* operon

i. z, y and *a* are structural genes.
ii. *p* is the promoter sequence.
iii. i is the regulatory gene.

Q.34. How are the DNA fragments separated and isolated for DNA fingerprinting? Explain.

Ans. Separation and Isolation of DNA Fragments (Gel Electrophoresis)

- **Gel electrophoresis** is a technique for separating DNA fragments based on their size.
- Firstly, the sample DNA is cut into fragments by restriction endonucleases.
- The DNA fragments being negatively charged can be separated by forcing them to move towards the anode under an electric field through a medium/matrix.
- Commonly used matrix is **agarose,** which is a natural linear polymer of D-galactose and 3, 6-anhydro-L-galactose which is extracted from sea weeds.
- The DNA fragments separate-out (resolve) according to their size because of the sieving property of agarose gel. Hence, the smaller the fragment size, the farther it will move.
- The separated DNA fragments are visualised after staining the DNA with **ethidium bromide** followed by exposure to **UV radiation**.
- The DNA fragments are seen as orange coloured bands.
- The separated bands of DNA are cut out and extracted from the gel piece. This step is called **elution**.
- The purified DNA fragments are used to form recombinant DNA which can be joined with cloning vectors.

Q.35. Forensic department was given three blood samples. Write the steps of the procedure carried to get the DNA fingerprinting done for the above samples.

Ans. Methodology and Technique

i. DNA is isolated and extracted from the cell or tissue by centrifugation.

ii. By the process of polymerase chain reaction (PCR), many copies are produced. This step is called **amplification**.
iii. DNA is cut into small fragments by treating with restriction endonucleases.
iv. DNA fragments are separated by agarose gel electrophoresis.
v. The separated DNA fragments are visualised under ultraviolet radiation after applying suitable dye.
vi. The DNA is transferred from electrophoresis plate to nitrocellulose or nylon membrane sheet. This is called **Southern blotting**.
vii. VNTR probes are now added which bind to specific nucleotide sequences that are complementary to them. This is called **hybridisation**.
viii. The hybridised DNA fragments are detected by autoradiography. They are observed as dark bands on X-ray film.

Q.36. The technique is DNA fingerprinting. It includes the following steps:

Ans.

Methodology and Technique

i. DNA is isolated and extracted from the cell or tissue by centrifugation.
ii. By the process of polymerase chain reaction (PCR), many copies are produced. This step is called **amplification**.
iii. DNA is cut into small fragments by treating with restriction endonucleases.
iv. DNA fragments are separated by agarose gel electrophoresis.
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vii. VNTR probes are now added which bind to specific nucleotide sequences that are complementary to them. This is called **hybridisation**.
viii. The hybridised DNA fragments are detected by autoradiography. They are observed as dark bands on X-ray film.

Q.37.

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.

Ans.

a. Y’ stands for Yeast and ‘B’ stands for Bacterial.
‘YAC’ and ‘BAC’ are used as vectors for cloning foreign DNA.

b. The total human genome percentage is (<) 2% and percentage of discovered genes is (<) 50%.
c. Single Nucleotide Polymorphism.

Q.38. What is *hn*RNA? Explain the changes *hn*RNA undergoes during its processing to form *m*RNA.

Ans.

*hn*RNA is the precursor of *m*RNA that is transcribed by RNA ploymerase II and is called heterogenous nuclear RNA.

Changes:

- The *hn*RNA undergoes two additional processes called capping and tailing.
- In capping, an unusual nucleotide, methyl guanosine triphosphate, is added to the 5'-end of *hn*RNA.
- In tailing, adenylate residues (about 200–300) are added at 3'-end in a template independent manner.
- Now the *hn*RNA undergoes a process where the introns are removed and exons are joined to form *m*RNA by the process called splicing. Fragments on one of the template strands.

Q.39.

a. Explain DNA polymorphism as the basis of genetic mapping of human genome.
b. State the role of VNTR in DNA fingerprinting.

Ans.

a. Genetic polymorphism means occurrence of genetic material in more than one form. It is of three major types, *i.e.*, allelic, SNP and RFLP.
Allelic polymorphism: Allelic polymorphism occurs due to multiple alleles of a gene. Allele possess different mutations which alter the structure and function of a protein formed by them as a result, change in phenotype may occur.
SNP or single nucleotide polymorphism: SNP is very useful for locating alleles, identifying disease-associated sequence and tracing human history.
b. Variable Number Tandem Repeats (VNTRs) are used in DNA fingerprinting as markers. VNTRs vary from person to person and are inherited from one generation to the next. Therefore, only closely related individuals have similar VNTRs.

Q.40. A number of passengers were severely burnt beyond recognition during a train accident. Name and describe a modern technique that can help to hand over the dead to their relatives.

Ans. DNA fingerprinting can help to hand over the dead to their relatives.

- **Methodology and Technique**

  i. DNA is isolated and extracted from the cell or tissue by centrifugation.
  ii. By the process of polymerase chain reaction (PCR), many copies are produced. This step is called **amplification**.
  iii. DNA is cut into small fragments by treating with restriction endonucleases.
  iv. DNA fragments are separated by agarose gel electrophoresis.
  v. The separated DNA fragments are visualised under ultraviolet radiation after applying suitable dye.
  vi. The DNA is transferred from electrophoresis plate to nitrocellulose or nylon membrane sheet. This is called **Southern blotting**.
  vii. VNTR probes are now added which bind to specific nucleotide sequences that are complementary to them. This is called **hybridisation**.
  viii. The hybridised DNA fragments are detected by autoradiography. They are observed as dark bands on X-ray film.

Q.41. A criminal blew himself up in a local market when was chased by cops. His face was beyond recognition. Suggest and describe a modern technique that can help establish his identity.

Ans. The identity can be established by the technique of DNA fingerprinting.

- DNA is isolated and extracted from the cell or tissue by centrifugation.
- By the process of polymerase chain reaction (PCR), many copies are produced. This step is called **amplification**.
- DNA is cut into small fragments by treating with restriction endonucleases.
- DNA fragments are separated by agarose gel electrophoresis.
- The separated DNA fragments are visualised under ultraviolet radiation after applying suitable dye.
- The DNA is transferred from electrophoresis plate to nitrocellulose or nylon membrane sheet. This is called **Southern blotting**.
- VNTR probes are now added which bind to specific nucleotide sequences that are complementary to them. This is called **hybridisation**.
- The hybridised DNA fragments are detected by autoradiography. They are observed as dark bands on X-ray film.

Q.42. 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.

Ans. DNA fingerprinting can help in identification of kinship.

- **Methodology and Technique**

  i. DNA is isolated and extracted from the cell or tissue by centrifugation.
  ii. By the process of polymerase chain reaction (PCR), many copies are produced. This step is called **amplification**.
  iii. DNA is cut into small fragments by treating with restriction endonucleases.
  iv. DNA fragments are separated by agarose gel electrophoresis.
  v. The separated DNA fragments are visualised under ultraviolet radiation after applying suitable dye.
  vi. The DNA is transferred from electrophoresis plate to nitrocellulose or nylon membrane sheet. This is called **Southern blotting**.
  vii. VNTR probes are now added which bind to specific nucleotide sequences that are complementary to them. This is called **hybridisation**.
  viii. The hybridised DNA fragments are detected by autoradiography. They are observed as dark bands on X-ray film.

Q.43. "A very small sample of tissue or even a drop of blood can help determine paternity". Provide a scientific explanation to substantiate the statement.

Ans.

i. DNA from all cells of an individual shows the same degree of polymorphism and therefore becomes a useful identification tool.
ii. Polymorphs are heritable and the child inherits 50% of the chromosome from each parent.
iii. With the help of PCR the small amount of DNA from blood can be amplified and be used in DNA finger printing to identify the paternity.

Q.44.

a. In human genome which one of the chromosomes has the most genes and which one has the fewest?
b. Scientists have identified about 1.4 million single nucleotide polymorphs in human genome. How is the information of their existence going to help the scientists?

Ans.

a. Chromosome 1 has most genes and the Y has the fewest gene.
b. The information regarding the occurrence of 1.4 million SNPs (single nucleotide polymorphism) revolutionise the processes of finding chromosomal locations for diseaseassociated sequences and tracing human ancestory (history).

Q.45. Answer the following questions based on Meselson and Stahl's experiment:

a. Write the name of the chemical substance used as a source of nitrogen in the experiment by them.
b. Why did the scientists synthesise the light and the heavy DNA molecules in the organism used in the experiment?
c. How did the scientists make it possible to distinguish the heavy DNA molecule from the light DNA molecule? Explain.
d. Write the conclusion the scientists arrived at after completing the experiment.

Ans.

a. Ammonium chloride (NH_4Cl).
b. To check if DNA replication was semi-conservative.
c. The heavy and light DNA molecules were distinguished by centrifugation in a cesium chloride density gradient.
d. The scientists concluded that DNA replicates semi-conservatively.

Q.46. The base sequence in one of the strands of DNA is TAGCATGAT.

i. Give the base sequence of its complementary strand.
ii. How are these base pairs held together in a DNA molecule?
iii. Explain the base complementarity rules. Name the scientist who framed this rule.

Ans.

i. The complementary strand is ATCGTACTA.
ii. The base pairs are held together by hydrogen bonds in a DNA molecule. A and T are held by two hydrogen bonds while G and C are held by three hydrogen bonds.
iii. Watson and Crick framed the base complementarity rule. The rule states that the ratios between adenine and thymine, and guanine and cytosine are constant and equals one.

Q.47. Given below is a part of the template strand of a structural gene:

i. Write its transcribed mRNA strand with its polarity.
ii. Explain the mechanism involved in initiation of transcription of this strand.

Ans.

i. Polarity is 5′-3′ ; — AUG GUA AUC CUA—
ii. DNA-dependent RNA polymerase, catalyses transcription of *m*RNA. The strand of DNA with polarity acts as the template. The RNA polymerase binds to the promoter site and starts the process of transcription.

Q.48. State the conditions when ‘genetic code’ is said to be

i. degenerate,
ii. unambiguous and specific,
iii. universal.

Ans.

i. Degenerate—When some amino acids are coded by more than one amino acids.
ii. Unambiguous and specific—When one codon codes for only one specific amino acid.
iii. A particular codon codes for same amino acid in all organisms except in mitochondria and few protozoa.

Q.49.

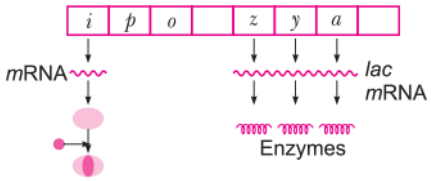
Study the mRNA segment given above which is complete to be translated into a polypeptide chain.

i. **Write the codons 'a' and 'b'.**
ii. **What do they code for?**
iii. **How is peptide bond formed between two amino acids in the ribosome?**

Ans.

i. a is AUG and b is UAA/UAG/UGA
ii. AUG codes for methionine (initiation codon).
UAA/UAG/UGA do not code for any amino acid, *i.e.*, stop or terminating codons.
iii. There are two sites (P-site and A-site) in the large subunit of ribosome, where subsequent amino acids bind to and thus are close enough to form peptide bond by peptidyl transferase enzyme. The ribosome also acts as a catalyst for the formation of peptide bond.

Q.50. Study the figure given below and answer the questions:



a. How does the repressor molecule get inactivated?
b. When does the transcription of lac mRNA stop?
c. Name the enzyme transcribed by the gene 'z'.

Ans.

a. When the inducer comes in contact with repressor, it is inactivated.
b. When lactose is lacking or absent, the transcription of *lac m*RNA stops.
c. β-galactosidase.

Short Answer Questions-II (OIQ)

[3 Marks]

Q.1. DNA separated from one cell, when introduced into another cell is able to bestow some of the properties of former to the latter. What is this change called in technical terms? Describe the experimental evidences which led to the discovery of the above phenomenon.

Ans. This change is called transformation.

Transforming Principle

- **Frederick Griffith** (1928) conducted experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
- He observed two strains of this bacterium—one forming smooth shiny colonies (S-type) with capsule, while other forming rough colonies (R-type) without capsule.
- When live S-type cells were injected into mice, they died due to pneumonia.
- When live R-type cells were injected into mice, they survived.
- When heat-killed S-type cells were injected into mice, they survived and there were no symptoms of pnuemonia.
- When heat-killed S-type cells were mixed with live R-type cells and injected into mice, they died due to unexpected symptoms of pneumonia and live S-type cells were obtained from mice.
- He concluded that heat-killed S-type bacteria caused a transformation of the R-type bacteria into S-type bacteria but he was not able to understand the cause of this bacterial transformation.

Q.2. Why did Hershey and Chase work with bacteriophages in their experiments to prove that DNA is the genetic material? Explain.

Ans. Hershey and Chase selected bacteriophage for their work because of the following reasons:

i. A bacteriophage has only two components—protein and DNA.
ii. They worked to find whether it was protein or DNA from the virus that entered the bacteria.
iii. The bacteriophage attaches to the bacteria.
iv. Its genetic material enters the bacterial cell.

v. The bacterial cell treats the viral genetic material as if it was its own and subsequently manufactures more virus particles.
vi. Proving DNA to be the genetic material/by tracing the radioactivity on DNA.

Q.3. Describe the discontinuous synthesis of DNA.

Ans. The discontinuous synthesis of DNA is as follows:

i. At the replication site, unwinding of double stranded DNA takes place by DNA gyrase and helicase.
ii. ssBPs (single-stranded binding proteins) bind to the separated strands to avoid recoiling or to provide stability.
iii. Since DNA polymerase can synthesise DNA only in 5′→3′ direction, DNA synthesis occurs discontinuously on the lagging strand.
iv. These small fragments of DNA are called Okazaki fragments.
v. The enzyme primase adds primers after every fragment is formed.
vi. These Okazaki fragments are then joined by DNA ligase.

Q.4. What are the three types of RNA? Mention their relation to protein synthesis.

Ans. Types of RNA

S. No.	Types of RNA	Functions
(*i*)	Messenger RNA (mRNA)	i. t stores the genetic information from DNA. ii. It decides the sequence of amino acid in a polypeptide.
(*ii*)	Transfer RNA (tRNA)	i. It acts as an adaptor molecule that at one end reads the code on mRNA and accordingly bind to amino acid on the other end. ii. It recognises the codon on mRNA by its anticodon and leaves amino acid at the protein synthesis site.
(*iii*)	Ribosomal RNA (rRNA)	i. It constitutes the ribosomal structure. ii. It helps to form peptide bond.

Q.5. State any two structural differences and one functional difference between DNA and *r*RNA.

Ans.

S. No.	DNA	*r*RNA
Structural		
(*i*) (*ii*) (*iii*)	It is a double-stranded structure. It contains nitrogen bases, A, T, G, C. It has deoxyribose sugar.	It is a single-stranded structure. It contains nitrogen base, A, U, G, C. It has ribose sugar.
Functional		
	It determines sequence of amino acid in a polypeptide by transcription and passes information from one generation to another.	It is the site of translation.

Q.6. DNA polymerase and RNA polymerase differ in their requirement while functioning. Explain.

Ans.

S. No.	RNA polymerase	DNA polymerase
(*i*) (*ii*) (*iii*)	It cannot carry out proofreading. RNA polymerase does not require RNA primer for synthesis of RNA. It uses ribonucleotides for RNA synthesis.	It carries out proofreading for DNA repairmechanism. DNA polymerase requires RNA primer for synthesis of DNA. It uses deoxyribonucleotides for DNA synthesis.

Q.7. A burglar in a huff forgot to wipe off his blood-stains from the place of crime where he was involved in a theft and fight. Name the technique which can help in identifying the burglar from the blood-stains. Describe the technique.

