Chapter

28 Molecular Basis of Inheritance

Nucleic acids (DNA and RNA) are the building blocks of genetic material. DNA is the genetic material in most of the organisms. DNA stands for deoxyribonucleic acid. RNA is the genetic material in some viruses. RNA stands for ribonucleic acid. It mostly functions as **messengers.**

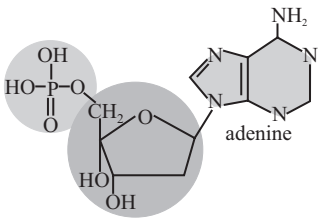
POLYNUCLEOTIDE CHAIN

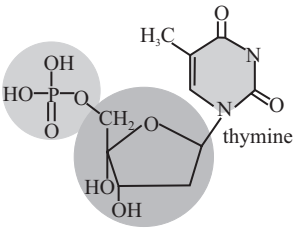
- They are polymers, composed of monomers called nucleotides.
- *A nucleotide has three components:*

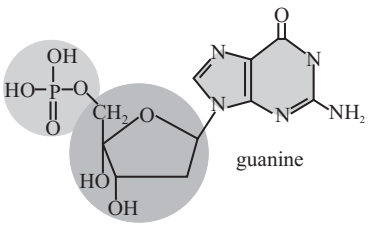
(i) A nitrogenous base

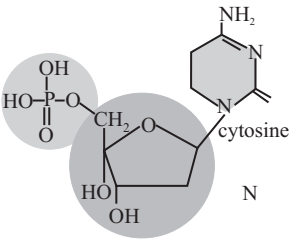
➢ **Purines** (double carbon-nitrogen rings):It includes Adenine (A) and Guanine (G).

➢ **Pyrimidines** (single carbon-nitrogen ring):It includes Cytosine (C), Thymine (T-only in DNA) and Uracil (U-only in RNA).

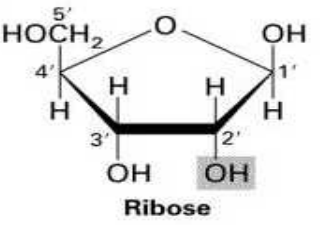


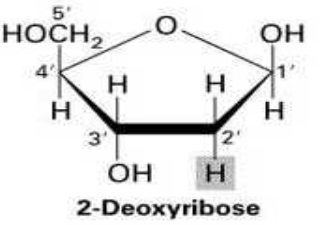






(ii) A pentose sugar: Ribose in RNA and deoxyribose in DNA.





➢ A nitrogen base is attached to the pentose sugar at C1 of pentose sugar by N-glycosidic linkage to form nucleoside.

Nitrogenous base + pentose sugar = nucleoside

According to the nature of pentose sugar, two types of nucleosides are formed ***ribonucleoside*** *and* ***deoxyribonucleotides.***

Ribonucleosides	Deoxyribonucleosides
• Adenosine	• Deoxyadenosine
• Guanosine	• Deoxyguanosine
• Cytidine	• Deoxycytidine
• Uridine	• Deoxythymidine.

(iii) Phosphate group : Phosphate group is linked to 5′-OH of a nucleoside through phosphodiester linkage to form nucleotide. (Ribonucleotide or deoxyribonucleotides depending on the sugar unit).

Nucleoside + Phosphate group = Nucleotide.

or **Nitrogen base + sugar + phosphate group = Nucleotide**

NUCLEOTIDE POLYMERISATION

- Nucleotides can join together by a condensation reaction (results in the removal of water) between the phosphate group of one nucleotide and the hydroxyl group on carbon 3 of the sugar of the other nucleotide. The bonds linking the nucleotides together are strong, covalent phosphodiester bonds. Many nucleotides form a polynucleotide.

- *Each polynucleotide chain has two distinct ends:*

(i) a 3′ end → carbon 3 of the deoxyribose is closest to the end

(ii) a 5′ end → carbon 5 of the deoxyribose is closest to the end

- Two nucleotides are joined by **3′-5′ phosphodiester linkage** to form dinucleotide.
- More than two nucleotides joined to form polynucleotide chain.

ERWIN CHARGAFF'S RULE

- Chargaff analyzed the base composition of DNA from a number of different organisms.
- He found that:
  - ➢ The base composition of DNA varies from one species to another.
  - ➢ Also he noted regularity in the ratios of nucleotide bases within a single species. This means,
    - ♦ Number of adenines approximately equalled the number of thymines.
    - ♦ Number of guanines approximately equalled the number of cytosines.
- This observation led to the formation of Chargaff's rule.
- It states that in any species, DNA molecule should have an equal ratio of pyrimidine (cytosine and thymine) and purine (adenine and guanine) *i.e.* the number of adenine molecules is equal to thymine molecules and the number of guanine molecules is equal to cytosine molecules.
- [A] + [G] = [T] + [C].

HISTORY OF DNA

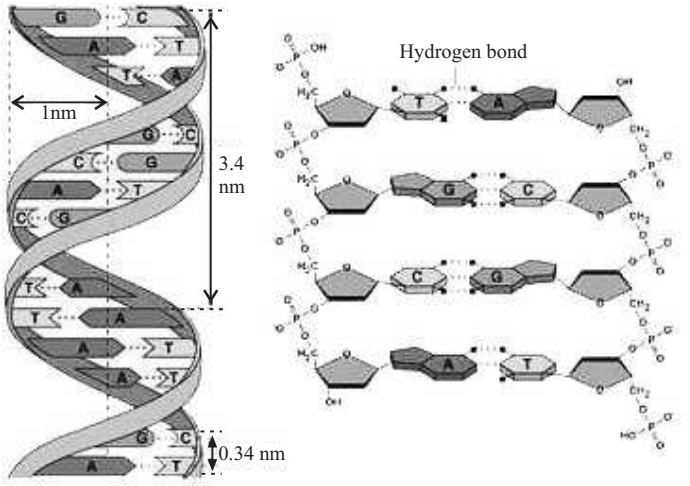
- DNA in the nucleus was first identified by Friedrich Meischer in 1869. He named it as 'Nuclein'.
- 1953, double helix structure of DNA was given by James Watson and Francis Crick, based on X-ray defraction data produced by Maurice Wilkins and Rosalind Franklin.
- Hallmark of their proposition was base pairing between two strands of polynucleotide chains. This was based on observation of Erwin Chargaff.
- Chargaff's observation was that for a double stranded DNA, the ratio between Adenine and Thymine, and Guanine and Cytosine are constant and equal one.

Important Information

- The Length of DNA is based on the number of nucleotides present in it. A pair of nucleotides is referred to as base pairs.
- 174 (a bacteriophage) has 5386 nucleotides.
- Bacteriophage lambda has 48502 base pairs (bp).
- *E. coli* has 4.6×10^6 bp.
- Haploid content of human DNA is 3.3×10^9 bp.

SALIENT FEATURES OF DOUBLE HELIX STRUCTURE OF DNA

- DNA is double-stranded, so there are two polynucleotide stands along side each other.
- The strands are antiparallel, *i.e.* they run in opposite directions (5′ → 3′ and 3′→5′)
- The two strands are wound round each other to form a double helix.
- The two strands are joined together by hydrogen bonds between the bases. The bases therefore form base pairs, which are like rungs of a ladder.
- H-bond confers stability of the helical structure of the DNA.
- Adenine of one strand pairs with thymine of another strand by two hydrogen bonds and vice-versa.
- Guanine of one strand pairs with cytosine of another strand by three hydrogen bonds and vice-versa.
- A=T (2 hydrogen bonds) C≡G (3 hydrogen bonds)
- The base pairs are specific. Purine comes opposite to a pyrimidine. This generates uniform distance between the 2 strands.
- Hence, A only binds to T (and T with A), and C only binds to G (and G with C). These are called complementary base pairs. This means that whatever the sequence of bases along one strand, the sequence of bases on the other strand must be complementary to it.
- The two chains are coiled in a right handed fashion.
- The pitch of the helix is 3.4 nm (34 Å) with 10 bp in each turn.
- Distance between adjacent base pairs is 0.34 nm (3.4 Å).



(a) (b)

Fig. (a) Double helical DNA strand.
(b) Arrangemnet of various constituents of DNA duplex.

Length of DNA = Number of base pairs × distance between two adjacent base pairs.
Number of base pairs in human = 6.6×10^9
Hence, the length of DNA = $6.6 \times 10^9 \times 0.34 \times 10^{-9}$
= 2.2 m
In *E. coli*, length of DNA = 1.36 mm = 1.36×10^{-3} m.
∴ The number of base pairs = 4×10^6bp

PACKAGING OF DNA HELIX

- **In prokaryotes** (*E.g. E. coli*)
  - ➢ The DNA is not scattered throughout the cell. DNA, being negatively charged, is held with some positively charged proteins and form 'nucleoid'.
- **In eukaryotes**
  - ➢ There is a set of positively charged, basic proteins called histones. Histones are rich in positively charged basic amino acid residues like lysines and arginines.
  - ➢ Histones are organised to form a unit of eight molecules called histone octamer.
- Negatively charged DNA is wrapped around histone octamer to form a structure callednucleosome.

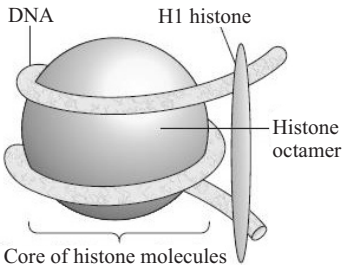


Fig. Nucleosome

- A typical nucleosome contains 200 bp of DNA helix.
- Therefore, the total number of nucleosomes in human $= \frac{6.6\times10^9 \text{bp}}{200} = 3.3\times10^7$
- Nucleosomes constitute the repeating unit of a structure in nucleus calledchromatin. Chromatin is the thread-like stained bodies.
- The nucleosomes are seen as **'beads-on-string'** structure when viewed under electron microscope.
- The beads on string structure in chromatin are packaged to form **chromatin fibres** that are further coiled and condensed at metaphase stage to form **chromosome.**
- The packaging of chromatin at higher level requires additional set of proteins called non-histone chromosomal (NHC) proteins.
- *Chromatin includes:*
  - ➢ **Euchromatin:** The region of chromatin, which is loosely packed and transcriptionally active. It stains light.
  - ➢ **Heterochromatin:** Heterochromatins are chromatin that is densely packed and transcriptionally inactive. It stains dark.

THE SEARCH FOR GENETIC MATERIAL

Griffith's Experiment (Transforming Principle)

- Griffith used mice and *Streptococcus pneumoniae*.
- *Streptococcus pneumoniae* has two strains:
  - ➢ **Smooth (S) strain (Virulent):** It has polysaccharide mucus coat and can cause pneumonia.They are pathogenic because they have a capsule that protects them from an animal's defense system
  - ➢ **Rough (R) strain (Non-virulent):** It has no mucous coat and are therefore non-pathogenic.
- To test for the trait of pathogenicity, Griffith injected mice with mixes of the two strains
  - ➢ S-strain → Inject into mice → Mice die
  - ➢ R-strain → Inject into mice → Mice live
  - ➢ S-strain (Heat killed) → Inject into mice → Mice live
  - ➢ S-strain (Heat killed) + R-strain (live) → Inject into mice → Mice die
- He concluded that some 'transforming principle', transferred from heat-killed S-strain to R-strain. It enabled R-strain to synthesize smooth polysaccharide coat and become virulent. This must be due to the transfer of some genetic material.
- However the biochemical nature of genetic material was not defined from his experiment.

Biochemical Characterization of Transforming Principle

- It was discovered by Oswald Avery, Colin MacLeod and Maclyn McCarty.
- They worked to determine the biochemical nature of 'transforming principle' in Griffith's experiment.
- They purified biochemicals (proteins, DNA, RNA etc.) from the heat killed S cells to see which ones could transform live R cells into S cells.
- They discovered that
  - ➢ DNA alone is transformed.
  - ➢ Proteases and RNases did not affect transformation.
  - ➢ Digestion with DNase inhibited transformation, suggesting that the DNA caused the transformation.
- They concluded that DNA is the hereditary material, but not all biologists were convinced.

The Hershey-Chase Experiment (Blender Experiment)

- In 1952, Alfred Hershey and Martha Chase performed experiment on bacteriophage (viruses that infect bacteria) and *E.coli* showing that DNA is the genetic material.
- They used different radioactive isotope to label DNA and protein coat of the bacteriophage.
- They grew some bacteriophage on a medium containing radioactive phosphorous P^{32} to identify DNA and some on medium containing radioactive sulphur S^{35} to identify protein.

- Then these radioactive labelled phages were allowed to infect E.coli bacteria. After infecting, the protein coat of the bacteriophage was separated from bacterial cell by blending and then subjected to the process of centrifugation.
- Since, the protein coat was lighter, it was found in the supernatant while the infected bacteria got settled at the bottom of the centrifuge tube. Hence, it was proved that DNA is the genetic material as it was transferred from virus to bacteria.

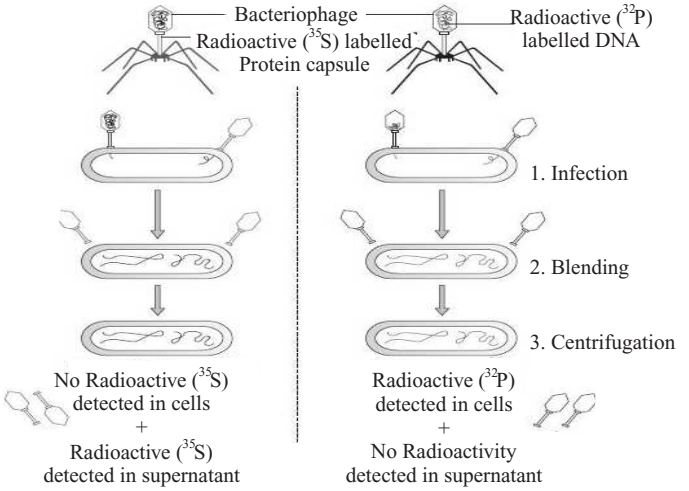


Fig. The Hershey-chase experiment

PROPERTIES OF GENETIC MATERIAL

- A genetic material should
  - ➢ Be able to generate its replica (Replication).
  - ➢ Be chemically and structurally stable.
  - ➢ Provide the scope for slow changes (mutations) that are required for evolution.
  - ➢ Be able to express itself as 'Mendelian Characters'.
- DNA is a better genetic material. It is because it is more stable than RNA.

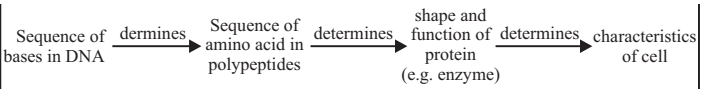
Reasons for stability (Less reactivity) of DNA	Reasons for mutability (High reactivity) of RNA
DNA is double stranded	RNA is single stranded
Presence of thymine in DNA	Presence of uracil in RNA
Absence of 2′- OH	Presence of 2′- OH, which is a highly reactive group, makes RNA labile and easily degradable.

Better Genetic Material : DNA or RNA?

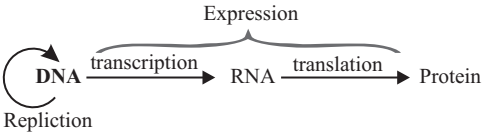
- Both DNA and RNA are able to mutate. In fact RNA being unstable mutatesand evolves at a faster rate.
- RNA can directly code for the protein synthesis, hence can easily express the characters. DNA, however, is dependent on RNA for protein synthesis.
- Both RNA and DNA can functions as genetic material, but DNA being more stable is preferred for storage of genetic information. For the transmission of genetic information RNA is better.

Function of DNA

- DNA is the genetic material, and genes are made of DNA. DNA therefore has two essential functions: replication and expression.
  - ➢ Replication means that the DNA, with all its genes, must be copied every time a cell divides.
  - ➢ Expression means that the genes on DNA must control characteristics. A gene was traditionally defined as a factor that controls a particular characteristic (such as flower colour), but a much more precise definition is that a gene is a section of DNA that codes for a particular protein. Characteristics are controlled by genes through the proteins they code for, like this:



  - ➢ Expression can be split into two parts:
    - ♦ Transcription (making RNA)
    - ♦ Translation (making proteins).
  - ➢ These two functions are summarised in this diagram (called the central dogma of genetics).



RNA WORLD

- RNA was the first genetic material.
- Essential life processes like metabolism, translation, splicing, etc. evolved around RNA.
- It acts as genetic material and catalyst. RNA being catalyst was reactive and hence unstable. Hence DNA has evolved from RNA with chemical modifications that make it more stable.
- DNA being double stranded and having complementary strand further resists changes by evolving a process of repair.

