Chemicals of life continued…

Structural Polysaccharides

Organisms build strong materials from structural polysaccharides. For example, the polysaccharide called cellulose is a major component of the tough walls that enclose plant cells.

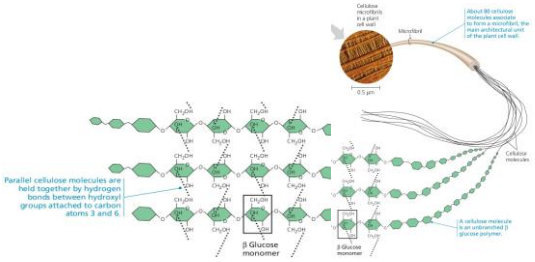
It is the most abundant organic compound on Earth. Like starch, cellulose is a polymer of glucose, but the glycosidic linkages in these two polymers differ.
The difference is based on the fact that there are actually two slightly different ring structures for glucose .When glucose forms a ring, the hydroxyl group attached to the number 1 carbon is positioned either below or above the plane of the ring. These two ring forms for glucose are called ***alpha (α)*** and ***beta (β)***, respectively.

Functional Approach page 65 fig 5.4

In starch, all the glucose monomers are in the α configuration. In contrast, the glucose monomers of cellulose are all in the β configuration, making every glucose monomer "upside down" with respect to its neighbors.

Functional Approach page 67 fig 5.8

Whereas certain starch molecules are largely helical, a cellulose molecule is straight. Cellulose is never branched, and some hydroxyl groups on its glucose monomers are free to hydrogen-bond with the hydroxyls of other cellulose molecules lying parallel to it. In plant cell walls, parallel cellulose molecules held together in this way are grouped into units called micro fibrils. These cable-like micro fibrils are a strong.



Enzymes that digest starch by hydrolyzing its α linkages are unable to hydrolyze the β linkages of cellulose because of the distinctly different shapes of these two molecules. Thus, although cellulose is not a nutrient for humans, it is an essential material in digestion since it stimulates the walls of the digestive tract to produce mucus.

Chitin

Is another important carbohydrate used by arthropods (insects, spiders, crustaceans, and related animals) to build their exoskeletons. Pure chitin is leathery and flexible, but it becomes hardened when encrusted with calcium carbonate, a salt.

Chitin is also found in many fungi, which use this polysaccharide rather than cellulose as the building material for their cell walls. Chitin is similar to cellulose, with β linkages, except that the glucose monomer of chitin has a nitrogen-containing appendage as shown below.

LIPIDS

Lipids are the one class of large biological molecules made up of elements such as carbon, hydrogen and oxygen. The hydrophobic behavior of lipids is based on their molecular structure. Although they may have some polar bonds associated with oxygen, lipids consist mostly of hydrocarbon regions. Lipids are varied in form and function.

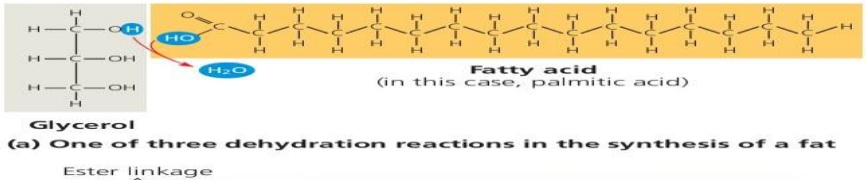
They include waxes and certain pigments, but most biologically important types of lipids: fats, phospholipids, and steroids.

Fats

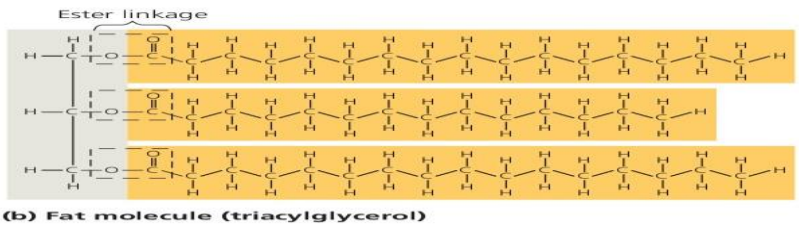
Although fats are not polymers, they are large molecules assembled from smaller molecules by dehydration reactions. A fat is constructed from two kinds of smaller molecules: glycerol and fatty acids. Glycerol is an alcohol; each of its three carbons bears a hydroxyl group. A fatty acid has a long carbon skeleton, usually 16 or 18 carbon atoms in length. The carbon at one end of the skeleton is part of a carboxyl group, the functional group that gives these molecules the name fatty acid. The rest of the skeleton consists of a hydrocarbon chain.

The relatively nonpolar C¬H bonds in the hydrocarbon chains of fatty acids are the reason fats are hydrophobic. Fats separate from water because the water molecules hydrogen bond to one another and exclude the fats. This is the reason that vegetable oil (a liquid fat) separates from the aqueous vinegar solution in a bottle of salad dressing.

In making a fat, three fatty acid molecules are each joined to glycerol by an ester linkage, a bond between a hydroxyl group and a carboxyl group. The resulting fat, also called a triacylglycerol, thus consists of three fatty acids linked to one glycerol molecule. (Still another name for a fat is triglyceride, a word often found in the list of ingredients on packaged foods.)



