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MOLECULAR BASIS OF INHERITANCE

SYLLABUS

Search for genetic material and DNA as genetic material; Structure of DNA and RNA; DNA packaging; DNA replication; Central dogma; Transcription, genetic code, translation; Gene expression and regulation-Lac Operon; Genome and human genome project; DNA finger printing.

KEY CONCEPTS

INTRODUCTION

* The fact that nucleus contains the units of inheritance was proposed by Oscar Hertwig in 1870.
* The mechanism was clearly understood with the development of Mendel's laws of inheritance.
* Further researchers proposed that cytoplasm also contains the hereditary material. The evidence for cytoplasmic inheritance was first presented by Correns in *Mirabilis Jalapa* and by Baur in *Pelargonium zonale* in 1908. The cytoplasm in such cases contain self perpetuating hereditary particles formed of DNA.
* Deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) are the two types of nucleic acids found in living systems.
* DNA acts as the genetic material in most of the organisms.
* RNA though it also acts as a genetic material in some viruses, mostly functions as a messenger.
* RNA has additional roles as well. It functions as adapter, structural, and in some cases as a catalytic molecule.

DNA (DEOXYRIBONUCLEIC ACID)

* Term was given by Zacharis.
* In bacteriophages and viruses there is a single molecule of DNA, which remains coiled and is enclosed in the protein coat.
* In bacteria, mitochondria, plastids and other prokaryotes, DNA is circular and lies naked in the cytoplasm but in eukaryotes it is found in nucleus and known as carrier of genetic information and capable of self replication.
* DNA is a long polymer of deoxyribonucleotides.
* The length of DNA is usually defined as number of nucleotides (or a pair of nucleotide referred to as base pairs) present in it. This also is the characteristic of an organism.
For example, a bacteriophage known as $\phi \times 174$ has 5386 nucleotides, Bacteriophage lambda has 48502 base pairs (bp), *Escherichia coli* has 4.6×10^6 bp, and haploid content of human DNA is 3.3×10^9 bp.
* DNA as an acidic substance present in nucleus was first identified by Friedrich Meischer in 1869. He named it as 'Nuclein'.
* In 1953 James Watson and Francis Crick, based on the X-ray diffraction data produced by Maurice Wilkins and Rosalind Franklin, proposed a very simple but famous **Double Helix** model for the structure of DNA.
* One of the hallmarks of their proposition was base pairing between the two strands of

polynucleotide chains. However, this proposition was also based on the observation of Erwin Chargaff that for a double stranded DNA, the ratios between **Adenine** and **Thymine** and **Guanine** and **Cytosine** are constant and equals one.

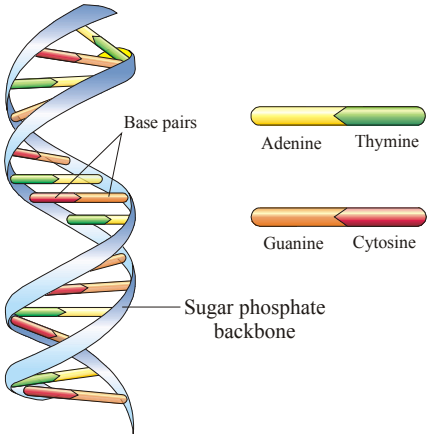


Figure : DNA double helix

* Chargaff (1950) made observations on the bases and other contents of DNA. These observations or generalizations are called **Chargaff's rules**.

(i) Purine and pyrimidine base pairs are in equal amount, *i.e.,* adenine + guanine = thymine + cytosine.

(ii) Molar amount of purine (adenine) is always equal to the molar amount of pyrimidine (thymine). Similarly, guanine is equalled by cytosine.

(iii) Sugar deoxyribose and phosphate occur in equimolar proportions.

(iv) The ratio of A + T/G + C is constant for a species (**Base ratio**, *e.g.,* 1.52 for human and 0.93 for *E.coli.*

* The base pairing is a very unique property of the polynucleotide chains.
* They are said to be complementary to each other, and therefore if the sequence of bases in one strand is known then the sequence in other strand can be predicted.
* If one DNA strand has A, the other would have T and if one has G, the other, would have C.
* If the base sequence of one strand is CAT TAG GAC, the base sequence of other strand would be GTA ATC CTG.
* The two polynucleotide strands are called complementary to one another.
* If each strand from a DNA or parental DNA acts as a template for synthesis of a new strand, the two double stranded DNA or daughter DNA produced would be identical to the parental DNA molecule.
* The chemical analysis has shown that DNA is composed of three different types of compound.

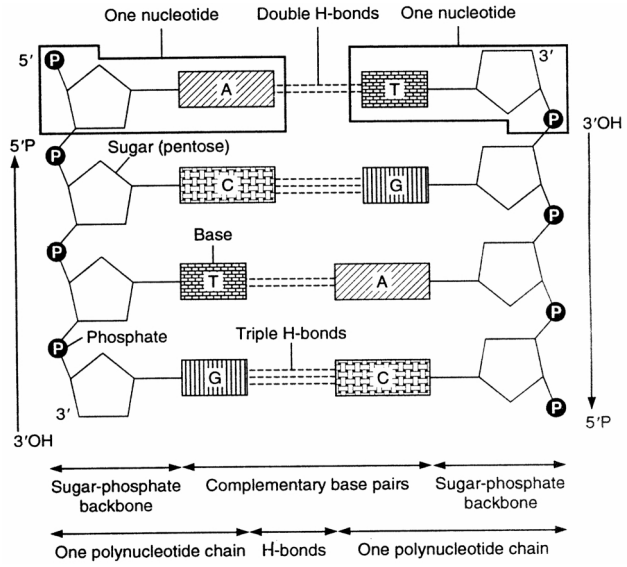


Figure : Polynucleotide chain

(i) Sugar molecule : Levene identified a five carbon sugar, ribose in nucleic acid in 1910. It is represented by a pentose sugar the deoxyribose or 2-deoxyribose which derived from ribose due to the deletion of oxygen from the second carbon.

(ii) Phosphoric acid : H_3PO_4 that makes DNA acidic in nature.

(iii) Nitrogeneous base : Kossel demonstrated the presence of two pyrimidines (**cytosine and thymine**) and two purines (**adenine and guanine**) in DNA & he was awarded Nobel Prize in 1910. These are nitrogen containing ring compound, which classified into two groups:

(a) Purines : Two ring compound namely as Adenine and Guanine.

(b) Pyrimidine : One ring compound included Cytosine and Thymine. In RNA Uracil is present instead of Thymine.

* **Nucleosides :** Nucleosides are formed by a purine or pyrimidine nitrogenous base and pentose sugar. DNA nucleosides are known as deoxyribosenucleosides.

* **Nucleotides :** In a nucleotide, purine or pyrimidine nitrogenous base is joined by deoxyribose pentose sugar (D), which is further linked with phosphate (P) group to form nucleotides.
* A nitrogenous base is linked to the OH of 1'C pentose sugar through a N-glycosidic linkage to form a nucleoside, such as adenosine or deoxyadenosine, guanosine or deoxyguanosine, cytidine or deoxycytidine and uridine or deoxythymidine.
* When a phosphate group is linked to OH of 5'C of a nucleoside through phosphoester linkage, a corresponding nucleotide (or deoxynucleotide depending upon the type of sugar present) is formed.
* Two nucleotides are linked through 3'-5' phosphodiester linkage to form a dinucleotide.
* More nucleotides can be joined in such a manner to form a polynucleotide chain. A polymer thus formed has at one end a free phosphate moiety at 5'-end of ribose sugar, which is referred to as 5'-end of polynucleotide chain. Similarly, at the other end of the polymer the sugar has a free 3' -OH group which is referred to as 3'- end of the polynucleotide chain.
* The backbone in a polynucleotide chain is formed due to sugar and phosphates. The nitrogenous bases linked to sugar moiety project from the backbone.
* In RNA, every nucleotide residue has an additional –OH group present at 2'-position in the ribose. Also, in RNA the uracil is found at the place of thymine (5-methyl uracil, another chemical name for thymine).

The salient features of the Double-helix structure of DNA

(i) It is made of two polynucleotide chains, where the backbone is constituted by sugar-phosphate, and the bases project inside.

(ii) The two chains have anti-parallel polarity. It means, if one chain has the polarity 5' → 3', the other has 3' → 5'.

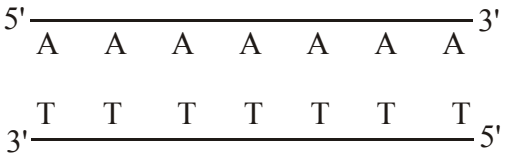
(iii) The bases in two strands are paired through hydrogen bond (H-bonds) forming base pairs (bp). Adenine forms two hydrogen bonds with Thymine from opposite strand and vice-versa. Similarly, Guanine is bonded with Cytosine with three H-bonds. As a result, always a purine comes opposite to a pyrimidine. This generates approximately uniform distance between the two strands of the helix.

(iv) The two chains are coiled in a right-handed fashion. The pitch of the helix is 3.4 nm (a nanometre is one billionth of a metre, that is 10^{-9} m) and there are roughly 10 bp in each turn. Consequently, the distance between a bp in a helix is approximately equal to 0.34 nm.

(v) The plane of one base pair stacks over the other in double helix. This, in addition to H-bonds, confers stability of the helical structure

Different morphological forms of DNA :

* Five different morphological forms of DNA double helix have been described. These are A, B, C, D and Z forms. Most of these forms (except B, and Z) occur in rigidly controlled experimental conditions. Watson and crick model represents commonest form, Biotic-form (B-form or B-DNA) of DNA. Some DNA forms are inter convertible also.
* **Promiscuous DNA :** Special type of DNA which makes movement between mitochondria, chloroplast and nucleus. It was discovered in 1983 in cambridge university in maize. It was later reported in yeast, mungbean, spinach and peas.
* **Repetitive DNA :** Multiple copies of DNA having same or almost same base pair sequence constitute repetitive DNA. In higher organisms 20% - 90% DNA is of this type.



* **Satellite DNA :** In some eukaryotes small highly repetitive DNA sequences have been found called satellite DNA, which differ in base composition.

* **Types of DNA and their comparison**

DNA types	Base pairs per turn (n)	Rotation	Vertical rise per bp	Helical diameter bp (h)
A	11	Right handed	2.56 Å	23 Å
B	10	Right handed	3.4 Å	20 Å
C	9.33	Right handed	3.3 Å	19 Å
Z	12	Left handed	3.8 Å	18.4 Å

* **Linear double-stranded DNA** in eukaryotes and PPLO (Monerans)
* **Palindromic DNA :** It has base sequence which reads the same on both strands either in 5' → 3' or 3' → 5' direction. Different types of palindromic sequences are recognized by restriction endonucleases, e.g.,
  5'-G A A T T C-3'
  3'-C T T A A G-5'
* **Denaturation and Renaturation :** Separation of two strands of DNA from each other due to breakage of H-bonds when it is exposed to high temperature, acid or alkali is called denaturation or melting.
  Reassociation of separated DNA by H-bonds formation is called renaturation or annealing. DNA with more A = T has low melting areas and denatured more easily. DNA with more G ≡ C than A = T has high melting areas.
* **C-value :** Total amount of DNA per genome.
* The amount of DNA is expressed in picogram.
  1 pg = 10^{-12} gm.
* **DNA functions:**

(a) Hereditary information
(b) Variations: It occurs due to crossing over at the time of meiosis.
(c) Mutations : Sudden inheritable variations due to change in genetic material.
(d) Autocatalytic function or DNA replication i.e., DNA → DNA synthesis
(e) Heterocatalytic function : DNA → RNA, proteins, hormones synthesis
(f) Control of metabolism. Growth and differentiation
(g) DNA fingerprinting

Packaging of DNA Helix:

(a) Packaging in prokaryotes:

* They do not have definite nucleus.
* The DNA is not scattered throughout the cell.
* DNA is held together with some proteins in a region is called 'nucleoid'.
* The DNA in nucleoid is organized in large loops held be proteins.

(b) Packaging in Eukaryotes:

* In eukaryotes the packaging is more complex.
* There is a set of positively charged, basic protein called **Histones.**
* Histones are positively charged being rich in basic amino acids like **Lysines** and **arginines.**
* Histones are organized to form a unit of eight molecules called **histone octamere.**
* Negatively charged DNA wrapped around positively charged histone octamere to form a structure called **nucleosome.**

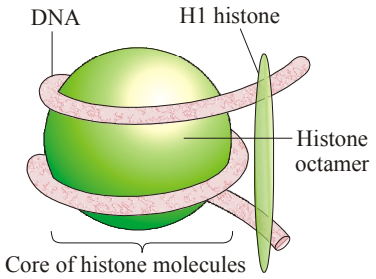


Figure : Nucleosome

* A typical nucleosome contains 200 bp of DNA helix.
* Nucleosome constitutes the repeating unit of a structure in nucleus called **chromatin**, thread like stained bodies seen in the nucleus.
* The nucleosomes are seen as **'beads-on-string'** structure when viewed under electron microscope.
* The chromatin is packaged to form **chromatin fibers** that are further coiled and condensed at metaphase stage to form **chromosome.**
* Packaging at higher level required additional set of proteins called **Non-histone Chromosomal (NHC) proteins.**
* In a typical nucleus some loosely coiled regions of chromatin (light stained) is called euchromatin.
* The chromatin that more densely packed and stains dark are called Heterochromatin.

* Euchromatin is **transcriptionally active** chromatin and heterochromatin is inactive.

Chemical Composition of Chromosome

* A chromosome consists of following chemical compositions:
  (a) DNA 40%
  (b) RNA 1.2%
  (c) Histone protein 50%
  (d) Acidic proteins 8.5%
  (e) Lipid traces
  (f) Ca^{+2}, Mg^{+2}, Fe^{+2} traces

DNA AS THE GENETIC MATERIAL

The following experiments conducted by the molecular biologists provide direct evidences of DNA being the genetic material.

(A) Bacterial transformation or Griffith's Experiments :

* In 1928, Frederick Griffith, in a series of experiments with Streptococcus pneumoniae (bacterium responsible for pneumonia), witnessed a miraculous transformation in the bacteria. During the course of his experiment, a living organism (bacteria) had changed in physical form.
* When *Streptococcus pneumoniae* (pneumococcus) bacteria are grown on a culture plate, some produce smooth shiny colonies (S) while others produce rough colonies (R). This is because the S strain bacteria have a mucous (polysaccharide) coat, while R strain does not. Mice infected with the S strain (virulent) die from pneumonia infection but mice infected with the R strain do not develop pneumonia.
  - Living S-strain Injected into mice → Mice killed
  - Living R-strain Injected into mice→Mice lived
  - Heat Killed S-strain Injected into mice → Mice lived
  - Living R-strain + Heat Killed S-strain Injected into mice → Mice killed
* Griffith was able to kill bacteria by heating them. He observed that heat-killed S strain bacteria injected into mice did not kill them.
* When he injected a mixture of heat-killed S and live R bacteria, the mice died. Moreover, he recovered living S bacteria from the dead mice.
* He concluded that the R strain bacteria had somehow been **transformed** by the heat-killed S strain bacteria.
* Some 'transforming principle', transferred from the heat-killed S strain, had enabled the R strain to synthesise a smooth polysaccharide coat and become virulent. This must be due to the transfer of the genetic material. However, the biochemical nature of genetic material was not defined from his experiments.

Biochemical Characterisation of Transforming Principle

* Prior to the work of Oswald Avery, Colin MacLeod and Maclyn McCarty (1933-44), the genetic material was thought to be a protein.
* They worked to determine the biochemical nature of 'transforming principle' in Griffith's experiment.
* They purified biochemicals (proteins, DNA, RNA, etc.) from the heat-killed S cells to see which ones could transform live R cells into S cells.
* They discovered that DNA alone from S bacteria caused R bacteria to become transformed.
* They also discovered that protein-digesting enzymes (proteases) and RNA-digesting enzymes (RNases) did not affect transformation, so the transforming substance was not a protein or RNA.
* Digestion with DNase did inhibit transformation, suggesting that the DNA caused the transformation. They concluded that DNA is the hereditary material.

(B) Evidence from bacteriophage infection :

Hershey and Chase (1952) conducted their experiment on T_2 bacteriophage, which attacks on *E.coli* bacterium. The phage particles were prepared by using radioisotopes of S^{35} and P^{32} in the following steps :

(i) Few bacteriophages were grown in bacteria containing ^{35}S. Which was incorporated into the cystein and methionine amino acids of proteins and thus these amino acids with ^{35}S formed the proteins of phage.

(ii) Some other bacteriophages were grown in bacteria having ^{32}P. Which was restricted to

DNA of phage particles. These two radioactive phage preparations (one with radioactive proteins and another with radioactive DNA) were allowed to infect the culture of *E.coli.* The protein coats were separated from the bacterial cell walls by shaking and centrifugation.

* The heavier infected bacterial cells during centrifugation pelleted to bottom.
* The supernatant had the lighter phage particles and other components that failed to infect bacteria.
* It was observed that bacteriophages with radioactive DNA gave rise to radioactive pellets with ^{32}P in DNA.
* However in the phage particles with radioactive protein (with ^{35}S) the bacterial pellets have almost nil radioactivity indicating that proteins have failed to migrate into bacterial cell. So, it can be safely concluded that during infection by bacteriophage T_2, it was DNA, which entered the bacteria.
* It was followed by an eclipse period during which phage DNA replicates numerous times within the bacterial cell.
* Towards the end of eclipse period phage DNA directs the production of protein coats assembly of newly formed phage particles.

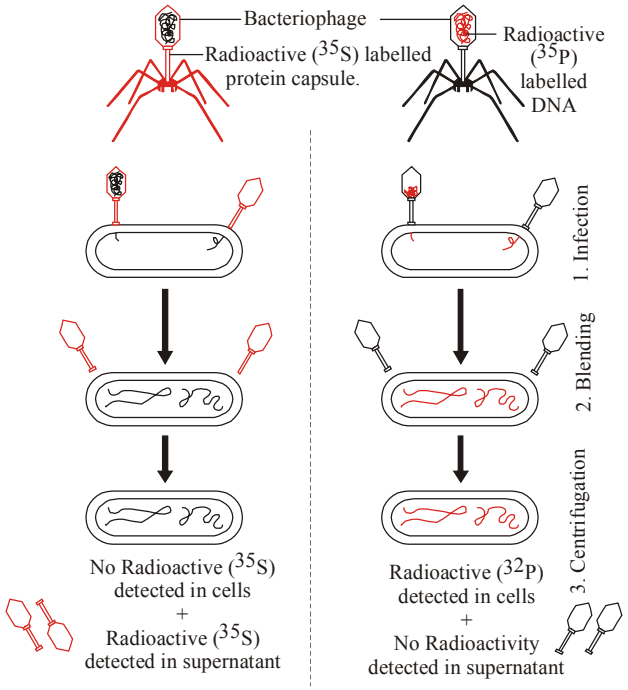


Figure : The Hershey-Chase experiment

* Lysozyme (an enzyme) brings about the lysis of host cell and release, the newly formed bacteriophages.
* The above experiment clearly suggests that it is phage DNA and not protein, which contains the genetic information for the production of new bacteriophages.
* However, in some plant viruses (like TMV), RNA acts as hereditary material (being DNA absent).

PROPERTIES OF GENETIC MATERIAL (DNA VERSUS RNA)

Criteria for genetic material:

* It should be able to generate its replica (replication)
* It should be chemically and structurally stable.
* It should provide the scope for slow changes (mutation) that required for evolution.
* It should be able to express itself in the form of 'Mendelian Character'.
* Protein does not fulfill the criteria hence it is not the genetic material.
* RNA and DNA fulfill the criteria.

RNA is unstable:

* 2'-OH group present at every nucleotide (ribose sugar) in RNA is a reactive group and makes RNA liable and easily degradable.
* RNA is also now known as **catalyst,** hence reactive.
* RNA is unstable and mutates faster. Consequently the viruses having RNA genome and having shorter life span mutate and evolve faster.

DNA is more stable:

* Stability as one of the properties of genetic material was very evident in Griffith's 'transforming principle' itself that heat, which killed the bacteria at least did not destroy some of the properties of genetic material.
* Two strands being complementary if separated by heating come together, when appropriate conditions are provided.
* Presence of Thymine in place of uracil confers additional stability to DNA.

* DNA is chemically less reactive and structurally more stable when compared to RNA.
* Therefore among the two nucleic acids the DNA is a better genetic material.

Better genetic material (DNA or RNA)

* Presence of thymine at the place of uracil confers more stability to DNA.
* Both DNA and RNA are able to mutate.
* In fact RNA being unstable mutate at a faster rate.
* RNA can directly code for the synthesis of proteins, hence easily express.
* DNA however depends on RNA for protein synthesis.
* The protein synthesis machinery has evolved around RNA.
* 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.

RNA WORLD

* RNA is the first genetic material. Essential life processes evolved around RNA.
* RNA used to act as a genetic material as well as catalyst.
* But 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.