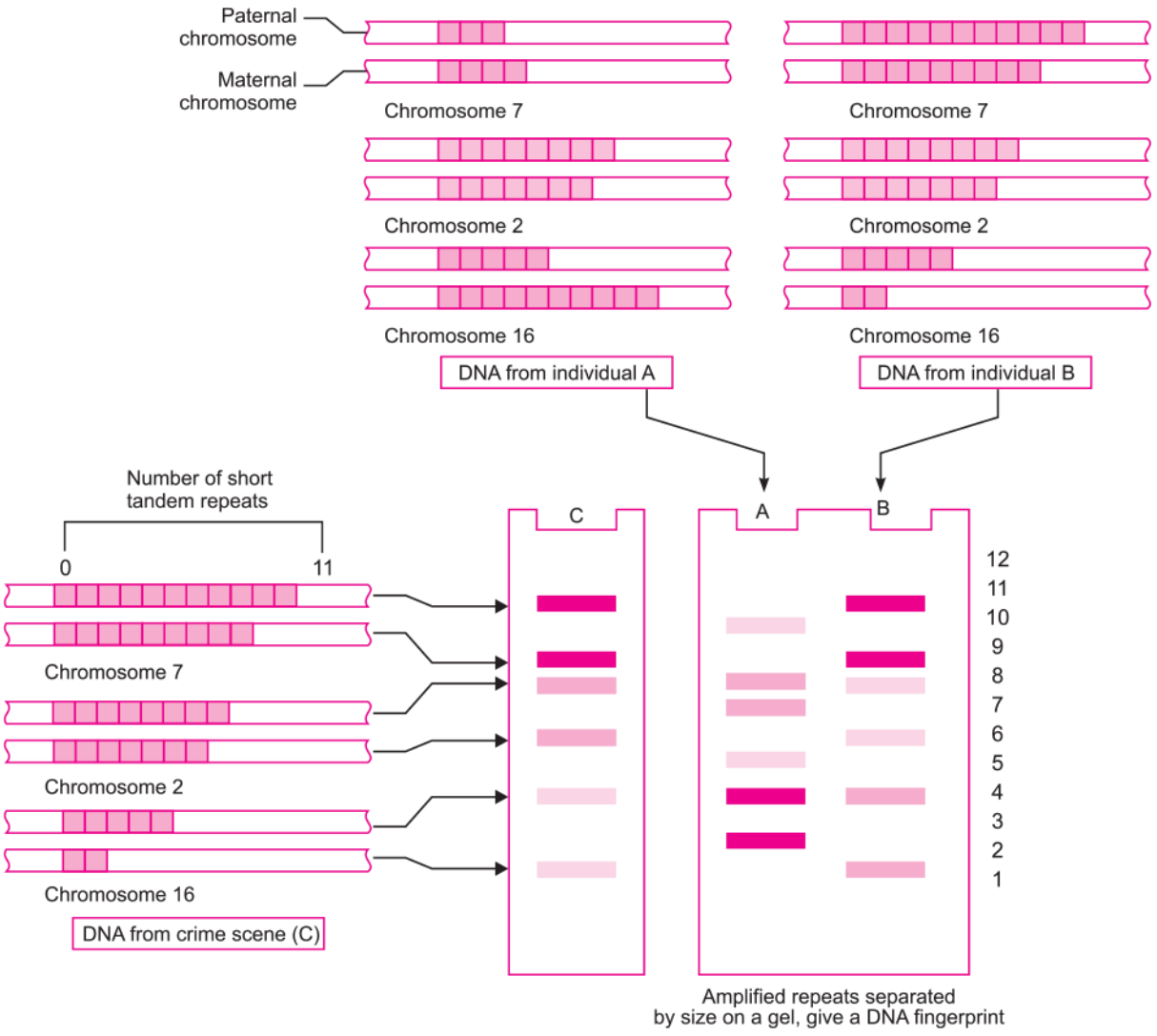
Ans. DNA Fingerprinting

- Dr. Alec Jeffreys developed the technique of DNA fingerprinting in an attempt to identify DNA marker for inherited diseases.
- DNA fingerprinting uses short nucleotide repeats called Variable Number Tandem Repeats (VNTRs) as markers. VNTRs vary from person to person and are inherited from one generation to the next. Only closely related individuals have similar VNTRs.

Methodology and Technique

i. DNA is isolated and extracted from the cell or tissue by centrifugation.

ii. By the process of polymerase chain reaction (PCR), many copies are produced. This step is called amplification.
iii. DNA is cut into small fragments by treating with restriction endonucleases.
iv. DNA fragments are separated by agarose gel electrophoresis.
v. The separated DNA fragments are visualised under ultraviolet radiation after applying suitable dye.
vi. The DNA is transferred from electrophoresis plate to nitrocellulose or nylon membrane sheet. This is called Southern blotting.
vii. VNTR probes are now added which bind to specific nucleotide sequences that are complementary to them. This is called hybridisation.
viii. The hybridised DNA fragments are detected by autoradiography. They are observed as dark bands on X-ray film.



Schematic representation of DNA fingerprinting: Few chromosomes have been shown to contain different copy number of VNTR. The two alleles (paternal and maternal) of a

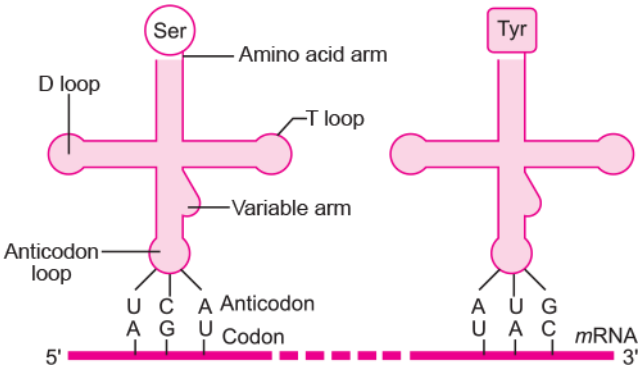
chromosome also contain different copy numbers of VNTR. It is clear that the banding pattern of DNA from crime scene matches with individual B and not with A.

Applications of DNA Fingerprinting

i. It is used as a tool in forensic tests to identify criminals and criminal investigations.
ii. It is used to settle paternity disputes and maternity disputes.
iii. It is used to determine population and genetic diversities to study evolution.
iv. It is used in the study of evolutionary biology.

Q.8. One of the codons on mRNA is AUG. Draw the structure of *t*RNA adaptor molecule for this codon. Explain the uniqueness of this *t*RNA.

Ans. This *t*RNA is specific for amino acid methionine and also acts as initiator *t*RNA.



Q.9. "The codon is a triplet and is read in a contiguous manner without punctuations." Provide the genetic basis for the statement.

Ans. Since there are only four bases which code for twenty amino acids, the code should be made up of three bases, *i.e.*, (4 × 4 × 4) = 64 codons; a number more than the required.
If the codon consists of four letters, only (4 × 4), only sixteen codons are possible, which is less than the required. Hence the codon is a triplet.
As the ribosome moves on *m*RNA, continuously without break, the codons are read in a contiguous manner.

Q.10. Answer the following questions:

Q. Differentiate between a template strand and coding strand of DNA.

Ans.

Role/Strand	Template strand	Coding strand
Function	Codes for the protein molecule	Does not code for anything

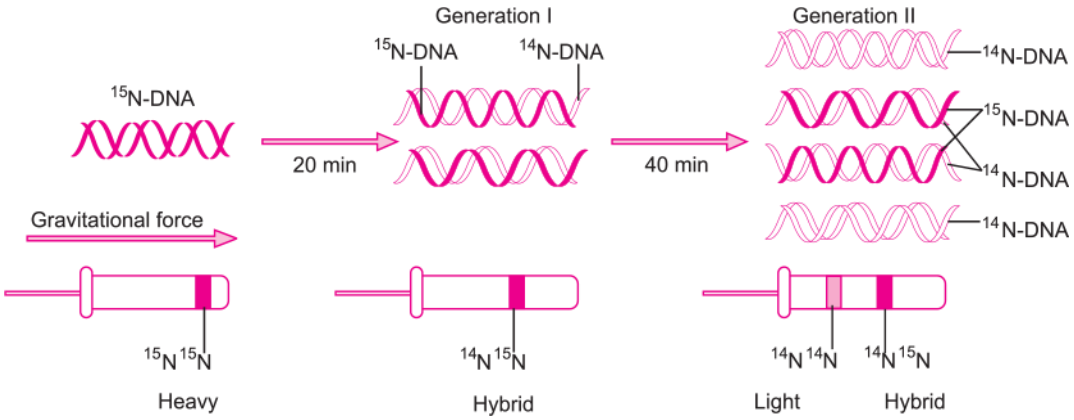
Polarity	3′ → 5′	5′ → 3′

Q.11. With respect to Messelson and Stahl's Experiment, answer the following questions:

a. Identify the method used to distinguish between heavy and light isotopes of nitrogen.
b. With the help of diagrams, compare the results for the DNA isolated after 20 minutes of experiment with the DNA which was isolated after 40 minutes.

Ans.

a. Centrifugation in a CsCl density gradient.
b.



Q.12. A tRNA is charged with amino acid phenylalanine.

i. At what end of the tRNA is the amino acid attached?
ii. What is the mRNA codon that codes for phenylalanine?
iii. Name the enzyme responsible for this attachment.

Ans.

i. At the 3′ end.
ii. UUU or UUC.
iii. Aminoacyl tRNA synthetase.

Q.13. A tRNA is charged with the amino acid methionine.

i. At what site in the ribosome will the tRNA bind?
ii. Give the anticodon of this *t*RNA.
iii. What is the *m*RNA codon for methionine?
iv. Name the enzyme responsible for this binding.

Ans.

i. If it behaves as starting codon it will bind at P site, otherwise it will bind at A site.
ii. UAC
iii. AUG
iv. Aminoacyl *t*RNA synthetase.

Q.14. The base sequence on one of the strands of DNA is ATGTCTATA.

i. Give the base sequence of its complementary strand.
ii. If an RNA strand is transcribed by this strand, what would be the base sequence of RNA?
iii. In what other respect, an RNA molecule differs from a DNA molecule?

Ans. (i) TACAGATAT

(ii) UACAGAUAU

(iii)

S. No.	DNA	RNA
(*a*)	It is a double-stranded structure.	It is a single-stranded structure.
(*b*)	It contains deoxyribose sugar.	It contains ribose sugar.
(*c*)	Bases are A, T, G, C	Bases are A, G, C, U

Long Answer Questions (PYQ)

[5 Marks]

Q.1. The average length of a DNA double helix in a typical mammalian cell is approximately 2.2 metres and the dimension of the nucleus is about 10^{-6} m.

Q. How is it possible that long DNA polymers are packed within a very small nucleus?

Ans. Packaging of DNA in eukaryotes

- The proteins associated with DNA are of two types—basic proteins (histone and protamine) and acidic non-histone chromosomal (NHC) proteins.
- The negatively charged DNA molecule wraps around the positively charged histone proteins to form a structure called **nucleosome**.
- The nucleosome core is made up of four types of histone proteins—H_2A, H_2B, H_3 and H_4— occurring in pairs.
- 200 bp of DNA helix wrap around the nucleosome by 1¾ turns, plugged by H_1 histone protein.

Q. Differentiate between euchromatin and heterochromatin.

Ans.

S. No.	Euchromatin	Heterochromatin
(*i*)	Regions of chromatin which are loosely packed during interphase are called euchromatin.	Regions of chromatin which are densely packed during cell division are called heterochromatin.
(*ii*)	When chromosomes are stained with Feulgen stain (specific for DNA), these appear as lightly stained chromatin.	When chromosomes are stained with Feulgen stain, these appear as intensely stained chromatin.
(*iii*)	Euchromatin contains active genes.	Heterochromatin contains inactive genes.
(*iv*)	They do not contain repetitive DNA sequences.	They are enriched with highly repetitive tandemly arranged DNA sequences.
(*v*)	It is transcriptionally active.	It is transcriptionally inactive.

Q. Mention the role of non-histone chromosomal protein.

Ans. The packaging of chromatin at higher level requires the presence of non-histone chromosomal protein.

Q.2. List the criteria a molecule that can act as genetic material must fulfill. 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.

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

- **i.** It should be able to generate its replica (Replication).
- **ii.** It should chemically and structurally be stable.
- **iii.** It should provide the scope for slow changes (mutation) that are required for evolution.
- **iv.** It should be able to express itself in the form of 'Mendelian Characters'.

In DNA the two stands being complementary if separated by heating come together, when appropriate conditions are provided. Further, 2'-OH group present at every nucleotide in RNA is also now known to be catalytic, hence reactive. Therefore DNA chemically is less reactive and structurally more stable when compared to RNA. Therefore, among the two nucleic acids, the DNA is a better genetic material. The presence of thymine at the place of uracil also confers additional stability to DNA.

Both DNA and RNA are able to mutate. In fact, RNA being unstable, mutate at a faster rate. 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.

Q.3. Describe the packaging of DNA helix in a prokaryotic cell and an eukaryotic nucleus.

Ans. Packaging of DNA

Packaging of DNA in eukaryotes

- The proteins associated with DNA are of two types—basic proteins (histone and protamine) and acidic non-histone chromosomal (NHC) proteins.
- The negatively charged DNA molecule wraps around the positively charged histone proteins to form a structure called **nucleosome**.
- The nucleosome core is made up of four types of histone proteins—H_2A, H_2B, H_3 and H_4— occurring in pairs.
- 200 bp of DNA helix wrap around the nucleosome by 1¾ turns, plugged by H_1 histone protein.
- Repeating units of nucleosomes form the chromatin in nucleus, which is a thread-like structure.
- The chromatin is packed to form a **solenoid structure** of 30 nm diametre.

Q.4.

a. How did Griffith explain the transformation of R-strain (non-virulent) bacteria into S-strain (virulent)?

b. Explain how MacLeod, McCarty and Avery determined the biochemical nature of the molecule responsible for transforming R-strain bacteria into S-strain bacteria.

OR

a. Describe the various steps of Griffith's experiment that led to the conclusion of the 'Transforming Principle'.
b. How did the chemical nature of the 'Transforming Principle' get established?

Ans.

(a) Transforming Principle

- **Frederick Griffith** (1928) conducted experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
- He observed two strains of this bacterium—one forming smooth shiny colonies (S-type) with capsule, while other forming rough colonies (R-type) without capsule.
- When live S-type cells were injected into mice, they died due to pneumonia.
- When live R-type cells were injected into mice, they survived.
- When heat-killed S-type cells were injected into mice, they survived and there were no symptoms of pnuemonia.
- When heat-killed S-type cells were mixed with live R-type cells and injected into mice, they died due to unexpected symptoms of pneumonia and live S-type cells were obtained from mice.
- He concluded that heat-killed S-type bacteria caused a transformation of the R-type bacteria into S-type bacteria but he was not able to understand the cause of this bacterial transformation.

(b) Biochemical Characterisation of Transforming Principle

- **Oswald Avery, Colin MacLeod** and **Maclyn McCarty** repeated Griffith's experiment in an in vitro system in order to determine biochemical nature of transforming principle.
- They reported that DNA from the heat-killed S-type bacteria caused the transformation of nonvirulent R-type bacteria into virulent S-type bacteria.
- They also discovered that proteases and RNases did not affect transformation while DNases inhibited the process.
- They concluded that DNA is the hereditary material.

Q.5.

(a) Write the scientific name of the bacterium used by Frederick Griffith in his experiment.

(b) How did he prove that some 'transforming principle' is responsible for transformation of the non-virulent strains of bacteria into the virulent form?

(c) State the biochemical nature of 'transforming principle'.

(d) Name the scientists who proved it.

Ans.

(a) *Streptococcus pneumoniae*

(b) Transforming Principle

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- He concluded that heat-killed S-type bacteria caused a transformation of the R-type bacteria into S-type bacteria but he was not able to understand the cause of this bacterial transformation.

(c) 'The transforming principle' was nucleic acid, *i.e.*, DNA.

(d) It was proved by O. Avery, C. MacLeod and M. McCarty.

Q.6.

(a) Explain the experiment performed by Griffith on Streptococcus pneumoniae. What did he conclude from this experiment?