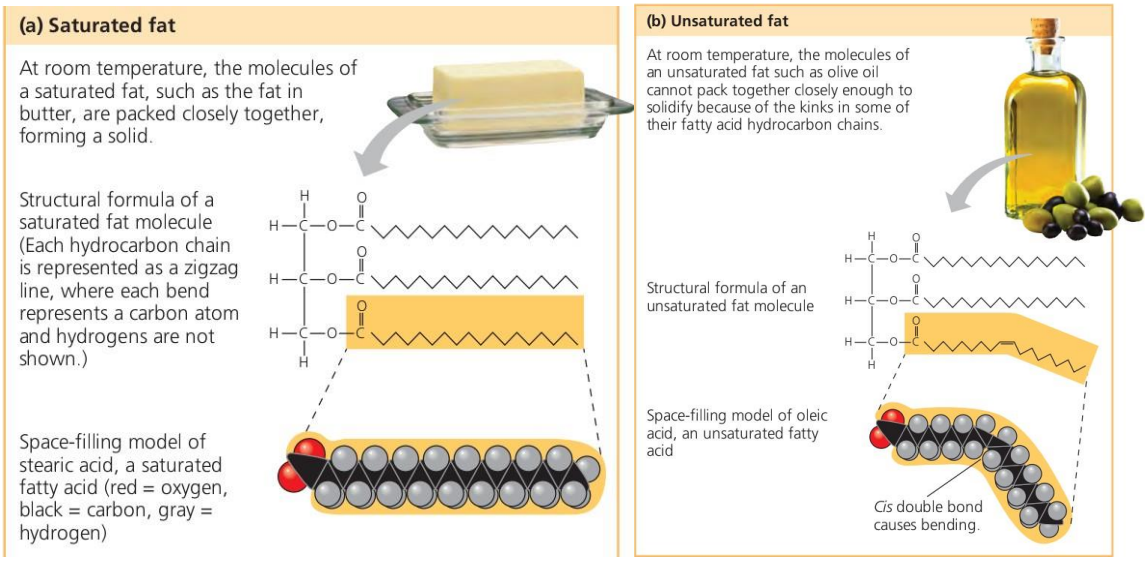
(a) One of three dehydration reactions in the synthesis of a fat



(b) Fat molecule (triacylglycerol)

The terms saturated fats and unsaturated fats refer to the structure of the hydrocarbon chains of the fatty acids. If there are no double bonds between carbon atoms in a chain, then the structure is said to be saturated with hydrogen, and the resulting fatty acid therefore called a saturated fatty acid.

An unsaturated fatty acid has one or more double bonds, nearly all double bonds in naturally occurring fatty acids are cis double bonds, which cause a kink in the hydrocarbon chain wherever they occur.



A fat made from saturated fatty acids is called a saturated fat. Most animal fats are saturated: The hydrocarbon chains of their fatty acids—the "tails" of the fat molecules—lack double bonds, and their flexibility allows the fat molecules to pack together tightly. Saturated animal fats—such as lard and butter are solid at room temperature.

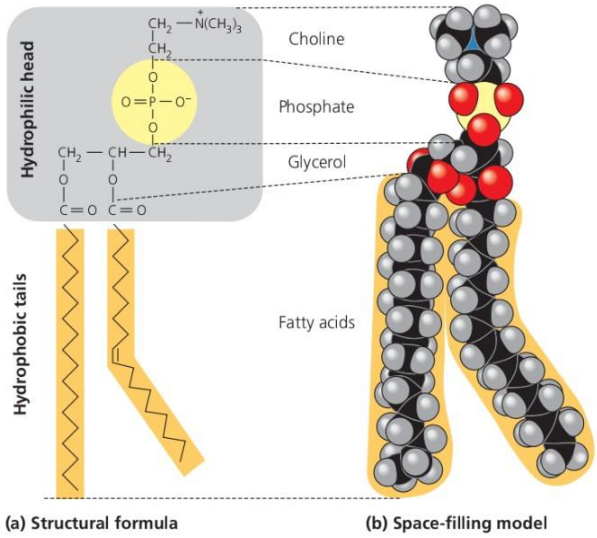
In contrast, the fats of plant and fishes are generally unsaturated, meaning that they are built of one or more types of unsaturated fatty acids. Usually liquid at room temperature, plant and fish fats are referred to as oils—olive oil and cod liver oil are examples. The kinks where the cis double bonds are located prevent the molecules from packing together closely enough to solidify at room temperature.

Phospholipids

Phospholipids are essential for cells because they make up cell membranes. Their structure provides a classic example of how it fits function at the molecular level. A phospholipid is similar to a fat molecule but has only two fatty acids attached to glycerol rather than three.

The third hydroxyl group of glycerol is joined to a phosphate group, which has a negative electrical charge in the cell. Additional small molecules, which are usually charged or polar, can be linked to the phosphate group to form a variety of phospholipids.

The two ends of phospholipids show different behavior toward water. The hydrocarbon tails are hydrophobic and are excluded from water. However, the phosphate group and its attachments form a hydrophilic head that has an affinity for water.(refer to the structure of a cell membrane).



Steroids

Different steroids, such as cholesterol and the vertebrate sex hormones, are distinguished by the particular chemical groups attached to this ensemble of rings. Cholesterol is a

crucial molecule in animals. It is a common component of animal cell membranes and is also the precursor from which other steroids are synthesized. In vertebrates, cholesterol is synthesized in the liver.

Waxs

These are formed by a combination of fatty acids with an alcohol other than glycerol. Their main function is water proofing in plants and animals.

TASK

- ★ Describe the functions of lipids (structural and physiological)
- ★ What properties do lipids possess as storage compounds?

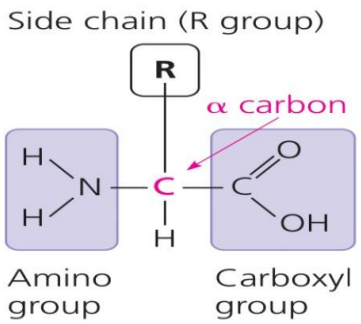
PROTEINS

These are organic compounds of large molecular mass. They are also made up of common elements eg carbon, hydrogen and oxygen. Its uniqueness is brought about by presence of nitrogen in its structure and usually Sulphur and sometimes phosphorus.

Proteins form the structural basis of all living cells. They are made up of amino acids as their building blocks.

Amino acids

All amino acids share a common structure. An amino acid is an organic molecule possessing both an amino group and a carboxyl group. The illustration below shows the general formula for an amino acid.



