NUCLEOSIDES

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A nucleoside is composed of purine and pyrimidine base and sugar. In the case of purine nucleosides, the sugar is attached to N-9 of purine ring where as in pyrimidine nucleosides, the sugar is attached to N-1 of pyrimidine ring (Fig.).

The type of linkage is N-glycosidic and sugar can be ribose or deoxyribose.

NOMENCLATURE OF NUCLEOSIDES

Nucleosides are named as derivatives of bases. For example, adenine linked to ribose is called as adenosine. Capital letter A is used to indicate adenine containing nucleoside.

- If adenine is linked to deoxyribose then it is named as deoxy adenosine and it is abbreviated as dA. Names and abbreviations of purine and pyrimidine nucleosides are given in the Table

Bases

- Purines-Adenine and Guanine
- Pyrimidines-Thymine and Cytosine

Base	Nucleosides	Abbreviation
Adenine	Adenosine	A
	Deoxyadenosine	dA
Guanine	Guanosine	G
	Deoxyguanosine	dG
Hypoxanthine	Inosine	I
Xanthine	Xanthosine	X

(Contd.)

Cytosine	Cytidine	C
	Deoxycytidine	dC
Thymine	Ribothymidine	T
	Deoxythymidine	dT
Uracil	Uridine	U
Dehydrouracil	Pseudouridine	Ψ
Orotic acid	Orotidine	O

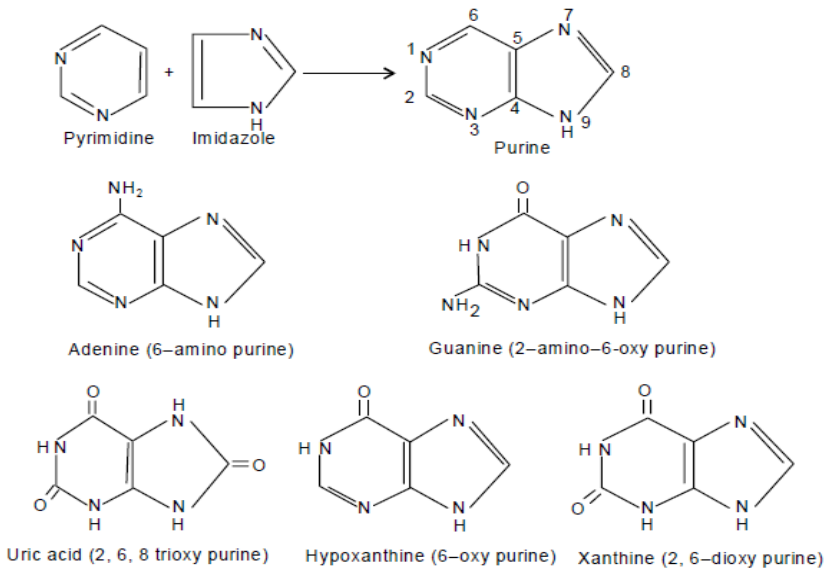

Fig: Structure of Purine bases

Purine bases

- They are derived from parent compound purine. Purine contains heterocyclic ring system.
- Fusion of pyrimidine ring with imidazole yields purine ring (Fig.). The carbon (c) and nitrogen (N) atoms of purine ring are numbered in anti-clockwise direction (Fig.).
- The purines present in nucleotides are adenine and guanine. The structures of adenine and guanine along with their systematic names are shown in Fig.
- Other purine bases are hypoxanthine and xanthine. They are intermediates in the formation of adenine and guanine nucleotides. Uric acid is another purine base. It is the end product of purine nucleotide catabolism

Pyrimidine bases

- Pyrimidine bases are derived from parent compound pyrimidine. Pyrimidine is a heterocyclic compound. The structure of pyrimidine ring along with numbering of atoms is shown in Fig. The C and N atoms are numbered in clockwise direction.
- The pyrimidine bases present in nucleotides are cytosine, uracil and thymine. The structures of these pyrimidines along with their systematic names are shown in Fig. Other pyrimidine bases are orotic acid and dihydroorotic acid. They are intermediates in the formation of pyrimidine nucleotides.

