UNIT 5 MACROMOLECULES OF THE CELL

Structure

5.1 INTRODUCTION

In Unit 4, you have learnt about the small basic molecules present in a cell-like water, amino acids, nucleotides, sugars and fatty acids and also about various techniques used for the isolation and purification of macromolecules.

In this unit you will study about large molecules present in various life forms ranging from bacteria to man. These macromolecules namely proteins, nucleic acids, lipids and carbohydrates have a common molecular organisation in different forms of life. These macromolecules of life are constantly in a state of flux. Here, you will study the various types of bonds and non-bonded interactions which help to unite the basic molecules to form these macromolecules and give them a structure and shape.

In the previous unit, you have studied about amino acids, which are the basic structural unit of proteins. Here, information is provided about how these molecules play a key role in all biological processes, and how polypeptides chains fold upon themselves and produce the specific three-dimensional structure of proteins. Proteins play an important role in carrying information from cytoplasm to nucleus, for example some promotors and repressor are proteins in nature. Proteins also mediate a wide range of other functions, such as mechanical support, transport and storage, coordinated movements, excitability, immune protection, and the control of growth and differentiation. The other important informational molecules in the cell are the nucleic acids which store, transmit and carry out the genetic information from one generation to the next. We will also discuss here about the structure and general properties of carbohydrates and lipids which are also called "non-informational molecules". Carbohydrates are the immediate source of energy, whereas lipids store energy and are the essential components of membrane structure.

Before you go in details of this unit, it is important that you must have studied Unit 4 carefully. You should also refresh your memory about the structure of an atom.

Objectives

After you have studied this unit you should be able to:

- explain different types of bonds that hold atoms and molecules together,
- identify the primary, secondary, tertiary and quaternary structures of a protein,
- distinguish between the structures of DNA and RNA,
- define polysaccharides, mucoplysaccharides, glycoproteins, proteoglycans, glycosaminoglycans, and
- list important lipids and the site of their occurrence.

5.2 TYPES OF BONDS

Macromolecules are held together by different types of chemical bonds. On the basis of energy required or released to break during bond formation or breakage, these bonds have been classified into two types, i.e., strong and weak bonds (Table 5.1). **Strong bonds** preserve the structure of macromolecules and require greater amount of energy to break. **Covalent bonds** are strong type of bonds (see Fig. 5.1(a)). Glycosidic, peptide, and nucleotide bonds are examples of covalent bonds. These are formed by sharing of electrons between two electronegative atoms. As you will proceed, you will study in detail about glycosidic, peptide and nucleotide bonds in Sections 5.3, 5.4 and 5.5. Hence, our main emphasis in this section will be on weak bonds. **Weak bonds,** called **non covalent bonds** help to carry the information and require much less energy to break. Weak bonds include hydrogen bonds, hydrophobic bonds, ionic bonds, and van der Waals forces (Table 5.1).

Table 5.1
Energies released/consumed during bond breakage/formation

Types of Bond		Bond energy kilojoules/mole
STRONG BONDS		
Covalent bonds		
Single bonds	O - H	462
	H - H	436
	S - S	426
	C - H	415
	C - O	356
	C - C	347
	C - N	292
Double bonds	C = O	723
	C = C	602
WEAK BONDS		
Ionic Bonds	NaCl	408
(In the absence of water)	NaI	304
Hydrogen Bonds		33 - 175
Hydrophobic Bonds (van der Waals attractions)		33

Hydrogen bonding is very common in biological systems. Hydrogen bonding is very important in maintaining three-dimensional structure of nucleic acids, protein molecules and specially of water (Fig 5.1b). In the absence of hydrogen bonding, water would have been in the gaseous state at room temperature and this would have made the existence of life impossible (Fig 5.1 c).

Non-polar molecules or groups tend to hold themselves together in the interior, when in water due to repulsion for water. These interactions are called **hydrophobic interactions** (hydro=water, phobia= repulsion). Dispersed oil droplets coming together in water to form a single large oil drop is a familiar example of hydrophobic interaction (Fig. 5.1 d).

Ionic or electrostatic bonds are formed by transfer of electrons between oppositely charged atoms, e.g., between Na^+ and Cl^-. Ionic bonds are very strong (like covalent bond) in the absence of water. However, they are quite weak (like hydrogen bond) in the presence of water (Fig. 5.1 e). Ionic bonds are very important in binding of enzyme and substrate.

Dipole: A molecule carrying positive and negative charges spatially separated at opposite ends of the structure.

When two atoms are not too far, i.e. distance between a pair of atoms is not more than one angstrom (1°A) they tend to interact due to the instantaneous dipoles induced. The fluctuating electrical charges set up between the nuclei and the electrons create a weak ionic interaction. This type of attraction is known as **van der Waals force** (Fig. 5.1 f). van der Waals forces break down easily when exposed to heat, because the strength of this bond is slightly more than the average molecular thermal energy at room temperature.

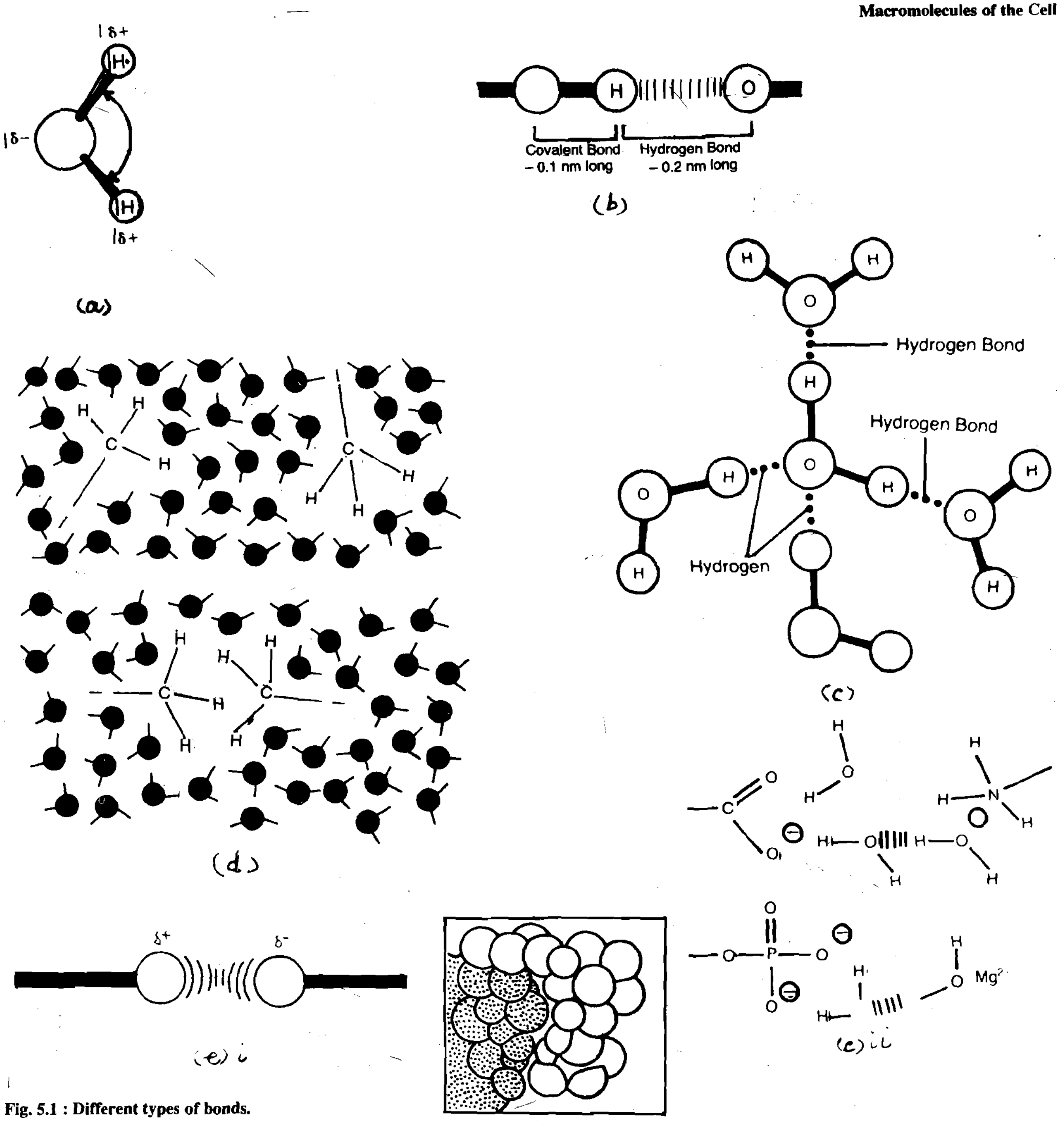

Fig. 5.1 : Different types of bonds.

a) Covalent bonds

Covalent bonds are strongest bonds formed by sharing of one or more electron pairs by the atoms. A water molecule consists of two hydrogen atoms and one oxygen atom joined by covalent bonds. The δ^+ and δ^- indicate a slight positive and negative charges on the molecules which is due to shifting of electrons to the more positively charged nucleus of oxygen.

b) Hydrogen bonds

For the formation of hydrogen bond a hydrogen atom is shared by two electronegative atoms, for example, the bond between an oxygen and nitrogen atoms and between two nitrogen atoms. Such bonds are predominantly found in proteins and nucleic acids.

c) Hydrogen bonds in water

Due to weak electrical charges, the water molecules are joined by hydrogen bonds transiently.

d) Hydrophobic bonds

A weak interacting force between water repelling, nonpolar residues and molecules, such as between fatty acid chains of membrane phospholipid or between aromatic bases in DNA.

e) Ionic bonds

These bonds are very strong in the absence of water. The force of attraction between the two charges, (+) and (–) is $F = \frac{q_1 q_2}{r^2 D}$. Where D= dielectric constant (1 for vacuum, 80 for water), r= distance between two molecules, q_1 and q_2 are the charges. Ionic bonds become weak in presence of water.

f) van der Waals force

A non specific, weak chemical interaction resulting from attractive forces produced two atoms or groups of atoms when they come near each other.

SAQ 1
Why do ionic bonds become weak in the presence of water?

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5.3 PROTEINS

Proteins are nitrogenous compounds of high molecular weight. These are the major building material of cells and take part in controlling different activities of living systems. Proteins are made-up of amino acids that are covalently linked with each other by peptide bonds. The number of amino acids in a peptide chain varies. Simple proteins consist of only amino acids, whereas complex proteins have other substances like lipids and carbohydrates also.

Proteins are classified into seven types on the basis of their biological functions (Table 5.2).

