5 CHAPTER

Molecular Basis of Inheritance

Level - 1 CORE SUBJECTIVE QUESTIONS

MULTIPLE CHOICE QUESTIONS (MCQs) (1 Mark)

1. Option (A) is correct

Explanation: According to Chargaff's rules, in DNA, A = T and G = C;

Thus, A + T + G + C =100

Given: T = 27% so A=T =27%

Thus A+T = 27 +27 =54%

Thus, G+C =100 – 54 = 46%

Since G = C so G = 46/2 =23%

2. Option (B) is correct

Explanation: Purines are heterocyclic- Adenine (A) and Guanine (G) are purine.

Pyrimidine are homocyclic- Cytosine (C) and Thymine (T) are pyrimidines.

Adenine form 2 hydrogen bond with thymine and guanine forms 3 hydrogen bond with cytosine.

So the correct sequence of nucleotide on first strand in 5′-3′ direction will be CGTA and on second strand TACG.

3. Option (B) is correct

Explanation: *E. coli* has 4.6×10^6 bp.

It completes replication process in 18 minutes i.e. 18×60 seconds.

Rate of polymerisation = $\frac{4.6 \times 10^6}{18 \times 60}$

= 4259.1 bp/s or approximately 4000b p/sec.

4. Option (A) is correct

Explanation: Lactose binds to the repressor and prevents it from binding to the operator. This in turn makes RNA polymerase free to bind to the promoter and transcribe the structural genes of lac operon.

5. Option (C) is correct

Explanation: The transcribed mRNA has same sequence as other strand (coding strand) except uracil at the place of thymine.

So, the transcribed mRNA can be represented by 5′ UAACGG 3′.

6. Option (C) is correct

Explanation: To determine the minimum number of bases required to form a codon for 96 different amino acids with 12 different bases, we use the formula n^k, where n is the number of bases and k is the number of bases in the codon.

We need $12^k \geq 96$:

- For $k = 1 : 12^1 = 12$ (not sufficient)
- For $k = 2 : 12^2 = 144$ (sufficient)
- For $k = 3 : 12^3 = 1728$ (excess)

Thus, the minimum number of bases required to form a codon is 2.

7. Option (C) is correct

Explanation: The schematic shows a polynucleotide chain, which consists of:

P: Phosphate group

S: Sugar (deoxyribose or ribose)

B: Nitrogenous base

The dotted line between the sugar (S) and base (B) represents the N-glycosidic linkage.

This bond connects the C_1' carbon of the sugar molecule to the nitrogen of the nitrogenous base in a nucleotide.

Hydrogen bonds occur between complementary nitrogenous bases in double-stranded DNA, not within a single polynucleotide chain.

Peptide bonds join amino acids in a polypeptide chain, not components of a nucleotide.

Phosphodiester bonds join the sugar-phosphate backbone of nucleotides in a polynucleotide chain, connecting the 3′ carbon of one sugar to the 5′ carbon of another.

8. Option (A) is correct

Explanation: The corresponding DNA sequence that would code for the polypeptide sequence (Alanine, Arginine, Lysine, Phenylalanine) is:

5′ - CGT GCT TTC AAA - 3′

9. Option (C) is correct

Explanation: In the double helical structure of a DNA molecule, the strands are described as anti-parallel and complementary. This means they run in opposite directions (one from 5′ to 3′ and the other from 3′ to 5′) and specific bases pair with each other: Adenine pairs with Thymine, and Cytosine pairs with Guanine.

10. Option (D) is correct

Explanation: In a transcription unit, the terminator is located towards the 3′ end of the coding strand. As transcription proceeds, RNA polymerase synthesises

RNA in the 5′ to 3′ direction, and upon reaching the terminator, transcription stops.

11. Option (C) is correct

Explanation: In a DNA fragment with 2000 nucleotides, where 140 are Adenine (A) and 140 are Thymine (T), the remaining bases are Cytosine (C) and Guanine (G). The total number of A and T bases is 140+140 = 280

Therefore, the number of remaining bases (C and G) is 2000−280 = 1720. Thus, the number of bases that have triple hydrogen bonds between them is 1720.

12. Option (C) is correct

Explanation: After six generations of *E. coli* grown in ^{15}N following initial growth in ^{14}N the CsCl density gradient centrifugation will show predominantly heavy DNA with a ratio of hybrid to heavy DNA being 1:31.

13. Option (A) is correct

Explanation: AUG serves as both the start codon (indicating the beginning of protein synthesis) and codes for the amino acid methionine. Hence, it has dual function.

14. Option (A) is correct

Explanation: In the 'lac' operon, the z gene codes for beta-galactosidase, which is primarily responsible for the hydrolysis of lactose. This enzyme catalyses the breakdown of lactose into its monosaccharide components, glucose and galactose, allowing the organism to utilise lactose as an energy source.

15. Option (C) is correct

Explanation: In the transcription process of prokaryotes:

- X is the promoter region where RNA polymerase binds to initiate transcription.
- Y is sigma factor, a protein that helps RNA polymerase recognise and bind to the promoter.
- Z is RNA polymerase. The enzyme that synthesises RNA from the DNA template.

