Chapter 24

Molecular Basis of Inheritance

Trend Analysis

Concepts name	NEET 2020 I Exam	NEET 2020 II Exam	NEET 2021	NEET 2022 I Exam	NEET 2022 II Exam	NEET 2023
The DNA, The Search For Genetic Material RNA World	4	6	7	4	4	3
Genetic Code, Gene Expression And DNA Fingerprinting and Protein Synthesis			2	4	3	4

Topic 1 The DNA, The Search For Genetic Material RNA World

Introduction

- Nucleic acids are the building blocks of genetic material.
- Nucleic acids are polymers of nucleotides.
- Deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) are the two types of nucleic acids found in living systems.
- DNA acts as the genetic material in most of the organisms. RNA acts as a genetic material in some viruses, mostly functions as a messenger.
- RNA also functions as adapter, structural, and in some cases as a catalytic molecule.

The DNA

- DNA is a long polymer of deoxyribonucleotides.
- The length of DNA is defined as number of nucleotides (or a pair of nucleotide referred to as base pairs) present in it. It is the characteristic of an organism.
- For example, a bacteriophage $\phi \times 174$ has 5386 nucleotides, bacteriophage lambda has 48502 base pairs (bp), *Escherichia coli* has 4.6×10^6bp, and haploid content of human DNA is 3.3×10^9bp.

Structure of Polynucleotide Chain

- A nucleotide has three components namely,

(a) A nitrogenous base

(b) A pentose sugar (ribose in case of RNA, and deoxyribose for DNA)

(c) A phosphate group.

- There are two types of nitrogenous bases namely,

(a) Purines (Adenine and Guanine)

(b) Pyrimidines (Cytosine, Uracil and Thymine).

- Cytosine is common for both DNA and RNA whereas Thymine is present in DNA and Uracil is present in RNA.
- A nitrogenous base is linked to the pentose sugar through an N-glycosidic linkage to form a nucleoside, such as adenosine or deoxyadenosine, guanosine or deoxyguanosine, cytidine or deoxycytidine and uridine or deoxythymidine.
- When a phosphate group is linked to 5'-OH of a nucleoside through phosphoester linkage, a nucleotide or deoxynucleotide is formed.
- Two nucleotides are linked through 3'-5' phosphodiester linkage to form a dinucleotide.
- More nucleotides can be joined to form a polynucleotide chain.
- A polymer formed has at one end a free phosphate moiety at 5'-end of ribose sugar, which is referred to as 5'-end of polynucleotide chain.
- At the other end of the polymer the ribose has a free 3'-OH group which is referred to as 3' -end of the polynucleotide chain.
- The backbone in a polynucleotide chain is formed due to sugar and phosphates.
- In RNA, every nucleotide residue has an additional –OH group present at 2' -position in the ribose.
- DNA as an acidic substance present in nucleus was first identified by Friedrich Meischer in 1869. He named it as 'Nuclein'.
- In 1953 James Watson and Francis Crick, based on the X-ray diffraction data produced by Maurice Wilkins and Rosalind Franklin, proposed double helix model for the structure of DNA.
- Base pairing between the two strands of polynucleotide chains was based on the observation of Erwin Chargaff.
- According to him, the ratios between Adenine and Thymine and Guanine and Cytosine are constant and equal one.
- A unique property of base pairing is that they are said to be complementary to each other and therefore if the sequence of bases in one strand is known, then the sequence in other strand can be predicted.
- If each strand from a DNA acts as a template for synthesis of a new strand, the two double stranded DNA produced would be identical to the parental DNA molecule.

⏩ Salient Features of Double Helix Model for the Structure of DNA

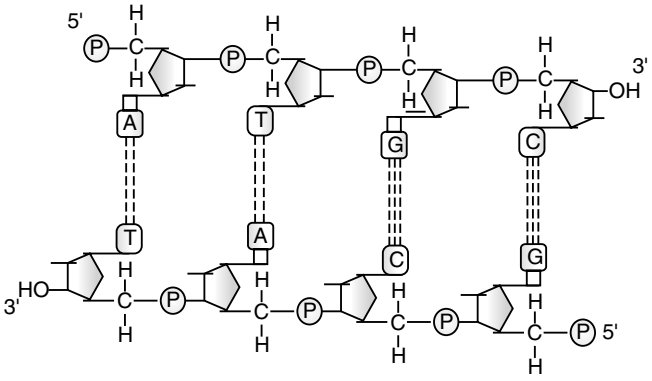
1. It is made of two polynucleotide chains.

2. The two chains have anti-parallel polarity.

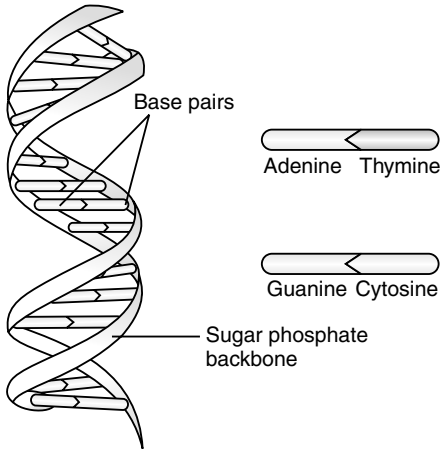
3. The bases in two strands are paired through hydrogen bond (H-bonds) forming base pairs (bp). Adenine forms two hydrogen bonds with Thymine from opposite strand similarly Guanine is bonded with Cytosine with three H-bonds. As a result, uniform distance between the two strands of the helix is formed.

4. The two chains are coiled in a right-handed fashion. The pitch of the helix is 3.4 nm. There are roughly 10 bp in each turn. The distance between a bp in a helix is approximately equal to 0.34 nm.

5. The plane of one base pair stacks over the other in double helix for the stability of the helical structure.



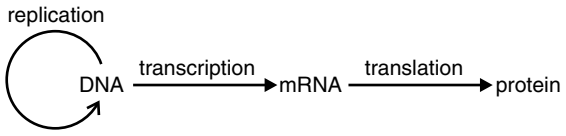
Double stranded polynucleotide chain



DNA double helix

Central Dogma

⏩ Francis Crick proposed the Central dogma in molecular biology, which states that the genetic information flows from DNA → RNA → Protein.



Central dogma

⏩ In some viruses the flow of information is in reverse direction *i.e.*, from RNA to DNA.

Packaging of DNA Helix

⏩ In prokaryotes, such as, *E. coli*, the DNA is not scattered throughout the cell.

⏩ DNA being negatively charged is held with some proteins having positive charges in a region termed as 'nucleoid'.

⏩ In eukaryotes, there is a set of positively charged, basic proteins called histones.

⏩ A protein acquires charge depending upon the abundance of amino acids residues with charged side chains.

⏩ Histones are rich in the basic amino acid residues lysines and arginines.

⏩ Both the amino acid residues carry positive charges in their side chains.

⏩ Histones are organised to form a unit of eight molecules called as histone octamer.

⏩ The negatively charged DNA is wrapped around the positively charged histone octamer to form a structure called nucleosome.

⏩ A nucleosome contains 200 bp of DNA helix.

⏩ Nucleosomes constitute the repeating unit of a structure in nucleus called chromatin, thread-like stained (coloured) bodies seen in nucleus.

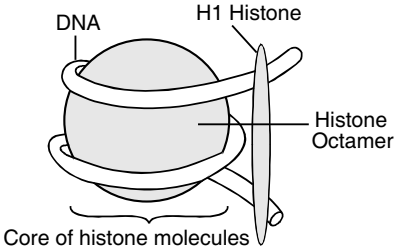
⏩ The nucleosomes in chromatin are seen as 'beads-on-string' structure to form chromatin fibers that further coils and condense at metaphase stage of cell division to form chromosomes.

⏩ The packaging of chromatin requires additional set of proteins referred to as Non-histone Chromosomal (NHC) proteins.

⏩ In a nucleus, some region of chromatin are loosely packed with light stains are referred to as euchromatin.

⏩ The chromatin that is more densely packed with dark stains is called as heterochromatin.

⏩ Euchromatin is said to be transcriptionally active chromatin, whereas heterochromatin is inactive.



Nucleosome

TRANSFORMING PRINCIPLE

⏩ In 1928, Frederick Griffith, in a series of experiments with *Streptococcus pneumoniae* (bacterium responsible for pneumonia), found a transformation in the bacteria in physical form.

⏩ When *Streptococcus pneumoniae* (pneumococcus) bacteria are grown on a culture plate, some produce smooth shiny colonies (S) while others produce rough colonies (R).

- This is because the S strain bacteria have a mucous (polysaccharide) coat, while R strain does not.
- Mice infected with the S strain (virulent) die from pneumonia infection but mice infected with the R strain do not develop pneumonia.

S strain ⟶ Inject into mice ⟶ Mice die
R strain ⟶ Inject into mice ⟶ Mice live

- Griffith was able to kill bacteria by heating them.
- He observed that heat-killed S strain bacteria injected into mice did not kill them.
- When he injected a mixture of heat-killed S and live R bacteria, the mice died.
- He recovered living S bacteria from the dead mice.