Table 5.2
Classification of Proteins according to Biological Functions

	Class	Example	Functions
i)	Enzymes	Ribonuclease, Trypsin	Help in catalysing chemical reactions in living cells
ii)	Transport proteins	Haemoglobin, Serum albumin, Myoglobin, —Lipoprotein	Involved in the transport of molecules and ions across the membranes
iii)	Nutrient and storage proteins	Gliadin (wheat), Ovalbumin (egg), Casein (milk), Ferritin	Provide the essential components by storing them in the body
iv)	Contractile or motile proteins	Actin, Myosin, Tubulin, Dynein	Coordinate movements such as movements of chromosomes in mitosis
v)	Structural proteins	Keratin, Fibroin, Collagen, Elastin, Proteoglycans	Essential components of various cells and tissues
vi)	Defence proteins	Antibodies, Fibrinogen, Thrombin, Dotulinus toxin, Diphtheria toxin, Snake venoms Ricin	Help in protection against harmful agents such as bacteria and virus
vii)	Regulatory proteins	Insulin, Growth hormone, Corticotropin, Repressors	Control of growth and differentiation

The polypeptides which form proteins after being synthesised on ribosomes in linear chains are biologically inactive. But within a few seconds after their synthesis, the folding of polypeptide chain occurs in specific forms to give functionally active proteins which have many levels of organisation. These levels are expressed as primary, secondary, tertiary and quaternary structures. The **primary structure** of a protein refers to the number, type, and position of the individual amino acids in a polypeptide chain. A peptide bond is a covalent bond between the carboxyl group of one amino acid and the amino group of the adjoining amino acid. One molecule of water is removed in the formation of one peptide bond. A polypeptide chain thus will have only one free amino(-N or -NH_2) terminal and one free carboxyl (-C or -COOH) terminal (Fig. 5.2 a).

Secondary structure: The local structure of a polypeptide or nucleic acid chain arising from chemical bonding between the neighbouring residues to produce forms such as stem and loop of transfer RNA and α helix or beta sheet configuration in polypeptides.

α - helix is a major secondary structure in polypeptides, characterised by regularly repeated hydrogen bonding between C = O and N - H groups in the chain.

Secondary structure of a protein is determined entirely by the primary structure. The secondary structure is formed by the folding of a polypeptide chain. The folded chain is held together by hydrogen and disulphide bonds. Hydrogen-bonding interactions between peptide bonds are responsible for regular folding pattern like α-helix and β sheets. In an α-helix such as in α-keratin fibres and myoglobin the chain itself turns regularly to make a rigid cylinder. The tightly coiled polypeptide main chain forms the inner part of the rod, and the side chains extend outward in a helical array. The helix is stabilised by hydrogen bonds between residue one and five of the amino acids (Fig. 5.2 b, i & ii). Number of amino acid residues per turn comes to 3.6. In a β sheet such as in silk fibroin and parts of immunoglobulin, the polypeptide chain itself folds back and forth. In β pleated sheet, all peptide linkages participate in the formation of hydrogen bonds to provide stability. Many beta sheets are slightly twisted, which are known as beta turns. The same polypeptide may form α-helix as well as β sheets (Fig. 5.2 b, iii & iv).

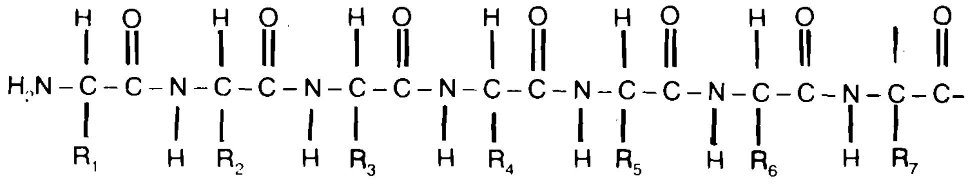
Tertiary structure of the protein is the characteristic overall shape assumed by arrangement and interrelationship of helical and non-helical regions of a polypeptide chain(s). It is the final folding of the chain involving non-covalent interactions between the distantly located residues. Functional regions of a protein are called domains such as the active site of an enzyme (Fig. 5.2 c).

Quaternary structure of a protein is made by the association of two or more polypeptide chains or subunits that fit together in a specific arrangement by non-covalent interactions—the stabilising force for such interactions. For example, haemoglobin molecule is formed by the association of two α polypeptide chains and two β chains (Fig. 5.2 d).

β pleated sheet is almost fully extended rather than being tightly coiled as in α helix. It is called β because it was their second structure. The α helix being the first.

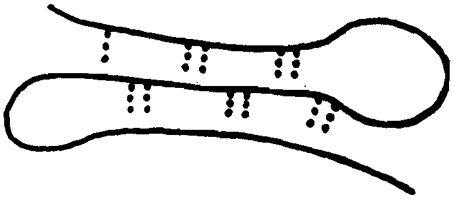
Tertiary structure: The three dimensional folding of a polypeptide or polynucleotide chain brought about by interactions among side groups or other residues at some distance from one another in the primary structure of the molecule.

Quaternary structure: Specific assemblies in a protein composed of two or more polypeptide chains that have different properties in the protein molecules than they would as individual chains.

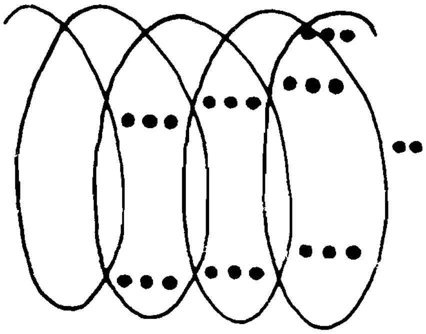


$$H_2N-\underset{R_1}{\overset{H}{C}}-\overset{O}{\overset{\|}{C}}-\underset{H}{N}-\underset{R_2}{\overset{H}{C}}-\overset{O}{\overset{\|}{C}}-\underset{H}{N}-\underset{R_3}{\overset{H}{C}}-\overset{O}{\overset{\|}{C}}-\underset{H}{N}-\underset{R_4}{\overset{H}{C}}-\overset{O}{\overset{\|}{C}}-\underset{H}{N}-\underset{R_5}{\overset{H}{C}}-\overset{O}{\overset{\|}{C}}-\underset{H}{N}-\underset{R_6}{\overset{H}{C}}-\overset{O}{\overset{\|}{C}}-\underset{H}{N}-\underset{R_7}{\overset{|}{C}}-\overset{O}{\overset{\|}{C}}-$$

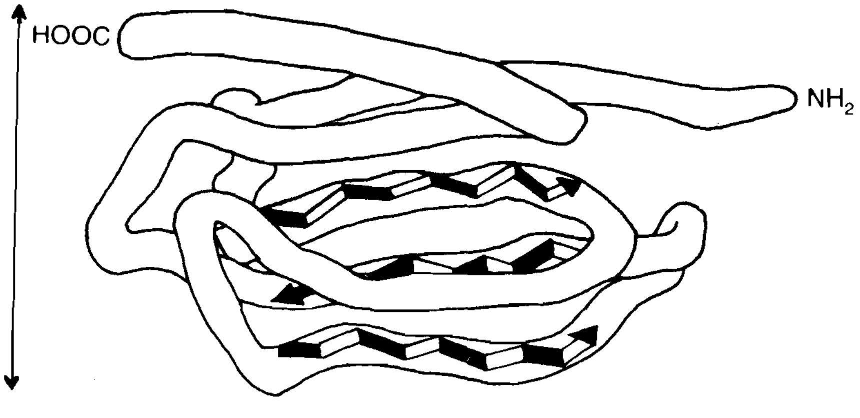
(a)