Types of RNA:

* In prokaryotes there are three major types of RNAs: **mRNA** (messenger), **tRNA** (transfer), and **rRNA** (ribosomal). All three RNAs are required to synthesize protein in a cell.
* The mRNA provides the template and having genetic information in the form of genetic code.
* The tRNA brings the amino acids and read the genetic code of mRNA.
* The rRNA is the structural part of the ribosome and also as catalytic role during process of translation. We will study translation in next section.
* **Table : Types of RNA**

S.N.	mRNA	rRNA	tRNA
1.	5% of total RNA in cell.	80%	15%
2.	Longest	Smaller	Smallest
3.	It is called template / nuclear / messenger or informational RNA as it carries genetic information provided by DNA	Has structural (forms ribosome) and catalytic role during translation.	Soluble or adapter RNA and carries amino acids.

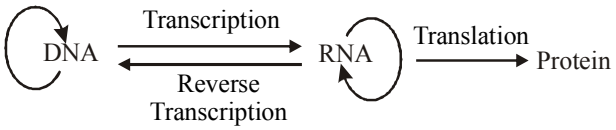
CENTRAL DOGMA

* Central dogma term was given by Crick.
* The formation (production) of RNA from DNA and then synthesis of protein from it, is known as Central Dogma.

DNA $\xrightarrow{\text{Transcription}}$ RNA $\xrightarrow{\text{Translation}}$ Protein

* It means, it includes transcription and translation.
* The central dogma scheme of protein synthesis was presented by Jacob and Monad.
* The detailed study of central dogma is done by Nirenberg, Mathai and Khorana.
* Beedle and Tatum studied central domag is a fungus Neurospora.

Replication



Reverse Transcription :

* The formation of DNA from RNA is known as Reverse transcription.
* It was discovered by Temin and Baltimore in Rous -sarcoma virus. So it is also called Teminism.
* ss-RNA of Rous-Sarcoma virus (Retro virus) produces ds-DNA in host's cell with the help of enzyme reverse transcriptase (DNA-polymerase). This DNA is called c-DNA (Complimentary DNA). Some times this DNA moves in host genome. Such mobile DNA is called Retroposon (Oncogene).

DNA REPLICATION

* D.N.A. is the only molecule capable of self duplication so it is termed as a Living molecule.
* All living beings have the capacity to reproduce because of this characteristic of D.N.A.
* D.N.A replication takes place in S-Phase of the cell cycle. At the time of cell division, it divides in equal parts in the daughter cells.

Semi conservative mode of D.N.A. replication :

* Semi conservative mode of D.N.A. replication was first theoretically proposed by Watson & Crick.
* Later on, it was experimentally proved by Meselson & Stahl (1958) on *E. Coli* and Taylor on Viccia faba.
* To prove this method, they used Radiotracer technique in which Radioisotope are used.
* Meselson and Stahl used N^{15} and Cairns (1963) used radioactive Thymidine (with H^3).

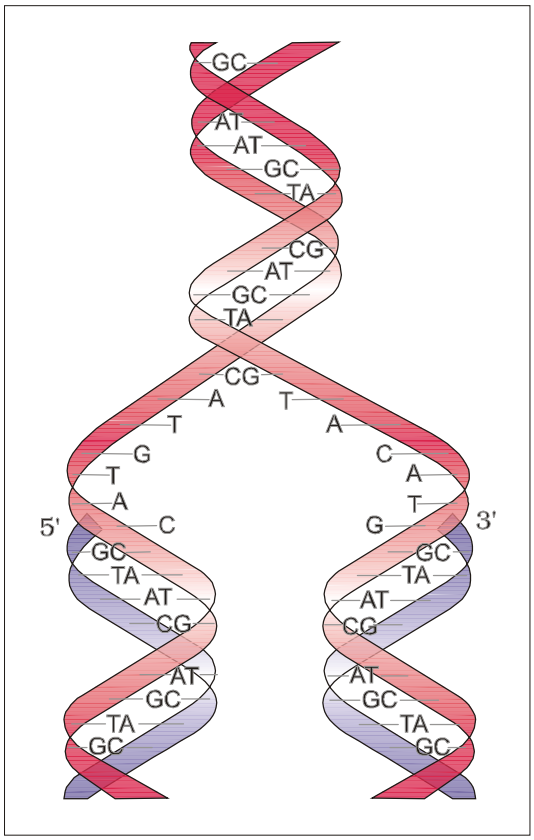


Figure : Watson-Crick model for semiconservative DNA replication

* Due to the replication of active Thymidine containing D.N.A., two D.N.A. molecules were obtained in which 50% radioactivity was found.
* When these two D.N.A. molecules containing active Thymidine were made to replicate, the next time four D.N.A. molecules were obtained. Out of these 4 D.N.A., 2 D.N.A. molecules were radioactive and remaining 2 were not radioactive.
* In the same sequence, the obtained D.N.A. molecules were further made to replicate then also, the no of radioactive D.N.A. remains 2.

The following steps are included in D.N.A. replication

Unzipping :

* The separation of 2 chains of D.N.A. is termed as unzipping. And it takes place due to the breaking of H bonds.
* The process of unzipping starts at a certain specific point which is termed as initiation point or origin of replication.
* In procaryotes there occur only one origin of replication but in eucaryotes there occur many origin of replication i..e. unzipping starts at many points simultaneously.
* At the place of origin, the topoisomerase enzyme (a type of endonuclease) induces a cut in one strand of DNA (Nicking) to relax the two strands of DNA.
* The enzyme responsible for unzipping (breaking the hydrogen bonds) is Helicase (= Swivelase).
* Mg^{+2} act as cofactor.

Unzipping takes place in alkaline medium.

* A protein, Helix destabilizing protein prevents recoiling of two separated strands during the process of replication.
* An another protein SSB (single stranded DNA binding protein) prevents the formation of bends or loops in separated strands.

DNA-Gyrase :

* A type of topoisomerase prevents supercoiling of DNA.

Note : The process of D.N.A. replication takes a few minutes in prokaryotes and a few hours in Eukaryotes.

Formation of New Chain :

* To start the synthesis of new chain, special type of R.N.A. is required which is termed as R.N.A. Primer.
* The formation of R.N.A. primer is catalysed by an enzyme - R.N.A. Polymerase (primase). Synthesis of RNA-primer takes place in 5' → 3' direction. After the formation of new chain, this R.N.A. is removed.
* For the formation of new chain Nucleotides obtained Nuceloplasm. In the nucleoplasm, Nucleotides are present in the form of triphosphates like dATP, dGTP, dCTP, dTTPetc.
* During replication, the 2 phosphate groups of all Nucleotides are separated.
* In this process energy is yielded which is consumed in DNA replication. So, it is clear that D.N.A. does not depend on mitochondria for it's energy requirements.
* The formation of new chain always takes place in 5'- 3' direction.
* As a result of this, one chain of DNA is continuously formed and it is termed as **Leading strand.**
* The formation of second chain begins from the centre and not from the terminal points, so this chain is discontinuous and is made up of small segments called **Okazaki Fragments**. This discontinuous chain is termed as **Lagging strand**.
* Ultimately all these segments joined together and a complete new chain is formed.

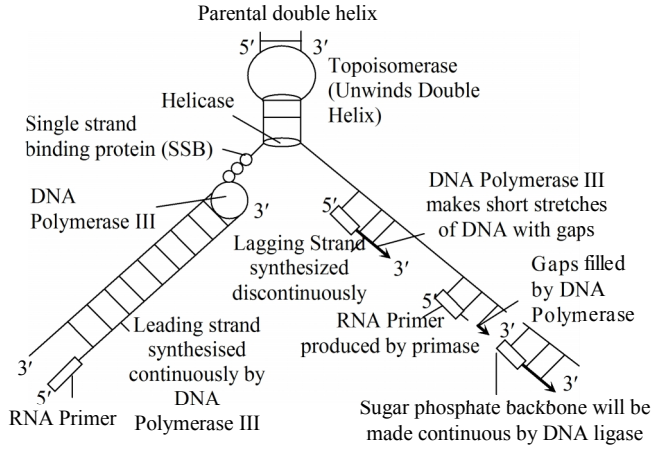


Fig : Showing continuous replication of a daughter DNA strand on leading strand and discontinuous replication of lagging strand

* 3' → 5' replication is **continuous**, while on the other (the template with polarity 5' → 3', it is **discontinuous.**
* The Okazaki segments are joined together by an enzyme DNA Ligase.(Khorana).
* The DNA polymerases on their own cannot initiate the process of replication.
* Also the replication does not initiate randomly at any place in DNA.
* There is a definite region in *E. coli* DNA where the replication originates. Such regions are termed as **origin of replication**.
* It is because of the requirement of the origin of replication that a piece of DNA if needed to be propagated during recombinant DNA procedures, requires a vector. The vectors provide the origin of replication.
* The formation of new chains is catalysed by an enzyme DNA Polymerase. In prokaryotes it is of 3 types:

(i) **DNA - Polymerase I :** This was discovered by Kornberg (1957). So it is also called as Kornberg's enzyme. Kornberg also synthesized DNA first of all, in the laboratory. This enzyme functions as exonuclease. It separates RNA primer from DNA and also fills the gap. It is also known as DNA-repair enzyme.

(ii) **DNA - Polymerase II :** It is least reactive in replication process. It is also helpful in DNA-repairing in absence of DNA-polymerase-I and DNA polymerase-III .

(iii) **DNA - Polymerase III :** This is the main enzyme in DNA-Replication. It is most important. It was discovered by Delucia and Cairns. The larger chains are formed by this enzyme. This is also known as Replicase.

DNA Polymerase III is a complex enzyme composed of seven polypeptides α, ε, θ, β, γ_1, δ, γ_2.

In Eucaryotes, there occur five types of DNA-polymerase enzyme.

(1) α-DNA - polymerase = Similar to DNA - polymerase I

(2) β-DNA - polymerase = .It concerned with DNA repair.

(3) γ-DNA - polymerase = It concerned with replication of cytoplasmic DNA.

(4) δ -DNA - polymerase =Similar to DNA - polymerase II

(5) ε - DNA polymerase = Similar to DNA - polymerase III

Thus DNA - Replication process is completed with the effect of different enzymes.

* In the semi conservative mode of replication each daughter DNA molecule receives one chain of polynucleotides from the mother DNA - molecule and the second chain is synthesized.

Note :

(a) All DNA polymerase I, II and III enzymes have 5'-3' polymerisation activity and 3'-5' exonucleas activity.

(b) A failure in cell division after DNA replication results into polyploidy (a chromosomal anomaly).

Meselson and Stahl's experiment :

* Meselson and Stahl (1958) cultured (*Escherichia coli*) bacteria in a culture medium containing N^{15} were isotopes of nitrogen.

* After these had replicated for a few generations in that medium both the strands of their DNA contained N^{15} as constituents of purines and pyrimidines.

* When these bacteria with N^{15} were transferred in cultural medium containing N^{14}, it was found that DNA separated from fresh generation of bacteria possesses one strand heavier than the other.

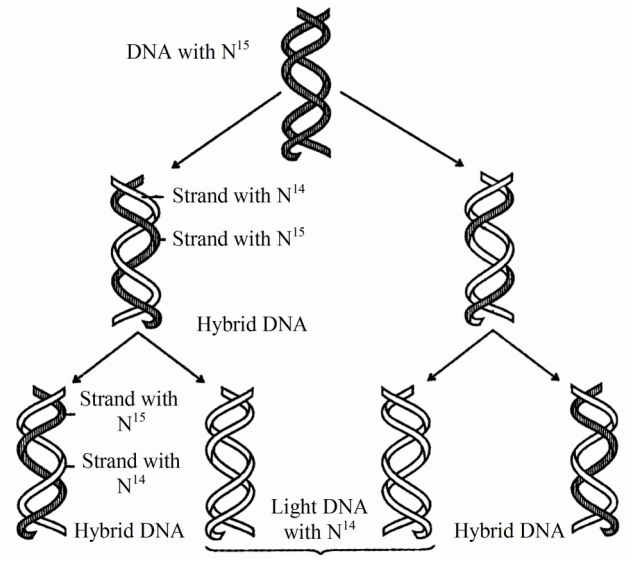


Fig : Second generation daughter molecules after DNA replication

* The heavier strand represents the parental strand and lighter one is the new one synthesized from the culture indicating semiconservative mode of DNA replication. circular form of replication on as characteristic of prokaryotes is theta replication discovered by J. Cairns.

MECHANISM OF PROTEIN SYNTHESIS

* The process of protein synthesis consists of two major steps:

(A) Transcription or synthesis of mRNA on DNA

(B) Translation or synthesis of proteins along mRNA

TRANSCRIPTION

* Formation of RNA over DNA templet is called transcription.

* The principle of complementarity governs the process of transcription, except the adenosine complements now forms base pair with uracil instead of thymine

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

* The segment of DNA involved in transcription is Cistron.

* Both the strands are not copied during transcription because

(i) If both strands act as a template, they would code for RNA molecule with different sequences (Remember complementarity does not mean identical), and in turn, if they code for proteins, the sequence of amino acids in the proteins would be different. Hence, one segment of the DNA would be coding for two different proteins, and this would complicate the genetic information transfer machinery.

(ii) The two RNA molecules if produced simultaneously would be complementary to each other, hence would form a double stranded RNA (dsRNA). This would prevent RNA from being translated into protein and the exercise of transcription would become a futile one.

* RNA polymerase enzyme involved in transcription. In eukaryotes there are three types of RNA polymerases.

– RNA polymerase-I for 28s rRNA, 18s rRNA, 5.8s rRNA.

– RNA polymerase-II for m-RNA.
– RNA polymerase-III for t-RNA, 5s rRNA. SnRNA

* In eucaryotes RNA polymerase enzyme composed of 10-15 polypeptide chains.
* Prokaryotes have only one type of RNA polymerase which synthesizes all types of RNAs.
* RNA polymerase of *E. Coli* has five polypeptide chains β, β ', α, α & σ
* σ polypeptide chain is also known as σ factor (sigma factor).
* Core enzyme+Sigma factor ⇒ RNA Polymerase
(β, β ', α, α) (σ)

Transcription Unit

* A transcription unit in DNA consists of three regions:

(i) A promoter : It is the binding site for RNA polymerase for initiation of transcription.

(ii) The structural gene : It codes for enzyme or protein for structural functions.

(iii) A terminator : It is the region where transcription ends.

* **DNA dependent RNA polymerase** catalyses the polymerization in only one direction that is 5'→3'.

Structural gene:

* 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.**

3'-ATGCATGCATGCATGCATGCATGC-5'
Template Strand
5'-TACGTACGTACGTACGTACGTACG-3'
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.

Promoter:

* **Promoter** and **Terminator** present on either side of structural gene.
* The promoter located towards 5' end **upstream**) of the structural gene.
* It is a short sequence of DNA that provides binding site for RNA polymerase.
* Presence of the promoter defines the template and coding strands.
* If the position of promoter is changed with terminator the definition of coding and template strand will be reversed.

Terminator:

* The **terminator** located towards 3' end (**down stream**) of coding strand.
* It terminates the process of transcription.

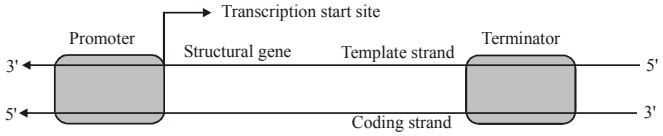


Figure : Schematic structure of a transcription unit

Transcription unit and the gene:

* Gene is defined as the functional unit of inheritance, located on the DNA.
* **Cistron:** a segment of DNA (structural gene) coding for a polypeptide.
* **Monocistronic:** most of eukaryotic structural gene codes for single polypeptide.
* **Polycistronic:** Most prokaryotic structural gene code for more than one polypeptides.
* In eukaryotes the monocistronic structural genes have interrupted coding sequences, the genes are said to be **split gene:**
The coding sequences or expressed sequences are called **Exons.**
Exons are interrupted by Introns.
* Exons are said to be those sequences that appear in mature or processed mRNA.
* Introns never appear in mature of processed mRNA. They are spliced out.

Process of transcription :

(1) Initiation :

* DNA has a "Promoter site or initiation site" where transcription begins and a "Terminator site", where transcription stops.
* Sigma factor (σ) recognises the promoter site of DNA.

* With the help of sigma factor RNA polymerase enzyme attached to a specific site of DNA called "Promoter site".
* In prokaryotes before the $10N_2$ base from Promoter site a sequence of 6 base pairs (TATAAT) is present on DNA, which is called Pribnow box.
* In eukaryotes before the $20N_2$ base from Promoter site a sequence of 7 base pairs (TATAAAA) or (TATATAT) is present on DNA, which is called "TATA box or Hogness box."
* At promoter site RNA polymerase enzyme breaks H-bonds between two DNA strands and separates them.
* One of them strand takes part in Transcription. Transcription proceeds in 5' → 3" direction.
* Ribonucleotide triphosphate come to lie opposite complementary nitrogen bases of anti sense strand.
* These Ribonucleotides present in the form of triphosphate ATP, GTP, UTP and CTP in nucleoplasm. When they used in transcription, pyrophosphatase hydrolyse two phosphates from each activated nucleotide. This releases energy.
* This energy used in process of transcription.

(2) Elongation :

* RNA polymerase enzyme establishes phosphodiester bond between adjacent ribonucleotides.
* Sigma factor separates and core enzyme moves along the anti sense strand till it reaches terminator site.

(3) Termination :

* When RNA polymerase enzyme reaches at terminator site, it separates from DNA templet.
* In terminator site on DNA, N_2 bases are resent in palindromic sequence.
* In most cases RNA polymerase enzyme can recognise the Terminator site and stop the synthesis of RNA chain, but in prokaryotes it recognises the terminator site with the help of Rho factor (ρ factor).
* Rho (ρ) factor is a specific protein which helps RNA polymerase enzyme to recognise the terminator site.

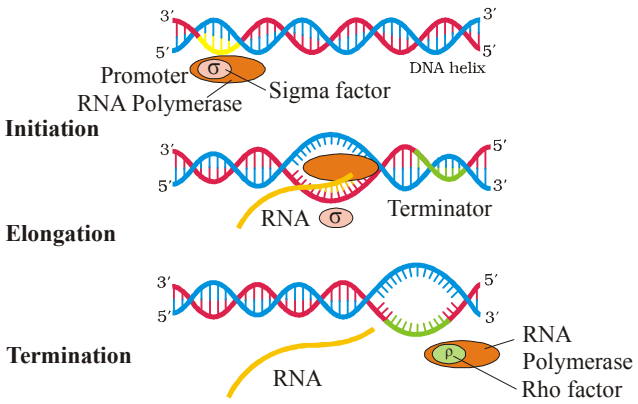


Figure : Process of transcription in bacteria

Transcription in Eukaryotes :

* In eukaryotes three types of RNA polymerases found in the nucleus are involved in transcription. **RNA Polymerase I :** Transcribes rRNAs. **RNA Polymerase II :** Transcribes hnRNA (which is precursor of mRNA). **RNA Polymerase III :** Transcribes tRNA, 5 srRNA and snRNA.
* The primary transcript has both **exon** and **intron** regions.
* Introns which are non-coding regions removed by a process called **splicing.**
* **hnRNA undergoes two additional processes:**

(a) Capping: An unusual nucleotide (methyl-guanosine triphosphate) is added to 5' end of hnRNA.

(b) Tailing : Adenylate residues (200-300) are added at 3'end.

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

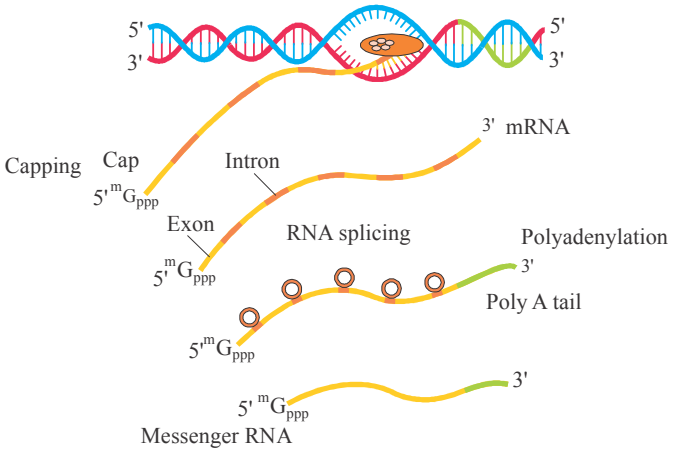


Figure : Process of transcription in Eukaryotes

GENETIC CODE

* Term Given by George Gamow.
* The relationship between the sequence of amino acids in a polypeptide chain and nucleotide sequence of DNA or m-RNA is called **genetic code.**
* There occur 20 types of amino acids which participate in protein synthesis. DNA contains information for the synthesis of any types of polypeptide chain. In the process of transcription, information transfers from DNA to m-RNA in the form of complementary N_2-base sequence.
* m-RNA contains code for each amino acid and it is called **codon**.
* A codon is the nucleotide sequence in m-RNA which codes for particular amino acid ; whereas the genetic code is the sequence of nucleotides in m-RNA molecule, which contains information for the synthesis of polypeptide chain.

Triplet Code :

* The main problem of genetic code was to determine the exact number of nucleotide in a codon which codes for one amino acid.
* There are four types of N_2-bases in m-RNA (A, U, G, C) for 20 types of amino acids.
* If genetic code is singlet i.e. codon is the combination of only one nitrogen base, then only four codons are possible A, C, G and U. These are insufficient to code for 20 types of amino acids.