(b) Name the three scientists who followed up Griffith's experiments.

(c) What did they conclude and how?

Ans.

(a) Transforming Principle

- **Frederick Griffith** (1928) conducted experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
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(b) Oswald Avery, Colin MacLeod and Maclyn McCarty.

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- They also discovered that proteases and RNases did not affect transformation while DNases inhibited the process.
- They concluded that DNA is the hereditary material.

Q.7.

(a) What did Meselson and Stahl observe when

i. they cultured *E. coli* in a medium containing $^{15}NH_4Cl$ for a few generations and centrifuged the content?
ii. they transferred one such bacterium to the normal medium of NH_4Cl and cultured for 2 generations?

(b) What did Meselson and Stahl conclude from this experiment? Explain with the help of diagrams.

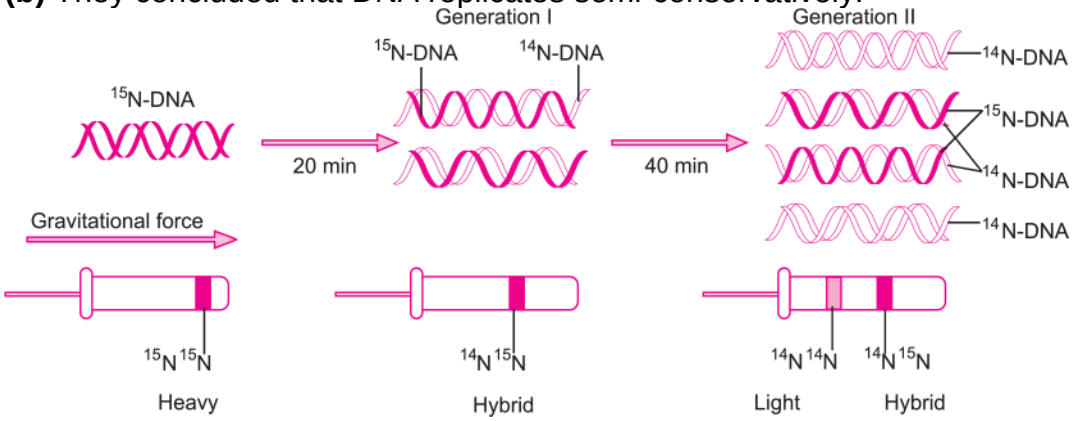
(c) Which is the first genetic material? Give reasons in support of your answer

Ans.

(a)

i. Meselson and Stahl observed that in the *E. coli* bacterium the DNA becomes completely labelled with ^{15}N medium after few generations.
ii. After two generations, they observed that density changed and showed equal amount of light DNA (^{14}N) and dark hybrid DNA (^{15}N–^{14}N).

(b) They concluded that DNA replicates semi-conservatively.



(c) RNA is the first genetic material.

Reasons:

i. RNA is highly reactive and acts as a catalyst as well as a genetic material.
ii. Essential life processes such as metabolism, translation and splicing evolved around RNA.
iii. It expresses itself through proteins.

Q.8. Describe the Hershey−Chase experiment. Write the conclusion they arrived at after the experiment.

OR

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

Ans. Proof for DNA as the Genetic Material

- **Hershey** and **Chase** conducted experiments on bacteriophage to prove that DNA is the genetic material.

Procedure:

i. Some bacteriophage virus were grown on a medium that contained radioactive phosphorus (^{32}P) and some in another medium with radioactive sulphur (^{35}S).
ii. Viruses grown in the presence of radioactive phosphorus (^{32}P) contained radioactive DNA.

iii. Similar viruses grown in presence of radioactive sulphur (^{35}S) contained radioactive protein.
iv. Both the radioactive virus types were allowed to infect *E. coli* separately.
v. Soon after infection, the bacterial cells were gently agitated in blender to remove viral coats from the bacteria.
vi. The culture was also centrifuged to separate the viral particle from the bacterial cell.

Observations and Conclusions:

i. Only radioactive ^{32}P was found to be associated with the bacterial cell, whereas radioactive ^{35}S was only found in surrounding medium and not in the bacterial cell.
ii. This indicates that only DNA and not protein coat entered the bacterial cell.
iii. This proves that DNA is the genetic material which is passed from virus to bacteria and not protein.

Q.9. Name the scientists who proved experimentally that DNA is the genetic material. Describe their experiment.

Ans. Alfred Hershey and Martha Chase proved that DNA is the genetic material.
Proof for DNA as the Genetic Material

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Q.10. How did Alfred Hershey and Martha Chase conclusively establish that DNA is the genetic material? Explain.

Ans. Proof for DNA as the Genetic Material

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Q.11. Who proposed that DNA replication is semi-conservative? How was it experimentally proved by Meselson and Stahl?

Ans. Watson and Crick had proposed the semi-conservative scheme for replication of DNA.

Experimental proof for semi-conservative mode of DNA replication

- **Matthew Meselson** and **Franklin Stahl** in 1958 performed experiments on *E. coli* to prove that DNA replication is semi-conservative.
- They grew *E. coli* in a medium containing $^{15}NH_4Cl$ (in which ^{15}N is the heavy isotope of nitrogen) for many generations.
- As a result, ^{15}N got incorporated into newly synthesised DNA.

- This heavy DNA can be differentiated from normal DNA by centrifugation in caesium chloride (CsCl) density gradient.
- Then they transferred the cells into a medium with normal $^{14}NH_4Cl$ and took the samples at various definite time intervals as the cells multiplied.
- The extracted DNAs were centrifuged and measured to get their densities.
- The DNA extracted from the culture after one generation of transfer from the ^{15}N medium to ^{14}N medium (*i.e.*, after 20 minutes; *E. coli* divides every 20 minutes) showed an intermediate hybrid density.
- The DNA extracted from culture after two generations (*i.e.*, after 40 minutes) showed equal amounts of light DNA and hybrid DNA.
- Similar experiment was performed by Taylor and colleagues in 1958, on *Vicia faba* to prove that the DNA in chromosome also replicate semi-conservatively.

Q.12. What is 'semi-conservative' DNA replication? How was it experimentally proved and by whom?

Ans. Watson and **Crick** in 1953 proposed a scheme that DNA replication was **semi-conservative**. According to the scheme, the two parental strands separate and each strand acts as a template for synthesising a complementary strand over it. After completion of replication, each DNA had one parental strand and one newly synthesised strand.

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Q.13. Describe Meselson and Stahl's experiment that was carried in 1958 on E.Coli. Write the conclusion they arrived at after the experiment.

Ans. Experimental proof for semi-conservative mode of DNA replication

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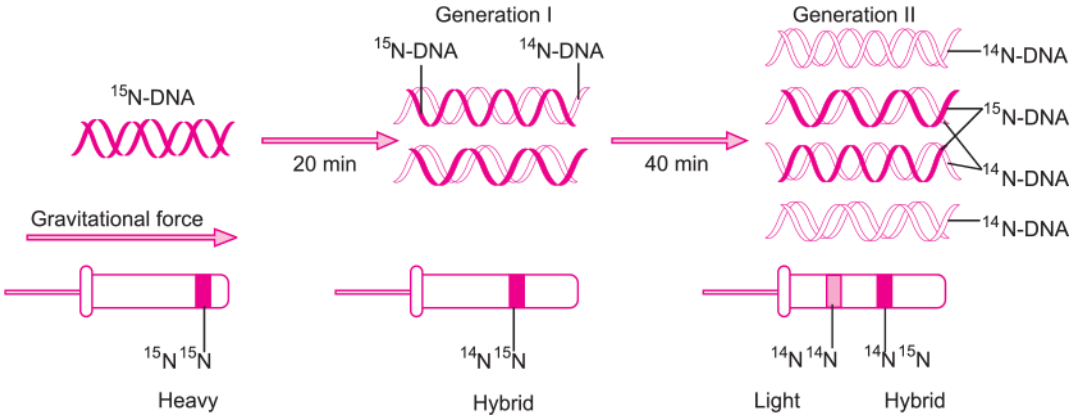


Meselson and Stahl's experiment

Q.14.

(a) Explain the observations of Meselson and Stahl when

i. **they cultured E. coli in a medium containing for a few generations and centrifuged the content.**
ii. **they transferred one such bacterium to the normal medium of**

(b) What does the above experiment prove?

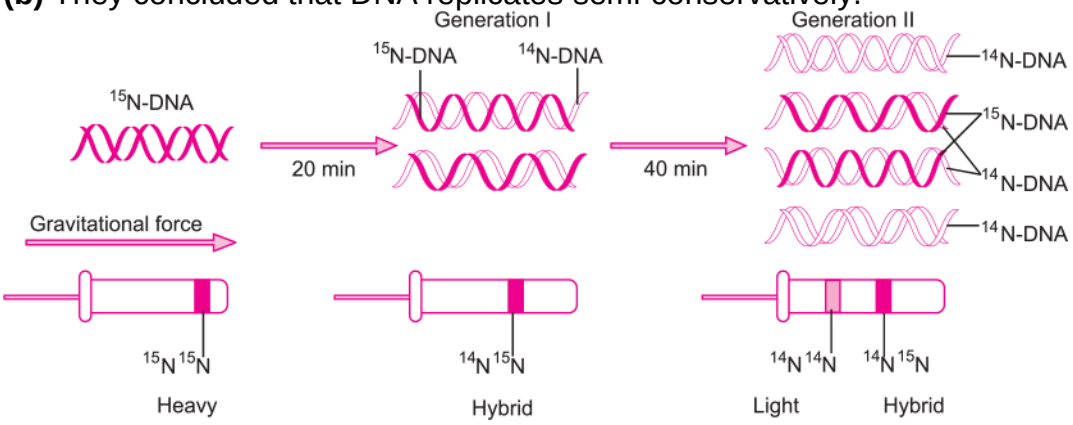
(c) Which is the first genetic material identified?

Ans.

(a)

i. Meselson and Stahl observed that in the E. coli bacterium the DNA becomes completely labelled with N medium by centrifugation for few generations.
ii. After two generations, density changed and showed equal amount of light DNA (N14) and dark hybrid DNA (N–N).

(b) They concluded that DNA replicates semi-conservatively.



(c) Ribonucleic acid (RNA) was the first genetic material.

Q.15.

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

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

(c) Why is DNA replication said to be semiconservative?

Ans.

(a) S-phase/synthetic phase (of interphase).

(b) Enzymes for DNA replication

- Various enzymes are required as catalysts during DNA replication in living cells.
- **DNA-dependent DNA polymerase:** It catalyses the polymerisation of deoxynucleotides on DNA template.
- **Helicase:** It unwinds the DNA strand to form the replication fork.
- **DNA ligase:** It joins the Okazaki fragments which are formed on the lagging strand.

(c) During DNA replication in the two newly synthesised daughter DNA one strand is parental (conserved) the other is newly synthesised. That is why it is called semiconservative.

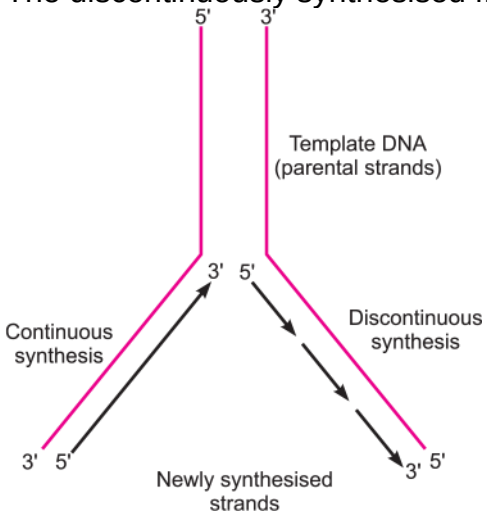
Q.16.

(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?

Ans.

(a) Replication of DNA begins at *ori*, to form a replication fork. DNA dependent DNA polymerase forms a new strand in 5′→ 3′ direction. The replication is continuous on the 3′ → 5′ strand whereas it is discontinuous on the 5′ → 3′ strand.
The discontinuously synthesised fragments are later joined by the enzyme DNA ligase.



(b) Replication occurs in S phase

If cell division is not followed after DNA replication, the cell will undergo polyploidy.

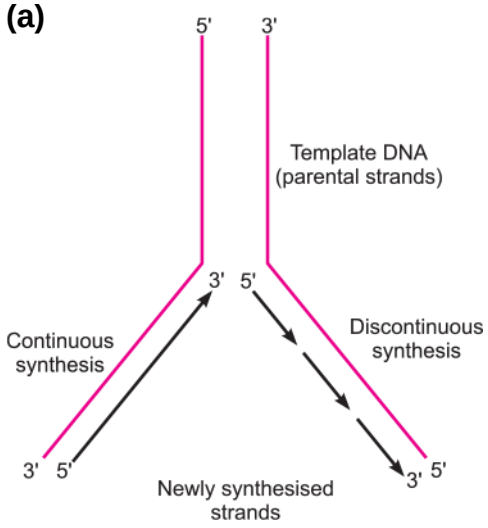
Q.17.

(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.

Ans.

(a)



The two strands of DNA cannot be separated in its entire length due to very high energy requirement. High amount of energy is required to break the hydrogen bonds holding the two strands. Therefore, the replication occurs in small opening of DNA strands called the replication fork.

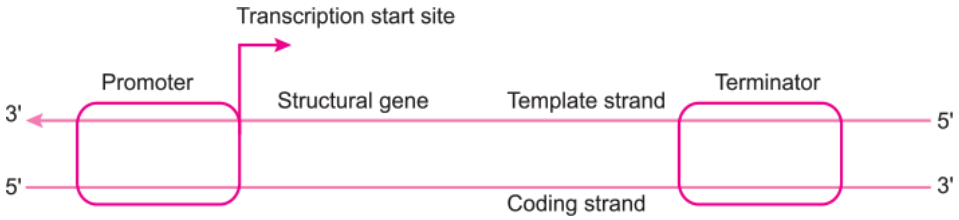
(b)

i. **DNA dependent DNA polymerase:** adds nucleotides only in 5 to 3 directions.
ii. **DNA ligase:** joins the discontinuously synthesised DNA fragments during replication.

Q.18. Draw a labelled schematic structure of a transcription unit. Explain the function of each component in the unit in the process of transcription.

Ans.

Schematic structure of a transcription unit:

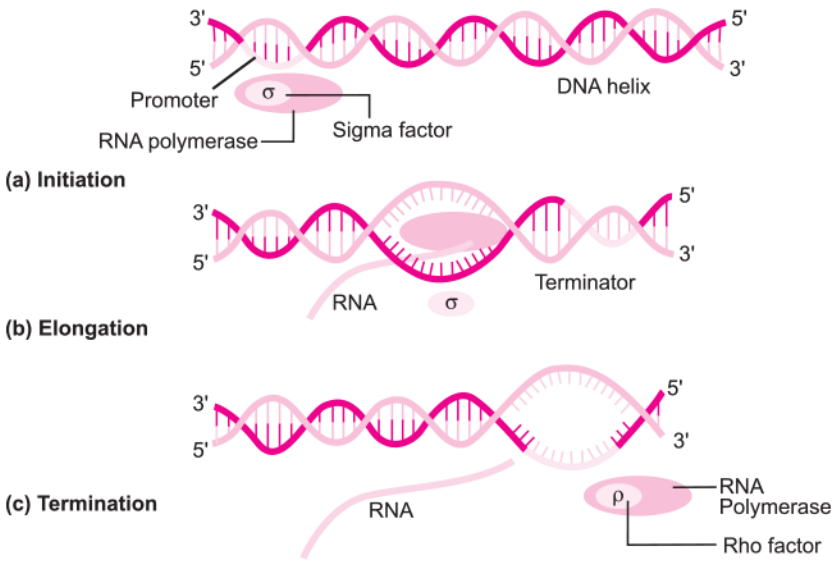


i. **Promoter:** It is the binding site for RNA polymerase for initiation of transcription.
ii. **Structural gene:** It codes for enzyme or protein for structural functions.
iii. **Terminator:** It is the region where transcription ends.