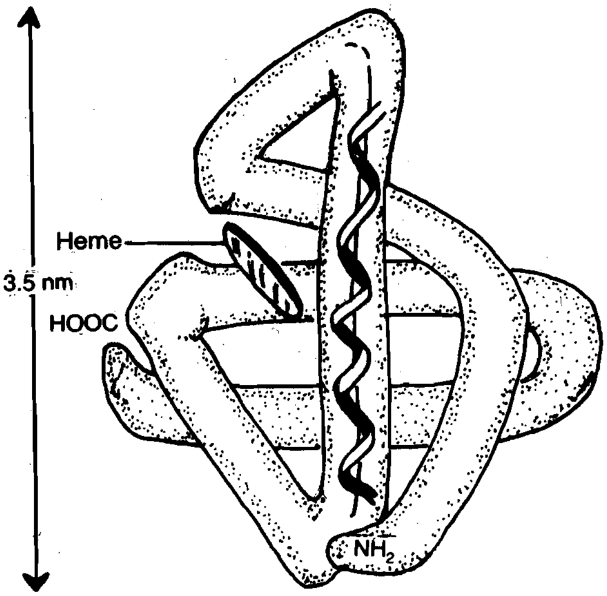


(b) i

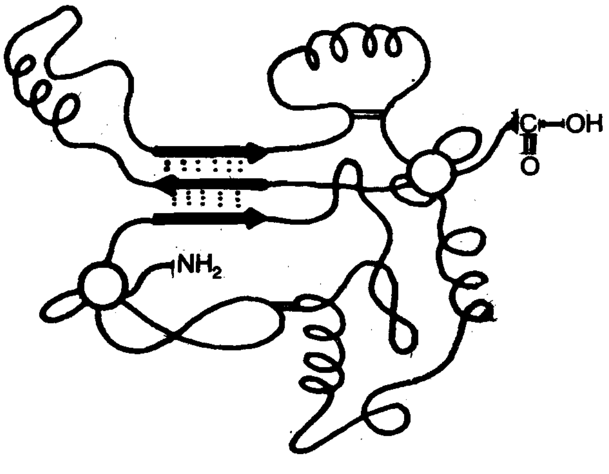


(b) ii

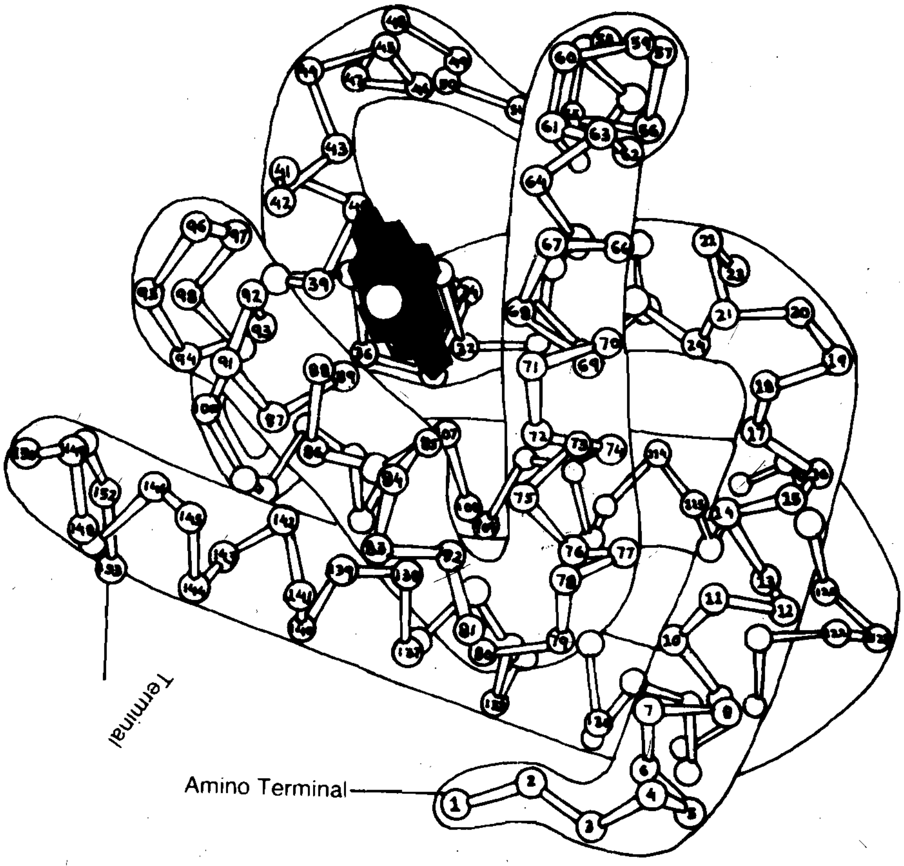




(b) iv



(c) i



(c) ii

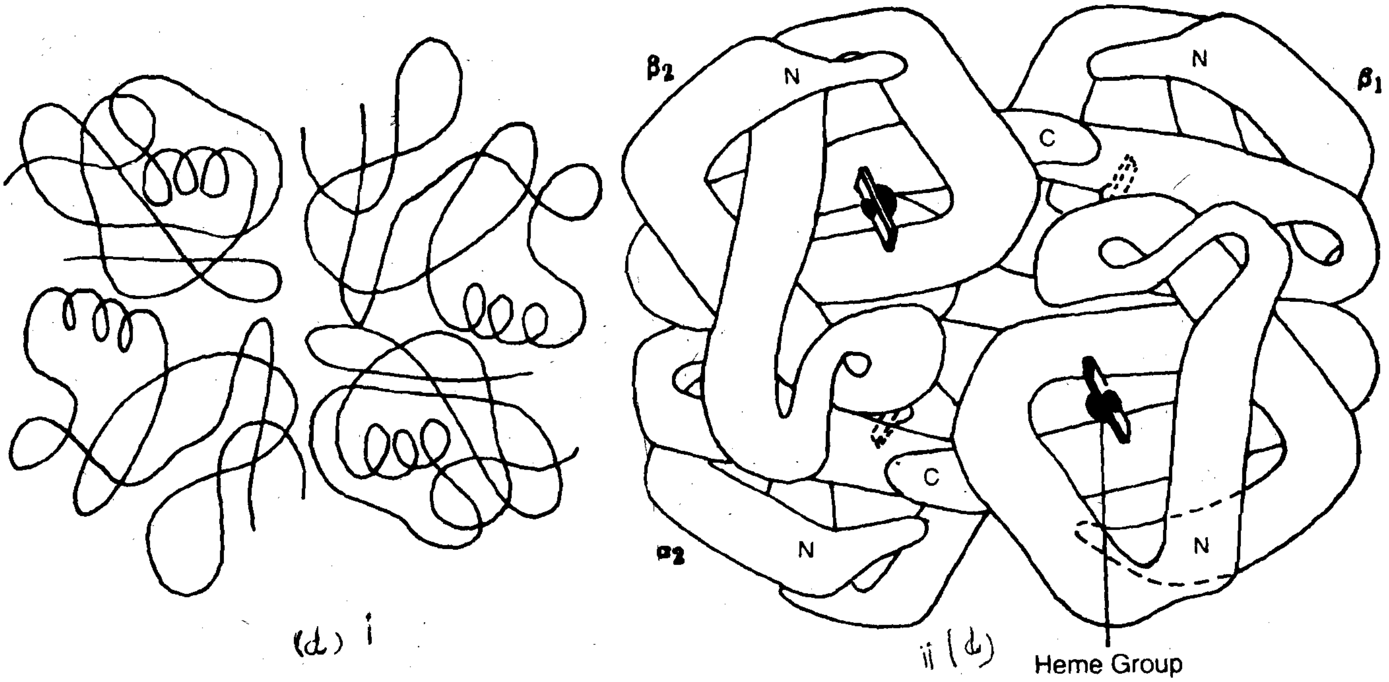


Fig. 5.2 : Different levels of protein structure
a) Primary structure. Amino acids in the chain are linked together by peptide bonds to form linear polypeptide chains with the removal of water molecule.
b) Secondary structure. In α-helix, the R groups of amino acids are directed radially away from the axis of helix. Every peptide bond is hydrogen bonded to a neighbour. Though the direction of helix can be right handed as well as left handed, right handed alpha helices are common. β-pleated arrangement of polypeptide are common and are present in many fibrous and most globular proteins.
c) Tertiary structure. Myoglobin molecule has eight helical segments. The spaces between loops of the chain are filled with R groups (not shown here).
d) Quaternary structure. The haemoglobin molecule consists of four polypeptide chains: two alpha globin and two beta globin chains. With each chain an oxygen binding heme group is attached.

Changes in pH or heating of protein molecules breaks protein polymers into monomers. The degradation results from loss of tertiary and secondary structure of monomers which leads to the loss of biological activity of the proteins. This disruption of native structure is termed as **denaturation**. Proteins regain their original structure when they return to their normal surroundings.

Diversity of protein molecules is due ~~to~~ the number, kinds and sequence of amino acids in a polypeptide chain. Change in amino acid sequence disrupts the structure of a protein, which thereby causes functional abnormality. For example, the change of even one amino acid residue in a chain of 146 residues of haemoglobin chain may bring about morphological and clinical changes in man causing the disease **sickle cell anemia** in which the capacity of red blood cells for oxygen uptake is impaired (Fig 5.3).

Residue: The main part of a molecule that is left after a small group has been removed in binding the molecule to another molecules.

	1	2	3	4	5	6	7	146
Hb A	Val –	His –	Leu –	Thr –	Pro –	$\boxed{\text{Glu}}$ –	Glu –	Lys – – – –
	Val –	His –	Leu –	Thr –	Pro –	$\boxed{\text{Val}}$ –	Glu –	Lys – – – –
Hb C	Val –	His –	Leu –	Thr –	Pro –	$\boxed{\text{Lys}}$ –	Glu –	Lys – – – –

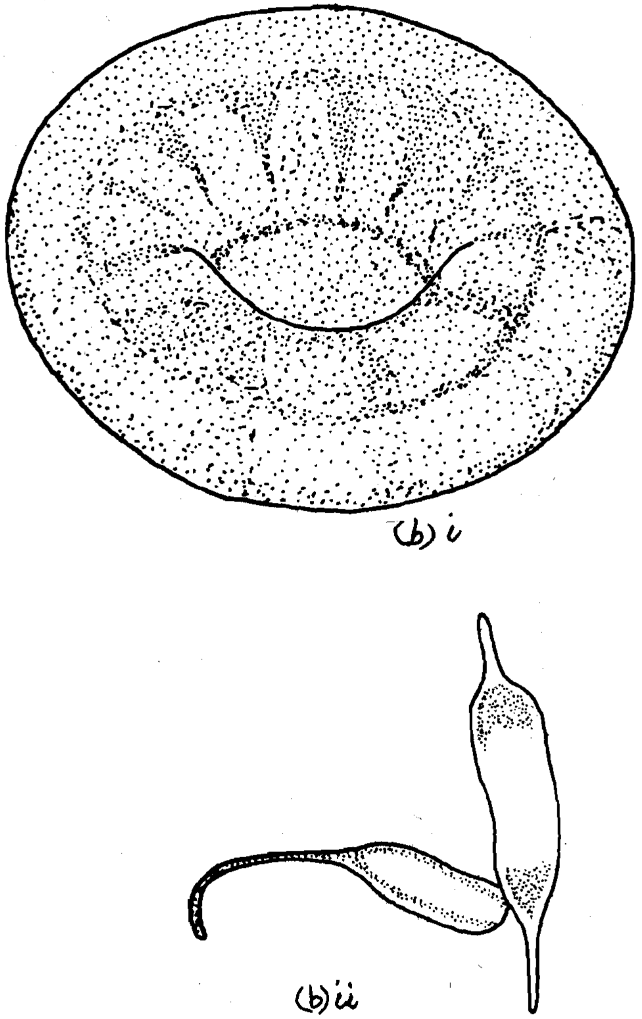


Fig. 5.3 : a) In normal haemoglobin of an adult (HbA), the sixth amino acid in the beta chain from the amino terminal is glutamic acid. In haemoglobin of the sickle cell (HbS), glutamic acid is replaced by valine, but the remaining 145 amino acids are unchanged.
b) Normal human red blood cells (i) are discoidal in shape; these-cells during low oxygen concentration become sickle shaped (ii) sickling of red blood cells causes the disease, known as sickle cell anaemia.

SAQ 2

Write the structure of the tetrapeptide derived from glutamic acid, lysine, asparagine and serine indicating the peptide bond clearly in the given space (see Section 4.2 of Unit 4 for structures of amino acids).

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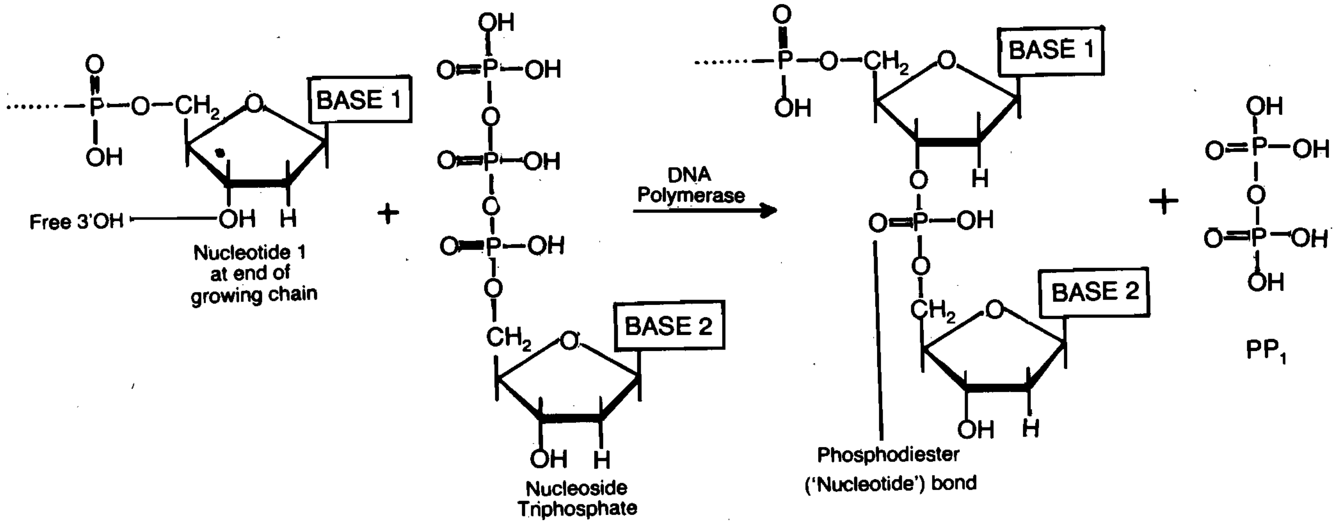
5.4 NUCLEIC ACIDS

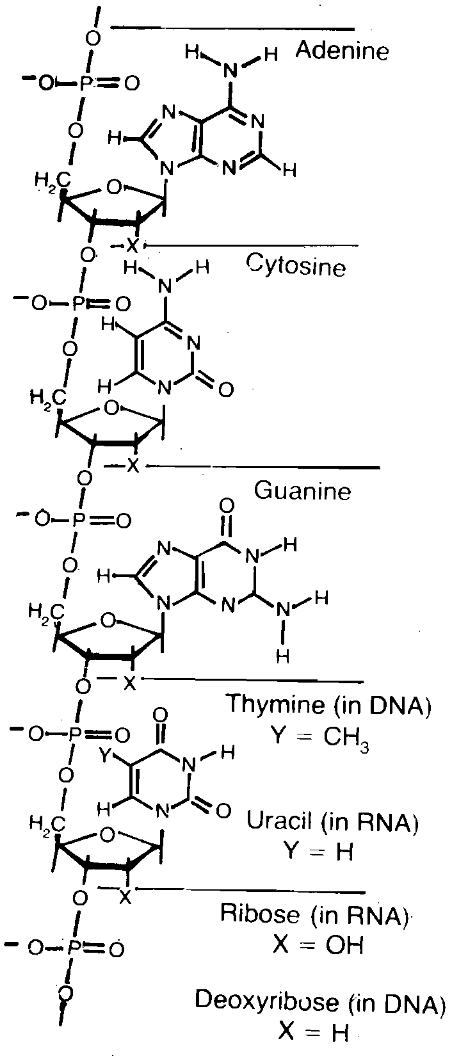
Nucleic acids are the genetic material in living organisms. Genetic information contained in each cell is encoded as polynucleotide in the form of nucleotide sequence. Information in the form of base pairing interactions of the nucleic acids is passed on from one generation to the next. There are two types of nucleic acids: deoxyribose nucleic acid (DNA) and ribose nucleic acid (RNA). In Unit 4, you have already studied about the monomers of nucleic acids, the nucleotides. We shall now discuss about the structure of nucleic acids in more detail.