At the center of the amino acid is an asymmetric carbon atom called the alpha (a) carbon. Its four different partners are an amino group, a carboxyl group, a hydrogen atom, and a variable group symbolized by R. The R group, also called the side chain, differs with each amino acid.

The carboxylic end of the amino acids acidic and the amino end is basic. These two ends ionse by losing and gaining a proton respectively hence becoming charged differently. The carboxyl side becomes negatively charged and the amino group becomes positively charged. Such ions are called ***Zwitter ions*** .

The negative and the positive charges exactly balance and the amino acid ion has no overall charge. In this case, when an amino acid is in an acidic solution, an amino acid acts like a base and in an alkaline solution acts as an acid. Therefore it acts as both acidic and alkali hence it is amphoteric.

Question: How do amino acids act as buffer solutions?

<u>Types of amino acid</u>

There are mainly two types of amino acids i.e essential and non-essential amino acids.

Essential amino acids are the ones which cannot be synthesized by the body and therefore got from the diet that an organism feeds on.

Non-essential amino acids are the ones that are synthesized by the body through a process called transamination.

There are mainly 20 amino acids in the body where 9 are essential and 11 non-essential.

(List both essential and non essential amino acids)

Protein are classified into two i.e High Biological Value proteins (HBV) which contain all the essential amino acids. These are mainly common to all animal products and in plants they are only found in soya beans.

The second one are the Low Biological Value proteins which are deficient in essential amino acids.

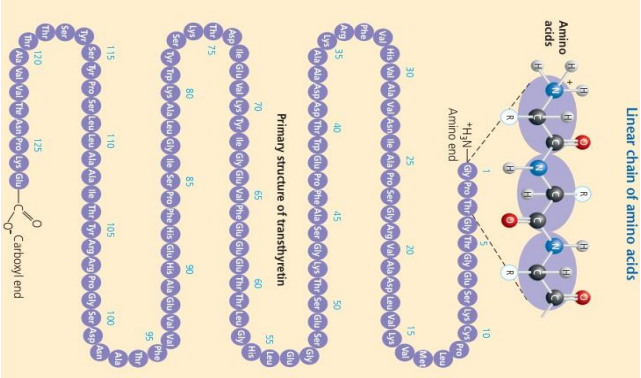
Question: Using amino acids as monomers, describe the formation of polypeptides.

POTEIN STRUCTURE.

There are 3 main protein structures i.e primary, secondary, tertiary and quaternary structure.

Primary structure;

The primary structure of a protein is a linked series of amino acids with a unique sequence. As an example, let's consider transthyretin, a globular blood protein that transports vitamin A and one of the thyroid hormones throughout the body.
The primary structure is like the order of letters in a very long word. If left to chance, there would be different ways of making a polypeptide chain of amino acids long. However, the precise primary structure of a protein is determined not by the random linking of amino acids, but by inherited genetic information. The primary structure in turn dictates secondary and tertiary structure, due to the chemical nature of the backbone and the side chains (R groups) of the amino acids positioned along the chain.



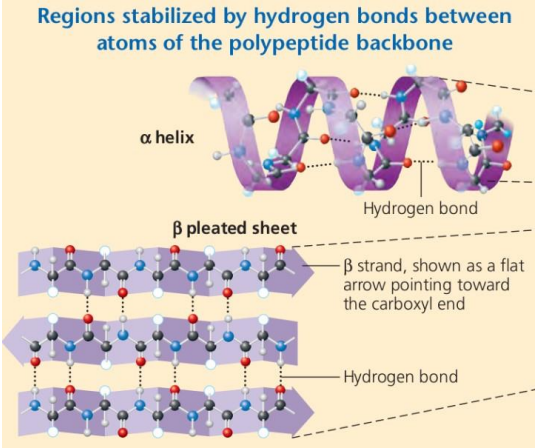
Secondary structure;

Most proteins have segments of their polypeptide chains repeatedly coiled or folded in patterns that contribute to the protein's overall shape. These coils and folds, collectively referred to as **secondary structure**, are the result of hydrogen bonds between the repeating constituents of the polypeptide backbone (not the amino acid side chains).

Within the backbone, the oxygen atom have a partial negative charge, and the hydrogen atoms attached to the nitrogens have a partial positive charge therefore, hydrogen bonds can form between these atoms.

Individually, these hydrogen bonds are weak, but because they are repeated many times over a relatively long region of the polypeptide chain, they can support a particular shape for that part of the protein.

One such secondary structure is the helix, a delicate coil held together by hydrogen bonding between every fourth amino acid. The secondary structure has two forms i.e the alpha (a) helix i.e keratin in hair and the beta (B) pleated beets e.g silk protein in spider web.



Tertiary structure;

The final folded shape of a globular protein, which positions the various motifs and folds nonpolar side groups into the interior, is called a protein's tertiary structure. A protein is driven into its tertiary structure by hydrophobic interactions with water.

The final folding of a protein is determined by its primary structure and by the chemical nature of its side groups. Many proteins can be fully unfolded ("denatured") and will spontaneously refold back into their characteristic shape.

A single polypeptide chain connects the domains of a protein, like a rope tied into several adjacent knots. Often the domains of a protein have quite separate functions i.e one domain of an enzyme might bind a cofactor, for example, and another to the enzyme's substrate.

Quotanart structure;

When two or more polypeptide chains associate to form a functional protein, the individual chains are referred to as subunits of the protein. The subunits need not be the same. Hemoglobin, for example, is a protein composed of two α-chain subunits and two β-chain subunits. A protein's subunit arrangement is called its quaternary structure.