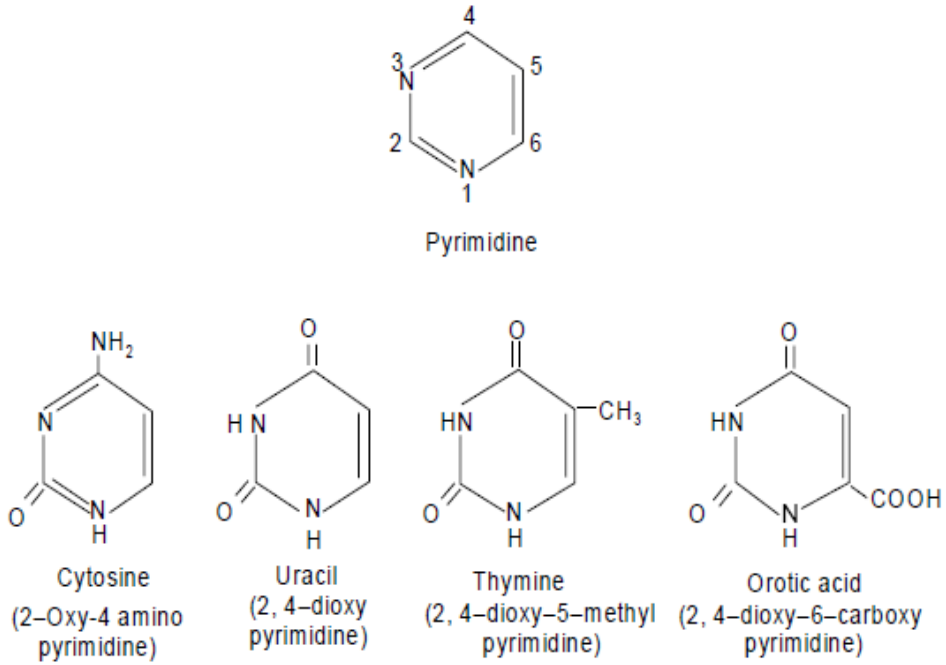

Fig: Structure of Pyrimidines

Sugars

Two types of pentose sugars are found in nucleotides. They are ribose and deoxy ribose.

- Nucleotides are named according to the type of sugar present. If the sugar is deoxyribose then nucleotide is named as deoxyribonucleotide. Similarly, if the sugar is ribose then nucleotide is named as ribonucleotide.

Some characteristic features of sugar present in nucleotides

1. Normally it is a 5-numbered furanose ring.

2. Only D-isomer is present.

3. Configuration around first carbon atom is ‘β’-form.

4. As mentioned earlier in deoxyribose, only hydrogen is present instead of OH group of 2 carbon atom of furanose ring (Fig.).

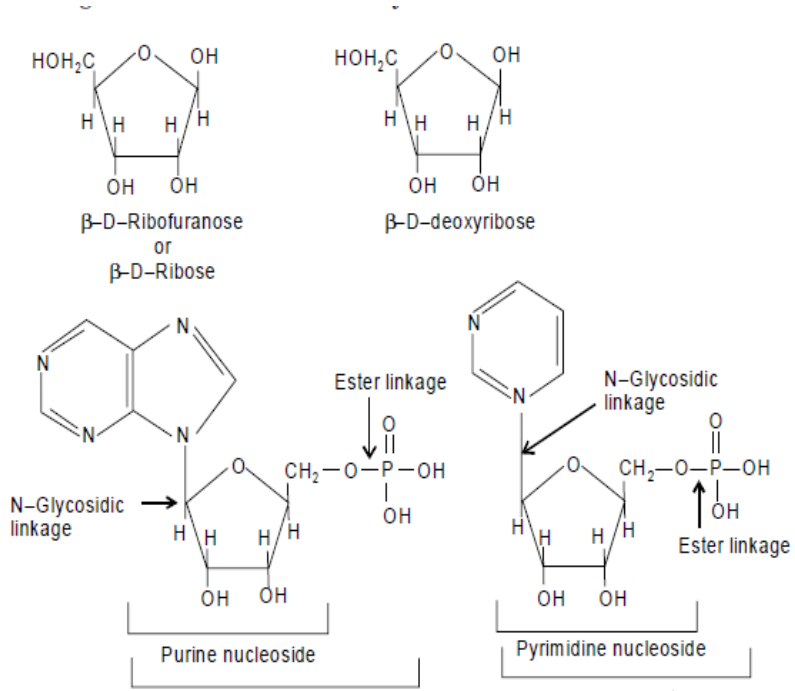

Fig: Structures of ribose, deoxyribose; purine and pyrimidine nucleosides and their corresponding nucleotides

Summary

The addition of a pentose sugar to a base through an N-glycosidic bond produces a nucleoside. If the sugar is ribose, a ribonucleoside is produced, and if the sugar is 2-deoxyribose, a deoxyribonucleoside is produced. The ribonucleosides of A, G, C, and U are named adenosine, guanosine, cytidine, and uridine, respectively. The deoxyribonucleosides of A, G, C, and T have the added prefix deoxy- (for example, deoxyadenosine). [Note: The compound deoxythymidine is often simply called thymidine, with the deoxy- prefix being understood, because it is incorporated into DNA only.] The carbon and nitrogen atoms in the rings of the base and the sugar are numbered separately.

[Note: Carbons in the pentose are numbered 1′ to 5′. Thus, when the 5′-carbon of a nucleoside (or nucleotide) is referred to, a carbon atom in the pentose, rather than an atom in the base, is being specified.]