16. Option (C) is correct

Explanation: In the given case, since child X shares key DNA segments with individuals 1 and 3, they are identified as the likely parents.

17. Option (C) is correct

Explanation: Meselson and Stahl's experiment to prove that DNA replication is semi-conservative involved several steps. They first grew bacteria in a ^{15}N medium for many generations, ensuring all DNA was labeled with the heavy isotope (step iii and iv). Next, they transferred the bacteria to a ^{14}N medium and sampled them every 20 minutes (step i). After one round of replication, they found that the bacteria contained hybrid DNA with one ^{15}N strand and one ^{14}N strand (step ii). Following two rounds of replication, some bacteria had all ^{14}N DNA, while others still had hybrid DNA (step v).

18. Option (D) is correct

Explanation: Lac operon was first gene which was isolated from *E. coli* in 1969.

ASSERTION-REASON QUESTIONS (1 Mark)

1. Option (C) is correct

Explanation: Deoxyribonucleoside triphosphates (dNTPs) do provide energy for DNA synthesis, but they do not serve as proofreaders. Proofreading is done by DNA polymerases.

2. Option (A) is correct

Explanation: RNA is generally unstable, making it more prone to degradation and mutations. The 2′-OH group in the ribose sugar of RNA nucleotides increases the molecule's susceptibility to hydrolysis, contributing to its instability compared to DNA, which has a deoxyribose sugar lacking this hydroxyl group.

3. Option (A) is correct

Explanation: Primary transcripts (pre-mRNA) contain both exons and introns. So, in eukaryotes, primary RNA transcripts undergo splicing, a process that removes introns (non-coding regions) to produce mature mRNA that only contains exons (coding regions).

4. Option (B) is correct

Explanation: The coding strand which has the polarity 5′ → 3′ does not directly code for proteins because it is not transcribed. Instead, the template strand (3′ → 5′) is transcribed into mRNA. The reason correctly states that reference points for transcription are made with respect to the code strand but this does not explain why the coding strand does not code for proteins.

5. Option (A) is correct

Explanation: In an operon, regulator and operator genes are not associated with constitutive genes. This is because constitutive genes are constantly expressed and do not rely on the regulatory mechanisms that involve the regulator and operator genes.

6. Option (A) is correct

Explanation: DNA is a very long polymer, which makes it necessary to fragment it for sequencing purposes.

VERY SHORT ANSWER TYPE QUESTIONS (2 Marks)

1. (i) I is point mutation; II is Frame shift

(ii) II as more codons are affected;

It is extremely likely to lead to large-scale changes to polypeptide length and chemical composition/ resulting in a non-functional protein that often disrupts the biochemical processes of a cell/Incorrect amino acids are inserted/ often premature termination occurs when a nonsense codon is read/ Frameshifts have very severe phenotypic effects. (any one)

2. (i) Translational unit in mRNA is the sequence of RNA that is flanked by the start codon (AUG) and the stop codon (UAA) and codes for a polypeptide/ AUG AUC UCG UAA.

(ii) Untranslated regions (UTR) are present at both 5′ -end (before start codon) and at 3′ -end (after stop codon). They are required for an efficient translation process.

3. (i) 8 amino acids.

Genetic code is read in triplets and there is no change in the number of triplets, i.e., no change in reading frame.

(ii) 3 amino acids , the 4th codon now reads as UGA – a stop codon.

4. The salient features of genetic code are:

(i) The codon is triplet.

(ii) 61 codons code for amino acids and 3 codons don't code for any amino acids hence they function as stop codons.

(iii) Some amino acids are coded by more than one codon, i.e., the genetic code is degenerate.

(iv) The codon is read in mRNA in a contiguous fashion, i.e., there are no punctuations.

(v) The code is nearly universal.

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

(vii) UAA, UAG, UGA are stop or terminator codons.

(Any Two)

5. (i) A- Replication

B- Transcription

C- Translation

(ii) Central dogma states the flow of genetic information in a cell. (DNA → RNA → Protein)

Viruses in which flows of information is in reverse direction that is from RNA to DNA, it is not applicable.

6. (i) 3 types

RNA polymerase –II transcribes hn RNA:

(ii) Splicing /Introns are removed and exons are joined in a definite order, undergoes capping /at 5′ end where unusual nucleotide (methyl guanosine triphosphate) is added, tailing/ at 3′ end where (200-300) adenylate residues are added.

7. A set of positively charged proteins called histones, due to presence of lysine and arginine (basic amino acids), holds the negatively charged DNA around it in a coiled manner. Histones are organised to form a unit of eight molecules (histone octamer). A typical nucleosome contains 200 bp of DNA helix. Nucleosomes constitute repeating units of a structure in nucleus called chromatin thread (like bodies as "beads on string" structure in a nucleus).