5.4.1 Deoxyribo Nucleic Acid (DNA)

DNA is a basic molecule found in the cells. In 1953 Watson and Crick of Cambridge University proposed a molecular model for DNA for which they were awarded the Nobel Prize in 1962. They based their model on the observation of X-ray diffraction studies and on chemical analysis. The total quantity of DNA in eucaryotic cells is much higher than in procaryotic cells (see Unit 1).



(a)



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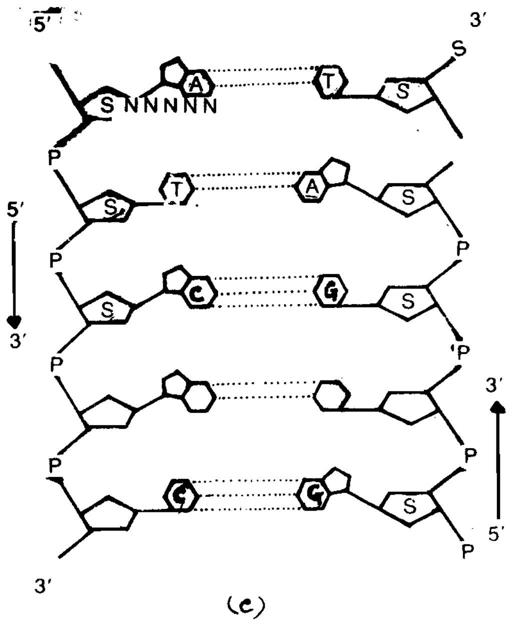

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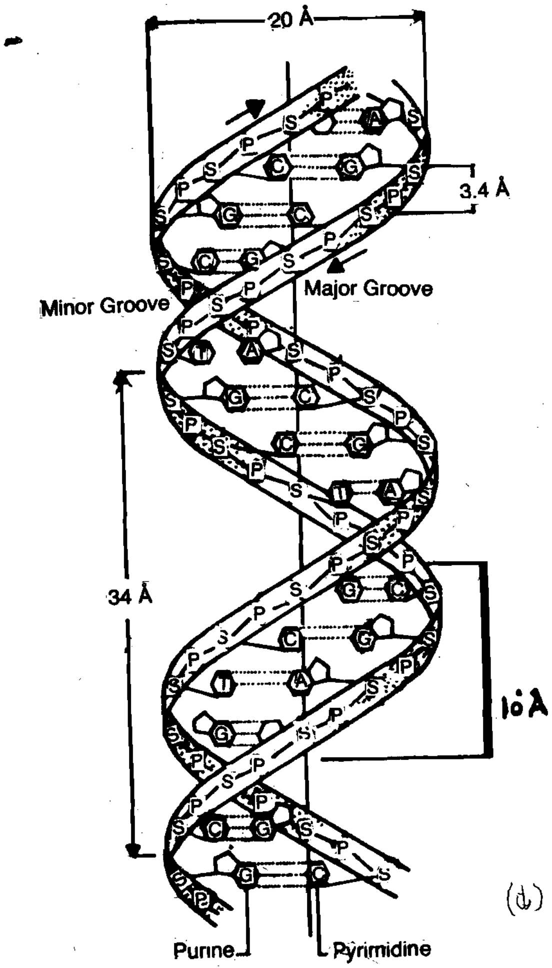

Fig. 5.4 : a) A nucleoside triphosphate. (Base 2) aligns itself to base 1 correctly. DNA polymerase enzyme links it to 3′ end and releases two phosphate groups as pyrophosphates (PPi).

b) A single nucleic acid chain showing the nucleotides. X=H in DNA (deoxyribose) and X=OH in RNA (Ribose). $Y=CH_3$ in DNA (Thymine) and Y=H in RNA (Uracil).

c) Molecular structure of DNA showing the pentose sugar (s)-phosphate(p) backbone of polynucleotide chain. The two strands are complementary and antiparallel in nature. By convention the base sequence in single strand of DNA is written from 5' end on left to 3' end on the right, or a p (for phosphate) is prefixed for free 5' making its - phosphoryl end.

d) DNA double helix showing major and minor grooves and some other molecular dimensions. The ribbons indicate phosphate deoxyribose backbones. Horizontal lines represent the base pairing. P=phosphate group, S=sugar.

The 5′ carbon of the deoxyribose sugar of one nucleotide is joined to 3′ carbon of deoxyribose sugar of the next nucleotide by a phosphodiester bond known as nucleotide bond or bridge (Fig 5.4 b). Phosphate group of the nucleotide can form an ester bond with both, the 3′ and 5′ -OH group of a pentose sugar and, therefore, the bond is known as **phosphodiester bond.**

A nucleic acid chain has one free 5' phosphoryl end and one free 3' hydroxyl end. The backbone of DNA is highly polar due to the presence of phosphate group which is acidic at the pH of the cell.

DNA molecule has two chains or strands which are known to be antiparallel as their 5'-3' polarity runs in opposite directions. Structure of a DNA molecule is helical and ladder-like, with steps made up of bases and the two sides (backbones) made up of sugar and phosphate residues (Fig. 5.4c). Nitrogenous bases of the two strands in a molecule are connected with each other by hydrogen bonds, which stabilise the DNA molecule.

Antiparallel: Alignment of the two DNA strands in a helix with their 3',5' phosphodiester linkages in opposite directions.

The base pairing is one of the most fundamental concepts of DNA structure and function and always occurs between a purine and pyrimidine due to the geometry of the double helical structure (see below). Adenine (A) forms hydrogen bonds only with thymine (T); and guanine (G) only with cytosine (C). This is called as **complementary base pairing**. Three hydrogen bonds are formed between G and C (G≡C) but only two between A and T (A=T). The GC pairing is, therefore, chemically more stable than AT pairing.

SAQ 3

If one strand of double helix of DNA has a base sequence of 5'-ATCGAACGT-3', what would be the base sequence of the complementary DNA strand?

(**Hint**: Complementary base pairing A-T and G-C.)

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DNA, The Double Helix

Double helix: Physical configuration typically adopted by the polynucleotide chains of DNA.

The two strands of the DNA form a helical structure, known as the **double helix**. It is important to mention here that DNA exists in five forms, i.e. A,B,C, D and E. Of these, B form is the most common about which we will discuss in detail here. It is a right handed helix and most commonly found in living system. The other forms have only minor differences. The spatial relationship between the two strands of the helix forms a major groove or wide groove and a minor groove or narrow groove (Fig. 5.4.d).

Each complete turn of helix is 3.4 nm long and contains 10 base pairs (bp). Therefore, the consecutive base pairs are 0.34 nm (3.4/10) apart and are inclined at 36° in relation to each other. The helix has a constant diameter of about 2 nm, hence, the dimensions of each base pair must be constant. Each base pair contains one two-ringed purine (1.2 nm long) and one single-ringed pyrimidine (0.8 nm long) so as to keep the dimensions of each base pair constant. A base pair formed by two purine bases or by two pyrimidine bases will, therefore, distort the helical structure.

DNA structure fulfils the basic requirement of the genetic material that means it must be copied accurately with every cell division. The accurate copying of DNA, i.e. DNA replication, is due to the complementary nature of the bases in the two strands of DNA: A pairing with T, and G pairing with C.

Complexes of DNA and Protein (Nucleosomes)

DNA in chromosomes is always associated with proteins and it coils on the protein to give rise to a highly compact tertiary structure.

A chromosome, which is a thread-like structure found in nucleus, consists of chromatin. Chromatin network contains about 60 per cent protein, 35 per cent DNA and 5 per cent RNA. On suitable treatment, chromatin can be seen under the electron microscope in its expanded form. It appears as "beads on a string" (Fig. 5.5) and these are known as **nucleosomes**. The "bead" or the nucleosome core is ellipsoidal in shape with a diameter of 11 nm, height of 6 nm and circumference of about 34 nm.

On biochemical analysis, a nucleosome is found to contain two molecules of each of the histones, H2A, H2B, H3 and H4 forming an octomeric protein disc, one molecule of histone H1 and a DNA strand of about 200 base pair long (Fig. 5.5).

DNA fragment of 140 base pairs is wrapped like a ribbon around the histone octamer. It is because this much length of DNA (67nm) may not be squashed (pressed) inside the small protein disc. Sensitivity of DNA to enzymes also supports the idea of DNA being on the outside of the protein disc of the 200 base pair DNA because the increased surface area of DNA will provide more space for enzyme reaction. About 140 base pair is sufficient to make two turns around the protein disc.

The remaining 60 base pair act as a linker or spacer DNA and joins the repeated nucleosome cores. Histone H1 is associated with DNA, at the entry and exit points of DNA from the core. It is involved in close packaging of the nucleosomes to form a 30 nm thick chromatin fibre.

5.4.2 Ribose Nucleic Acid (RNA)

Transcription: Process by which an RNA molecule is synthesised on a DNA template with the aid of various enzymes.

