লাল-সবুজে দাগানো

TEXT BOOK

Botany

UNMESH

Medical & Dental Admission Care

It is also crucial that reproductive cells, such as eggs and sperm, contain the right number of chromosomes and that those chromosomes have the correct structure. If not, the resulting offspring may fail to develop properly. For example, people with **Down syndrome** have three copies of chromosome 21, instead of the two copies found in other people. In humans, defective chromosomes made up of joined pieces of broken chromosomes cause one type of **leukaemia** and some other **cancers**.

For an organism to grow and function properly, cells must constantly divide to produce new cells to replace old, worn-out cells. During cell division, it is essential that DNA remains intact and evenly distributed among cells. Chromosomes are a key part of the process that ensures DNA is accurately copied and distributed in the vast majority of cell divisions.

1.5 Genetic materials or Hereditary materials

Heredity is the passing of traits to offspring from its parents or ancestors. This is the process by which an offspring cell or organism acquires or becomes predisposed to the characteristics of its parent cell or organism. Heritable traits are known to be passed from one generation to the next via the materials are known as **hereditary** or **genetic materials.** The molecules **nucleic acids** that encode genetic information and found in the chromosome of the cells are recognized as hereditary materials of the organisms.

Definition of nucleic acid

Nucleic acids are the naturally occurring long chain polymers present in the nucleus of the cell, capable of being broken down to yield phosphoric acid, sugars and a mixture of organic bases and play the prime role in inherited characteristics of every living organisms by directing the process of protein synthesis.

These are the largest and significant biomolecules of the cell and carrying all the traits of heredity, hence known as **master molecules**. Although nucleic acids are mainly present in the nucleus of the cell, they also found in mitochondria, plastid, ribosome and cytoplasm.

Discovery:

Nucleic acid was discovered as **nuclein** by Swiss physician and biologist **Friedrich Miescher** in 1869 from the nuclei of white blood cells. **Altmann** (1889) named the nuclein as nucleic acids. **Albrecht Kossel** (1894) isolated and described the nitrogenous bases, sugar and phosphoric acids of nucleic acids. For this discovery, he was awarded the Nobel Prize in Physiology or Medicine in 1910. **Theodore Levene** (1921) characterized the different forms of nucleic acids, DNA from RNA.

Functions:

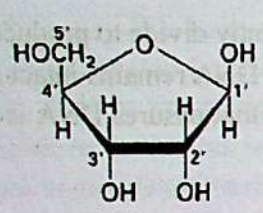
- The main functions is to store and transfer genetic information.
- To use the genetic information to direct the synthesis of new protein.

Chemical structure

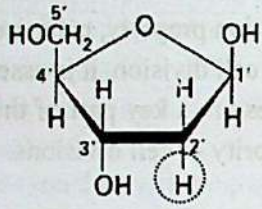
Chemically nucleic acid is a polymer of nucleotide molecule. Each nucleotide composed of the following molecules:

1. One molecule of pentose sugar,
2. One molecule of inorganic phosphoric acid and
3. One molecule of nitrogenous base.

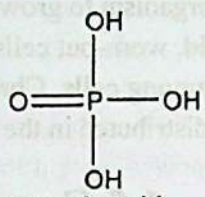
1. Pentose sugar: Each nucleic acid has a 5-carbon sugar as a part of its polymer backbone called pentose sugar. Nucleic acid has two types of pentose sugar, *viz.*, ribose and deoxyribose. β-D ribose or deoxyribose sugar of cyclic structure contribute to form nucleic acid. Both have the similar molecular structure but in deoxyribose sugar an oxygen atom is lacking in carbon 2 position of pentose structure (*deoxy*=lack of oxygen). Hence, it is also known as 2-β-D deoxyribose sugar.



ribose sugar



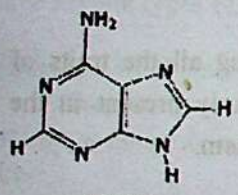
deoxyribose sugar



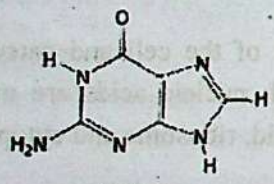
phosphoric acid

2. Inorganic phosphoric acid: The another part of the nucleic acid is a phosphoric acid (H_3PO_4). It is attached to the sugar molecule in place of the -OH group on the 5' carbon.

3. Nitrogenous base: Nucleic acid has two types of nitrogenous base,- purine bases and pyrimidine bases. Purine bases have two rings of atoms and chemical formula $C_5H_4N_4$. Nucleic acid has two purine bases as adenine and guanine. Pyrimidine bases have a single ring of atoms and chemical formula $C_4H_4N_2$. Nucleic acid has three pyrimidine bases as Cytosine, Thymine and Uracil. The nitrogen bases of nucleic acid are abbrebiated with their first letter (- A=Adenine, G=Guanine, C=Cytosine, T= Thymine and U= Uracil) when to write genetic codes. A nucleic acid of any type (DNA or RNA) has any four of nitrogen bases.

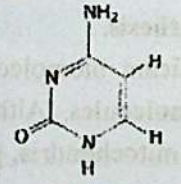


Adenine

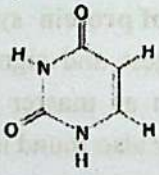


Guanine

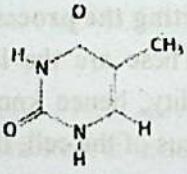
PURINES



Cytosine



Uracil



Thymine

PYRIMIDINES

❒ **Nucleoside:** One molecule pentose sugar bounds to a nitrogenous base (adenine, guanine, cytosine, thymine, or uracil) with β-glycosidic likage to form a nucleoside molecule. The nucleosides with ribose and deoxyribose sugar are called **ribonucleoside** and **deoxyribonucleoside,** respectively. Based on the sugar and nitrogenous bases the nucleosides are of following types:

Nitrogen bases	Ribonucleoside	Deoxyribonucleoside
Adenine (A)	Adenosine	Deoxyadenosine
Guanine (G)	Guanosine	Deoxyguanosine
Cytosine (C)	Cytidine	Deoxycytidine
Thymine (T)	-	Deoxythymidine
Uracil (U)	Uridine	-

❒ **Nucleotide:** One molecule inorganic phosphate bounds to a nucleoside to form a nucleotide. Actually, nucleotide consists of a nitrogenous base, a sugar (ribose or deoxyribose) and a phosphate.

groups. Nucleotides are building blocks of nucleic acids (DNA and RNA), i.e. nucleic acid is the polymer of nucleotides. The nucleotides with ribose and deoxyribose sugar are called **ribonucleotide** and **deoxyribonucleotide**, respectively. Based on the sugar and nitrogenous bases the nucleotides are of following types:

Nitrogen bases	Ribonucleoside	Deoxyribonucleoside
Adenine (A)	Adenosine monophosphate (AMP)	Deoxyadenosine monophosphate (dAMP)
Guanine (G)	Guanosine monophosphate (GMP)	Deoxyguanosine monophosphate (dGMP)
Cytosine (C)	Cytidine monophosphate (CMP)	Deoxycytidine monophosphate (dCMP)
Thymine (T)	-	Deoxythymidine monophosphate (dTMP)
Uracil (U)	Uridine monophosphate (UMP)	-

Nucleotide triphosphate (NTP): When a nucleotide contains a phosphate group then called nucleotide monophospahte (NMP), when it contains two phosphate group then called nucleotide diphosphate (NDP) and it contains three phosphate group then called nucleotide triphosphate (NTP). Thus there are five types of NTP, as:

AMP + P=ADP	ADP + P= ATP (Adenosine triphosphate)
GMP + P=GDP	GDP + P= GTP (Guanosine triphosphate)
CMP + P=CDP	CDP + P= CTP (Cytidine triphosphate)
UMP + P=UDP	UDP + P= UTP (Uridine triphosphate)
TMP + P=TDP	TDP +P= TTP (Thymidine triphosphate)

Functions of nucleotides:

1. Nucleotides are basically the building blocks of DNA and RNA.
2. They are carriers of chemical energy in the cell (as ATP, GTP), components of cofactors (as NAD, FAD),
3. They are also intermediates in cellular communication and signal transduction (as cAMP, cGMP), and last but not the least, donor substrates for glycobiology (as UDPG).