8. A molecule that can act as a genetic material must fulfil the following criteria:

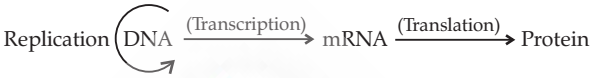
(i) It should be able to generate its replica (Replication).

(ii) It should be stable chemically and structurally.

(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'.

9.



10. (i) The human genome contains 3164.7 million nucleotide bases.

(ii) The average gene consists to 3000 bases, but sizes vary greatly, with the largest known human gene being dystrophin at 2.4 million bases.

(iii) The total number of genes is estimated at 30,000 – much lower than previous estimates of 80,000 to 1,40,000 genes. Almost all (99.9 percent) nucleotide bases are exactly the same in all people.

(iv) The functions are unknown for over 50 per cent of the discovered genes.

(v) Less than 2 per cent of the genome codes for proteins.

(vi) Repeated sequences make up very large portion of the human genome.

(vii) Repetitive sequences are stretches of DNA sequences that are repeated many times, sometimes hundred to thousand times. They are thought to have no direct coding functions, but they shed light on chromosome structure, dynamics and evolution.

(viii) Chromosome 1 has most genes (2968), and the Y has the fewest (231).

(ix) Scientists have identified about 1.4 million locations where single base DNA differences (SNPs single nucleotide polymorphism, pronounced as 'snips') occur in humans. This information promises to revolutionise the processes of finding chromosomal locations for disease associated sequences and tracing human history.

(Any four)

SHORT ANSWER TYPE QUESTIONS (3 Marks)

1. (A) During replication, Adenine pairs with thymine in DNA; during transcription, adenine pairs with uracil in RNA.

(B) In retrovirus the nucleic acid is RNA and it is used to synthesise DNA; the process is called reverse transcription.

(C) It is a highly energy-rich process/ or as per the need only the gene coding for a specific protein is transcribed.

2. (i) Satellite DNA / Repetitive DNA/ VNTR

The characteristics are:

(1) Do not code for any protein.

(2) It form a large portion of human genome.

(3) It show high degree of polymorphism.

(Any two)

(ii) (1) It is useful in forensic applications.

(2) It helps in determining population and genetic diversities.

(3) It forms the basis of paternity testing.
(4) It is used to study evolution.
(5) It is used to trace path of hereditary diseases.
(Any two)

3. (i) 'Beads on String' / Nucleosomes in Chromatin.
It was viewed under Electron microscope

(ii) Dark spots are – Nucleosomes.
8 molecules of positively charged histone proteins are organised to form histone octamer, and negatively charged DNA is wrapped around it to form nucleosome.
To accommodate very long DNA helix in nucleus, such an organised structure is formed.

4. DNA fingerprinting is the basis of paternity testing, high degree of polymorphism in DNA, the polymorphisms are inheritable.
Isolation of DNA and amplification by PCR, bigestion of DNA, separation of DNA fragments by electrophoresis, blotting and hybridisation, detection of hybridised fragments by autoradiography, matching the DNA bands of father and child.

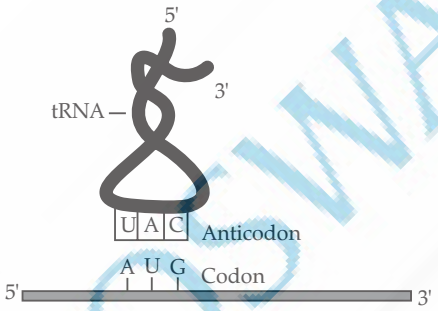
5. (i) Amino acids are activated in the presence of ATP, and linked to their cognate tRNA – a process called charging of tRNA or aminoacylation of tRNA.

(ii) At the end of translation a release factor binds to the stop codon terminating translation. When ribosome moves to the stop codon (UAA/UAG/UGA) release factor binds to the stop codon terminating translation.

(iii) Untranslated regions (UTR). UTRs are present at both 5′ – end (before start codon/ AUG) and at 3′ end (after stop codon) of mRNA.

6. (i) RNA polymerase – III / RNA polymerase

(ii)



(iii) It recognises the start codon (AUG) and bind to mRNA.

7. (i) (1) Identify all the approximately 20,000 – 25,000 genes in human DNA.
(2) Determine the sequences of the 3 billion chemical base pairs that make up human DNA.
(3) Store this information in databases.
(4) Improve tools for data analysis.
(5) Transfer related technologies to other sectors, such as industries.
(6) Address the ethical / legal / social issues (ELSI) that may arise from the project. **(Any four)**

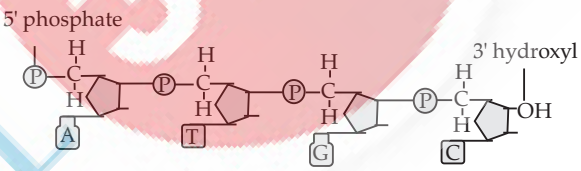
(ii) *Caenorhabditis elegans* / *Drosophila*.

8. (i)

'R' Strain	'S' Strain
Non-Virulent	Virulent
No polysaccharide	Have polysaccharide coat.