Q.19. Explain the process of transcription in prokaryotes. How is the process different in eukaryotes?

Ans. Transcription in Prokaryotes

- **Initiation:** σ (sigma) factor recognises the start signal and promotor region on DNA which then along with RNA polymerase binds to the promoter to initiate transcription.
- **Elongation:** The RNA polymerase after initiation of RNA transcription loses the σ factor but continues the polymerisation of ribonucleotides to form RNA.
- **Termination:** Once the RNA polymerase reaches the termination region of DNA, the RNA polymerase is separated from DNA–RNA hybrid, as a result nascent RNA separates. This process is called termination which is facilitated by a termination factor ρ (**rho**).



Process of transcription in bacteria

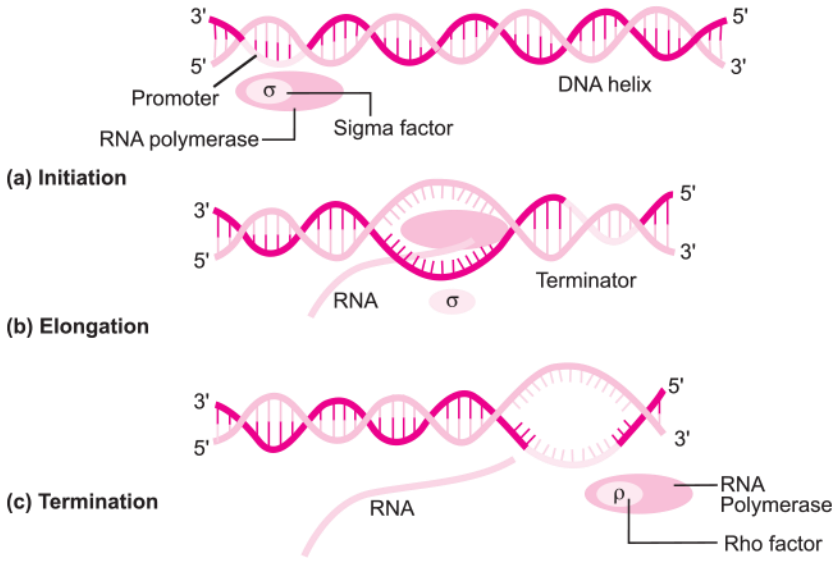
Transcription in Eukaryotes

- The structural genes are monocistronic in eukaryotes.
- The process of transcription is similar to that in prokaryotes.
- It takes place in the nucleus.
- Coding gene sequences called exons form the part of *m*RNA and non-coding sequence called introns are removed during RNA splicing.
- In eukaryotes, three types of RNA polymerases are found in the nucleus:
  i. **RNA polymerase I** transcribes *r*RNAs (28S, 18S, and 5.8S).
  ii. **RNA polymerase II** transcribes the precursor of *m*RNA (called heterogeneous nuclear RNA or *hn*RNA).
  iii. **RNA polymerase III** transcribes *t*RNA, 5S *r*RNA and *sn*RNAs (small nuclear RNAs).

Q.20. Explain the process of transcription in Eukaryotes.

Ans. Transcription in Prokaryotes

- In prokaryotes, the structural gene is polycistronic and continuous.
- In bacteria, the transcription of all the three types of RNA (mRNA, tRNA and rRNA) is catalysed by single DNA-dependent enzyme, called the RNA polymerase.
- In E. coli bacterium, the RNA polymerase has co-factors β, β′, a, a′ and w along with s (sigma) factor, to catalyse the process.
- The transcription is completed in three steps: initiation, elongation and termination.
- **Initiation:** s (sigma) factor recognises the start signal and promotor region on DNA which then along with RNA polymerase binds to the promoter to initiate transcription.
- **Elongation:** The RNA polymerase after initiation of RNA transcription loses the s factor but continues the polymerisation of ribonucleotides to form RNA.
- **Termination:** Once the RNA polymerase reaches the termination region of DNA, the RNA polymerase is separated from DNA–RNA hybrid, as a result nascent RNA separates. This process is called termination which is facilitated by a termination factor r (rho).
- In prokaryotes, mRNA does not require any processing, so both transcription and translation occur in the cytosol. It can be said that transcription and translation are coupled together.



Process of transcription in bacteria

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iii. **RNA polymerase III** transcribes *t*RNA, 5S *r*RNA and *sn*RNAs (small nuclear RNAs).**Post-transcriptional modifications**

- The primary transcripts are non-functional, containing both the coding region, exon, and region, intron, in RNA and are called heterogenous RNA or *hn*RNA.
- The *hn*RNA undergoes two additional processes called **capping** and **tailing**.
- In capping, an unusual nucleotide, methyl guanosine triphosphate, is added to the 5′-end of *hn*RNA.
- In tailing, adenylate residues (about 200–300) are added at 3′-end in a template independent manner.
- Now the *hn*RNA undergoes a process where the introns are removed and exons are joined to form *m*RNA by the process called **splicing**.

Q.21. Explain the role of RNA polymerase in transcription in bacteria.

Ans.

- In E. coli bacterium, the RNA polymerase has co-factors β, β′, α, α′ and ω along with σ (sigma) factor, to catalyse the process.
- The transcription is completed in three steps: initiation, elongation and termination.
- **Initiation:** σ (sigma) factor recognises the start signal and promotor region on DNA which then along with RNA polymerase binds to the promoter to initiate transcription.

Q.22. How do RNA, *t*-RNA and ribosomes help in the process of translation?

Ans.

*m*RNA provides a template with codons for specific amino acids to be linked to form a polypeptide/ protein.

*t*RNA brings amino acid to the ribosomes reads the genetic code with the help of its anti-codons, initiator *t*RNA is responsible for starting polypeptide formation in the ribosomes *t*RNAs are specific for each amino acid.

Ribosomes-(Cellular factories for proteins synthesis) its smaller sub unit binds with *m*RNA to initiate protein synthesis at the start codon AUG, in its larger sub unit there are two sites present which brings two amino acids close to each other helping them to form peptide bond. Ribosomes moves from codon to codon along *m*RNA, amino acids are added one by one to form polypeptide/ protein.

Q.23. Name the major types of RNAs and explain their role in the process of protein synthesis in a prokaryote.

Ans.

The three major types of RNAs are—*m*RNA, *t*RNA and *r*RNA. ***m*RNA:** It provides the template for protein synthesis. It also provides site to initiate and terminate the process of protein synthesis ***t*RNA:** Its anticodon loop reads the genetic code on *m*RNA and brings the corresponding amino acid bound to its amino acid binding end on to the *m*RNA. ***r*RNA:** It forms a structural component of ribosome (23S RNA) and acts as a catalyst for the formation of peptide bond.

Q.24. Where do transcription and translation occur in bacteria and eukaryotes respectively? Explain the complexities in transcription and translation in eukaryotes that are not seen in bacteria.

Ans.

Transcription and translation in bacteria occur in the cytoplasm of the cell, whereas in eukaryotes, transcription occurs in the nucleus and translation occurs in the cytoplasm.

Complexities in transcription in eukaryotes

i. The structural genes are monocistronic and split in eukaryotes.
ii. The genes of eukaryotic organisms have coding or expressed sequences called exons that form the part of *m*RNA and non-coding sequences called introns, that do not form part of the *m*RNA and are removed during RNA splicing.
iii. In eukaryotes, apart from the RNA polymerase found in the organelles, three types of RNA polymerases are found in the nucleus.
iv. RNA polymerase I transcribes *r*RNAs (28S, 18S, and 58S).
v. RNA polymerase II transcribes the precursor of *m*RNA (called as heterogeneous nuclear RNA (*hn*RNA).
vi. RNA polymerase III helps in transcription of *t*RNA, 5S *r*RNA, and *sn*RNAs (small nuclear RNAs).
vii. The primary transcripts contain both the coding regions called exons and non-coding regions called intron in RNA and are non-functional called *hn*RNA.
viii. The *hn*RNA undergoes two additional processes called capping and tailing.
ix. In capping, an unusual nucleotide is added to the 5′-end of *hn*RNA *i.e.* methyl guanosine triphosphate.
x. In tailing, about 200-300 adenylate residues are added at 3′-end in a template independent manner.
xi. Now the *hn*RNA undergoes a process where the introns are removed and exons are joined to form *m*RNA called splicing.

Translation in both eukaryotes and prokaryotes is similar

Q.25.

a. **Explain the process of aminoacylation of *t*RNA. Mention its role in translation.**
b. **How do ribosomes in the cells act as factories for protein synthesis?**
c. **Describe ‘initiation’ and ‘termination’ phases of protein synthesis.**

Ans.

a. Aminoacylation is the process by which amino acids become activated by binding with its aminoacyl *t*RNA synthetase in the presence of ATP.
If two charged *t*RNAs come close during translation process, the formation of peptide bond between them in energetically favourable.

b. The cellular factory responsible for synthesising proteins is the ribosome. The ribosome consists of structural RNAs and about 80 different proteins. In its inactive state, it exists as two subunits: a large subunit and a small subunit. When the small subunit encounters an *m*RNA, the process of translation of the *m*RNA to protein begins. There are two sites in the large subunit, for subsequent amino acids to bind to and thus, be close enough to each other for the formation of a peptide bond. The ribosome also acts as a catalyst (23S *r*RNA in bacteria is the enzyme ribozyme) for the formation of peptide bond.

c.

Translation

- Translation is the process of synthesis of protein from *m*RNA with the help of ribosome.
- A translational unit in *m*RNA from 5' → 3' comprises of a start codon, region coding for a polypeptide, a stop codon and untranslated regions (UTRs) at both 5'-end and 3'-end for efficient process.
- There are three stages of protein synthesis:
    i. **Initiation**
        - Assembly of ribosome on *m*RNA.
        - Activation of amino acids and its delivery to *t*RNA
    ii. **Elongation**
        - Repeated cycle of amino acid delivery.
        - Peptide bond formation and movement along the *m*RNA called **translocation**.
    iii. **Termination**
        - The release of a polypeptide chain.

i. **Initiation**

- In prokaryotes, initiation requires the large and small ribosome subunits, the *m*RNA, initiation *t*RNA and three initiation factors (IFs).
- **Activation of amino acid:** Amino acids become activated by binding with aminoacyl *t*RNA synthetase enzyme in the presence of ATP.
- **Transfer of amino acid to *t*RNA:** The AA–AMP–Enzyme complex formed reacts with specific *t*RNA to form aminoacyl-*t*RNA complex. AA–AMP–Enzyme complex + *t*RNA → AA–*t*RNA + AMP + Enzyme.
- The cap region of mRNA binds to the smaller subunit of ribosome.
- The ribosome has two sites, A-site and P-site.

- The smaller subunit first binds to the initiator *m*RNA and then binds to the larger subunit so that initiation codon (AUG) lies on the P-site.
- The initiation *t*RNA, *i.e.*, methionyl *t*RNA then binds to the P-site.

ii. **Elongation of polypeptide chain**

- Another charged aminoacyl tRNA complex binds to the A-site of the ribosome at the second codon.
- A peptide bond is formed between carboxyl group (—COOH) of amino acid at P-site and amino group (—NH) of amino acid at A-site by the enzyme **peptidyl transferase**.
- The ribosome slides over *m*RNA from codon to codon in the 5′→3′ direction.
- According to the sequence of codons, amino acids are attached to one another by peptide bonds and a polypeptide chain is formed.

iii. **Termination of polypeptide**

- When the A-site of ribosome reaches a termination codon which does not code for any amino acid, no charged tRNA binds to the A-site.
- Dissociation of polypeptide from ribosome takes place, which is catalysed by a **'release factor'**.
- There are three **termination codons** namely UGA, UAG and UAA.

Q.26.

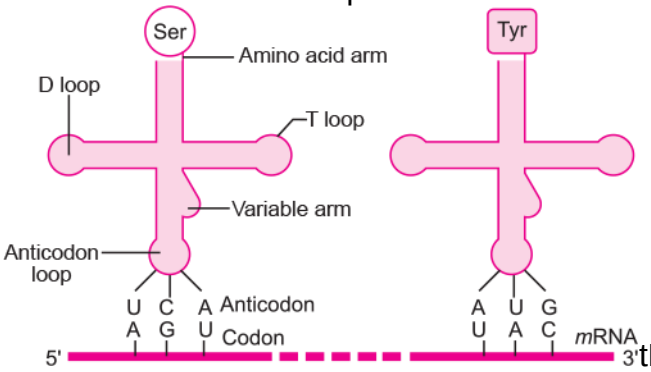
a. Name the scientist who postulated the presence of an adapter molecule that can assist in protein synthesis.
b. Describe its structure with the help of a diagram. Mention its role in protein synthesis.

Ans.

a. Francis Crick
b.

- **Francis Crick** proposed the presence of an adaptor molecule which could read the code on one end and on the other end would bind to the specific amino acids.
- However, *t*RNA was known before genetic code was postulated and was then called *s*RNA (soluble RNA). Its role as an adaptor molecule was reported later.**Structure**
- The secondary structure of tRNA is clover-leaf like but the three-dimensional tertiary structure depicts it as a compact inverted L-shaped molecule.
- *t*RNA has five arms or loops:
  i. **Anticodon loop,** which has bases complementary to the code.
  ii. **Amino acid acceptor end** to which amino acids bind.
  iii. **T loop,** which helps in binding to ribosome.
  iv. **D loop,** which helps in binding aminoacyl synthetase.
  v. **Variable loop**.

- Each *t*RNA is specific for a particular amino acid.
- A specific *t*RNA for initiation is called initiator *t*RNA.
- There is no *t*RNA for stop codons.



tRNA—the adapter molecule***t*RNA—the Adaptor Molecule**

The adapter molecule reads code with the help of anticodon loop and on the other end binds specific amino acids by peptide bond.

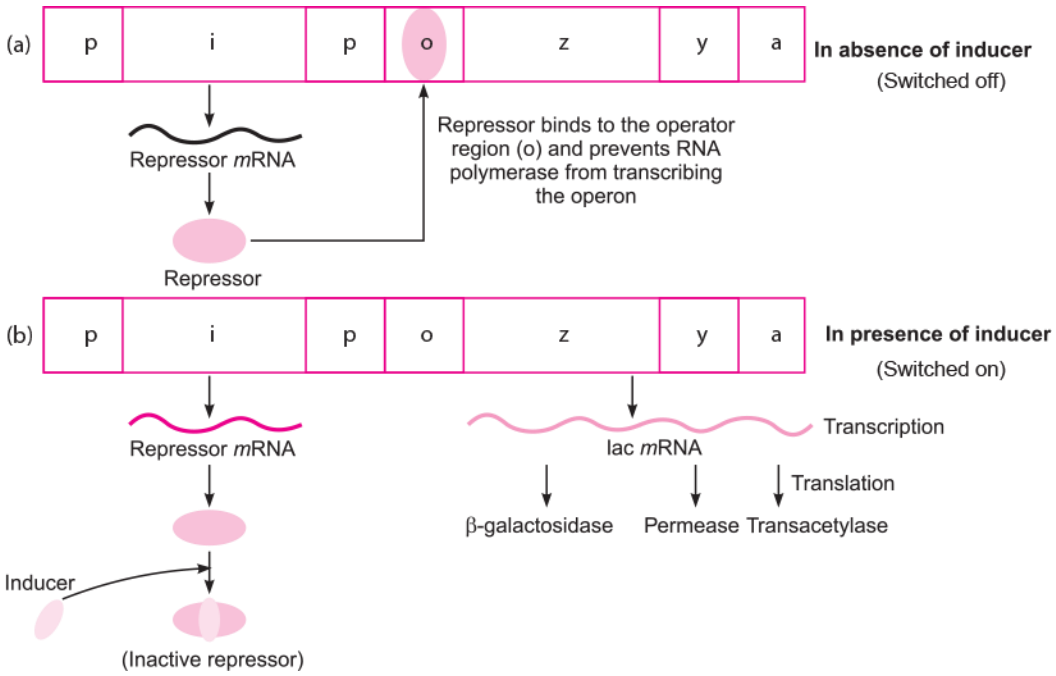
Q.27.

a. **What is an operon?**
b. **Explain how a polycistronic structural gene is regulated by a common promoter and a combination of regulatory genes in a lac-operon.**

Ans.

a. An operon is a polycistronic structural gene which is regulated by a common promoter and regulator gene.
b. **The lac Operon**

- *lac* operon consists of **three structural genes** (*z, y, a*), operator (*o*), promoter (*p*) and a separate regulatory gene (*i*). Lactose is the inducer in lac operon.
- The three structural genes (z, y, a) transcribe a polycistronic *m*RNA.



a.