Types of nucleic acids

Based on pentose sugar structure nucleic acids are of two types, *viz.*-

1. **Deoxyribo nucleic acid (DNA)**- Having sugar molecule of deoxyribose type, and
2. **Ribo nucleic acid (RNA)**- Having sugar molecule of ribose type.

Deoxyribonucleic acid or DNA

Definition

The nucleic acid of living cell having **deoxyribose sugar** in its nucleotide, carrying hereditary traits, controlling all biological activities of cell and capable of replication and mutation is known as deoxyribonucleic acid or DNA.

Where found?

DNA is the main chemical structure of chromosome of eukaryotic cells. It is also found in mitochondria, chloroplasts of eukaryotes and cytoplasm of prokaryotes and in some viruses.

Discovery

In 1869, the Swiss physician **Friedrich Miescher** first isolated DNA. In 1928, **Frederick Griffith** realized that DNA might actually hold genetic information. In 1953, **James D. Watson** and **Francis Crick** proposed the idea that the DNA's structure was a double-helix.

Chemical Structure of DNA

DNA molecule is a polymer of deoxyribonucleotide. Each deoxyribonucleotide composed of the following molecules:

1. One molecule of deoxyribose pentose sugar,
2. One molecule of inorganic phosphoric acid and
3. One molecule of nitrogenous base.

1. Pentose sugar: DNA contains 2-β-D type deoxyribose pentose sugar in which an oxygen atom is lacking in carbon 2 position of pentose structure (*deoxy*=lack of oxygen).

2. Inorganic phosphoric acid: The another part of the DNA is a phosphoric acid. It is attached to the sugar molecule in place of the -OH group on the 5' carbon.

3. Nitrogenous base: Each nucleotide in a DNA molecule has one of four nitrogenous bases: adenine, guanine, thymine, and cytosine. The first two are called **purine bases** because their structure consists of two rings of atoms and chemical formula $C_5H_4N_4$. The latter two are known as **pyrimidine bases,** since they have a single ring of atoms and chemical formula $C_4H_4N_2$.

One molecule deoxyribose sugar bounds to a nitrogen base to form a **nucleoside**. A nucleoside bounds to a phosphoric acid and thus form a **nucleotide**. Actually, DNA is the polymer of nucleotide molecules.

Physical Structure of DNA

American scientist **James D. Watson** and **Francis Crick** described the model of physical structure of DNA in 1953. This model is known as **double helix model**. The double-helix model of DNA structure based upon the crucial X-ray diffraction image of **Rosalind Franklin** and **Maurice H. F. Wilkins.** Crick, Wilkins, and Watson awarded the Nobel Prize in 1962 in Physiology and Medicine for their contributions to the discovery. (*Franklin died in 1958 and thus was ineligible to be nominated for a Nobel Prize.*)

James Dewey Watson, 1928 ...

Francis Harry C. Crick, 1916-2004

M.H. Frederick Wilkins, 1916-2004

Rosalind Franklin

The double helix of DNA of **Watson** and **Crick** has the following features:

1. DNA molecule contains two polynucleotide strands wound around each other. It is look like a twisted ladder.
2. The two stands are complementary each other. The sequences of base along one strand specify the sequence of base along the other strand.
3. The backbone of each consists of alternating deoxyribose and phosphate group.
4. The phosphate group bonded to the 5' carbon atom of one deoxyribose is covalently bonded to the 3' carbon of the next.

5. The two strands are antiparallel, that is, one strand runs 5′ to 3′ while the other runs 3′ to 5′.

6. The purine or pyrimidine attached to each deoxyribose projects in toward the axis of the helix.

7. Each base forms hydrogen bonds with the one directly opposite it, forming base pairs. Adenine (A) always connected with thymine (T) by two hydrogen bonds (A=T) and guanine (G) is connected with cytosine (C) with three hydrogen (G≡C) bonds. This is called **Chargaff's** rule.

8. 3.4 Å separate the planes in which adjacent base pairs are located.

9. The double helix makes a complete turn in just over 10 nucleotide pairs, so each turn takes a little more (35.7 Å to be exact) than the 34 Å shown in the diagram.

10. The diameter of the helix is 20 Å.

11. The path taken by the two backbones forms a major groove and a minor groove.

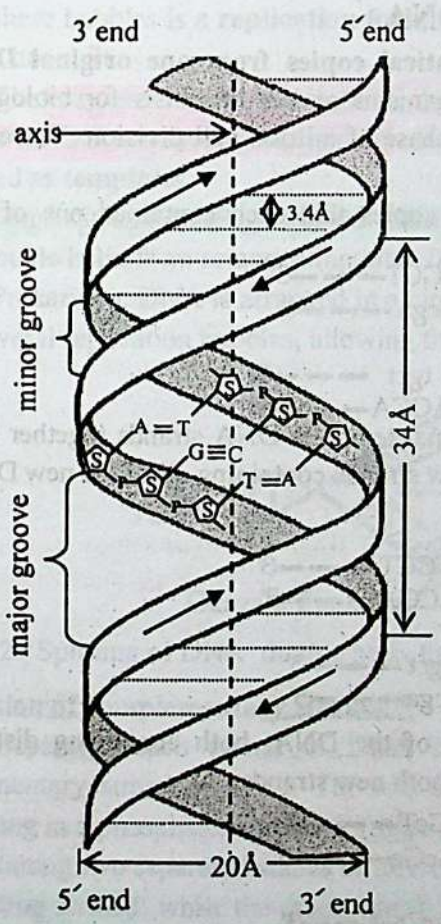


Fig. 1.25 Double helix model of DNA

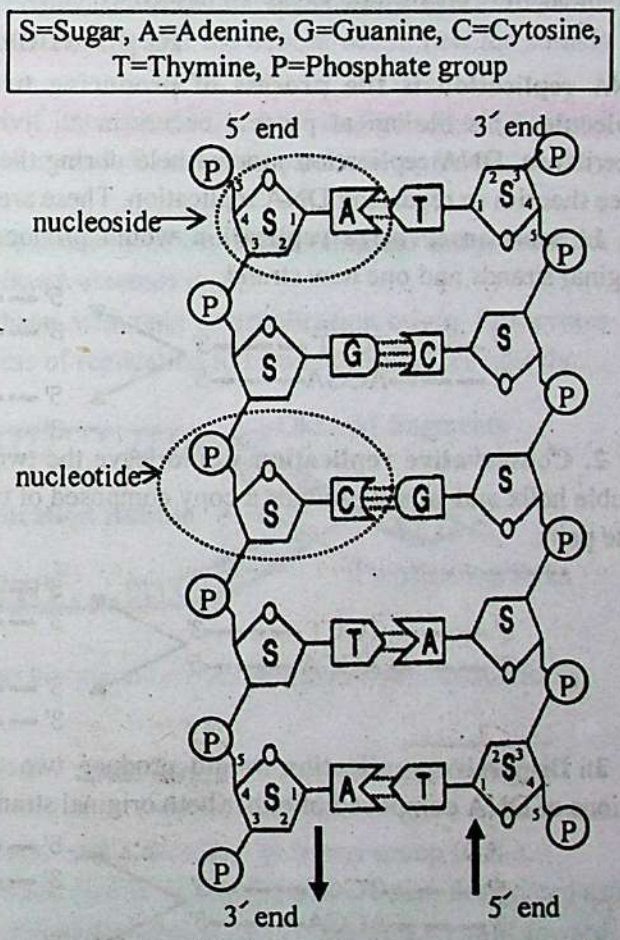


Fig. 1.26 Molecular model of DNA

The double helical structure of DNA is essential to its function-

The genetic material must perform four important functions:

1. It must be able to store all of an organism's genetic information.
2. It must be susceptible to mutation.
3. It must be precisely replicated in the cell division cycle.
4. It must be expressible as the phenotype.