  Singlet code = $4^1 = 4$ codons

A
C
G
U

Codons

Singlet code

* If genetic code is doublet (i.e. codon is the combination of two nitrogen bases) then 16 codons are formed.

  Doublet code = $4^2 = 4 \times 4 = 16$ codons.

  16 codons insufficient for 20 amino acid.

AA	AC	AG	AU
CC	CA	CG	CU
GG	GA	GC	GU
UU	UA	UG	UC

Double code

Gamow :

* (1954) Pointed out the possibility of three letter code [Triplet code).
* Genetic code is triplet i.e. one codon consists of three nitrogen bases

  Triplet code = $4^3 = 4 \times 4 = 64$ codons
* In this case there occurs 64 codons in dictionary of genetic code.
* 64 codons are sufficient to code 20 types of amino adds.
* The chemical method developed by **Har Gobind Khorana** was instrumental in synthesising RNA molecules with defined combinations of bases (homopolymers and copolymers).
* Marshall Nirenberg's cell-free system for protein synthesis finally helped the code to be deciphered.
* Severo Ochoa enzyme (polynucleotide phosphorylase) was also helpful in polymerising RNA with defined sequences in a template independent manner (enzymatic synthesis of RNA).

Table : The Codons for the Various Amino Acids

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

Characteristics of Genetic Code :

(i) Triplet in Nature :

A codon is composed of three adjacent nitrogen bases which specifies the one amino acid in polypeptide chain.

For Ex. :

* In m-RNA if there are total 90 N_2 - bases.
* Then this m-RNA determines 30 amino acids in polypeptide chain.
* In above example, number of Nitrogen bases are 90 so codons $\Rightarrow$ 30 and 30 codons decide 30 amino acid in polypeptide chain.

(ii) Universality :

* The genetic code is applicable universally.
* The same genetic code is present in all kinds of living organism including viruses, bacteria, unicellular and multicellular organism.

(iii) Non - Ambiguous :

* Genetic code is non ambiguous i.e. one codon specifies only one amino acid and not any other.
* In this case one codon never code two different amino acids. Exception GUG codon which code both Valine and methionine amino acid.

(iv) Non - Overlapping :

* A nitrogen base is a constituent of only one codon.

(v) Commaless :

* There is no punctuation (comma) between the adjacent codon i.e. each codon is immediately followed by the next codon.
* If a nucleotide is deleted or added, the whole genetic code read differently.
* A Polypeptide chain having 50 amino acids shall be specialized by a linear sequence of 150 nucleotides. If a nucleotide is added in the middle of this sequence, the first 25 amino acids of polypeptide will be same but next 25 amino acids will be different.

(vi) Degeneracy of Genetic code :

* There are 64 codons for 20 types of amino acids, so most of the amino acids (except two) can be coded by more than one codon.
* Single amino acid coded by more than one codon is called Degeneracy of genetic code. This incident was discovered by Baumfield and Nirenberg.
* Only two amino acids Tryptophan and Methionine are specified by single codon.

  UGG for Tryptophan ; AUG for methionine
* All the other amino acids are specified or coded by 2 to 6 codons.
* Leucine, serine and arginine are coded or specified by 6-codons.

  Leucine = CUU, CUC, CUA, CUG, UUA & UUG

  Serien = UCU, UCC, UCA, UCG, AGU, AGC

  Arginine = CGU, CGC, CGA, CGG, AGA, AGG
* Degeneracy of genetic code is related to third position (3'-end of triplet codon) of codon. The third base is described as "Woobly base".

Chain initiation and chain termination codon :

* Polypeptide chain synthesis is signalled by two initiation codons AUG or GUG.
* AUG codes methionine amino acid in evacaryotes and in prokaryotes AUG codes N-formyl methionine.
* Some times GUG also functions as start codon it codes for valine amino acid normally but when it is present at starting position it code for methionine amino acid.
* Out of 64 codons 3-codons are **stopping** or **nonsense or termination codon.**

  Nonsense codons do not specify any amino acid.

  UAA (Ochre)
UAG (Amber)
UGA (Opal) } Non-sense Codon
* So only 61 codons are sense codons which specify 20 amino acid.

Wobble Hypothesis

* It is propounded by Crick.
* Normally an anticodon recognises only one codon, but sometimes an anticodon recognises more than one codon.

  This is known as Wobbling. Wobbling normally occurs for third nucleotide of codon.

* For e.g. Anticodon AAG can recognise two anticodons i.e. UUU and UUC, both stand for phenyl alalnine.

Types of m-RNA -

m-RNA is of 2 types -

(1) **Monocistronic :** The m-RNA in which genetic signal is present for the formation of only one polypeptide chain.

(2) **Polycistronic :** The m-RNA, in which genetic signal is present for the formation of more than one polypeptide chains.
Non sense codons lie found in middle position in polycistronic m-RNA.

Mutation and Genetic code:

* Mutation is defined as the sudden inheritable change in the genetic material.

(i) **Point mutation:**

- It occurs due to replacement nitrogen base within the gene.
- It only affects the change of particular amino acid.
- Best understood the cause of **sickle cell anemia.**

(ii) **Frame shift mutation:**

- It occurs due to insertion or deletion of one or more nitrogen bases in the gene.
- There is change in whole sequence of amino acid from the point of insertion or deletion.
- Best understood in **β-thalasemia.**

(a) **Insertion :** It is the addition of one or more nucleotides in the DNA segment. Insertion of three or its multiple bases do not change the reading frame but add a new amino acid.

(b) **Deletion :** It is the removal of one or more nucleotides from the DNA segment. Deletion of three or its multiple bases do not change the reading frame but remove one or more amino acids.

Normal DNA : ATC GAT CGA,

Insertion : ATC C G A TCG,

Deletion : ATC ATC GA

tRNA-the Adaptor molecule:

* The tRNA is called sRNA (soluble RNA)
* It acts as an adapter molecule.
* tRNA has an **anticodon loop** that base complementary to the codon.
* It has an **amino acid accepter** end to which it binds with amino acid.
* Each tRNA bind with specific amino acid i.e 61 types of tRNA found.
* One specific tRNA with anticodon UAC called **initiator tRNA.**

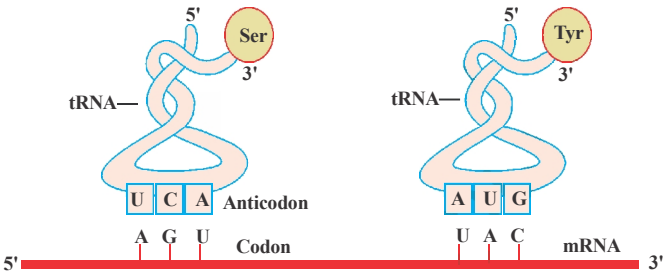


Figure : tRNA - The Adapter molecule

* There is no tRNA for stop codons. (UAA, UGA, UAG)
* The secondary structure is like clover-leaf.
* The actual structure of tRNA is compact, looks like inverted 'L'.

TRANSLATION

* It refers to the process of polymerization of amino acids to form a polypeptide. The order and sequence of amino acids are defined by the sequence of bases in the mRNA.
* The amino acids are joined by a bond which is known as a peptide bond.
* Amino acids are activated in the presence of ATP and linked to their specific tRNA is called **charging of tRNA or aminoacylation of tRNA.**

Amino acid + ATP $\xrightarrow{\text{Amino acyl t-RNA synthatase}}$
Amino acyl AMP-enzyme complex + PP
Amino acyl AMP-enzyme complex + t-RNA
→Amino acyl t-RNA complex + AMP + enzyme

* Ribosome is the cellular factory for protein synthesis.
* Ribosome consists of structural rRNA and 80 different proteins.

* In inactive state, ribosome(70S) present in two subunits:-
  - A large sub unit 50S.
  - A small sub unit 30S.

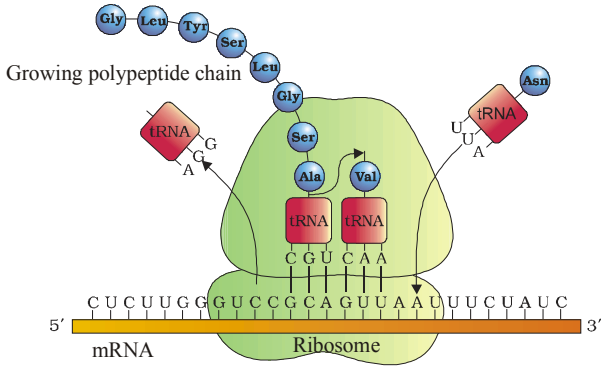


Figure : Translation

Steps :

(a) Initiation:

* The process of translation or protein synthesis begins with attachment of mRNA with small subunit of ribosome.
* The ribosome binds to the mRNA at the start codon (AUG).
* AUG is recognized by the initiator tRNA.

(b) Elongation:

* Larger subunit attached with the initiation complex.
* Larger subunit has two site 'A' site and 'P' site. Initiator tRNA accommodated in 'P' site of large subunit, the subsequent amino-acyl-tRNA enters into the 'A' site.
* The subsequent tRNA selected according to the codon of the mRNA.
* Codon of mRNA and anticodon of tRNA are complementary to each other.
* Formation of peptide bond between two amino acids of 'P' and 'A' site, catalyzed by **ribozyme,** (23S rRNA in bacteria). The moves from codon to codon along the mRNA is called translocation.

(c) Termination:

* Elongation continues until a stop codon arrives at 'P' site.
* There is no tRNA for stop codon.
* A **release factor** binds to the stop codon.
* Further shifting of ribosome leads to separation of polypeptide.
* An mRNA also has some additional sequences that are not translated called **untranslated regions (UTR).**

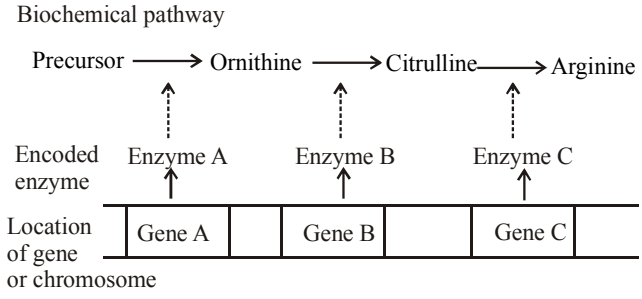
ONE GENE ONE ENZYME HYPOTHESIS

* The concept that genes have the information to produce enzymes, or gene metabolism relationship was experimentally proved by Beadle and Tatum (1948), on the basis of experiments conducted on pink bread mould (Neurospora crassa).
* This mould can normally grow in a simple minimal medium containing salts and sugar, making all other chemicals such as amino acids, purines, pyrimidines etc. through enzyme catalysed reactions. This wild type of the mould is called **prototroph**.
* Beadle and Tatum exposed the pink bread mould to X-rays, which can bring about a change in the nucleotide sequence of DNA and thus causes mutation.
* They found that the mutants were unable to grow on a minimal medium.
* Each type of mutant required some extra nutrient in the minimal medium for it's normal growth.
* Such nutritional mutants are called **auxotrophs.**
* They obtained different nutritional mutants requiring amino acids ornithine or citrulline or arginine for growth.
* The mutants could be classified into three types:

(i) **Mutant I :** Some could grow on ornithine -, or citrulline -, or arginine- containing medium,

(ii) **Mutant II :** some could grow on citrulline - or arginine containing medium, and

(iii) **Mutant III :** some could grow only on arginine supplemented medium.



* This shows that all mutants could grow on arginine supplemented medium suggesting that arginine is the final product of this pathway.
* The mutant of class I, could grow on ornithine, citrulline or arginine, suggesting that they lacked the capacity to synthesize ornithine, but beyond that they could complete the pathway.
* Similarly, mutants of class II, could not convert ornithine to citrulline, but if supplied citrulline could synthesize arginine.
* The last mutants of class III could not convert citrulline to arginine and had to be supplied later for growth.
* Beadle and Tatum reasoned that these defects could arise due to defective enzymes in each case.
* Since such changes were mutational, they held that one gene controls one enzyme in a pathway leading to their famous 'one gene one enzyme hypothesis'.

Types of genes

* All the genes do not play the same role nor all genes are active all the time. With regard to their role and activity, the genes are of following types:

(i) **Homeotic genes :** Homeotic gene regulates the organ differentiation in embryo. Homeobox related to transcription of homeotic gene.
If mutation takes place in homeotic gene organ formation is disturbed.

(ii) **Constitutive genes (House-keeping genes):** These genes are expressed constantly, because their products are constant needed for cellular activity. e.g. genes for glycolysis, gene of ATPase enzyme.

(iii) **Non-constitutive genes (Smart gene or Luxary gene) :**

* These genes remain silent and are expressed only when the gene product is needed.
* They are switched 'on' or 'off' according to the requirement of cellular activities.
* Non-constitutive genes are of two types (a) inducible and (b) repressible.
* The inducible genes are switched on in presence of a chemical substance called inducer, required for the functioning of gene activity.
* The repressible genes continue to express themselves till a chemical, often an end product of the metabolism inhibits or represses their activity. Such type of inhibition is called feed back inhibition or feed back repression.

(iv) **Overlapping gene :** A few genes in certain bacteria and animal viruses code for two different polypeptides. These are called overlapping genes. For example-in $\phi \times 174$ virus, SV-40 virus.

(v) **Pseudoallele :**

* Gene which is located on non homologous chromosome or gene which is located on different locus on homologous chromosome produces almost same phenotype called as pseudoallele.
* Pseudo allele is non allelic gene produced identical phenotype in cis-trans position. eg. Duplicate gene.

(vi) **Isoallele :** If several alleles exhibit same phenotype then they are said to Isoallele. In Drosophila allele W^{+C}, W^{+S}, $W^{+g} \rightarrow$ produce red eye colour.

(vii) **Hybrid vigour/Heterosis :**

* Superiority of offsprings over it's parents is called as Hybrid vigour & it develops due to Heterozygosity.
* Hybrid vigour can be maintained for long time in vegetatively propagated crops.
* Hybrid vigour can be lost by inbreeding (selfing) because inbreeding induces the Homozygosity in offsprings.
* Loss of Hybrid vigour due to inbreeding, is called as **inbreeding depression.**
* Inbreeding depression mainly related to cross pollinated crops.

(viii) **Jumping genes :**

* It is a segment of DNA which moves from one chromosome to another chromosome within the genome of an individual. McClintock (1983) got nobel prize for the discovery of jumping gene in maize.
* Two transposable controlling elements (Ds) and activator (Ac), which can jump to any chromosome from their original location on chromosome 9.

* Also in bacteria plasmid transposone carry gene for antibiotic resistance (ampicillin).
* **Other Examples :** Transposable elements (TE) in Drosophila- As much as 10% of the genome consist of transposons, most important of these are copia like element, Fold back (FB) (for eye colour) , and P and I element (for sterlity). Ty-element in yeast.

REGULATION OF GENE EXPRESSION

* All the genes are not needed constantly. The genes needed only sometimes are called regulatory genes and are made to function only when required and remain nonfunctional at other times. Such regulated genes, therefore required to be switched 'on' or 'off' when a particular function is to begin or stop.
* Regulation of gene expression in eukaryotes takes place in different level:

(i) Transcriptional level (formation of primary transcript)
(ii) Processing level (regulation of splicing)
(iii) Transport of mRNA from nucleus to the cytoplasm.
(iv) Translational level.

Operon concept :

* Proposed by Jacob & Monad.
* Segment of genetic material that act as a regulated unit is called operon.
* It is a group of gene. It is of two types-
  (1) Inducible operon
  (2) Repressible operon

1. Inducible operon : Normally remain inactive when inducer come this operon become active.
Eg.- Lac operon of *E. coli.*

Structure of lac operon of *E. coli.* Lac operon of E. coli have four component

(a) Regulatory gene : Synthesize the repressor that attach with the operator gene & block the passage of RNA polymerase.

(b) Promotor gene : It provide site for attachment to RNA polymerase enzyme and form the initiating point for the transcription.

(c) Operator gene : Control the activities of structure gene and provide the passage to the RNA polymerase enzyme.

(d) Structure gene : It has three structural genes cistron-Z, cistron - Y, cistron -X.

* Cistron Z is responsible for the synthesis of β galactocidase enzyme.
* Cistron- Y is responsible for synthesis of permease enzyme.
* Cistron-X is responsible for the synthesis of transacetylase enzyme.
* This lac operon normally remain inactive when lac operon contact with lactose, the lactose act as a inducer. Lactose combine with the repressor so repressor is detached from operator gene and RNA polymerase enzyme gets its passage and reached to the structural genes and transcription started. Structural gene form the polycistronic mRNA and form the β-galactocidase enzyme and permease and transacetylase enzyme. β-galatocidase enzyme hydrolyses the lactose. Permease enzyme increase the entry of lactose inside the bacterial cell. Transacetylase enzyme has no role in lactose hydrolysis.

Inducer (Lactose) + Repressor → Switched on

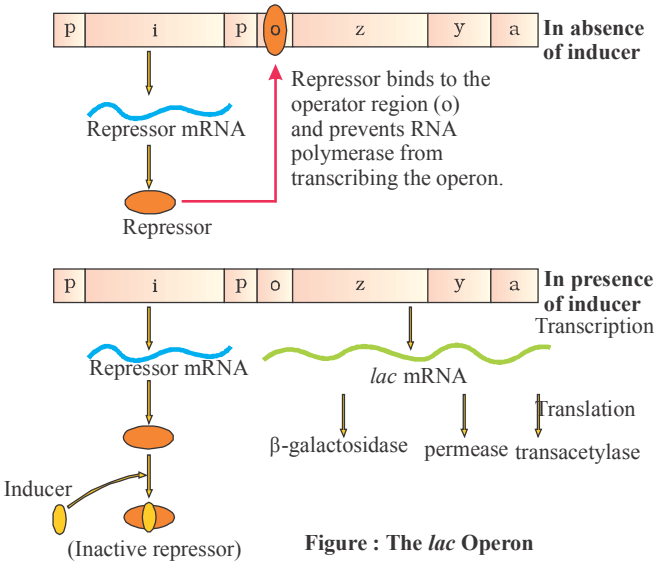


Figure : The *lac* Operon

2. Repressible operon : Operon that remain generally active and synthesize product when product cross the threshold value operon become inactive.
Eg.- Tryptophan operon (Trp. operon)

Trp. operon consist of four component.

(a) **Regulatory gene :** That synthesize the aporepressor. Aporepressor can not combine with the operator gene and does not block the passage of RNA polymerase enzyme.

(b) **Promotor gene :** Which is the initial point of transcription provide site for attachment to RNA polymerase enzyme.

(c) **Operator gene :** Which control the activity of structural genes and provide the passage to the RNA polymerase enzyme.

(d) **Structural gene :**

* Structural gene of Trp. operon are five type. Cistron - E, D, C, B, A.
* In Trp. operon passage of RNA polymerase enzyme generally open and transcription continuously occur.
* All the cistron of Trp. operon form the polycistronic mRNA which synthesize the tryptophan.
* When tryptophan cross the threshold value. Then act as a corepressor.
* Corepressor combine with the aporepressor and form the repressor.
* Repressor attached with the operator gene and block the passage of RNA polymerase enzyme and transcription stops and thus operon become inactive.

Gene expression in Eukaryotes :

1. In eukaryotes, functionally related genes may not be clustered together constituting an operon.

2. The most popular model is known as 'Britten-Davidson model' or 'Gene battery model' proposed by Britten and Davidson in 1969.

3. A set of structural genes controlled by one sensor site is termed as battery.

4. Gene-battery model assumes the presence of four classes of sequences:

(i) **Producer gene:** A producer gene is comparable to structural gene of prokaryotic operon.

(ii) **Receptor site:** A receptor site is comparable to operator gene of bacterial operon and one such receptor site is assumed to be present adjacent to each producer gene.

(iii) **Integrator gene:** Integrator gene is comparable to regulator gene and is responsible for synthesis of an activator RNA. It activates the receptor site.

(iv) **Sensor site:** A sensor site regulates the activity of integrator gene. Activator gene can be transcribed only when the sensor site is activated. The sensor sites are recognized by agents which change the patterns of gene expression like hormones and proteins. When a transcription factor (protein, hormone) bind to the sensor site it cause the transcription of integrator.

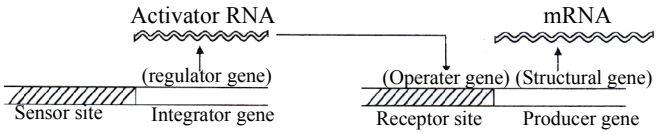


Figure : Britten-Davidson model or Gene-battery model

HUMAN GENOME PROJECT

* Genetic make-up of an organism or an individual lies in the DNA sequences. If two individuals differ, then their DNA sequences should also be different, at least at some places. These assumptions led to the quest of finding out the complete DNA sequence of human genome.
* With the establishment of genetic engineering techniques where it was possible to isolate and clone any piece of DNA and availability of simple and fast techniques for determining DNA sequences, a very ambitious project of sequencing human genome was launched in the year 1990.
* Human genome is said to have approximately 3×10^9 bp, and if the cost of sequencing required is US $ 3 per bp (the estimated cost in the beginning), the total estimated cost of the project would be approximately 9 billion US dollars. Further, if the obtained sequences were to be stored in typed form in books, and if each page of the book contained 1000 letters and each book contained 1000 pages, then 3300 such books would be required to store the information of DNA sequence from a single human cell. HGP was closely associated with the rapid development of a new area in biology called as **Bioinformatics.**
* The project was completed in 2003.