(ii) S strain → Inject into mice → Mice die
R strain → Inject into mice → Mice live
S stain (heat killed) → Inject into mice → Mice live
S stain (heat killed) + R stain → Inject into mice → Mice die
Conclusion: He concluded that the R strain bacteria had somehow been transformed by the heat-killed S strain bacteria. Some 'transforming principle' transferred from heat killed S strain and transform R strain into S strain.

9.



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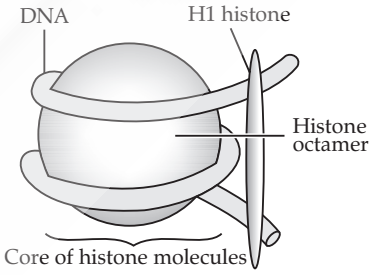


There are about 200 base pairs of DNA in a normal nucleosome. The nucleosomes in chromatin are seen as 'beads-on-string'. Histone proteins are abundant in lysine and arginine residues, which are basic amino acid residues with a positive charge in their side chains.

LONG ANSWER TYPE QUESTIONS (5 Marks)

1.
- Isolation of DNA.
- Digestion of DNA by restriction endonucleases.
- Separation of DNA fragments by electrophoresis.
- Transferring (blotting) of separated DNA fragments to synthetic membranes, such as nitrocellulose or nylon.
- Hybridisation using labelled VNTR probe, and
- Detection of hybridised DNA fragments by autoradiography.

2. Frederick Griffith
He took two strains of *Streptococcus pneumoniae* bacteria and inject them into mice
- R strain – Rough and non–virulent

- S strain – Smooth and virulent (with mucous coat)

S strain → Inject into mice → Mice die

R strain → Inject into mice → Mice live

S strain → Inject into mice → Mice live

(heat - killed)

S strain

(heat - killed)

\+ → Inject into mice → Mice die

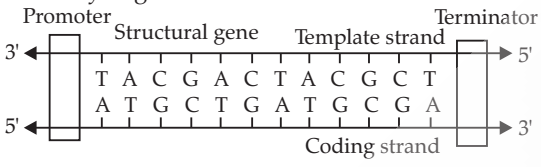
R strain

(live)

Conclusion:

- R–strain bacteria had been transformed by heat killed S – strain.
- 'Transforming principle' transferred from heat killed S-Strain and enabled R–strain to synthesise a smooth polysaccharide coat. This must be due to the transfer of the genetic material.
- Heat which killed bacteria did not destroy some of the properties of genetic material which shows stability of genetic material.

3. (i)

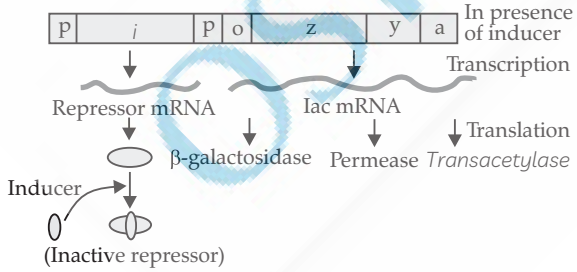


(ii) By switching the position of promoter and terminator the coding strand becomes template strand.

(iii)

- If both strands acts as template, they would code for RNA molecule with complementary sequences hence would form a dsRNA and prevent translation.
- If both strands act as template, they would code for RNA molecules with different sequences and if they code for proteins, they will make different proteins. Hence one segment of DNA would be coding for two different proteins and complicate genetic information transfer machinery.
- Single stranded RNA molecule is required for the process of translation. **(Any Two)**

4. (i)



(ii) The regulation of lac operon is referred to as negative regulation because repressor binds to operator to inhibit the gene expression.

5. Griffith selected 'S' strain and 'R' strain bacteria *Streptococcus pneumoniae*,

'S' strain – Virulent causes pneumonia,

'R' strain – Non-virulent does not cause pneumonia

'S' strain $\xrightarrow{\text{Inject into mice}}$ mice die

'R' strain $\xrightarrow{\text{Inject into mice}}$ mice live

'S' strain (heat - killed) $\xrightarrow{\text{Inject into mice}}$ → mice live

Heat killed 'S' strain + 'R' strain (live) $\xrightarrow{\text{Inject into mice}}$ mice die.

Griffith concluded that the 'R' strain bacteria had somehow been transformed by the heat killed 'S' strain bacteria.

They purified biochemicals (Proteins, DNA, RNA etc.) from the heat killed 'S' cells and the fractions were added individually to the culture of the live 'R' cells.

DNA was able to cause transformation of 'R' cells into 'S' cells. They found that protein digesting enzyme or RNA digesting enzymes did not affect transformation or digestion with DNase did inhibit transformation indicating that the transforming substance is not a protein or RNA.

This suggests that the DNA is the "genetic material".

6. (i)

- Since Sulphur is component of protein so they used radioactive Sulphur to label protein coat of the virus.
- Since Phosphorus is the component of the DNA so they used radioactive Phosphorus to label DNA.