The simple, double-helical structure of DNA, with the two strands linked by complementary base pairs, lends itself well to the first three of these functions. DNA is also well suited to expression as a phenotype, though this function is not inherent in the structure of the molecule.

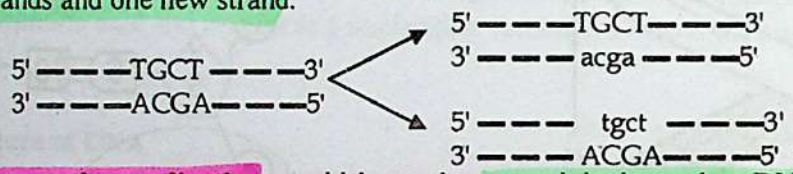
Function of DNA

1. **Control of cell activities:** To produce characteristics of an individual and species DNA controls all activities of cell.
2. **DNA inheritance:** DNA is important in terms of heredity. It packs in all the genetic information and passes it on to the next generation. The basis for this lies in the fact that DNA makes genes and genes make chromosomes.
3. **Coding for proteins:** DNA is read by the messengers that break it open into single stranded polynucleotide chains and is copied into RNA.

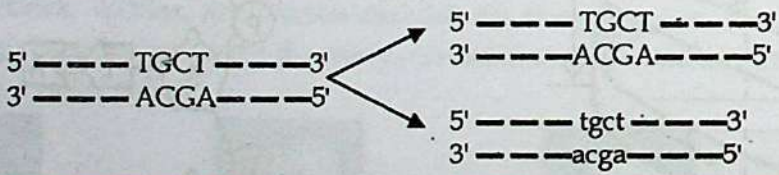
Replication of DNA

DNA replication is the process of producing two identical copies from one original DNA molecule. This biological process occurs in all living organisms and is the basis for biological inheritance. DNA replication process held during the interphase of mitosis cell division. There are three theories in regarding DNA replication. These are:

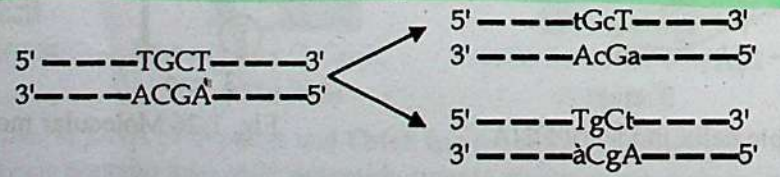
1. **Semiconservative replication** would produce two copies that each contained one of the original strands and one new strand.



2. **Conservative replication** would leave the two original template DNA strands together in a double helix and would produce a copy composed of two new strands containing all of the new DNA base pairs.



3. **Dispersive replication** would produce two copies of the DNA, both containing distinct regions of DNA composed of either both original strands or both new strands.



Among these theories, semiconservative theory is widely accepted.

Semiconservative Replication of DNA

Watson and **Crick** in 1953 propose the semiconservative model of replication. **Meselson-Stahl** (1958) have proved semiconservative replication of prokaryotic cells in a series of elegant experiments with *E. coli* bacteria. **Herber Taylor** (1960) has proved semiconservative replication

of eukaryotic cells performing experiments with root tip cells of the bean plant. This process is completed by **three** consecutive stages. The stages are-

1. Separating of strands

❒ The first major step for the DNA replication to take place is the breaking of hydrogen bonds between bases of the two **antiparallel** strands. Before this the *topoisomerase* enzyme relaxes the DNA from its super-coiled nature.

❒ Replication begins at a site called **'origin of replication'** or **'ori'** along a DNA molecule, where the DNA is unzipped when paired nitrogenous bases are separated from each other. The separation happens in places of the chains which are rich in A-T, because there are only two bonds between adenine and thymine.

❒ The openings in the DNA are called **'replication bubbles'** or **'replication eyes.'** At either end of these bubbles is a **replication fork**, a 'Y'-shaped region of the bubble where new the strands of DNA are built.

❒ The enzyme *helicase* breaks the hydrogen bond between the bases of nucleotides of DNA and untwists the DNA at the replication fork. Both DNA strands take part in replication process, so they are called as **templates.**

❒ *Single-Strand Binding Proteins* (SSBP) binds to each DNA strand or template and prevent the DNA double helix from re-annealing after *DNA helicase* unwinds it.

❒ Prokaryotic DNA is arranged in a circular shape, with only one replication origin. Eukaryotes form several replication bubbles, allowing the process of replication to be completed more quickly.

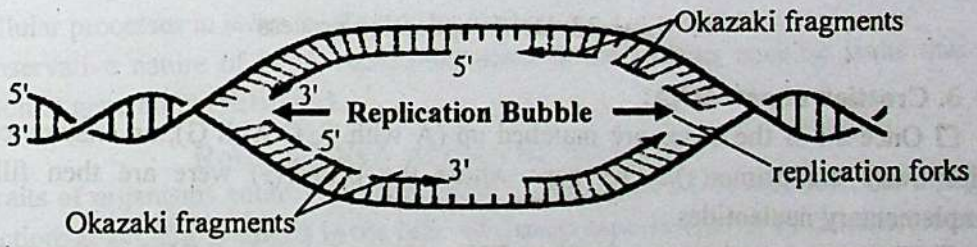


Fig 1.27 Splitting of DNA double helix that forms a replication bubble and two replication forks

2. Creation of complementary strands

❒ Separated each strand of DNA serves as a **template** to guide the synthesis of its complementary strand of DNA. The end of each strand is distinct, with the 5' (five prime) end terminating in a phosphate, and the 3' (three prime) end with a dangling hydroxyl group (OH-).

❒ Among two separated stands of DNA, one strand runs from the ***5' end to 3' end***, designated as the **'leading strand'** while the other runs ***3' end to 5' end*** designated as the **'lagging strand'** toward the replication fork.

❒ The **RNA primer** made by the *primase* enzyme binds at the end of leading strand and various points of lagging strand. The primer is a short sequence of several base of RNA that acts as the starting point for DNA synthesis.

❒ The essential nucleotides of DNA are exist in nucleoplasm. With the help of *DNA polymerase* and Mg^{2+} these nucleotides attach to the template by phosphodiaster bonds.

❒ *DNA polymerase* can only add nucleotides continuously at the free 3' end of a leading strand, always forming the new DNA strands in the 5' to 3' direction only.