* Knowledge about the effects of DNA variations among individuals can lead to revolutionary new ways to diagnose, treat and someday prevent the thousands of disorders that affect human beings. Besides providing clues to understanding human biology, learning about non-human organisms, DNA sequences can lead to an understanding of their natural capabilities that can be applied toward solving challenges in health care, agriculture, energy production, environmental remediation.
* Many non-human model organisms, such as bacteria, yeast, Caenorhabditis elegans (a freeliving non-pathogenic nematode), Drosophila (the fruit fly), plants (rice and Arabidopsis), etc., have also been sequenced.

Goals of HGP

Some of the important goals of HGP are as follows :

* Identify all the genes in human DNA.
* Determine the sequences of the 3 billion chemical base pairs that make up human DNA.
* Store this information in databases.
* Improve tools for data analysis.
* Transfer related technologies to other sectors, such as industries.
* Address the ethical, legal, and social issues (ELSI) that may arise from the project.

Methodologies:

* The methods involved two major approaches.

(1) **Epressed Sequence Tags (ESTs)** Identifying all the genes that expressed as RNA.

(2) **Sequence Annotation** - The blind approach of simply sequencing the whole set of genome that contained all the coding and non-coding sequence, and later assigning different regions in the sequence with functions.

* For sequencing, the total DNA from a cell is isolated and converted into random fragments of relatively smaller sizes (recall DNA is a very long polymer, and there are technical limitations in sequencing very long pieces of DNA) and cloned in suitable host using specialised vectors. The cloning resulted into amplification of each piece of DNA fragment so, that is subsequently could be sequenced with ease.
* The commonly used hosts were bacteria and yeast, and the vectors were called as **BAC (bacterial artificial chromosomes)**, and **YAC (yeast artificial chromosomes).**
* The fragments were sequenced using automated DNA sequencers that worked on the principle of a method developed by Frederick Sanger. (Remember, Sanger is also credited for developing method for determination of amino acid sequences in proteins). These sequences were then arranged based on some overlapping regions present in them. This required generation of overlapping fragments for sequencing. Alignment of these sequences was humanly not possible. Therefore, specialised computer based programmes were developed. These sequences were subsequently annotated and were assigned to each chromosome.
* The sequence of chromosome I was completed only in May 2006 (this was the last of the 24 human chromosomes-22 autosomes and X and Y to be sequenced).
* Another challenging task was assigning the genetic and physical maps on the genome. This was generated using information on polymorphism of restriction endonuclease recognition sites, and some repetitive DNA sequences known as microsatellites.

Salient Features of Human Genome

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

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

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

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

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

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

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

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

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

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

	Base pair	Gene No.
Bateriophage	10,000	------ / -----
Lily	106 Billion B.P.	------
E.coli	4.7 million B.P.	4,000
S. cerviceae	12 Million B.P.	6,000
D. melangaster	180 Million B.P.	13,000
Caenorhabditis elegans	97 Million B.P.	18,000
Human	3 Billion B.P.	30,000

(a) First prokaryotes in which complete genome was sequenced is *Haemophilus influenzae.*

(b) First Eukaryote in which complete genome was sequenced is *Saccharomyces cerviceae* (Yeast).

(c) First plant in which complete genome was sequenced is *Arabidopsis thaliana* (Small mustard plant).

(d) First animal in which complete genome was sequenced is *Caenorhabditis elegans* (Nematode).

β-globin and insulin gene are less than 10 kilo base pair T.D.F. gene is the smallest gene (14 base pair) and Duchenne muscular Dystrophy gene is made up of 2400 kilo base pair.(Longest gene).

Gene Banks :

* A gene bank is a store house of clones of known DNA fragments, genes, gene maps, seeds, spores, frozen sperms or eggs or embryos.
* These are stored for possible use in genetic engineering and breeding experiments where species have become extinct.
* The need of gene banks is being increasingly felt as the rate of extinction is increasing day by day. The human genome project is the most remarkable contribution in this field.

DNA FINGER PRINTING

* DNA finger printing is a very quick way to compare the DNA sequences of any two individual.
* DNA fingerprinting involves identifying differences in some specific regions in DNA called **repetitive DNA**, because in these sequences, a small stretch of DNA is repeated many times.
* During centrifugation the bulk DNA forms major peak and the other small peaks are called **satellite DNA.**
* Depending on base composition (A:T rich or G:C rich), length of segment, and number of repetitive units, the satellite DNA classified into many types, such as mini -satellite and micro - satellite.
* 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.**

The process:

* DNA fingerprinting was initially developed by Alec Jeffreys.
* 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)

* The VNTR belongs to a class of satellite DNA referred to as mini-satellite.
* The size of VNTR varies from 0.1 to 20 kb.
* 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 DNA from a single cell is enough to perform DNA fingerprinting.

Different steps of DNA fingerprinting are:-

* **Extraction of DNA** - using high speed refrigerated centrifuge.
* **Amplification** - many copies are made using PCR
* **Restriction Digestion** - using restriction enzymes DNA is cut into fragments.
* **Separation of DNA fragments** - using electrophoresis-agarose polymer gel.
* **Southern Blotting :** Separated DNA sequences are transferred onto nitrocellulose or nylon membrane.
* **Hybridisation :** The nylon memberane exposed to radio active probes.
* **Autoradiography :** The dark bands develop at the probe site.

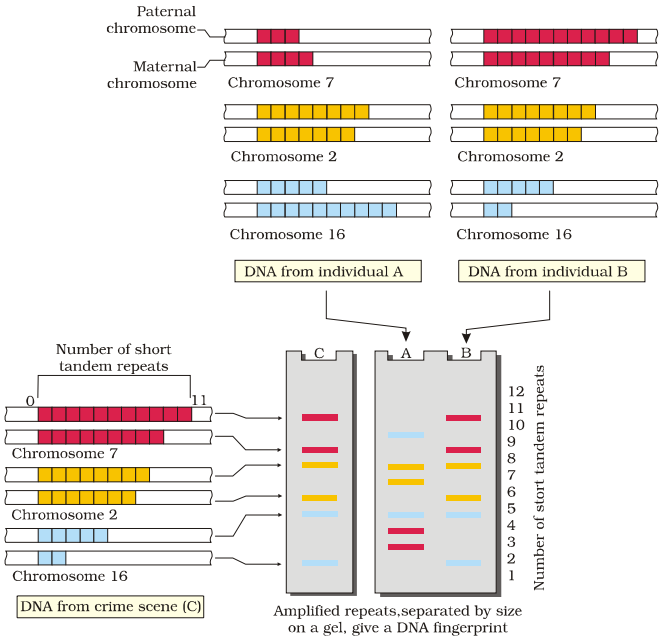


Figure : Schematic representation of DNA fingerprinting:

Applications of DNA Fingerprinting

(i) Identify criminals in forensic labs.
(ii) Determine paternity
(iii) Verify whether a hopeful immigrant is really close relative of an already established resident.
(iv) Identify racial graps to rewrite biological evolution.

CONCEPT REVIEW

* Nucleotide monomers constitutes a polymer called **nucleic acid.** It is of two types RNA and DNA.
* While DNA is **store house** of information, RNA helps in **transfer** and **expression** of information.
* As DNA is structurally and chemically more **stable,** it is better genetic material. Although both DNA and RNA serves as genetic material.
* RNA was **first to evolve,** and DNA was derived from it.
* Bases in two DNA strands show hydrogen bonding (A = T, G = C) and follow **Chargaff's rule,** so that both the strands are complementary and its replication is semi-conservative.
* Segment of DNA that codes for an RNA is known as **gene.** During transcription, one DNA strand acts as template which directs the synthesis of complementary RNA.
* In prokaryotes, transcription and translation is a continuous process. In eukaryotes, the genes are split **exons are interupted by introns.** Introns are removed and exons are joined, to produce functional RNA.
* The mRNA contains genetic code In combination of three (triplet code) to code for an amino acid. This genetic code is read by t-RNA which act as an **adapter molecule.**
* There is specific t-RNA for each amino acid. Each t-RNA binds to amino acid at one end and with codons by H-bonding at another end.
* Translation occurs at ribosome, here **ribozyme** (rRNA enzyme) acts as catalyst which helps in peptide bond formation. Process of translation has evolved around RNA, which shows that life began around RNA.

* Since transcription and translation are **energetically** very expensive; they are tightly regulated, *e.g.*, ***lac*** **operon** which is regulated by amount of lactose in medium, *i.e.*, regulation of enzyme synthesis by its substrate.
* Human genome project is aimed for sequencing every base in human genome. DNA finger printing is used for this which is based upon **principle of polymorphism** in DNA sequence.

IMPORTANT POINTS

* Transcription involves synthesis of RNA over DNA.
* Usual method of DNA replication is semiconservative.
* Functional unit of gene that specifies synthesis of one polypeptide is cistron.
* Enzyme required for transcription is RNA polymerase.
* Site of tRNA that binds to mRNA molecule is anticodon.
* Ligase = Joins short DNA segments.
  Helicase = Breaks H-bonds between complementary DNA strands.
* Arrangement of three successive bases in genetic code signifies amino acid.
* Lac operon is inducible operon.
* Okazaki segments are formed during replication.
* Khorana synthesised the first artificial gene.
* tRNA recognises amino acyl synthetase enzymed by DHU loop.
* Transposable elements (genes) were first discovered in maize.
* DNA helicase –
  (i) Separate DNA strands and establish replication forks.
  (ii) ATP requiring unwinding enzymes.
  (iii) Hydrolyse ATP
* Site for protein synthesis is ribosome.
* Thymine is absent in RNA.
* Purines of DNA are adenine and guanine.
* mRNA is synthesised over DNA template in direction 5' → 3'.
* Central dogma of protein synthesis consists of

$$DNA \xrightarrow{\text{Transcription}} mRNA \xrightarrow{\text{Translation}} \text{Protein.}$$

* Enzyme catalysing peptide formation is located in larger subunit of ribosome.
* The smallest RNA is tRNA.
* The most abundant RNA of cell is rRNA.
* Exon part of mRNA has code for polypeptide.
* Teminism is reverse transcription.
* During transcription, RNA polymerase binds to DNA site promoter.
* Structural gene = Codes for enzyme proteins.
  Operator gene = Binding site for repressor protein
  Promoter gene = Binding site for RNA-polymerase.
  Regulator gene = Codes for repressor protein.
* Helicase = Opening of DNA
  Gyrase = Unwinding of DNA
  Primase = RNA priming
  DNA polymerase III = Joining of nucleotides.
* AUG = Methionine
  UAA = Termination
  UUU = Phenylalanine
  UGG = Tryptophan
* In lac operon system, lac gene-i codes for β-galactosidase.
* mRNA is shorted lived.
* Process used by Meselson and Stahl for studying semiconservative replication of DNA was density gradient centrifugation.
* 450-700 genes = *Mycoplasma*
  4000 genes = *Escherichia coli*
  13000 genes = *Drosophila melanogaster.*
  32000-50000 genes = *Oryza sativa*
  35000-45000 genes = *Homo sapiens*
* Enzyme responsible for DNA chain elongation is DNA polymerase III.
* Okazaki fragment during DNA replication, Polymerise in
  5' → 3' direction and explain 3' → 5' DNA replication.
* Association of mRNA with many ribosomes is polysome.
* $RNA \xrightarrow{\text{Reverse Transcription}} DNA \xrightarrow{\text{Replication}} DNA \xrightarrow{\text{Transcription}} mRNA \xrightarrow{\text{Translation}}$ Polypeptide
* RNA polymerase III transcribes tRNA.

* HIV does not follow central dogma of molecular biology.
* Chargaff's rule is applicable to A-T.
* Process of translation is related to protein synthesis.
* Reverse transcriptase is RNA dependent DNA polymerase.

Nitrogenous base	Nucleoside (Base + Sugar)	Nucleotide (Base + Sugar + Phosphate)
DNA Adenine = A	Deoxyadenosine	Deoxyadenosine monophosphate or Adenine deoxyribose nucleotide
Guanine = G	Deoxyguanine	Deoxygunine monophosphate or Guanine deoxyribose-nucleotide
Thyamine = T	Thymidine	Deoxythymidine monophosphate or Thymidine deoxyribose nucleotide
Cytosine = C	Deoxycitidine	Deoxycytidine monophosphate or Cytosine deoxyribose nucleotide
RNA Adenine = A	Adenosine	Adenosine monophosphate or Adenine ribose nucleotide
Guanine = G	Guanosine	Guanosine monophosphate or Guanine ribose nucleotide
Uracil = U	Uridine	Uridine monophosphate or Uracil ribose nucleotide
Cytosine = C	Cytidine	Cytidine monophosphate or Cytosine ribose nucleotide

* Repetitive DNA and Satellite DNA

S.No.	Repetitive DNA	Satellite DNA
1.	Repetitive DNA are DNA sequences that contain small segments, which are repeated many times.	Satellite DNA are DNA sequences that contain highly repetitive DNA.

* mRNA and tRNA

S.No.	mRNA	tRNA
1.	mRNA or messenger RNA acts as a template for the process of transcription.	tRNA or transfer RNA acts as an adaptor molecule that carries a specific amino acid to mRNA for the synthesis of polypeptide.
2.	It is a linear molecule.	It has clover leaf shape.

* Template strand and Coding strand

S.No.	Template strand	Coding strand
1.	Template strand of DNA acts as a template for the synthesis of mRNA during transcription.	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).
2.	It runs from 3' to 5'.	It runs from 5'to 3'.

QUESTION BANK

EXERCISE - 1 (LEVEL-1) [NCERT EXTRACT]

SECTION - 1 (VOCABULARY BUILDER)

Choose one correct response for each question.
For Q.1-Q.4
Match the column I with column II.

Q.1 Match the following columns.

	Column I	Column II
a.	RNAdigesting enzymes	i. Lipase
b.	Protein digesting enzymes	ii. DNase
c.	DNAdigesting enzymes	iii. Protease
d.	Fat digesting enzymes	iv. RNase

Codes
(A) (a) – (iii), (b) – (iv), (c) – (ii), (d) – (i)
(B) (a) – (i), (b) – (ii), (c) – (iv), (d) – (iii)
(C) (a) – (iv), (b) – (iii), (c) – (ii), (d) – (i)
(D) (a) – (i), (b) – (ii), (c) – (iii), (d) – (iv)

Q.2 Match the following columns.

	Column I	Column II
a.	F. Miescher	i. DNA double helix
b.	Griffith	ii. Nuclein
c.	Hershey and Chase	iii. *Streptococcus pneumoniae*
d.	Watson and Crick	iv. Bacteriophage
e.	Wilkins and Franklin	v. X-ray diffraction studies

Codes
(A) (a) – (v), (b) – (iv), (c)–(iii), (d)–(i), (e)–(ii)
(B) (a) – (i), (b) – (iv), (c)–(iii), (d)–(ii), (e)–(v)
(C) (a) – (ii), (b) – (iii), (c)–(iv), (d)–(i), (e)–(v)
(D) (a) – (i), (b) – (iii), (c)–(iv), (d)–(ii), (e)–(v)

Q.3 Match the following columns.

	Column I	Column II
a.	tRNA	i. Linking of amino acids
b.	mRNA	ii. Transfer of genetic information
c.	rRNA	iii. Nucleolar organising region
d.	Peptidyl transferase	iv. Transfer of amino acid from cytoplasm to ribosome.

Codes
(A) (a) – (iv), (b) – (ii), (c) – (iii), (d) – (i)
(B) (a) – (i), (b) – (iv), (c) – (iii), (d) – (ii)
(C) (a) – (i), (b) – (ii), (c) – (iii), (d) – (iv)
(D) (a) – (i), (b) – (iii), (c) – (ii), (d) – (iv)

Q.4 Match the following columns.

	Column I	Column II
a.	Termination	i. Aminoacyl tRNA synthatase
b.	Translation	ii. Okazaki fragments
c.	Transcription	iii. GTP dependent release factor
d.	DNA replication	iv. RNA polymerase

Codes
(A) (a) – (iii), (b) – (i), (c) – (iv), (d) – (ii)
(B) (a) – (ii), (b) – (iii), (c) – (i), (d) – (iv)
(C) (a) – (iv), (b) – (iii), (c) – (i), (d) – (ii)
(D) (a) – (ii), (b) – (i), (c) – (iii), (d) – (iv)

SECTION - 2 (BASIC CONCEPTS BUILDER)

For Q.5 to Q.31 :

Choose one word for the given statement from the list.

DNA polymerase, heterochromatin, 2.2, DNA helicase, DNA ligase, Sugar-phosphate, Chargaff's rule, telomerase, 3, operator, mRNA, primase, Sigma, DNA polymerase, Exons

Q.5 ____ catalyzes the unwinding of the DNA double helix.

Q.6 ____ produces an RNA strand that acts as a starting point for DNA replication.

Q.7 ____ connects Okazaki fragments in the lagging strand.

Q.8 _____ adds repeating units to the end of chromosomes.

Q.9 _____ may be responsible for cancer cell development

Q.10 ____ adds nucleotides only at the 3' end of an existing nucleotide chain

Q.11 The length of DNA in diploid human cell is ___m.

Q.12 ____ forms the backbone of DNA double helix.

Q.13 During DNA replication, primer is formed by __.

Q.14 Initiation of prokaryotic transcription is performed by _____ factor after binding with _____ site.

Q.15 DNA has an equal number of adenine and thymine residues (A = T) and equal number of guanine and cytosine (G = C). These relationships are known as _____.

Q.16 Fully processed hnRNA is called _____.

Q.17 Part of chromatin which is densly packed and stain darkly is called _____.

Q.18 The main enzyme which use a DNA template to catalyse the polymerisation of deoxynucleotides is _____.

Q.19 The accessibility of the promoter regions of prokaryotic DNA is (in many cases) regulated by the interaction of proteins with the sequences termed as _____.

Q.20 In *lac* operon model, all time or constitutively working gene is _____.

Q.21 Number of nitrogenous bases in a codon is/are _____.

Q.22 Sequences that appears in the mature or processed RNA are called _____.

Q.23 Base pairing in DNA is the same as the one used by RNA polymerase for making mRNA. **[True / False]**

Q.24 Enzymes used for transcription are same in prokaryotic and eukaryotic cells. **[True / False]**

Q.25 Transcription takes place in the cytoplasm of prokaryotic cells and in the nucleus of eukaryotic cells. **[True / False]**

Q.26 Only one ribosome can translate an mRNA at one time. **[True / False]**

Q.27 In eukaryotes, RNA polymerase binds directly to the promoter sequence. **[True / False]**

Q.28 In both, prokaryotic and eukaryotic cells,gene regulation takes place mostly at the transcription level. **[True / False]**

Q.29 The hnRNA is primary transcript produced in prokaryotes. **[True / False]**

Q.30 In total, there are five punctuation codons. **[True / False]**

Q.31 Promoter for inhibition gene and structural genes in *lac*-operon is common. **[True / False]**

SECTION - 3 (ENHANCE PROBLEM SOLVING SKILLS)

Choose one correct response for each question.

PART - 1 : THE DNA

Q.32 Name the pyrimidine, which is present only in RNA.
(A) Adenine (B) Guanine
(C) Thymine (D) Uracil

Q.33 Which additional group is present at the 2' position of the ribose sugar in RNA?
(A) R – H (B) CHO
(C) OH (D) COOH

Q.34 According to Chargaff's rule
(A) A = C (B) G = T
(C) A + G = T + C (D) $\frac{A+T}{C+G}=1$

Q.35 What is the difference between adenosine and deoxyadenosine?
(A) Only sugar (B) Only purine
(C) Only phosphate (D) All of these

Q.36 Nitrogenous bases are linked to sugar by –
(A) hydrogen bond
(B) phosphodiester bond
(C) N-glycosidic bond
(D) covalent bond

Q.37 Hallmark of the Watson and Crick 3-dimensional DNA model was based upon the findings of
(A) Wilkins and Franklin
(B) Erwin Chargaff
(C) Hershey and Chase
(D) Meselson and Stahl

Q.38 Positively charged basic proteins that are found in eukaryotes are called –
(A) histones (B) protamine
(C) arginine (D) lysine

Q.39 Thymine is also called –
(A) 2 methyl uracil (B) 3 methyl uracil
(C) 4 methyl uracil (D) 5 methyl uracil

Q.40 a ↻ DNA $\xrightarrow{b}$ mRNA $\xrightarrow{c}$ Proteins
Choose the correct option for a, b, c and d.
(A) a-Replication, b-Transcription,c-Translation
(B) a-Translation, b-Transcription, c-Reverse transcription
(C) a-Translation, b-Transcription,c-Replication
(D) a-Transcription, b-Translation,c-Replication

Q.41 H_1 histone is also called
(A) junk histone (B) linker histone
(C) neutral histone (D) basic histone

Q.42 Which of the following DNA form has maximum number of base pairs per turn?
(A) A-DNA (B) B-DNA
(C) C-DNA (D) Z-DNA

Q.43 The process of reverse transcription was discovered by –
(A) Temin and Baltimore (B) Watson and Crick
(C) Alfred Hershey (D) None of these

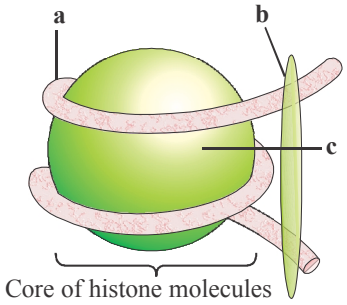
Q.44 How many base pairs of DNA helix are contained in a typical nucleosome?
(A) 400 (B) 300
(C) 200 (D) 100

Q.45 Central dogma states that genetic information flows from
(A) DNA → RNA → Fat
(B) DNA → RNA → Protein
(C) RNA → DNA → Protein
(D) RNA → DNA → Amino acid

Q.46 Choose the correct option w.r.t. chemical composition of chromosome
(A) DNA-40%, RNA-8.5%
(B) DNA-50%, Histone-40%
(C) RNA-1.2%, Histone-50%
(D) RNA-1.2%, Histone-40%

Q.47 The packaging of chromatin at higher level requires an additional set of proteins that are collectively referred to as
(A) histone proteins
(B) non-histone proteins
(C) basic proteins
(D) acidic packaging proteins

Q.48 In the given diagram, identify a, b and c.