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

S strain (heat-killed) + R strain (live) ⟶ Inject into mice ⟶ Mice die

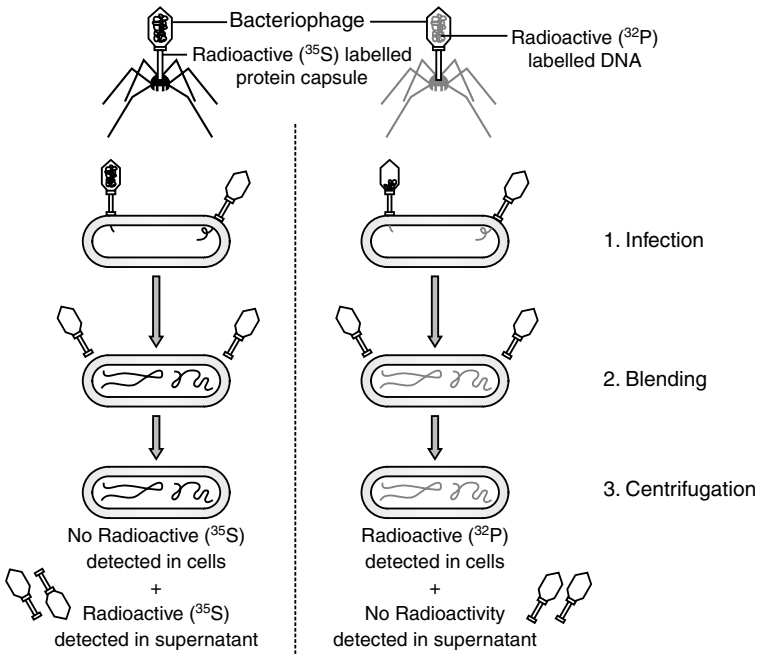
- Thus, he concluded that some transforming principle transferred from the heat-killed S strain had enabled the R strain to become virulent. This must be due to the transfer of the genetic material.
- However, the biochemical nature of genetic material was not defined from his experiments.

Biochemical Characterisation of Transforming Principle

- Prior to the work of Oswald Avery, Colin MacLeod and Maclyn McCarty (1933–44), the genetic material was thought to be a protein.
- They worked to determine the biochemical nature of 'transforming principle' in Griffith's experiment.
- They purified biochemicals such as proteins, DNA, RNA, etc., from the heat-killed S cells to see which could transform live R cells into S cells and found that DNA 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.
- DNase did inhibit transformation suggesting that the DNA caused the transformation.
- Hence, they concluded that DNA is the hereditary material.

The Genetic Material is DNA

- The unequivocal proof that DNA is the genetic material came from the experiments of Alfred Hershey and Martha Chase (1952).
- They worked with viruses that infect bacteria called bacteriophages.
- The bacteriophage attaches to the bacteria and its genetic material enters the bacterial cell.
- The bacterial cell manufactures more viral genetic particles.
- Hershey and Chase worked to discover whether it was protein or DNA from the viruses that entered the bacteria.
- Viruses grown in the presence of radioactive phosphorus contained radioactive DNA but not radioactive protein because DNA contains phosphorus but protein does not.
- On the other hand, viruses grown on radioactive sulphur contained radioactive protein but not radioactive DNA because DNA does not contain sulphur.
- Radioactive phages were allowed to attach to *E. coli* bacteria.
- As the infection proceeded, the viral coats were removed from the bacteria by agitating them in a blender.
- The virus particles were separated from the bacteria by spinning them in a centrifuge.
- Virus infected bacteria had radioactive DNA were radioactive, indicating that DNA was the material that passed from the virus to the bacteria.
- Virus infected bacteria that had radioactive proteins were not radioactive.
- This indicated that proteins did not enter the bacteria from the viruses.
- DNA is therefore the genetic material that is passed from virus to bacteria.



Properties of Genetic Material (DNA versus RNA)

- RNA is the genetic material in Tobacco Mosaic Viruses, QB bacteriophage, etc.
- DNA is the predominant genetic material whereas RNA performs dynamic functions of messenger and adapter.
- A molecule that can act as a genetic material must fulfill the following criteria:

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

Due to rule of base pairing and complementarity, both the nucleic acids (DNA and RNA) have the ability to direct their duplications.

However, proteins fail to fulfill first criteria itself.

2. It should chemically and structurally be stable.

The genetic material should not change with different stages of life cycle, age or with change in physiology of the organism.

Stability as one of the properties of genetic material was evident in Griffith's 'transforming principle' which showed that the two strands of DNA being complementary if separated by heating come together under appropriate conditions.

Further, 2'-OH group present at every nucleotide in RNA is a reactive group and makes RNA labile and easily degradable.

RNA is also now known to be catalytic, hence reactive.

Therefore, DNA chemically is less reactive and structurally more stable when compared to RNA. DNA is a better genetic material.

The presence of thymine at the place of uracil provides additional stability to DNA.

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

Both DNA and RNA are able to mutate.

RNA being unstable, mutate at a faster rate.

Thus, viruses having RNA genome and shorter life span will mutate and evolve faster.

4. It should be able to express itself in the form of 'Mendelian Characters'.

RNA can directly code for the synthesis of proteins and hence can easily express the characters.

DNA is dependent on RNA for synthesis of proteins.

Both RNA and DNA can function as genetic material.

However, DNA being more stable is preferred for storage of genetic information while RNA is preferred for the transmission of genetic information.

RNA WORLD

- RNA was the first genetic material.
- RNA used to act as a genetic material as well as a catalyst.
- Since RNA being a catalyst is reactive and hence unstable.
- DNA has evolved from RNA with chemical modifications that make it more stable.
- Further, DNA being double and complementary stranded resists changes by repair.

REPLICATION

- After proposing the double helical structure for DNA, Watson and Crick proposed a scheme for replication of DNA.
- The scheme suggested that the two strands would separate and act as a template for the synthesis of new complementary strands.
- After the completion of replication, each DNA molecule would have one parental and one newly synthesised strand. This scheme was termed as semiconservative DNA replication.

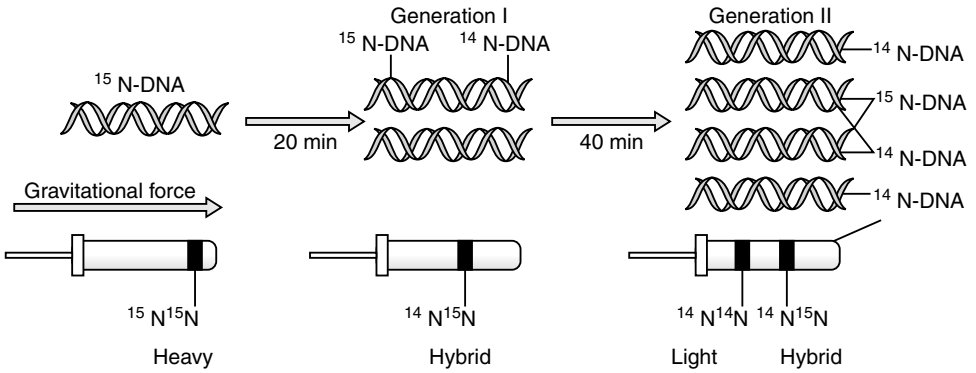
The Experimental Proof

- DNA replicates semi-conservatively was shown first in *Escherichia coli*.
- Matthew Meselson and Franklin Stahl performed the following experiment in 1958:

(a) They grew *E. coli* in a medium containing $^{15}NH_4Cl$ in which ^{15}N is the heavy isotope of nitrogen. This resulted ^{15}N to synthesize new DNA. This heavy DNA molecule could be distinguished from the normal DNA by centrifugation in a cesium chloride (CsCl) density gradient.

(b) 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.

(c) The DNA extracted from the culture one generation after the transfer from ^{15}N to ^{14}N medium had a hybrid or intermediate density. DNA extracted from the culture after another generation was composed of equal amounts of the hybrid DNA and of 'light' DNA.



⏩ Experiments involving use of radioactive thymidine to detect distribution of newly synthesised DNA in the chromosomes was performed on *Vicia faba* (faba beans) by Taylor and colleagues in 1958.

The Machinery and the Enzymes

⏩ In *E. coli*, the process of replication requires a set of catalysts (enzymes).

⏩ The main enzyme is referred to as DNA-dependent DNA polymerase, since it uses a DNA template to catalyse the polymerisation of deoxynucleotides.

⏩ These enzymes are highly efficient in a very short time. *E. coli* that has only 4.6×10^6 bp completes the process of replication within 38 minutes i.e., the average rate of polymerisation is approximately 2000 bp per second.

⏩ These polymerases have to be fast and catalyse the reaction with high degree of accuracy.

⏩ Any mistake during replication would result into mutations.

⏩ Energetically replication is a very expensive process.

⏩ Deoxyribonucleoside triphosphates serve dual purposes as follows:

(a) Act as substrates

(b) They provide energy for polymerisation reaction

⏩ There are many additional enzymes required to complete the process of replication with high degree of accuracy.

⏩ In long DNA molecules, the two strands of DNA cannot be separated in its entire length as it requires high energy.

⏩ Thus, the replication occurs within a small opening of the DNA helix, referred to as replication fork.

⏩ The DNA-dependent DNA polymerases catalyse polymerisation only in one direction (5' → 3').

⏩ So, on the template with polarity 3' → 5', the replication is continuous, while on the other 5' → 3', it is discontinuous.

⏩ The discontinuously synthesized fragments are joined by the enzyme DNA ligase.

⏩ The DNA polymerases cannot initiate the process of replication and does not initiate randomly at any place in DNA on their own.

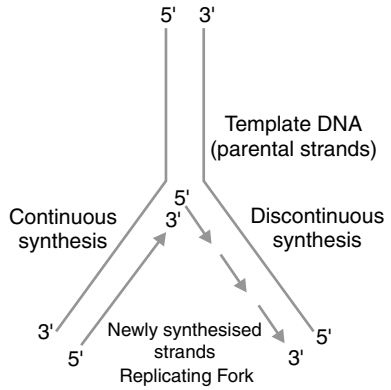
⏩ Therefore, there is a definite region called origin of replication in *E. coli* DNA where the replication originates.

⏩ If a piece of DNA is needed to be propagated during recombinant DNA procedures, it requires a vector which provides the origin of replication.

⏩ In eukaryotes, the replication of DNA takes place at S-phase of the cell-cycle.