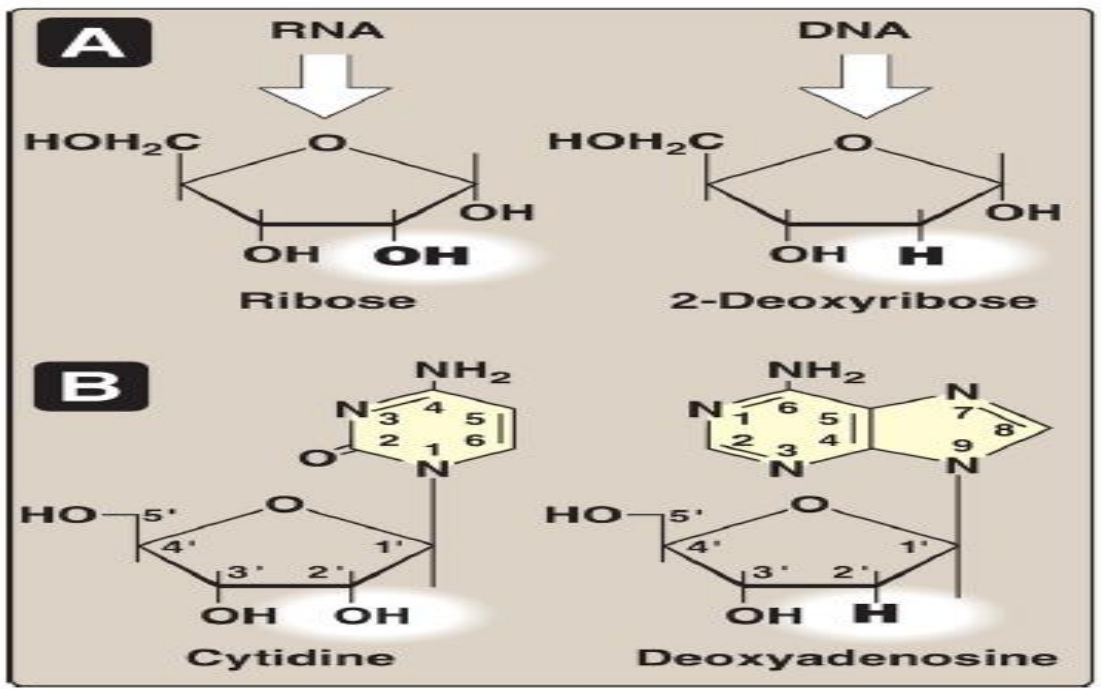

Fig: Pentoses found in nucleic acids. B. Examples of the numbering systems for purine- and pyrimidine-containing nucleosides.

NUCLEOTIDES

The addition of one or more phosphate groups to a nucleoside produces a nucleotide. The first phosphate group is attached by an ester linkage to the 5′-OH of the pentose, forming a nucleoside 5′-phosphate or a 5′-nucleotide.

The type of pentose is denoted by the prefix in the names 5′-ribonucleotide and 5′-deoxyribonucleotide. If one phosphate group is attached to the 5′-carbon of the pentose, the structure is a nucleoside monophosphate, like adenosine monophosphate (AMP, or adenylate). If a second or third phosphate is added to the nucleoside, a nucleoside diphosphate (for example, adenosine diphosphate [ADP] or triphosphate, for example, ATP) results (Fig.). The second and third phosphates are each connected to the nucleotide by a “high-energy bond” (a bond with a large, negative change in free energy [–ΔG] of hydrolysis). [Note: The phosphate groups are responsible for the negative charges associated with nucleotides and cause DNA and RNA to be referred to as nucleic acids.]

Chemical nature of nucleotides

Hydrolysis of nucleotides produces nitrogen bases, sugars and phosphate.

Nitrogenous bases. Nucleotides contain two types of nitrogenous bases. They are purine bases and pyrimidine bases.

Physicochemical properties of purine bases

1. Purine bases are sparingly soluble in water. Uric acid and xanthine tend to crystalize at physiological pH at high concentration.

2. Purine bases absorb light in UV region at 260 nm. This property is used for detection and quantitation of purine nucleotides.

3. Purine bases are capable of forming hydrogen bonds.

4. Purine bases like guanine exhibit keto-enol tautomerism at body pH. The keto form predominates. However, small amount of enol form is present.