(A) a-DNA, b-H_1 Histone, c-Histone octamer
(B) a-RNA, b-H_1 Histone, c-Histone octamer
(C) a-DNA, b-H_1 Histone, c-Histone tetramer
(D) a-RNA, b-H_1 Histone, c-Histone tetramer

Q.49 Erwin Chargaff stated that for double-stranded DNA, the ratio between adenine and thymine and guanine and cytosine is –
(A) constant and equals to one
(B) constant and equals to 1.5
(C) not constant at all
(D) not constant for DNA only

PART - 2 : GENETIC MATERIAL

Q.50 Who introduced the transforming principle?
(A) Frederick Griffith (B) Oswald Avery
(C) Colin Macleod (D) Maclyn McCarty

Q.51 Which of the following types of bacteria were used in Grifith's transformation experiment?
(A) *Diplococcus,* R-III and S-II type
(B) *Pneumococcus,* T2 phage
(C) *Streptococcus,* R-II and S-III type
(D) *Diplococcus, E. coli*

Q.52 Stability of DNA is impacted by
(A) deoxyribose sugar
(B) presence of thymine in place of uracil
(C) Both (A) and (B)
(D) None of the above

Q.53 Adenosine is a
(A) nitrogenous base (B) nucleotide
(C) ribonucleoside (D) ribonucleotide

Q.54 Bacteriophage protein coat was labelled by growing *E. coli* on –
(A) ^{35}S labelled sulphate
(B) ^{32}S labelled sulphate
(C) ^{30}S labelled sulphate
(D) ^{32}P labelled sulphate

Q.55 The biochemical nature of transforming principle was defined by
(A) Griffith
(B) Avery, Macleod, McCarty
(C) Watson and Crick
(D) Taylor

Q.56 Which of the following process is associated with synthesis of enzymes?
(A) Translation (B) Replication
(C) Transduction (D) Transformation

Q.57 Which group present in RNA nucleotide is very reactive and makes RNA liable and easily degradable than DNA?
(A) 2–OH' group on the purine base
(B) 2–OH' group on ribose sugar
(C) 3–OH' group on ribose sugar
(D) 4–OH' group on ribose sugar

Q.58 In Hershey and Chase experiment, the protein of T2 phage was made radioactive by using
(A) S^{32} (B) P^{31}
(C) S^{35} (D) P^{32}

Q.59 Hershey and Chase concluded that viral infecting agent in their experiment was –
(A) Protein (B) DNA
(C) RNA (D) Both (B) and (C)

PART - 3 : THE RNA WORLD

Q.60 Which of the following is a genetic RNA?
(A) mRNA
(B) rRNA
(C) hn-RNA
(D) RNA present in plant viruses

Q.61 Processes like metabolism, splicing and translation are evolved around
(A) DNA (B) RNA
(C) protein (D) nucleus

Q.62 Ribozymes are
(A) RNA acting as enzymes.
(B) DNA acting as enzymes.
(C) DNA acting as molecular scissors.
(D) RNA acting as molecular scissors.

Q.63 Choose the correct option w.r.t. RNA.
(A) Presence of thymine in place of uracil
(B) Absence of free 2'OH in sugar
(C) Mutates at faster rate
(D) Is non-catalytic

PART - 4 : REPLICATION

Q.64 Who experimentally proved the semiconservative mode of DNA replication?
(A) Mathew Meselson (B) Franklin Stahl
(C) Both (A) and (B) (D) Watson and Crick

Q.65 Telomerase works at the –
(A) end of prokaryotic chromosome
(B) end of eukaryotic chromosome
(C) middle of eukaryotic chromosome
(D) start point of prokaryotic chromosome

Q.66 DNA replication is –
(A) Semi-conservative, continuous
(B) Conservative, continuous
(C) Semi-conservative, semi-discontinuous
(D) Semi-continuous, conservative

Q.67 On which strand of DNA, replication is discontinuous?
(A) 5' - 3' polarity strand
(B) 3' - 5' polarity strand
(C) on both strand of DNA
(D) discontinuous replication doesn't takes place in replication.

Q.68 Any mistake during replication would result into
(A) duplication (B) inversion
(C) mutation (D) polyploidy

Q.69 How many types of DNA polymerases are associated with eukaryotic cell
(A) Three (B) Four
(C) Five (D) Two

Q.70 Name the heavy isotope used by Meselson and Stahl for proving the semiconservative mode of DNA.
(A) $^{15}NH_4Cl$ (B) $^{14}NH_3Cl_2$
(C) $^{13}NH_2Cl_3$ (D) All of these

Q.71 In Hershey and Chase experiment, radioactive ^{32}P was used to culture bacteriophage which resulted in radioactive –
(A) Viral DNA
(B) Bacterial capsule
(C) Viral protein
(D) Plasma membrane of bacteria

Q.72 Which of the following acts as substrate as well as provide energy for DNA polymerisation?
(A) Ribonucleoside
(B) Deoxyribonucleoside
(C) Ribonucleotide
(D) Deoxyribonucleoside triphosphate

Q.73 The replication occur within the small opening of DNA helix referred to as –
(A) replication fork (B) duplication fork
(C) DNA fork (D) RNA fork

Q.74 Semiconservative DNA replication was proved by Messelson & Stahl, in which DNA was made
(A) Radioactive using N15
(B) Heavy using N14
(C) Heavy using 15 NH_4Cl
(D) Radioactive using 14 NH_4Cl

Q.75 Reverse transcriptase is
(A) DNA dependent DNA polymerase.
(B) RNA dependent DNA polymerase.
(C) DNA dependent RNA polymerase
(D) RNA dependent RNA polymerase

PART - 5 : TRANSCRIPTION

Q.76 Transcription involves the formation of
(A) DNA from DNA (B) RNA from DNA
(C) RNA from RNA (D) Protein from RNA

Q.77 The term 'genetic RNA' refers to –
(A) Genetic material of RNA viruses
(B) RNA that carries genetic massage
(C) RNA that helps gene regulation is lac operon
(D) RNA present in mitochondria

Q.78 How many types of RNA participate in eukaryotic transcription?
(A) three types of RNA
(B) two types of RNA
(C) only one type of RNA
(D) four types of RNA

Q.79 Polycistronic transcriptional unit codes for
(A) one polypeptide
(B) many polypeptides
(C) two polypeptides
(D) recombinant polypeptide

Q.80 Template strand is also called
(A) non-coding strand (B) antisense strand
(C) master strand (D) All of these

Q.81 RNA polymerase II transcribes
(A) hnRNA (heterogenous nuclear RNA)
(B) 50S rRNA
(C) 30S rRNA
(D) 40S rRNA

Q.82 Regulatory sequence may be present at –
(A) only upstream to the promoter.
(B) only down stream to the promoter.
(C) upstream or down stream to the promoter.
(D) None of the above

Q.83 A gene that takes part in synthesis of polypeptide
(A) regulator gene (B) structural gene
(C) operator gene (D) promoter gene

Q.84 (–) sign and (+) sign for DNA strand stands for
(A) non-coding strand and coding strand.
(B) template strand and non-template strand.
(C) antisense strand and sense strand.
(D) All of the above

Q.85 RNA polymerase associates transiently with ____ factor and _____ factor to initiate and terminate the process of transcription respectively.
(A) initiator; terminator
(B) terminator; initiation
(C) sigma (σ); rho (ρ)
(D) Both (A) and (C)

Q.86 The regulatory genes are located –
(A) along with the structural genes.
(B) in between operator and the structural genes
(C) in the middle of the structural genes
(D) in front of the structural genes

Q.87 DNA dependent RNA polymerase catalyses the polymerisation in
(A) 5' - 3' direction (B) 3'- 5' direction
(C) 3'- 2' direction (D) 2' - 3' direction

Q.88 RNA polymerase I transcribes
(A) 28S r RNA (B) 18S rRNA
(C) 5.8S rRNA (D) All of these

Q.89 Consider the following statements, in eukaryotes
I. RNA polymerase I transcribes rRNAs
II. RNA polymerase II transcribes SnRNAs
III. RNA polymerase III transcribes hnRNA
IV. RNA polymerase II transcribes hnRNA
Which of the statements given above are correct?
(A) I and II (B) I and III
(C) I, II and IV (D) I and IV

Q.90 Monocistronic transcriptional unit codes for
(A) single polypeptide
(B) double polypeptides
(C) no polypeptide
(D) triple polypeptides

Q.91 Splicing takes place in
(A) prokaryotes only (B) eukaryotes only
(C) Protista only (D) plants only

Q.92 RNA polymerase binds to the
(A) regulator gene (B) promoter gene
(C) operator gene (D) structural gene

Q.93 Which one of the following enzyme makes use of RNA as a template to synthesise DNA?
(A) Reverse trancriptase
(B) DNA dependant RNA polymerase
(C) DNA polymerase
(D) RNA polymerase

Q.94 If the coding strand have the sequences 5 '-AGGCCT -3' then find out the sequence in the strand of mRNA transcribed.
(A) 5'-AGGCCU -3' (B) 3'-AGGCCU -5'
(C) 3'-UCCGGA-5' (D) 5'-ACCGGU -3'

Q.95 Why both the strands of DNA are not copied during transcription?
(A) Because RNA molecule with different sequences will be formed.
(B) Because RNA molecule with same sequences will be formed.
(C) Because RNA molecule with identical sequences will be formed.
(D) Because DNA molecule with different sequences will be formed.

PART - 6 : GENETIC CODE

Q.96 Credit of disclosing genetic code goes to
(A) Nirenberg (B) Matthaei
(C) Both (A) and (B) (D) Khorana

Q.97 The nucleotide sequence of an anticodon is complementary to nucleotide sequence of–
(A) tRNA (B) mRNA
(C) rRNA (D) DNA

Q.98 Which mutation of the genetic bases gives the proof that codon is triplet and reads in a contagious manner?
(A) frameshift mutation (B) point mutation
(C) Both (A) and (B) (D) inversion mutation

Q.99 Codons are degenerate, means some amino acid are coded by –
(A) more than the codons
(B) only one codon
(C) two codons
(D) more than 8 codons

Q.100 Stop or non-sense codons are
(A) two in number (B) three in number
(C) four in number (D) one in number

Q.101 In the protein synthesis, tRNA carrying the amino acid enters from which site of the ribosome?
(A) A-site (B) P-site
(C) anticodon site (D) R-site

Q.102 Before the genetic code was postulated, the tRNA was called –
(A) rRNA(ribosomal RNA)
(B) mRNA (messenger RNA)
(C) sRNA(soluble RNA)
(D) sRNA (sedimentary RNA)

Q.103 How many codons codes for amino acid?
(A) 25 (B) 50
(C) 61 (D) 60

Q.104 The four nitrogenous base sequences, which forms the code words for DNA language are
(A) UTAC (B) ACTU
(C) AGCU (D) ATCG

Q.105 Starting codon for all eukaryotes is
(A) GUA (B) GAU
(C) AUG (D) AGU

PART - 7 : TRANSLATION

Q.106 Translation refers to the –
(A) formation of amino acid from RNA
(B) formation of RNA from DNA
(C) formation of DNA from DNA
(D) polymerisation of amino acid

Q.107 What is the purpose of untranslated regions present on mRNA?
(A) To stop the process of translation.
(B) To start the process of translation.
(C) For efficient translation
(D) For DNA recognition

Q.108 Which of the following process is associated with the synthesis of enzymes and proteins?
(A) Translation (B) Replication
(C) Transduction (D) Transcription

Q.109 Anticodon is a base triplet on –
(A) mRNA complementary to base sequence on rRNA.
(B) mRNA complementary to base sequence on tRNA.
(C) tRNA complementary to base sequence on rRNA.
(D) tRNA complementary to base sequence on mRNA.

Q.110 Where does the peptide synthesis takes place?
(A) Chloroplast (B) Leucoplast
(C) Golgi body (D) Ribosome

Q.111 A particular ____ that carries the information for making a particular polypeptide out of ____ can be used to make any polypeptide.
(A) gene and mRNA; a ribosome and tRNA
(B) gene and ribosome; a tRNA & mRNA
(C) ribosome and mRNA; a gene and tRNA
(D) gene and t RNA; a ribosome and mRNA

Q.112 Amino acids are activated by
(A) ADP (B) AMP
(C) ATP (D) Special proteins

Q.113 In 125 amino acid sequence, if 25 amino acids are mutated to UAA, then –
(A) a polypeptide of 124 amino acid will be formed.
(B) a polypeptide of 25 amino acid will be formed.
(C) a polypeptide of 24 amino acid will be formed.
(D) any of the above is possible.

Q.114 Ribosome that acts as a catalyst or ribozyme is
(A) 40S rRNA (B) 50S rRNA
(C) 70S rRNA (D) 23S rRNA

PART - 8 : REGULATION OF GENE EXPRESSION

Q.115 In *E.coli*, hydrolysis of disaccharide, lactose into galactose and glucose is performed by
(A) permease (B) catalase
(C) β-galactosidase (D) transacylase

Q.116 Who gave the 1st operon system?
(A) Francois Jacob (B) Jacob and Monod
(C) Bateson (D) Both (A) and (B)

Q.117 How many structural genes are present in *lac-operon* of *E. coli?*
(A) 4 (B) 3
(C) 2 (D) 1

Q.118 Positively regulatory proteins are called
(A) activator (B) repressors
(C) necessary proteins (D) accessory proteins

Q.119 In *lac* operon model, lactose acts as –
(A) repressor (B) terminator
(C) Inducer (D) None of these

Q.120 Which type of regulation takes place in *lac* operon?
(A) Positive regulation (B) Neutral regulation
(C) Negative regulation (D) Both (A) and (C)

Q.121 Inducer molecule in *lac*-operon of *E coli* is chemically a/an
(A) Disaccharide (B) Amino acid
(C) Protein (D) RNA

Q.122 Regulatory gene are also called
(A) i-gene (B) r-gene
(C) s-gene (D) o-gene

Q.123 Lactose is transported into cells through
(A) β-galactosidase (B) permease
(C) transacetylase (D) transferase

Q.124 Operon is –
(A) a set of closely linked genes, regulating a metabolic pathway in prokaryotes.
(B) the sequence of three nitrogen bases determining a single amino acid.
(C) the sequence of nitrogen bases in mRNA, which codes for a single amino acid.
(D) a gene responsible for switching on or off other genes.

Q.125 Choose the correct option w.r.t. the chemical nature of apo-repressor and co-repressor respectively in *trp*-operon?
(A) Protein, Amino acid (B) Amino acid, Protein
(C) Lipoidal, Sugary (D) Sugary, Lipoida

Q.126 In a *lac* operon model, operator region is present
(A) adjacent to regulatory genes
(B) adjacent to promoter genes
(C) adjacent to structural genes
(D) adjacent to introns

Q.127 Function of operator is to bind with
(A) repressor (B) RNA polymerase
(C) DNA polymerase (D) inducer

Q.128 Tryptophan operon is
(A) Catabolicsystem (B) Repressible system
(C) Inducible system (D) 3 structural genes

Q.129 Lactose is a substrate for
(A) galactosidase (B) α-galactosidase
(C) β-galactosidase (D) γ-galactosidase

PART - 9 : HUMAN GENOME PROJECT

Q.130 Commonly used host for cloning in human genome project were.
I. YAC (Yeast Artificial Chromosome)
II. BAC (Bacterial Artificial Chromosome)
III. PAC (Plasmic Artificial Chromosome)
IV. GMO (Genetically Modified Organism)
Choose the correct combination of given options.
(A) I and II (B) II and III
(C) III and IV (D) IV and I

Q.131 ELSI stands for (in reference to HGP)
(A) Ethical Legal and Social Issue
(B) Embedded Low Software Index
(C) Endonuclease Ligase Surface Immunity
(D) Ear Lung Spleen Immunity

Q.132 Total % of genes, which codes for proteins is –
(A) 2% (B) 3%
(C) 4% (D) 5%

Q.133 How genetic and physical maps were generated in HGP?
(A) By using DNase
(B) By using RNase
(C) By using restriction endonuclease
(D) By using automated DNA sequences

Q.134 SNPs can be used for –
(A) finding chromosome locations for disease associated sequences.
(B) tracing human history
(C) evolution
(D) All of the above

PART - 10 : DNA FINGERPRINTING

Q.135 DNA fingerprinting involves identifying the differences in some specific regions in DNA sequence called
(A) non- repetitive DNA (B) coding DNA
(C) non-codinq DNA (D) repetitive DNA

Q.136 The sensitivity of DNA fingerprinting can be increased by –
(A) using intron sequences.
(B) using exon sequences.
(C) using polymerase chain reactions.
(D) All of the above

Q.137 Polymorphism occurs at
(A) genetic level (B) individual level
(C) Both (A) and (B) (D) None of the above

Q.138 Satellite DNA or repetitive DNA
(A) do not code for any protein
(B) forms a large portion of human genome
(C) shows high degree of polymorphism
(D) All of the above

EXERCISE - 2 (LEVEL-2)

Choose one correct response for each question.

Q.1 DNA Replication occurs at –
(A) G_0 & G_{-1} (B) G_2 - stage
(C) S - Stage (D) Mitotic phase

Q.2 RNA synthesis is controlled by –
(A) Rho- factor (B) Sigma factor
(C) Endo nuclease (D) RNA-polymerase

Q.3 Duplication of DNA is called –
(A) Replication (B) Transduction
(C) Transcription (D) Translation

Q.4 A DNA molecule in which both strands have radioactive thymidine is allowed to duplicate in an environment containing non- radioactive thymidine. What will be the exact number of DNA molecules that contains the radio active thymidine after 3 duplications
(A) One (B) Two
(C) Four (D) Eight

Q.5 A bacterium with completely radioactive DNA was allowed to replicate in a non- radioactive medium for two generation what % of the bacteria should contain radioactive DNA –
(A) 100% (B) 50%
(C) 25% (D) 12.5 %

Q.6 In the base sequence of one strand of DNA is GAT, TAG, CAT, GAC what shall be the sequence of its complementary strand –
(A) CAT, CTG, ATC, GTA
(B) GTA, ATC, CTG, GTA
(C) ATC, GTA, CTG, GTA
(D) CTA, ATC, GTA, CTG

Q.7 In Griffith experiment, what would be the effect of following conditions on mice?

Form of *Pneumococcus* Injected	**Effect on Mice**
I. Live rough non-capsulated	(a)
II. Live smooth capsulated	(b)
III. Heat-killed smooth	(c)
IV. Heat-killed smooth + live rough	(d)

Choose the correct option for effect on mice.
(A) a-Survived, b-Died, c-Died, d-Survived
(B) a-Survived, b-Died, c-Survived, d-Died
(C) a-Died, b-Survived, c-Survived, d-Died
(D) a-Died, b-Survived, c-Died, d-Died

Q.8 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) UCG - Start (B) UUU - Stop
(C) UGU - Leusine (D) UAC - Tyrosine

Q.9 During translation initiation in prokaryotes, a GTP molecule is needed in –
(A) Formation of formyl-met-tRNA.
(B) Binding of 30S subunit of ribosome with mRNA.
(C) Association of 30 S-mRNA with formyl-met tRNA.
(D) Association of 50 S subunit of ribosome with initiation complex.

Q.10 In recent years, DNA sequences (nucleotide sequence) of mt-DNA and Y chromosomes were considered for the study of human evolution, because –
(A) They are small, and therefore, easy to study.
(B) They are uniparental in origin and do not take part in recombination.
(C) Their structure is known in great detail.
(D) They can be studied from the samples of fossil remains.

Q.11 Degeneration of a genetic code is attributed to the –
(A) First member of a codon
(B) Second member of a codon
(C) Entire codon
(D) Third member of a codon

Q.12 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 24 amino acids will be formed.