- Gene z codes for β-galactosidase (β-gal) enzyme which breaks lactose into galactose and glucose.
- Gene *y* codes for permease, which increases the permeability of the cell to lactose.
- Gene *a* codes for enzyme transacetylase, which catalyses the transacetylation of lactose in its active form.
- **When Lactose is Absent**
    i. When lactose is absent, *i* gene regulates and produces repressor *m*RNA which translate repression.
    ii. The repressor protein binds to the operator region of the operon and as a result prevents RNA polymerase to bind to the operon.
    iii. The operon is switched off.
- **When Lactose is Present**
    i. Lactose acts as an inducer which binds to the repressor and forms an inactive repressor.
    ii. The repressor fails to bind to the operator region.
    iii. The RNA polymerase binds to the operator and transcribes *lac m*RNA.
    iv. *lac m*RNA is polycistronic, *i.e.*, produces all three enzymes, β-galactosidase, permease and transacetylase.
    v. The *lac* operon is switched on.

Q.28. Study the schematic representation of the genes involved in the lac operon given below and answer the questions that follow:

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

Ans. *i* gene is the regulatory gene and codes of repressor which acts as inhibitor as inhibits the transcription of structural genes.

The repressor of the operon is synthesised from the *i* gene. The repressor protein in the absence of an inducer (lactose or allolactose) binds to the operator region of the operon and prevents RNA polymerase from transcribing the structural genes. Thus 'switching off ' the operon.

Q. Why is lac operon's regulation referred to as negative regulation?

Ans. Regulation by *lac* operon is referred to as negative regulation because the repressor binds to the operator for 'switching off ' the operon.

Q. Name the inducer molecule and the products of the genes 'z' and 'y' of the operon. Write the functions of these gene products.

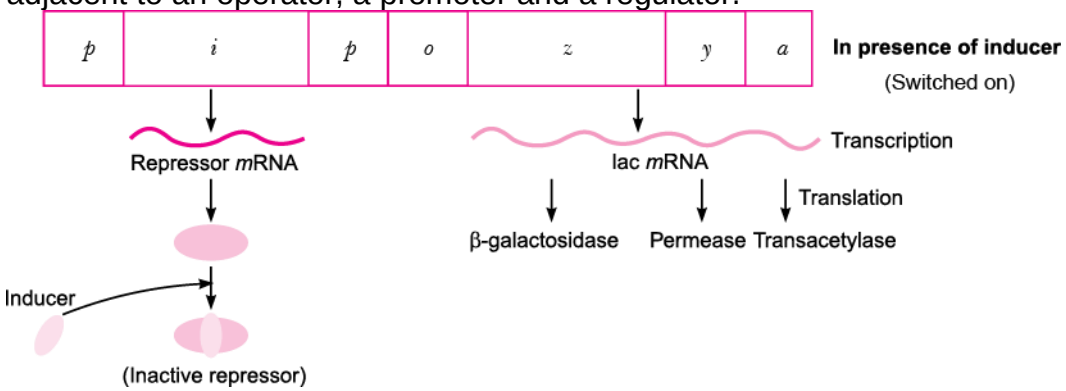
Ans. Lactose or allolactose acts as an inducer. Gene *z* codes for β-galactosidase (gal) enzyme which breaks lactose into galactose and glucose. Gene *y* codes for permease, which increases the permeability of the cell to lactose.

Q.29.

a. **State the arrangement of different genes that in bacteria is referred to as 'operon'.**
b. **Draw a schematic labelled illustration of *lac* operon in a 'switched on' state.**
c. **Describe the role of lactose in *lac* operon.**

Ans.

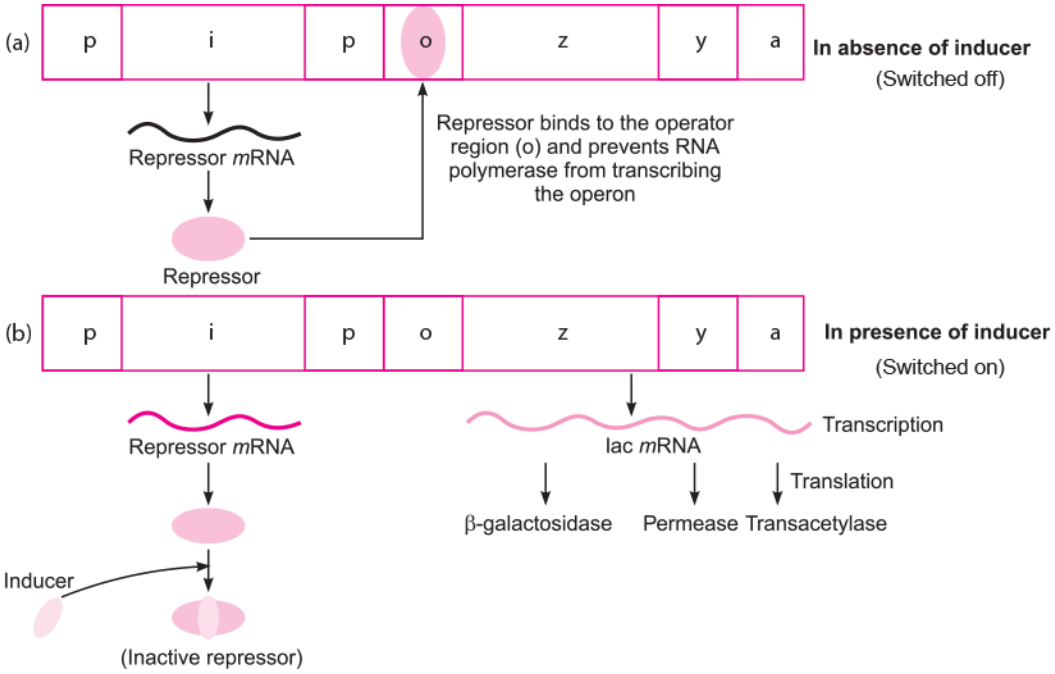
a. The operon has polycistronic structural genes, *i.e.*, three structural genes adjacent to an operator, a promoter and a regulator.



b.
c. Lactose is the inducer that inactivates repressor. This allows RNA polymerase to access promoter and initiate transcription of the structural genes or switch on the operon.

Q.30. Describe how the lac operon operates, both in the presence and absence of an inducer in *E.coli*.

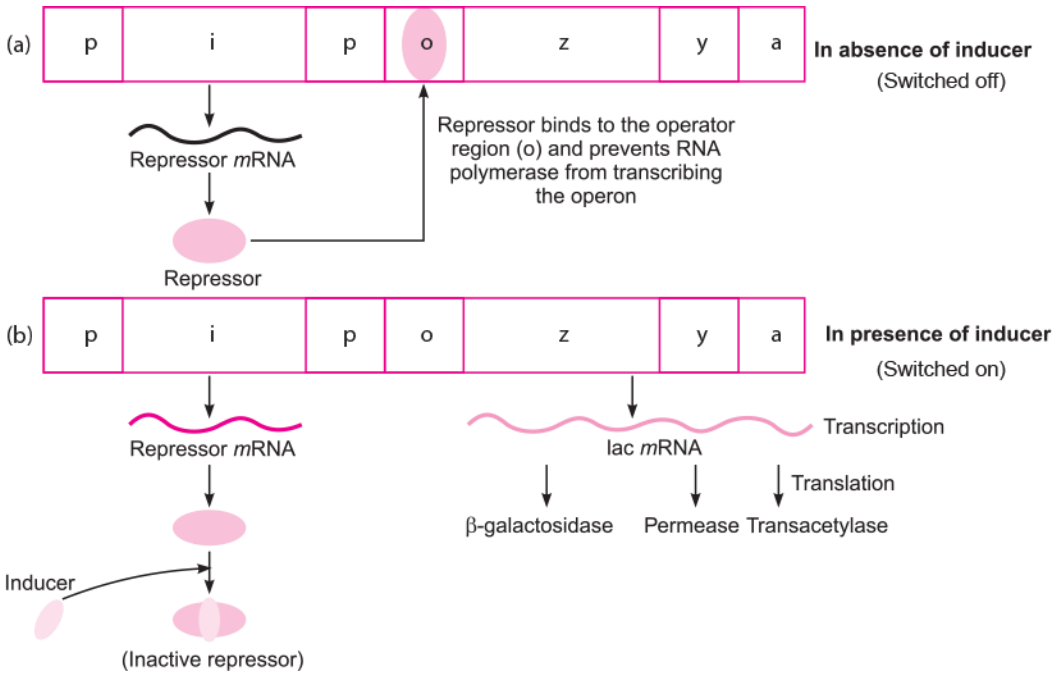
Ans.



The repressor is synthesised form the *i* gene. The repressor protein binds to the operator region and prevents RNA polymerase from transcribing the structural genes *zya*. In the presence of an inducer, the repressor is inactivated by interaction with inducer. This allows RNA polymerase access to promotor and transcription proceeds.

Q.31. Explain the role of lactose as an inducer in a *lac* operon.

Ans. The lac Operon



The *lac* operon

- **When Lactose is Absent**
  i. When lactose is absent, *i* gene regulates and produces repressor *m*RNA which translate repression.
  ii. The repressor protein binds to the operator region of the operon and as a result prevents RNA polymerase to bind to the operon.
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  i. Lactose acts as an inducer which binds to the repressor and forms an inactive repressor.
  ii. The repressor fails to bind to the operator region.
  iii. The RNA polymerase binds to the operator and transcribes *lac m*RNA.
  iv. *lac m*RNA is polycistronic, *i.e.*, produces all three enzymes, β-galactosidase, permease and transacetylase.
  v. The *lac* operon is switched on.

Q.32. Explain the steps of DNA fingerprinting that will help in processing of the two blood samples A and B picked up from the crime scene.

Ans. **DNA Fingerprinting**

Methodology and Technique

i. DNA is isolated and extracted from the cell or tissue by centrifugation.
ii. By the process of polymerase chain reaction (PCR), many copies are produced. This step is called **amplification**.
iii. DNA is cut into small fragments by treating with restriction endonucleases.
iv. DNA fragments are separated by agarose gel electrophoresis.

v. The separated DNA fragments are visualised under ultraviolet radiation after applying suitable dye.
vi. The DNA is transferred from electrophoresis plate to nitrocellulose or nylon membrane sheet. This is called **Southern blotting**.
vii. VNTR probes are now added which bind to specific nucleotide sequences that are complementary to them. This is called **hybridisation**.
viii. The hybridised DNA fragments are detected by autoradiography. They are observed as dark bands on X-ray film.

Q.33.

i. DNA polymorphism is the basis of DNA fingerprinting technique. Explain.
ii. Mention the causes of DNA polymorphism.

Ans.

i. Allelic sequence variation has traditionally been described as a DNA polymorphism if its frequency is greater than 0.01. Simply, if an inheritable mutation is observed in a population at high frequency, it is referred to as DNA polymorphism. DNA fingerprinting is a technique of determining nucleotide sequences of certain areas of DNA which are unique to each individual. Although the DNA from different individuals is more alike than different, there are many regions of the human chromosomes that exhibit a great deal of diversity. Such variable sequences are termed “polymorphic” (meaning many forms)
A special type of polymorphism, called VNTR (variable number of tandem repeats), is composed of repeated copies of a DNA sequence that lie adjacent to one another on the chromosome.Since polymorphism is the basis of genetic mapping of human genome, therefore it forms the basis of DNA fingerprinting too.
ii. The probability of such variations to be observed in non-coding DNA sequences would be higher as mutations in these sequences may not have any immediate effect in an individual’s reproductive ability. These mutations keep on accumulating generation after generation and form one of the basis of variability. There is a variety of different types of polymorphisms ranging from single nucleotide change to very large scale changes. For evolution and speciation, such polymorphisms play very important role.
The single nucleotide polymorphisms are used in locating diseases and tracing of human history. DNA polymorphisms are due to mutations.

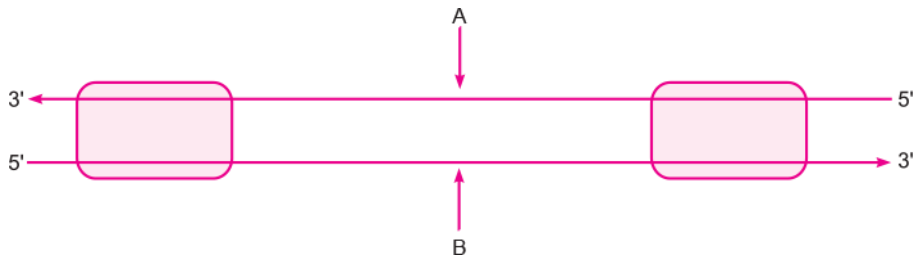
Q.34. Two blood samples A and B picked up from the crime scene were handed over to the forensic department for genetic fingerprinting. Describe how the technique of genetic fingerprinting is carried out. How will it be confirmed whether the samples belonged to the same individual or to two different individuals?

Ans. Methodology and Technique

i. DNA is isolated and extracted from the cell or tissue by centrifugation.
ii. By the process of polymerase chain reaction (PCR), many copies are produced. This step is called **amplification**.
iii. DNA is cut into small fragments by treating with restriction endonucleases.
iv. DNA fragments are separated by agarose gel electrophoresis.
v. The separated DNA fragments are visualised under ultraviolet radiation after applying suitable dye.
vi. The DNA is transferred from electrophoresis plate to nitrocellulose or nylon membrane sheet. This is called **Southern blotting**.
vii. VNTR probes are now added which bind to specific nucleotide sequences that are complementary to them. This is called **hybridisation**.
viii. The hybridised DNA fragments are detected by autoradiography. They are observed as dark bands on X-ray film.

On comparing the DNA prints of blood samples A and B, it can be confirmed that the blood sample picked up from the crime scene belongs to the same individual or to two different individuals by matching the position and thickness of the bands.

Q.35.



a. Identify strands 'A' and 'B' in the diagram of transcription unit given above and write the basis on which you identified them.
b. State the functions of Sigma factor and Rho factor in the transcription process in a bacterium.
c. Write the functions of RNA polymerase-I and RNA polymerase-III in eukaryotes.

Ans.

a. A—Template strand
B—Coding strand
The templates are identified on the basis of polarity with respect to promoter. Template strand has polarity 3′ → 5′ and coding strand has polarity 5′ → 3′.
b. In initiation sigma factor associates with RNA polymerase to initiate transcription and Rho factor gets associated to RNA polymerase to terminate transcription.
c. RNA polymerase-I transcribes *r*RNAs.
RNA polymerase-III transcribes *t*RNA, 5*sr*RNA and *sn*RNA.

Q.36. Answer the following questions:

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

i. **Histone octomer**
ii. **Nucleosome**
iii. **Chromatin**

Ans.

i. Eight molecules of positively charged basic proteins called histones are organised to form histone octomer.
ii. Negatively charged DNA is wrapped around positively charged histone octamer to give rise to nucleosome.
iii. Nucleosome constitute the repeating unit of a structure called chromatin.

Q. Differentiate between Euchromatin and Heterochromatin.

Ans.

Euchromatin	Heterochromatin
1. Loosely packed 2. Stains light 3. Transcriptionally active	1. Densely packed 2. Stains dark 3. Transcriptionally inactive

Q.37. Answer the following questions:

Q. Describe the series of experiments of F. Griffith. Comment on the significance of the results obtained.

Ans.