⏩ The replication of DNA and cell division cycle should be highly coordinated.

⏩ A failure in cell division after DNA replication results into polyploidy.



TRANSCRIPTION

⏩ The process of copying genetic information from one strand of the DNA into RNA is termed as transcription.

⏩ The principle of complementarity governs the process of transcription, except the adenosine which forms base pair with uracil.

⏩ In transcription, only a segment of DNA and only one of the strands is copied into RNA.

⏩ This would demarcate the region and the strand of DNA that would be transcribed.

⏩ Both the strands are not copied during transcription. This is because:

(a) The code for proteins is different in both strands. This complicates the translation.

(b) The two RNA molecules if produced simultaneously, would be complementary to each other and hence would form a double stranded RNA. This would prevent RNA from being translated into protein.

Transcription Unit

⏩ A transcription unit in DNA is differentiated into three regions namely:

(a) A Promoter

(b) The Structural gene

(c) A Terminator

⏩ Since the two strands of DNA have opposite polarity and the DNA-dependent RNA polymerase catalyse the polymerisation in only one direction (5' → 3'), the strand that has the polarity 3' → 5' acts as a template, and is referred to as template strand.

⏩ The other strand which has the polarity (5' → 3') is referred to as coding strand.

⏩ For example – a hypothetical sequence from a transcription unit is represented below:

3'-ATGCATGCATGCATGCATGCATGC-5' Template Strand

5'-TACGTACGTACGTACGTACGTACG-3' Coding Strand

⏩ The promoter and terminator play an important role in transcription unit.

⏩ The promoter is located towards 5'-end in the upstream of the structural gene.

⏩ It is a DNA sequence that provides binding site for RNA polymerase.

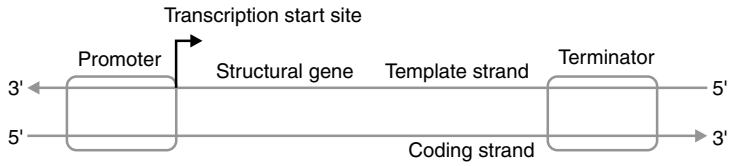
⏩ The promoter defines the template and coding strands.

⏩ By switching its position with terminator, the coding and template strands could be reversed.

⏩ The terminator is located towards 3'-end in the downstream of the coding strand and defines the end of the process of transcription.

⏩ Inheritance of a character is also affected by promoter and regulatory sequences of a structural gene.

⏩ Hence, regulatory sequences are loosely defined as regulatory genes, though these do not code for any RNA or protein.



Transcription Unit and the Gene

⏩ A gene is defined as the functional unit of inheritance.

⏩ It is the DNA sequence coding for tRNA or rRNA molecule.

⏩ Cistron: A segment of DNA coding for a polypeptide.

⏩ Structural gene in a transcription unit are of two types:

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

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

Steps of Transcription in Prokaryotes

⏩ It includes three steps namely,

(a) Initiation

(b) Elongation

(c) Termination

Initiation:

⏩ Here, the enzyme RNA *polymerase* binds at the promoter site of DNA. This causes the local unwinding of the DNA double helix. An *initiation factor* (σ *factor*) present in RNA polymerase initiates the RNA synthesis.

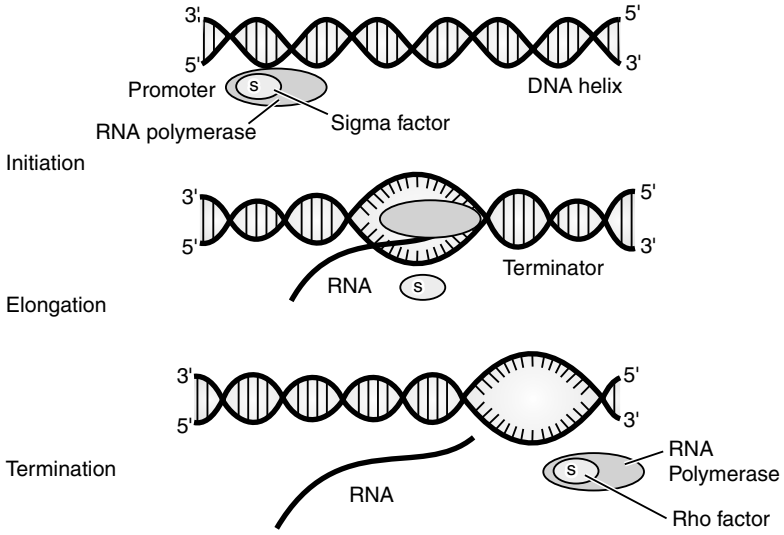
Elongation:

⏩ The RNA chain is synthesized in the 5′-3′ direction. In this process, activated ribonucleoside triphosphates (ATP, GTP, UTP & CTP) are added. This is complementary to the base sequence in the DNA template.

Termination:

⏩ A *termination factor* (ρ *factor*) binds to the RNA polymerase and terminates the transcription.

⏩ In bacteria, translation can begin much before the mRNA is fully transcribed since the mRNA does not require any processing to become active, and transcription and translation take place in the same compartment due to absence of a well defined nucleus.



Process of Transcription in Bacteria

Steps of Transcription in Eukaryotes

⏩ In eukaryotes, the monocistronic structural genes have interrupted coding sequences – the genes in eukaryotes are split.

⏩ The coding sequences or expressed sequences are defined as exons.

⏩ Exons are said to be those sequence that appear in mature or processed RNA.

⏩ The exons are interrupted by introns.

⏩ Introns or intervening sequences do not appear in mature or processed RNA.

⏩ In eukaryotes, there are two additional complexities:

(a) There are three RNA polymerases in the nucleus in addition to the RNA polymerase found in the organelles.

(i) The RNA polymerase I: It transcribes rRNAs (28S, 18S, and 5.8S)

(ii) The RNA polymerase II: It is the precursor of mRNA, the heterogeneous nuclear RNA (hnRNA).

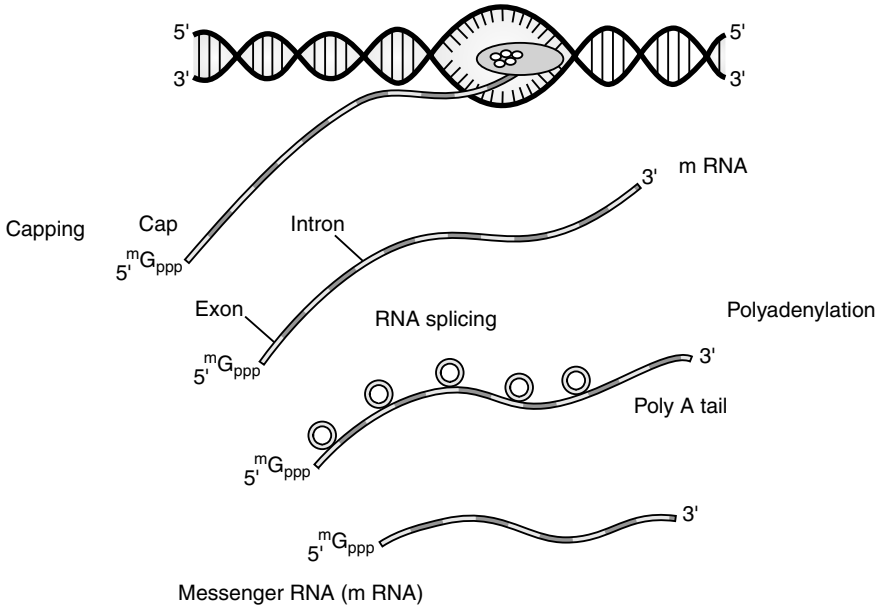
(iii) The RNA polymerase III: It is responsible for transcription of tRNA, 5SrRNA, and snRNAs(small nuclear RNAs).

(b) The primary transcripts (hnRNA) contain both the exons and the introns and are non-functional. In order to remove the introns, it undergoes the following processes:

(i) Splicing: The introns are removed from hnRNA and exons are joined together.

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

(iii) Tailing (Polyadenylation): Here, adenylate residues (200-300) are added at 3′-end.



Process of Transcription in Eukaryotes

⏩ The fully processed hnRNA is now called mRNA that is transported for translation.

Significance of the Split-gene Arrangements in Eukaryotes

(a) It represents an ancient feature of the genome.
(b) The presence of introns is reminiscent of antiquity, and the process of splicing represents the dominance of RNA-world.

Topic 2 Genetic Code, Gene Expression and DNA Fingerprinting and Protein Synthesis

Revision Notes

Genetic Code

⏩ The process of translation requires transfer of genetic information from a polymer of nucleotides to a polymer of amino acids. This led to the proposition of genetic code.

⏩ Genetic code is the sequence of nucleotides (nitrogen bases) in mRNA that contains information for protein synthesis (translation).

⏩ There are 20 amino acids involved in translation as follows:

Alanine (Ala)	Leucine (Leu)
Arginine (Arg)	Lysine (Lys)
Asparagine (Asn)	Methionine (Met)
Aspartic acid (Asp)	Phenyl alanine (Phe)
Cystein (Cys)	Proline (Pro)
Glutamine (Gln)	Serine (Ser)
Glutamic acid (Glu)	Threonine (Thr)
Glycine (Gly)	Tryptophan (Trp)
Histidine (His)	Tyrosine (Tyr)
Isoleucine (Ile)	Valine (Val)

Scientists Involved in Genetic Code

George Gamow:

⏩ He suggested that for coding 20 amino acids, the code should be made up of 3 nucleotides.

Har Gobind Khorana:

⏩ He developed the chemical method of synthesizing RNA molecules with defined combinations of bases (homopolymers & copolymers).

Marshall Nirenberg:

⏩ He developed cell-free system for protein synthesis.