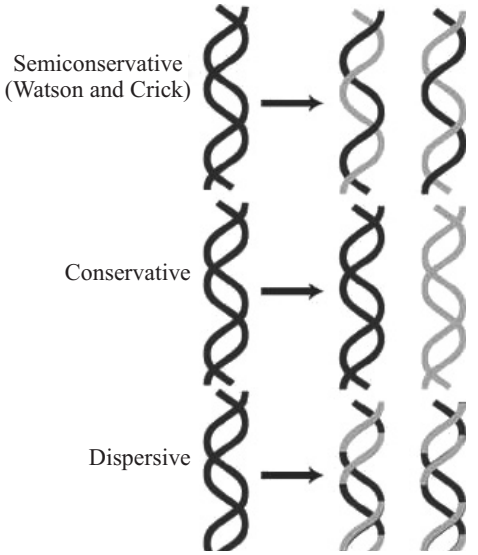
MECHANISM OF DNA REPLICATION

- Replication is the copying of DNA from parental DNA strand.
- Watson and Crick observed that the two strands of DNA are anti-parallel and complementary to each other with respect to base sequences.
- This type of arrangement of DNA molecule led to the hypothesis that DNA replication is semi-conservative. It means that the double stranded DNA molecules separates and then, each of the separated strand acts as a template for the synthesis of a new complementary strand. As a result, each DNA molecule would have one parental strand and a newly synthesized daughter strand.
- Meselson and Stahl experimentally proved it.

Competing Models Included

(i) **Conservative model:** The 2 parental strands re-associate after acting as templates for new strands, thus restoring the parental double helix

(ii) **Dispersive model:** Each strand of both daughter molecules contains a mixture of old and newly synthesized DNA.



Messelson and Stahl's Experiment

- They used the bacterium *E. coli* together with the technique of density gradient centrifugation, which separates molecules on the basis of their density.
- They cultured *E.coli* in a medium containing N salts labeled with ^{14}N (a lighter isotope of nitrogen). ^{14}N was incorporated in both strands of DNA and became lighter.
- Then they cultured *E.coli* in a medium containing $^{15}NH_4Cl$ for many generations. (^{15}N is the heavy isotope of Nitrogen).
- **Result:** ^{15}N was also incorporated into both strands of bacterial DNA and the DNA became heavier.
- The two types of DNA can be separated by centrifugation in a CsCl density gradient.
- Then, they took *E.coli* cells from ^{15}N medium and transferred to ^{14}N medium.
- After one generation, they isolated and centrifuged the DNA. Its density was intermediate between ^{15}N DNA and ^{14}N DNA. This shows that the newly formed DNA one strand is old (^{15}N type) and one strand is new (^{14}N type). This confirms semi-conservative replication.

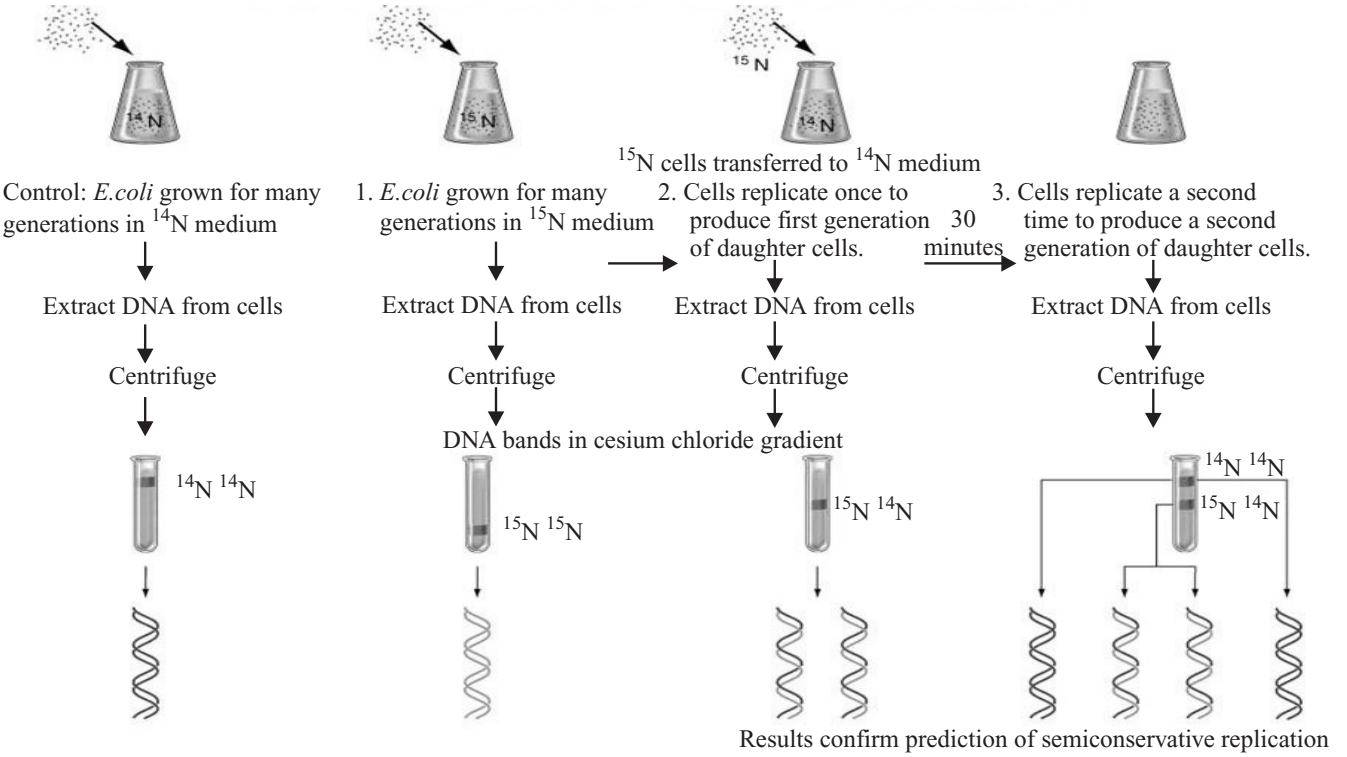


Fig. Meselson and Stahl's experiment

The Machinery and Enzymes for Replication

- The process of DNA replication begins at a point called the **origin of replication (ori)**.
- A unit of replication with one origin is called a **replicon.**
  - ➢ *E.coli* chromosome is circular with a single origin of replication.
  - ➢ A eukaryotic chromosome may have 100s-1000s of origins of replication. It helps to speed up DNA replication of very long DNA molecules.
- An enzyme called **helicase** unwinds the DNA double helix and separates it into two strands.
- A Y-shaped replication forkwill form as the double unwinds.
- As the parental strand separates, single-stranded DNA binding proteins help keep the strands separate and prevent the strands from getting back together.
- The untwisting of the double helix causes tighter twisting and strain ahead of the replication fork.
- **Topoisomerase** corrects this "over winding" ahead of replication forks by breaking, swivelling, and re-joining DNA strands.
- The separated strands act as templates for the synthesis of new strands.
- DNA replicates in the 5′→3′ direction.
- Deoxyribonucleoside triphosphates(dATP, dGTP, dCTP & TTP) act as substrate and also provide energy for polymerization.
- DNA polymerase is an enzyme that assembles a new DNA strand that is complementary to the template strand.
- A primer, which is a short single strand of RNA, is needed in order for the DNA replication to start. Primers are synthesized by primase.
- Primers bind to the origin of replication and initiate the synthesis of new strands.
- Then the DNA polymerase begins adding nucleotides to the 3′ end of the primer.
- DNA polymerase can only add a nucleotide to the 3' end.
- DNA polymerase continues to move along the template strand and add new nucleotides to the growing or complement strand until the entire genome is replicated.
- Remember, replication occurs in both directions because the two DNA strands are anti-parallel.
- The DNA polymerase forms one new strand (leading strand) in a continuous stretch in the 5′→3′ direction (Continuous synthesis).
- The other new strand is formed in small stretches (Okazaki fragments) in 5′→3′ direction (Discontinuous synthesis).
- The Okazaki fragments are then joined together to form a new strand by an enzyme, DNA ligase. This new strand is called lagging strand.
- If a wrong base is introduced in the new strand, DNA polymerase can do proof reading.
- *E.coli* completes replication within 38 minutes. *i.e.* 2000 bp per second.
- In eukaryotes, the replication of DNA takes place at S-phase of the cell cycle. Failure in cell division after DNA replication results in polyploidy.

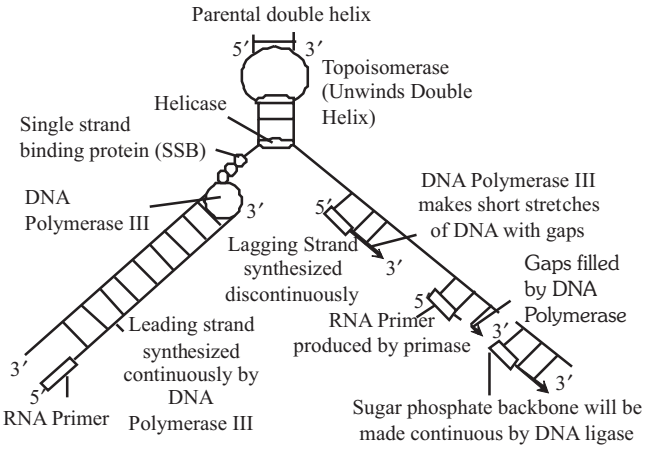


Fig. Continuous replication of a daughter DNA strand on leading strand and discontinuous replication of lagging strand

Table: Bacterial DNA replication Proteins and their functions

Proteins/Enzymes	Functions
Helicase	Unwinds parental double stand at replication forks.
Single stranded binding proteins	Binds to and stabilizes single stranded DNA until it can be used as a template.
Topoisomerases	Relieves "over-winding"strain ahead of replication forks by breaking, swivelling and rejoicing DNA strands
Primase	Synthesizes an RNA primer at 5'end of leading strand and of each Okazaki fragment of lagging strand.
DNA polymerase III	It synthesises new DNA strand by covalently adding nucleotide to the 3' end of pre-existing DNA strand or RNA primer.
DNA polymerase I	Removes RNA nucleotides of primer from 5'end and replaces them with DNA nucleotides
DNA ligase	It joins the okazaki fragments of lagging strand.

- There are two different types of nucleic acid polymerases:
  - **(i) DNA dependent DNA polymerases:** It uses a DNA template for synthesizing a new strand of DNA.
  - **(ii) DNA dependent RNA polymerases:** It used DNA template strand for synthesizing RNA.

CENTRAL DOGMA OF MOLECULAR BIOLOGY

Transcription

- It is the process of synthesis of RNA from DNA template. A segment of DNA gets copied into mRNA during this process.
- Here, adenine pairs with uracil instead of thymine.

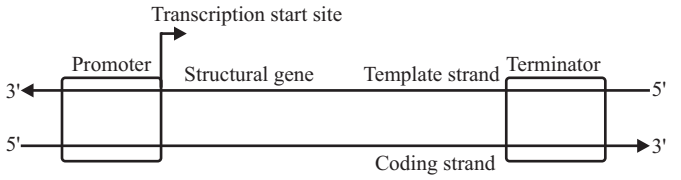
- *Both strands are not copied during transcription, because*
  - ➢ If both strand of DNA acts as template, they would be translated into two RNA of different sequences and in turn if they code for proteins, the sequence of amino acids in the protein would be different. Hence one segment of DNA would be coding for two different proteins.
  - ➢ The two RNA molecules, if produced simultaneously, would be complementary to each other, hence will form double stranded RNA. This would prevent RNA translation into protein.

Transcription vs. replication

- Principle of complementarity governs the process of transcription except adenosine of DNA forms base pair with the uracil instead of thymine. During replication adenine pairs with thymine instead of uracil.
- During replication once started the whole DNA is duplicated, whereas transcription takes place only a segment of DNA.
- In replication both strand acts as template, whereas in transcription only one strand is acts as template to synthesize RNA.
- In replication DNA copied from a DNA, whereas in transcription RNA copied from the DNA.

Transcription unit

- The process of transcription starts from at the promoter region of the template and terminates at the terminator regions. The region of DNA between these two regions is known as transcription unit. It consists of three regions:
  - **(i) A promoter (Transcription start site):** It is the binding site for RNA polymerase.
  - **(ii) The structural gene:** It is the region between promoter and terminator where transcription takes place.
  - **(iii) A terminator:** It is the end of the process of transcription.



(i) *Promoter*

- The promoter is located towards 5′ end (upstream) of the structural gene.
- It is a short sequence of DNA that provides binding site for RNA polymerase. (mostly TATA , Commonly called TATA box)
- The presence of promoter defines the template and coding strands.

(ii) *Structural gene*

- Structural gene is the region between promoter and terminator, where transcription takes place.
- The DNA strand having polarity 3′→5′ is called template strand for transcription.
- The other strand of DNA having polarity 5′→3′ is called coding strand.
- The sequences of nitrogen base in the RNA transcribed from the template strand are same as the coding strand of DNA except having thymine in place of uracil.
- All the reference point defining a transcription unit is made with the coding strand only, not the template strand.

(iii) Terminator

- The terminator located towards 3' end (downstream) of coding strand.
- It terminates the process of transcription.
- It is also a short segment of DNA which recognizes the termination factor. (ρ-factor)
- If the position of promoter is changed with terminator the definition of coding and template strand will be reversed.
- Since the 2 strands have opposite polarity and the DNA-dependent RNA polymerasecatalyse the polymerization in only one direction, *i.e.* 5′→3′.
- 3′→5′ acts as template strand. 5′→3′ acts as coding strand.
- 3′-ATGCATGCATGCATGCATGCATGC-5′ Template strand.

5′-TACGTACGTACGTACGTACGTACG-3′ Coding strand.

Transcription unit and gene

- Gene is defined as thefunctional unit of inheritance. It is the DNA sequence coding for RNA molecule.
- Cistron is a segment of DNA coding for a polypeptide.
- Structural gene in a transcription unit is monocistronic (in eukaryotes) or polycistronic (in prokaryotes).
  - ➢ **Monocistronic genes:** They code for single polypeptide. They have interrupted coding sequences called split genes.
    - ♦ The coding sequences or expressed sequences that transcribe for proteinsare called as exons.
    - ♦ The exons are interrupted by introns. Introns are intervening sequences.
  - ➢ **Polycistronic genes:** They code for more than one polypeptide.
    - ♦ In polycistronic, there are no split genes.

RNA (Ribonucleic acid)

- They are single stranded molecule.
- RNA is found in nucleus and cytoplasm.
- It contains ribose sugar and the nitrogen base uracil (U) instead of thymine, so A pairs with U.
- Base pairings are A-U and C-G.
- There are three types of RNA: mRNA, tRNA, and rRNA.

(i) mRNA (Messenger RNA)

- Single, uncoiled, straight strand of nucleic acid.
- It is found in the nucleus and cytoplasm.
- The mRNA provides the template for protein synthesis (translation) and has genetic information in the form of genetic code.

- It copies DNA's instructions and carries them to the ribosomes where proteins can be made.
- mRNA's base sequence is translated into the amino acid sequence of a protein.
- Three consecutive bases on mRNA called a codon (e.g. UAA, CGC, AGU).

(ii) tRNA (Transfer RNA)

- The tRNA is called sRNA (soluble RNA).
- It acts as an adapter molecule.
- It is the single stranded molecule containing 80 nucleotides in the shape of a cloverleaf.
- The tRNA brings the amino acids to ribosomes and read the genetic code of mRNA.
- tRNA has an
  - ➢ Anticodon loop that base complementary to the codon. Three bases on tRNA that are complementary to a codon on mRNA are called anticodons(*e.g.* codon- UUA; anticodon- AAU).
  - ➢ Amino acid accepterend to which it binds with amino acid.
- Each tRNA bind with specific amino acid i.e. 61 types of tRNA are found.
- One specific tRNA with anticodon UAC is called initiator tRNA.
- There is no tRNA for stop codons. (UAA, UGA, UAG)
- Secondary (2-D) structure of tRNA looks like a clover-leaf. 3-D structure looks like inverted 'L'.

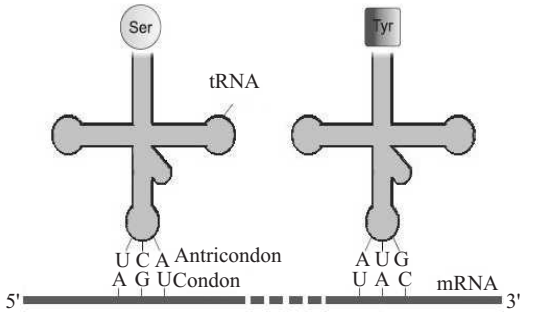


Fig. tRNA - the adapter molecule

(iii) rRNA (Ribosomal RNA)

- It is globular shape.
- It helps make up the structure of the ribosomes.
- rRNA and protein make up the large and small subunits of ribosomes.
- Ribosomes are the site of translation (making polypeptides).
- It aids in moving ribosomes along the mRNA strand as amino acids are linked together to make a protein.