- **Frederick Griffith** (1928) conducted experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
- He observed two strains of this bacterium—one forming smooth shiny colonies (S-type) with capsule, while other forming rough colonies (R-type) without capsule.
- When live S-type cells were injected into mice, they died due to pneumonia.
- When live R-type cells were injected into mice, they survived.
- When heat-killed S-type cells were injected into mice, they survived and there were no symptoms of pnuemonia.
- When heat-killed S-type cells were mixed with live R-type cells and injected into mice, they died due to unexpected symptoms of pneumonia and live S-type cells were obtained from mice.
- He concluded that heat-killed S-type bacteria caused a transformation of the R-type bacteria into S-type bacteria but he was not able to understand the cause of this bacterial transformation.

Q. State the contribution of Macleod, McCarty and Avery.

Ans. Biochemical Characterisation of Transforming Principle

- **Oswald Avery, Colin MacLeod** and **Maclyn McCarty** repeated Griffith's experiment in an in vitro system in order to determine biochemical nature of transforming principle.
- They reported that DNA from the heat-killed S-type bacteria caused the transformation of nonvirulent R-type bacteria into virulent S-type bacteria.
- They also discovered that proteases and RNases did not affect transformation while DNases inhibited the process.
- They concluded that DNA is the hereditary material.

Q.38. Answer the following questions:

Q. Describe the experiment which demonstrated the existence of "transforming principle".

Ans. Transforming Principle

- **Frederick Griffith** (1928) conducted experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
- He observed two strains of this bacterium—one forming smooth shiny colonies (S-type) with capsule, while other forming rough colonies (R-type) without capsule.
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- He concluded that heat-killed S-type bacteria caused a transformation of the R-type bacteria into S-type bacteria but he was not able to understand the cause of this bacterial transformation.

Q. How was the biochemical nature of this "transforming principle" determined by Avery, MacLeod and McCarty?

Ans. Biochemical Characterisation of Transforming Principle

- **Oswald Avery, Colin MacLeod** and **Maclyn McCarty** repeated Griffith's experiment in an in vitro system in order to determine biochemical nature of transforming principle.
- They reported that DNA from the heat-killed S-type bacteria caused the transformation of nonvirulent R-type bacteria into virulent S-type bacteria.
- They also discovered that proteases and RNases did not affect transformation while DNases inhibited the process.
- They concluded that DNA is the hereditary material.

Q.39. Answer the following questions:

Q. Write the conclusion drawn by Griffith at the end of his experiment with *Streptococcus pneumoniae*.

Ans. At the end of his experiments Griffith concluded that transformation of R strain by the heatkilled S strain indicated the presence of a transforming principle or genetic material. This transforming principle made the R strain virulent.

Q. How did O. Avery, C MacLeod and M. McCarty prove that DNA was the genetic material? Explain.

Ans. They purified biochemicals (proteins, DNA, RNA, etc.) from the heat-killed 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, so the transforming substance was not a protein or RNA. Digestion with DNase did inhibit transformation, suggesting that the DNA caused the transformation. They concluded that DNA is the hereditary material.

Q.40. Answer the following questions:

Q. Explain the process of DNA replication that occurs in a replication fork in *E. coli*.

Ans. Process of DNA Replication

- DNA replication begins at a unique and fixed point called **origin of replication** or **'ori'**.**Initiation**

- The complementary strands of DNA double helix are separated by two enzymes, DNA gyrase and DNA helicase. This is called **unwinding** of double-stranded DNA.
- The separated strands tend to rewind, therefore these are stabilised by proteins called **single strand binding proteins (ssBPs),** which bind to the separated strands.
- Unwinding of double-stranded DNA forms a Y-shaped configuration in the DNA duplex, which is called **replication fork**.

Elongation

- An enzyme called **primase** initiates replication of the strand oriented in the 3′ (towards origin)→5′ (towards fork) direction. This generates 10–60 nucleotides long primer RNA (replicated in 5′→3′ direction).
- The free 3′–OH of this RNA primer provides the initiation point for DNA polymerase for sequential addition of deoxyribonucleotides.
- DNA polymerase progressively adds deoxyribonucleotides to the free 3′-end of the growing polynucleotide chain so that replication of the 3′→5′ strand of the DNA molecule is continuous (growth of the new strand in 5′→3′ direction).
- The replication of 3′→5′ strand is continuous and it is called **leading strand,** while the replication of second strand (5′→3′ strand) of the DNA molecules is discontinuous and it is known as the **lagging strand**.
- The replication of lagging strand generates small polynucleotide fragments called **'Okazaki fragments'** (after R. Okazaki, who first identified them).

- These Okazaki fragments are then joined together by enzyme called DNA **ligase**.

Q. How are translational unit and untranslated regions in *m*RNA different from each other?

Ans. A translational unit in *m*RNA from 5' → 3' comprises of a start codon, region coding for a polypeptide, a stop codon and untranslated regions (UTRs). UTRs are present at both 5'-end and 3'-end of *m*RNA.

Q.41. Answer the following questions:

Q. Why is DNA molecule a more stable genetic material than RNA? Explain.

Ans. In DNA, presence of thymine at the place of uracil confers more stability to DNA. In RNA, the −OH group is a reactive group that makes RNA labile and degradable, while its absence in DNA makes DNA chemically less reactive and more stable.

Q. "Unambiguous", "degenerate" and "universal" are some of the salient features of genetic code. Explain.

Ans.

Unambiguous: One codon specifies only one particular amino acid hence it is called unambiguous.

Degenerate: Some amino acids are coded by more than one codons hence the code is said to be degenerate.

Universal: A particular codon coding for an amino acid is same in all organisms except in mitochondria and protozoa.

Q.42. Answer the following questions:

Q. Write the specific features of the genetic code AUG.

Ans. AUG is the starting codon and codes for methionine.

Q. Genetic codes can be universal and degenerate. Write about them, giving one example of each.

Ans.

The genetic code is universal, *i.e.*, a particular codon codes for the same amino acid in all organisms. For example, UUU codes for phenylalanine in all organisms.

Some amino acids are coded by more than one codon, hence the code is degenerate. For example, UUU and UUC both code for phenylalanine.

Q. Explain aminoacylation of the *t*RNA.

Ans. Amino acids become activated by binding with aminoacyl *t*RNA synthetase enzyme in the presence of ATP.

$$\text{Amino } acid(AA) + \text{ATP} \xrightarrow{\text{Aminoacyl tRNA synthetase}} AA\text{–}AMP\text{–}Enzyme \text{ complex} + \text{Pi}$$

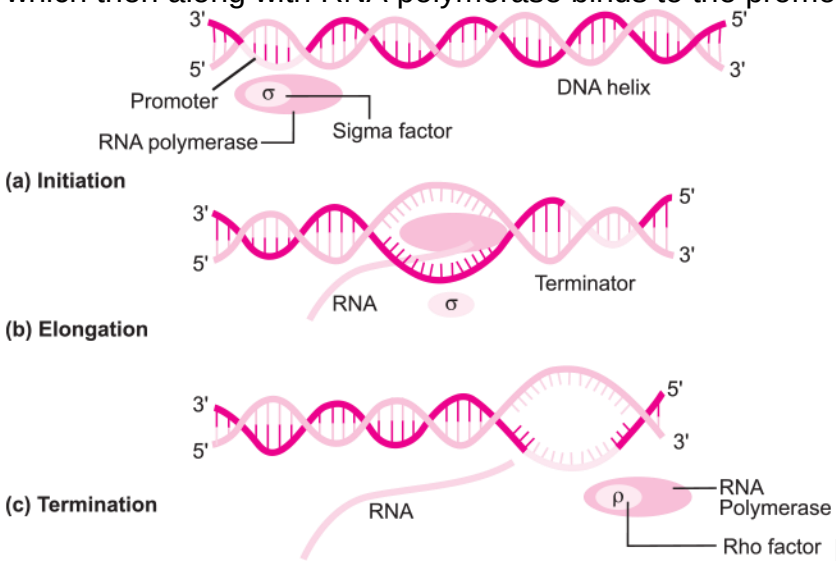
These activated amino acids are then linked to their cognate tRNA to form aminoacylated *t*RNA.

Q.43. Answer the following questions:

Q. Describe the process of transcription in bacteria.

Ans. Transcription in Prokaryotes

- **Initiation:** σ (sigma) factor recognises the start signal and promotor region on DNA which then along with RNA polymerase binds to the promoter to initiate transcription.



Process of transcription in bacteria

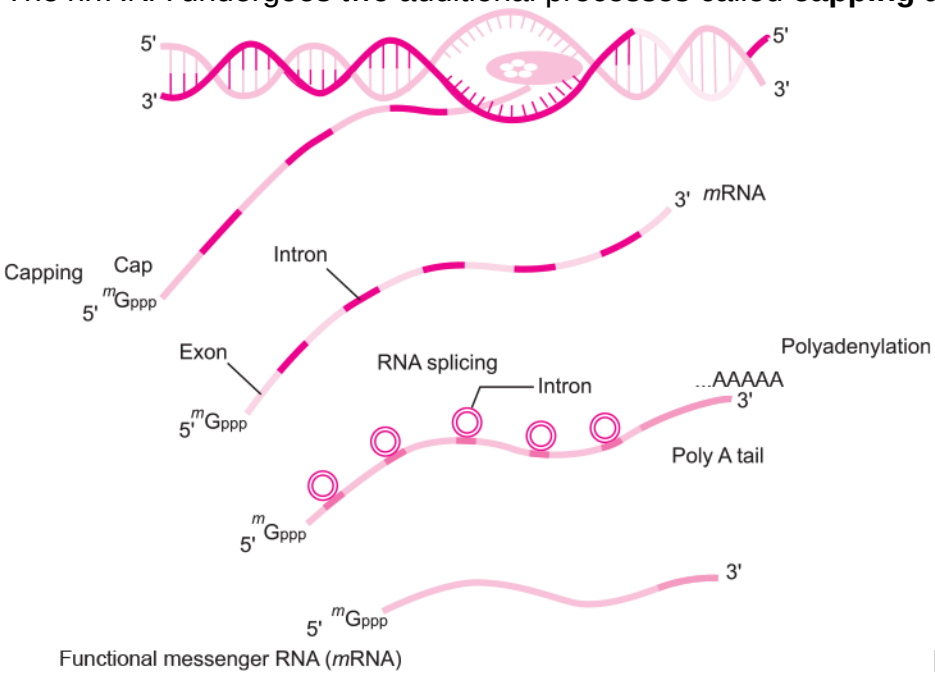
- **Elongation:** The RNA polymerase after initiation of RNA transcription loses the σ factor but continues the polymerisation of ribonucleotides to form RNA.
- **Termination:** Once the RNA polymerase reaches the termination region of DNA, the RNA polymerase is separated from DNA–RNA hybrid, as a result nascent RNA separates. This process is called termination which is facilitated by a termination factor ρ (**rho**).
- In prokaryotes, *m*RNA does not require any processing, so both transcription and translation occur in the cytosol. It can be said that transcription and translation are coupled together.

Q. Explain the processing the *hn*RNA needs to undergo before becoming functional *m*RNA in eukaryotes.

Ans. Transcription in Eukaryotes

- The structural genes are monocistronic in eukaryotes.
- The process of transcription is similar to that in prokaryotes.
- It takes place in the nucleus.
- Coding gene sequences called exons form the part of *m*RNA and non-coding sequence called introns are removed during RNA splicing.
- In eukaryotes, three types of RNA polymerases are found in the nucleus:
  i. **RNA polymerase I** transcribes *r*RNAs (28S, 18S, and 5.8S).
  ii. **RNA polymerase II** transcribes the precursor of *m*RNA (called heterogeneous nuclear RNA or *hn*RNA).
  iii. **RNA polymerase III** transcribes *t*RNA, 5S *r*RNA and *sn*RNAs (small nuclear RNAs).**Post-transcriptional modifications**

    - The primary transcripts are non-functional, containing both the coding region, exon, and region, intron, in RNA and are called heterogenous RNA or *hn*RNA.
    - The *hn*RNA undergoes two additional processes called **capping** and **tailing**.



Functional messenger RNA (*m*RNA)

Post-transcriptional modifications in eukaryotes

    - In capping, an unusual nucleotide, methyl guanosine triphosphate, is added to the 5′-end of *hn*RNA.
    - In tailing, adenylate residues (about 200–300) are added at 3′-end in a template independent manner.
    - Now the *hn*RNA undergoes a process where the introns are removed and exons are joined to form *m*RNA by the process called **splicing**.

Q.44. Answer the following questions:

Q. Explain the role of DNA dependent RNA polymerase in initiation, elongation and termination during transcription in bacterial cell.

Ans. The DNA dependent RNA polymerase helps in DNA replication by catalysing the polymerisation in only one direction, *i.e.*, 5′→3′. In bacteria, the RNA polymerase has co-factors β, β′, α, α′, ω and σ which catalyse the process.

Transcription in Prokaryotes

- In prokaryotes, the structural gene is polycistronic and continuous.
- In bacteria, the transcription of all the three types of RNA (*m*RNA, *t*RNA and *r*RNA) is catalysed by single DNA-dependent enzyme, called the **RNA polymerase**.
- In *E*. *coli* bacterium, the RNA polymerase has co-factors β, β′, α, α′ and ω along with σ (sigma) factor, to catalyse the process.
- The transcription is completed in three steps: initiation, elongation and termination.
- **Initiation:** σ (sigma) factor recognises the start signal and promotor region on DNA which then along with RNA polymerase binds to the promoter to initiate transcription.
- **Elongation:** The RNA polymerase after initiation of RNA transcription loses the σ factor but continues the polymerisation of ribonucleotides to form RNA.
- **Termination:** Once the RNA polymerase reaches the termination region of DNA, the RNA polymerase is separated from DNA–RNA hybrid, as a result nascent RNA separates. This process is called termination which is facilitated by a termination factor ρ (rho).
- In prokaryotes, mRNA does not require any processing, so both transcription and translation occur in the cytosol. It can be said that transcription and translation are coupled together.

Q. How is transcription a more complex process in eukaryotic cells? Explain.

Ans. Transcription in Eukaryotes

- The structural genes are monocistronic in eukaryotes.
- The process of transcription is similar to that in prokaryotes.
- It takes place in the nucleus.
- Coding gene sequences called exons form the part of *m*RNA and non-coding sequence called introns are removed during RNA splicing.
- In eukaryotes, three types of RNA polymerases are found in the nucleus:
  i. **RNA polymerase I** transcribes *r*RNAs (28S, 18S, and 5.8S).
  ii. **RNA polymerase II** transcribes the precursor of *m*RNA (called heterogeneous nuclear RNA or *hn*RNA).
  iii. **RNA polymerase III** transcribes *t*RNA, 5S *r*RNA and *sn*RNAs (small nuclear RNAs).

Q.45. Answer the following questions:

Q. Describe the process of synthesis of fully functional mRNA in an eukaryotic cell.

Ans. Transcription in Eukaryotes

- The structural genes are monocistronic in eukaryotes.
- The process of transcription is similar to that in prokaryotes.
- It takes place in the nucleus.
- Coding gene sequences called exons form the part of *m*RNA and non-coding sequence called introns are removed during RNA splicing.
- In eukaryotes, three types of RNA polymerases are found in the nucleus:
  i. **RNA polymerase I** transcribes *r*RNAs (28S, 18S, and 5.8S).
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  iii. **RNA polymerase III** transcribes *t*RNA, 5S *r*RNA and *sn*RNAs (small nuclear RNAs).**Post-transcriptional modifications**

    - The primary transcripts are non-functional, containing both the coding region, exon, and region, intron, in RNA and are called heterogenous RNA or *hn*RNA.
    - The *hn*RNA undergoes two additional processes called **capping** and **tailing**.