(B) Two polypeptides of 24 and 25 amino adds will be formed.
(C) A polypeptide 6f 49 amino acids will be formed.
(D) A polypeptide of 25 amino acids will be formed.

Q.13 A completely radioactive double stranded DNA molecule undergoes two round of replication in a non radioactive medium. What will be the radioactive status of the four daughter molecules
(A) All four still contain radioactivity
(B) Radioactivity is lost from all four
(C) Out of four, three contain radioactivity
(D) Half of the number contain no radioactivity

Q.14 Consider the following sequence on m-RNA AUGGCAGUGCCA. Assuming that genetic code is overlap then how many number of codon may be present on this genetic code
(A) 9 (B) 10
(C) 8 (D) 11

Q.15 A normal DNA molecule is continuously replicate in N^{15} medium than what is the % of nonradioactive DNA in 4th generation.
(A) 12.5% (B) 25%
(C) 0% (D) 6.25%

Q.16 Which word would best describe the operon?
(A) respiration (B) transport
(C) regulation (D) nutrition

Q.17 Khorana synthesized two RNAs (a) with repeat sequence of AB and (b) with repeat sequence of ABC the polypeptides coded by (a) & (b) are respectively :
(A) Homopolypeptides in both (a) and (b).
(B) Heteropolypeptides in both.
(C) Homopolypeptide in (a) & peptide heteropoly in (b).
(D) Heteropolypeptide in (a) & peptide homopoly in (b).

Q.18 Which of the following m-RNA is translated completely :
(a) 5' AUG UGA UUA AAG AAA 3'
(b) 5' AUG AUA UUG CCC UGA 3'
(c) 5' AGU UCC AGA CUC UAA 3'
(d) 5' AUG UAC AGU AAC UAG 3'
(A) (a) and (b) (B) (b) and (d)
(C) (c) and (d) (D) (a) and (d)

Q.19 Identify the stop codons in given options.
(A) UAA, UAG, UGA
(B) UCA, UCC, UCA
(C) UGC, UCG, UCC
(D) UUU, UAT, UTA

Q.20 Given below is sequence of the processed mRNA ready for translation : 5'-AUG CUA UAC UAA CUG CCA UGC UAG-3'
How many amino acids will present in polypeptide chain corresponding to this mRNA
(A) 7 (B) 8
(C) 6 (D) 3

Q.21 Which one of the following makes use of RNA as a template to synthesize DNA -
(A) DNA dependant RNA polymerase
(B) DNA polymerase
(C) Reverse transcriptase
(D) RNA polymerase

Q.22 Protein synthesis in an animal cell occurs –
(A) On ribosomes present in cytoplasm as well as in mitochondria.
(B) On ribosomes present in the nucleolus as well as in cytoplasm.
(C) Only on ribosomes attached to the nuclear envelope and endoplasmic reticulum.
(D) Only on the ribosomes present in cytosol.

Q.23 Hershey and Chase used ^{35}S and ^{32}P to prove that DNA is the genetic material. Their experiments proved that DNA is genetic material because –
(A) progeny viruses retained ^{32}P but not ^{35}S.
(B) retention of ^{32}P in progeny viruses indicated that DNA was passed on.
(C) loss of ^{35}S in progeny viruses indicated that proteins were not passed on.
(D) All of the above

Q.24 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) CAAT box (B) GGIT box
(C) AAAT box (D) TATA box

Q.25 Triplet for inhibiting process of translation is –
(A) UAG (B) UAA
(C) UAC (D) UGG

Q.26 cDNA probes are copied from the messenger RNA molecules with the help of –
(A) Restriction enzymes
(B) Reverse transcriptase
(C) DNA polymerase
(D) Adenosine deaminase

Q.27 Which one of the following statement is true for protein synthesis (translation) –
(A) Amino acids are directly recognized by m-RNA.
(B) The third base of the codon is less specific.
(C) Only one codon codes for an amino acid.
(D) Every t-RNA molecule has more than one amino acid attachment site.

Q.28 E.coli cells with a mutated z gene of the lac operon cannot grow in medium containing only lactose as the source energy because –
(A) In the presence of glucose, E.coli cells do not utilize lactose.
(B) They cannot transport lactose from the medium into the cell.
(C) The lac operon is constitutively active in these cells.
(D) They cannot synthesize functional beta galactosidase.

Q.29 Amino acid sequence, in protein synthesis is decided by the sequence of –
(A) tRNA (B) mRNA
(C) cDNA (D) rRNA

Q.30 One gene one enzyme hypothesis was postulated by –
(A) R. Franklin (B) Hershey and Chase
(C) A.Garrod (D) Beadle and Tatum

Q.31 Which one of the following pair is correctly matched –

(A) Van Helmont	Discovered mutations
(B) Louis Pasteur	Wrote "The Origin of Species"
(C) T.H. Morgan	Studied sex-linked inheritance
(D) H. Khorana	Studied DNA replication

Q.32 During protein synthesis in an organism, at one point the process comes to a halt. Select the group of the three codons from the following from which anyone of the three could bring about this halt -
(A) UUU, UCC, UAU (B) UUC, IIA, UAC
(C) UAG, UGA, UAA (D) UUG, UCA, UCG

Q.33 Molecular basis of organ differentiation depends on the modulation in transcription by –
(A) RNA polymerase (B) Ribosome
(C) Transcription factor (D) Anticodon

Q.34 The Okazaki fragments in DNA chain growth –
(A) Result in transcription.
(B) Polymerize in lie 3'-to-5' direction and forms replication fork.
(C) Prove semi-conservative nature of DNA replication.
(D) Polymerize in the 5'-to-3' direction and explain 3'-to-5' DNA replication.

Q.35 Ligase helps in –
(A) Removal of few genes
(B) Translation
(C) Inserting few genes in DNA
(D) Bringing transversion in chromosomes

Q.36 Proved that DNA replicates by semiconservative replication
(A) Hershey and Chase (B) Watson and Crick
(C) Meselsohn and Stahl (D) Rosalind Franklin

Q.37 Proved that the nuclear material in a bacteriophage, not the protein coat, infects a bacterium
(A) Hershey and Chase (B) Watson and Crick
(C) Meselsohn and Stahl (D) Rosalind Franklin

Q.38 The first to analyze DNA by X-ray crystallography
(A) Hershey and Chase
(B) Watson and Crick
(C) Meselsohn and Stahl
(D) Rosalind Franklin

Q.39 A scientist used a template of polyuridylic acid chain for translation then he found that only one type of amino acid in whole polypeptide chain and also observed that no. of amino acid is one-third of total no. of N_2 bases in the polyuridylic acid chain, this prove.
(A) Genetic code consists of three N_2 base.
(B) Genetic code consists of three N_2 base and for a particular amino acid, required a special sequence of N_2 base.
(C) Genetic code is information of DNA transcription.
(D) Translation occur in cytoplasm.

Q.40 In one DNA molecule amount of adenine is 26 % then the cell will be –
(A) Prokaryotic (B) Eukaryotic
(C) Both (D) Data insufficient

Q.41 Segments of DNA Which are capable of moving in and out of a chromosome are termed as –
(A) Transposons (B) Recon
(C) Muton (D) Replicon

Q.42 In DNA when AGCT occurs, their association is per which of the following pair?
(A) AG-CT (B) AC-GT
(C) AT -GC (D) All of these

Q.43 In prokaryotes the genetic material is –
(A) Linear DNA without histones
(B) Linear DNA with histones
(C) Circular DNA without histones
(D) Circular DNA with histones

Q.44 Which of the following RNAs picks up specific amino acids from amino acid pool in the cytoplasm to ribosome during protein synthesis
(A) t-RNA (B) m-RNA
(C) r-RNA (D) s-RNA

Q.45 The maximum formation of m-RNA occurs in –
(A) Cytoplasm (B) Ribosome
(C) Nucleolus (D) Nucleoplasm

Q.46 Transcription begins when one of the following enzymes binds to promoter site –
(A) DNA polymerase (B) RNA polymerase
(C) Helicase (D) Gyrase

Q.47 Amino acyl synthase enzyme takes parts in :
(A) Attachment of m-RNA of 30s ribosome
(B) Transfer of activated amino acid to t-RNA
(C) Activation of amino-acid
(D) Hydrolysis of ATP to AMP

Q.48 These are 64 codon in genetic code dictionary because –
(A) There are 64 types of t-RNA, found in the cell.
(B) There are 44 meaningless and 20 codons for amino acid.
(C) There are 64 amino acids to be coded
(D) Genetic code is triplet.

Q.49 An unfertilized egg stores a lot of mRNA whose translation is blocked until after the sperm has fused with it. The proteins that block mRNA are called the _____ proteins.
(A) repressor (B) masking
(C) activator (D) enzyme

Q.50 DNA replication can best be described as –
(A) semiconservative (B) conservative
(C) degenerate (D) comparative

Q.51 Discovered transformation in bacteria
(A) Hershey and Chase (B) Watson and Crick
(C) Meselsohn and Stahl (D) Griffith

Q.52 How many nucleosomes are found in helical coil of 30 nm chromatin fibre –
(A) 10 (B) 12
(C) 6 (D) 9

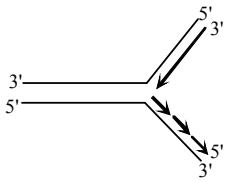
Q.53 Because most of the amino acid are represented by more than one codon, the genetic code is –
(A) Overlapping (B) Wobbling
(C) Degenerate (D) Generate

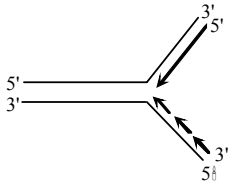
Q.54 Tryptophan (Trp) operon is –
(A) Inducible system
(B) Repressible system
(C) Controlled by regulator genes
(D) controlled by three structural genes.

Q.55 An amino acid binds to tRNA at the:
(A) 5' end (B) 3' end
(C) anticodon (D) any of these

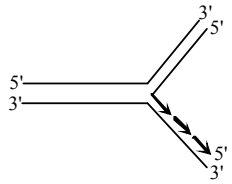
Q.56 In which of the following DNA not directly involved –
(A) Replication (B) Transcription
(C) Translation (D) Transformation

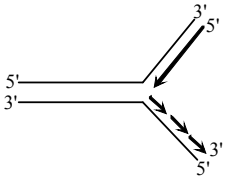
Q.57 Which one of the following correctly represents the manner of replication of DNA
(A) (B)





(C) (D)





Q.58 Polytene chromosomes in salivary glands of Drosophila are formed as a result of –
(A) Endoduplication
(B) Duplication without separation
(C) Replication of DNA without cell division
(D) All the above

Q.59 In 1980, F. Sanger was awarded Nobel prize second time to be shared by Gilbert and Maxum for their work on –
(A) Genetic mapping of chromosomes
(B) Determining amino acid sequence of insulin
(C) Determining base sequence of DNA of virus
(D) Determining the structure of DNA

Q.60 Bacteria were grown in a medium containing heavy isotope of nitrogen (N^{15}) for many generations and all their DNA contained many heavy nitrogen only. A bacterium of this type was transferred to normal medium and allowed to duplicate. After two divisions of heavy DNA is likely to be
(A) Only one daughter cell will have heavy DNA.
(B) Two daughter cells have normal DNA and other two have both normal and heavy DNA.
(C) All daughter cells have heavy DNA.
(D) Half daughter cells have heavy DNA and other half have normal DNA.

Q.61 In his experiments on the chemistry of DNA, Chargaff estimated the base composition of human sperms and found that Adenine constituted 31 % and Guanine 19%. The quantity of Cytosine in the DNA of human somatic cell is
(A) 31% (B) 19%
(C) 38% (D) 68%

Q.62 In DNA if 10% guanine is present, how much thymine is
(A) 10% (B) 40%
(C) 80% (D) 20%

Q.63 What function is performed by sigma factor and rho factor in the process of transcription
(A) Of initiation and termination
(B) Of initiation and elongation
(C) Of charging tRNA and elongation
(D) None of the above

Q.64 Gene regulation occurs at
I. translational level.
II. transcriptional level.
III. post transcriptional level.
IV. post translation level.
Choose the correct combination.
(A) I and II (B) III and IV
(C) I and IV (D) I, II, III and IV

Q.65 Consider the following
1. Structural gene 2. Messenger RNA
3. Ribosomes 4. Transcription
5. Translation
Which of the following is the correct sequence for protein synthesis
(A) 1, 4, 3, 2, 5 (B) 1, 4, 5, 2, 3
(C) 1, 4, 2, 3, 5 (D) 3, 5, 4, 2, 1

Q.66 RNA polymerase is involved in –
(A) Translation (B) Transcription
(C) Translocation (D) Replication

Q.67 Experiments of DNA replication identified that the daughter DNA consisted of one strand of parent DNA and one strand of new DNA. This type of replication is –
(A) semiconservative (B) conservative
(C) dispersive (D) semidisruptive

Q.68 When DNA is replicating, a nucleotide can only be added to the end of an existing nucleotide chain.
(A) 3' (B) 5'
(C) either 3' or 5' (D) phosphodiester end

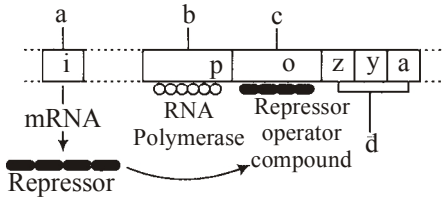
Q.69 The method developed by Matthew Meselson and Franklin Stahl to separate heavy DNA with ^{15}N from DNA with ^{14}N, for providing evidence for semi-conservative replication of DNA is
(A) ion exchange chromatography
(B) density gradient centrifugation
(C) isopycnic centrifugation
(D) gel filtration.

Q.70 Activity in which enzyme would indicate that DNA was about to replicate?
(A) topoisomerase (B) DNA polymerase
(C) primase (D) DNA helicase

Q.71 Find out the number of base pairs in in *E.coli* DNA if its DNA is 1.36 mm long
(A) 4×10^6 bp (B) 3×10^6 bp
(C) 2×10^6 bp (D) 7×10^6 bp

Q.72 Consider the following statements.
I. rRNA provides the template for synthesis of proteins.
II. tRNA brings amino acids and reads the genetic code.
III. RNA polymerase binds to promoter and initiates transcription.
IV. A segment of DNA coding for polypeptide is called intron.
Which of the statements given above are correct?
(A) I and III (B) I and II
(C) I, II and III (D) II and III

Q.73 Identify a, b, c and d.



(A) a-Regulatory gene, b-Promoter, c-Operator, d-Structural gene
(B) a-Regulatory gene, b-Promoter, c-Structural gene, d-Operator
(C) a-Regulatory gene, b-Structural gene, c-Promoter, d-Operator
(D) a-Regulatory gene, b-Structural gene, c-Operator gene, d-Promoter gene

Q.74 Which of the following statements about Hershey and Chase experiment are correct?
I. Sulphur is present in proteins but not in DNA.
II. Phosphorus is present in DNA but not in protein.
III. ^{32}P will end up in the supernatant after centrifugation.
IV. Progeny generation of T_2-bacteriophage contain ^{32}P.
V. Progeny generation of T_2-bacteriophage contain ^{35}S.
(A) I and II (B) II and III
(C) IV and V (D) I, II and IV

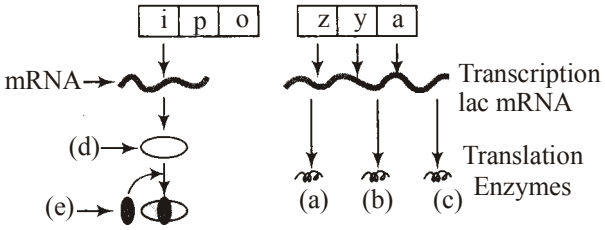
EXERCISE - 3 (LEVEL-3)

Choose one correct response for each question.

Q.1 If the replication fork were blocked, the activity of would be affected first.
(A) helicase (B) DNA polymerase
(C) primase (D) DNA ligase

Q.2 If DNA proofreading fails, ____ may occur
(A) transformations (B) mutations
(C) telomerization (D) mismatch base pairing

Q.3 Given is the diagram of the lac operon showing an operon of inducible enzymes. Identify components and enzymes (a, b, c, d and e).



(A) a-Galactosidase, b-Permease, c-Transacetylase, d-Repressor protein, e-Inducer (lactose)
(B) a-Galactosidase, b-Permease, c-Transacetylase, d-Inducer (lactose), e-Repressor protein
(C) a-Galactosidase, b-Transacetylase, c-Permease, d-Repressor protein, e-Inducer (lactose)
(D) a-Permease, b-Transacetylase, c-Galactosidase, d-Repressor protein, e-Inducer (lactose)

Q.4 If you wanted to study DNA replication in a eukaryote, the most likely portion of the chromosome to look for changes in activity would be the –
(A) heterochromatin (B) nucleoid
(C) nucleosome (D) euchromatin

Q.5 Arrange the steps of transcription :
a. The new mRNA temporarily binds to DNA template.
b. RNA polymerase binds to the promoter region.
c. The enzyme reaches the end of the transcription unit.
d. The enzyme moves along transcription unit.
e. The enzyme unwinds the two strands of DNA.
f. mRNA and the enzyme are released from DNA.
g. Corresponding nucleotides are added.
(A) bdegacf (B) bfegcad
(C) dbegafc (D) bdgeafc

Q.6 In eukaryotic transcript, all of the following are present except –
(A) introns and exons. (B) 5' GTP cap.
(C) methionine. (D) 3' poly A tail.

Q.7 Which of the following helps in splicing pre-mRNA in eukaryotic cells?
(A) snRNP (B) ribosome
(C) RNA polymerase (D) tRNA

Q.8 Arrange the various steps of DNA fingerprinting technique in the correct order.
(i) Separation of DNA fragments by electrophoresis.
(ii) Digestion of DNA by restriction endonucleases.
(iii) Hybridization using labelled VNTR probe.
(iv) Isolation of DNA.
(v) Detection of hybridized DNA fragments by auto radiography.
(vi) Transferring the separated DNA fragments to nitrocellulose membrane.
(A) (iv) → (ii) → (i) → (vi) → (iii) → (v)
(B) (iv) → (i) → (ii) → (iii) → (vi) → (v)
(C) (ii) → (i) → (iv) → (vi) → (iii) → (v)
(D) (iii) → (v) → (iv) → (ii) → (i) → (vi)

Q.9 Which of the following has the anticodon?
(A) mRNA (B) DNA
(C) tRNA (D) rRNA

Q.10 In DNA replication, the role of DNA polymerase is to
(A) bring two separate strands back together after new ones are formed.

(B) join the RNA nudeotides together to make the primer
(C) build a new strand of DNA from 5' to 3'
(D) unwind the tightly wound helix

Q.11 Which is NOT used in the normal replication of DNA?
(A) RNA primer (B) ligase
(C) restriction enzymes (D) polymerase

Q.12 Which of the following site in the ribosome allows aminoacyl-tRNA to bind?
(A) A (B) P
(C) E (D) D

Q.13 At which site in ribosome does the polypeptide grow?
(A) A (B) P
(C) E (D) D

Q.14 In trp operon, tryptophan acts as a/an
(A) repressor (B) corepressor
(C) activator (D) inducer

Q.15 Which of the following are universally involved in packing DNA to form chromatin in eukaryotes?
(A) repressors (B) activators
(C) histones (D) inducers

Q.16 A repressible operon codes for the enzymes of the following pathway. Which component of the pathway is most likely to be the corepressor for that operon?

$$A \xrightarrow[\text{Enzyme 1}]{} B \xrightarrow[\text{Enzyme 2}]{} C \xrightarrow[\text{Enzyme 3}]{} D$$

(A) substance A (B) substance B or C
(C) substance D (D) enzyme 1

Q.17 An mRNA molecule transcribed from the lac operon contains nucleotide sequences complementary to
(A) structural genes coding for enzymes
(B) the operator region
(C) the promoter region
(D) the repressor gene

Q.18 Hormones are able to exert their affect on several genes due to the presence of the same ___ sequence before all those genes.
(A) regulatory (B) promoter
(C) operator (D) repressor

Q.19 Which refers to spreading of the cancer cells?
(A) dedifferentiation (B) benign
(C) metastasis (D) mutation

Q.20 Topoisomerases
(A) synthesize DNA
(B) synthesize RNA primers
(C) join Okazaki fragments
(D) break & rejoin DNA to resolve knots that have formed

Q.21 A phosphate in DNA
(A) hydrogen-bonds to a base
(B) covalently links to two bases
(C) covalently links to two deoxyriboses
(D) hydrogen-bonds to two additional phosphates

Q.22 Identify the correct match between the codons and coding functions.