Process of transcription in prokaryotes

- The process by which the DNA message is copied into a strand of mRNA is called transcription.
- It takes place in the nucleus.
- The transcription requires RNA polymerase enzyme, a DNA template, four types of Ribonucleotides and certain co-factors such as Mg^{2+}.
- There is a single DNA dependent RNA polymerase that catalyses transcription or synthesis of all three types of RNAs in prokaryotes.
- *The process of transcription is completed in three steps:*

(i) Initiation: Here, the enzyme RNA polymerasebinds at the promoter site of DNA and initiates the process of transcription. It causes the local unwinding of the DNA double helix. An initiation factor (σ)present in RNA polymerase initiates the RNA synthesis.

(ii) Elongation: The RNA chain is synthesized in the 5'-3' direction.

- ♦ RNA polymerase unzips the DNA double helix and forms an open loop.
- ♦ One of the strands, called sense strand, acts as template for mRNA synthesis.
- ♦ The enzyme, RNA polymerase, utilizesribonucleoside triphosphates(ATP, GTP, UTP and CTP) as substrate and polymerizes them to form mRNA following the rule of complementarity.
- ♦ This process of opening of helix and elongation of polynucleotide chain continues until the enzyme reaches the terminator gene.

(iii) Termination:

- ♦ RNA polymerase recognizes the terminator gene by a termination-factor called rho (ρ) factor.
- ♦ After RNA polymerase reaches the terminator region, the newly synthesized mRNA transcript along with enzyme is released.
- ♦ The proceeded mRNA leaves the nucleus and enters the cytoplasm.

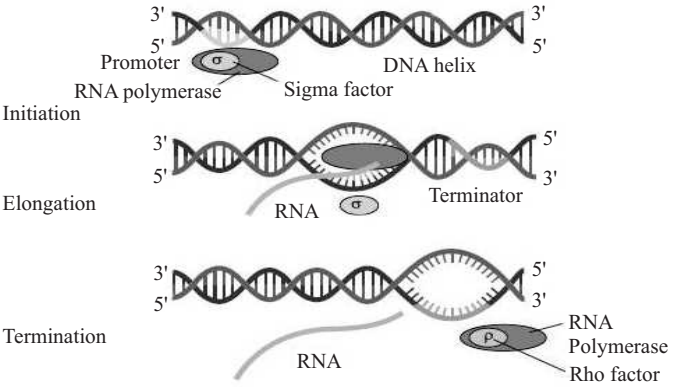


Fig. Process of transcription in bacteria

- *In bacteria (Prokaryotes) transcription and translation are coupled because*
  - ➢ mRNA requires no processing to become active.
  - ➢ Transcription and translation take place in the same compartment (no separation of cytosol and nucleus). Translation can begin before mRNA is fully transcribed.
- *In eukaryotes, there are two additional complexities:*

(i) There are three RNA polymerases:

(a) RNA polymerase I: It transcribes rRNAs (28S, 18S and 5.8S).

(b) RNA polymerase II: It transcribes the heterogeneous nuclear RNA (hnRNA). hnRNA is the precursor of mRNA.

(c) RNA polymerase III: It transcribes tRNA, 5S rRNA and snRNAs (small nuclear RNAs).

(ii) Post transcriptional processing: (occurs inside the nucleus)

(a) Splicing:

- The primary transcript (hn RNA) contain both exons and introns and required to be processed before they become translationally active (mRNA).
- The introns are removed by a process called RNA processing or RNA splicing.
- This process is catalysed by large complex of SnRNP, called spliceosome that excises theintrons exons are joined together.

(b) Capping:

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

(c) Tailing (Polyadenyaltion):

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

- The processed hnRNA is now called mRNA and transported out of the nucleus for translation.

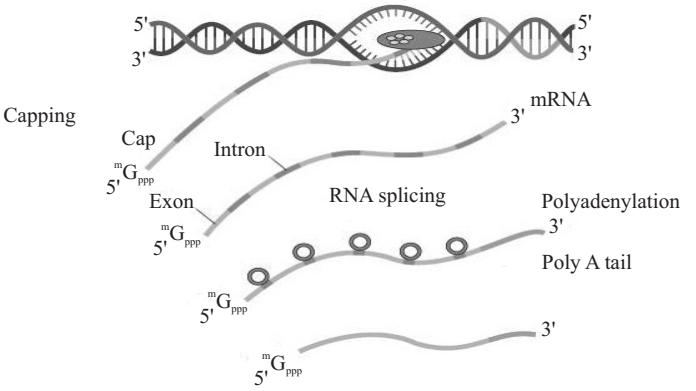


Fig. Process of transcription in eukaryotes

Difference between template strand and coding strand

- **Template strand:** Template strand of DNA acts as a template for the synthesis of mRNA during transcription. It runs from 3′ to 5′.
- **Coding strand:** Coding strand is a sequence of DNA that has the same base sequence as that of mRNA (except thymine that is replaced by uracil in DNA.

GENETIC CODE

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

20 amino acids involved in translation are:

1. Alanine (Ala)
2. Arginine (Arg)
3. Asparagine (Asn)
4. Aspartic acid (Asp)
5. Cystein (Cys)
6. Glutamine (Gln)
7. Glutamic acid (Glu)
8. Glycine (Gly)
9. Histidine (His)
10. Isoleucine (Ile)
11. Leucine (Leu)
12. Lysine (Lys)
13. Methionine (Met)
14. Phenyl alanine (Phe)
15. Proline (Pro)
16. Serine (Ser)
17. Threonine (Thr)
18. Tryptophan (Trp)
19. Tyrosine (Tyr)
20. Valine (Val)

History of Genetic Code

- The process of replication and transcription based on complementarity.
- The process of translation is the transfer of genetic information from a polymer of nucleotides to a polymer of amino acids. There is no complementarity exist between nucleotides and amino acids.
- If there is change in the nucleic acid (genetic material) there is change in amino acids in proteins.
- Therefore, there must be a genetic code that could direct the sequence of amino acids in proteins during translation.
- **George Gamow** proposed the code should be combination of bases, he suggested that in order to code for all the 20 amino acids, the code should be made up of three nucleotides.
- **Har Govind Khorana** developed the chemical method insynthesizing RNA molecules with desired combinations of bases **(homopolymer and copolymers).**
- **Marshall Nirenberg's** developed cell – free system for protein synthesis, which finally helped in the discovery of genetic code.
- **Severo Ochoa** enzyme **(polynucleotide phosphorylase) is used to** polymerize RNA with desired sequences in a template independent manner (enzymatic synthesis of RNA).

Salient Features of Genetic Code

- There are 64 codons. 61 codes for amino acids and 3 codons are stop codon.
- The codon is triplet (three-letter code). Three nitrogen base sequences constitute one codon.
- The genetic code is non-ambiguous *i.e.* one codon specify only one amino acid.
- **Degeneracy:** A single amino acid is represented by many codons. Such codons are called **degenerate codons**.
- **Comma less:** The codon is read in mRNA in a continuous fashion. There is no punctuation.
- **Universal:**Genetic code is universal.From bacteria to human, UUU codes for phenyl alanine.
- **Non-overlapping:** The genetic code reads linearly.
- **Direction:** the code only read in 5' → 3' direction.
- **Anticodon:** Each codon has a complementary anticodon on tRNA.
- **Initiation codon:** AUG is the initiator codon. In eukaryotes, methionine is the first amino acid and *formyl methionine* in prokaryotes.
- Termination codons (non-sense codons/stop codons) are UAA, UAG and UGA. They do not indicate any amino acids.

MUTATION

- Relationship between DNA and genes are best understood by mutation.

(i) Point mutation:

- It occurs due to change in a single base pair of DNA, by substitution, deletion or insertion of a single nitrogenous base.
- *E.g.* sickle cell anaemia. It involves mutation in a single base pair in the beta globin chain of haemoglobin pigment in the blood. Glutamic acid in short arm of chromosome II gets replaced with valine at the sixth position.

(ii) Frame shift mutation:

- It occurs due to loss (deletions) or gain (insertion/ duplication) of a DNA segment.
- There is change in whole sequence of amino acid from the point of insertion or deletion.
- *E.g.* β-thalassemia.

TRANSLATION (PROTEIN SYNTHESIS)

- It refers to polymerization of amino acids to form a polypeptide.
- The triplet sequence of base pairs in mRNA defines the order and sequence of amino acids in a polypeptide chain.
- It takes place in ribosomes. Ribosome is the cellular factory for protein synthesis.
- **Important functions of ribosome during translation:**
  - ➢ Ribosome acts as the site where protein synthesis takes place from individual amino acids. It is made up of two subunits. The smaller subunit comes in contact with mRNA and forms protein synthesizing complex whereas the smaller subunit acts as an amino acid binding site.
  - ➢ Ribosome acts as a catalyst for forming peptide bond. For example, 23 rRNA in bacteria acts as ribozyme.

Process of Translation

1. Charging of tRNA (Aminoacylation of tRNA)

- Here, amino acids are activated (amino acid + ATP) and linked to their cognate tRNA in the presence of aminoacyl tRNA synthetase. This process is commonly known as charging of tRNA or aminoacylation of tRNA.

2. Initiation

- Translation is initiated by formation of an initiation complex consisting of 30S ribosomal subunit, formyl-methionyl (fMet) tRNA, and mRNA.
- It begins at the 5'-end of mRNA in the presence of an initiation factor.
- The mRNA binds to the small subunit of ribosome. AUG is recognized by the initiator tRNA.
- Initiation codon for methionine is AUG. So methionyl tRNA complex would have UAC at the Anticodon site.
- Now the large subunit (50S) binds to the small subunit to complete the initiation complex.
- Large subunit (70S) has two binding sites to which tRNA-carrying amino acids can bind. One is called aminoacyl tRNA binding site (A site) and the other is called peptidyl site (P site).
- There is also a third site called the exit or E site where tRNAs are released.
- Initiation codon for methionine is AUG. So methionyl tRNA complex would have UAC at the Anticodon site.

3. Elongation

- The initiating tRNA carrying fomyl methionine binds, to the P site.
- 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, peptidyltransferase.
- The ribosome now advances a distance of one codon and the tRNA that carried the formyl methionine is released at the E-site.
- A tRNA carrying the next amino acid now moves to the A site where the anticodon on the tRNA matches the codon on the mRNA. This is called translocation.
- The ribosome shifts down by a distance of one codon. As the shift occurs, the two amino acids on the tRNA in the P site are transferred to the new amino acid and the second tRNA is released from the E site.
- The ribosome continues to move along the mRNA and new amino acids are added to the growing polypeptide chain.
- A group of ribosomes associated with a single mRNA for translation is called a polyribosome (polysomes).

4. Termination

- Elongation of a polypeptide is terminated when a stop codon moves into the A site. A stop codon does not specify an amino acid and does not have a corresponding tRNA.
- When aminoacyl tRNA reaches the termination codon like UAA, UAG andUGA, known as stop codon, the termination of translation occurs. The polypeptide and tRNA are released from the ribosomes.
- The ribosome dissociates into large (50S) and small (30S) subunits at the end of protein synthesis.
- An mRNA has additional sequences that are not translated (untranslated regions or UTR). UTRs are present at both 5′-end (before start codon) and 3′-end (after stop codon). They are required for efficient translation process.

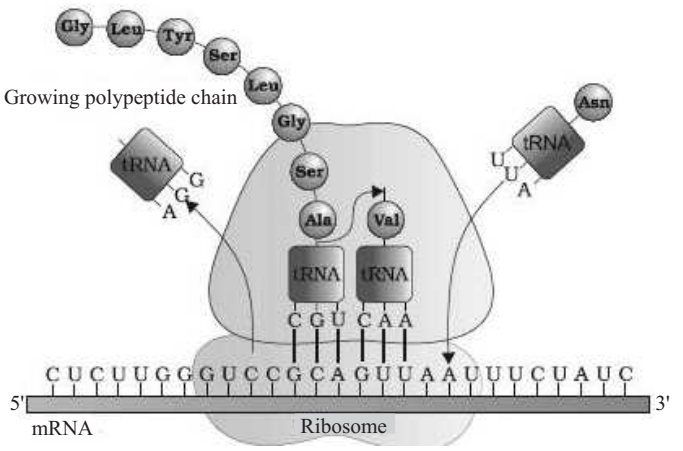


Fig.: Translation

REGULATION OF GENE EXPRESSION

- Gene expression results in the formation of a polypeptide.
- *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 metabolic, physiological and environmental conditions regulate expression of genes. *E.g.*
  - ➢ In *E.coli* the enzyme, beta-galactosidase hydrolyses lactose into galactose and glucose. If the bacteria do not have lactose the synthesis of beta-galactosidase stops.
  - ➢ The development and differentiation of embryo into adult are a result of the expression of several set of genes.

OPERON CONCEPT

- *It states that "Each metabolic reaction is controlled by a set of genes".*
- **Francois Jacob** and **Jacque Monod** were the first to describe a transcriptionally regulated system of gene expression.
- 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

- It is the operon that controls the lactose metabolism.
- The lac operon consists of
  - ➢ One regulatory gene (i-gene), which codes for repressor.
  - ➢ Three structural genes (z, y and a).

(i) **z-gene:** Codes for β-galactosidase, which hydrolyze lactose to galactose and glucose.
(ii) **y-gene:** Codes for Permease, which increases the permeability of the cell to lactose.
(iii) **a-gene:** Codes for a transacetylase.

- The genes present in the operon function together in the same or related metabolic pathway. There is an operator region for each operon.
- In *lac* operon, lactose acts as an inducer. The lactose is transported into the *E.coli* cells by the action of permease.
- **In the presence of lactose (inducer):**
  - ➢ Lactose (inducer) binds with repressor protein and inactivates it. So repressor protein cannot bind to operator gene. The operator gene becomes free and induces the RNA polymerase to bind with promoter gene. Hence, three structural genes express their product and respective enzymes are produced. These enzymes act on lactose so that lactose is metabolized into glucose and galactose.
- **In the absence of lactose (inducer):**
  - ➢ When the level of inducer decreases as it is completely metabolised by enzymes, it causes synthesis of repressor from repressor gene. The repressor binds to the operator gene and blocks RNA polymerase from transcribing the operon. Hence, the transcription is stopped. This type of regulation is known as negative regulation.

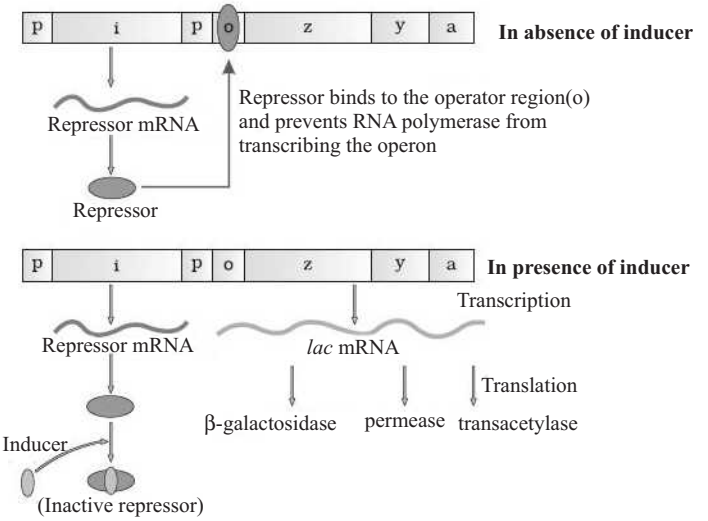


Fig. The *lac* operon

HUMAN GENOME PROJECT (HGP)

- Genome is the entire DNA in the haploid set of chromosome of an organism.
- In human genome, DNA is packed in 23 chromosomes.
- Human genome project (1993-2006) was considered mega project because it had a specific goal to sequence every base pair present in the human genome.

- It was a 13 year project coordinated by the U.S. Department of energy and National Institute of Health and got accomplished in the year 2006.
- It is the first effort in identifying the sequence of nucleotides and mapping of all the genes in human genome.
- Human genome contains about 3×10^9 bp.

Goals of HGP

- To identify all the estimated genes in human DNA
- To determine the sequences of the 3 billion chemical base pairs that makes up human DNA.
- To store this information in databases.
- To improve tools for data analysis.
- To transfer related technologies to other sectors.
- To address the ethical, legal and social issues (ELSI) that may arise from the project.

Methodologies of HGP

There were two major approaches

- **Expressed sequence tags (ESTs):** It focused on identifying all the genes that are expressed as RNA.
- **Sequence annotation:** It was the blind approach of simply sequencing the whole set of genome containing all the coding and non-coding sequence and later assigning different regions in the sequence with functions.
- The commonly used hosts for sequencing were bacteria and yeast and vectors were called as **BAC** (bacterial artificial chromosome) and **YAC** (yeast artificial chromosome).

Procedure:

- Isolate total DNA from a cell → Convert them into random fragments → Clone in suitable host (*e.g.* BAC and YAC) for amplification → Fragments are sequenced using Automated DNA sequencers (using Frederick Sanger method) → Sequences are arranged based on overlapping regions → Alignment of sequences using computer 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).