❒ The other new strand, the lagging strand, must be made in a piecemeal fashion, as small 3' to 5' bits and pieces, called **Okazaki fragments**, add discontinuously and ultimately joined together by the enzyme *DNA ligase*. In this case both strands the enzyme ***RNA primase*** adds more **RNA primers.**

[**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. Okazaki fragments are between 1000 and 2000 nucleotides long in *Escherichia coli* and are approximately 150 nucleotides long in eukaryotes. Okazaki fragments were discovered by Japanese scientist **Reiji Okazaki** and his wife **Tsuneko Okazaki** in 1968]

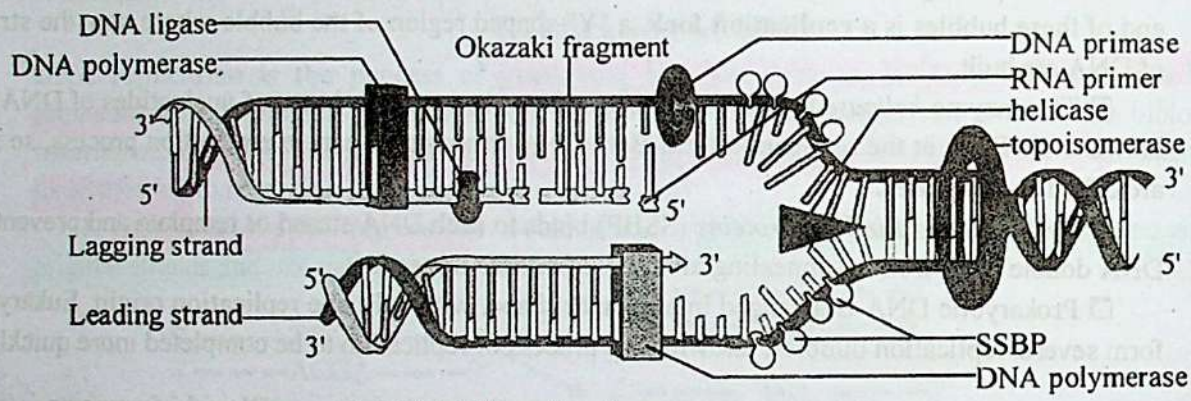


Fig1.28: DNA replication process

3. Creation of new DNA:

❒ Once all of the bases are matched up (A with T, C with G), an enzyme called *exonuclease* strips away the primer(s). The gaps where the primer(s) were are then filled by yet more complementary nucleotides.

❒ The new strand is proofread to **DNA mismatch repair** (MMR) in the new DNA sequence. Enzymes like *nucleases* remove the wrong nucleotides and the DNA polymerase fills the gaps.

[DNA mismatch repair (MMR) deficiency is one of the best understood forms of genetic instability in **colorectal cancer** (CRC), and is characterized by the loss of function of the MMR pathway.]

❒ Finally, an enzyme called *DNA ligase* seals up the sequence of DNA into two continuous double strands.

❒ The result of DNA replication is two DNA molecules consisting of one new and one old chain of nucleotides. This is why DNA replication is described as semi-conservative, half of the chain is part of the original DNA molecule, half is brand new.

❒ Following replication, the new DNA automatically winds up into a double helix.

Replisome or Replication complex

At the replication fork, many replication enzymes assemble on the DNA into a complex molecular machine called the **replisome** or the **replication complex.** The following is a list of major DNA replication enzymes that participate in the replisome:

Enzyme	Function in DNA replication
DNA Helicase	Unwinds the DNA double helix at the replication fork.
DNA Polymerase	Builds a new duplex DNA strand by adding nucleotides in the 5' to 3' direction. Also performs proof-reading and error correction.
DNA Clamp	A protein which prevents elongating DNA polymerases from dissociating from the DNA parent strand.
Single-Strand Binding Proteins (SSBP)	Bind to ssDNA and prevent the DNA double helix from re-annealing after DNA helicase unwinds it.
Topoisomerase	Relaxes the DNA from its super-coiled nature.
DNA Gyrase	Relieves strain of unwinding by DNA helicase.
DNA Ligase	Re-anneals the semi-conservative strands and joins Okazaki fragments of the lagging strand.
Primase	Provides a starting point of RNA (or DNA) for DNA polymerase to begin synthesis of the new DNA strand.
Telomerase	Lengthens telomeric DNA by adding repetitive nucleotide sequences to the ends of eukaryotic chromosomes.

Biological significance of DNA replication

1. DNA replication needs to occur so that during cell division, new cells will also have a copy of the organism's DNA.
2. DNA is necessary to make all the RNA and proteins needed for cells carry out necessary reactions and cellular processes in order for them to survive.
3. Semiconservative nature of DNA replication ensures the species specific traits that pass through generation to generation unchanged.

Roles of DNA as genetic material

All hereditary traits of organisms control by gene. Gene is part of DNA of chromosome that gives necessary instructions to protein synthesis in the cell. Different experiments of F. Griffith (1928). O. T. Avery, C. M. MacLeod, and M. McCarthy (1944) have provided information that gene is the part of DNA i.e. DNA is the gene. DNA is the permanent largest molecule of chromosome. All of the biochemical reactions in the cell are regulated by the DNA, hence it is called **the master molecule.** Traits of parent pass to offspring as chemical component of DNA. For this reason, DNA is known as **the chemical basis of heredity.** Of the following reasons, DNA is called holder and carrier of heredity:

1. All genetic information of organism storage in DNA.
2. Gene expression held through the phenomenon central dogma as from DNA to RNA to proteins
3. DNAs are capable of synthesis all types of proteins essential for cells.
4. It is capable of carrying all biological symbols of heredity.
5. During meiosis cell division DNA produced exact copy of DNA that passes to the germ cell.
6. DNA is species specific and unchangeable; only mutation can change the structure of DNA.
7. If any change happen in DNA by mutation that should be express in the next generation of organism.

2. Ribonucleic acid or RNA

The nucleic acid of living cell having ribose sugar in its nucleotides and perform multiple vital roles in the coding, decoding, regulation, and expression of genes is called **ribonucleic acid** or **RNA.** In prokaryotic cell these are found in cytoplasm, chromosome, ribosome, nucleolus, plastid and mitochondria. In eukaryotic cells 90% RNA present in cytoplasm and 10% in other structures. In some viruses RNA exists as genetic material.

Physical structure: Primarily RNA is single-stranded but in their secondary structure there are several U shaped loops.

Chemical Structure of RNA: RNA molecule is a polymer of ribonucleotide. Each ribonucleotide consists of the following molecules:

1. One molecule of ribose pentose sugar,
2. One molecule of inorganic phosphoric acid and
3. One molecule of nitrogenous base.

Each nucleotide in a DNA molecule has one of four nitrogenous bases: adenine, guanine, cytosine and uracil. The first two are **purine** bases and the latter two are **pyrimidine** bases.