⏩ Severo Ochoa

⏩ He used polynucleotide phosphorylase enzyme to polymerize RNA with defined sequences in a template independent manner.

Codons for Amino Acids

⏩ The checker board below shows the codons for the various amino acids.

	U		C		A		G		
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys	C
	UUA	Leu	UCA	Ser	UAA	Stop	UGA	Stop	A
	UUG	Leu	UCG	Ser	UAG	Stop	UGG	Trp	G
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC	Leu	CCC	Pro	CAC	His	CGC	Arg	C
	CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg	A
	CUG	Leu	CCG	Pro	CAG	Gln	CGG	Arg	G
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser	C
	AUA	Ile	ACA	Thr	AAA	Lys	AGA	Arg	A
	AUG	Met	ACG	Thr	AAG	Lys	AGG	Arg	G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U
	GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly	C
	GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly	A
	GUG	Val	GCG	Ala	GAG	Glu	GGG	Gly	G

Salient Features of Genetic Code

1. The codon is triplet.

2. 61 codons code for amino acids while 3 codons i.e., UAA, UAG & UGA do not code for any amino acids, hence they function as stop codons or non-sense codons.

3. Genetic code is unambiguous and specific. i.e., one codon specifies only one amino acid.

4. A single amino acid is represented by many codons (except AUG for methionine & UGG for tryptophan). Such codons are called degenerate codons.

5. No punctuations between adjacent codons (comma less code). The codon is read in mRNA in a contiguous fashion.

6. Genetic code is universal. e.g., From bacteria to human UUU codes for Phenylalanine. Some exceptions are found in mitochondrial codons, and in some protozoans.

7. AUG has dual functions. It codes for Methionine (Met), and also acts as initiator codon. In eukaryotes, methionine is the first amino acid and *formyl methionine* in prokaryotes.

Mutation and Genetic Code

- The effect of large deletions, addition and rearrangements in a segment of DNA results in loss or gain of a gene that can be easily comprehended.
- Example of point mutation is a change of single base pair in the gene for beta globin chain that changes amino acid residue glutamate to valine resulting in a diseased condition called as sickle cell anaemia.
- Insertion or deletion of one or two bases changes the reading frame from the point of insertion or deletion.
- e.g., – Insertion or deletion of three or its multiple bases insert or delete one or multiple codon hence one or multiple amino acids, and reading frame remains unaltered from that point onwards. Such mutations are referred to as frame-shift insertion or deletion mutations. This forms the genetic basis of proof that codon is a triplet and it is read in a contiguous manner.

Types of RNA

- In prokaryotes such as bacteria, there are three major types of RNAs namely,

(a) mRNA (messenger RNA)

(b) tRNA (transfer RNA)

(c) rRNA (ribosomal RNA).

- All three RNAs are needed to synthesise a protein in a cell.
- The mRNA provides the template, tRNA brings amino acids and reads the genetic code, and rRNAs play structural and catalytic role during translation.
- There is single DNA-dependent RNA polymerase that catalyses transcription of all types of RNA.

The tRNA, the Adapter Molecule

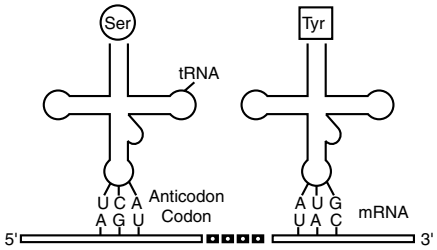
- Francis Crick postulated the presence of an adapter molecule that would on one hand read the code and on other hand would bind to specific amino acids as amino acids have no structural specialities to read the code.
- The tRNA, then called sRNA (soluble RNA) play the role as an adapter molecule.
- The tRNAs are specific for each amino acid.
- The tRNA is a compact molecule having the following:

(a) An anticodon loop that has bases complementary to the code.

(b) An amino acid acceptor end to which amino acid binds.

(c) Initiator tRNA for initiation and no tRNAs for stop codons.

(d) Secondary (2-D) structure of tRNA looks like a clover-leaf while 3-D structure looks like inverted 'L'.



t-RNA the adapter molecule

TRANSLATION

- It is the process of polymerisation of amino acids to form a polypeptide.
- The order and sequence of amino acids are defined by the sequence of bases in the mRNA.
- The amino acids are joined by a bond which is known as a peptide bond.

Steps Involved in Translation

- The translation involves the following steps:

(a) Charging of tRNA

(b) Initiation

(c) Elongation

(d) Termination

Charging of tRNA or Aminoacylation of tRNA

(a) Formation of peptide bond requires energy obtained from ATP.

(b) So, amino acids are activated (amino acid + ATP) and linked to their cognate tRNA in the presence of *aminoacyl* tRNA *synthetase*.

(c) Hence, the tRNA becomes charged.

(d) The presence of a catalyst would enhance the rate of peptide bond formation.

Initiation

(a) It begins at the 5'-end of mRNA in the presence of an *initiation factor.*

(b) The mRNA binds to the small subunit of ribosome.

(c) Later the large subunit binds to the small subunit to complete the initiation complex.

(d) The large subunit has 2 binding sites for tRNA-aminoacyl tRNA binding site (A site) and peptidyl site (P site).

(e) Initiation codon and the codon for methionine is AUG. So methionyl tRNA complex would have UAC at the anticodon site.

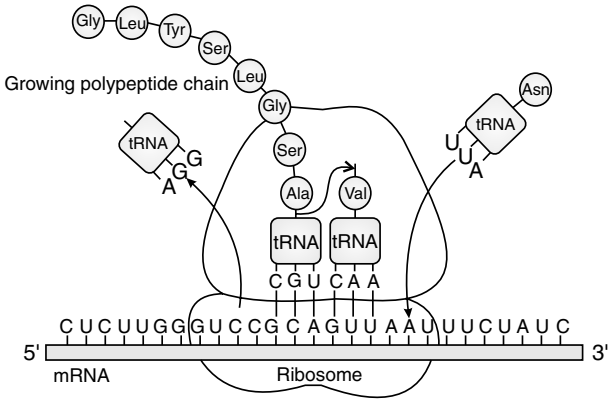
Elongation

(a) At the P site the first codon of mRNA binds with anticodon of methionyl-tRNA complex.

(b) Another aminoacyl-tRNA complex with an appropriate amino acid enters the ribosome and attaches to A site. Its anticodon binds to the second codon on the mRNA and a peptide bond is formed between first and second amino acids in presence of an enzyme, peptidyl transferase.
(c) First amino acid and its tRNA are broken and the tRNA is removed from P site.
(d) The second tRNA from A site is pulled to P site along with mRNA. This is called translocation.
(e) Now, the third codon comes into A site and a suitable tRNA with third amino acid binds at the A site. This process is repeated.
(f) A group of ribosomes associated with a single mRNA for translation is called a polyribosome (polysomes).

Termination

(a) When aminoacyl-tRNA reaches the termination codon like UAA, UAG & UGA, the termination of translation occurs.
(b) The ribosome dissociates into large and small subunits at the end of protein synthesis.
(c) An mRNA has additional sequences that are not translated (untranslated regions or UTR).
(d) UTRs are present at both 5′-end (before start codon) and 3′-end (after stop codon) and are required for efficient translation process.
(e) At the end, a release factor binds to the stop codon, terminating translation and releasing the complete polypeptide from the ribosome.



Translation

Regulation of Gene Expression

- Gene expression results in the formation of a polypeptide.

Eukaryotes

- In eukaryotes, the regulation includes the following levels:

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

- The genes are expressed to perform a particular function or a set of functions.
- Example 1 – In bacteria like *E. coli*, the enzyme *beta-galactosidase* hydrolyses lactose into galactose and glucose.
- In the absence of lactose, the synthesis of beta-galactosidase stops.
- Example 2 – The development and differentiation of embryo into adult are a result of the coordinated regulation of expression of several set of genes.
- The metabolic, physiological and environmental conditions regulate expression of genes.

Prokaryotes

- In prokaryotes, the expression of gene is done at transcriptional level.
- Here, the activity of RNA polymerase at a given promoter is regulated by interaction with accessory proteins, which affect its ability to recognize start sites.
- These regulatory proteins can act both positively (activators) and negatively (repressors).
- The accessibility of promoter regions of prokaryotic DNA is regulated by the interaction of proteins with sequences termed operators.
- The operator region is adjacent to the promoter elements and the sequences of the operator bind a repressor protein.
- Each operon has its specific operator and specific repressor.
- For example, *lac* operator is present only in the *lac* operon and it interacts only with *lac* repressor.

OPERON CONCEPT

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

Lac Operon in *E. coli*

- The operon controls lactose metabolism. It consists of two genes namely,

(a) A regulatory or inhibitory gene (i)
(b) Three structural genes
(i) *z* gene
(ii) *y* gene
(iii) *a* gene

- The inhibitory gene (*i* gene) codes for the repressor.
- The '*z*' gene codes for □ *galactosidase* and helps in hydrolyzing lactose to galactose and glucose.
- The '*y*' gene codes for *permease* and helps to increase the permeability of the cell to lactose.
- The '*a*' gene codes for a *transacetylase*.
- In most other operons, the genes present in the operon function together in the same or related metabolic pathway.
- There is an operator region for each operon.
- If there is no lactose (inducer), *lac* operon remains switched off.
- The regulator gene synthesizes mRNA to produce the repressor protein.
- This protein binds to the operator genes and blocks RNA polymerase movement. So, the structural genes are not expressed.
- If lactose is provided in the growth medium, the lactose is transported into the *E. coli* cells by the action of permease.

⏩ The repressor protein binds to the operator region of the operon and prevents RNA polymerase from transcribing the operon.

⏩ In the presence of an inducer, such as lactose, the repressor is inactivated. This allows RNA polymerase access to the promoter and transcription proceeds.