Salient Features of Human Genome

- The human genome contains 3164.7 million nucleotide bases.
- The total numbers of genes were about 30,000.
- Average gene consists of 3000 bases, but sizes vary. The largest known human gene called dystrophin on X-chromosome contains 2.4 million bases.
- 99.9% nucleotide bases are identical in all people. 0.1% is what makes each of us unique.
- The functions of over 50% of discovered genes are unknown.
- Chromosome I has most genes (2968) and Y has the fewest (231).
- Less than 2% of the genome codes for proteins.
- Repeated sequences make up very large portion of human genome. Repetitive sequences are stretches of DNA sequences that are repeated many times. They have no direct coding functions, but they shed light on chromosome structure, dynamics and evolution.
- About 1.4 million locations where single-base DNA differences (known as SNPs- Single nucleotide polymorphism or 'snips') occur in humans.

BIOINFORMATICS

- HGP was closely associated with Bioinformatics.
- Bioinformatics is the application of computational and statistical techniques to the field of molecular biology.
- It solves the practical problems arising from the management and analysis of biological data.
- The field of bioinformatics developed after the completion of Human geneome project. This is because enormous amount of data has been generated during the process of HGP that has to be managed and store for easy access and interpretation for future use by various scientists.
- Hence, bioinformatics involves the creation of biological databases that store vast information of biology.
- It develops certain tools for easy and efficient access to the information and utilisation. Bioinformatics has developed new algorithms and statistical methods to find out the relationship between the data, to predict protein structure and their functions, and to cluster protein sequences into their related families.

DNA FINGERPRINTING (DNA PROFILING)

- It is the technique to identify the similarities of the DNA fragments of two individuals.
- It was developed by Alec Jeffreys in 1985.

Basis of DNA Fingerprinting

- DNA fingerprinting involves identifying differences in some specific regions in DNA called **repetitive DNA** variable number tandem repeats (VNTR)**,** because in these sequences, a small stretch of DNA is repeated many times.

- The size of VNTR varies in size from 0.1 to 20 kb. This number of repeats is specific from person to person.
- These 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-satellitesetc) based on base composition (A:T rich or G:C rich), length of segment and number of repetitive units.
- These sequences dose not code for any proteins.
- These sequences show high degree of polymorphism and form basis of DNA fingerprinting.
- Polymorphism in DNA sequence is the basis of genetic mapping of human genome as well as of DNA fingerprinting.
- Polymorphism (variation at genetic level) arises due to mutations.
- If an inheritable mutation is observed in a population at high frequency it is referred as DNA polymorphism.
- Polymorphism is higher in non-coding DNA sequence. Because mutations in these sequences may not have any immediate effect in an individual's reproductive ability.
- These mutations accumulate generation after generation and cause polymorphism. For evolution and speciation, polymorphisms play important role.

Difference between repeated DNA and satellite DNA

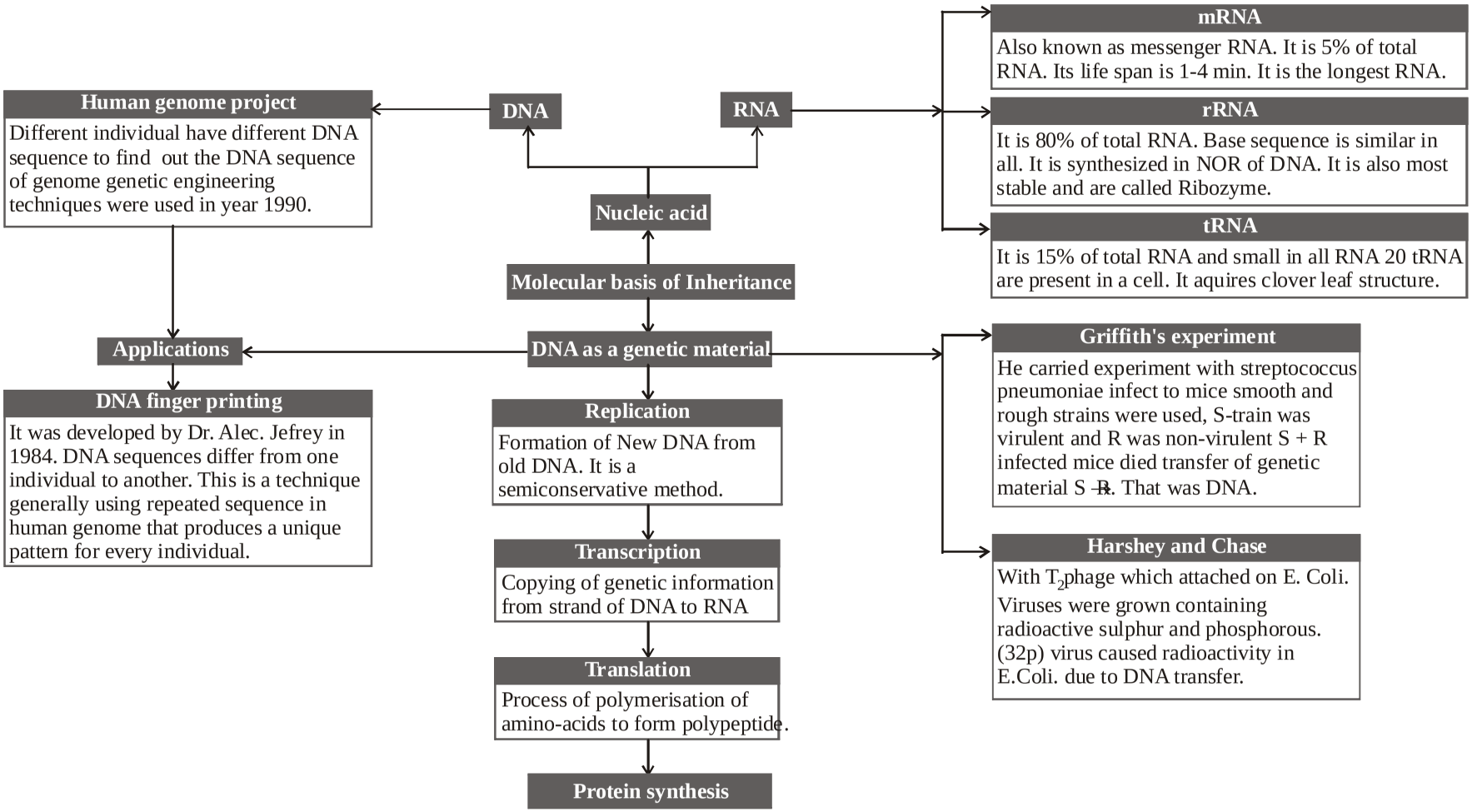
- Repetitive DNA is DNA sequences that contain small segments, which are repeated many times.
- Satellite DNA is DNA sequences that contain highly repetitive DNA.

Steps of DNA Fingerprinting

- He used satellite DNA as the basis of DNA fingerprinting that shows very high degree of polymorphism. It was called as Variable Number Tandem Repeats (VNTR).
- Different steps of DNA fingerprinting are:-
  - ➢ Isolation of DNA. (From any cells like blood stains, semen stains or hair roots).
  - ➢ Make copies (amplification) of DNA by polymerase chain reaction (PCR).
  - ➢ Digestion of DNA by restriction endonucleases.
  - ➢ Separation of DNA fragments by gel electrophoresis.
  - ➢ Transferring (blotting) of separated DNA fragments to synthetic membranes, such as nitrocellulose or nylon and then baked in a vacuum oven at 80°C for 3-5 hours (to fix the DNA fragment on the membrane).
  - ➢ Double stranded DNA made single stranded.
  - ➢ Hybridization using labeled VNTR probe.
  - ➢ Detection of hybridized DNA fragments by autoradiography. After hybridization with VNTR probe the autoradiogram gives many bands of different sizes. These bands give a characteristic pattern for an individual DNA. It differs from individual to individual.
  - ➢ The image (in the form of dark & light bands) obtained is called DNA fingerprint.
- The DNA from a single cell is enough to perform DNA fingerprinting.

Application of DNA fingerprinting

- It is used in forensic science to identify potential crime suspects.
- It is used to establish paternity and family relationships.
- It is used to identify and protect the commercial varieties of crops and livestocks.
- It is used to find out evolutionary history of an organism and trace out the linkages between various groups of organisms.


Human genome project
Different individual have different DNA sequence to find out the DNA sequence of genome genetic engineering techniques were used in year 1990.
DNA
RNA
mRNA
Also known as messenger RNA. It is 5% of total RNA. Its life span is 1-4 min. It is the longest RNA.
rRNA
It is 80% of total RNA. Base sequence is similar in all. It is synthesized in NOR of DNA. It is also most stable and are called Ribozyme.
tRNA
It is 15% of total RNA and small in all RNA 20 tRNA are present in a cell. It aquires clover leaf structure.
Nucleic acid
Molecular basis of Inheritance
Applications
DNA as a genetic material
Griffith's experiment
He carried experiment with streptococcus pneumoniae infect to mice smooth and rough strains were used, S-train was virulent and R was non-virulent S + R infected mice died transfer of genetic material S → R. That was DNA.
DNA finger printing
It was developed by Dr. Alec. Jefrey in 1984. DNA sequences differ from one individual to another. This is a technique generally using repeated sequence in human genome that produces a unique pattern for every individual.
Replication
Formation of New DNA from old DNA. It is a semiconservative method.
Harshey and Chase
With T2phage which attached on E. Coli. Viruses were grown containing radioactive sulphur and phosphorous. (32p) virus caused radioactivity in E.Coli. due to DNA transfer.
Transcription
Copying of genetic information from strand of DNA to RNA
Translation
Process of polymerisation of amino-acids to form polypeptide.
Protein synthesis

EXERCISE - 1
Conceptual Questions

1. What does "*lac*" refer to in what we call the *lac* operon?
(a) The number 1,00,000 (b) Lactose
(c) Lactase (d) *Lac* insect

2. DNA fingerprinting refers to
(a) molecular analysis of profiles of DNA samples
(b) analysis of DNA samples using imprinting devices
(c) techniques used for molecular analysis of different specimens of DNA
(d) techniques used for identification of fingerprints of individuals.

3. In negative operon
(a) co-repressor binds with repressor
(b) co-repressor does not bind with repressor
(c) co-repressor binds with inducer
(d) cAMP have negative effect on *lac* operon

4. Genes that are involved in turning on or off the transcription of a set of structural genes are called
(a) Operator genes (b) Redundant genes
(c) Regulator genes (d) Polymorphic genes

5. If the gene encoding the *lac* repressor is mutated so that it can no longer bind the operator, will transcription of that operon occur?
(a) Yes, but only when lactose is present.
(b) No, because RNA polymerase is need to transcribe the genes.
(c) Yes, because the operator will not be bound by repressor and RNA polymerase can transcribe the *lac* operon.
(d) No, because cAMP levels are low when the repressor is nonfunctional.

6. The error rate of changing an incorrect base with another incorrect base during proofreading is
(a) 1 in 10 bases (b) 1 in 100 bases
(c) 1 in 1,000 bases (d) 1 in 10,000 bases

7. Transcriptional regulation in prokaryotes can occur by
(a) a repressor binding an operator and preventing transcription.
(b) an activator binding upstream from a promoter and positively affecting transcription.
(c) different promoter sequences binding RNA polymerase more tightly, resulting in more effective transcriptional initiation.
(d) All of the above

8. Which of the following is the first thing that happens when a signal molecule acts on a target cell?
(a) A transcription factor acts on the DNA.
(b) The signal molecule binds to RNA.
(c) A new protein is made in the target cell.
(d) The signal molecule binds to a receptor.

9. Process used for amplication or multiplication of DNA for finger printing is
(a) polymerse chain reaction
(b) nesslerisation
(c) southern blotting
(d) northern blotting

10. Lactose operon produces enzymes
(a) β-galactosidase, permease and glycogen synthetase.
(b) β-galactosidase, permease and transacetylase.
(c) Permease, glycogen synthetase and transacetylase.
(d) β-galactosidase, permease and phosphoglucose isomerase.

11. The most common way of gene expression is regulated in both prokaryotes and eukaryotes is through the
(a) control of mRNA translation.
(b) breakdown of proteins formed by translation.
(c) prevention of DNA uncoiling prior to transcription.
(d) control of gene transcription.

12. Satellite DNA
(a) is classified in many categories such as micro-satellites, minisatellites, etc. on the basis of base composition length of segments and number of repetitive units.
(b) normally does not code for any protein.
(c) shows polymorphism.
(d) forms the basis of DNA finger printing.

13. What are the three major properties of genes that are explained by the structure of DNA?
(a) They contain information, direct the synthesis of proteins, and are contained in the cell nucleus.
(b) They contain nitrogenous bases, direct the synthesis of RNA, and are contained in the cell nucleus
(c) They encode the organisms phenotype, are passed on from one generation to the next, and contain nitrogenous bases.
(d) They contain information, replicate exactly, and change to produce a mutation.

14. In prokaryotes, gene regulation occurs at the level of
(a) transcription (b) translation
(c) post-transcription (d) post-translation

15. The regulation of tryptophan synthesis in *E. coli* is an example of affecting gene expression through
(a) translational control.
(b) transcriptional control.
(c) homeotic gene control.
(d) breaking down mRNA molecules.

16. Which of the following findings derived from recent analysis of the human genome does not illustrate our genetic relationships to other, more "primitive," organisms?
(a) Only 35,000 genes are required to make a human.
(b) Human DNA contains hundreds of bacterial genes.
(c) Numerous homeotic genes are shared among humans and other animals.
(d) There are over 40 newly identified disease genes.

17. Determination of one amino acid by more than one codon is due to
(a) redundancy of genetic code.
(b) continuous nature of genetic code.
(c) punctuation in genetic code.
(d) universal nature of genetic code.

18. If a nucleotide lacking a hydroxyl group at the 3' end is added to a PCR, what would be the outcome?
(a) No additional nucleotides would be added to a growing strand containing that nucleotide.
(b) Strand elongation would proceed as normal.
(c) Nucleotides would only be added at the 5' end.
(d) *T. aquaticus* DNA polymerase would be denatured.

19. SNP which is pronounced as "snips" stands for
(a) small nuclear protein
(b) single nucleotide particle
(c) single nucleotide polymorphism
(d) small nicking points

20. The process of transfer of genetic information from DNA to RNA/formation of RNA from DNA is
(a) transversion (b) transcription
(c) translation (d) translocation

21. Transcription in prokaryotic cell is :
(a) initiated at a promoter using one of three RNA polymerases (RNA polymerase II).
(b) initiated at a start codon with the help of initiation factors and the small subunit of the ribosome.
(c) initiated at a promoter and uses only one strand of DNA, the template strand, to synthesize a complementary RNA strand.
(d) is terminated at stop codons.

22. What would happen if a mutation occurred in the DNA such that the second codon of a polypeptide, UGC, was changed to a UAG?
(a) Nothing. The ribosome would skip that codon and translation would continue.
(b) Translation would continue, but the reading frame of the ribosome would be shifted.
(c) Translation would stop at the second codon and no functional protein would be made.
(d) Translation would continue, but the second amino acid in the protein would be different.

23. A functional piece of mRNA has 66 codons. What is the maximum number of amino acids that could be present in the protein coded for by this mRNA?
(a) 22 (b) 64
(c) 65 (d) 66

24. Termination of polypeptide chain is brought about by
(a) UUG, UAG and UCG (b) UAA, UAG and UGA
(c) UUG, UGC and UCA (d) UCG, GCG and ACC

25. Nucleotide arrangement in DNA can be seen by
(a) X-ray crystallography (b) electron microscope
(c) ultracentrifuge (d) light microscope

26. The primary function of DNA polymerase is to
(a) add nucleotides to the growing daughter strand.
(b) seal nicks along the sugar-phosphate backbone of the daughter strand.
(c) unwind the parent DNA double helix.
(d) prevent reassociation of the denatured parent DNA strands.

27. The lagging daughter strand of DNA is synthesized in what appears to be the "wrong" direction. This synthesis is accomplished by
(a) ligating (connecting) short Okazaki fragments that are synthesized in short spurts in the "right" direction.
(b) primase.
(c) using multiple primers and DNA polymerase I.
(d) Both (a) and (b)

28. RNA primers are necessary in DNA synthesis because
(a) DNA polymerase can only add to an existing strand of nucleotides.
(b) DNA polymerase can only add to an existing DNA strand.
(c) DNA primase is the first enzyme in the replication complex.
(d) All of the above

29. Proof reading and repair occur
(a) at anytime during or after synthesis of DNA.
(b) only before DNA methylation occurs.
(c) only in the presence of DNA polymerase.
(d) only in the presence of an excision repair mechanism.

30. DNA replication is an _____ process and _____ energy.
(a) exergonic; does not require
(b) endothermic; does require
(c) endergonic; does require
(d) endothermic; does not require

31. Information flow or central dogma of modern biology is
(a) RNA $\rightarrow$ Proteins $\rightarrow$ DNA
(b) DNA $\rightarrow$ RNA $\rightarrow$ Proteins
(c) RNA $\rightarrow$ DNA $\rightarrow$ Proteins
(d) DNA $\rightarrow$ RNA $\rightarrow$ Proteins.