As you have studied in the previous section, DNA stores the genetic information which is transferred from nucleus to cytoplasm by transcribing to the RNA molecules. These RNA molecules translate the information to synthesise proteins. The primary structure of RNA is

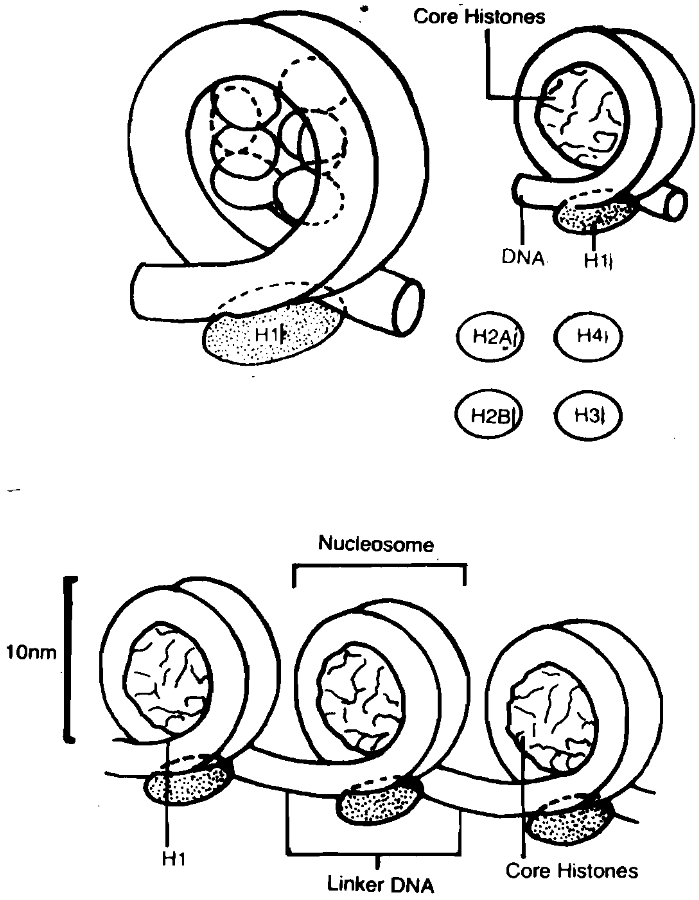


Fig. 5.5 : Chromatin appearing as beads on a string. Each nucleosome bead is connected to its neighbour by a linker DNA. Beads are released from chromatin by digestion of the linker DNA with micrococcal nuclease enzymes. Each bead has an octamer histone core around which 146 base pair DNA is wrapped.

comparable to that of DNA: a polynucleotide chain with 5′–3′ sugar phosphate backbone. But it differs from DNA as the pentose sugar in RNA is ribose instead of deoxyribose. Further, thymine is substituted by uracil in RNA (Table 5.3). All RNAs exist as non-helical single stranded structure. The molecules are much shorter than DNA and the ratio of purines and pyrimidines is not 1:1. However, RNA molecules may have complementary intramolecular regions. The complementary sequences in an RNA strand may fold back upon itself to form an antiparallel duplex structure known as the hairpin loop. Such complementary sequences are palindromic in nature. Palindrome is a stretch of DNA in which the base sequences read the same from the 3′ or 5′ end. In these regions, hydrogen bonds may be formed between A and U, and G and C. As in the case of DNA, base pairing provides stability to the RNA also.

Translation: Process by which a protein is synthesised from amino acids according to specifications encoded in the mRNA

Palindrome: A sequence of duplex DNA that is the same when the two strands are read in opposite direction such as **Malayalam** is a palindromic word with the sequence of letters on both sides of y being the same.

Table 5.3
Difference between DNA and RNA

Feature	DNA	RNA
1) Pentose sugar	Deoxyribose	Ribose
2) Nitrogenous base	Adenine, Thymine, Cytosine, Guanine	Adenine, Uracil, Cytosine, Guanine
3) Ratio of purines to pyrimidines	One	Variable
4) Secondary structure	Double stranded and helical	Single stranded and non-helical
5) Role in a eucaryotic cell	Carries genetic information	Synthesis of proteins
6) Localisation	Primarily in nucleus; also in mitochondria and chloroplast	Largely in cytoplasm, synthesised in nucleolus
7) No. of nucleotides	Contains a larger number of nucleotides, upto a few millions.	Contains much smaller number of nucleotides, upto a few thousands.

There are three major classes of ribonucleic acids (RNA) which can be distinguished structurally and functionally. These are messenger RNA (mRNA), transfer RNA (tRNA) and ribosomal RNA (rRNA). All these types of RNA are synthesised in the nucleus and are involved in protein synthesis.

The mRNA carries the genetic message, and it is a single stranded polymer. The length of mRNA depends upon the number of polypeptides it codes for.

The tRNA molecule serves as adaptor for the translation of genetic information in the sequences of mRNA into specific amino acids. The primary structure of tRNA is a single stranded nucleotide which folds back to align with the complementary regions to form a secondary structure like a clover leaf. You will study the structure of tRNA in detail in Units 13 and 14 with reference to protein synthesis.

The rRNA is a component of ribosome. The ribosome has a nucleoprotein structure and is the site for protein synthesis.

A comparison of 'three kinds of RNA' is made in Table 5.4. You will study about all these types of RNAs in detail in Units 13 and 14.

Table 5.4
Comparison among three kinds of RNA

Property	Ribosomal RNA	Messenger RNA	Transfer RNA
Sedimentation coefficient (S units)	5-7, 18, 28	8	4
Number of nucleotides	120-5500	900-12000	75-85
Molecular weight	$0.5\text{-}1.1 \times 10^6$	500,000	25,000
Unusual bases	small amount of methylated bases	small amount of unusual bases	large amount of unusual bases
Percentage of total cellular RNA	about 80	upto about 5	about 15-20
Site of synthesis	nucleolus	nucleolus	nucleolus
Role	serves as template for synthesis of ribosomal proteins	carries genetic information from chromosomal DNA to cytoplasmic ribosomes where it participates in protein synthesis.	acts as adaptor for specific amino acid attachment and transfer to mRNA template.

SAQ 4

Which of the following statements (i-iv) apply to

a) DNA only
b) RNA only
c) Both DNA and RNA

Write your answer (s) in the space provided.

[**Hint**: If a particular statement applies to DNA only then the answer will be (a) and if to RNA only then the answer will be (b) and if to both DNA and RNA, then the answer will be (c).]

Statements

i) Found mainly in the nucleus.

....

ii) Polynucleotide chain in which sugar is ribose.

....

iii) Contains equal number of purine and pyrimidine bases.

....

iv) Contains linked nucleotides.

....

5.5 CARBOHYDRATES

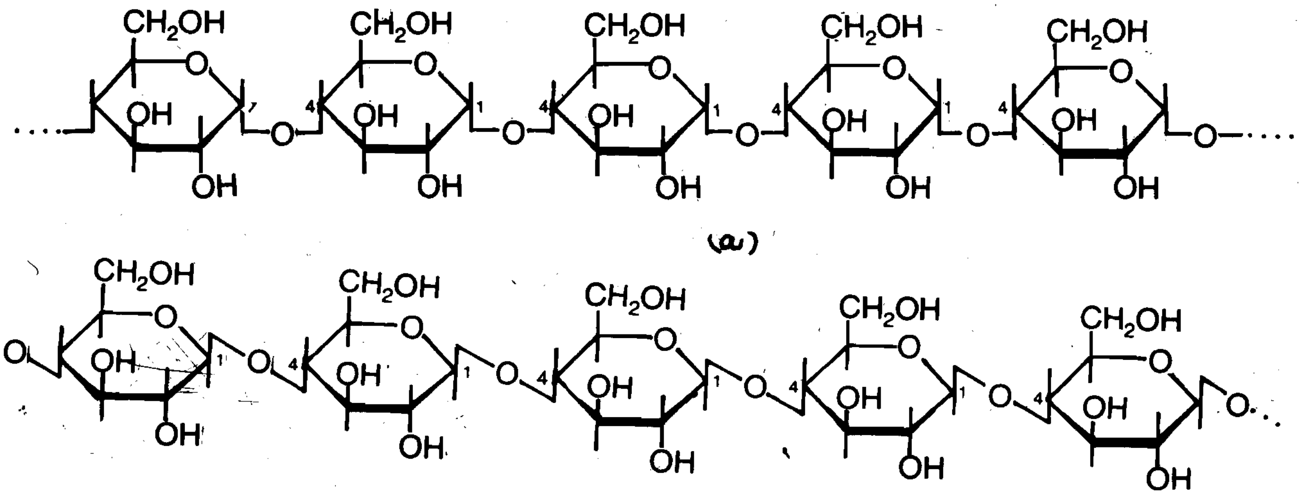
Carbohydrates, composed of carbon, hydrogen and oxygen, are the main source of cellular energy and are important structural components of cell walls and intercellular materials. Carbohydrates are classified into monosaccharides, disaccharides and polysaccharides according to the number of monomers they contain. You have studied in detail about monosaccharides and disaccharides in Unit 4, so we will discuss about the structure and function of polysaccharides in this unit.

Polysaccharides have the general formula $(C_6H_{10}O_5)_n$. They are polymers formed by condensation of large number of monomers such as glucose, fructose, etc. Major functions of polysaccharides are concerned with food storage and maintenance of cellular structure. In eucaryotes two structural polysaccharides are cellulose and chitin. Cellulose is found in plant cell wall, as well as in many algae and fungi. Chitin forms the exo-skeleton of many animals like arthropods (e.g. insects), many other invertebrates and also in many plants, e.g. fungi (Table 5.5).

Table 5.5
Some Naturally Occurring Polysaccharides

Distribution	Name	Chemical composition	Biological role
PLANTS	Cellulose	homopolymer of glucose, unbranched	the main structural component of plant cell walls
	Amylose	homopolymer of glucose, unbranched	food store : a component of starch
	Amylopectin	homopolymer of glucose, unbranched	food store : a component of starch
ANIMALS	Glycogen	homopolymer of glucose, more branched than amylopectin	food store, mainly in muscles and liver
	Chitin	unbranched non-glucose homopolymer of acetyl glucosamine and glucuronic acid	forms horny exo-skeleton in arthropods
	Chondroitin Sulphate	complex heteropolymer of galactosamine	structural component of cartilage

You have already learnt the structure of some common monosaccharides in Unit 4. Each monomeric unit is linked to the other by a glycosidic bond. The bond may be between carbon atom 1 of one monosaccharide and carbon atom 4 or 6 of the other monosaccharide. These may be α- or β-glycosidic bonds depending on the position of hydroxyl group at carbon atom -1. Amylose, cellulose and glycogen are all polymers of glucose molecules but differ in the way they are joined together (Fig. 5.6). Unlike mono and disaccharides (sugars), the polysaccharides are relatively insoluble in water and are therefore not sweet in taste.