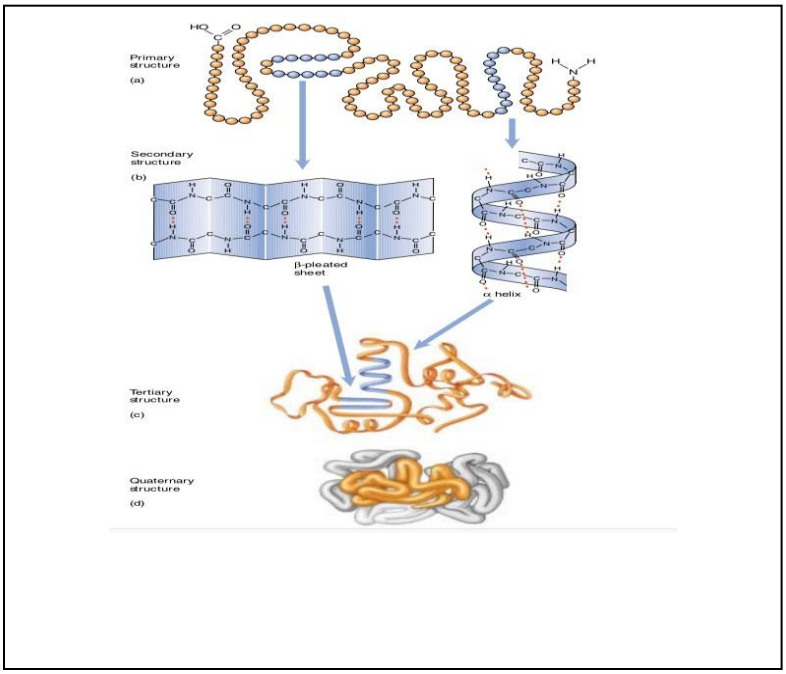


FIGURE: Levels of protein structure. The amino acid sequence of a protein is called its (a) primary structure. Hydrogen bonds form between nearby amino acids,producing (b) fold-backs called beta-pleated sheets and coils called alpha helices. These fold-backs and coils constitute the protein's secondary structure. A globular protein folds up on itself further to assume a threedimensional (c) tertiary structure. Many proteins aggregate with other polypeptide chains in clusters; this clustering is called the (d) quaternary structure of the protein.

Task;

Give and describe the three types of proteins.

How does the molecular structure of proteins relate to their roles?

ENZYMES

The chemical reactions within living organisms are regu lated by controlling the points at which catalysis takes place. Life itself is, therefore, regulated by catalysts. The agents that carry out most of the catalysis in living organ isms are proteins called enzymes.

An enzyme is an organic compound, protein in nature that speeds up the rate of biochemical reactions in the body of an organism and remains unchanged at the end of the reaction.

Structure of enzymes.

Like all the other proteins, enzymes are made up of polypeptide chains hence they have a tertiary structure of proteins hence known as globular proteins. The polypeptide chains are highly folded obtaining a particular shape.

In its folds it has a groove of a particular shape known as an active site into which a particular substrate fixes during a biochemical reaction.

Question; Give classes of enzymes

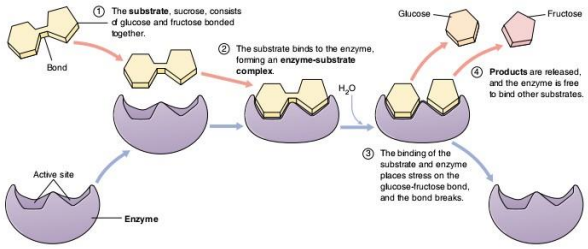
Enzymatic action

There are mainly two hypotheses which explain action of an enzyme i.e Lock and key hypothesis and induced fit hypothesis

The lock and key hypothesis

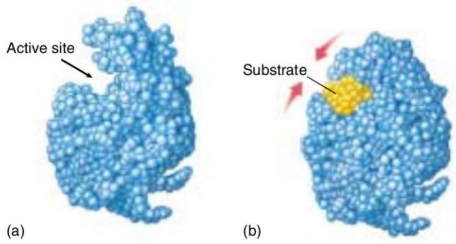
The hypothesis suggests that the enzyme(with a fixed shape) acts as a lock with an active site having a specific shape into which the substrate with a complementary shape fits in as a key. This results into formation of an enzyme-substrate complex.

When that happens, amino acid side groups of the enzyme end up in close proximity to certain bonds of the substrate. These side groups interact chemically with the substrate, usually stressing or distorting a particular bond and consequently lowering the activation energy needed to break the bond. The substrate, now a product, then dissociates from the enzyme.



Induced fit hypothesis

Proteins are not rigid as suggested in the lock and key hypothesis. The binding of a substrate induces the enzyme to adjust its shape slightly, leading to a better induced fit between enzyme and substrate. There fore this is the most accepted hypothesis of enzymatic action.



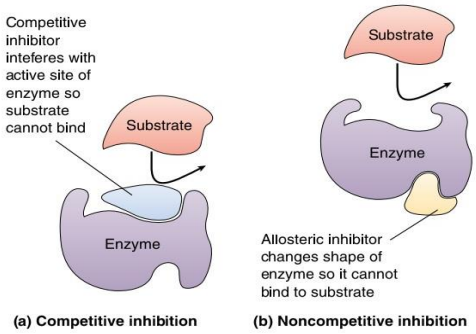
Enzyme in hibition

Enzyme activity is sensitive to the presence of specific substances that bind to the enzyme and cause changes in its shape. Through these substances, a cell is able to regulate which enzymes are active and which are inactive at a particular time.

A substance that binds to an enzyme and decreases its activity is called an inhibitor. Very often, the end product of a biochemical pathway acts as an inhibitor of an early reaction in the pathway, a process called feedback inhibition.
Enzyme inhibition occurs in two ways:

Competitiveinhibitors; compete with the substrate for the same binding site, displacing a percentage of substrate molecules from the enzymes.

noncompetitive inhibitors; bind to the enzyme in a location other than the active site, changing the shape of the enzyme and making it unable to bind to the substrate. Most noncompetitive inhibitors bind to a specific portion of the enzyme called an **allosteric site** (Greek allos, "other" + steros, "form").