32. Triplet UUU codes for
(a) leucine (b) methionine
(c) phenylalanine (d) glycine

33. Which of the following statements about DNA replication is false?
(a) Okazaki fragments are the initiators of continuous DNA synthesis along the leading strand.
(b) Replication forks represent areas of active DNA synthesis on the chromosomes.
(c) Error rates for DNA replication are often less than one in every billion base pairings.
(d) Ligases and polymerases function in the vicinity of replication forks.

34. The key finding of the Hershey and Chase experiments on the mechanism of viral replication was that
(a) protein, not DNA, is the hereditary material.
(b) DNA, not protein, is the hereditary material.
(c) protein and DNA play an equal role in determining inheritance.
(d) neither protein nor DNA play a role in determining inheritance.

35. Which of the following statements about the process of DNA replication is false?
(a) Many different enzymes are needed for the process to function properly.
(b) Mistakes can be corrected at multiple steps in the process.
(c) Uncorrected mistakes introduce mutations into the DNA base sequence.
(d) Mistakes in the copying process are very common occurrences.

36. Assume that you chemically label both strands within a molecule of DNA. You then allow this DNA to replicate using unlabelled nucleotides. Which of the following statements about the two resulting DNA molecules is false?
(a) Both will have the chemical label.
(b) One will have the chemical label, the other will not.
(c) One strand within each molecule will have the chemical label.
(d) Assuming no replication errors, both molecules will be genetically identical.

37. In order for the information contained in a gene to be used to produce a functioning protein, the
(a) DNA must be replicated.
(b) information must be transcribed into mRNA and then translated into amino acids.
(c) tRNA must be transcribed into rRNA and then translated into amino acids.
(d) ribosome must be converted from rRNA into mRNA.

38. DNA is acidic due to
(a) sugar (b) purine
(c) phosphoric acid (d) pyrimidine

39. Nucleosome is
(a) intron interrupted DNA
(b) double helix DNA
(c) negatively charged DNA wrapped around positively charged histone octomer
(d) satellite DNA

40. Genes can be inactivated by
(a) inaccurate removal of introns.
(b) transposable genetic elements.
(c) movement of genes to heterochromatic regions of the chromosome.
(d) All of the above

41. Which of the following mechanisms of gene regulation operates after mRNA transcription but before translation of mRNA into protein?
(a) mRNA splicing
(b) DNA packing
(c) Repressors and activators
(d) Protein degradation

42. In humans, the hormone testosterone enters cells and binds to specific proteins, which in turn bind to specific sites on the cells' DNA. These proteins probably act to
(a) help RNA polymerase transcribe certain genes.
(b) alter the pattern of DNA splicing.
(c) stimulate protein synthesis.
(d) unwind the DNA so that its genes can be transcribed.

43. During transcription, the DNA site at which RNA polymerase binds is called
(a) enhancer (b) promoter
(c) regulator (d) receptor

44. During translation initiation in prokaryotes, a GTP molecule is needed in
(a) association of 50 S subunit of ribosome with initiation complex
(b) formation of formyl-met-tRNA
(c) binding of 30 S subunit of ribosome with mRNA
(d) association of 30S-mRNA with formyl-met-tRNA

45. Which one of the following triplet codes, is correctly matched with its specificity for an amino acid in protein synthesis or as 'start' or 'stop'codon ?
(a) UAC – Tyrosine (b) UCG – Start
(c) UUU – Stop (d) UGU – Leucine

46. *t*RNA takes part in
(a) transfer of genetic code to cytoplasm.
(b) carry amino acids to ribosomes.
(c) collection of RNA in ribosomes.
(d) copy the genetic code from DNA in nucleus.

47. Lactose operon produces enzymes
(a) β-galactosidase, permease and glycogen synthetase.
(b) β-galactosidase, permease and transacetylase.
(c) Permease, glycogen synthetase and transacetylase.
(d) β-galactosidase, permease and phosphoglucose isomerase.

48. What would happen if in a gene encoding a polypeptide of 50 amino acids, 25th codon (UAU) is mutated to UAA?
(a) A polypeptide of 25 amino acids will be formed
(b) A polypeptide of 24 amino acids will be formed
(c) Two polypeptides of 24 and 25 amino acids will be formed
(d) A polypeptide of 49 amino acids will be formed

49. Protein synthesis occurs
(a) on ribosmes present in cytosol as well as in mitochondria
(b) only on ribosomes attached to the nuclear envelope and endoplasmic reticulum
(c) only on the ribosomes present in cytosol
(d) on ribosomes present in the nucleolus as well as cytoplasm

50. Which step of translation does not consume a high energy phosphate bond ?
(a) Translocation
(b) Amino acid activation
(c) Peptidyl-transferase reaction
(d) Aminoacyl tRNA binding to active ribosomal site

51. Degeneration of a genetic code is attributed to the
(a) third member of a codon
(b) first member of a codon
(c) second member of a codon
(d) entire codon

52. In a mutational event, when adenine is replaced by guanine, it is a case of
(a) frame shift mutation (b) transcription
(c) transition (d) transversion

53. Reverse transcriptase is
(a) RNA dependent RNA polymerase
(b) DNA dependent RNA polymerase
(c) DNA dependent DNA polymerase
(d) RNA dependent DNA polymerase

54. Crossing over that results in genetic recombination in higher organisms occurs between
(a) sister chromatids of a bivalent
(b) non-sister chromatids of a bivalent
(c) two daughter nuclei
(d) two different bivalents

55. The following ratio is generally constant for a given species:
(a) $\frac{A+G}{C+T}$ (b) $\frac{T+C}{G+A}$
(c) $\frac{G+C}{A+T}$ (d) $\frac{A+C}{T+G}$

56. The telomeres of eukaryotic chromosomes consist of short sequences of
(a) thymine rich repeats (b) cytosine rich repeats
(c) adenine rich repeats (d) guanine rich repeats

57. How many base pairs (bp) are found in the haploid genome of humans?
(a) 2.9×10^9 (b) 4×10^8
(c) 7×10^9 (d) 3×10^9

58. Eukaryotic chromosomes
(a) are circular and contain origin and terminator sequences.
(b) are linear and have origins and telomeres.
(c) contain coding and non-coding sequences.
(d) Both (b) and (c)

59. The processes by which DNA forms *m*RNA and *m*RNA forms protein are respectively
(a) translation and transcription
(b) transcription and replication
(c) transcription and translation
(d) replication and translation.

60. In lac operon, structural gene 'Z' synthesises
(a) β-galactosidase
(b) galactosidase permease
(c) galactosidase transacetylase
(d) None of the above

61. Chromatin structure must be altered in order for gene expression to occur because
(a) condensed chromatin is replicated but not transcribed.
(b) condensed chromatin makes most DNA sequence inaccessible to the transcription complex.
(c) decondensed chromatin has more nucleosomes per DNA molecule.
(d) heterochromatin is actively transcribed and euchromatin is not transcribed.

62. Which of the following would you not expect to find in prokaryotic DNA?
(a) Millions of base pairs.
(b) Histone proteins around which the DNA is coiled.
(c) Functionally related genes grouped together in the same section of DNA.
(d) A majority of DNA that codes for protein or RNA.

63. The primary purpose of Griffith's experiments on the *Streptococcus pneumoniae* bacterium was to
(a) find a cure for pneumonia in humans.
(b) prevent cancers caused by exposure to ultraviolet light.
(c) determine if DNA is the hereditary material.
(d) discover the molecular structure of DNA.

64. Which of the following parts of a DNA molecule are held together by hydrogen bonds?
(a) The carbons within the sugar–phosphate group.
(b) The carbons within the nitrogen-containing bases.
(c) Nucleotide bases on opposite strands of the helix.
(d) Successive nucleotides within a single strand of the helix.

65. Operon is
(a) sequence of three nitrogen bases determining a single amino acid.
(b) a set of closely placed genes regulating a metabolic pathway in prokaryotes.
(c) segment of DNA specifying a polypeptide.
(d) gene responsible for switching on and switching off of other genes.

66. The primary reason DNA was first thought to be a poor candidate for the hereditary material was that
(a) Griffith's experiments showed that protein, not DNA, caused transformation.
(b) viruses lack DNA yet still pass genetic information between generations.
(c) DNA was believed to have a simple chemical structure with little variability.
(d) the work of Hershey and Chase showed that protein was the genetic material.

67. Consider Griffith's experiments on transformation in *Streptococcus pneumoniae*. Now imagine that you are extending these experiments by injecting a mixture of heat-killed strain R bacteria and live strain S bacteria into a mouse. The result will be that the mouse will _____, and you will find live strain _____ bacteria in its blood.
(a) die; R (b) live; R
(c) die; S (d) live; S

68. Telomerase is an enzyme which is a
(a) simple protein (b) RNA
(c) ribonucleoprotein (d) repetitive DNA

69. A murder has occurred, and you are asked to help solve it. The police bring you a sample from the crime scene of what they believe is the killer's DNA and ask you for a chemical analysis. Your study of this sample reveals the presence of adenine, thymine, ribose, and uracil, leading you to conclude that the sample is
(a) pure DNA.
(b) pure RNA.
(c) probably a mixture of DNA and RNA.
(d) probably a mixture of rRNA and mRNA.

70. Prior to mutation, a sequence of DNA reads GAGCCTATGCCAGTA. After the mutation, the sequence reads GAGCGTACGCCATTA. Which of the following best explains the change in DNA that has occurred?
(a) There was a single base deletion.
(b) There was a single base substitution.
(c) There were multiple base deletions.
(d) There were multiple base substitutions.

71. Experiments by Avery, McLeod, and McCarty supported DNA as the genetic material by showing that
(a) both protein and DNA samples provided the transforming factor.
(b) DNA was not complex enough to be the genetic material.
(c) only samples with DNA provided activity.
(d) even though DNA was molecularly simple, it provided adequate variation to act as the genetic material.

72. Chargaff's rules of base pairing states that
(a) the ratio of purines to pyrimidmes is roughly equal in all tested organisms.
(b) the ratio of A to T is roughly equal in all tested organisms.
(c) the ratio of A + T and G + C is roughly equal in all tested organisms.
(d) Both (a) and (b)

73. Thirty percent of the bases in a sample of DNA extracted from eukaryotic cells is adenine. What percentage of cytosine is present in this DNA?
(a) 10% (b) 20%
(c) 30% (d) 40%

74. A sequential expression of a set of human genes
(a) messenger RNA (b) DNA sequence
(c) ribosome (d) transfer RNA

75. Removal of introns and joining the exons in a defined order in a transcription unit is called:
(a) tailing (b) transformation
(c) capping (d) splicing

EXERCISE - 2
Applied Questions

1. During replication of a bacterial chromosome DNA synthesis starts from a replication origin site.
(a) RNA primers are involved
(b) is facilitated by telomerase
(c) moves in one direction of the site
(d) moves in bi-directional way

2. In transgenics, expression of transgene in target tissue is determined by
(a) enhancer (b) transgene
(c) promoter (d) reporter

3. *E.coli* cells with a mutated z gene of the *lac* operon cannot grow in medium containing only lactose as the source of energy because:
(a) the *lac* operon is constitutively active in these cells
(b) they cannot synthesize functional beta-galactosidase
(c) in the presence of glucose, *E.coli* cells do not utilize lactose
(d) they cannot transport lactose from the medium into the cell

4. During transcription holoenzyme RNA polymerase binds to a DNA sequence and the DNA assumes a saddle like structure at that point. What is that sequence called?
(a) AAAT box (b) TATA box
(c) GGTT box (d) CAAT box

5. Which one of the following makes use of RNA as a template to synthesize DNA?
(a) DNA polymerase
(b) RNA polymerase
(c) Reverse transcriptase
(d) DNA dependant RNA polymerase

6. A short sequence of bases on one strand of DNA is AGTCTACCGATAGT. If this sequence serves as a template for the formation of a new strand of DNA, what will be the corresponding base sequence in the new strand?
(a) AGTCTACCGATAGT (b) TCAGATGGCTATCA
(c) TGATAGCCATCTGA (d) GACATCGATTCGAT

7. One gene -one enzyme hypothesis was postulated by
(a) Hershey and Chase (b) A. Garrod
(c) Beadle and Tatum (d) R. Franklin

8. The okazaki fragments in DNA chain growth
(a) polymerize in the 3' - to - 5' direction and forms replication fork
(b) prove semi-conservative nature of DNA replication
(c) polymerize in the 5' - to - 3' direction and explain 3' - to - 5' DNA replication
(d) result in transcription.

9. The length of DNA molecule greatly exceeds the dimensions of the nucleus in eukaryotic cells. How is this DNA accommodated?
(a) super-coiling in nucleosomes
(b) DNase digestion
(c) through elimination of repititive DNA
(d) deletion of non-essential genes

10. One gene-one enzyme relationship was established for the first time in
(a) *Salmonella typhimurium*
(b) *Escherichia coli*
(c) *Diplococcus pneumoniae*
(d) *Neurospora crassa*

11. Molecular basis of organ differentiation depends on the modulation in transcription by
(a) ribosome (b) transcription factor
(c) anticodon (d) RNA polymerase

12. In the DNA molecule
(a) the total amount of purine nucleotides and pyrimidine nucleotides is not always equal
(b) there are two strands which run parallel in the $5' \rightarrow 3'$ direction
(c) the proportion of adenine in relation to thymine varies with the organism
(d) there are two strands which run anti-parallel one in $5' \rightarrow 3'$ direction and other in $3' \rightarrow 5'$

13. Which one of the following pairs of codons is correctly matched with their function or the signal for the particular amino acid?
(a) GUU, GCU-Alanine
(b) UAG, UGA-Stop
(c) AUG, ACG-Start/Methionine
(d) UUA, UCA-Leucine

14. Which one of the following pairs of nitrogenous bases of nucleic acids, is wrongly matched with the category mentioned against it?
(a) Thymine, Uracil - Pyrimidines
(b) Uracil, Cytosine - Pyrimidines
(c) Guanine, Adenine - Purines
(d) Adenine, Thymine - Purines

15. Haploids are more suitable for mutation studies than the diploids. This is because
(a) haploids are reproductively more stable than diploids
(b) mutagens penetrate in haploids more effectively than diploids
(c) haploids are more abundant in nature than diploids
(d) all mutations, whether dominant or recessive are expressed in haploids

16. T.O. Diener discovered a:
(a) free infectious DNA (b) infectious protein
(c) bacteriophage (d) free infectious RNA

17. What is not true for genetic code?
(a) It is nearly universal
(b) It is degenerate
(c) It is unambiguous
(d) A codon in mRNA is read in a non contiguous fashion

18. Semi-conservative replication of DNA was first demonstrated in:
(a) *Escherichia coli*
(b) *Streptococcus pneumoniae*
(c) *Salmonella typhimurium*
(d) *Drosophila melanogaster*

19. Whose experiments cracked the DNA and discovered unequivocally that a genetic code is a 'triplet'?
(a) Hershey and Chase (b) Morgan and Sturtevant
(c) Beadle and Tantum (d) Nirenberg and Mathaei

20. The one aspect which is not a salient feature of genetic code, is its being:
(a) degenerate (b) ambiguous
(c) universal (d) specific

21. Satellite DNA is useful tool in:

(a) organ transplantation (b) sex determination
(c) forensic science (d) genetic engineering

22. The telomeres of eukaryotic chromosomes consist of short sequences of
(a) thymine rich repeats
(b) cytosine rich repeats
(c) adenine rich repeats
(d) guanine rich repeats

23. What does "lac" refer to in what we call the lac operon?
(a) The number 1,00,000
(b) Lactose
(c) Lactase
(d) Lac insect

24. In transgenics, expression of transgene in target tissue is determined by
(a) enhancer (b) transgene
(c) promoter (d) reporter

25. In the genetic code dictionary, how many codons are used to code for all the 20 essential amino acids ?
(a) 60 (b) 20
(c) 64 (d) 61

26. Degeneration of a genetic code is attributed to the
(a) third member of a codon
(b) first member of a codon
(c) second member of a codon
(d) entire codon

27. Transformation experiment was first performed on which bacteria?
(a) *E.coli*
(b) *Diplococcus pneumoniae*
(c) *Salmonella*
(d) *Pasteurella pestis*

28. Exon part of m- RNAs have code for
(a) protein (b) lipid
(c) carbohydrate (d) phospholipid

29. Which one of the following does not follow the central dogma of molecular biology?
(a) Pea (b) *Mucor*
(c) *Chlamydomonas* (d) HIV

30. Which one of the following also acts as a catalyst in a bacterial cell ?
(a) 5 s rRNA (b) sn RNA
(c) hn RNA (d) 23 s rRNA

31. For transformation, micro-particles coated with DNA to be bombarded with gene gun are made up of :
(a) Silver or Platinum (b) Platinum or Zinc
(c) Silicon or Platinum (d) Gold or Tungsten