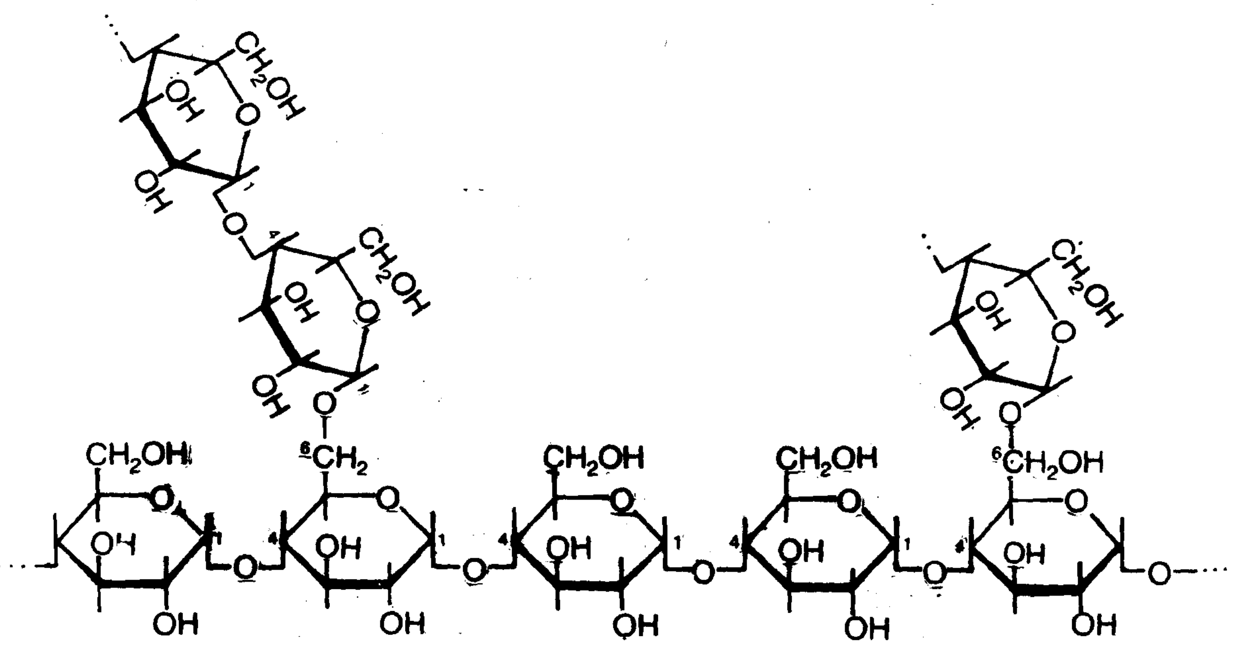


Fig. 5.6 : a) The 1-4 glycosidic bond between two glucose molecules showing a part of amylose molecule.
b) The 1-4 glycosidic bond between two glucose molecules showing a part of a cellulose molecule.
c) The 1-4 and 1-6 glycosidic bonds between glucose molecules which give rise to branched molecules of glycogen and amylopectin. Glycogen is highly branched, the ratio of 1,4 to 1,6 bonds being from 12 to 18, while amylopectin is less branched.

SAQ 5

Which carbon atoms of glucose are most commonly involved in glycosidic bond formation? Write your answer in 2-3 lines.

……………………………………………………………………………………………………

……………………………………………………………………………………………………

……………………………………………………………………………………………………

Complex Polysaccharides

In some of the hexoses, the hydroxyl group is replaced by amino, acetylamino, carboxyl or sulphate groups to form derivatives of monosaccharides (Fig. 5.7). These derivatives of monosaccharides combine together to form complex polysaccharides. Complex polysaccharides are important in molecular organisation. They are often found in combination with proteins or lipids.

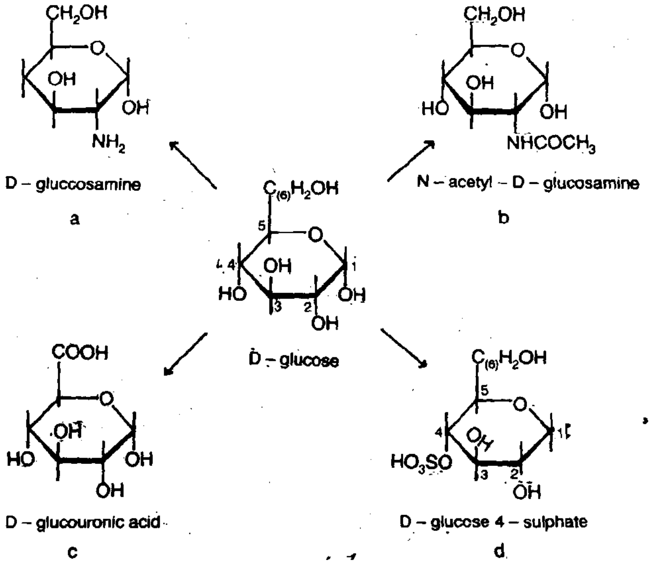


Fig. 5.7 : Derivatives of monosaccharides. The replacement of –OH group of D-glucose by –NH_2 (amino) group forms D-glucosamine (a); by -$NHCOCH_3$, (acetylamino) groups forms N-acetyle D-glucosamine (b); by-COOH (carboxyl)group forms D-glucouronic acid (c); and by OSO_3H sulphate group, forms D-glucose 4-sulphate (d).

Glycosaminoglycans, Proteoglycans and **glycoproteins** are examples of complex polysaccharides. Glycosaminoglycans are built up of repeating disaccharides units, generally composed of an amino sugar (either glucosamine or galactosamine) and a uronic acid (e.g. glucouronic acid). Glycosaminoglycans were formerly called mucopolysaccharides. Hyaluronic acid, chondroitin sulphate and heparin are a few examples of this class. Numerous glycosaminoglycan molecules in combination with small amounts of protein form proteoglycans, formerly known as mucoprotein.

The glycoproteins, on the other hand, are protein molecules with a few short or long carbohydrate side chains. It may be noted that proteoglycans are mainly glycans whereas glycoproteins are mainly proteins.

5.6 LIPIDS

Lipids are major structural components of the cells, and are a class of chemically diverse compounds with a common property. They are all insoluble in polar solvents such as water but are soluble in non-polar organic solvents such as ether and alcohol. This is because lipids contain hydrocarbon chains which are non-polar and hydrophobic. Since they contain fatty acids (about which you have studied in detail in Section 4.2 of Unit 4) with a free carboxyl end, they can undergo saponification (soap formation). Some of the commonly known lipids are classified in three groups (Table 5.6).

Table 5.6
Classification of Lipids

Lipid group	Class name	Cellular location of compounds
Fatty acids*	Fatty acids	Cytosol, mitochondria, glyoxysome of fatty seeds
Simple lipids (Esters of fatty acids with alchools)	Neutral fats (Triacylglycerols)	Fat storage in cytoplasm
Compound lipids (Simple lipids containing other group(s) in addition to fatty acids)	Phospholipids	Membranes
	Sphingolipids	Membranes
	Glycolipids	Membranes
Derived lipids	Steroids	Membranes
	Terpenes (Essential oils, caretenoinds)	Plant cytosol and chloroplast

* Fatty acids as such are not lipids but they are the essential components of lipids.

5.6.1 Simple Lipids

You have already studied the structure of fatty acids in Section 4.2 of Unit 4. Simple lipids are triacylglycerols, which are formed by the combination of three fatty acid molecules with a glycerol molecule (Fig. 5.8a). Triacylglycerols are non-polar, hydrophobic molecules and since they do not contain any charged groups, they are named as neutral fats. When oxidised, these fats produce energy more than twice of that given by carbohydrates or proteins.

In simple triacylglycerols such as tristearate glycerol or tripalmityl glycerol all the three fatty acid molecules (R_1, R_2, R_3) are of one type (Fig. 5.8 b). But in mixed triacylglycerols such as 1,2 distearopalmitin, more than one type of fatty acid molecules are joined to the same glycerol molecule (Fig. 5.8 c).

Most of the neutral fats, such as those in butter and olive oil are mixtures of simple and mixed triacylglycerols. Neutral fats containing only saturated fatty acids are solids at room temperature. Fats with largely unsaturated fatty acids like oleic and linoleic acid etc. remain liquid at room temperature and are known as oils. Oils are converted into fats by hydrogenation of the double bonds. That is how the vegetable ghee is produced. Oils, such as groundnut oil which contain unsaturated fatty acids are easily oxidised because of the presence of a large number of double bonds and hence they are spoiled easily. Saturated fats have better keeping quality.

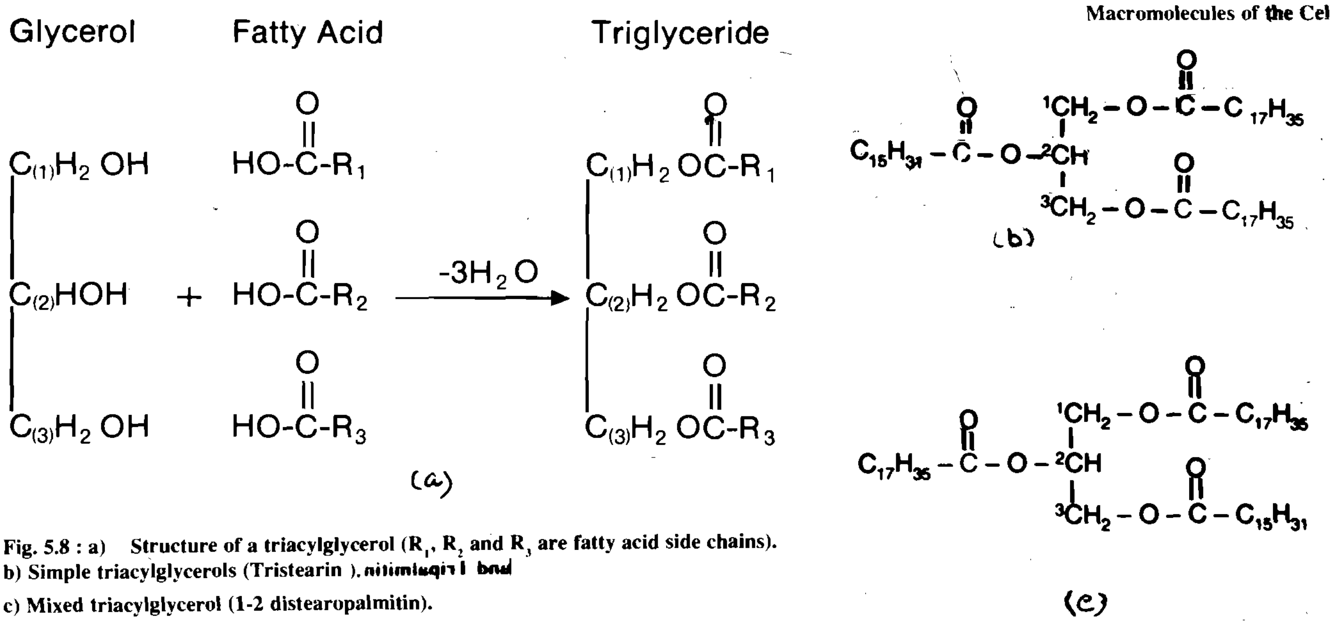
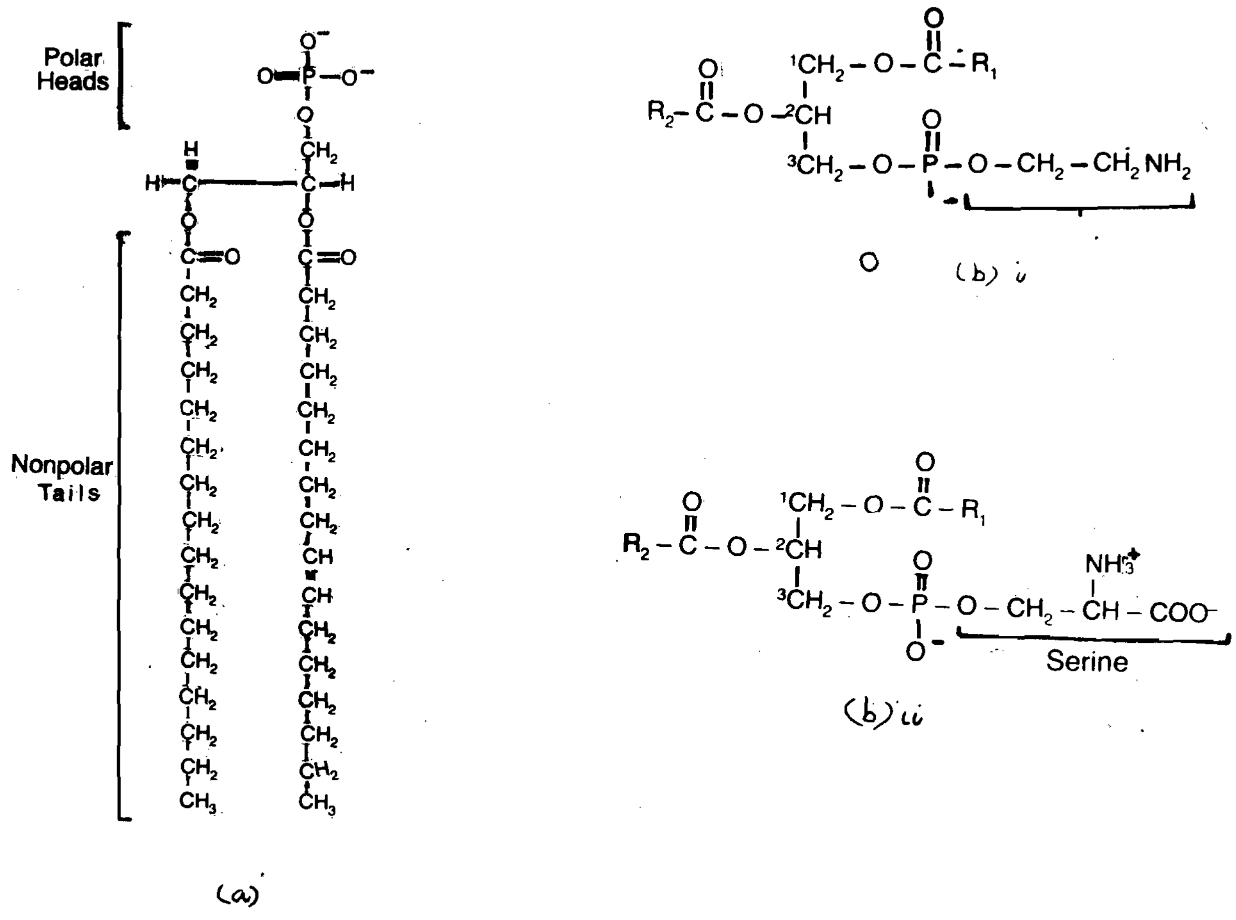