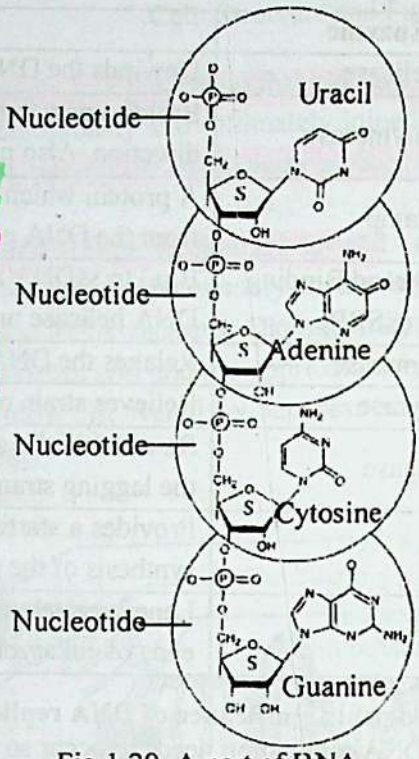


Fig 1.29 A part of RNA

Types of RNA

RNA are of two main types, *viz*;-

1. **Genetic RNA or gRNA:** When RNA functions as genetic material, *e.g.* RNA of some viruses.
2. **Non-genetic RNA:** When RNA took part in only protein synthesis, *e.g.* RNA of eukaryotic and prokaryotic cells. There are three types of non-genetic RNA:

(i) Ribosomal RNA or rRNA: It makes up about 80% of the total RNA in a cell. These are synthesized in nucleolus and occur in ribosome. Ribosomal RNA composed of unbranched, flexible polynucleotide chain. This chain remains coil in low ionic concentration but its nitrogen bases form helical pair in high ionic concentration. In such case adenine bound with uracil and guanine bound with cytosine.

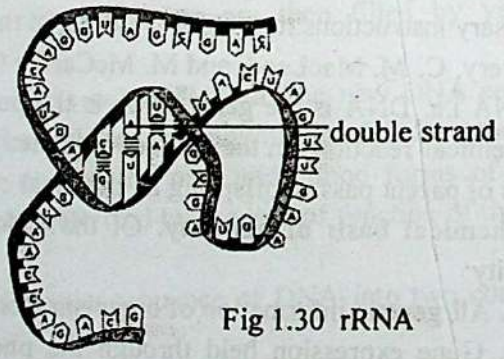


Fig 1.30 rRNA

Eukaryotic rRNA is of four types *viz*:-28S rRNA, 18S rRNA, 5.8S rRNA and 5S rRNA.

Functions: Ribosomal RNA provides a mechanism for decoding mRNA into amino acids and interacts with tRNAs during translation. It comprises the predominant material within the ribosome.

(ii) Messenger RNA or mRNA: An RNA produced by transcription that carries the code for a particular protein from the nuclear DNA to a ribosome in the cytoplasm and acts as a template for the formation of that protein called **messenger RNA.** It makes up 3-5% of the total RNA in a cell.

Jacob and **Monod** coined the name mRNA. Messenger RNA is a single strand made of up to several thousand nucleotides. It is created as complementary strand of DNA hence, it has base sequences as like as in DNA. In its linear structure mRNA have two non-coding ends and middle coding zone. The two ends of mRNA recognized as **5′ leader** and **3′ trailer** end.

Functions: mRNA transcribed from a DNA template, and carries coding information to the sites of protein synthesis in the ribosomes.

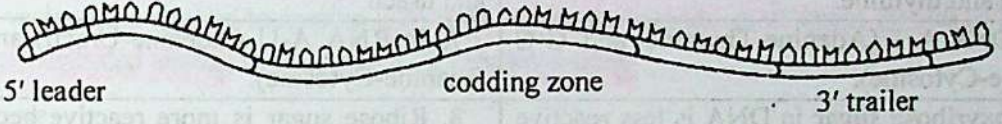


Fig 1.31. An mRNA

(iii) Transfer RNA or tRNA: A relatively small, clover leaf forms of RNA that transfers a particular amino acid to a growing polypeptide chain at the ribosomal site of protein synthesis during translation is called transfer RNA or tRNA. The tRNA is made up of 70 to 90 nucleotides. **Robert William Holley *et al.*** (1965) proposed the clover leaf model structure of tRNA. He awarded the Nobel Prize in Physiology or Medicine in 1968 with **Har Gobind Khorana** and **Marshall Warren Nirenberg** for describing this model. According to this model the single polenucleotide chain of tRNA is folded upon itself to form five arms. The arms are: (i) Acceptor arm, (ii) Dihydrouridine (DHU) arm or D arm, (iii) Anticodon arm, (iv) Variable arm and (v) Thymine pseudocytosine or TψC arm.

Transfer RNA also has DHU loop, variable loop, anticodon loop, TψC loop and amino acid acceptor end. It has four normal bases A, G, U, C and some unknown bases like isonine (I), dihydrouridine, pseudouradine etc. Both end of single chain of tRNA (5′→3′) exist aside.

Functions:

1. Transfer RNA mediates recognition of the codon and provides the corresponding amino acid.
2. It mainly recognized for carrying amino acids.
3. It then gives to it mRNA to translate the nucleotides proteins.

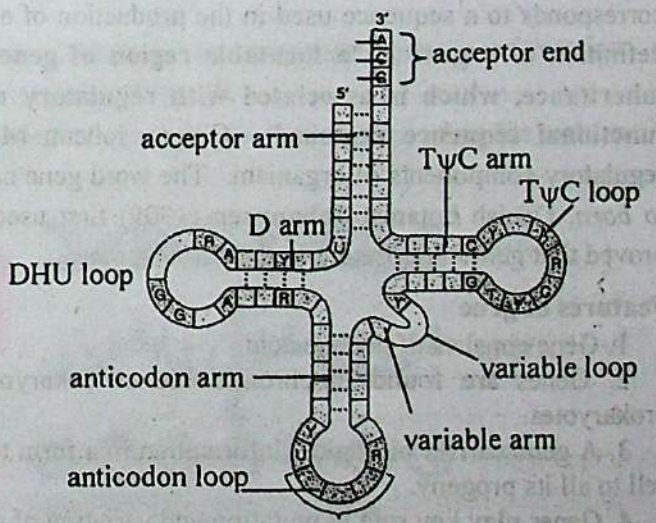


Fig1.32 Clover leaf model of tRNA

Differences between DNA and RNA

DNA	RNA
1. DNA is deoxyribonucleic acid.	1. RNA is ribonucleic acid.
2. DNA is the medium of long-term storage and transmission of genetic information.	2. RNA transfer the genetic code needed for the creation of proteins from the nucleus to the ribosome.

3. The helix geometry of DNA is of β-form.	3. The helix geometry of RNA is of α-form.
4. DNA is protected in the nucleus, as it is tightly packed.	4. RNA strands are continually made, broken down and reused.
5. DNA can be damaged by exposure to ultra-violet rays.	5. RNA is more resistant to damage by ultra-violet rays.
6. DNA has deoxyribose sugar, phosphate backbone, and four bases *viz.*, adenine, guanine, cytosine and thymine.	6. RNA has ribose sugar, phosphate backbone and four bases *viz.*, adenine, guanine, cytosine, and uracil
7. In DNA A-T (Adenine-Thymine) and G-C (Guanine-Cytosine).	7. In RNA A-U (Adenine-Uracil) and G-C(Guanine-Cytosine).
8. Deoxyribose sugar in DNA is less reactive because of C-H bonds. Stable in alkaline conditions.	8. Ribose sugar is more reactive because of C-OH (hydroxyl) bonds. Not stable in alkaline conditions.
9. DNA has smaller grooves, which makes it harder for enzymes to attack DNA.	9. RNA has larger grooves, which makes it easier to be attacked by enzymes
10. DNA is self-replicating.	10. RNA is synthesized from DNA when needed.