32. Methyl guanosine triphosphate is added at 5' end of hn RNA in a process of
(a) tailing (b) splicing
(c) capping (d) None of these

33. 5' end of a polynucleotide contains
(a) hydroxyl group (b) methyl group
(c) carboxyl group (d) phosphate group

34. Variable part of DNA molecule is
(a) phosphate (b) sugar
(c) nitrogen base (d) All of these

35. Supercoiled DNA occurs in
(a) prokaryotes as well as eukaryotes
(b) prokaryotes only
(c) eukaryotes only
(d) None of these

36. Nucleotide arrangement in DNA can be seen by
(a) X-ray crystallography (b) electron microscope
(c) ultracentrifuge (d) light microscope

37. Which enzymes will be produced in a cell in which there is a nonsense mutation in the lac Y gene?
(a) Lactose permease
(b) Transacetylase
(c) Lactose permease and transcetylase
(d) β- galactosidase

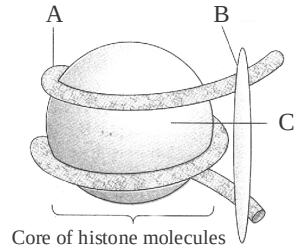
38. Uridine, present only in RNA is a
(a) Pyrimidine (b) Nucleoside
(c) Nucleotide (d) Purine

39. Which of the following is not a property of the genetic code?
(a) Universal (b) Non-overlapping
(c) Ambiguous d) Degeneracy

40. One of the most frequently used techniques in DNA fingerprinting is
(a) AFLP (b) VNTR
(c) SSCP (d) SCAR

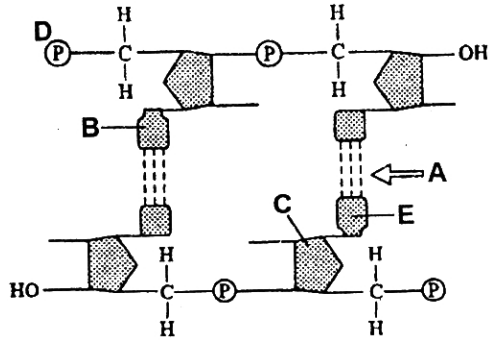
41. In an inducible operon, the genes are
(a) Always expressed
(b) Usually not expressed unless a signal turns them "on"
(c) Usually expressed unless a signal turns them "off"
(d) Never expressed

42. Identify A, B and C of a nucleosome.



(a) A – DNA; B – H1 histone; C – Histone octamer
(b) A – H1 histone; B – DNA; C – Histone octamer
(c) A – Histone octamer; B – RNA; C – H1 histone
(d) A – RNA; B – H1 histone; C – Histone octamer

43.



(a) A–Hydrogen bonds, B–Pyrimidine, C–Hexose (deoxyribose) sugar, D–5' end, E–Purine base

(b) A–Hydrogen bonds, B–Purine base, C–Hexose (deoxyribose) sugar, D–5' end, E–Pyrimidine

(c) A–Hydrogen bonds, B–Pyrimidine, C–Pentose (deoxyribose) sugar, D–5' end, E–Purine base

(d) A–Hydrogen bondsm, B–Purine base,C–Pentose (deoxyribose) sugar, D– 5' end, E– Pyrimidin**e**

44. Match Column-I with Column-II

Column I		**Column II**	
A.	Helicase	**1.**	Joining of nucleotides
B.	Gyrase	**2.**	Opening of DNA
C.	Primase	**3.**	Unwinding of DNA
D.	DNA polymerase III	**4.**	RNA priming

(a) A → (2); B → (1); C → (3); D → (4)

(b) A → (2); B → (1); C → (4); D → (3)

(c) A → (4); B → (3); C → (1); D → (2)

(d) A → (2); B → (3); C → (4); D → (1**)**

45. Match Column-I with Column-II

Column I		**Column II**	
A.	Operator sit**e**	**1.**	Binding site for RNA polymerase
B.	Promoter sit**e**	**2.**	Binding site for repressor molecule
C.	Structural gen**e**	**3.**	Codes for enzyme protein
D.	Regulator gen**e**	**4.**	Codes for repressor molecules

(a) A → (2); B → (1); C → (3); D → (4)

(b) A → (2); B → (1); C → (4); D → (3)

(c) A → (4); B → (3); C → (1); D → (2)

(d) A → (2); B → (3); C → (1); D → (4)

46. Select the two correct statements out of the four (a–d) given below about *lac* operon.

1. Glucose or galactose may bind with the repressor and inactivate it.

2. In the absence of lactose the repressor binds with the operator region.

3. The z-gene codes for permease.

4. This was elucidated by Francois Jacob and Jacque Monod.

(a) 2 and 3 (b) 1 and 3

(c) 2 and 4 (d) 1 and 2

47. The differene(s) between mRNA and tRNA is / are that –

1. mRNA has more elaborated 3-dimensional structure due to extensive base - pairing.

2. tRNA has more elaborated 3-dimensional structure due to extensive pairing.

3. tRNA is usually smaller than mRNA.

4. mRNA bears anticodon but tRNA has codons.

(a) 1 and 3 (b) All of these

(c) 2 and 3 (d) 1, 2 and 3

48. Which one(s) is / are correct?

1. In prokaryotes single type of RNA polymerase can transcribe mRNA, tRNA and rRNA.

2. In eukaryotes RNA polymerase I transcribes rRNA (28S, 18S and 5.8S) whereas RNA pol III is responsible for transcription of tRNA, 5S rRNA and Sn RNAs.

3. RNA pol II transcribes hnRNA in eukaryotes.

4. Ribosomal large subunit has P and A-sites.

(a) 1 and 3 (b) All of these

(c) 2, 3 and 4 (d) 1, 2 and 3

DIRECTIONS for Qs. 49 and 50 : Each question contains STATEMENT-1 (Assertion) and STATEMENT-2 (Reason). Each question has 4 choices (a), (b), (c) and (d) out of which ONLY ONE is correct.

(a) Statement- 1 is True, Statement-2 is True, Statement-2 is a correct explanation for Statement -1

(b) Statement -1 is True, Statement -2 is True ; Statement-2 is NOT a correct explanation for Statement - 1

(c) Statement - 1 is True, Statement- 2 is False

(d) Both the Statements are False.

49. **Statement 1 :** One of the two strands of DNA is called sense strand and other is called antisense strand.

Statement 2 : Sense strand of DNA forms complementary RNA.

50. **Statement 1 :** UAA, UAG and UGA terminate protein synthesis.

Statement 2 : They are not recognised by tRNA.

EXERCISE - 3
Exemplar & Past Years NEET/AIPMT Questions

Exemplar Questions

1. In a DNA strand the nucleotides are linked together by
(a) glycosidic bonds (b) phosphodiester bonds
(c) peptide bonds (d) hydrogen bonds

2. Nucleoside differs from a nucleotide. It lacks the :
(a) base (b) sugar
(c) Phosphate group (d) Hydroxyl group

3. Both deoxyribose and ribose belong to a class of sugars called
(a) Trioses (b) hexoses
(c) Pentoses (d) Polysaccharides

4. The fact that a purine always paired base through hydrogen bonds with a pyrimidine base leads to, in the DNA double helix.
(a) the antiparallel nature
(b) the semiconservative nature
(c) uniform width throughout DNA
(d) uniform length in all DNA

5. The net electric charge on DNA and histones is
(a) both positive (b) both negative
(c) both (a) and (b) (d) zero

6. The promoter site and the terminator site for transcription are located at
(a) 3' (downstream) end and 5' (upstream) end, respectively of the transcription unit
(b) 5' (upstream) end and 3' (downstream) end, respectively of the transcription unit
(c) 5' (upstream) end
(d) 3' (downstream) end

7. Which of the following statements is the most apporpriate for sickle-cell anaemia?
(a) It cannot be treated with iron supplements
(b) It is molecular disease
(c) It confers resistance to acquiring malaria
(d) All of the above

8. One of the following is true., with respect to AUG
(a) It codes for methionine only
(b) It is also an initiation codon
(c) It code for methionine in both prokaryotes and eukaryotes
(d) All of the above

9. The first genetic material could be
(a) Protein (b) Carbohydrates
(c) DNA (d) RNA

10. With regard to mature mRNA in eukaryotes
(a) exons and introns do not appear in the mature RNA
(b) exons appear but introns do not appear in the mature RNA
(c) introns appear but exons do not appear in the mature RNA
(d) Both exons and introns appear in the mature RNA

11. The human chromosome with the highest and least number of genes in them are respectively
(a) chromosome 21 and Y (b) chromosome 1 and X
(c) chromosome 1 and Y (d) chromosome X and Y

12. Who amongst the following scientists had no contribution in the development of the double helix model for the structure of DNA ?
(a) Rosalind franklin (b) Maurice Wilkins
(c) Erwin Chargaff (d) Meselson and Stahl

13. DNA is a polymer of nucleotides are linked to each other by 3'–5' phosphodiester bond. To prevent polymerisation of nucleotides, which of the following modifications would you choose ?
(a) Replace purine with pyrimidines
(b) Remove/ Replace 3' OH group in deoxyribose
(c) Remove/ Replace 2' OH group with some other group in deoxyribose
(d) Both (b) and (c)

14. Discontinuous synthesis of DNA occurs in one strand, because
(a) DNA molecule being synthesised is very long
(b) DNA dependent DNA polymerase catalyses polymerisation only in one direction (5′→3′)
(c) It is a more efficient process
(d) DNA ligase has to have a role

15. Which of the following steps in transcription is catalysed by RNA polymerase ?
(a) Initiation (b) Elongation
(c) Termination (d) All of these

16. Control of gene expression takes place at the level of
(a) DNA- replication (b) transcription
(c) Translation (d) None of these

17. Regulatory proteins are the accessory proteins that interact with RNA polymerase and affect its role in transcription. Which of the following statements is correct about regulatory protein?
(a) They only increase expression
(b) They only decrease expression
(c) They interact with RNA polymerase but do not affect the expression
(d) They can act both as activators and as repressors

18. Which was the last human chromosome to be compeletely sequenced?
(a) chromosome 1 (b) chromosome 11
(c) chromosome 21 (d) chromosome X

19. Which of the following are the functions of RNA?
(a) It is carrier of genetc information from DNA to ribosomes synthesising polypeptide
(b) It carries amino acids to ribosomes
(c) It is a constituent of ribosomes
(d) All of the above

20. While analysing the DNA of an organism a total number of 5386 nucleotides were found out of which the proportion of different bases were Adenine = 29% Guanine = 17% Cytosine = 32%, Thymine = 17%. Considering the Chargaffs rule it can be concluded that
(a) it is double-stranded circular DNA
(b) it is single-stranded DNA
(c) it is a double-linear DNA
(d) No conclusion can be drawn

21. In some viruses, DNA is synthesised by using RNA as template. Such a DNA is called.
(a) A-DNA (b) B-DNA
(c) cDNA (d) rDNA

22. If meselson and Stahl's experiment is continued for four generations in bacteria, the ratio of $15_N/15_N : 15_N/14_N : 14_N/14_N$ containing in the fourth generation would be
(a) 1 : 1 : 0 (b) 1 : 4 : 0
(c) 0 : 1 : 3 (d) 0 : 1 : 7

23. If the sequence of nitrogen bases of the coding strand of DNA in transcription unit is
5′-ATGAATG-3′
The sequence of bases in its RNA transcript would be
(a) 5′-AUGAAUG-3′ (b) 5′-UACUUAC-3′
(c) 5′-CAUUCAU-3′ (d) 5′-G UAAGUA-3′

24. The RNA polymerase holoenzyme transcribes
(a) The promoter structural gene and the terminator region
(b) the promoter and the termintor region
(c) The structural gene and the terminator regions
(d) the structure gene only

25. If the base sequence of a codon in mRNA is 5'-AUG-3' the sequence of tRNA pairing with it must be
(a) 5′- UAC -3′ (b) 5′- CAU -3′
(c) 5′- AUG -3′ (d) 5′- GUA -3′

26. The amino acid attaches to the tRNA at its
(a) 5′-end (b) 3′-end
(c) anti codon site (d) DHU loop

27. To initiate translation, the mRNA first binds to
(a) the smaller ribosomal sub-unit
(b) the larger ribosomal sub-unit
(c) the whole ribosome
(d) No such specificity exists

28. In *E.coil* the lac operon gets switched on when
(a) lactose is present and it binds to the repressor
(b) repressor binds to operator
(c) RNA polymerase binds to the operator
(d) lactose is present and it binds to RNA polymerase

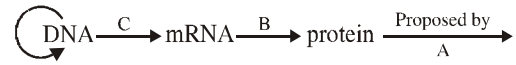
NEET/AIPMT (2013-2017) Questions

29. Which enzymes will be produced in a cell in which there is a nonsense mutation in the lac Y gene? ***[2013]***
(a) Lactose permease
(b) Transacetylase
(c) Lactose permease and transcetylase
(d) β- galactosidase

30. Uridine, present only in RNA is a ***[NEET Kar. 2013]***
(a) Pyrimidine (b) Nucleoside
(c) Nucleotide (d) Purine

31. Which of the following is **not** a property of the genetic code? ***[NEET Kar. 2013]***
(a) Universal (b) Non-overlapping
(c) Ambiguous (d) Degeneracy

32. One of the most frequently used techniques in DNA fingerprinting is ***[NEET Kar. 2013]***
(a) AFLP (b) VNTR
(c) SSCP (d) SCAR

33. 

The figure gives an important concept in the genetic implication of DNA. Fill the blanks A, B and C. ***[NEET Kar. 2013]***
(a) A – Francis Crick; B – translation; C – transcription
(b) A – Maurice Wilkins; B – transcription; C – translation
(c) A – James Watson; B – replication; C – extension
(d) A – Erwin Chargaff; B – translation; C – replication

34. In an inducible operon, the genes are ***[NEET Kar. 2013]***
(a) Always expressed
(b) Usually not expressed unless a signal turns them "on"
(c) Usually expressed unless a signal turns them "off"
(d) Never expressed

35. Which one of the following is **wrongly** matched? ***[2014]***
(a) Transcription – Writing information from DNA to tRNA.
(b) Translation – Using information in mRNA to make protein
(c) Repressor protein – Binds to operator to stop enzyme synthesis.
(d) Operon – Structural genes, operator and promoter.

36. Transformation was discovered by: ***[2014]***
(a) Meselson and Stahl (b) Hershey and Chase
(c) Griffith (d) Watson and Crick

37. Select the correct option: ***[2014]***
Direction of RNA Direction of reading of synthesis the template DNA strand
(a) 5′—3′ 3′—5′
(b) 3′—5′ 5′—3′
(c) 5′—3′ 5′—3′
(d) 3′—5′ 3′—5′

38. In sea urchin DNA, which is double stranded, 17% of the bases were shown to be cytosine. The percentages of the other three bases expected to be present in this DNA are :- ***[2015 RS]***
(a) G-17%; A-16.5%; T-32.5%
(b) G-17%; A-33%; T-33%
(c) G-8.5%; A-50%; T-24.5%
(d) G-34%; A-24.5%; T-24.5%

39. The movement of a gene from one linkage group to another is called : ***[2015 RS]***
(a) Duplication (b) Translocation
(c) Crossing over (d) Inversion

40. Gene regulation governing lactose operon of *E.coli* that involves the lac I gene product is : ***[2015 RS]***
(a) Negative and inducible because repressor protein prevents transcription
(b) Negative and repressible because repressor protein prevents transcription
(c) Feedback inhibition because excess of b-galactosidase can switch off trascription
(d) Positive and inducible because it can be induced by lactose

41. Which one of the following is not applicable to RNA? ***[2015 RS]***
(a) 5' phosphoryl and 3' hydroxyl ends
(b) Heterocyclic nitrogenous bases
(c) Chargaff's rule
(d) Complementary base pairing

42. Satellite DNA is important because it : ***[2015 RS]***
(a) shows high degree of polymorphism in population and also the same degree of polymorphism in an individual, which is heritable from parents to children.
(b) does not code for proteins and is same in all members of the population
(c) codes for enzymes needed for DNA replication
(d) codes for proteins needed in cell cycle.

43. A complex of ribosomes attached to a single strand of RNA is known as ***[2016]***
(a) Polysome (b) Polymer
(c) Polypeptide (d) Okazaki fragment

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

45. Which one of the following is the starter codon? ***[2016]***
(a) AUG (b) UGA
(c) UAA (d) UAG

46. Which of the following is required as inducer(s) for the expression of Lac operon? ***[2016]***
(a) Glucose (b) Galactose
(c) Lactose (d) Lactose and galactose

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

48. DNA fragments are: ***[2017]***
(a) Negatively charged
(b) Neutral
(c) Either positively or negatively charged depending on their size
(d) Positively charged

49. If there are 999 bases in an RNA that codes for a protein with 333 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? ***[2017]***
(a) 11 (b) 33
(c) 333 (d) 1

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

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

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

53. The association of histone H1 with a nucleosome indicates: ***[2017]***
(a) DNA replication is occurring.
(b) The DNA is condensed into a Chromatin Fibre.
(c) The DNA double helix is exposed.
(d) Transcription is occurring.