	Column I	**Column II**
a.	AUG	1. Phenylalanine
b.	UAA	2. Methionine
c.	UUU	3. Tryptophan
d.	UGG	4. Termination

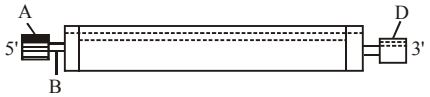
(A) a-1, b-4, c-2, d-3 (B) a-2, b-4, c-1, d-3
(C) a-4, b-3, c-2, d-1 (D) a-4, b-1, c-3, d-2

Q.23 Which of the following depicts the relative arrangement of the complementary strands of a DNA double helix?
(A) 5'–5' / 3'–3' (B) 3'–5' / 3'–5'
(C) 3'–3' / 3'–3' (D) 3'–5' / 5'–3'

Q.24 A lagging strand forms by –
(A) joining primers
(B) joining Okazaki fragments
(C) joining leading strands
(D) breaking up a leading strand

Q.25 The immediate source of energy for DNA replication is
(A) the hydrolysis of the nucleotides, with the release of two phosphates.
(B) the oxidation of NADPH
(C) the hydrolysis of ATP
(D) electron transport

Q.26 Identify a, b, c & d in the given diagram of mRNA.



(A) a-Methylated cap, b-Initiation codon, c-Termination codon, d-Poly A tail
(B) a-PolyA tail, b-Termination codon, c-Initiation codon, d-Methylated cap
(C) a-Methylated cap, b-Non-coding region, c-Coding region, d-Poly A tail
(D) a-Methylated cap, b-Coding region, c-Non-coding region, d-PolyA tail

Q.27 Which of the following statements about eukaryotic chromosomes is false?
(A) Eukaryotic chromosomes have free ends.
(B) Telomeres contain protein-coding genes.
(C) Telomerase lengthens telomeric DNA.
(D) Telomere shortening may contribute to cell aging.

Q.28 Which of the following is/are not found in a bacterial mRNA molecule?
(A) stop codon
(B) upstream leader sequences
(C) downstream trailing sequences
(D) promoter sequences

Q.29 Which of the following is/are typically removed from pre-mRNA during nuclear processing in eukaryotes?
(A) upstream leader sequences (B) poly-A tail
(C) introns (D) exons

Q.30 Which of the following is a spontaneous process, with no direct requirement for ATP or GTP?
(A) formation of a peptide bond.
(B) translocation of the ribosome.
(C) formation of aminoacyl tRNA
(D) A and B

Q.31 The role of tRNA is to transport –
(A) amino acids to the ribosome.
(B) amino acids to the nucleus.
(C) initiation factors to the ribosome.
(D) mRNA to the ribosome.

Note (Q.32-Q.Q.33) :
(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) Statement -1 is False, Statement -2 is False.

Q.32 **Statement 1 :** Regulator and operator genes are not associated with constitutive genes.
Statement 2 : Constitutive genes need not be repressed.

Q.33 **Statement 1 :** Genetic code is universal.
Statement 2: Genetic code is same for all organisms.

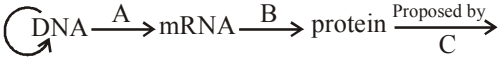
Q.34 DNA replication enzymes are given below.
Select their correct sequence in DNA replication.
I. Helicase II. SSB
III. Primase IV. DNA polymerase
V. DNA ligase
(A) I → V → IV → III → II
(B) I → II → III → V → IV
(C) V → IV → III → II → I
(D) I → II → III → IV → V

EXERCISE - 4 (PREVIOUS YEARS AIPMT/NEET EXAM QUESTIONS)

Choose one correct response for each question.

Q.1 Which enzyme will be produced in a cell in if there is a nonsense mutation in the lac Y gene ? **[NEET 2013]**
(A) Transacetylase
(B) Lactose permease and transacetylase
(C) β-galactosidase
(D) Lactose permease

Q.2 The diagram shows an important concept in the genetic implication of DNA. Fill in the blanks A to C **[NEET 2013]**



(A) A-Transcritpion, B-Translation, C-Francis Crick

(B) A-Translation, B-Extension, C-Rosalind Franklin
(C) A-Transcription, B-Replication, C-James Watson
(D) A-Translation, B-Transcription, C-Ervin Chargaff

Q.3 Which one of the following is wrongly matched?
(A) Transcription - Writing information from DNA to tRNA. **[AIPMT 2014]**
(B) Translation - Using information in m-RNA to make protein.
(C) Repressor protein - Binds to operator to stop enzyme synthesis.
(D) Operon - Structural genes, operator and promoter.

Q.4 Transformation was discovered by
(A) Meselson and Stahl **[AIPMT 2014]**
(B) Hershey and Chase
(C) Griffith
(D) Watson and Crick

Q.5 Select the correct option **[AIPMT 2014]**

	Direction of RNA synthesis	Direction of reading of the template DNA strand
(A)	5' – 3'	3' – 5'
(B)	3' – 5'	5' – 3'
(C)	5' – 3'	5' – 3'
(D)	3' – 5'	3' – 5'

Q.6 Gene regulation governing lactose operon of E.coli that involves the lac I gene product is **[AIPMT 2015]**
(A) Negative and repressible because repressor protein prevents transcription
(B) Feedback inhibition because excess of β-galactosidase can switch off transcription
(C) Positive and inducible because it can be induced by lactose
(D) Negative and inducible because repressor protein prevents transcription.

Q.7 The movement of a gene from one linkage group to another is called – **[AIPMT 2015]**
(A) Translocation (B) Crossing over
(C) Inversion (D) Duplication

Q.8 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
(A) G 17%, A 33%, T 33% **[AIPMT 2015]**
(B) G 8.5%, A 50%, T 24.5%
(C) G 34%, A 24.5%, T 24.5%
(D) G 17%, A 16.5%, T 32.5%

Q.9 Which is not applicable to RNA ?
(A) Heterocyclic nitrogenous bases
(B) Chargaff's rule **[RE-AIPMT 2015]**
(C) Complementary base pairing
(D) 5'phosphoryl and 3'hydroxyl ends

Q.10 Balbiani rings are sites of – **[RE-AIPMT 2015]**
(A) Polysaccharide synthesis
(B) RNA and protein synthesis
(C) Lipid synthesis
(D) Nucleotide synthesis

Q.11 Identify the correct order of organisation of genetic material from largest to smallest **[RE-AIPMT 2015]**
(A) Genome, chromosome, gene, nucleotide
(B) Chromosome, genome, nucleotide, gene
(C) Chromosome, gene, genome, nucleotide
(D) Genome, chromosome, nucleotide, gene

Q.12 Satellite DNA is important because it **[RE-AIPMT 2015]**
(A) Does not code for proteins and is same in all members of the population
(B) Codes for enzymes needed for DNA replication
(C) Codes for proteins needed in cell cycle
(D) Shows high degree of polymorphism in population and also the same degree of polymorphism in an individual, which is heritable from parents to children.

Q.13 Which of the following is required as inducer(s) for the expression of Lac operon? **[NEET 2016 PHASE 1]**
(A) Glucose (B) Galactose
(C) Lactose (D) Lactose & Galactose

Q.14 A complex of ribosomes attached to a single strand of RNA is known **[NEET 2016 PHASE 1]**
(A) Polysome (B) Polymer
(C) Polypeptide (D) Okazaki fragment

Q.15 Which of the following is not required for any of the techniques of DNA fingerprinting available at present? **[NEET 2016 PHASE 1]**
(A) Polymerase chain reaction
(B) Zinc finger analysis
(C) Restriction enzymes
(D) DNA-DNA hybridization

Q.16 Which one of the following is the starter codon? **[NEET 2016 PHASE 1]**
(A) AUG (B) UGA
(C) UAA (D) UAG

Q.17 Taylor conducted the experiments to prove semiconservative mode of chromosome replication on – **[NEET 2016 PHASE 2]**
(A) *Vinca rosea* (B) *Vicia faba*
(C) *Drosophila melanogaster* (D) *E. coli*

Q.18 The equivalent of a structural gene is **[NEET 2016 PHASE 2]**
(A) Muton (B) Cistron
(C) Operon (D) Recon

Q.19 Which of the following rRNAs acts as structural RNA as well as ribozyme in bacteria? **[NEET 2016 PHASE 2]**
(A) 5 S rRNA (B) 18 S rRNA
(C) 23 S rRNA (D) 5.8 S rRNA

Q.20 A molecule that can act as a genetic material must fulfill the traits given below, except **[NEET 2016 PHASE 2]**
(A) It should be able to express itself in the form of 'Mendelian characters'.
(B) It should be able to generate its replica.
(C) It should be unstable structurally and chemically.
(D) It should provide the scope for slow changes that are required for evolution.

Q.21 DNA-dependent RNA polymerase catalyzes transcription on one strand of the DNA which is called the – **[NEET 2016 PHASE 2]**
(A) Template strand (B) Coding strand
(C) Alpha strand (D) Antistrand

Q.22 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? **[NEET 2017]**
(A) 1 (B) 11
(C) 33 (D) 333

Q.23 The final proof for DNA as the genetic material came from the experiments of **[NEET 2017]**
(A) Griffith
(B) Hershey and Chase
(C) Avery, Mcleod and McCarty
(D) Hargobind Khorana

Q.24 The association of histone H1 with a nucleosome indicates: **[NEET 2017]**
(A) Transcription is occurring
(B) DNA replication is occurring
(C) The DNA is condensed into a Chromatin Fibre
(D) The DNA double helix is exposed

Q.25 Which of the following RNAs should be most adundant in animal cell? **[NEET 2017]**
(A) r-RNA (B) t-RNA
(C) m-RNA (D) mi-RNA

Q.26 During DNA replication, Okazaki fragments are used to enlongate **[NEET 2017]**
(A) The leading strand towards replication fork.
(B) The lagging strand towards replication fork.
(C) The leading strand away from replication fork.
(D) The lagging strand away from the replication fork.

Q.27 The experimental proof for semiconservative replication of DNA was first shown in a **[NEET 2018]**

(A) Plant (B) Bacterium
(C) Fungus (D) Virus

Q.28 Select the correct match **[NEET 2018]**

(A) Matthew Meselson and F. Stahl - *Pisum sativum*
(B) Alfred Hershey and Martha Chase - TMV
(C) Alec Jeffreys - *Streptococcus pneumoniae*
(D) Francois Jacob and Jacques Monod - Lac operon

Q.29 All of the following are part of an operon except **[NEET 2018]**

(A) an enhancer (B) structural genes
(C) an operator (D) a promoter

Q.30 AGGTATCGCAT is a sequence from the coding strand of a gene. What will be the corresponding sequence of the transcribed mRNA? **[NEET 2018]**

(A) ACCUAUGCGAU
(B) UGGTUTCGCAT
(C) AGGUAUCGCAU
(D) UCCAUAGCGUA

Q.31 Expressed Sequence Tags (ESTs) refers to : **[NEET 2019]**

(A) Genes expressed as RNA.
(B) Polypeptide expression.
(C) DNA polymorphism
(D) Novel DNA sequences

Q.32 Match the following genes of the Lac operon with their respective products : **[NEET 2019]**

(a) i gene	(i) β-galactosidase
(b) z gene	(ii) Permease
(c) a gene	(iii) Repressor
(d) y gene	(iv) Transacetylase

Select the correct option.

(A) a-(i), b-(iii), c-(ii), d-(iv)
(B) a-(iii), b-(i), c-(ii), d-(iv)
(C) a-(iii), b-(i), c-(iv), d-(ii)
(D) a-(iii), b-(iv), c-(i), d-(ii)

Q.33 Under which of the following conditions will there be no change in the reading frame of following mRNA? 5'AACAGCGGUGCUAUU3' **[NEET 2019]**

(A) Insertion of G at 5^{th} position
(B) Deletion of G from 5^{th} position
(C) Insertion of A and G at 4^{th} and 5^{th} positions respectively.
(D) Deletion of GGU from 7^{th}, 8^{th} and 9^{th} positions

ANSWER KEY

EXERCISE-1 (SECTION-1&2)

(1) (C) **(2)** (C) **(3)** (A) **(4)** (A)
(5) DNA helicase
(6) primase
(7) DNA ligase
(8) telomerase
(9) telomerase
(10) DNA polymerase
(11) 2.2 metres
(12) Sugar-phosphate
(13) Primase
(14) Sigma
(15) Chargaff's rule
(16) mRNA
(17) Heterochromatin
(18) DNA polymerase
(19) Operator
(20) Regulator
(21) 3
(22) Exons
(23) False
(24) False
(25) True
(26) False
(27) False
(28) False
(29) False
(30) True
(31) False

EXERCISE - 1 [SECTION-3]

Q	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51
A	D	C	C	A	C	B	A	D	A	B	D	A	C	B	C	B	A	C	C	A
Q	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71
A	B	A	C	B	D	B	A	C	C	B	C	A	C	C	A	A	A	B	B	A
Q	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91
A	A	B	D	A	C	B	D	D	D	A	D	A	B	B	C	B	A	A	B	A
Q	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111
A	C	D	C	A	C	A	A	C	D	C	D	B	A	C	D	A	A	B	A	A
Q	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131
A	B	C	A	A	C	D	D	C	D	A	A	B	A	A	B	A	B	C	A	A
Q	132	133	134	135	136	137	138													
A	A	C	D	D	C	C	D													

EXERCISE - 2

Q	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
A	C	D	A	B	B	D	B	D	C	B	D	A	D	B	C	C	D	B	A	D
Q	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
A	C	A	D	D	B	B	B	D	B	D	C	C	C	D	C	C	A	D	B	B
Q	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
A	A	C	C	A	D	B	C	D	B	A	D	C	C	B	B	C	D	D	C	B
Q	61	62	63	64	65	66	67	68	69	70	71	72	73	74						
A	B	B	A	D	C	B	A	A	B	D	A	D	A	D						

EXERCISE - 3

Q	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
A	C	B	A	D	A	C	A	A	C	C	C	A	B	B	C	C	A	A	C	D
Q	21	22	23	24	25	26	27	28	29	30	31	32	33	34						
A	C	B	D	B	A	C	B	D	C	A	A	A	A	B						

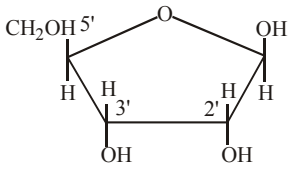
EXERCISE - 4

Q	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
A	C	A	A	C	A	D	A	A	B	B	A	D	C	A	B	A	B	B	C	C
Q	21	22	23	24	25	26	27	28	29	30	31	32	33							
A	A	C	B	C	A	D	B	D	A	C	A	C	D							

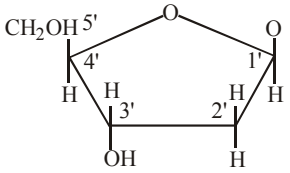
SOLUTIONS

EXERCISE-1

(1) (C) **(2)** (C) **(3)** (A) **(4)** (A)
(5) DNA helicase **(6)** primase
(7) DNA ligase **(8)** telomerase
(9) telomerase **(10)** DNA polymerase
(11) 2.2 metres
(12) Sugar-phosphate **(13)** Primase
(14) Sigma **(15)** Chargaff's rule
(16) **mRNA.** hn (histonuclear) RNA is the raw form of mRNA after splicing and post transcriptional modification of hnRNA, mRNA is formed.
(17) Heterochromatin **(18)** DNA polymerase
(19) Operator **(20)** Regulator
(21) **3.** Number of nitrogenous base in a codon is three.
(22) Exons
(23) **False.** In DNA, A pairs with T and G pairs with C, whereas RNA polymerase places U against A.
(24) **False**. Prokaryotic cells have only one type of RNA polymerase that transcribes protein-coding and non-protein-coding genes, whereas in eukaryotic cells, RNA polymerase II transcribes protein coding genes, and RNA polymerase I and III transcribes non-protein-coding genes.
(25) **True.** Prokaryotic cells do not have compartments or organelles and therefore all process take place in the cytoplasm, whereas in eukaryotic cells, most of the DNA is located in the nucleus and therefore transcription takes place in the nucleus.
(26) **False.** An mRNA can be read by several ribosomes at the same time.
(27) **False.** In eukaryotes, RNA polymerase binds only after the transcription factors have attached to the promoter sequence.
(28) **False.** In prokaryotes, most of the regulation of gene expression takes place at the transcription level, whereas in eukaryotes, control can be at transcription, posttranscription, translation, or posttranslation level.
(29) False **(30)** True **(31)** False
(32) **(D).** Uracil is present in RNA in place of thymine.
(33) **(C).** RNA has ribose sugar.



DNA has deoxyribose sugar.



(34) **(C).**
(35) **(A).** Nitrogenous bases attached to pentose sugar by N-glycoside bond. If the sugar is ribose then it is called nucleoside and when the sugar is deoxyribose then it is called deoxynucleoside. i.e., adenoside (sugar is ribose), deoxyadenosine (sugar is deoxyribose), cytidine, deoxycytidine, uridine or deoxythymine.
(36) (C) **(37)** (B)
(38) **(A).** Histone are the basic proteins. Together with DNA they compact the size of DNA and gives the nucleosomal model of DNA. They are of two kinds
(i) linker histone – H_1
(ii) non-linker histone – H_2A and H_2B
core histones – H_3 and H_4
(39) **(D).** Thymine and uracil, both have similar structures (pyrimidine). Thymine ring has one additional methyl group at 5' position in its pyrimidine ring.
(40) (A)
(41) **(B).** H_1 histone is called the linker histone protein. It connects the two nucleosome octamers.
(42) (D)
(43) **(A).** The process of reverse, transcription was discovered by Temin and Baltimore. The process of reverse transcription is also called Teminism.
(44) **(C).** A typical nucleosome contains 140-200 base pair of DNA helix.
(45) **(B).** Genetic information flows from
DNA $\rightarrow$ RNA $\rightarrow$ Protein

(46) (C) **(47)** (B) **(48)** (A) **(49)** (A)
(50) (A) **(51)** (C) **(52)** (C) **(53)** (C)
(54) (A) **(55)** (B) **(56)** (A) **(57)** (B)
(58) (C) **(59)** (B) **(60)** (D) **(61)** (B)

(62) **(A).** RNAworking as enzymes are called ribozymes.In splicing (removal of introns), RNAwork as ribozyme. Ribozymes also works in protein synthesis (23S RNA).

(63) (C) **(64)** (C)

(65) **(B).** Telomerase is the special enzyme found in eukaryotes. During the replication telomerase maintains the terminal part of the chromosomes. **(66)** (C)

(67) **(A).** On 5'-3' polarity strand, the replication is continuous.

(68) (C) **(69)** (C)

(70) **(A).** ^{15}N is not radioactive isotope. It is a heavy isotope of ^{14}H and can be separated from ^{14}N by density gradient centrifugation.

(71) **(A).** An Hershey and Chase radioactive ^{32}P was used to culture bacteriophage which resulted in radioactive viruses. Hershey and Chase used virus, which infected bacteria called bacteriophage. The bacteriophage attaches to the bacteria and its genetic material enters into the bacterial cell.

(72) (D)

(73) **(A).** Whole of DNA do not open in one stretch due to very high energy requirement. The point of separation proceeds slowly towards both the directions. In each direction, it gives the appearance of Y-shaped structure called replication fork. **(74)** (C)

(75) **(B).** Formation of DNA from RNA is called reverse transcription.

(76) **(B).** The process of copying genetic information from one strand of the DNA to RNA is called transcription.
The principle of complementarity governs the process of transcription, except the adenosine forms base pair with uracil instead of thymine.

(77) **(A).** Genetic RNA refers to the RNA, which is used as genetic material. There are certain viruses like HIV (retrovirus), in which DNA is formed from RNA.

(78) (A)

(79) **(B).** When it codes for many peptide.

(80) (D)

(81) **(A).** RNA polymerase II transcribes hnRNA (mRNA).

(82) **(C).** Regulatory sequences are the part of transcriptional unit, which regulate the transcription. Regulatory sequences are also present at the replication and translational level. Their positions are not fixed. They may be present at the upstream or downstream.

(83) **(B).** Structural genes are the functional part of transcriptional unit. Rest of the part like promoter or terminator are the regulatory part of transcriptional unit.

(84) **(D).** Non coding strand, minus (–) strand, templete strand, antisense strand all these. These are the synonyms used for 3'–5' strand. Coding strand, non-templete strand, sense strand, positive (+) strand, all there are the synonyms used for 5'–3' strand.

(85) (D)

(86) **(D).** The regulatory genes are located at the starting point of the transcriptional unit (5' end). They are called promoters. They lie in front of structural genes.

(87) (A)

(88) **(D).** There are atleast three types of RNAs in eukaryotes

Name of RNA	**Functions**
RNA polymerase I	Making of rRNA (28S,18S, 5.8S RNA)
RNA polymerase II	hnRNA (mRNA)
RNA polymerase III	5-S rRNA and tRNA, SnRNAs

(89) (D)

(90) **(A).** **Monocistron :** When transcription unit codes only for single polypeptide. It is mostly found in eukaryotes.
Polycistron : When transcriptional unit codes for many polypeptide. It is mostly found in prokaryotes.
Exon : The gene or transcriptional unit split into coding part called exon and non-coding part called intron. Introns are the intervening sequences, which don't appear in mature or processed RNA.

(91) **(B).** Splicing takes place in eukaryotes because introne are found only in case of eukaryotes. Before processing, exons needs to be removed out. This process is called splicing,

(92) **(B).**

(93) **(A).** Reverse transcriptase or RNA dependant DNA polymerase uses RNA as a templete to synthesise DNA.

(94) **(C).**

(95) **(A).** The strands in the DNA are complementary to each other, not identical. If the two RNAs are formed from both strands then RNAs with different sequences would be formed.