Fig. 5.8 : a) **Structure of a triacylglycerol (R_1, R_2 and R_3 are fatty acid side chains).**
b) Simple triacylglycerols (Tristearin). nitimlaqirT bna
c) Mixed triacylglycerol (1-2 distearopalmitin).

5.6.2 Compound Lipids

These are the lipids which are composed of glycerol, fatty acids, phosphoric acid and a nitrogenous compound such as choline, serine, ethanolamine etc. Major types of compound lipids are phospholipids, glycolipids, and sphingolipids. In phospholipids, one fatty acid molecule in a triacylglycerol is substituted by a phosphoric acid molecule. Thus, all phospholipids have a hydrophobic tail consisting of two fatty acid chains and a hydrophilic head made up of negatively charged phosphoric acid residue (Fig. 5.9 a). Consequently, they are amphipathic in nature as they have both hydrophobic and hydrophilic region in the same molecule. They are the major constituents of the cell membrane.

Amphipathic: Molecules that have both hydrophilic and hydrophobic groups.



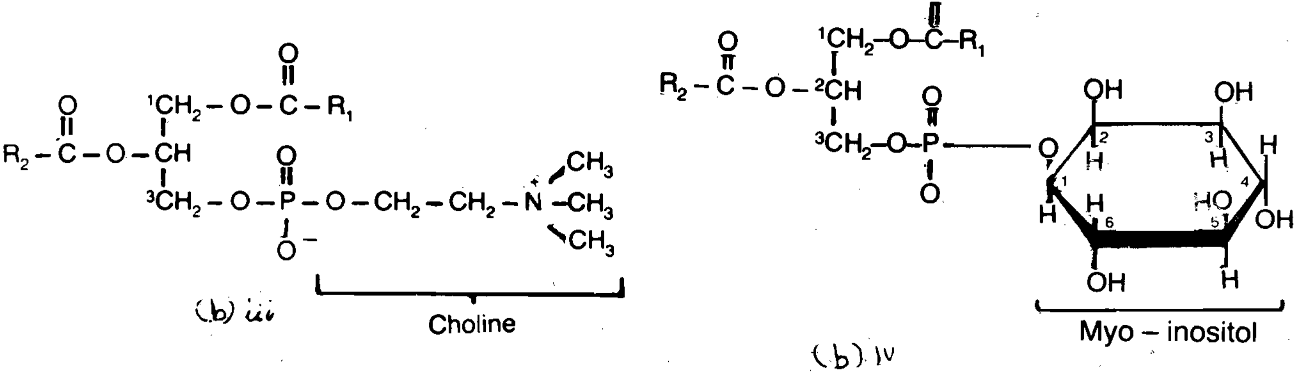


Fig. 5.9 : a) A phosphoglyceride. Two fatty acid molecules are esterified to the first and second hydroxyl groups of glycerol. Phosphoric acid is esterified to third hydroxyl group of glycerol.
b) Different types of phosphoglycerides.

The most abundant phospholipids are phosphatidylethanolamine (cephalin), phosphatidylcholine (lecithin), phosphatidylserine and phosphatidylinositol (Fig. 5.9 b). Sphingolipids and glycolipids are also amphipathic molecules and are main constituents of cell membranes. These are the main components of brain and nervous tissues.

5.6.3 Derived Lipids

Derived lipids contain no fatty acids. Therefore, they cannot be converted into soaps (non-saponifiable). These include steroids and terpenes.

All the steroids have parent nucleus called as **cyclopentanoperhydrophenantherene** ring (Fig. 5.10). This structure is composed of four rings A,B,C and D which are fused with each other. A, B and C rings constitute phenanthrene ring and to them the cyclopentane ring D is attached.

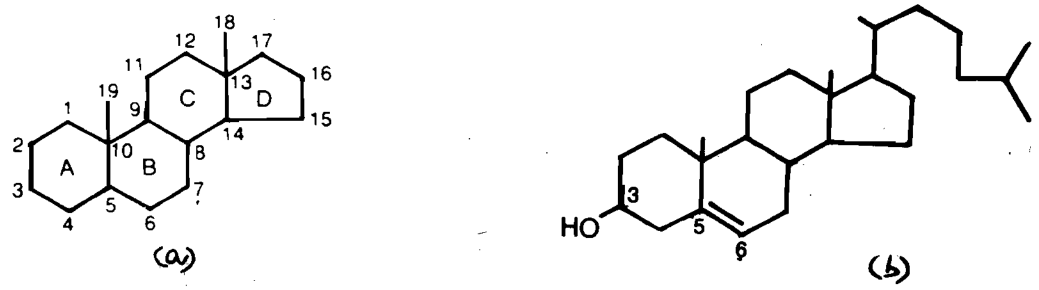


Fig. 5.10 : a) Cyclopentanoperhydrophenantherene nucleus with numbered carbon atoms. Three cyclohexane rings (A,B and C) and a terminal cyclopentane ring (D) form the basic structure of steroid.
b) Cholesterol. The hydroxyl group is polar and rest of the molecule is non-polar in nature.

The most important members of steroids are cholesterol, bile acids and sex hormones. Cholesterol is only found in animal tissues and is the parent compound which produces ergosterol, a precursor for the formation of vitamin D (Fig. 5.10).

Terpenes are synthesised by polymerisation of the five carbon unit called isoprene unit. These units are bound in head to tail organisation. Terpenes include certain fat soluble vitamins like Vitamin A, E, K, plant pigments like carotenoids, chlorophyll and certain co-enzymes (coenzyme Q, ubiquinone). Terpenes are major components of the essential oils.

5.7 SUMMARY

In this unit, you have studied:

- Types of chemical bonds and formation of macromolecules,
- Structure of proteins which are formed from amino acids bonded together by covalent peptide bonds. Proteins have four levels of structural organisation i.e. primary, secondary, tertiary and quarternary structures. Proteins are of major importance in the living system as they are the major cellular components and are involved in several vital functions such as enzyme formation and transport of substance etc.
- Nucleic acids, the genetic material, are the linear polymers of nucleotides.
- Deoxyribonucleic acid (DNA) consists of two complementary strands joined by hydrogen bonds and is coiled to form a double helical structure. Ribonucleic acid (RNA) is a single stranded structure having a ribose sugar and nitrogenous base uracil in place of thymine.
- Polysaccharides may be branched or unbranched chains formed by monosaccharides joined together by glycosidic linkages. The most important storage polysaccharides are starch in plants and glycogen in animals. Cellulose is the main component of plant cell wall. Chitin forms the exo-skeleton in most invertebrates.
- Lipids are water-insoluble components of cells. Neutral fats are simple lipids and serve as storage fats. Phospholipids, sphingolipids and glycolipids are structural elements of membranes and are amphipathic in nature.
- Sex hormones and cholesterol, are some examples of steroids, which are non-saponifiable lipids. Terpenes are major components of essential oil and chlorophyll.

5.8 TERMINAL QUESTIONS

1) Why is the tertiary structure of a protein lost on heating to 80° whereas the primary structure remains unchanged? Give your answer in 3-4 lines.

....

....

....

....

2) a) How many nucleosomes would be formed by 4×10^5 bp long DNA and why?

....

....

b) How many molecules each of histones H1,H2A, H2B, H3 and H4 would be required to form the nucleosomes for the above DNA?

....

....

3) In a fragment of DNA double helix there are 60 pyrimidine bases and 20 adenine bases. Calculate the number of each of the following in the fragment giving reasons.

a) Thymine bases

....

....

b) Total number of bases

....

....

c) Cytosine bases

....

....

d) Nucleotides

....

....

e) Complementary base pairs

....

....

4) Cellulose, amylose, amylopectin and glycogen are all polymers of only one monosaccharide, i.e. glucose. Then how do they differ from each other in their structure and properties? Give four reasons.

....

....

....

....

5) Write the structural formula of dipalmitinstearic glycerol in the given space.
(**Hint**: See the structures of palmitic acid and stearic acid in Section 4.2 of Unit 4.)

....

....

....

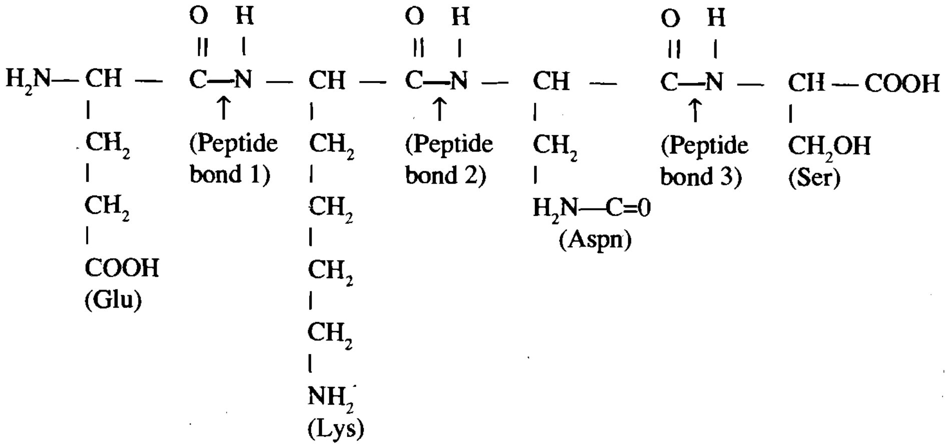
....