Gene

Gene is a small molecular unit in the cell that control all the hereditary traits of living organism. **A gene can be defined as a region of DNA that controls a hereditary characteristic.** It usually corresponds to a sequence used in the production of a specific protein or RNA. A modern working definition of a gene is **"a locatable region of genomic sequence, corresponding to a unit of inheritance, which is associated with regulatory regions, transcribed regions, and or other functional sequence regions."** Gregor Johann Mendel used the term factor for these traits regulatory components of organism. The word gene came from the Greek word *genos* which means *to born*. Danish botanist **Johannsen** (1909) first used the term gene. **T. H. Morgan** (1912) have proved that genes are present in the chromosome.

Features of gene

1. Gene consists of nucleic acid.
2. Genes are found in chromosome of eukaryotes and in nucleo materials or plasmid in prokaryotes.
3. A gene carries biological information in a form that must be copied and transmitted from each cell to all its progeny.
4. Genes play key role in mutation and variation of organism.
5. Different genes determine the different characteristics, or traits, of an organism.
6. Each chromosome of each species has a definite number and arrangement of genes.
7. Genes can be as short as 1000 base pairs or as long as several hundred thousand base pairs.
8. Genes have the power of self-replication.

Nature of gene

Genes hold the information to build and maintain an organism's cells and pass genetic traits to offspring. Two genes of same nature present in a locus of homologous chromosome of diploid cell. Genes code for proteins, which might result in identifiable traits. As one gene can regulate more

than one trait, one trait is also control by several genes. Genes are involved in different functions due to their structural diversities.

The structure of gene could be changed by any natural or artificial factor. Any extensive change held in gene could express in organism traits. Genes of eukaryotic organism have coding and non ooding regions known as **axon** and **intron** respectively. Axons are responsible for protein synthesis.

The total amount of gene in a set of chromosomes of all type of an organism is known as genome. German botanist **Hans Winkler** (1920) first used the term genome. The number of genes in the genome varies from species to species. The human genome is made up of about 20,000 to 25,000 genes which distributed among 24 (22A+1X+1Y) chromosomes.

Action of gene

A gene may determine a characteristic of an individual by specifying a polypeptide chain that forms a protein or part of a protein. Action of gene may be defined as the process of protein synthesis of genes. A structural gene, an operator gene and a promoter gene take part in protein synthesis. These genes are called together as **operon.** The gene, which regulates the operon, is called the **regulator gene.** Gene actions held always within the cell to continuous supply of protein in the body.

Gene actions carry out in the cell by three successive processes:

1. Replication: Replication is the process of producing two identical copies from one original DNA molecule. It conserves all genetical information generation to generation. DNA replication held in synthesis (S) stage of cell cycle.

2. Transcription: DNA transcription is a process that involves transcribing genetic information from DNA during replication to mRNA. It held in nucleus of the cell.

3. Translation: Translation is the process where ribosomes synthesize proteins using the mature mRNA transcript produced during transcription.

Central Dogma

The flow of genetic information through the three stages of gene action (replication, transcription and translation) from DNA to RNA to protein is termed as "**central dogma**". The idea of central dogma of molecular biology was first stated by **Francis Crick** in 1958 and restated in a *Nature* paper published in 1970.

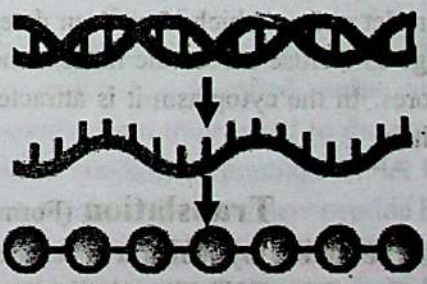


Fig: 1.33 The central dogma

Transcription (Formation of messenger RNA)

Transcription is the process by which a complementary mRNA copy is made of the specific region of the DNA molecule, which codes for a polypeptide. Transcription held in nucleus of the cell including following consecutive stages-

1. Initiation phase: At first *RNA polymerase* enzyme recognizes a specific base sequence in the DNA called a **promoter** and binds to it. From that point, a specific region of the DNA molecule, called a **cistron,** unwinds. This unwinding is the result of hydrogen bonds between base pairs in the DNA double helix being broken with action of *RNA polymerase*. This exposes the bases along each

strand. Each base along 3'-5' strand (this strand is called as **sense-strand** and another is called as **anti-sense** strand) attracts its complementary RNA nucleotide, i.e. a free guanine base on the DNA will attracts an RNA nucleotide with a cytosine base and a uracil (not thymine) is attracts to adenine.

2. Chain elongation phase: In the presence of Mg^{++} or Mn^{++} the *RNA polymerase* assembles bases (ATP, GTP, UTP and CTP) that are complimentary to the DNA 3©-5© strand (sense strand) being copied and elongated the mRNA strand. Actually 3'-5' strand of DNA used as a template of mRNA transcription, because after assembling complimentary bases to the mRNA the *RNA polymerase* reforms the DNA helix as like as before.

3. Termination phase: At the end of transcription *RNA polymerase* enzyme faces a specific base sequence in the DNA called a **terminator,** which indicate termination of the gene encoding region of DNA. The mRNA produced is called a ***pre mRNA.***

4. Processing the pre mRNA: In eukaryotic cells, the newly-formed pre mRNA must be further modified before it can be used. A **cap** (guanine nucleotide) is added to the 5' end and a poly-A tail (50-250 adenine) is added to the 3'end of the molecule. The newly-formed pre mRNA has regions that do not contain a genetic message. These regions are called ***introns*** and must be removed. Their function is unknown. The remaining portions of mRNA are called ***exons***. They are spliced together to form a ***mature mRNA***, a process is called the **splicing** with the help of a chemical complex **spliceosome.**

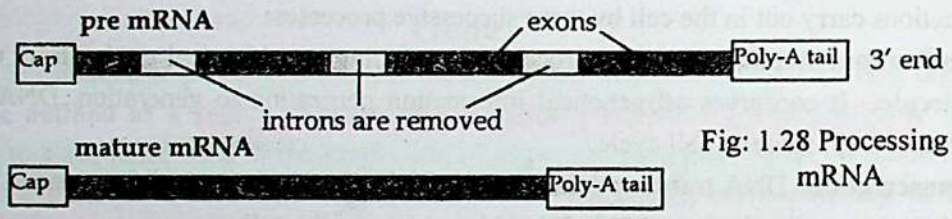


Fig: 1.28 Processing of mRNA

Fig: 1.34 Processing the pre mRNA

Adding of **cap** (called capping) and **poly-A tail** (called tailing) to the mRNA facilitates it passing out through nuclear pore and adhere to the ribosomes. Along the mature mRNA is a sequence of triplet codes, which have been determined by the DNA. Each triplet is called a **codon.** Being too large to diffuse across the nuclear membrane, the mature mRNA leaves instead through the nuclear pores. In the cytoplasm it is attracted to the ribosomes for the process of translation of polypeptide chain.