(96) **(C).** Nirenberg and Mathaei (1961) argued that the single code (one amino acid specified by one nitrogenous base) can specify only 4 acids, a double-code only for 16 (4^2). While triplet code can specify up to 64 amino acid (4^3). As there are no amino acids in a triplet code, there nitrogen bases for one amino acid can be operative.

(97) **(B).** Nucleotide sequence of anticodon on tRNA is complementary to the mRNA sequence.

(98) **(A).** Frame shift mutation (deletion or addition) gives the genetic bases of proof that codon is triplet and reads in contagious manner. Deletion or addition of base pair disturb the reading frame of DNA or mRNA.

(99) **(A).** One amino acid codes by more than one codon called degenerated code. Only methionine and tryptophan are coded by only one codon. Rest of amino acids codes for more than one codons.

(100) **(B).** Stop codons are three in number.

(101) **(A).** In the protein synthesis, tRNA carrying the amino acids enters to the A-site of the ribosome. Peptide bonds that are formed between the amino acids are present on P and A-site.

(102) **(C).** tRNA was known before the genetic code was postulated later on tRNA was then called sRNA (soluble RNA). Its role as an adaptor molecule was reported later.

(103) **(C).** There are 64 codon. 61 codon codes for amino acid and some non-sense codons also exists. Non-sense codon are used to stop translation. They are also called stop codon.

(104) **(D).** ATCG (adenine, thymine, cytosine and guanine).

(105) **(C).** AUG is the starting codon for both eukaryotes and prokaryotes.

(106) **(A).** Translation refers to the polymerisation of amino acids to form a polypeptide.

(107) (C) **(108)** (A) **(109)** (D)

(110) **(A).** Chloroplast as it is highly enzymatic body just like mitochondria.

(111) **(A).**

(112 **(C).** Amino acids are activated by ATP.

(113) **(C).** **Non-sense mutation :** This mutation changes the codon to stop codon, which prematurely ends translation when mRNA transcript is being read by the ribosomes.

(114) **(D).** The 23S rRNA is 2904 base pair long and it is a component of bacterial ribosome. Ribosomal peptidyl transferase activity resides in 23S rRNA for peptide bond formation between two amino acid during translation. Some naturally occurring ribozymes include (i) Peptidy transferase 23S RNA (ii) RNase (iii) Group I and group II introns.

(115) **(C).** $\text{Lactose} \xrightarrow{\beta\text{-galactosidase}} \text{Galactose} + \text{Glucose}$

(116) (D) **(117)** (B)

(118) **(A).** The operon is regulated in both negative and positive way.

Negative Control : The product of the regulatory genes shuts off the expression of genes under its control.

Positive Control : The product of the regulatory genes activates the expression of genes under its control.

(119) **(C).** **Inducer:** It is a chemical (substrate, hormone or some other metabolite) which, after coming in contact with the repressor, changes the latter into non-DNA binding state so as to free the operator gene. The inducer for *lac* operon of *Escherichia coli* is lactose (actually allolactose or metabolite or lactose).

(120) **(D).** Regulation of *lac* operon by the repressor is referred to as negative regulation. *Lac* operon is under the control of positive regulation as well, by CAP (Catabolic Activator Protein). It exerts a positive control in lac operon because in its absence, RNA polymerase is unable to recognise the promoter gene and switch off the *lac* operon.

(121) (A) **(122)** (A) **(123)** (B)

(124) **(A).** Operon is a set of closely linked genes, regulating a metabolic pathway in prokaryotes. **(125)** (A)

(126) **(B).** Operator region/gene present beside the promoter region. It lies in between the operator and the structural genes.

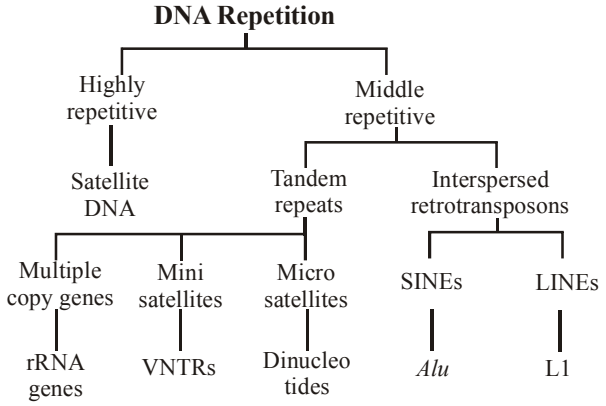
(127) **(A).** Repressor binds with the operator.

(128) (B) **(129)** (C)

(130) **(A).** BAC-Bacterial Artificial Chromosome.
YAC-Yeast Artificial Chromosome.
These two vectors are generally used in human genome project for cloning the large fragments of human DNA.

(131) (A) **(132)** (A) **(133)** (C) **(134)** (D)

(135) **(D).** Most of the human DNA is repetitive DNA there are several kinds of repetitive DNA. They may be classified on the basis of frequency of repetition.



(136) **(C).** PCR (Polymerase Chain Reaction). It is the technique in which the many copy of DNA can be produced in a short period of time. It increases the sensitivity of DNA fingerprinting.

(137) **(C).** Polymorphism as name indicates means multiple form. It is the sum of variation at the genetic level and individual level. These variations arises due to the mutation. DNA polymorphism is the basis of genetic mapping of human genome as well as DNA fingerprinting.

(138) **(D).** Satellite DNA or repetitive DNA do not, code for any protein. Repetitive DNA forms the major part of DNA.

EXERCISE-2

(1) **(C).** S-phase (synthesis phase) is the part of the cell cycle in which DNA is replicated, occurring between G1 phase and G2 phase.

(2) (D)

(3) **(A).** DNA replication is the process by which DNA makes a copy of itself during cell division.

(4) (B) **(5)** (B) **(6)** (D) **(7)** (B)

(8) (D) **(9)** (C) **(10)** (B)

(11) **(D).** Degeneracy of codons is the redundancy of the genetic code, exhibited as the multiplicity of three-codon combinations specifying an amino acid.

(12) (A) **(13)** (D) **(14)** (B) **(15)** (C)

(16) **(C).** The operon is the means by which prokaryotes regulate gene expression. An operon consists of a cluster of related genes and the DNA that controls them, such as, a promoter and operator.

(17) (D) **(18)** (B)

(19) **(A).** UAA, UAG, UGA are stop codon.

(20) (D) **(21)** (C)

(22) **(A).** The synthesis of proteins from RNA is known as translation. In eukaryotes, translation occurs in the cytoplasm, where the ribosomes are located. Ribosomes are made of a small and large subunit that surround the mRNA.

(23) **(D).**

(24) **(D).** A TATA box is a DNA sequence that indicates where a genetic sequence can be read and decoded. It is a type of promoter sequence, which specifies to other molecules where transcription begins. Transcription is a process that produces an RNA molecule from a DNA sequence.

(25) **(B).** UAA and UGA is termination codons. This is the final step during which the process of protein synthesis is stopped.

(26) (B) **(27)** (B)

(28) **(D).** The enzyme like lactase or β-galactosidase which is formed in response to the presence of its called inducible enzyme.

(29) (B) **(30)** (D)

(31) **(C).** The concept of sex-linked inheritance was introduced by Thomas H. Morgan in 1910, while working on Drosophila melanogaster.

(32) (C)

(33) **(C).** A transcription factor (sometimes called a sequence-specific DNA-binding factor) is a protein that binds to specific DNA sequences, thereby controlling the rate of transcription of genetic information from DNA to messenger RNA.

(34) **(D).** Okazaki fragments are short, newly synthesized DNA fragments that are formed on the lagging template strand during DNA replication. They are complementary to the lagging template strand, together forming short double-stranded DNA sections.

(35) **(C).** DNA ligase is a specific type of enzyme, a ligase, that facilitates the joining of DNA strands together by catalyzing the formation of a phosphodiester bond.

(36) **(C).** Semiconservative replication was hypothesized by Watson and Crick and confirmed experimentally by Meselsohn and Stahl.

(37) **(A).** Hershey & Chase carried our experiments where they tagged bacteriophages with ^{32}P and ^{35}S. They proved that the DNA from the viral (phage) nucleus, not ptotein from the viral coat, was infecting bacteria and producing thousands of progeny.

(38) **(D).** Rosalind Franklin, while working in the lab of Maurice Wilkins, carried out the X-ray crystallography analysis of DNA that showed DNA to be a helix.

(39) (B) **(40)** (B) **(41)** (A) **(42)** (C)

(43) **(C).** Most prokaryotes carry a small amount of genetic material in the form of a single molecule, or chromosome, of circular DNA. The DNA in prokaryotes is contained in a central area of the cell called the nucleoid, which is not surrounded by a nuclear membrane.

(44) (A) **(45)** (D)

(46) **(B).** RNA polymerase is an enzyme that is responsible for making RNA from a DNA template. In all cells RNAP is needed for constructing RNA chains from a DNA template, a process termed transcription.

(47) (C) **(48)** (D)

(49) **(B).** Masking proteins inactivate mRNA in an unfertilized egg.

(50) **(A).** Replication of DNA is semiconservative. This means that when one double helix makes a copy of itself, the two new DNA molecules each consist of one new strand and one old strand. This was hypothesized by Watson and Crick and confirmed experimentally by Meselsohn and Stahl.

(51) **(D).** Griffith discovered bacterial transformation in 1927.

(52) **(C).** According to Radial loop model. Each chromosome has one or two interconnected scaffolds made of non histone chromosomal proteins. The scaffold bears a large member of lateral loop all over it. Each lateral loop is 30 nm thick fibre similar to chromatin fibre. It develops through solenoid coiling of nucleosome chain with about six nucleosomes per turn.

(53) (C) **(54)** (B)

(55) **(B).** Each type of tRNA molecule can be attached to only one type of amino acid, so each organism has many types of tRNA (in fact, because the genetic code contains multiple codons that specify the same amino acid, there are several tRNA molecules bearing different anticodons which also carry the same amino acid).
The covalent attachment to the tRNA 3' end is catalyzed by enzymes called aminoacyl tRNA synthetases. **(56)** (C)

(57) **(D).** The new strands of DNA are formed in the $5' \rightarrow 3'$ direction from the $3' \rightarrow 5'$ template DNA by the addition of deoxyribo-nucleotides to the 3' end of primer RNA.

(58) **(D).** The chromosome is formed by somatic pairs between homologous chromosomes and repeated replication or endomitosis of chromonemata.

(59) **(C).** For determination of nucleotide sequence of genes in virus.

(60) **(B).** After two divisions, four bacterial cells are formed in which two daughter bacterial cells have normal DNA and other two have both normal and heavy DNA because DNA replicates by semiconservative method in bacteria.

(61) **(B).** 19%; because 'G' is always attached with 'C' (G ≡ C), thus percentage of C will always be equal to G.

(62) **(B).** C is always equal to G and T is always equal to A in DNA.
If G = 10%, then C = 10%
∴ T and A = 80%.
Hence T = 40% and A = 40%

(63) **(A).** Sigma (σ) factor recognises the start signal or promoter region of DNA. Rho (ρ) or termination factor is required for termination of transcription.

(64) **(D).** Genes are regulated both in eukaryotes and prokaryotes. They are regulated at four level
I. Transcriptional level (regulatory genes).
II. Post-transcriptional level (splicing, capping, etc.).
III. Translational level (operon model).
IV. Post-translational level (modification in proteins).

(65) **(C).** Structural gene - transcription - mRNA - ribosomes translation; this process is central dogma of protein synthesis.

(66) **(B).** Transcription occurs with the help of enzyme RNA polymerase (RNAP).

(67) **(A).** The daughter DNA is new and part is conserved from the parent DNA; (B) and (C) are two types of replication that were shown to be incorrect in the Meselson and Stahl experiments; (D) is a type of replication that does not exist.

(68) **(A).** DNA polymerase can only add nucleotides in this fashion; (B) and (C) are incorrect because the DNA polymerase is not able to add nucleotides to the 5' end; (D) is incorrect because phosphodiester is a bond, not an end of either strand of DNA.

(69) (B)

(70) **(D).** (D) is the enzyme necessary for the unwinding of DNA; the other enzymes are involved in steps of DNA replication after the DNA unwinds.

(71) **(A).** Average distance between two base pairs of DNA is 3.4 Å. Length of *E. coli's* DNA is = 1.36×10^7 Å
So, number of nucleotides

$$= \frac{1.36 \times 10^7}{3.4 \times \text{Å}} \text{A} = 0.39 \times 10^7$$

$= 3.9 \times 10^6 = 4 \times 10^6$

(72) **(D).** tRNA brings amino acid and reads the genetic code. RNA polymerase binds to promoter and initiates transcription.

(73) (A)

(74) **(D).** In Hershey and Chase experiment, it was finally proved that DNA is the genetic material not proteins. So, the statements given, ^{32}P found in supernatant after centrifugation and progeny generation of T_2-bacteriophage contain ^{32}S are wrong.

EXERCISE-3

(1) **(C).** Primase lays down short RNA primers at the replication fork; the other enzymes are used at different steps in DNA replication.

(2) **(B).** Mutations occur if there is an error that occurs in the final product of DNA replication; (A) is when DNA is put into another organism; (C) doesn't exist; (D) is a mismatch.

(3) **(A).**

(4) **(D).** This is an area of loosely packed DNA that is available for expression and replication; (A) represents blocks of DNA that are inactive or highly condensed; nucleoids are masses of circular DNA found in prokaryotes; (C) is the structure that contains both histone proteins and DNA.

(5) (A)

(6) **(C).** A transcript is a RNA. Methionine is an amino acid.

(7) **(A).** snRNP are small nuclear ribonucleoproteins that splices pre-mRNA in eukaryotic cells.

(8) (A)

(9) **(C).** tRNA has the anticodon that matches the codon on mRNA.

(10) **(C).** DNA polymerase builds a new strand of DNA from the 5' end to the 3' end (of the new strand). DNA polymerase can only add nucleotides to an existing strand of DNA.

(11) **(C).** Restriction enzymes are a laboratory tool for cutting pieces of DNA at specific restriction sites.

(12) **(A).** A site is the first site where tRNA enters with its specific amino acid.

(13) **(B).** P is the second site where a tRNA attaches it amino acid to the growing chain of amino acids.

(14) **(B).** Tryptophan acts as a corepressor and binds to the repressor, making it active and then blocking the transcription of the cluster of genes.

(15) **(C).** Histones are known to be the proteins that pack DNA into nucleosome.

(16) (C) **(17)** (A)

(18) **(A).** Systems where multiple genes need to be controlled at the same time; it is now known that they have the same regulatory sequence to turn them on.

(19) **(C).** Metastasis is a term for spreading of malignant tumor or cancer cells.

(20) **(D).** Topoisomerases are enzymes that regulate the overwinding or underwinding of DNA.

(21) (C) **(22)** (B) **(23)** (D)

(24) **(B).** On the lagging strand template, a primase "reads" the template DNA and initiates synthesis of a short complementary RNA primer. A DNA polymerase extends the primed segments, forming Okazaki fragments. The RNA primers are then removed and replaced with DNA, and the fragments of DNA are joined together by DNA ligase.

(25) (A) **(26)** (C) **(27)** (B) **(28)** (D)

(29) (C) **(30)** (A) **(31)** (A) **(32)** (A)

(33) (A)

(34) (B)

EXERCISE-4

(1) **(C).** If nonsense mutation occurs in lacY gene on that time it forms only Z-cistron (gene) and when Z-cistron (gene) translated it forms β-galactosidase

(2) **(A).** Central Dogma.

$$DNA \xrightarrow[A]{\text{Transcription}} mRNA \xrightarrow[B]{\text{Translation}} protein \xrightarrow[C]{\text{Francis Crick}}$$

(3) **(A).** Transcription is writing information from DNA to m-RNA.

(4) **(C).** In 1928, Frederick Griffith performed transformation experiment by using *Streptococcus pneumoniae*.

(5) **(A).** RNA Polymers catalyse polymerisation only in one direction, that is 5' → 3' and the strand that has the polarity 3' → 5' act as a template.

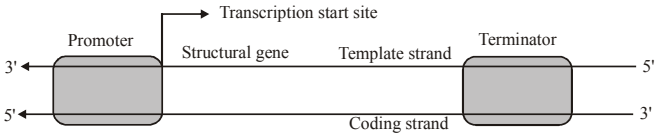


Figure : Schematic structure of a transcription unit

(6) **(D).** Lac I gene produces an inhibitor or rerpressor and negative regulation of lac operon is induced. The repressor binds to the operator gene and stops its working. Repressor is meant to block the operator gene so that structural genes are unable to form mRNA thus stopping the transcription of genes.

(7) **(A).** The movement of a gene from one linkage group to another called translocation.

(8) **(A).** Chargaff's rule states that purine and pyrimidine base paires are present in equal amount, i.e.

$A = T, G = C ; \quad (A + T) = (G + C)$

$$\therefore \quad \frac{A + T}{G + C} = 1$$

Cytosine = 17%

If A + G + C + T = 100 and G = C, A = T then

$A + 17 + 17 + T = 100 \quad \therefore G = 17\%$

$A + T + 34 = 100 ; \; A + T = 100 - 34 = 66$

$A = T = 33\% = 66$

Hence, if cytosine is 17%, then G = 17%

A and T will be 33% each.

(9) **(B).** Chargaff's rule is applicable only for DNA.

(10) **(B).** Balbiani rings are the large chromosome puff of polytene chromosomes. These are the sites of RNA and protein synthesis.

(11) **(A).** Order of organisation of genetic material
Genome (haploid set of chromosome) (Largest)
→ Chromosome (Condensed chromatin)
→ Gene (Segment of DNA; unit of inheritance)
→ Nucleotide (Made up of pentose sugar, nitrogen base and phosphate) [smallest]

(12) **(D).** Satellite DNA are the repetitive DNA which do not code for any protein. They show high degree of polymorphism and form basis of DNA fingerprinting. Since DNA from every tissue from an individual show the same degree of polymorphism, they become very useful identification tool in forensic applications.

(13) **(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.

(14) **(A).** In prokaryotes, several ribosomes may attach to single mRNA and form a chain called polyribosomes or polysomes.

(15) **(B).** A zinc finger is a small protein structural motif that characterised by the co-ordination of one or more Zn ions in order to stabilise the folds.

(16) **(A).** AUG is the start codon.
UAA, UAG and UGA are stop codons.

(17) **(B).** Semiconservative mode of chromosome replication was proved by Taylor in Vicia faba.

(18) **(B).** Cistron is a segment of DNA coding for a polypeptide. Eukaryotic structural gene is monocistronic whereas prokaryotic structural gene is polycistronic.

(19) **(C).** 23S rRNA is a component of larger subunit of ribosome and it act as peptidyl transferase (ribozyme).

(20) **(C).** A molecule which is unstable structurally and chemically cannot act as a genetic material.

(21) **(A).** The DNA-dependent RNA polymerase catalyze the polymerisation in only one direction that is 5'→ 3', the strand with polarity 5'→ 3' act as template and is called as template strand.

(22) **(C).** If deletion occurs at 901st position the remaining 98 bases specifying for 33 codons of amino acids will be altered.

(23) **(B).** Hershey and Chase gave unequivocal proof which ended the debate between protein and DNA as genetic material.

(24) **(C).** The association of H1 protein indicates the complete formation of nucleosome.
Therefore the DNA is in condensed form.

(25) **(A).** rRNA is most abundant in animal cell. It constitutes 80% of total RNA of the cell.

(26) **(D).** Two DNA polymerase molecules work simultaneous at the DNA fork, one on the leading strand and the other on the lagging strand.
Each Okazaki fragment is synthesized by DNA polymerase at lagging strand in 5' → 3' direction.
New Okazaki fragments appear as the replication fork opens further.
As the first Okazaki fragment appears away from the replication fork, the direction of elongation would be away from replication fork.

(27) **(B).** Semi-conservative DNA replication was first shown in Bacterium Escherichia coli by Matthew Meselson and Franklin Stahl.

(28) **(D).** Francois Jacob and Jacque Monod proposed model of gene regulation known as operon model/lac operon.
– Alec Jeffreys – DNA fingerprinting technique.
– Matthew Meselson and F. Stahl – Semiconservative DNA replication in E. coli.
– Alfred Hershey and Martha Chase – Proved DNA as genetic material not protein

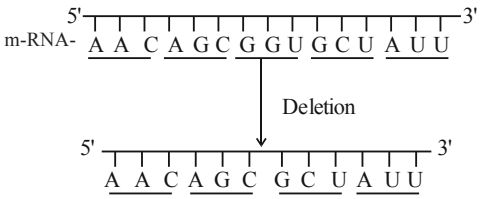
(29) **(A).** Enhancer sequences are present in eukaryotes. Operon concept is for prokaryotes

(30) **(C).** Coding strand and mRNA has same nucleotide sequence except, 'T' – Thymine is replaced by 'U'–Uracil in mRNA.

(31) **(A).** Expressed Sequence Tags (ESTs) are DNA sequences (genes) that are expressed as mRNA for protein synthesis. These are used in human Genome Project.

(32) **(C).** In lac operon
i gene – Repressor
z gene – β-galactosidase
y gene – Permease
a gene – Transacetylase

(33) **(D).**



No change in reading frame of m-RNA.