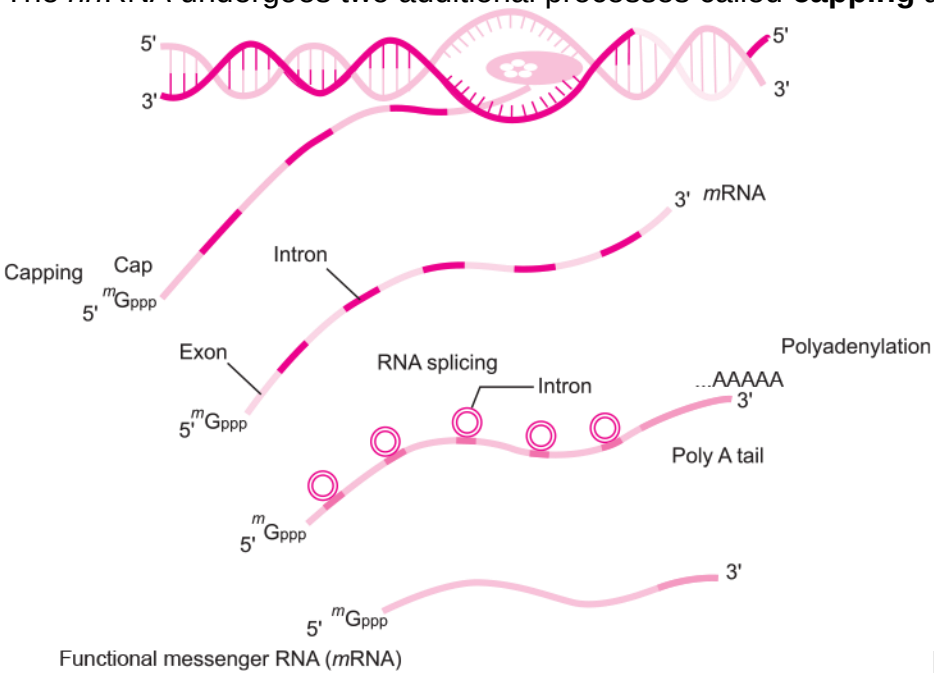


Fig. 6.12 Post-transcriptional modifications in eukaryotes

    - In capping, an unusual nucleotide, methyl guanosine triphosphate, is added to the 5′-end of *hn*RNA.
    - In tailing, adenylate residues (about 200–300) are added at 3′-end in a template independent manner.
    - Now the *hn*RNA undergoes a process where the introns are removed and exons are joined to form *m*RNA by the process called **splicing**.

Q.46. Answer the following questions based on Meselson and Stahl's experiment:

a. Why did the scientists use $^{15}NH_4Cl$ and $^{14}NH_4Cl$ as sources of nitrogen in the culture medium for growing E. coli?
b. Name the molecule(s) that ^{15}N got incorporated into.

c. How did they distinguish between ^{15}N labelled molecules from ^{14}N ones?
d. Mention the significance of taking the E. coli samples at definite time intervals for observations.
e. Write the observations made by them from the samples taken at the end of 20 minutes and 40 minutes respectively.
f. Write the conclusion drawn by them at the end of their experiment.

Ans.

a. ^{15}N is the heavy isotope of nitrogen and it can be separated from ^{14}N based on the difference in their densities.
b. ^{15}N was incorporated into newly synthesised DNA.
c. The two molecules were distinguished by cesium chloride centrifugation in which these two separated into two different bands at different positions based on their densities.
d. *E*. *coli* culture is taken at equal intervals to know the progress of the experiment as generation time of *E. coli* is 20 minutes.
e. After 20 minutes the culture had an intermediate density showing a band in the middle tube and after 40 minutes, the culture had equal amounts of hybrid DNA and the light DNA showing two bands, one in the centre and one at the bottom.
f. They concluded that DNA replicates semi-conservatively.

Q.47. Answer the following questions based on Hershey and Chases's 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.

Ans.

a. They worked with bacteriophage because when it attacks a bacteria it only inserts its genetic material in its body.
b. They grew some viruses on a medium that contained radioactive phosphorus and some others on medium that contained radioactive sulphur. 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 to agitate the bacteria to remove the viral coats from them. Centrifuge was used to separate virus particle from the bacteria.
d. Bacteria which was infected with viruses that had radioactive DNA were radioactive, indicating that DNA was the material that passed from the virus to the bacteria. Bacteria that were infected with viruses that had radioactive proteins

were not radioactive. This indicates that proteins did not enter the bacteria from the viruses. DNA is therefore the genetic material that is passed from virus to bacteria.

Q.48. 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

i. Identify and name the regulatory gene in this operon. Explain its role in 'switching off' the operon.
ii. Why is lac operon's regulation referred to as negative regulation?
iii. Name the inducer molecule and the products of the genes 'z' and 'y' of the operon. Write the functions of these gene products.

Ans.

i. *i* gene is the regulatory gene and codes of repressor which acts as inhibitor as inhibits the transcription of structural genes.
The repressor of the operon is synthesised from the i gene. The repressor protein in the absence of an inducer (lactose or allolactose) binds to the operator region of the operon and prevents RNA polymerase from transcribing the structural genes. Thus 'switching off' the operon.
ii. Regulation by lac operon is referred to as negative regulation because the repressor binds to the operator for 'switching off' the operon.
iii. Lactose or allolactose acts as an inducer. Gene *z* codes for β-galactosidase (gal) enzyme which breaks lactose into galactose and glucose. Gene *y* codes for permease, which increases the permeability of the cell to lactose.

Long Answer Questions (OIQ)

[5 Marks]

Q.1. What background information did Watson and Crick had available with them for developing a model of DNA? What was their own contribution?

Ans. Watson and Crick had the following informations which helped them to develop a model of DNA:

i. Chargaff 's Law suggesting A=T and C G.
ii. Wilkins and Franklin's X-ray diffraction studies on DNA's physical structure.

Based on these information, Watson and crick proposed

i. complementary base-pairing of nitrogenous bases
ii. semi-conservative mode of replication
iii. occurrence of mutation through tautomerism.

Q.2. DNA separated from one cell, when introduced in another cell, is able to bestow some of the properties of the former to the latter. What is this change called in technical terms? Describe the experiment evidences which led to the discovery of the above phenomenon.

Ans. The change is called transformation.

Transforming Principle

- **Frederick Griffith** (1928) conducted experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
- He observed two strains of this bacterium—one forming smooth shiny colonies (S-type) with capsule, while other forming rough colonies (R-type) without capsule.
- When live S-type cells were injected into mice, they died due to pneumonia.
- When live R-type cells were injected into mice, they survived.
- When heat-killed S-type cells were injected into mice, they survived and there were no symptoms of pnuemonia.
- When heat-killed S-type cells were mixed with live R-type cells and injected into mice, they died due to unexpected symptoms of pneumonia and live S-type cells were obtained from mice.
- He concluded that heat-killed S-type bacteria caused a transformation of the R-type bacteria into S-type bacteria but he was not able to understand the cause of this bacterial transformation.

Q.3. What are the characteristics of DNA?

Ans. Following are some features of DNA:

i. DNA is made up of two polynucleotide chains, where the backbone is made up of sugar and phosphate groups and the nitrogenous bases project towards the centre.
ii. There is complementary base pairing between the two strands of DNA.
iii. The two strands are coiled in right-handed fashion and are anti-parallel in orientation. One chain has a 5′→3′ polarity while the other has 3′→5′ polarity.
iv. The diameter of the strand is always constant due to pairing of purine and pyrimidine, *i.e.*, adenine is complementary to thymine while guanine is complementary to cytosine.
v. The distance between two base pairs in a helix is 0.34 nm and a complete turn contains approximately ten base pairs. The pitch of the helix is 3.4 nm and the two strands are righthanded coiled.

Q.4. Describe in detail the steps involved in the replication of DNA.

Ans. Process of DNA Replication

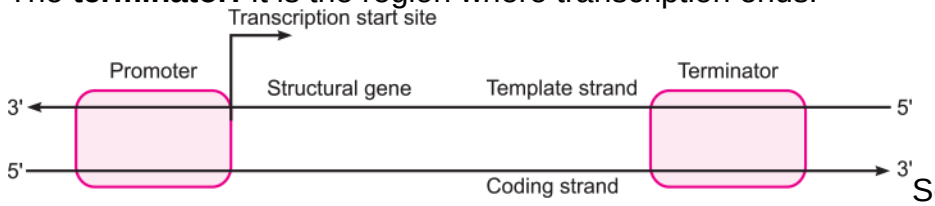
- DNA replication begins at a unique and fixed point called **origin of replication** or **'ori'**.**Initiation**

- The complementary strands of DNA double helix are separated by two enzymes, DNA gyrase and DNA helicase. This is called **unwinding** of double-stranded DNA.
- The separated strands tend to rewind, therefore these are stabilised by proteins called **single strand binding proteins (ssBPs),** which bind to the separated strands.
- Unwinding of double-stranded DNA forms a Y-shaped configuration in the DNA duplex, which is called **replication fork**.**Elongation**
- An enzyme called **primase** initiates replication of the strand oriented in the 3′ (towards origin)→5′ (towards fork) direction. This generates 10–60 nucleotides long primer RNA (replicated in 5′→3′ direction).
- The free 3′–OH of this RNA primer provides the initiation point for DNA polymerase for sequential addition of deoxyribonucleotides.
- DNA polymerase progressively adds deoxyribonucleotides to the free 3′-end of the growing polynucleotide chain so that replication of the 3′→5′ strand of the DNA molecule is continuous (growth of the new strand in 5′→3′ direction).
- The replication of 3′→5′ strand is continuous and it is called **leading strand,** while the replication of second strand (5′→3′ strand) of the DNA molecules is discontinuous and it is known as the **lagging strand**.
- The replication of lagging strand generates small polynucleotide fragments called **'Okazaki fragments'** (after R. Okazaki, who first identified them).
- These Okazaki fragments are then joined together by enzyme called DNA **ligase**.

Q.5. Draw a labelled schematic structure of a transcription unit. Explain the function of each component in the unit in the process of transcription.

Ans. Transcription unit

- The transcription unit of DNA contains three regions in the DNA:
  i. The **promoter:** It is the binding site for RNA polymerase for initiation of transcription.
  ii. The **structural gene:** It codes for enzyme or protein for structural functions.
  iii. The **terminator:** It is the region where transcription ends.



Schematic structure of a transcription unit

Q.6.

i. **Describe the role of RNA polymerases in transcription in bacteria and in eukaryotes.**
ii. **Name the scientist who postulated the role of an 'adaptor' in protein synthesis. Name the adaptor molecule.**

Ans.

i. Role of polymerase in transcription in bacteria
   a. **Initiation:** σ (sigma) factor recognises the start signal and promotor region on DNA and the σ (sigma) with RNA polymerase binds to the promoter and initiates transcription.
   b. **Elongation:** The RNA polymerase after initiation of RNA transcription loses the σ-factor but continues the process of RNA formation.
   c. **Termination:** Once the RNA polymerase reaches the termination region of DNA, the RNA polymerase is separated from DNA-RNA hybrid, as a result nascent RNA separates. This process is called termination which is facilitated by certain termination factor .

   Role of polymerase in transcription in eukaryotes

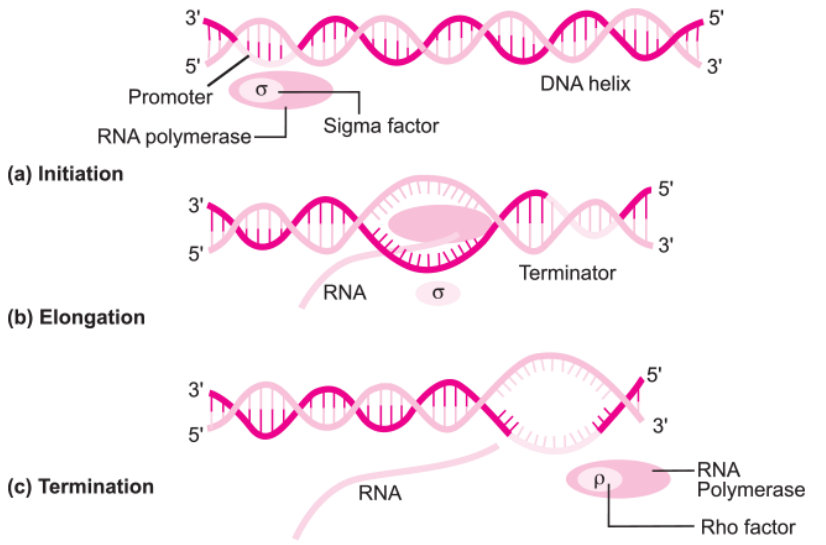
   a. In eukaryotes, apart from the RNA polymerase found in the organelles, three types of RNA polymerases are found in the nucleus.
   b. RNA polymerase II transcribes the precursor of mRNA (called as heterogeneous nuclear RNA (hnRNA).
   c. RNA polymerase III helps in transcription of tRNA, 5S rRNA, and snRNAs (small nuclear RNAs).

ii. Francis Crick postulated the role of an adaptor. tRNA or transfer RNA is the adaptor molecule.

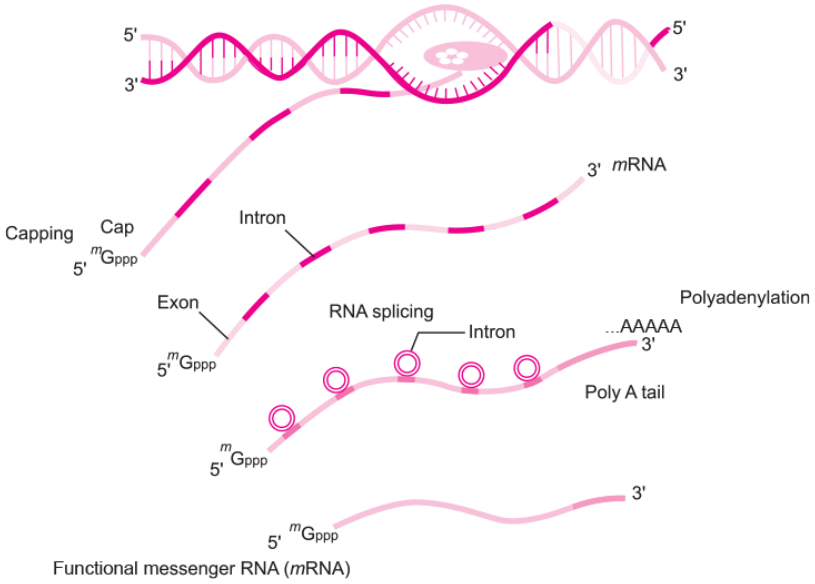
Q.7. Transcription in eukaryotes is more complex process than in prokaryotes. Justify and compare the initiation, elongation and termination in bacterial cells with eukaryotes.

Ans. Transcription is more complex in eukaryotes due to following reasons:

- In prokaryotes only one type of RNA polymerase is involved whereas in eukaryotes three types of RNA polymerases are involved.
- For Description of processing of *hn*RNA involving-introns/exons/splicing in eukaryotes and for Description of capping and tailing, Refer to Basic Concepts Point 17.



Process of transcription in bacteria



Post-transcriptional modifications in eukaryotes

Q.8.

i. **What are the three types of RNA?**
ii. **Which one of these has the shape of a clover-leaf in two dimensional structure?**
iii. **How is each RNA related in the information flow during protein synthesis? Explain.**

Ans.