Translation (Formation of amino acid chain)

Translation is the means by which a specific sequence of amino acids is formed in accordance with the codons on the mRNA. Translation involves the following processes:

1. Activation of amino acid: First step of translation is the activation of amino acid. In presence of *amino acyl tRNA synthetage enzyme* (aa-tRNA synthetage) and Mg^{++} amino acids of the cytoplasm combined to the ATPs to form active amino acyl adenosine monophosphates (AA~AMPs) and pyrophosphate (PP). About 20 amino acids involve in protein synthesis process each of which has a specific aa-tRNA synthetage enzyme.

$$\underset{\text{amino acid}}{AA} + ATP \xrightarrow[Mg^{++}]{\textit{aa-tRNA}\text{ synthetage}} \underset{\text{active amino acid}}{AA\sim AMP} + \underset{\text{pyrophosphate}}{PP}$$

2. Transfer of activated amino acid to tRNA: There are about 100 types of tRNA in the cell. Each active amino acid has specific tRNA, such as Met-tRNA for methionine. The active amino acid combined to its specific tRNA with the help of amino acyl adenylate synthetage enzyme (*aaa*-synthetage) and produce amino acyl tRNA complex (aa-tRNA complex), adenosine monophosphate (AMP) and enzyme. In this reaction –COOH of amino acid bonding the –OH of ribose sugar of tRNA of 3'end.

$$\underset{\text{active amino acid}}{\text{AA}\sim\text{AMP}} + \text{tRNA} \xrightarrow{(aaa\text{- synthetage})} \underset{\text{aa-tRNA complex}}{\text{AA}\sim\text{tRNA}} + \text{AMP} + \text{enzyme}$$

3. Initiation of protein synthesis: Some factors are essential for initiation of protein synthesis. Methionine is the initial N-ending amino acid of a polypeptide chain. So specific methionine with tRNA initiates the process of protein synthesis. In this process *N-formylmethionine complex* or *fMet-tRNA complex* is formed. It is followed in eukaryotic cell by the formation of ***40S initial complex*** by assembling of mRNA, 40S ribosomal subunit, fMet-tRNA complex, GTP and three initiative factors (IF-1. IF-2 and IF-3).

At the end of initiation of protein synthesis 60S ribosomal subunit combine to the 40S initial complex and thus formed an ***80S complex***. The 60S ribosomal subunit has two atachment sites, viz., *A* site or acceptor site and *P* site polymerization site. Functional a ribosome can provide place for two codons (6nucleotides) at a time. The fMet-tRNA is attach to the P site and other tRNAs are attached first to the A site and then transferred to the P site.

4. Elongation of the polypeptide chain: Some soluble protein factors (EF-T, EF-G) a requiring for elongation of the polypeptide chain. These factors are called elongation factors (EF). The initial amino acid combined to the second one (amino acid) through the formation of peptide bond. In this time, tRNA of fMet-tRNA removed from the P site. The second amino acid held together with its tRNA through carboxyl group. The peptide bond is form with the assistance of peptidyl trnasferage complex of 60S ribosome.

The tRNA which adhere the elongated polypeptide chain is called **peptidyl tRNA**. It is attached to the P site of ribosome. The tRNA which carry amino acid is called **amino acyle tRNA** (aa_2-tRNA). During formation of peptide bonds the peptide chain transferred to the amino acyle tRNA from peptidyl tRNA. In this time the carboxyl ester bonding of peptidyl tRNA break down and combined to the amino acid of amino acyle tRNA in course of forming new peptide bond.

The movement of ribosome along the mRNA is called translocation. The ribosome move along the mRNA in 5'-3' direction. In each step, it moves a single codon distance from the initial end to the ending code.

During first step of translocation, the attached amino acyle tRNA complex transferred from A site to P site. The empty A site then refill by the third amino acyle tRNA complex (aa_3-tRNA). This process occurs repeatedly and thus elongated the polypeptide chain.

5. Chain termination: The ribosomal movement continues along the mRNA until it reaches one of the terminal codes (UAA, UGA, UAG) at which point the polypeptide is cut off. In this way, many identical polypeptides are produced simultaneously. The ribosome, mRNA and polypeptide chain segregated each other. The polypeptide chains are then used in formation of complex protein molecule. The process of transcription and translation is summarized in the figure 1.29

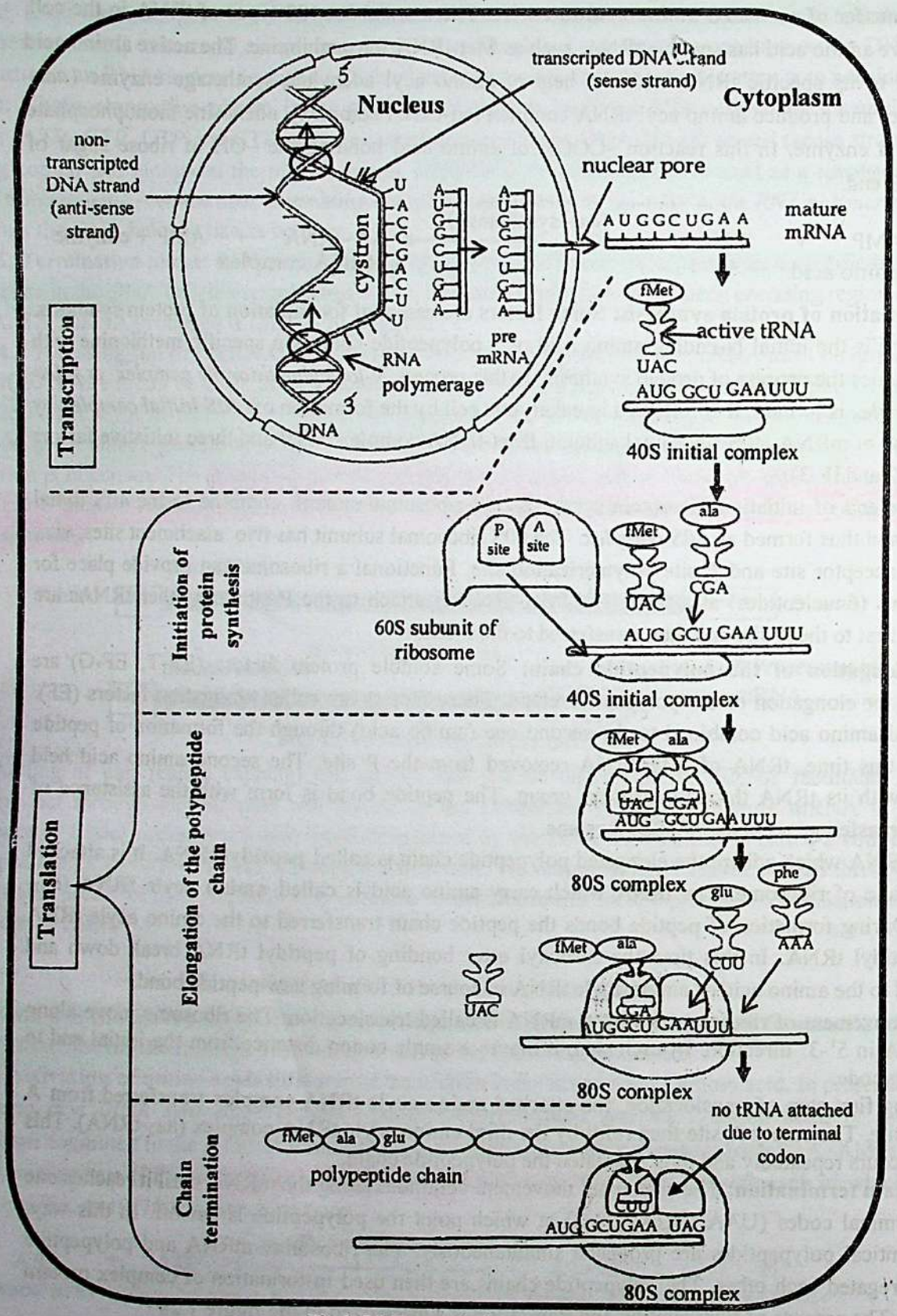


Fig 1.35 Transcription and translation

Differences between Transcription and Translation

Transcription	Translation
1. In transcription, RNA is made from DNA template.	1. Synthesis of proteins occurs in translation.
2. It occurs inside the nucleus in eukaryotes and cytoplasm in prokaryotes.	2. It occurs inside the ribosome in eukaryotes and cytoplasm in prokaryotes.
3. The template is antisense strand of DNA.	3. The template is mRNA.
4. Transcription requires RNA polymerases and some transcription factors.	4. Translation requires initiation, elongation and translocase factors.
5. Polymerase moves over the template.	5. Ribosome moves over mRNA.
6. An adapter molecule is not required in transcription	6. Adapter molecules bring amino acids over the template.
7. Product often requires splicing.	7. Splicing is absent.
8. The product undergoes processing that involves cutting, modification of nitrogen bases, folding and attaching of specific groups at the ends.	8. Processing involves occasional modification of amino acids, combining with other substances (e.g., glycosylation) and packing.