⏩ Regulation of *lac* operon by repressor is called negative regulation.

HUMAN GENOME PROJECT

⏩ The entire DNA in the haploid set of chromosome of an organism is called a genome.

⏩ In Human genome, DNA is packed in 23 chromosomes.

⏩ Human Genome Project (1990-2003) was the first effort in identifying the sequence of nucleotides and mapping of all the genes in human genome.

⏩ Human genome contains about 3×10^9bp.

⏩ HGP was closely associated with bioinformatics.

Bioinformatics

⏩ It is the application of computer science and information technology to the field of biology and medicine.

⏩ It helps to analyze DNA sequence data.

Goals of HGP

(a) Identify all the estimated genes in human DNA

(b) Determine the sequences of the 3 billion chemical base pairs that make up human DNA.

(c) Store this information in databases.

(d) Improve tools for data analysis.

(e) Transfer related technologies to other sectors.

(f) Address the ethical, legal and social issues (ELSI) that may arise from the project.

Methodologies of HGP

⏩ The methods of HGP involve two major approaches namely,

(a) Expressed sequence tags (ESTs)

(b) Sequence annotation

Expressed Sequence Tags [ESTs]

⏩ It focusses on identifying all the genes that expressed as RNA (referred to as Expressed Sequence Tags (ESTs).

Sequence Annotation

⏩ It sequences the whole set of genome containing all the coding and non-coding sequence, and assigning different regions in the sequence with functions (a term referred to as Sequence Annotation).

Procedure

⏩ For sequencing, the total DNA from a cell is isolated and converted into random fragments.

⏩ These fragments are then cloned in suitable host using specialised vectors.

⏩ This results in the amplification of each piece of DNA fragment so that it could be sequenced with ease.

⏩ The fragments were sequenced using automated DNA sequencers using Frederick Sanger method.

⏩ These sequences were then arranged based on some overlapping regions present in them.

⏩ Alignment of these sequences is done using specialized computer based programs.

⏩ Genetic and physical maps on the genome were generated using information on polymorphism of restriction endonuclease recognition sites and some repetitive DNA sequences (microsatellites).

⏩ The commonly used hosts were bacteria and yeast, and the vectors were called as BAC (bacterial artificial chromosomes), and YAC (yeast artificial chromosomes).

Salient Features of Human Genome

(a) The human genome contains 3164.7 million nucleotide bases.

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

(c) The total number of genes is estimated at 30,000.

(d) Almost all (99.9%) nucleotide bases are exactly the same in all people.

(e) The functions of 50% of discovered genes are unknown.

(f) Less than 2% of the genome codes for proteins.

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

(h) Repetitive sequences are stretches of DNA sequences that are repeated many times, sometimes hundred to thousand times. They have no direct coding functions, but help in understanding chromosome structure, dynamics and evolution.

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

(j) About 1.4 million locations where single-base DNA differences (SNPs- Single nucleotide polymorphism or 'snips') occur in humans.

DNA FINGERPRINTING OR DNA PROFILING

⏩ It is the technique to identify the similarities of the DNA fragments of 2 individuals.

⏩ It was developed by Alec Jeffreys (1985).

⏩ DNA carries some non-coding sequences called repetitive sequence [variable number tandem repeats (VNTR)

The VNTR belongs to a class of satellite DNA referred to as mini-satellite. A small DNA sequence is arranged tandemly in many copy numbers.

⏩ Number of repeats is specific from person to person.

⏩ The size of VNTR varies from 0.1 to 20 kb.

⏩ Repetitive DNA are separated from bulk genomic DNA as different peaks during density gradient centrifugation.

⏩ The bulk DNA forms a major peak and the other small peaks are called as satellite DNA.

⏩ Satellite DNA is classified into many categories, (micro-satellites, mini-satellites etc.) based on base composition (A:T rich or G:C rich), length of segment and number of repetitive units.

⏩ An inheritable mutation observed in a population at high frequency is called DNA polymorphism (variation at genetic level).

⏩ Polymorphism is higher in non-coding DNA sequence. This is because, the mutations in these sequences may not have any immediate effect in an individual's reproductive ability.

⏩ These mutations accumulate generation after generation and cause polymorphism.

⏩ Polymorphism plays an important role in evolution and speciation.

Application of DNA Fingerprinting

(a) Forensic tool to solve paternity, rape, murder etc.

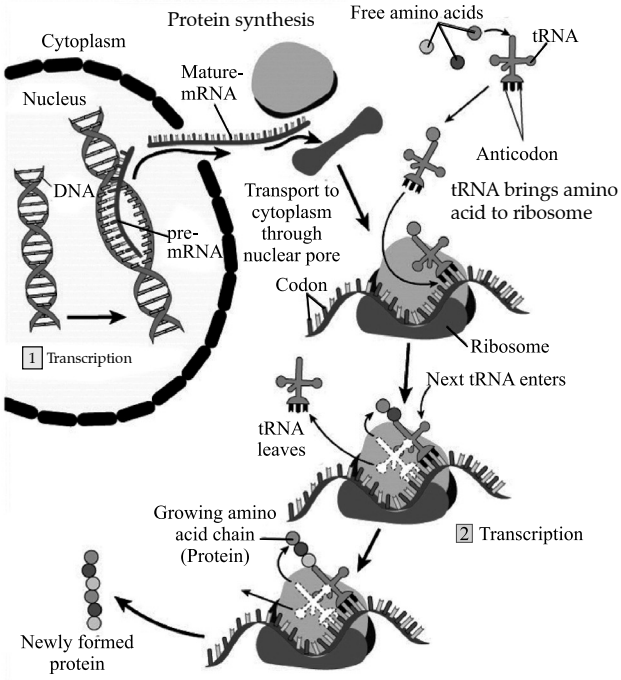
(b) For the diagnosis of genetic diseases.

(c) To determine phylogenetic status of animals.

Protein Biosynthesis

1. Transcription:

⏩ During transcription also, one of the strands of DNA acts a template to direct the synthesis of complementary RNA the details of which we have already discussed earlier.



2. Translation:

⏩ Translation takes place in ribosomes, which can be found in the cytoplasm or attached to the endoplasmic reticulum (ER) in eukaryotic cells.

⏩ Translation refers to the process of polymerisation of amino acids to form a polypeptide. The order and sequence of amino acids are defined by the sequence of bases in the mRNA.

3. Protein Folding:

⏩ Once the polypeptide chain is synthesized, it begins to fold into a three-dimensional structure.

⏩ Protein folding is driven by various chemical interactions, including hydrogen bonds, hydrophobic interactions, ionic bonds, and disulfide bridges.

⏩ Proper folding is crucial for the protein to achieve its functional conformation.

⏩ Molecular chaperones assist in protein folding and prevent misfolding.

4. Post-Translational Modifications:

⏩ Many proteins undergo post-translational modifications to acquire their final functional form.

⏩ These modifications include phosphorylation (addition of phosphate groups), glycosylation (addition of sugar groups), acetylation (addition of acetyl groups) and lipidation (addition of lipid groups), among others.

⏩ Post-translational modifications can alter a protein's stability, activity and interactions with other molecules.

5. Regulation:

⏩ Protein biosynthesis is tightly regulated at multiple levels:

• Transcriptional control regulates when and how often a gene is transcribed.

• Post-transcriptional control involves mRNA stability and processing.

• Translation control regulates the rate at which mRNA is translated into protein.

⏩ Cells can adjust protein production in response to changing environmental conditions and cellular needs.

◇◇◇

Topic 1: Previous Year's Questions

1. Unequivocal proof that DNA is the genetic material was first proposed by [NEET 2023]

(a) Alfred Hershey and Martha Chase

(b) Avery, MacLeod and McCarty

(c) Wilkins and Franklin

(d) Frederick Griffith

2. Given below are two statements:

Statement 1: In prokaryotes, the positively charged DNA is held with some negatively charged proteins in a region called nucleoid.

Statement II: In eukaryotes, the negatively charged DNA is wrapped around the positively charged histone octamer to form nucleosome.

In the light of the above statements, the correct answer from the options given below: [NEET 2023]

(a) Both the **Statements I** and **Statement II** are false.

(b) Statement I is correct but **Statement II** is false.

(c) Statement I incorrect but **Statement II** is true.

(d) Both **Statement I** and **Statement II** are true.

3 Given below are two statements:

Statement I: DNA polymerases catalyse polymerisation only in one direction, that is 5' → 3'

Statement II: During replication of DNA, on one strand the replication is continuous while on other strand it is discontinuous.