(ii) **(1)** To remove viral coats from bacteria or *E. coli* by agitating.

(2) The viral particles were separated from bacteria or *E. coli* by spinning in a centrifuge.

(iii)

- No radioactive S^{35} detected in the cells but detected in the supernatant in case of radioactive S^{35} labelled protein capsule of bacteriophage.
- Radioactive P^{32} detected in cells but not in the supernatant in case of viruses having radioactive P^{32} labelled DNA.

(iv) DNA is the genetic material.

7. (i) **Initiation:** DNA dependent RNA polymerase attaches at 3'-end of the DNA template using sigma factor.

Elongation: By using nucleotide triphosphates as substrate polymerisation in template dependent fashion occurs by following rule of complementarity.

Termination: On reaching terminator region, polymerase binds with rho factor leads to separation of nascent RNA and polymerase.

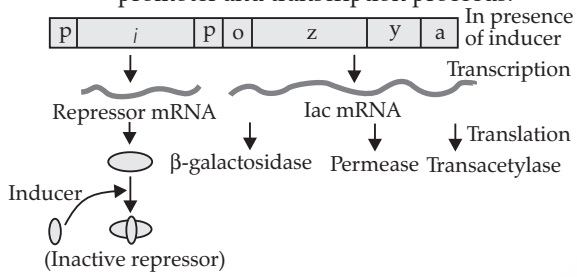
(ii) **(1)** one in prokaryotes.

(2) Three in eukaryotes.

8. (i) Switching 'on' of the lac operon

- The lac operon consists of one regulatory gene and three structural genes (z, y and a)
- The *i* gene codes for the repressor of the lac operon.
- The z gene codes for beta – galactosidase (β – gal). Beta galactosidase is responsible for hydrolysis of (disaccharide) lactose into galactose and glucose.

- y gene codes for permease which increases the permeability of the cell to β-galactosides/ lactose.
- The repressor protein binds to the operator region and prevents RNA polymerase from transcribing the operon.
- Lactose is the inducer and regulates switching on and off of the operon.
- In the presence of inducer, lactose or allolactose, the repressor is inactivated by interaction with the inducer.
- This allows RNA polymerase to access the promoter and transcription proceeds.



(ii) Repressor binds to the operator to inhibit gene expression therefore, it is referred to be negatively regulated.

9. The two strands of DNA are complementary to each other and highly stable. The presence of thymine at the place of uracil makes DNA more stable. 2′OH group present at every nucleotide in RNA is a reactive group and makes RNA labile and easily degradable. RNA mutates at faster rate than DNA. DNA being more stable is preferred for storage of genetic information.

10. (i) Lactose acts as an inducer molecule. In its absence repressor protein binds to the operator region. RNA polymerase is prevented from transcribing the operon.

(ii) (1) By preventing formation of primary transcript.

(2) By preventing splicing.

(3) By preventing transport of mRNA from nucleus to the cytoplasm

(4) By preventing formation of protein from mRNA. **(Any Two)**

11. (i) Normal nitrogen/ ^{14}N, heavy nitrogen/ ^{15}N to produce two types of DNA / light and heavy DNA respectively.

(ii) *E. coli* has generation time of 20 minutes so the samples were taken at intervals of 20 minutes, to understand the mode of replication when *E. coli* with ^{15}N DNA was cultured in medium ^{14}N (normal) nitrogen.

(iii) To distinguish or separate heavy DNA from light DNA on the basis of density.

(iv) Mode of DNA replication is semi conservative.

12. tRNA: Act as adaptor molecule, with amino acid binding site and anticodon loop. Brings specific amino acid to the amino acid binding site on the ribosome. Initiator t-RNA starts the process of translation.

mRNA: Act as a template for protein synthesis, carries. Information in the form of codon. It has the initiator codon /start codon /AUG to initiate the process. It has the stop codon/UAA/UAG/UGA for termination of the protein synthesis.

rRNA: rRNA organises itself into ribosomes. There are two sites in the large sub-unit in which one site is for binding the incoming t-RNA with the corresponding amino acid and second site for peptide bond formation. When the small sub-unit of rRNA (ribosomes) encounters the mRNA, the process of translation begins. Ribosome also acts as a catalyst for the formation of peptide bond.

13. DNA fingerprinting

Steps:

(i) Isolation of DNA.

(ii) Digestion of DNA by restriction endonuclease enzyme.

(iii) Separation of DNA fragments, by electrophoresis.

(iv) Transferring of separated DNA fragments to synthetic membrane such as nitrocellulose or nylon.

(v) Hybridisation, using labelled VNTR probe.

(vi) Detection of hybridised DNA fragments by autoradiography.