Genetic code

Genetic code is the linear sequence of nucleotide triplets in messenger RNA (mRNA out as the sequence of nucleotides in DNA molecule to determine the specific sequence in the synthesis of proteins. It is also known as the mRNA code. It is the basis of heredity and nearly universal in all organisms.

Explanation: RNA molecule has four nitrogenous bases as Adenine (A), Guanine (G), Uracil (U) and Cytosine (C). Each of the base is the part of a nucleotide and nucleotides are arranged in RNA as polynucleotide chain. Nitrogenous bases are designated in the polynucleotide as their first letter. Theses four letters alphabet form genetic codes, which are responsible for infinite number of protein synthesis.

Twenty (20) types of amino acids are involved in protein synthesis and nitrogenous bases of mRNA provide essential codes. When one base defines a singlet code only 4 types coding is possible. When two bases define a doublet code 16 types coding is possible but insuffient to production of 20 amino acids. It is only possible to synthesis 20 types of amino acid when three nitrogenous bases define a triplet code. That is why each triplet nucleotide is known as mRNA codon. **Actually genetic code means a triplet code.**

In this way 4×4×4=64 types of permutation and combination is possible. **Watson and** introduced the triplet concept. **Nirenberg** and **Matthaei** invent 64 triplet codes for amino acids.

Types of Codon:

The genetic code consists of 64 triplets of nucleotides. These triplets are called **codons.** With *three* exceptions, each codon encodes for one of the 20 amino acids used in the synthesis of proteins. The codons are of three types, *viz:*

1. Sense Codon: Those codons that code for amino acids are called sense codons. There are 61 sense codons in the genetic code which code for 20 amino acids.

2. Start Codons: The codon which starts the translation process is known as start codon. It is also known as **initiation codon** because it initiates the synthesis of polypeptide chain. Example of this codon is AUG. This codon also codes for the amino acid methionine. In eukaryotes, the starting amino acid is **methionine,** while in prokaryotes it is **N-formyl methionine.**

3. Stop Codons: Those codons that provide signal for termination of polypeptide chain are known as stop codons. These codons are also known as **termination codons** because they provide signal for the termination and release of polypeptide chain. Examples of stop codons are UAA, UAG and UGA. Since stop signal codons do not code for any amino acid they were earlier called as **non-sense codons.**

1st letter (5′)	2nd letter: U	2nd letter: C	2nd letter: A	2nd letter: G	3rd letter (3′)
U	UUU phenyle-alanine	UCU serine	UAU tyrosine	UGU cysteine	U
	UUC phenyle-alanine	UCC serine	UAC tyrosine	UGC cysteine	C
	UUA leucine	UCA serine	UAA STOP ocher	UGA STOP opal	A
	UUG leucine	UCG serine	UAG STOP amber	UGG tryptophan	G
C	CUU leucine	CCU proline	CAU histidine	CGU arginine	U
	CUC leucine	CCC proline	CAC histidine	CGC arginine	C
	CUA leucine	CCA proline	CAA glutamine	CGA arginine	A
	CUG leucine	CCG proline	CAG glutamine	CGG arginine	G
A	AUU isoleucine	ACU Threonine	AAU asparagine	AGU serine	U
	AUC isoleucine	ACC Threonine	AAC asparagine	AGC serine	C
	AUA isoleucine	ACA Threonine	AAA lysine	AGA arginine	A
	AUG START met	ACG Threonine	AAG lysine	AGG arginine	G
G	GUU valine	GCU alanine	GAU aspartic acid	GGU glycine	U
	GUC valine	GCC alanine	GAC aspartic acid	GGC glycine	C
	GUA valine	GCA alanine	GAA glutamic acid	GGA glycine	A
	GUG valine	GCG alanine	GAG glutamic acid	GGG glycine	G

Fig. 1.36 Genetic code table

Characteristics of Genetic Code

1. The genetic code is a triplet code where three adjacent bases of mRNA form a codon, specify one amino acid.

2. Genetic code always non-overlapping, adjacent codons do not overlap each other.

3. There is no punctuation in the genetic code i.e., genetic code is comma (,) less.

4. The genetic code is universal i.e., a given codon specifies the same amino acid in all protein synthesizing organisms.

5. The genetic code lacks specificity and one amino acid often has more than one code triplet. This phenomenon is known as **redundancy or degeneracy.**

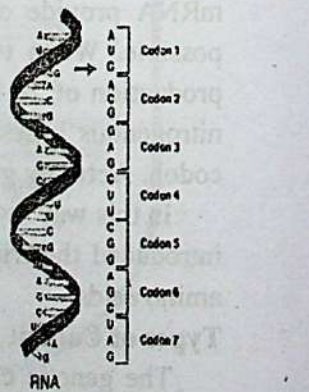


Fig. 1.37 Genetic code

For example, the amino acid phenylalanine (Phe) is specified by the codons UUU and UUC, and the amino acid leucine (Leu) is specified by the codons CUU, CUC, CUA, and CUG.

6. Each codon codes for only one amino acid, none for more than one.

7. Three of the 64 codons, names UAA, UAG and UGA do not specify any amino acid but signal the end of the message. They are called **nonsense** or **terminator codons.**

8. The codon AUG is called the initiation or start codons as they begin the synthesis of polypeptide.

9. The genetic codes have definite 5→3 polarity.

Did You Know?

- Eukaryotic cells are 10 times larger than prokaryotic cells, simply because they have a nucleus
- We have approximately 100 trillion cells in our body! A typical cell is 10 micrometers in size and 1 nanogram in mass.
- The longest cells in the human body are the motor neurons. They can be up to 4.5 feet (1.37 meters) long and run from the lower spinal cord to the big toe.
- Prokaryotic single-celled organisms were the earliest and most primitive forms of life on earth.
- Scientists have estimated that about 95% of all the cells in the body are bacteria. The vast majority of these microbes can be found within the digestive tract.
- When a cell becomes damaged or undergoes some type of infection, it will self destruct by a process called apoptosis. Apoptosis works to ensure proper development and to keep the body's natural process of mitosis in check. A cell's inability to undergo apoptosis can result in the development of cancer.
- The mitochondria can quickly change shape and move around the cell when needed. It can reproduce by growing larger and then dividing, when the cell needs more energy
- If you put all the DNA molecules in your body end to end, the DNA would reach from the Earth to the Sun and back over 600 times
- If you could type 60 words per minute, eight hours a day, it would take approximately 50 years to type the human genome.
- The DNA in every cell of human body is damaged 1,000 to 1 million times every single day. Luckily, our body has an elaborate system of repairing those damaged DNAs constantly. When the repairing mechanism fails events like cellular death or cancer formation takes place.
- Important functions such as coding and decoding, transcription, regulation and expression of genes, protein binding etc. are carried out by RNA.