In the light of the above statements, choose the correct answer from the options given below: [NEET (Phase-II) 2022]

(a) Both Statement I and Statement II are correct

(b) Both Statement I and Statement II are incorrect

(c) Statement I is correct but Statement II is incorrect

(d) Statement I is incorrect but Statement II is correct

4. Match List-I with List-II:

List - I	List - II
(a) Bacteriophage □ × 174	**(i)** 48502 base pairs
(b) Bacteriophage lambda	**(ii)** 5386 nucleotides
(c) *Escherichia coli*	**(iii)** 3.3 × 109 base pairs
(d) Haploid content of human DNA	**(iv)** 4.6 × 106 base pairs

Choose the correct answer from the options given below: [NEET (Phase-II) 2022]

(a) (a) - (i), (b) - (ii), (c) - (iii), (d) - (iv)

(b) (a) - (ii), (b) - (iv), (c) - (i), (d) - (iii)

(c) (a) - (ii), (b) - (i), (c) - (iv), (d) - (iii)

(d) (a) - (i), (b) - (ii), (c) - (iv), (d) - (iii)

5. If DNA contained sulphur instead of phosphorus and proteins contained phosphorus instead of sulfur, what would have been the outcome of Hershey and Chase experiment? [NEET (Phase-II) 2022]
(a) No radioactive sulfur in bacterial cells
(b) Both radioactive sulfur and phosphorus in bacterial cells
(c) Radioactive sulfur in bacterial cells
(d) Radioactive phosphorus in bacterial cells

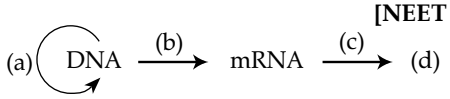
6. If A and C make 30% and 20% of DNA, respectively, what will be the percentage composition of T and G? [NEET (Phase-II) 2022]
(a) T: 20%, G: 30% **(b)** T: 30%, G: 20%
(c) T: 30%, G: 30% **(d)** T: 20%, G: 20%

7. Read the following statements and choose the set of correct statements:
(a) Euchromatin is loosely packed chromatin
(b) Heterochromatin is transcriptionally active
(c) Histone octamer is wrapped by negatively charged DNA in nucleosome.
(d) Histones are rich in lysine and arginine.
(e) A typical nucleosome contains 400 bp of DNA helix.
Choose the correct answer from the options below: [NEET (Phase-I) 2022]
(a) (b), (d), (e) Only **(b)** (a), (c), (d) Only
(c) (b), (e) Only **(d)** (a), (c), (e) Only

8. If the length of a DNA molecule is 1.1 metres, what will be the approximate number of base pairs? [NEET (Phase-I) 2022]
(a) 3.3×10^9 bp **(b)** 6.6×10^9 bp
(c) 3.3×10^6 bp **(d)** 6.6×10^6 bp

9. Ten *E. coli* cells with ^{15}N - dsDNA are incubated in medium containing ^{14}N nucleotide. After 60 minutes, how many *E. coli* cells will have DNA totally free from ^{15}N? [NEET (Phase-I) 2022]
(a) 20 cells **(b)** 40 cells
(c) 60 cells **(d)** 80 cells

10. Complete the flow chart on central dogma. [NEET 2021]



(a) (a)-Transduction; (b)-Translation; (c)-Replication; (d)-Protein
(b) (a)-Replication; (b)-Transcription; (c)-Transduction; (d)-Protein
(c) (a)-Translation; (b)-Replication; (c)-Transcription; (d)-Transduction
(d) (a)-Replication; (b)-Transcription; (c)-Translation; (d)-Protein

11. If Adenine makes 30% of the DNA molecule, what will be the percentage of Thymine, Guanine and Cytosine in it? [NEET 2021]
(a) T: 20 ; G: 25 ; C: 25 **(b)** T: 20 ; G: 30 ; C: 20
(c) T: 20 ; G: 20 ; C: 30 **(d)** T: 30 ; G: 20 ; C: 20

12. Which one of the following statements about Histones is wrong? [NEET 2021]
(a) Histones carry positive charge in the side chain.
(b) Histones are organized to form a unit of 8 molecules.
(c) The pH of histones is slightly acidic.
(d) Histones are rich in amino acids - Lysine and Arginine.

13. The term 'Nuclein' for the genetic material was used by [NEET (Phase-II) 2020]
(a) Franklin. **(b)** Meischer.
(c) Charagaff. **(d)** Mendel.

14. In the polynucleotide chain of DNA, a nitrogenous base is linked to the –OH of [NEET (Phase-II) 2020]
(a) 2'C pentose sugar. **(b)** 3'C pentose sugar.
(c) 5'C pentose sugar. **(d)** 1'C pentose sugar.

15. *E. coli* has only 4.6×10^6 base pairs and completes the process of replication within 18 minutes; then the average rate of polymerisation is approximately [NEET (Phase-II) 2020]
(a) 2000 base pairs/second
(b) 3000 base pairs/second
(c) 4000 base pairs/second
(d) 1000 base pairs/second

16. Which of the following statement is correct? [NEET (Phase-I) 2020]
(a) Adenine pairs with thymine through one H-bond.
(b) Adenine pairs with thymine through three H-bonds.
(c) Adenine does not pair with thymine.
(d) Adenine pairs with thymine through two H-bonds.

17. If the distance between two consecutive base pairs is 0.34 nm and the total number of base pairs of a DNA double helix in a typical mammalian cell is 6.6×10^6 kb, then the length of the DNA is approximately. [NEET (Phase-I) 2020]
(a) 2.5 meters **(b)** 2.2 meters
(c) 2.7 meters **(d)** 2.0 meters

18. Purines found in the DNA and RNA are [NEET 2019]
(a) adenine and guanine.
(b) guanine and cytosine.
(c) cytosine and thymine.
(d) adenine and thymine.

19. The experimental proof for semi-conservative replication of DNA was first shown in a: [NEET 2018]
(a) Plant **(b)** Bacterium
(c) Fungus **(d)** Virus

20. Which of the following RNAs should be most abundant in animal cell? [NEET 2017]
(a) *r*-RNA **(b)** *t*-RNA
(c) *m*-RNA **(d)** *mi*-RNA

21. The final proof for DNA as the genetic material came from the experiments of: [NEET 2017]
(a) Griffith
(b) Hershey and Chase
(c) Avery, Mcleod and McCarty
(d) Hargobind Khorana

22. The association of histone H1 with a nucleosome indicates: [NEET 2017]
(a) Transcription is occuring
(b) DNA replication is occuring
(c) The DNA is condensed into a chromatin fibre
(d) The DNA double helix is exposed

23. A molecule that can act as a genetic material must fulfill the traits given below, except:
[NEET (Phase-II) 2016]

(a) It should be able to generate its replica
(b) It should be unstable structurally and chemically
(c) It should provide the scope for slow changes that are required for evolution
(d) It should be able to express itself in the form of Mendelian characters

24. Taylor conducted the experiments to prove semi-conservative mode of chromosome replication on:
[NEET (Phase-II) 2016]

(a) *Vicia faba* **(b)** *Drosophila melanogaster*
(c) *E. Coli* **(d)** *Vinca rosea*

Answer Key

1.	(a)	**2.**	(c)	**3.**	(a)	**4.**	(c)	**5.**	(c)	**6.**	(b)
7.	(b)	**8.**	(a)	**9.**	(c)	**10.**	(d)	**11.**	(d)	**12.**	(c)
13.	(b)	**14.**	(d)	**15.**	(a)	**16.**	(d)	**17.**	(b)	**18.**	(a)
19.	(b)	**20.**	(a)	**21.**	(b)	**22.**	(c)	**23.**	(b)	**24.**	(a)

Answers with Explanation

1. (a) The proof that DNA is the genetic material came first time from the experiment of Alfred Hershey and Martha Chase. Avery, Macleod and McCarty gave the biochemical characterisation of the Transforming Principle. The transformation experiments using *Pneumococcus* were conducted by Frederick Griffith. Wilkins and Franklin produced X-ray diffraction data of DNA.

2. (c) In prokaryotes, the negatively charged DNA is held by some positively charged non-histone proteins in a region known as the nucleoid. In eukaryotes, nucleosome represents the structure that is formed by the negatively charged DNA wrapped around the positively charged histone octamer.

3. (a) DNA polymerase can read template DNA in only one direction i.e., 3' → 5' thus DNA replication can continue only in 5' → 3' direction, thus it can continue only on one strand of DNA. The DNA stand on which replication is continuous is called leading strand whereas the strand on which replication is discontinuous is said to be lagging strand.

4. (c)

Organism	**Genome size**
Bacteriophage □ × 174	5386 Nucleotides (SS)
Bacteriophage lambda	48502 bp
E. coli	4.6×10^6 bp
Haplid content of Human DNA	3.3×10^9 bp

5. (c) If **Sulphur and Phosphorus** change their presence in DNA and protein respectively the result of **Hershey** and **Chase** experiment will be reversed. Bacteria with radioactive sulphur formed at the base of Test Tube.

6. (b)
A → 30% = T → 30%
C → 20% = G → 20%
According to chargaff's rule, Adenine (A) pairs with Thymine (T) and Cytosine (C) pairs with Guanine (G). So, The ds DNA have equal percentage of A and T or G and C.

7. (b) Euchromatin is loosely packed and enriched in genes, hence it is responsible for the active transcription. A typical nucleosome contains about 200 base pairs (bp) of the DNA helix. Heterochromatin is highly condensed and is transcriptionally silent.

8. (a) The total length of double helix DNA = total number of base pairs × distance between two base pairs.
The length between two base pair is = 0.34 nm = 0.34×10^{-9} m
The length of given DNA molecule is = 1.1m.
1.1 = total number of base pairs × 0.34×10^{-9} m

$$\text{Total number of base pairs} = \frac{1.1}{0.34 \times 10^{-9}} = 3.23 \times 10^9$$

$3.23 \times 10^9 = \square 3.3 \times 10^9$.

9. (c) A new hybrid $^{15}N - {}^{14}N$ is formed after 20 minutes. After 40 minutes equal hybrids of high density DNA and low density DNA will be formed.
After 60 minutes, all the DNA strands will be containing ^{14}N nucleotide.

10. (d) Francis Crick proposed the Central dogma in molecular biology. It states the flow of genetic information from DNA to RNA to Protein. The transfer of information from DNA to DNA is called replication. The transfer of information from DNA to primary transcript (*m*RNA) is called transcription. It contains coding regions called exons and non-coding regions called introns. The process of synthesising a protein from *m*RNA is called translation. So, the complete flow chart of central dogma is in the order of a) Replication; b) Transcription; c) Translation; and d) Protein.