Hints & Solutions

EXERCISE - 1

1. (b) Lactose operon in *E.coli* is a catabolic pathway in which the structural genes remain switched off unless the inducer (Lactose) is present in the medium.
2. (a) DNA fingerprinting is the technique of determining nucleotide sequences of certain areas of DNA which are unique to each individual. DNA contains non cistronic hypervariable repeat sequences called VNTR. DNA fingerprinting involves the identification of these VNTRs.
3. (a) In negative (repressible) operon, the repressor co-repressor complex binds with the operator. The free repressor cannot bind to the operator.
4. (a) Operator gene allows the functioning of the operon.
5. (c) If the *lac* repressor is non functional, it cannot bind the operator site and transcription of the *lac* operon will occur at all times, whether or not lactose is present.
6. (d)
7. (d) Option *a* refers to the *lac* and *trp* repressors, option *b* to the CRP protein, and option *c* refers to promoter that have different transcriptional efficiencies.
8. (d) The first effect of any signal molecule must involve the binding of the molecule to a receptor.
9. (a) 10. (b)
11. (d) All of these are ways that gene expression can be regulated, but transcriptional control is clearly the most common mechanism.
12. (b) 13. (d) 14. (a)
15. (b) The presence or absence of tryptophan determines whether the genes that code the necessary enzymes in tryptophan synthesis will even be transcribed.
16. (d) The fact that numerous disease genes have been discovered relationships between organisms.
17. (a)
18. (a) A hydroxyl group at the 3' position of a nucleotide is necessary for the binding of any additional nucleotides. If this hydroxyl group were absent, no other nucleotides could be added to a growing strand.
19. (c) 20. (b)
21. (c) Option (a) describes transcription in eukaryotic cells; Option (b) describes translation.
22. (c) UAG is a stop codon and translation would terminate at that site.
23. (c) A functional strand of mRNA must have a start and a stop codon. The start codon often also codes for the amino acid methionine, which may or may not end up being a part of the final protein. However, the stop codon would not code for an amino acid. Thus, with 66 codons in the mRNA, there could be as many as 65 amino acids in the protein product.
24. (b) 25. (a)
26. (a) DNA polymerase adds nucleotides to an existing nucleotide strand.
27. (d) Okazaki fragments are short pieces of newly synthesized DNA. The production of each of these fragments is dependent on a beginning RNA primer. The small fragments are ultimately ligated (connected) together to form the lagging strand.
28. (a) DNA polymerase cannot initiate the building of a nucleotide strand; it can only add to an existing strand. Thus, RNA primers are necessary to begin DNA synthesis.
29. (a) For the integrity of DNA to be maintained, repair mechanisms must be active during synthesis, modification, and utilization of DNA.
30. (c) DNA replication is an energy-consuming process that must have an input of energy to proceed. Energy is provided in the breaking of the triphosphate tails of each nucleotide.
31. (d) 32. (c)
33. (a) Okazaki fragments are found only along the lagging strand.
34. (b) Hershey and Chase used radioactive labeling of sulphur and phosphorus to clearly demonstrate that DNA, and not protein, is the material that carries hereditary information.
35. (d) Even though DNA replication typically occurs millions of times during the life of a multicellular organism, it is remarkably error-free. Those errors that do occur are usually corrected with a high degree of reliability.
36. (c) In DNA replication, each strand of the original molecule serves as a template for the formation of a new strand, thus, each new molecule will have half of its nucleotides (and the chemical label) from the original molecule.
37. (b) Protein synthesis is a two-step process involving transcription in the cell nucleus followed by translation in the cytoplasm. All the other choices are either factually inaccurate or, if accurate, need not necessarily take place for protein synthesis to occur.
38. (c) 39. (c)
40. (d) Inaccurate removal of introns can create mRNAs that are missing coding sequence or that have extra non-coding sequences. Transposable genetic elements can move into the coding regions of genes, inactivating those gene products. Moving a gene to a heterochromatic (transcriptionally inactive) region of a chromosome results in that DNA beings inaccessible to the transcription complex.
41. (a) RNA processing occurs after transcription and before translation.
42. (a) The presence of testosterone enables RNA polymerase to transcribe certain male-specific genes.

43. (b) Regulator is a gene which forms a biochemical for suppressing the activity of operator gene. Promoter is the gene which provides the point of attachment to RNA polymerase required for transcription of structural genes.
44. (d) For the formation of initiation complex during translation of *m*RNA, GTP is also required. The initiator AUG codes for the formylmethionine in prokaryotes.
45. (a) AUG is initiating codon. UCG codes for serine, UUU codes for phenylalanine, UGU codes for cysteine.
46. (b) 47. (b)
48. (b) UAA is the stop codon. Therefore at 25th amino acid the synthesis of polypeptide stops. So, a polypeptide of 24 Amino acid is formed.
49. (a) Ribosomes are the sites of protein synthesis. Mitochondria being a semi autonomous organelle has its own protein synthesizing machinery.
50. (d) During the activation of amino acids, in the presence of Mg^{2+} and ATP an amino acid gets attached to a specific enzyme aminoacyl t-RNA synthetase. Pyrophosphate is released which breaks up to release energy. During translocation, in the presence of the enzyme translocase and energy from GTP the ribosome moves in such a way that the peptidyl bearing t-RNA of A - site comes to lie on the P-site, exposing a new codon at A - site. In the peptidyl transferase reaction energy is provided by GTP.
51. (a) According to the Wobble hypothesis, tRNA anticodon has the ability to wobble at its 5′end by pairing with even non-complementary base of mRNA codon. It corresponds to third base degeneracy of the codons.
52. (c) In transition substitution a purine is replaced by another purine base (A with G or vice versa). In transversion substitution a purine is replaced by a pyrimidine base or vice versa. Frameshift mutation is a type of mutation where the reading of codons is changed due to insertion or deletion of nucleotides. Transition is the formation of RNA over the template of DNA.
53. (d)
54. (b) Crossing over occurs between non–sister chromatids of two homologous chromosomes. Homologous chromosomes form bivalent. Crossing over occurs between chromosomes in a nucleus.
55. (c) According to Chargaff purines and pyrimidines are in equal amounts. Purine (adenine) is equimolar with pyrimidine (thymine) and purine (guanine) is equimolar with pyrimidine (cytosine). Base ratio is specific for species.
56. (c)
57. (a) The number of base pairs (bp) found in the haploid genome of humans is 2.9×10^9.
58. (d) Prokaryotic chromosomes are circular and contain termination sequences.
59. (c) 60. (a)
61. (b) Nucleosomes condense the DNA. Heterochromatin is transcriptionally inactive, while euchromatin is transcriptionally active.
62. (b) Histone proteins are used to coil the large amount of DNA found in eukaryotes so that it can be packaged more efficiently within the cell. Prokaryotes do not face this problem because they have much less DNA.
63. (a) Griffith was a physician trying to find a way to effectively treat or cure pneumonia. Nothing much was known about the structure or function of DNA at the time he did his work.
64. (c) Hydrogen bonds connect the bases on opposite strands of the DNA molecule, which is the reason that the helix can be unwound and separated relatively easily. All other bonds in file molecule are covalent.
65. (b)
66. (c) Since the building blocks of DNA were thought to be structurally simple and few number, biologists prior to the 1940s thought that only proteins could have the necessary complexity and diversity to be the hereditary material.
67. (c) Since strain R bacteria do not harm the mouse, this experiment is the equivalent of injecting the virulent strain S only. Thus the mouse will die, and you will find living strain S bacteria in its blood.
68. (c) Telomerase is a ribonucleoprotein which synthesize the rich strand of telomeres in DNA. **Telomerase** is an enzyme that adds specific DNA sequence repeats ("TTAGGG" in all vertebrates) to the 3' end of DNA strands in the telomere regions, which are found at the ends of eukaryotic chromosomes.
69. (c) The available evidence indicates that both DNA and RNA are present in the sample. The logic here is that thymine is unique to DNA, and both ribose and uracil are found only in RNA. With this evidence, however, you can say nothing about the types of RNA present in the sample, or whether the sample is actually from the killer.
70. (d) Since the total number of bases is the same, either no deletions or insertions occurred, or an equal number of each must have occurred. In this case, however, simply comparing each strand base-for-base shows that the more likely, explanation is that multiple substitutions took place along the sequence.
71. (c) These researchers were able to isolate nearly pure DNA samples. It was only these samples that provided transformation activity.
72. (d) Chargaff found that the relative ratios of purine to pyrimidines were equal. Adenine and guanine are purines and cytosine and thymine are pyrimidines; therefore, ratios of adenine and thymine should be equal. Chargaff also found that there is no conserved ratio between specific pairs (*e.g.*, A + T and G + C).
73. (b) If 30 percent of DNA is adenine, then by Chargaff's rule 30 percent will be thymine. The remaining 40 percent of the DNA is cytosine and guanine. Since the ratio of cytosine to guanine must be equal, then each accounts for 20 percent of the bases.

74. (b) A sequential expression of a set of human genes is the DNA sequence. Because gene is the functional part of DNA sequence.

75. (d) Splicing is the removal of introns and joining the exons in a defined order in a transcription unit. In molecular biology, splicing is a modification of RNA after transcription, in which introns are removed and exons are joined.

EXERCISE - 2

1. (d) Replication begins at the *Ori* - origin of replication and proceeds on both sides from the *Ori*. Unidirectional replication is rare. RNA primers are involved in both prokaryotes and eukaryotes.

2. (b)

3. (b) Operons are segments of genetic material which function as regulated unit or units that can be switched on and switched off. An operon consists of one to several structural genes. (Three in *lac* operon).
These are genes which produce mRNAs for forming polypeptides / proteins / enzymes. Z (produces enzyme β-galactosidase for splitting lactose into glucose and galactose). Y (produces enzyme galactoside permease required in entry of lactose). A (produces enzyme thiogalactoside trans-acetylase).
The three structural genes of the operon produce a single polycistronic mRNA.

4. (b) About 28 base pairs from transcription start site are TATA boxes. After 40 bases from TATA boxes appears LAAT boxes. Both of these sequence serve as recognition site in eukaryotic promoters (Transcription in eukaryotic genes in a far more complicated process than in prokaryotes).

5. (c) Reverse transcriptase (RNA dependent DNA polymerase) is present in some retroviruses e.g. HIV virus.

6. (b) The complementary base will pair with each base on the template to form the specific sequence shown.

7. (c) Beadle & Tatum postulated the theory of 'One-gene-one-enzyme' in which they stated that in any living cell there are number of genes present on chromosomes in a linear fashion. One single gene controls the synthesis of one particular enzyme (or protein) in the cell which is responsible for its phenotypic character.

8. (c) Okazaki fragments in DNA are linked up by the enzyme DNA *ligase*. Replication always occur in 5' - 3' direction. Okazaki fragments synthesized on 3' - 5' DNA template, join to form lagging strand which grows in 3' - 5' direction.

9. (a) The nucleosome model explains the packaging of histone proteins and DNA in the chromatin material which forms the chromosome.

10. (d) It was given by Geneticists George W. Beadle and E. L. Tatum which states that each gene in an organism controls the production of a specific enzyme. It is these enzymes that catalyze the reactions that lead to the phenotype of the organism.

11. (d) The process of formation of protein sequence from DNA strand is called transcription which requires RNA polymerase chain. RNA polymerase chains are of 3-types in eukaryotes
(i) RNA polymerase-I
(ii) RNA polymerase II
(iii) RNA polymerase-III

12. (d) In the DNA molecule, there are two strands which run anti-parallel one is 5' - 3' direction and other in 3' -5' direction, the two chains are held together by hydrogen bonds between their bases. Adenine (A), a purine of one chain is exactly opposite thymine (T), a pyramidine of the other chain. Similarly, cytosine (C), a pyrimidine lies opposite guanine (G), a purine. This allows a sort of lock & key arrangement between large sized purine & small sized pyrimidine. It is strengthened by the appearance of hydrogen bonds between the two.

13. (b) GCU indicates alanine but GUU indicates valine.
Stop codons are UAG, UGA and UAA
AUG is the most common start codon
which does for methionine.
UUA indicates leucine but UCA indicates serine.

14. (d) Purine is an organic nitrogenous base sparingly soluble in water, that gives rise to a group of biologically important derivatives, notably adenine and guanine, which occur in nucleotides and nucleic acids (DNA and RNA).

15. (d) Haploid describes a nucleus cell or organism with a single set of unpaired chromosomes. The haploid number is designated as X. Reproductive cells, formed as a result of meiosis are diploid. Fusion of two such cells restores the normal diploid number. Therefore, haploids are more suitable for mutation studies than the diploids. This is because all mutations, whether dominant or recessive are expressed in haploids.

16. (d) Theodor O. Diener discovered the Potato Spindle Tuber Viroid ("PSTVd"), the first viroid ever identified, in 1971. PSTVd is a small, circular RNA molecule. Dr. Diener discovered that the pathogen causing potato spindle tuber disease is not a virus, as previously believed, but a much smaller, free RNA molecule.

17. (d) The genetic code consists of 64 triplets of nucleotides. These triplets are called codons. With three exceptions, each codon encodes for one of the 20 amino acids used in the synthesis of proteins. That produces some redundancy in the code. Most of the amino acids being encoded by more than one codon. The genetic code can be expressed as either RNA codons or DNA codons.

18. (a) Semiconservative replication of DNA was first demonstrated in *Escherichia coli*. *E. coli* is a common type of bacteria

that can get into food, like beef and vegetables. The strange thing about these bacteria is that they are not always harmful to you. *E. coli* normally lives inside your intestines, where it helps your body breakdown and digest the food you eat.

19. (d) Nirenberg and Mathaei (1961) experimentally proved that a single amino acid is determined by a sequence of three nitrogen bases. The sequence of three nitrogen bases determining a single amino acid is called a triplet code. Nirenberg and Mathaei experiments cracked the DNA and discovered unequivocally that a genetic code is a triplet.
20. (b) Genetic code is non ambiguous. There is no ambiguity for a particular codon. A particular codon will always code for the same amino acid, where ever it is found.
21. (c) Satellite DNA is useful in forensic science. The polymorphism of minisatellite, microsatellite and minivariant repeats is analysed for DNA finger printing, DNA profiling. It helps in the resolution of crimes, legal disputes etc.
22. (c) Telomeres are non sticky terminal ends of the chromosomes. It has heterochromatin and repetitive DNA.
23. (b) Lactose operon in *E.coli* is a catabolic pathway in which the structural genes remain switched off unless the inducer (Lactose) is present in the medium.
24. (b) Transgenic organisms are genetically modified organisms.
25. (d) Out of a total of 64 codons, 3 codons do not make any sense. Hence only 61 codons are used in the formation of the 20 essential amino acids (polypeptides).
26. (a) According to the Wobble hypothesis, tRNA anticodon has the ability to wobble at its 5′end by pairing with even non-complementary base of mRNA codon. It correspond to third base degeneracy of the codons.
27. (b) Transformation is change in genetic material of an organism by obtaining genes from outside.
28. (a) Exons are the coding part of mRNA.
29. (d) HIV viruses do not follow central dogma. Central dogma is a one way flow of information from DNA to mRNA and then to protein.

$$\text{DNA} \underset{\text{reverse transcription}}{\overset{\text{transcription}}{\rightleftarrows}} \text{mRNA} \xrightarrow{\text{translation}} \text{Protein}$$

30. (d) 23s rRNA acts as a catalyst in a bacterial cell.
31. (d) For gene transfer into the host cell without using vector microparticles made of tungsten and gold coated with foregin DNA are bombarded into target cells at a very high velocity.
32. (c) 33. (d) 34. (c) 35. (a)
36. (a) In 1953 Wilkins obtained very fine X-ray crystallographic pictures of DNA from which Watson and Crick developed the double helix model of DNA.
37. (d) A nonsense mutation is the one which stops polypeptide synthesis due to formation of a terminating or non sense codon. e.g. ATT(UAA), ATC (UAG), ACT(UGA) . The lactose or lac operon of *Esherichia coli* contains structural genes (Z, Y, A) . If Y codes for termination of polypeptide chain then only the product of 'Z' gence teranscribe to form β galactosidase.
38. (b) The combination of pentose sugar with nitrogenous bases (purines or pyrimidines) is called nucleoside. Examples are adenosine, guanosine, cytidine, thymidine and uridine.
39. (c) Genetic code is the relationship of amino acid sequence in a polypeptide and nucleotide/base sequence in mRNA/ antisense strand of DNA.
It is **universal,** *i.e.*, a codon specifies the same amino acid in all organisms, **non-overlapping**, *i.e.*, adjacent codons are independent with no base being member of two codons, **degeneracy**, *i.e.*, some amino acids are coded by more than one codon, hence the code is degenerate, **unambiguous,** *i.e.*, one codon codes for only one amino acid.
40. (b) The technique of DNA fingerprinting was developed by Dr. Alec Jeffrey in 1984. It is a technique generally using repeated sequences (repetitive DNA) in the human genome that produces a pattern of band that is unique for every individuals. These short nucleotide repeats vary in number from person to person and are called **variable number of tandem repeat (VNTR).** VNTR belongs to class of satellite DNA referred to as minisatellite.
41. (b) Inducible operons are usually switched off. This is a type of operon which is switched on when a chemical called inducer is present. The inducer is almost always a substrate**.**
42. (a) 43. (d) 44. (d) 45. (a)
46. (c) **Jacob** and **Monod** proposed the *lac* operon of *E. coli*. The *lac* operon contains a promoter, an operator, and three structural genes called Z, Y, and A, coding for the enzyme, β galactosidase, permease and transacetylase respectively. The *lac* regulator gene, designated as *i* gene, codes for repressor. In the absence of the inducer, the repressor binds to the *lac* operator, preventing RNA polymerase from binding to the promoter and thus transcribing the structural gene.
47. (c) 48. (b)
49. (b) Only one of the two strands of DNA possesses correct hereditary information. It is known as sense strand. Its complementary strand is called antisense strand. Antisense RNA that is made from the DNA strand that means it is complementary to the sense strand of the DNA.
50. (a)