These sites serve as chemical on/off switches. The binding of a substance to the site can switch the enzyme between its active and inactive configurations. A substance that binds to an allosteric site and reduces enzyme activity is called an allosteric inhibitor.

On the other side, **enzyme activators** bind to allosteric sites and keep the enzymes in their active configurations, thereby increasing enzyme activity.

Task: List properties of enzymes.

Describe the factors that affect enzyme activities.activities

NUCLEIC ACIDS

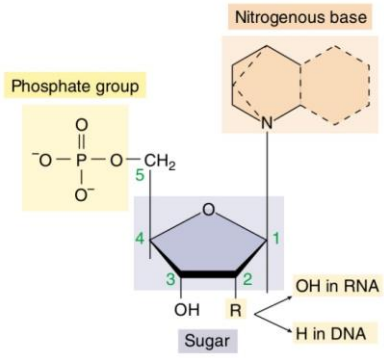
Nucleic acids are long polymers of repeating subunits called nucleotides. There are mainly two types of nucleic acids i.e **DNA** (Deoxyribo Nucleic Acid) and **RNA** (Ribo Nucleic Acid).

Each nucleic acid consists of monomers known as **nucleotides.** Each nucleotide is made up of three components:

A five-carbon sugar (ribose in RNA and deoxyribose in DNA)

A phosphate (—PO_4) group; and

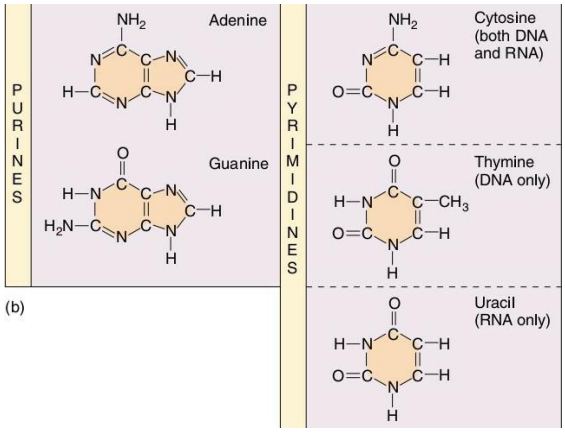
An organic nitrogen containing base



When a nucleic acid polymer forms, the phosphate group of one nucleotide binds to the hydroxyl group of another, releasing water and forming a phosphodiester bond. A nucleic acid, then, is simply a chain of five-carbon sugars linked together by phosphodiester bonds with an organic base protruding from each sugar.

Two types of organic bases occur in nucleotides. The first type, **purines**, are large, double-ring molecules found in both DNA and RNA. They are adenine (A) and guanine (G).

The second type, **pyrimidines**, are smaller, single-ring molecules. They include cytosine (C, in both DNA and RNA), thymine (T, in DNA only), and uracil (U, in RNA only).



Ribo Nucleic Acid (RNA)

The RNA molecule is made up of a long chain of nucleotides. It consists of a Penrose sugar ribose and any of the four bases i.e adenine or guanine (purines) and cytosine or uracil (pyramidines). RNA chains exist as a single strand.

RNA exists in 3 types;

- *Messenger RNA (mRNA)*
- *Transfer RNA (tRNA)*
- *Ribosomal RNA (rRNA)*

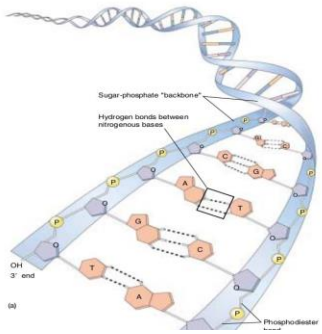
Task; Describe the structure and functions of the three types of RNAs.

Deoxyribose Nucleic Acid (DNA)

DNA molecule is made up of a sugar-phosphate backbone and a nitrogenous bases attached to the sugars forming a long chain of nucleotides (nucleic acid chain). Nitrogenous bases on one chain of nucleotides communicates to another antiparallel polynucleotide through hydrogen bonding.

The bases are attached in such a way that a purine to a pyrimidine e.g Adenine to Thymine using two hydrogen bonds, while Guanine to Cytosine using three hydrogen bonds. The two polynucleotide chains of DNA form a right helical spiral about an axis forming a DNA double helix. The DNA molecule has a large molecular mass and stable to metabolism.

Therefore the DNA is a suitable molecule to store information of hereditary from one generation to another.



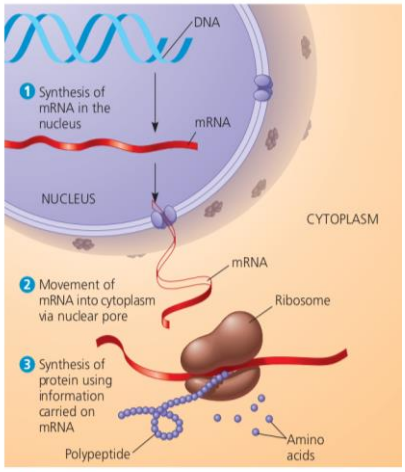
Task; compare and contrast the structure of DNA and RNA.

Protein synthesis

This process involves the conversion of the stored information in the DNA inform of cordons to polypeptide chains required to make a particular protein needed by the cell. Since the DNA cannot move out of the nucleus, this information is transferred to the cytoplasm by a type of RNA known as messenger RNA to the ribosomes in the cytoplasm of the cell where a polypeptide chains required are synthesized.

The process involves three major steppes;

Transcription
Amino acid activation
Translation



▲ **Figure 5.25 DNA → RNA → protein.** In a eukaryotic cell, DNA in the nucleus programs protein production in the cytoplasm by dictating synthesis of messenger RNA (mRNA). (The cell nucleus is actually much larger relative to the other elements of this figure.)