11. (d) According to Chargaff's rule, DNA consists of a 1:1 (base pair rule) ratio of pyrimidine and pyrine bases. The amount of guanine is equal to the amount of cytosine. Similarly, the amount of thymine is equal to adenine.
Number of Adenine = number of thymine
If the number of (A) is 30%, then the number of thymine would be 30%
Therefore = 100 – (A+T)
= 100 – (30 + 30)
= 100 – 60 = 40
The percentage of (C) and (G) = 40
Then (C) and (G) would be 20%.
T=30%, A=30%, G=20%, and C=20%

12. (c) Histone octamers consist of units of 8 histone molecules with a pair of each protein H_2A, H_2B, H_3, and H_4. H1 histone present outside of the octamer connects the DNA with the octomer. Histones consist of basic amino acid residues such as lysine and arginine with a side chain. They have a positive charge in the side chain. But they are not acidic.

13. (b) Nuclein was used by Friedrich Miescher to describe the nuclear material he discovered in 1869, which today is known as DNA.

14. (d) In the polynucleotide chain of DNA, a nitro-genous base is linked to the –OH of 1'C pentose sugar.

15. (a) The average rate of polymerisation of DNA in *E. coli* is 2000 bp per second. It has only 4.6×10^6 bp and completes the process of replication within 18 minutes.

16. (d) Adenine pairs with thymine through two hydrogen bonds. Cytosine pairs with guanine through three hydrogen bonds.

17. (b) Length of DNA = $[0.34 \times 10^{-9}]$m $\times 6.6 \times 10^9$ bp = 2.2 m
Distance between 2 base pair in DNA helix
= 0.34 nm
= 0.34×10^{-9} m Total number of base pair
= 6.6×10^9 bp.

18. (a) Purines (double carbon-nitrogen rings) include Adenine (A) and Guanine (G) while pyrimidines (single carbon-nitrogen ring) include Cytosine (C), Thymine (T-only in DNA) and Uracil (U-only in RNA).

19. (b) Semi-conservative DNA replication was first shown in bacterium *Escherichia coli* by Meselson and Stahl.

20. (a) *r*RNA is the most abundant in animal cell and constitutes 80% of the total RNA.

21. (b) Hershey and Chase gave the unequivocal proof that the DNA is the genetic material.

22. (c) The association of H1 protein indicates the complete formation of nucleosome because of which the DNA is condensed form.

23. (b) A molecule that can act as genetic material must fulfill certain criteria, and one of them is stability. The genetic material needs to be stable to ensure accurate transmission of genetic information from one generation to the next. Unstable molecules would lead to frequent errors and mutations, jeopardising the fidelity of genetic information transfer. Therefore, stability is a crucial trait for a molecule to function as genetic material.

24. (a) Taylor conducted treated root tip cells of Vicia faba with radioactive thymidine to label the DNA and then grew them in the normal medium to demonstrate semi- conservative mode of chromosome replication.

Topic 2: Previous Year's Questions

1. Given below are two statements: One is labelled as Assertion A and the other is labeled as Reason R:
Assertion A: The genetic code is degenerate, allowing multiple codons to code for the same amino acid.
Reason R: Degeneracy in the genetic code provides redundancy and protects against the harmful effects of mutations.
In the light of the above statements, choose the correct answer from the options given below:
(a) Both A and R are true but R is NOT the correct explanation of A.
(b) A is true but R is false.
(c) A is false but R is true.
(d) Both A and R are true and R is the correct explanation of A.

2. Given below are two statements: One is labelled as Assertion A and the other is labeled as Reason R:
Assertion A: During translation, the small subunit of the ribosome binds to the mRNA and moves along it until it finds the start codon.
Reason R: The start codon, AUG, codes for the initiation of translation and the incorporation of the first amino acid in the polypeptide chain.
In the light of the above statements, choose the correct answer from the options given below:
(a) Both A and R are true but R is NOT the correct explanation of A.
(b) A is true but R is false.
(c) A is false but R is true.
(d) Both A and R are true and R is the correct explanation of A.

3. Given below are two statements: One is labelled as Assertion A and the other is labeled as Reason R:
Assertion A: The release factor plays a crucial role in terminating translation.
Reason R: The release factor recognises the stop codon on the mRNA and causes the release of the polypeptide chain from the ribosome, concluding the translation process.
(a) Both A and R are true but R is NOT the correct explanation of A.
(b) A is true but R is false.
(c) A is false but R is true.
(d) Both A and R are true and R is the correct explanation of A.

4. What is the role of RNA polymerase III in the process of transcription in eukaryotes? [NEET 2023]
(a) Transcription of tRNA, 5 srRNA and snRNA
(b) Transcription of precursor of mRNA
(c) Transcription of only snRNAs
(d) Transcription of rRNAs (28S, 18S, and 5.8S)

5. Expressed Sequence Tags (ESTs) refers to [NEET 2023]
(a) All genes that are expressed as proteins.
(b) All genes whether expressed or unexpressed.
(c) Certain important expressed genes.
(d) All genes that are expressed as RNA.

6. Match List I with List II.

List I		List II	
A.	Gene '*a*'	I.	β-galactosidase
B.	Gene '*y*'	II.	Transacetylase
C.	Gene '*i*'	III.	Permease
D.	Gene '*z*'	IV.	Repressor protein

Choose the correct answer from the options given below: [NEET 2023]
(a) A-II, B-III, C-IV, D-I **(b)** A-III, B-IV, C-I, D-II
(c) A-III, B-I, C-IV, D-II **(d)** A-II, B-I, C-IV, D-III

7. Which one of the following is the sequence on corresponding coding strand, if the sequence on *mRNA* formed follows
***5′AUCGAUCGAUCGAUCGAUGG AUcg AUCG* 3′? [NEET 2023]**
(a) 3′ UAGCUAGCUAGCUAGCUA GCUAGCUAGC 5′
(b) 5′ ATCGATCGATCGATCGATCG ATCGATCG 3′
(c) 3′ ATCGATCGATCGATCGATG ATCGATCG 5′
(d) 5′ UAGCUAGCUAGCUAGCUA GCUAGC UAGC 3′

8. Against the codon 5' UAC 3', what would be the sequence of anticodon on tRNA? [NEET (Phase-II) 2022]
(a) 5' AUG 3' **(b)** 5' ATG 3'
(c) 5' GTA 3' **(d)** 5' GUA 3'

9. DNA polymorphism forms the basis of: **[NEET (Phase-I) 2022]**
(a) Genetic mapping
(b) DNA fingerprinting
(c) Both genetic mapping and DNA finger- printing
(d) Translation

10. The process of translation of mRNA to proteins begins as soon as: **[NEET (Phase-I) 2022]**
(a) The small subunit of ribosome encounters mRNA
(b) The larger subunit of ribosome encounters mRNA
(c) Both the subunits join together to bind with mRNA
(d) The tRNA is activated and the larger subunit of ribosome encounters mRNA

11. If a geneticist uses the blind approach for sequencing the whole genome of an organism, followed by assignment of function to different segments, the methodology adopted by him is called as: **[NEET (Phase-I) 2022]**
(a) Sequence annotation
(b) Gene mapping
(c) Expressed sequence tags
(d) Bioinformatics

12. In an *E. coli* strain *i* gene gets mutated and its product cannot bind the inducer molecule. If growth medium is provided with lactose, what will be the outcome? **[NEET (Phase-I) 2022]**
(a) Only *z* gene will get transcribed
(b) *z*, *y*, *a* genes will be transcribed
(c) *z*, *y*, *a* genes will not be translated
(d) RNA polymerase will bind the promoter region

13. Statement I: The codon 'AUG' codes for methionine and phenylalanine.
Statement II: 'AAA' and 'AAG' both codons code for the amino acid lysine.
In the light of the above statements, choose the correct answer from the options given below. **[NEET 2021]**
(a) Statement I is incorrect but Statement II is true.
(b) Both Statement I and Statement II are true.
(c) Both Statement I and Statement II are false.
(d) Statement I is correct but Statement II is false.

14. Identify the correct statement. **[NEET 2021]**
(a) Split gene arrangement is characteristic of prokaryotes.
(b) In capping, methyl guanosine triphosphate is added to the 3' end of hnRNA.
(c) RNA polymerase binds with Rho factor to terminate the process of transcription in bacteria.
(d) The coding strand in a transcription unit is copied to an mRNA.

15. What is the role of RNA polymerase III in the process of transcription in eukaryotes? **[NEET 2021]**
(a) Transcribes only snRNAs
(b) Transcribes rRNAs (28S, 18S and 5.8S)
(c) Transcribes tRNA, 5s rRNA and snRNA
(d) Transcribes precursor of mRNA

16. DNA fingerprinting involves identifying differences in some specific regions in DNA sequence, called as **[NEET 2021]**
(a) Polymorphic DNA. **(b)** Satellite DNA.
(c) Repetitive DNA. **(d)** Single nucleotides.

17. Which is the "Only enzyme" that has "Capability" to catalyse Initiation, Elongation and Termination in the process of transcription in prokaryotes? **[NEET 2021]**
(a) DNase
(b) DNA dependent DNA polymerase
(c) DNA dependent RNA polymerase
(d) DNA Ligase

18. Which is the basis of genetic mapping of human genome as well as DNA finger printing? **[NEET 2020 (Phase-II)]**
(a) Polymorphism in DNA sequence
(b) Single nucleotide polymorphism
(c) Polymorphism in hnRNA sequence
(d) Polymorphism in RNA sequence

19. Name the enzyme that facilitates opening of DNA helix during transcription. **[NEET 2020 (Phase-I)]**
(a) DNA helicase **(b)** DNA polymerase
(c) RNA polymerase **(d)** DNA ligase

20. The first phase of translation is **[NEET 2020 (Phase-I)]**
(a) recognition of DNA molecule.
(b) aminoacylation of tRNA.
(c) recognition of an anti-codon.
(d) binding of mRNA to ribosome

21. Under which of the following conditions will there be no change in the reading frame of following mRNA? **[NEET 2019]**
5' AACAGCGGUGCUAUU 3'
(a) Deletion of G from 5th position
(b) Insertion of A and G at 4th and 5th positions respectively
(c) Deletion of GGU from 7th, 8th and 9th positions
(d) Insertion of G at 5th position.