14. (i)
- Heterogenous nuclear RNA
- Eukaryotic cells
- RNA polymerase-II

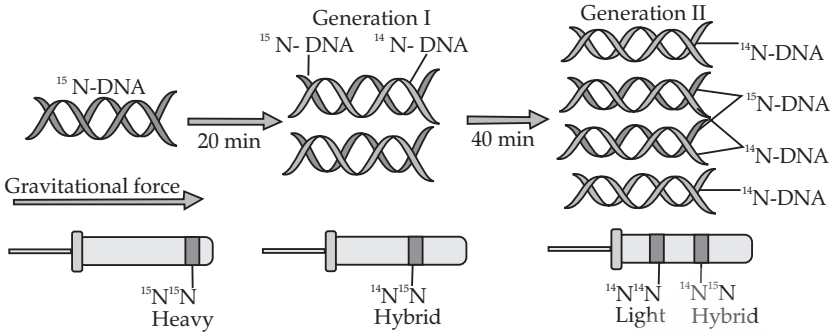
(ii)
- Yes
- hnRNA is subjected to a process called splicing where the introns are removed and exons are joined in a defined order. It capping an unusual nucleotide (methyl guanosine triphosphate) is added to the 5′ - end of hnRNA. In tailing adenylate residues (200 - 300) are added at 3′ - end.
- mRNA

(iii)

mRNA	tRNA
Provide template for protein synthesis.	Act as adaptor molecule/brings amino acids and read genetic code.

15. They grew *E. coli* in a medium containing $^{15}NH_4Cl$ (^{15}N is the heavy isotope of nitrogen) as the only nitrogen source of many generations, the result was that ^{15}N was incorporated into newly synthesised DNA (as well as other nitrogen containing compounds). This heavy DNA molecule could be distinguished from the normal DNA by centrifugation (in a cesium chloride (CsCl) density gradient), then they transferred the cells into a medium with normal $^{14}NH_4Cl$, and took samples at various definite time intervals as the cells multiplied, and extracted the DNA that remained as double-stranded helices. The various samples were separated independently on CsCl gradients to measure the densities of DNA. Thus the DNA that was extracted from the culture one generation after the transfer from ^{15}N to ^{14}N medium [that is after 20 minutes], DNA extracted from the culture after another generation [that is after 40 minutes II generation], was composed of equal amounts of this hybrid DNA, and of 'light' DNA.

(Separation of DNA by Centrifugation)



Meselson and Stahl's experiment

Level - 2 ADVANCED COMPETENCY FOCUSED QUESTIONS

MULTIPLE CHOICE QUESTIONS (MCQs) (1 Mark)

1. Option (C) is correct

   Explanation: In DNA fingerprinting, repetitive DNA sequences, particularly VNTRs (Variable Number Tandem Repeats) or STRs (Short Tandem Repeats), are analysed. These regions do not code for proteins but vary highly between individuals, making them ideal for identification in forensic science. Exons and coding sequences are largely similar among individuals. RNA segments are not used in DNA fingerprinting. Hence, repetitive DNA is used to generate a unique genetic profile.

2. Option (A) is correct

   Explanation: During DNA replication, RNA primers are laid down initially to start DNA synthesis. These primers must be removed and replaced with DNA. DNA polymerase I (in prokaryotes) removes the RNA primers using its 5′ → 3′ exonuclease activity and fills the gap with DNA using its polymerase activity.

3. Option (B) is correct

   Explanation: Semi-conservative replication means that during DNA replication the double-stranded DNA separates into two single strands. Each original (parent) strand serves as a template for the synthesis of a new complementary strand. As a result, each daughter DNA molecule consists of one original (parental) strand, and one newly synthesised strand.

4. Option (C) is correct

   Explanation: The promoter region is a specific DNA sequence upstream (before) the coding part of a gene. It is the binding site for RNA polymerase and transcription factors. Mutations in the promoter can disrupt or reduce the binding of RNA polymerase, leading to problems in initiating transcription.

5. Option (B) is correct

   Explanation: Retroviruses (like HIV) have RNA as their genetic material. They follow a unique flow of genetic information using an enzyme called reverse transcriptase:

   RNA is reverse transcribed into DNA

   The DNA is integrated into the host genome

   Host machinery then transcribes it into RNA, which is translated into proteins

6. Option (C) is correct

   Explanation: When a segment of foreign DNA (e.g., a human gene) is introduced into a bacterial cell, and the bacteria starts producing a human protein, it is an example of recombinant DNA technology. Recombinant DNA Technology involves joining DNA from two different sources, commonly used to produce insulin, growth hormones, and vaccines. Bacteria are often used as host organisms because they grow quickly and can express inserted genes.

7. Option (A) is correct

   Explanation: Splicing is the process where introns are removed and exons are joined together. This results in a mature mRNA that is ready for translation into a protein.

ASSERTION-REASON QUESTIONS (1 Mark)

1. Option (A) is correct

   Explanation: Assertion is true. The term semi-conservative refers to the mechanism of DNA replication where each newly formed DNA molecule retains one strand from the original DNA and synthesises one new complementary strand. This ensures genetic consistency across generations.

   Reason is also true. This is the defining feature of semi-conservative replication. The original DNA double helix separates, and each single strand acts as a template for forming a new complementary strand.