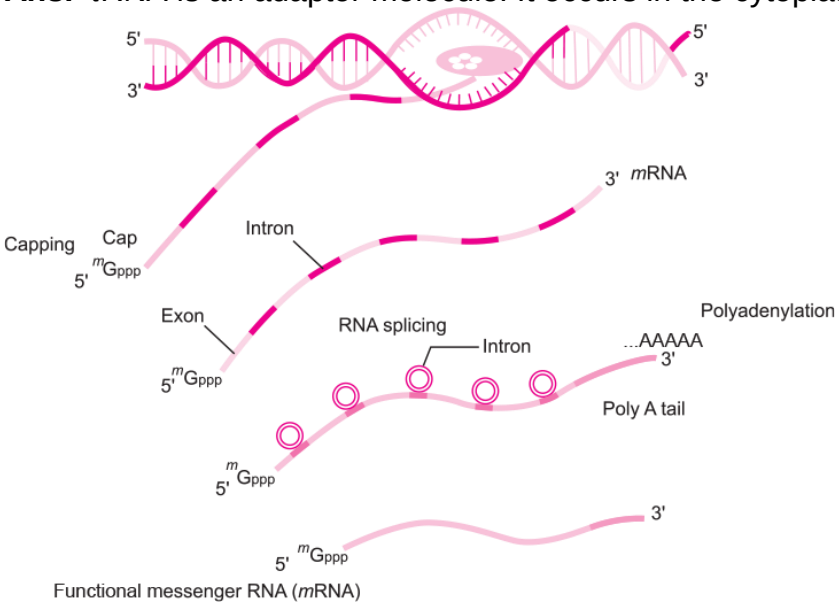
i. The three types of RNA are:
   a. Messenger RNA (*m*RNA)
   b. Transfer RNA (*t*RNA)
   c. Ribosomal RNA (*r*RNA).

ii. *t*RNA.

iii. The genetic information in DNA is transcribed into messenger RNA (*m*RNA). It stores the genetic information from DNA and decides the sequence of amino acid in a polypeptide.
Transfer RNA (*t*RNA) acts as an adaptor molecule that at one end reads the code on *m*RNA and accordingly bind to amino acid on the other end. It recognises the codon on *m*RNA by its anticodon and leaves amino acid at the site of protein synthesis.
Ribosomal RNA (*r*RNA) constitutes the ribosomal structure and helps to form peptide bond.

Q.9. What is *t*RNA? Where does it occur in a cell? Show by diagram the structure of *t*RNA. Write a note on the activation of amino acids and the involvement of *t*RNA in it?

Ans. *t*RNA is an adaptor molecule. It occurs in the cytoplasm.



Functional messenger RNA (*m*RNA)

Post-transcriptional modifications in eukaryotes
For activation of amino acids, \

Initiation

- In prokaryotes, initiation requires the large and small ribosome subunits, the *m*RNA, initiation *t*RNA and three initiation factors (IFs).
- **Activation of amino acid:** Amino acids become activated by binding with aminoacyl *t*RNA synthetase enzyme in the presence of ATP.

- **Transfer of amino acid to *t*RNA:** The AA–AMP–Enzyme complex formed reacts with specific *t*RNA to form aminoacyl-*t*RNA complex. AA–AMP–Enzyme complex + *t*RNA → AA–*t*RNA + AMP + Enzyme.
- The cap region of mRNA binds to the smaller subunit of ribosome.
- The ribosome has two sites, A-site and P-site.
- The smaller subunit first binds to the initiator *m*RNA and then binds to the larger subunit so that initiation codon (AUG) lies on the P-site.
- The initiation *t*RNA, *i.e.*, methionyl *t*RNA then binds to the P-site.

Q.10. Explain the steps involved in a polypeptide synthesis. How are the amino acids activated during polypeptide synthesis?

Ans.

i. **Initiation**

- In prokaryotes, initiation requires the large and small ribosome subunits, the *m*RNA, initiation *t*RNA and three initiation factors (IFs).
- **Activation of amino acid:** Amino acids become activated by binding with aminoacyl *t*RNA synthetase enzyme in the presence of ATP.
- Aminoacid(AA)+ATP−→−−−synthetasesAminoacyltRNAAA–AMP–Enzymecomplex+Pi
- **Transfer of amino acid to *t*RNA:** The AA–AMP–Enzyme complex formed reacts with specific *t*RNA to form aminoacyl-*t*RNA complex. AA–AMP–Enzyme complex + *t*RNA → AA–*t*RNA + AMP + Enzyme.
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- The smaller subunit first binds to the initiator *m*RNA and then binds to the larger subunit so that initiation codon (AUG) lies on the P-site.
- The initiation *t*RNA, *i.e.*, methionyl *t*RNA then binds to the P-site.

ii. **Elongation of polypeptide chain**

- Another charged aminoacyl tRNA complex binds to the A-site of the ribosome at the second codon.
- A peptide bond is formed between carboxyl group (—COOH) of amino acid at P-site and amino group (—NH) of amino acid at A-site by the enzyme **peptidyl transferase**.
- The ribosome slides over *m*RNA from codon to codon in the 5′→3′ direction.
- According to the sequence of codons, amino acids are attached to one another by peptide bonds and a polypeptide chain is formed.

Q.11. Explain the process of protein synthesis from processed *m*RNA.

Ans. Translation

- Translation is the process of synthesis of protein from *m*RNA with the help of ribosome.

- A translational unit in *m*RNA from 5' → 3' comprises of a start codon, region coding for a polypeptide, a stop codon and untranslated regions (UTRs) at both 5'-end and 3'-end for efficient process.
- There are three stages of protein synthesis:
  i. **Initiation**
    - Assembly of ribosome on *m*RNA.
    - Activation of amino acids and its delivery to *t*RNA
  ii. **Elongation**
    - Repeated cycle of amino acid delivery.
    - Peptide bond formation and movement along the *m*RNA called **translocation**.
  iii. **Termination**
    - The release of a polypeptide chain.

i. **Initiation**
- In prokaryotes, initiation requires the large and small ribosome subunits, the *m*RNA, initiation *t*RNA and three initiation factors (IFs).
- **Activation of amino acid:** Amino acids become activated by binding with aminoacyl *t*RNA synthetase enzyme in the presence of ATP.
- **Transfer of amino acid to *t*RNA:** The AA–AMP–Enzyme complex formed reacts with specific *t*RNA to form aminoacyl-*t*RNA complex. AA–AMP–Enzyme complex + *t*RNA → AA–*t*RNA + AMP + Enzyme.
- The cap region of mRNA binds to the smaller subunit of ribosome.
- The ribosome has two sites, A-site and P-site.
- The smaller subunit first binds to the initiator *m*RNA and then binds to the larger subunit so that initiation codon (AUG) lies on the P-site.
- The initiation *t*RNA, *i.e.*, methionyl *t*RNA then binds to the P-site.

ii. **Elongation of polypeptide chain**
- Another charged aminoacyl tRNA complex binds to the A-site of the ribosome at the second codon.
- A peptide bond is formed between carboxyl group (—COOH) of amino acid at P-site and amino group (—NH) of amino acid at A-site by the enzyme **peptidyl transferase**.
- The ribosome slides over *m*RNA from codon to codon in the 5′→3′ direction.
- According to the sequence of codons, amino acids are attached to one another by peptide bonds and a polypeptide chain is formed.

iii. **Termination of polypeptide**
- When the A-site of ribosome reaches a termination codon which does not code for any amino acid, no charged tRNA binds to the A-site.
- Dissociation of polypeptide from ribosome takes place, which is catalysed by a **'release factor'**.
- There are three **termination codons** namely UGA, UAG and UAA.

Q.12. Where do transcription and translation occur inside a living cell? Briefly describe the three steps involved in the process of translation?

Ans.

	Prokaryotes	Eukaryotes
Transcription	Occurs in cytosol	Occurs in nucleus
Translation	Occurs in cytosol	Occurs in cytoplasm

Translation

- Translation is the process of synthesis of protein from *m*RNA with the help of ribosome.
- A translational unit in *m*RNA from 5' → 3' comprises of a start codon, region coding for a polypeptide, a stop codon and untranslated regions (UTRs) at both 5'-end and 3'-end for efficient process.
- There are three stages of protein synthesis:
  i. **Initiation**
    - Assembly of ribosome on *m*RNA.
    - Activation of amino acids and its delivery to *t*RNA
  ii. **Elongation**
    - Repeated cycle of amino acid delivery.
    - Peptide bond formation and movement along the *m*RNA called **translocation**.
  iii. **Termination**
    - The release of a polypeptide chain.

Q.13. What does the *lac* operon consist of ? How is the operator switch on and off in the expression of gene in this operon? Explain.

Ans. The *lac* operon consists of structural genes, promoter, operator, repressor, and inducer.

When Lactose is Absent

i. When lactose is absent, *i* gene regulates and produces repressor *m*RNA which translate repression.
ii. The repressor protein binds to the operator region of the operon and as a result prevents RNA polymerase to bind to the operon.
iii. The operon is switched off.

When Lactose is Present

i. Lactose acts as an inducer which binds to the repressor and forms an inactive repressor.
ii. The repressor fails to bind to the operator region.
iii. The RNA polymerase binds to the operator and transcribes *lac m*RNA.
iv. *lac m*RNA is polycistronic, *i.e.*, produces all three enzymes, β-galactosidase, permease and transacetylase.
v. The *lac* operon is switched on.

Q.14. You are repeating the Hershey–Chase experiment and are provided with two isotopes: ^{32}P and ^{15}N (in place of ^{35}S in the original experiment). How do you expect your results to be different?

Ans. Use of ^{15}N will be inappropriate because method of detection of ^{35}P and ^{15}N is different (^{32}P being a radioactive isotope while ^{15}N is not radioactive but is the heavier isotope of nitrogen). Even if ^{15}N was radioactive then its presence would have been detected both inside the cell (^{l5}N incorporated as nitrogenous base in DNA) as well as in the supernatant because ^{15}N would also get incorporated in amino group of amino acids in proteins). Hence, the use of ^{15}N would not give any conclusive results.

Q.15. There is only one possible sequence of amino acids when deduced from a given nucleotide. But multiple nucleotide sequences can be deduced from a single amino acid sequence. Explain this phenomenon.

Ans. Some amino acids are coded by more than one codon (known as degeneracy of codon), hence on deducing a nucleotide sequence from an amino acid sequence, multiple nucleotide sequences will be obtained.

For example, isoleucine has three codons AUU, AUC and AUA. Hence a dipeptide Met–Ile can have any of the following nucleotide sequences:

i. AUG–AUU
ii. AUG–AUC
iii. AUG–AUA

If we deduce amino acid sequences of the above nucleotide sequences, all the three will code for Met–Ile.

Q.16. Which methodology is used while sequencing the total DNA from a cell? Explain it in detail.

Ans. Methodologies of HGP

- The methods involve two major approaches:
    i. **Expressed sequence tags (ESTs):** This method focusses on identifying all the genes that are expressed as RNA.
    ii. **Sequence annotation:** It is an approach of simply sequencing the whole set of genome that contains all the coding and non-coding sequences, and later assigning different regions in the sequence with functions.
- For sequencing, the total DNA from cell is first isolated and broken down in relatively small sizes as fragments.
- These DNA fragments are cloned in suitable host using suitable vectors. When bacteria is used as vector, they are called **bacterial artificial chromosomes** (BAC) and when yeast is used as vector, they are called **yeast artificial chromosomes** (YAC).

- Frederick Sanger developed a principle according to which the fragments of DNA are sequenced by automated DNA sequences.
- On the basis of overlapping regions on DNA fragments, these sequences are arranged accordingly.
- For alignment of these sequences, specialised computer-based programmes were developed.
- Finally, the genetic and physical maps of the genome were constructed by collecting information about certain repetitive DNA sequences and DNA polymorphism, based on endonuclease recognition sites.

Q.17. Answer the following questions:

Q. Explain what DNA replication refers to.

Ans. DNA replication refers to DNA synthesis.

Q. State the properties of DNA replication model.

Ans. DNA replication is :

i. Semi-conservative,
ii. Semi-discontinuous,
iii. Unidirectional

Q. List any three enzymes involved in the process along with their functions.

Ans. Enzymes for DNA replication

- Various enzymes are required as catalysts during DNA replication in living cells.
- **DNA-dependent DNA polymerase:** It catalyses the polymerisation of deoxynucleotides on DNA template.
- **Helicase:** It unwinds the DNA strand to form the replication fork.
- **DNA ligase:** It joins the Okazaki fragments which are formed on the lagging strand.

Q.18. Illustration below is a DNA segment, which constitutes a gene:

i. Name the shaded and unshaded regions of gene.
ii. Explain how these genes are expressed.
iii. How is this gene different from prokaryotic gene in its expression? [HOTS]

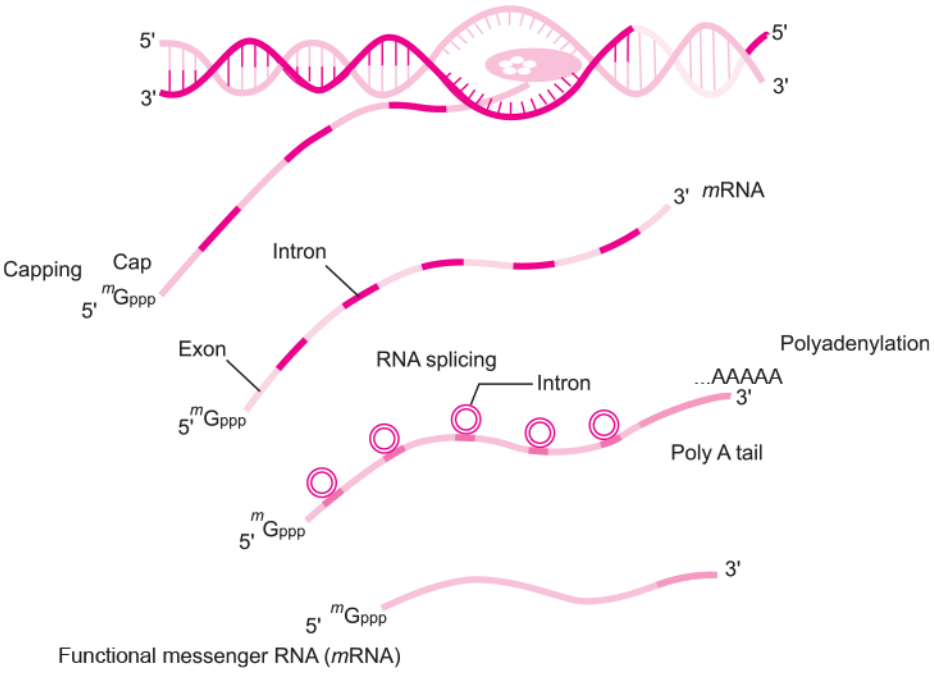
Ans.

(i) The shaded portions are introns and unshaded portions are exons.

(ii) The primary RNA contains both introns and exons. By the mechanism of splicing, introns are removed and exons are joined to form functional mRNA after capping and tailing.

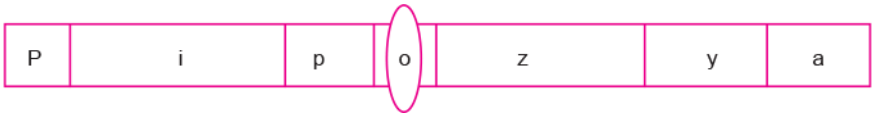
Post-transcriptional modifications

- The primary transcripts are non-functional, containing both the coding region, exon, and non-coding region, intron, in RNA and are called heterogenous RNA or hnRNA.
- The hnRNA undergoes two additional processes called capping and tailing.
- 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 by the process called splicing.



(iii) In prokaryotes, the structural gene is continuous and is not differentiated into exons and introns unlike eukaryotes. In prokaryotes, transcription is followed by translation without RNA splicing mechanism.

Q.19. Observe the representation of genes involved in the lac operon given below:



a. Identify the region where the repressor protein will attach normally.
b. Under certain conditions repressor is unable to attach at this site. Explain.
c. If repressor fails to attach to the said site what products will be formed by z, y and a?
d. Analyse why this kind of regulation is called negative regulation.

Ans.

a. The repressor protein will attach to operator region, *o*.
b. In presence of an inducer, lactose, repressor is unable to attach.
c. *z*-β galactosidase.
   y-permease
   a-Transacetylase
d. It is called negative regulation as it involves constitutive (all the time) repressor. The operon is always in off position due to presence of repressor and is switched on only in presence of an inducer. Inducer Lactose or allolactose interacts with repressor making it inactive.