Transcription

This is the process by which the information in the DNA is converted into a long chain of mRNA having anticodons to the strand of DNA that is copied.

The process is initiated by an enzyme known as helicase which moves along the DNA double helix and breaks down the hydrogen bonds between the two wound parallel strands of the DNA. This results into the unwinding of the DNA double helix.

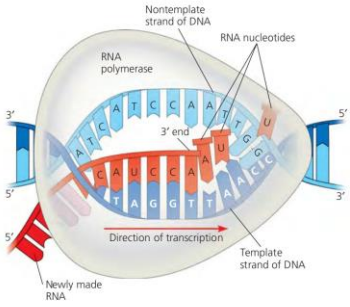
Another key enzyme in protein synthesis known as RNA polymerase enzyme attaches its self on one of the DNA strand, and move along its template. The strand onto which the RNA polymerase enzyme is moving is called the coding strand while the other one is called the non-coding strand.

As DNA polymerase enzyme moves along the coding strand, it brings about the arrangement of free nucleotides in the nucleolus into long chain polynucleotide known as mRNA. The mRNA strand formed has anticodons as compared to the coded strand of the DNA.

The mRNA formed then leaves the nucleus via the nuclear pores to the ribosomes in the cytoplasm of the cell where Translation occurs.

Amino acid activation.

Amino acids are the basic units of proteins, therefore these are very important during protein synthesis. In a cellular cytoplasm, there are only 20 types of amino acids i.e both



▲ **Figure 17.9 Transcription elongation.** RNA polymerase

essential and non-essential amino acids. These are transported by a particular RNA known as transporter RNA (tRNA) to the site of protein synthesis. During this process, a particular amino acid attaches its self to the antenna end of tRNA with a specific codon.

This process requires energy from ATP and it results into formation of tRNA amino acid complex which moves to the mRNA on the ribosomes hence a process of Translation.

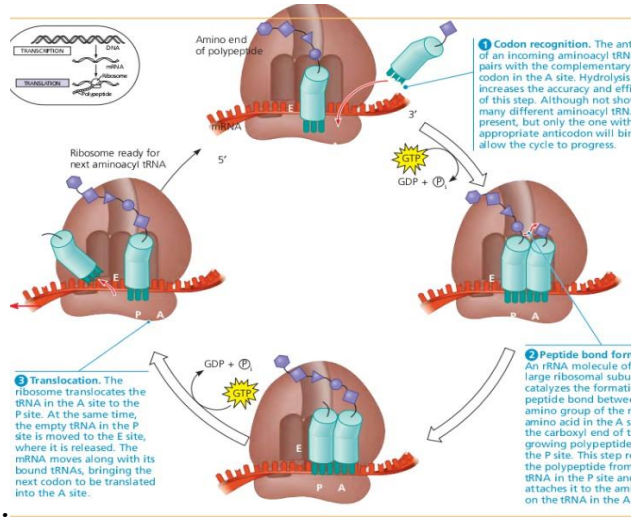
Translation

This is a process by which the information on the mRNA inform of cordons is converted to a polypeptide chain. This process occurs on the ribosomes in the cytoplasm of the cell.

The ribosome has three sites i.e A, P and E but it can hold only two tRNA amino acid complex and the mRNA strand. The first two cordons of mRNA attracting the tRNA amino acid complex enter the ribosome i.e into site A and P. The two tRNA amino acid complex having anticodons to those of the mRNA also enter the ribosome. The amino acids carried by the tRNA then form a polypeptide bond.

This triggers the movement of the ribosome one codon ahead on the mRNA attracting the next tRNA amino acid complex with an anticodon. The first tRNA carrying the first amino acid (methionine) leaves the amino acid behind and moves to site E from where it exits the ribosome to the cytoplasm for further activation.

The process continues until a terminator cordon is reached. The polypeptide chain formed then leaves the ribosome to the Golgi apparatus for more complication.



N.B

Since the mRNA is very long, only one ribosomes will take a long period of time to form a polypeptide chain. Therefore many ribosomes will attach on different lengths of mRNA hence forming polysomes.

The first cordon attracting the tRNA amino acyl complex is called the initiator codon.

THE GENETIC MATERIAL

This is the material that is responsible for the transmission of hereditary traits or characteristics from one generation to another.

Characteristics of a hereditary material

i) It should be able to carry out self-replication i.e. make exact copies of itself for the onward transmission of its features to the off springs.

ii) It should be stable in structure i.e. it should not change erratically losing its structure during transmission.

iii) It should have the capacity to change i.e. to provide new material for creation of a new inheritance feature that can improve linkage of off springs. This can be done through mutation.

iv) It should have the capacity to store information correctly preferably in a code which can be read and interpreted at an appropriate time.

v) It should be strategically located in the part of the body where it can be protected against metabolic reactions but have the ease to transmit information to all body parts e.g. in the nucleus.

Evidence of DNA as a hereditary material

Early researchers scrutinized many molecules in the body to find out which ones could have characteristics that fit the hereditary material. Proteins were seen as the best candidates since they were versatile in nature and were dominant in body parts. Proteins however are unstable as they constantly change and they are metabolically active and even not self-replicating.

Friedrich later eliminated proteins as the best candidate and identified a macro molecule he named 'nuclein' which appeared to satisfy most of the essential characteristics. Nuclein

was later renamed DNA.

Characteristics of DNA as a genetic material

i) Consistency of DNA content in the nucleus. Diploid nuclei from cells in any species and at different stages of mitosis all contain the same quantity of DNA.

ii) The gamete nuclei contain half the quantity as expected.
iii) Unlike other cell components, DNA remains stable and intact as a large molecule.
iv) DNA is not metabolized at any stage.
v) DNA has the capacity to mutate. Mutagens like U.V. light bring about changes in the DNA molecule which acts as a basis for new material of inheritance. Mutation is however limited and does not change the whole organism.
vi) Presence of DNA in chromosomes which are the materials of hereditary.
vii) Ability of DNA to replicate.