2. Option (A) is correct

   Explanation: Assertion is true. In eukaryotic cells, the primary mRNA transcript (pre-mRNA) undergoes several post-transcriptional modifications before becoming mature mRNA:Capping at the 5′ end (addition of 7-methylguanosine cap), Splicing (removal of introns and joining of exons), and Tailing at the 3′ end (addition of poly-A tail)

Reason is also true. These modifications increase mRNA stability (poly-A tail protects from degradation), help in export of mRNA from the nucleus to the cytoplasm, aid in ribosome binding and efficient translation, and ensure accurate coding by removing non-coding introns.

3. Option (A) is correct

Explanation: Assertion is true. The genetic code is called degenerate because multiple codons can specify the same amino acid. For example:Leucine is coded by six different codons: UUA, UUG, CUU, CUC, CUA, and CUG.

Reason is also true. This statement accurately explains what "degenerate" means in the context of the genetic code. It is the reason why the code is considered degenerate.

4. Option (C) is correct

Explanation: Assertion is true. tRNA (transfer RNA) is called an adapter molecule because it brings the correct amino acid to the ribosome and matches it with the corresponding codon on mRNA using its anticodon. It plays a crucial role in translating the genetic code into proteins.

Reason is false. tRNA does not carry mRNA codons. Instead mRNA carries codons to the ribosome. tRNA carries amino acids and has anticodons that pair with mRNA codons during translation.

5. Option (D) is correct

Explanation: Assertion is false. DNA polymerase cannot initiate DNA synthesis on its own.

It requires a primer (usually an RNA strand synthesised by primase) that provides a free 3′-OH group to begin adding nucleotides.

Reason is true. The 3′-OH group is essential for DNA polymerase to form a phosphodiester bond with incoming nucleotides during DNA replication.

VERY SHORT ANSWER TYPE QUESTIONS (2 Marks)

1. • Start codon anticodon: 5′ - UAC - 3′
   • tRNA molecule does not have a stop codon.
2. (i) **Restriction digestion:** DNA being very long, had to be broken into smaller pieces, which could be done using restriction digestion.
   (ii) **rDNA technology:** The small sequences of DNA had to be amplified for sequencing and since the sequence was not known, it had to be cloned in a suitable host using vectors for amplification.
3. (i) RNA consists of ribose sugars where the hydroxyl group (-OH) is exposed to hydrolysis and degradation whereas DNA consists of deoxyribose sugars.
   (ii) RNA is single-stranded whereas DNA is double-stranded with complementary bases forming hydrogen bonds that release free energy making it thermodynamically stable. (Any one)
4. The DNA is transcribed into an mRNA sequence which is present in the nucleus whereas translation is done by ribosomes which are present in the cytoplasm or on the rough endoplasmic reticulum.

SHORT ANSWER TYPE QUESTIONS (3 Marks)

1. (i) DNA fingerprinting is a technique used to identify individuals based on the unique patterns in their DNA, especially in the non-coding, repetitive sequences.
   (ii) The applications of DNA fingerprinting in real life are:
   (1) Forensic Science: Used to identify suspects in criminal investigations by matching DNA found at the crime scene with that of suspects.
   (2) Paternity and Maternity Disputes: Used to establish biological relationships between individuals.
   (iii) Alec Jeffreys developed this technique in 1985.

CASE BASED QUESTIONS (4 Mark)

1. **(i)** Option (C) is correct

Explanation: The DNA profile of S_3 shows the greatest match (50% match) with the DNA found under the victim's fingernails, indicating that she is likely the murderer.

(ii) Option (B) is correct

Explanation: The DNA profiling indicates a direct match between S_3's DNA and the DNA found at the crime scene, providing strong evidence that she was involved in the murder.

(iii) Option (B) is correct

Explanation: Since the DNA profiles of S_1 and S_2 do not match completely, it indicates they could be non-identical twins, as identical twins would share the same DNA profile.

(iv) Option (B) is correct

Explanation: The fact that S_1 and S_2's DNA profiles show differences suggests that they are not identical twins, as identical twins have identical genetic makeup.

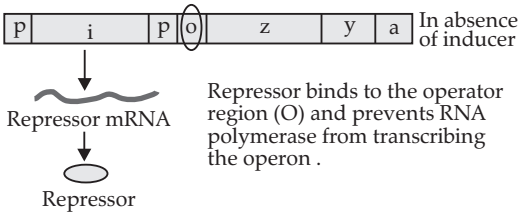
2. **(i)** In presence of lactose repressor protein dose not bind to the operator region (O) and allow RNA polymerase to transcribe the operon.

In absence of lactose repressor protein binds to the operator region (O) and prevent RNA polymerase from transcribing the operon.

(ii) Presence of Permease enzyme coded by gene '*y*' is required that allows lactose to enter the cell for switching on the operon / so that lactose enter inside the cell.