5.9 ANSWERS

Self-assessment Questions

1) Ionic bonds become weak in the presence of water because water molecules prevent the interaction between ions by increasing the distance of separation between charged molecules.

2)



$$\begin{array}{lllllll}
 & \mathrm{O}\quad\mathrm{H} & & \mathrm{O}\quad\mathrm{H} & & \mathrm{O}\quad\mathrm{H} & \\
 & \| \quad | & & \| \quad | & & \| \quad | & \\
\mathrm{H_2N{-}CH} - & \mathrm{C{-}N} - & \mathrm{CH} - & \mathrm{C{-}N} - & \mathrm{CH} - & \mathrm{C{-}N} - & \mathrm{CH{-}COOH} \\
\quad | & \uparrow & | & \uparrow & | & \uparrow & | \\
\quad \mathrm{CH_2} & \text{(Peptide} & \mathrm{CH_2} & \text{(Peptide} & \mathrm{CH_2} & \text{(Peptide} & \mathrm{CH_2OH} \\
\quad | & \text{bond 1)} & | & \text{bond 2)} & | & \text{bond 3)} & \text{(Ser)} \\
\quad \mathrm{CH_2} & & \mathrm{CH_2} & & \mathrm{H_2N{-}C{=}0} & & \\
\quad | & & | & & \text{(Aspn)} & & \\
\quad \mathrm{COOH} & & \mathrm{CH_2} & & & & \\
\quad \text{(Glu)} & & | & & & & \\
 & & \mathrm{CH_2} & & & & \\
 & & | & & & & \\
 & & \mathrm{NH_2} & & & & \\
 & & \text{(Lys)} & & & &
\end{array}$$

3) 3′-TAGCTTGCA-5′

4) i) a
ii) b
iii) a
iv) c

5) Carbon atom 1 and 4 or carbon atom 1 and 6 of glucose are most often involved in glycosidic bond formation.

Terminal Questions

1) The tertiary structure of proteins is stabilised by weak hydrogen bonds which break at 80°, whereas the primary structure is stabilised by covalent bonds which are too strong to be affected at this temperature.

2) a) 2×10^3, as 200 bp length of DNA comprises one nucleosome.

   b) 2×10^3 of H1 and 4×10^3 each of H2A, H2B, H3, and H4.

3) a) 20. By the base pair rule of A-T and G-C.

   b) 120. As there are 60 pyrimidine bases, there must be 60 purine bases that is 120 (60 +60) bases altogether.

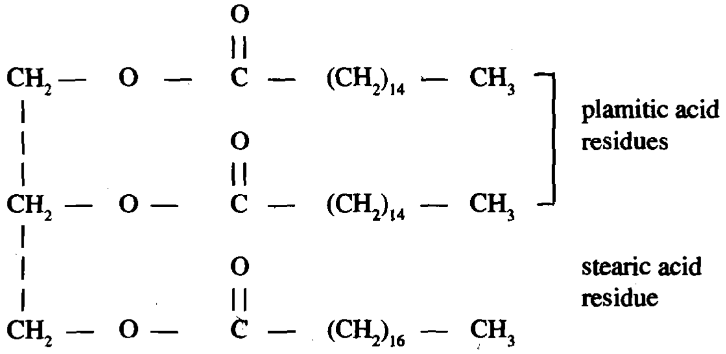
   c) 40. As pyrimidine bases (T+C) are 60, and thymine bases are 20, so cytosine bases are 40 (60-20).

   d) 120. As the total number of bases is 120.

   e) 60. As total number of bases is 120, the number of base pair must be half.

4) This is due to (i) branched or unbranched structures, (ii) sequences of different lengths (iii) 1–4 or 1–6 glycosidic bond and (iv) different types (α or β) of glucose molecules.

5)



$$\begin{array}{l}
CH_2-O-C(=O)-(CH_2)_{14}-CH_3 \\
CH_2-O-C(=O)-(CH_2)_{14}-CH_3 \\
CH_2-O-C(=O)-(CH_2)_{16}-CH_3
\end{array}$$

(The order of fatty acid residues may differ.)

GLOSSARY

affinity chromatography: a technique for separating macromolecules based on the biological affinity of the molecule for a matrix bound ligand.

autophagy: digestion of cellular material by the cell's own enzymes; part of normal regeneration and turn over of eucaryotic cellular components.

autoradiography: determining the location of radioactive tracers introduced into cell by exposure of photographic emulsions placed in contact with the cells.

basal body: an organelle located at the base of cilia and believed to be involved in the organisation of ciliary microtubules.

cell culture: a population of cells grown *in vitro*.

centromere : the primary construction of a chromosome to which the spindle fibers remain attached.

chloroplasts: membranous organelles of plant cells containing chlorophyll wherein photosynthesis occurs.

cilia (sing: cilium): locomotor organelles located at the cell surface.

cisterna (pl. cisternae): a flattened membranous sac filled with fluid.

codon: a sequence of three nucleotides of messenger RNA that codes for an amino acid or for chain termination.

complementary base pairing : hydrogen bond formation between a particular purine and a particular pyrimidine in nucleic acids, for example, guanine and cytosine and adenine and thymine.

core particle: result of partial digestion of a nucleosome leaving the histone octamer and 146 base pair of DNA.

covalent bond : bond between atoms formed by sharing of electrons.

cristae: infoldings of the mitochondrial inner membrane and the site of enzymes of oxidative phosphorylation and electron transport.

cytoskeleton: an intracellular framework composed of filaments and microtubules.

cytosol: the fluid portion of the cytoplasm in which the organelles are suspended.

deoxyribonucleic acid (DNA) : the genetic material of all cells and many viruses.

dictyosome: a stack of cisternae that forms part of the Golgi apparatus. In plant cells, the term is often used for the entire Golgi apparatus.

endocytosis: intake of solutes or particles by a cell by enclosing them in an infolding of the plasma membrane.

exocytosis: a mode of transport of substances out of the cell by enclosure in a vesicle, fusion of the vesicle with the plasma membrane and subsequent expulsion of the vesicle's contents.

ferritin: an iron-rich protein found in the liver, spleen and bone-marrow.

flagella (sing flagellum): locomotor organelles ultra structurally similar to cilia but usually longer and present in smaller numbers per cell.

fluorescent antibody technique: detection of selected antigens in cells by staining with specific antibody that has been conjugated with a fluorescent dye.

GERL: Golgi associated endoplasmic reticulum involved in the production of lysosomes.

hairpin loops: a folded region of single-stranded DNA or RNA formed by the pairing of two neighbouring complementary stretches of bases.

helix : a spiral structure having a repeating pattern described by two simultaneous operations—rotation and translation. It is the natural conformation of many biological polymers.

heterophagy : the process of forming a heterophagic vacuole.

histone: a protein component of the chromosome having a high content of basic amino acids. Eight histones comprise the core of a nucleosome.

hydrophobic bond : the associations formed by hydrophobic groups when surrounded by water.

in vitro (Latin-"in glass") : experiments carried out with isolated cells, tissues or cell free extracts.

in vivo (Latin-"in life"): experiments carried out using the intact organism.

lipid: class of organic compounds that are poorly soluble or insoluble in water but soluble in nonaqueous solvents such as ether or acetone.

lysosomes: intracellular organelles that contain a large variety of hydrolytic enzymes.

macromolecules: molecules having molecular weights in the range of few thousand to hundreds of millions of molecular weight units.

microbody: a membrane bounded cytoplasmic organelle with varied enzyme content and functions e.g. peroxisomes and glyoxysomes.

neutral fats : glycerides, fatty acid esters of glycerol, a major storage form of fats.

nucleic acid : polymer of nucleotides in an unbranched chain, DNA and RNA.

nucleoid : a region in the cytosol of procaryotic cells that contains nuclear material but is not segregated by membranes.

nucleoside: molecule containing a purine or pyrimidine linked to a pentose sugar.

nucleosomes: spherical particles seen along decondensed chromatin, each nucleosome is composed of eight histones around which there are nearly two turns of DNA.

nucleotide: a phosphorylated nucleoside.

organelle: a subcellular component, a discrete structural differentiation of the cell containing particular enzymes and performing particular functions for the whole cell; e.g. mitochondria, ribosome, etc.

peptidoglycan: macromolecule formed from both protein and carbohydrate parts, abundant in the cell walls of bacteria.

phagocytosis: a form of endocytosis in which large amounts of particulate material, even whole cells are enclosed in endocytic vesicles.

phosphodiester linkage: a covalent linkage involving esterification to phosphoric acid.

phospholipids: lipids that contain charged, hydrophilic phosphate groups; primary components of cell membranes.

photorespiration: uptake of oxygen and release of carbon dioxide by photosynthetic cells or whole plants in the light.

pinocytosis: endocytosis of small molecules in an aqueous medium.

plastid : eucaryotic cell organelle that stores pigments or carbohydrates.

polynucleotide: a linear sequence of nucleotides in which the sugar of one nucleotide is linked through a phosphate group to the sugar on the adjacent nucleotide.

procaryotes: organisms such as bacteria, blue green algae and mycoplasmas in which the nucleus is not separated from the cytoplasm by membranes.

purine: parent compound of the nitrogen containing bases adenine and guanine

pyrimidine: parent compound of the nitrogen containing bases cytosine, thymine and uracil.

radioactive isotope: isotope with an unstable nucleus that emits electrons (undergo beta decay) and are used as labels or tracers in biology.

residual bodies: secondary lysosomes containing undigested residues, membrane fragments and whorls.

ribonucleic acid (RNA): nucleic acids that function in transcription and translation. The genetic material of certain viruses.

rough ER(RER): portion of the endoplasmic reticulum bearing ribosomes.

smooth ER(SER): portion of the endoplasmic reticulum devoid of ribosomes.

steroids: compounds that are derivatives of a tetracyclic structure composed of a cyclopentane ring fused to a substituted phenantherne nucleus.

stroma: unstructured matrix of the chloroplast in which the grana and stroma thylakoids are suspended.

template: a molecule which contains information from which other molecules can be synthesised.

thylakoid: a membranous sac present in chloroplasts that may be disc shaped (in the grana) or elongated, it is the site of reactions of the photosynthesis requiring light and CO_2.

ultracentrifuge: centrifuge capable of producing rotor speeds up to 100,00. rmp and able to rapidly sediment tiny particles and macromolecules.

van der Waals force: a weak, attractive force between atoms, particularly important in hydrophobic bonding of amino acids in proteins.

wobble: capability of the third base in the tRNA anticodon (5' end) to form a hydrogen bond with any two or three bases at 3' end of the mRNA codon.

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