DNA Replication.

DNA replication is the process by which DNA makes a copy of itself during cell division.

There are three hypotheses put toward to explain the process of DNA replication i.e

- Semi-coservative hypothesis
- Conservative hypothesis
- Dispersive hypothesis

Of the above, Semi-conservative hypothesis is the most accepted hypothesis for DNA replication during cell division.

The following is the way how DNA replication occurs;

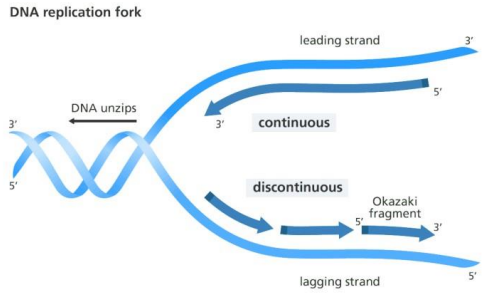
1. The first step in DNA replication is to 'unzip' the double helix structure of the DNA molecule.

2. This is carried out by an enzyme called ***helicase*** which breaks the hydrogen bonds holding polynucleotide chains of the DNA together (A with T, C with G).

3. The separation of the two single strands of DNA creates a 'Y' shape called a replication 'fork'. The two separated strands will act as templates for making the new strands of DNA.

4. One of the strands is oriented in the 3' to 5' direction (towards the replication fork), this is the ***leading strand*** . The other strand is oriented in the 5' to 3' direction (away from the replication fork), this is the **laging strand**

. As a result of their different orientations, the two strands are replicated differently:



An illustration to show replication of the leading and lagging strands of DNA.

Leading strand

5. A short piece of RNA called a primer (produced by an enzyme called primase) comes along and binds to the end of the leading strand. The primer acts as the starting point for DNA synthesis.

6.DNA polymerase binds to the leading strand and then 'moves' along it, adding new complementary nucleotides with bases (A, C, G and T) to the strand of DNA in the 5' to 3' direction. This sort of replication is continuous.

Lagging strand

5. Numerous RNA primers are made by the primase enzyme and bind at various points along the lagging strand.

6. Chunks of DNA, called Okazaki fragments, are then added to the lagging strand also in the 5' to 3' direction.

7. This replication is discontinuous as the Okazaki fragments will need to be joined up later.

8. 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.

9. The new strand is proofread to make sure there are no mistakes in the new DNA sequence.

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

11. 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.

The other two hypotheses follow the same principal but differ in the way of incorporation of the new and old DNA strands as follows;

The conservative hypothesis

Here, no unwinding occurs but the DNA molecule acts as a stimulant to direct the reaction. All the DNA strands formed are directly similar but not complementary to the parental strands. This hypothesis has not received any scientific backing and appears impractical.

The Dispersive hypothesis

According to the hypothesis, DNA initially disintegrates and then re-assembles alongside with the new complementary nucleotides adding to form new helices.

DNA AND THE CHROMOSOME STRUCTURE

The chromosome structure depends upon the complexity of an organism. There are two levels of complexity and two types of chromosomes:

i) Prokaryotic chromosomes:

Prokaryotes have simple chromosomes but with a naked structure. Simple chromosomes are also found in chloroplasts, mitochondria of higher plants, blue green algae (cyanophyta).

ii) Eukaryotic chromosomes:

They are in higher plants and animals. Each cell contains several pairs of chromosomes. The chromosomes are large and they change their form and structural organization at different stages of the cell cycle.

Each chromosome is made up DNA and an equal quantity of protein weight by weight. The DNA protein complex found in chromosomes is known as nucleoprotein or chromatin.

Proteins in a chromosome

There are two types:

1) Histones:

These are basic or non-acidic proteins that form the back bone structure of a chromosome on which the DNA is wrapped. The back bone structure of the chromosome on which the DNA is wrapped is called octamer. The types of histones are H1, H2A, H2B, H3 and H4.

2) DNA:

Eukaryotic chromosomes contain double helical DNA in large quantities. Replication of DNA in eukaryotic chromosomes occurs by the semiconservative method but would be very slow due to its length taking about 16 days to manufacture one strand.

To avoid the slow speed, DNA opens up as many as 6000 replication forks. Replication takes place at all the forks almost concurrently and the cycle is completed in 3-4 minutes.

DNA AND GENES

The genetic code

This refers to the way genetic information is encoded or arranged on the DNA strand. It is a known fact that a lot of genetic information is stored and transmitted by the DNA molecule.

Such information is arranged in form of a code of base pairs on the DNA strand. To be able to utilize this information e.g. during the manufacture of amino acids, proteins, enzymes, hormones, etc. the code must be read and interpreted correctly and the secret information released and transformed into products.

Reading the code

A code (DNA) is usually located in the nucleus yet the products of reading it are found in the cytoplasm. Therefore, information has to be transferred from the nucleus to the cytoplasm in order to make the products. Both transfer and utilization of information is done through a special molecule called RNA. This is a nucleic acid that has the capacity to move out of the nucleus therefore transfer information.

What is a gene?

It is a unit of hereditary located on the positions called gene loci on the chromosome. Genes who code for polypeptides are of two groups:

1) *Structural genes:* these code for function of proteins e.g. enzymes, hormones, antibodies, etc.

2) *Regulatory genes:* these serve to control the activity of other genes.