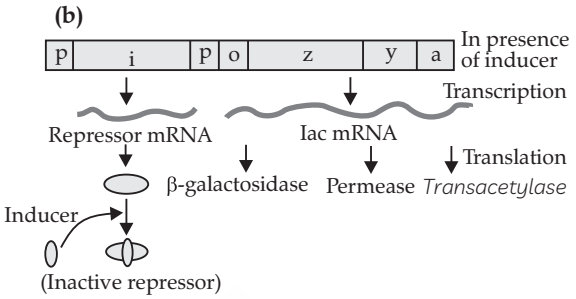
(iii) '*i*' stands for 'inhibitor. This gene transcribes repressor protein which binds to the 'operator' site and switch off the operon.

(iv) **(a)**



OR

(b)



LONG ANSWER TYPE QUESTIONS (5 Marks)

1. (i) DNA is a double helix composed of two antiparallel strands made up of nucleotides, each consisting of:

(1) A deoxyribose sugar,

(2) A phosphate group, and

(3) A nitrogenous base (A, T, G, C).

The strands are held together by hydrogen bonds a pairs with T (2 H-bonds), G pairs with C (3 H-bonds).

This complementary base pairing allows accurate copying of genetic information during DNA replication, ensuring traits are inherited from one generation to the next.

(ii) (1) Initiation: DNA unwinds at specific origins with the help of helicase, forming a replication fork. Single-stranded binding proteins (SSBs) stabilise the unwound strands. Topoisomerase relieves tension ahead of the fork.

(2) Primer Binding:Primase synthesises short RNA primers.

(3) Elongation:DNA Polymerase III adds nucleotides in the 5′ → 3′ direction.

Leading strand is synthesised continuously; lagging strand forms Okazaki fragments.

(4) Primer Removal and Joining:DNA Polymerase I replaces RNA primers with DNA. DNA Ligase joins the Okazaki fragments to form a continuous strand.

(5) Proofreading and Correction:DNA polymerase checks and corrects errors.

(iii) A point mutation (change in a single base pair) can alter the structure or function of a protein. For example: Sickle Cell Anaemia is caused by a substitution of A → T in the β-globin gene, changing the codon from GAG (glutamic acid) to GTG (valine).

This causes haemoglobin to polymerize under low oxygen, deforming red blood cells into a sickle shape, impairing oxygen transport.

2. (i) DNA fingerprinting is based on the fact that certain regions of DNA, called Variable Number Tandem Repeats (VNTRs) or Short Tandem Repeats (STRs), vary greatly between individuals. These repetitive sequences are inherited and differ in number from person to person, making each individual's DNA unique (except in identical twins).

(ii) (1) Isolation of DNA:DNA is extracted from the cells (blood, hair, semen, etc.).

(2) Cutting DNA with Restriction Enzymes: Specific restriction enzymes cut DNA at specific recognition sites to generate fragments.

(3) Separation by Gel Electrophoresis:The DNA fragments are separated by size using agarose gel electrophoresis.

(4) Southern Blotting:DNA fragments are transferred onto a nylon or nitrocellulose membrane.

(5) Hybridisation with DNA Probes:Radioactive or fluorescent DNA probes specific to VNTR regions are added. These bind to complementary DNA sequences on the membrane.

(6) Detection of DNA Pattern:The pattern of bands formed is visualised on X-ray film (autoradiography) or digitally scanned. Each person has a unique banding pattern – the DNA fingerprint.

(iii) Paternity disputes:DNA fingerprints of the child are compared with the mother and alleged father. The father's DNA must match half of the child's bands.

Criminal investigations:DNA found at crime scenes (blood, hair, etc.) can be matched with suspects.

Identifying missing persons or disaster victims:Helps in identification when physical recognition isn't possible.

Inheritance and property claims:Confirms biological relationships legally.

3. (i) β-thalassemia is caused by mutations in the HBB gene, which codes for the β-globin chain of hemoglobin. These mutations lead to reduced

(β^+) or absent (β^o) synthesis of β-globin chains, resulting in defective haemoglobin, leading to anaemia, fatigue, and other symptoms. It is an autosomal recessive disorder, so a person must inherit two defective alleles (one from each parent) to show the disease.

(ii) Molecular diagnosis involves techniques like PCR (Polymerase Chain Reaction) and

DNA sequencing or RFLP (Restriction Fragment Length Polymorphism).

These tests detect mutations in the HBB gene even in asymptomatic carriers, allow carrier screening in high-risk families, are used for prenatal diagnosis (e.g., using fetal cells from amniotic fluid or chorionic villus). Thus, early detection helps in informed decision-making and genetic counselling.

(iii) Gene therapy aims to insert a normal copy of the β-globin gene into the patient's bone marrow stem cells, allowing them to produce functional haemoglobin.

Steps:

(1) Stem cells are collected from the patient.

(2) A normal β-globin gene is introduced using viral vectors (e.g., lentivirus).

(3) Modified cells are returned to the patient's body.

(4) The new cells produce normal red blood cells with healthy haemoglobin.

(5) Though still under clinical trials, gene therapy offers long-term hope for curing β-thalassemia.

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