EXERCISE - 3

Exemplar Questions

1. (b) In a DNA strand the nucleotides are linked together by 3'–5' phosphodiester linkage (bonds) to form a dinucleotide. To form a polynucleotide chain, more nucleotides can be joined.
2. (c) A nitrogenous base is attached to the pentose sugar by an N- glycosidic linkage to form a nucleoside, i.e., Nucleoside = Nitrogen base + Pentose sugar. When a phosphate group is attached to the 5'-OH of a nucleoside through phosphodiester linkage, a nucleotide is formed, *i.e*. Nucleotide = Nitrogen base + Pentose sugar + phosphate (PO_4)
   So, a nucleoside differs from a nucleotide as it lacks the phosphate group.
3. (c) Both deoxyribose and ribose belong to the class pentoses as it contains '5' carbon atoms.
4. (a) The diameter of the strand always constant due to a pairing of purine (adenine and guanine) and pyrimidine (cytosine and thymine). The specific bonding gives uniformity and keep strands together.
5. (c) DNA consists of a nitrogenous base, pentose sugar and phosphate group. Due to the presence of phosphate group $\left(PO_4^{3-}\right)$, DNA has negative charge
   Histones are rich in the basic amino acid lysines and arginines, that carry positive charges in their side chains, Therefore, histones are positively charged.
6. (b) The promoter is a DNA sequence that provides the binding site for RNA polymerase for initiation of transcription. The promoter is located towards 5'-end (upstream) of structural gene and terminator site is located towards 3 end (downstream of the coding strand).
7. (d) Sickel- cell anaemia is an autosome linked recessive trait. Only the homozygous individuals for $Hb^s{}_2$ *i.e.*, $Hb^s\ Hb^s$ show the diseased phenotype. The heterozygous individuals (Hb^s / Hb^A) are carriers.
   It is also known that heterozygous, having both types of haemoglobin. It shows resistance to malaria infection because the body targets the *P. falciparum* (protozoan) infected cells for destruction of RBC.
8. (d) Polypeptide synthesis is signalled by two initiation codons commonly AUG or methionine codon and rarely GUG or valine codon. Since there are 64 triplet codons and only 20 amino acids, the insertion of some amino must get influenced by more than one codon.
   Only tryptophan (UGG) and methonine (AUG) are specified by single codons. AUG codes for methionine in both prokaryotes and eukaryotes.
9. (d) The first genetic material was considered as RNA. There are now enough evidence to suggest that essential life processes (such as metabolism, translation, splicing etc.) evolved around RNA.
   It acts as a genetic material as well as catalyst (there are some important biochemical reactions in living systems that are catalysed by RNA catalysts and not by protein enzymes). But, RNA being a catalyst was reactive and hence unstable and not by protein enzymes) but, RNA being a catalyst was reactive and hence unstable.
   Therefore, DNA has evolved from RNA with chemical modifications that make it more stable.
10. (b) The coding sequence or expressed sequences are defined exons. The exons appear in mature or processed RNA and are interrupted by introns or intervening sequence which do not appear in mature or processed RNA.
11. (c) In human chromosome 1 has highest genes (2968 approx.) and the Y has the fewest (231 aprox). genes
12. (d) In 1953 **James Watson** and **Francis Crick**, based on the X-ray diffraction data produced by **Maurice Wilkins** and **Rasalind Franklin** proposed a double helix model of DNA.
    Erwin chargaff observed that, in double-stranded DNA, the ratios between adenine and thymine and guanine and cytosine are constant and equal. **Metthew Meselson** and **franklin stahl** in 1958 performed experiments on *E. Coli* to prove that DNA replicates semiconservatively. But had no contribution it the development of double helix model.
13. (b) The enzyme called DNA polymerase progressively adds deoxyriboncleotides to the free 3′– end of the growing polynucleotide chain so, that replication of he 3'–5' strand of the DNA molecule is continous (growth of the new strand in 5′→3′ direction). So, to prevent polymerisation of nucleotides 3 OH group in deoxyribose should be replaced/ removed.
14. (b) DNA polymerase adds deoxyribonucleotides to the free 3′- end of the growing polynucleote chain so that replication of the 3′→5′ strand of the DNA molecule is continuous (growth of the new strand occurs in 5′→ 3′ direction)
    Since, DNA dependent DNA polymerase catalyses polymerisation only in one direction (5′→ 3′) discontinuous synthesis of DNA occurs in the other strand.
15. (b) The DNA dependent RNA polymerase helps in elongation of DNA by catalysing the polymerisation in only one direction, *i.e*., 5′→ 3′.
16. (b) Considering that gene expression results in the formation of a polypeptide, and can be regulated at several levels. In eukaryotes, the regulation could be at transcriptional level (formation of primary transcript, processing level (regulation of splicing), transport of mRNA from nucleus to the cytoplasm and translational level.
    While, in prokaryotes control of the rate of transcriptional initiation is the predominant site for control of gene expression.
17. (d) Regulatory sequences (proteins) control the functions of structural genes and are called regulatory genes. The important regulatory genes are promoters, terminators, operators and repressor.

To regulate the process of transcription, trancription factors (a sequence of specific DNA-binding factor) alone or with other proteins. promoter (as on activator) or stop as a repress or the binding site of RNA polymerase to DNA.

18. (a) Chromosome 1 was the last completed chromosome, sequenced two decades after the beginning of the human Genome project (hGP). It is for the largest human chromosome.

19. (d) rRNA, mRNA and tRNA are major classes of RNAs which are involved in gene expression. rRNAs bind protein molecules and give rise to ribosomes.
mRNA carries coded information for translation into polypeptide formation.
tRNA is called soluble or adaptor RNA that carries amino acids to mRNA during protein synthesis.

20. (b) According to chargaff's rules of base pairing
(i) The amount of adenine is always equal to the amount of thymine and the amount of guanine is always equal to the amount of cytosine.
(ii) Adenine is joined to thymine with two hydrogen bonds and guanine is jointed to cytosine by three hydrogen bonds.
(iii) The ratio of adnine to thymine and that of guanine to cytosine is always equal to one.
i.e., $\frac{A}{T}=\frac{G}{C}=1$
In the given organism, the DNA is not following the Chargaff's rule, hence it can be concluded that it is a single- stranded DNA not double- stranded.

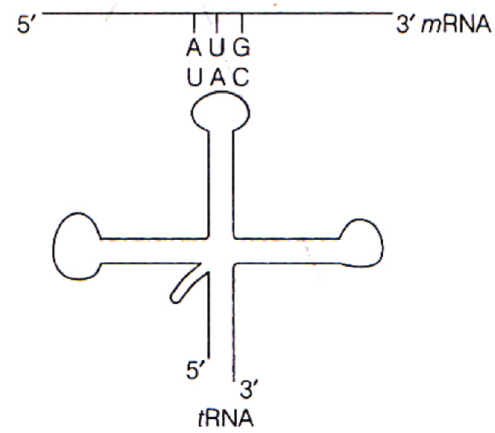
21. (c) In viruses, like retroviruses (e.g., HIV), an enzyme called reverse transcriptase is used to generate complementary DNA (cDNA) from and RNA template. This process is termed as reverse transcription.

22. (d) Meselson and stahl observed that DNA of the first generation was hybrid or intermediate (^{15}N and ^{14}N). It settled caesium chloride at a level higher than the fully labelled DNA of parent bacteria (^{15}N ^{15}N). After 40 minutes the second generation of bacteria, contained two types of DNA i.e.50% light (N^{14} N^{14}) and 50% intermediate (N^{15} N^{14}). The third generation of bacteria after 60 minute contained two type of DNA, 25% intermediate (N^{15} N^{14}) and 75% light (N^{14} N^{14}) in 1:3 ratio. The fourth generation after 80 minutes contained 12.5% N^{15} N^{14} and 87.5% DNA in 1: 7 ratio.

23. (a) 5′-A T G A T G-3′ (coding strand)
↓
5′-T ACT TAC-3′ (complementary strand)
↓
5′-A U G A A U G-3′ (RNA)

24. (c) The RNA polymerase are associated transiently with initiation factor (σ) and terminaton factor (ρ). This is only the enzyme that is capable of catalysing the process of elongation and also catalyses all types of RNA in bacteria. It binds to the promoter and initiates the transcription. After initiation, it also facilitates unwindng of helix and elongation continues. When polymerases reaches the terminator region the nascent RNA fall of so as RNA polymerase. As a result termination of transcription occurs.

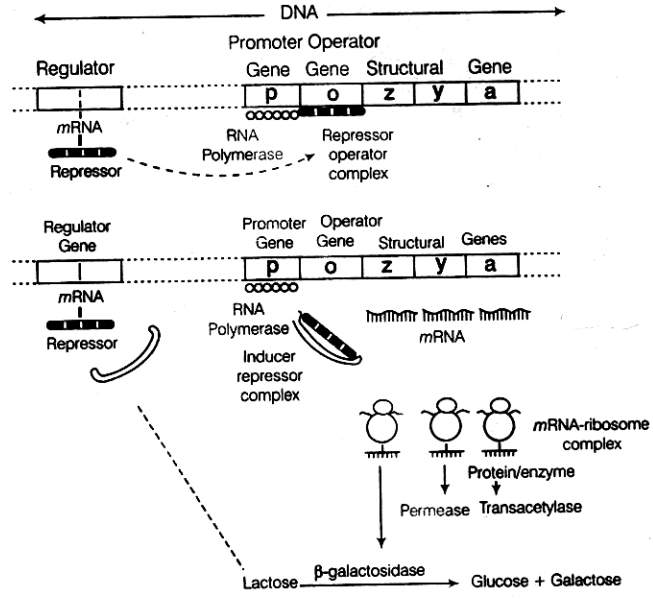
25. (a) 5′- AUG -3′ (codon in mRNA)
| | |
5′- UAC -3′ (tRNA)



26. (b) AA- binding site (amino acid binding site) lies at the 3′ end opposite the anticodon and has CCA-OH group. It is the site where amino acid attached to the tRNA.

27. (a) The ribosome consists of structural RNAs and about 80 different proteins. In its inactive state, it exists as two subunits, a larger subunit and a smaller subunit. When the smaller subunit encounters the m RNA, the process of translation of the mRNA to protein begins.

28. (a) In the presence of lactose



Jacob and Monod model of an inducible operon

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

In the absence of lactose

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

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29. (d) A nonsense mutation is the one which stops polypeptide synthesis due to formation of a terminating or non sense codon. e.g. ATT(UAA), ATC (UAG), ACT(UGA) . The lactose or lac operon of *Esherichia coli* contains structural genes (Z, Y, A). If Y codes for termination of polypeptide chain then only the product of 'Z' gene transcribe to form β galactosidase.

30. (b) The combination of pentose sugar with nitrogenous bases (purines or pyrimidines) is called nucleoside. Examples are adenosine, guanosine, cytidine, thymidine and uridine.

31. (c) Genetic code is the relationship of amino acid sequence in a polypeptide and nucleotide/base sequence in mRNA/ antisense strand of DNA.
It is **universal,** *i.e.*, a codon specifies the same amino acid in all organisms, **non-overlapping**, *i.e.*, adjacent codons are independent with no base being member of two codons, **degeneracy**, *i.e.*, some amino acids are coded by more than one codon, hence the code is degenerate, **unambiguous,** *i.e.*, one codon codes for only one amino acid.

32. (b) The technique of DNA fingerprinting was developed by Dr. Alec Jeffrey in 1984. It is a technique generally using repeated sequences (repetitive DNA) in the human genome that produces a pattern of band that is unique for every individuals. These short nucleotide repeats vary in number from person to person and are called **variable number of tandem repeat (VNTR).** VNTR belongs to class of satellite DNA referred to as minisatellite.

33. (a) In this question A is Franis Crick, B is translation and C is transcription. It is unidirectional flow of information DNA to mRNA (transcription) and then decoding the information present in mRNA in the formation of polypeptide chain or protein (translation).

34. (b) Inducible operons are usually switched off. This is a type of operon which is switched on when a chemical called inducer is present. The inducer is almost always a substrate.

35. (a) Process of copying genetic information from DNA to RNA is called **transcription**. At a time only one DNA strand is being transcribed into RNA. The strand of DNA with polarity 3' → 5' act as **template strand** and the DNA strand with polarity 5' → 3' act as **coding strand**.

36. (c) Frederick Griffith (in 1928), a British Medical officer described the phenomenon of **bacterial transformation**. He carried out experiment with ***Streptococcus pneumoniae*** (bacterium causing pneumonia) which is used to infect mice. By using S Strain (heat killed) and R strain (live) it was concluded that R strain has been transformed by some material of S strain which makes R strain virulent and enable to synthesize smooth polysachharide.

37. (a) Synthesis of RNA exhibits several features that are synonymous with DNA replication. RNA synthesis requires accurate and efficient initiation, elongation proceeds in the 5'→3' direction (i.e. the polymerase moves along the template strand of DNA in the 3'→5' direction), and RNA synthesis requires distinct and accurate termination. Transcription exhibits several features that are distinct from replication.

38. (b) Chargaff's rule states that A = T and G ≡ C. The molar amount of adenine = molar amount of thymine. The molar amount of guanine = molar amount of cytosine.
Hence, G is 17%, so, C = 17%
A = 33%, so, T = 33%

39. (b) In translocation, the movement of a gene takes place from one linkage group to another between non-homologous chromosomes.

40. (a) Lac operon under control of repressor shows a negative regulation. Operon has inducible nature.

41. (c) Chargaff's rule is not applicable to RNA.

42. (a) Satellite DNA displays high degree of polymorphism in population and also the same degree of polymorphism in an individual, which is inherited from parents to children (offsprings).

43. (a) A polysome or polyribosome is a complex of an mRNA molecule and two or more ribosomes, which is formed during the active translation process. They were initially named as ergosomes in 1963. However, further research by Jonathan Warner and Alex Rich characterized polysome.

44. (b) Zinc-finger analysis is used for protein analysis. The zinc finger proteins are a super family of proteins involved in numerous activities of plant growth and development.

45. (a) The start codon is the first codon of a messenger RNA (mRNA) transcript translated by a ribosome. The start codon always codes for methionine in eukaryotes and a modified Met (fMet) in prokaryotes. The most common start codon is AUG.
46. (c) Lac operon is an inducible operon. Lactose is the substrate for the enzyme beta-galactosidase and it also regulates switching on and off of the operon. Hence, it is termed as inducer. Inducers function by disabling repressors. The gene is expressed because an inducer binds to the repressor. The binding of the inducer to the repressor prevents the repressor from binding to the operator. RNA polymerase can then begin to transcribe operon genes.
47. (a) Hershey and Chase proved that DNA as genetic material. They used bacteriophage for their experiment.
48. (a) DNA fragments are negatively charged because of presence of phosphate group.
49. (b) If deletion happen at 901st position than the remaining 98 bases specifying for 33 codons of amino acids will be altered.
50. (c) Two DNA polymerase molecules simultaneously work at the DNA fork, one on the leading strand and the other on the lagging strand.
    DNA polymerase synthesizes each Okazaki fragment at lagging strand in 5′-3′ direction. As the replication fork opens further, new Pkazaki fragments appear. The first Okazaki fragment appears away from the replication fork and thus the direction of elongation would be away from replication fork.
51. (d) Ribosomal RNA (rRNA) is most abundant in animal cell. It constitutes 80% of total RNA of the cell.
52. (c) In eukaryotes spliceosomes are used in removal of introns during post-transcriptional processing of hnRNA. They are absent in prokaryotes.
53. (b) The association of H1 protein indicates the complete formation of nucleosome which requires DNA condensation. The DNA is therefore in condensed form.