22. Which of the following features of genetic code does allow bacteria to produce human insulin by recombinant DNA technology? **[NEET 2019]**
(a) Genetic code is redundant
(b) Genetic code is nearly universal
(c) Genetic code is specific
(d) Genetic code is not ambiguous

23. Select the correct match: **[NEET 2018]**
(a) Mathew Meselson and F. Stahl — *Pisum sativum*
(b) Alfred Hershey and Martha Chase — TMV
(c) Alec Jeffreys — *Streptococcus pneumoniae*
(d) Francois Jacob and Jacques Monod — *Lac* Operon

24. All of the following are part of an operon except: **[NEET 2018]**
(a) enhancer **(b)** structural genes
(c) an operator **(d)** a promoter

25. AGGTATCGCAT is sequence from the coding strand of a gene. What will be the corresponding sequence of the transcribed *m*RNA? **[NEET 2018]**
(a) ACCUAUGCCU **(b)** UGTUTCGCAT
(c) AGGUAUCGCAU **(d)** UCCAUAGCGUA

26. Spliceosomes are not found in cells of: **[NEET 2017]**
(a) Plants **(b)** Fungi
(c) Animals **(d)** Bacteria

27. If there are 999 bases in an RNA that codes for a protein with 33 amino acids, and the base at position 901 is deleted such that the length of the RNA becomes 998 bases, how many codons will be altered? [NEET 2017]
(a) 1 **(b)** 11
(c) 33 **(d)** 333

28. During DNA replication, Okazaki fragments are used to elongate: [NEET 2017]
(a) The leading strand towards replication fork
(b) The lagging strand towards replicaton fork
(c) The leading strand away from replication fork
(d) The lagging strand away from the replication fork

29. DNA dependent RNA polymerase catalyses transcription on one strand of DNA which is called the [NEET (Phase-II) 2016]
(a) Antistrand **(b)** Template strand
(c) Coding strand **(d)** Alpha strand

30. Which of the following is not required for any of the techniques of DNA fingerprinting available at present? [NEET Phase I 2016]
(a) DNA – DNA hybridization
(b) Polymerase chain reaction
(c) Zinc finger analysis
(d) Restriction enzymes

31. Satellite DNA is important because it: [RE AIPMT 2015]
(a) Codes for enzymes needed for DNA replication
(b) Codes for proteins needed in cell cycle.
(c) Shows high degree of polymorphism in population and also the same degree of polymorphism in an individual which is heritable from parents to children.
(d) Does not code for proteins and is same in all members of the population.

Answer Key

1.	(d)	**2.**	(d)	**3.**	(a)	**4.**	(a)	**5.**	(d)	**6.**	(a)
7.	(b)	**8.**	(d)	**9.**	(c)	**10.**	(a)	**11.**	(a)	**12.**	(c)
13.	(a)	**14.**	(c)	**15.**	(c)	**16.**	(c)	**17.**	(c)	**18.**	(a)
19.	(c)	**20.**	(b)	**21.**	(c)	**22.**	(b)	**23.**	(d)	**24.**	(a)
25.	(c)	**26.**	(d)	**27.**	(c)	**28.**	(d)	**29.**	(b)	**30.**	(c)
31.	(c)										

Answers with Explanation

1. (d) The genetic code is indeed degenerate, meaning that multiple codons can code for the same amino acid. This degeneracy provides redundancy, which is advantageous in protecting against the harmful effects of mutations. Even if there is a mutation in a codon, it might still code for the same amino acid, maintaining the integrity of the protein.

2. (d) The small subunit of the ribosome indeed binds to the mRNA and moves along it until it encounters the start codon, AUG. This start codon initiates translation, and the ribosome begins the process of synthesizing the polypeptide chain, incorporating the first amino acid.

3. (a) The release factor does play a crucial role in terminating translation by recognizing the stop codon on the mRNA. However, the reason provided correctly explains this role, as the release factors recognition of the stop codon leads to the release of the polypeptide chain from the ribosome, concluding translation.

4. (a) In eukaryotes, there are three major types of RNA polymerases.
RNA polymerase I help in the transcription of 5.8S, 18S, and 28S rRNAs.
RNA polymerase II helps in the transcription of hnRNAs (precursor of mRNA).
RNA polymerase III helps in the transcription of tRNAs, ScRNA, 5S rRNA and snRNA.

5. (d) All the genes that are expressed as RNA are known as Expressed Sequence Tags (ESTs).

6. (a) In a *lac* operon,
Gene *a* codes for enzyme transacetylase.
Gene *y* codes for enzyme permease.
Gene *i* codes for a repressor protein
Gene *z* codes for enzyme beta-galactosidase.

7. (b) The sequence of the coding strand is the same as transcribed mRNA except for thymine at the place of uracil.
Template strand → 3′-TAGCTAGCTAGCTAGCTAGCT AGCTAGC-5′
Coding strand → 5′-ATCGATCGATCGATCGATCGAT CGATCG-3′
mRNA → 5′ AUCGAUCGAUCGAUCGAUCGAUCGA UCG 3′

8. (d) 5' UAC 3' code on mRNA can be complemented by 5' GUA 3' on anticodon loop of tRNA.
Codon anticodon pairing between mRNA and rRNA is the key of translation process.

9. (c) Polymorphism is the presence of two or more variant forms of a specific DNA sequence occuring in different individuals or populations. It forms the basis of both genetic mapping and DNA fingerprinting.

10. (a) As soon as the small sub-unit of ribosome encounters mRNA, the process of translation (mRNA to proteins) begins.

11. (a) Sequence annotation is the process of identifying the boundaries between genes and other features in a DNA sequence. This methodology is adopted by the geneticist for sequencing the whole genome of an organism.

12. (c) If the *i* gene of *E. coli* strain get mutated and its product can not bind the inducer molecule or lactose, then *i* gene will code for repressor, and due to mutation *z*, *y*, a gene will not be translated.

13. (a) The code which has at least three letters is called the triplet code. There are about 64 codons to code for 20 amino acids. Among them, AUG has an initiator dual function. It codes for Methionine and also acts as an initiator codon. The codon 'AAA' and 'AAG' code for amino acid lysine. So, statement I is incorrect, but statement II is correct.

14. (c) The process of copying genetic information from one strand of the DNA into RNA is called transcription. It is carried out by the transcription unit.

The transcription unit has three regions in DNA called a promoter, structural gene, and terminator. RNA polymerase can catalyze the process of elongation in transcription. But the initiation and termination depend on the initiation factor and termination factor. The termination factor can also be called the Rho factor. When RNA polymerase binds to the Rho factor, the process of transcription is terminated in bacteria.

15.(c) There are three types of RNA polymerases in the nucleus. They are RNA polymerase I, II, and III. RNA polymerase I transcribe rRNA. RNA polymerase II transcribes the precursor of mRNA, which PSII, while in the stroma lamellae membrane, is also called heterogeneous nuclear RNA. RNA polymerase III transcribes tRNA, 5S rRNA, and small nuclear RNAs.

16.(c) DNA fingerprinting can identify the differences in certain specific regions of DNA sequences called repetitive DNA. These small stretches of DNA are repeated several times to form a bulk peak of DNA called satellite DNA. Based on the composition of the base, length of a segment, and the number of repetitive units, the satellite DNA is of several types like micro-satellite and mini-satellite, etc.

17.(c) The single DNA-dependent RNA polymerase can catalyze the transcription of all varieties of RNA in bacteria. It is also called a holoenzyme made up of several polypeptides. These all together can catalyze the process of initiation, elongation, and termination in the process of transcription.

18.(a) Polymorphism in DNA sequence is the basis of genetic mapping of human genome as well as DNA finger printing.

19.(c) DNA helix is opened during transcription by RNA polymerase.

20.(b) The first phase of translation involves activation of amino acid in the presence of ATP and linked to their cognate tRNA-a process commonly called as charging of tRNA or aminoacylation of tRNA.

21.(c) In case of deletion of GGU from 7th, 8th and 9th position, there will be no change in the reading frame of mRNA.

22.(b) In recombinant DNA technology, a bacterium can produce human insulin because genetic code is nearly universal.

23.(d) Francois Jacob and Jacques Monod proposed the model of gene regulation known as lac operon.

24.(a) Operon concept is for prokaryotes and enchancer sequences are present in eukaryotes.

25.(c) Coding strand and *m*RNA has same nucleotide sequence except, 'T'-Thymine is replaced by 'U'-Uracil in *m*RNA.

26.(d) Spliceosomes are found in cells of eukaryotes only as split genes are absent in prokaryotes. They are used in removal of introns during post-transcriptional processing of *hn*RNA.

27.(c) If deletion takes place at 901^{st} position the remaining 98 bases specifying for 33 codons of amino acids will be altered.

28.(d) Each Okazaki fragment is synthesised by DNA Polymerase at lagging strand in 5′ $\longrightarrow$ 3′ direction. New Okazaki fragments appear in the replication fork opens further. As the first Okazaki fragment appears away from the replication fork, the direction of elongation would be away from replication fork.

29.(b) DNA-dependent RNA polymerase catalyzes transcription on one strand of DNA, which is called the Template strand.

30.(c) The sensitivity of the DNA fingerprinting technique has been increased by use of polymerase chain reaction. The DNA fingerprinting technique involves Southern blot hybridisation using radiolabelled VNTR as a probe. The digestion of DNA by restriction endonucleases.

31.(c) Satellite DNAs in eukaryotes has long repetitive sequences. They do not code for any protein but exhibit polymorphism on which DNA finger printing is based.

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