The DNA strand has two regions;

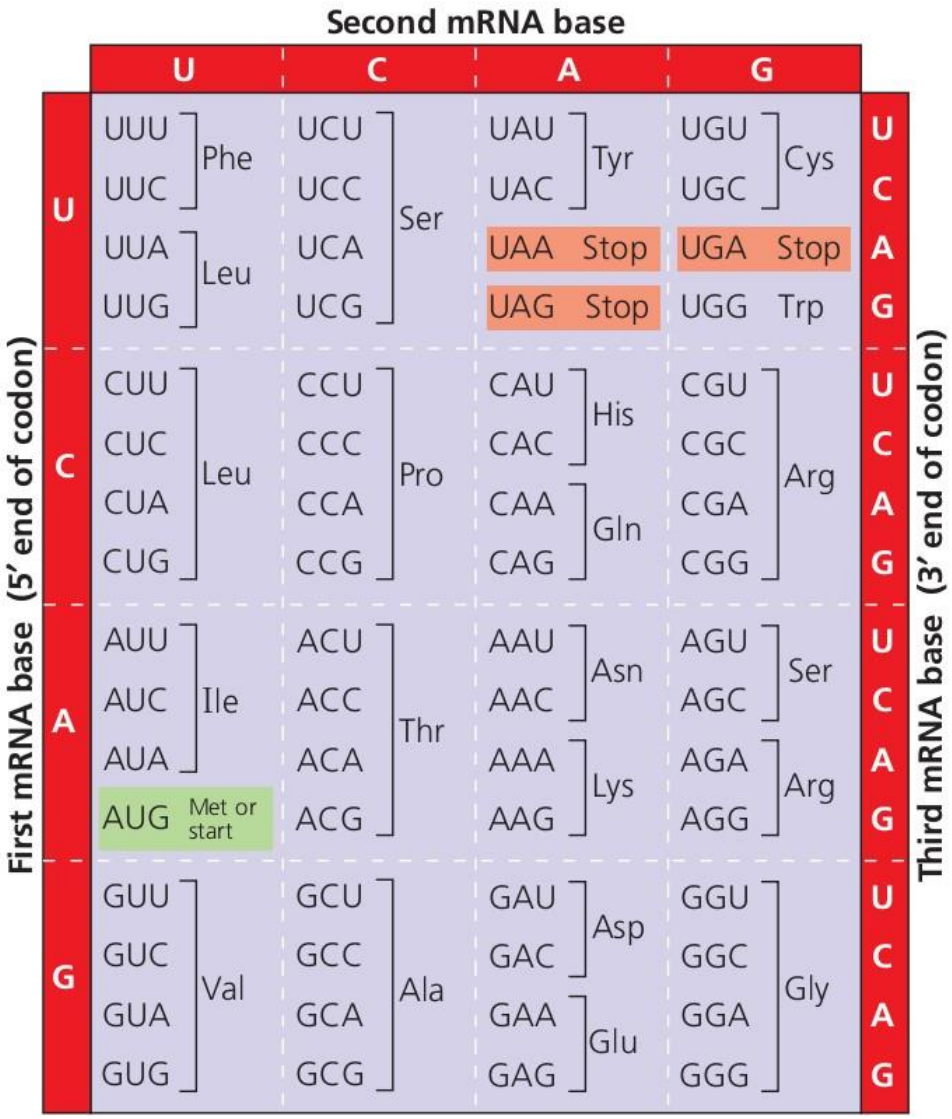
i) The split gene area, which is the coded area and made up of coding sequences known as exons.

ii) The non-coding area is made up of redundant DNA and is composed of non-coding sequences called introns. The function of introns is unknown.

The code dictionary/genetic code

The genetic code is a set of rules by which information encoded within genetic material is translated into proteins by living cells. There are four bases on the DNA strand that are used for coding of amino acids. Their combination ought to give a coding total of 20 amino acids found in the body. If each base was on its own codes for an amino acid, only four amino acids would be coded. If the bases acted in pairs only 16 amino acids would be coded. In both cases, 20 amino acids are not arrived at it. It therefore appears reasonable to theorize that 3 base pairs

are required for coding an amino acid.



Having established that each amino acid is determined by a triplet base pair, it has been used to establish and read the code dictionary. The three base pair hypothesis means that to code for the 20 amino acids occurring in the body, 64 possible combinations exist. The 44 combinations are not used in amino acid coding and are referred to as degenerate or nonsense codons/stop codons. Because of this, more than one but nearly similar triplet can code for an amino acid.

The three bases of an mRNA codon are designated here as the first, second, and third bases, reading in the 5` to 3` direction along the mRNA. () the codon AUG not only

stands for the amino acid methionine (met) but also functions as a "start" signal for ribosomes to begin translating the mRNA at that point. Three of the 64 codons function as "stop" signals, marking the end of a genetic message.

General characteristics of the genetic code

i) **Universal**: This means that the same codons are used to specify the same amino acids in all forms of life.

ii) The code is **degenerate** i.e. more than one codon can code for one amino acid. Some amino acids like methionine and tryptophan are coded by only one codon but many others are coded by several codons. Therefore, a code has excess codons. These codons are known as synonymous.

iii) The code is **non-ambiguous** i.e. no one codon can code for more than one amino acid.

iv) The genetic code is **triplet** i.e. it has got three bases.

v) The principle of **co-linearity:** It is collinear because the sequence of codons on the mRNA corresponds to that of the amino acid on the polypeptide chain. The linear order of nucleotides in DNA determines the linear order of codons in mRNA.

vi) **Non-over lapping** except in some viruses. From the starting of mRNA the sequence of bases read in blocks of three, correspond to the sequence of amino acids, without any overlapping of bases. For example if the bases from the starting are AUGCCAAUC the sequence of codons is AUG/CCA/AUC and not AUG/GCC/CAA/AUG. No single base in a sequence takes part in the formation of more than one codon.

vii) **Non sense/termination codons:** Some triplets do not code for any amino acids i.e. they punctuate the process of protein synthesis. They include UAA, UAG and UGA.

viii) The genetic code has **initiation or start codons**. AUG specifies methionine, AUG

when present at the first position of the mRNA, acts as a start signal thus called start codon. It means all polypeptides begin with the first amino acid as methionine which is later removed enzymatically. If AUG appears in the middle of mRNA, it simply codes for methionine.