5. Purine bases exhibit amino-imino tautomerism at body pH. However, amino form predominates

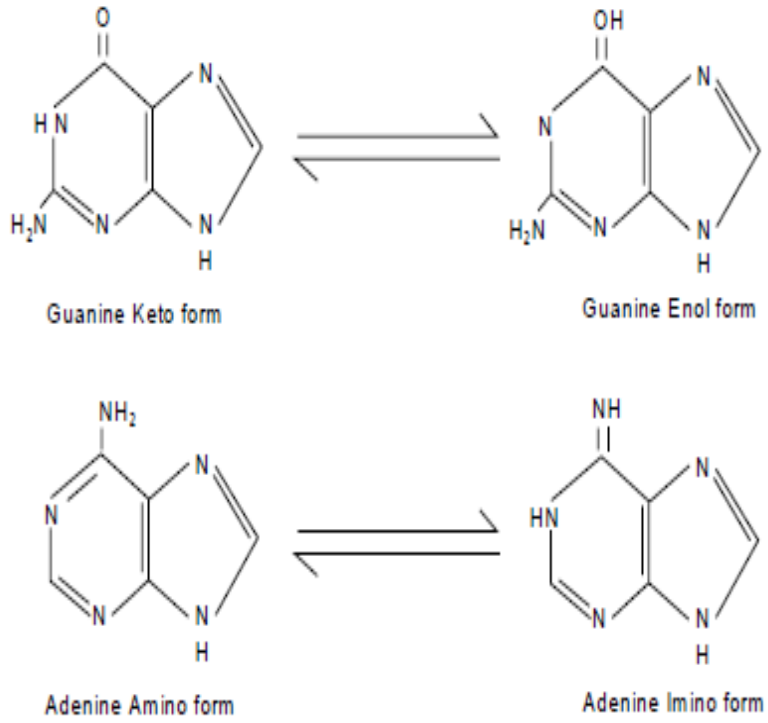

Fig: Types of tautomerism of purine bases

Physicochemical properties of pyrimidine bases

1. Pyrimidine bases are soluble in water at body pH.

2. Pyrimidine bases also absorb UV light at 260 nm. This property is used to detect and estimate pyrimidine nucleotides.

3. They are capable of forming hydrogen bonds.

4. They too exhibit keto-enol tautomerism as well as amino-imino tautomerism like purine bases.

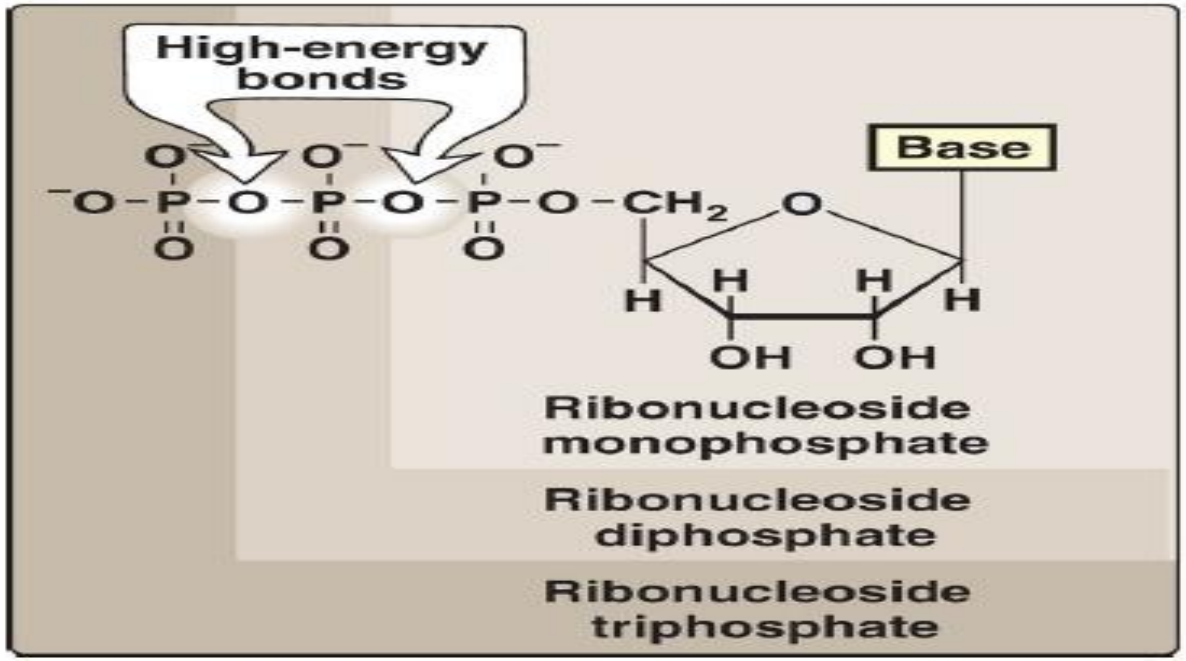

Fig: Ribonucleoside monophosphate, diphosphate, and triphosphate.

PURINE NUCLEOTIDE SYNTHESIS

The atoms of the purine ring are contributed by a number of compounds, including amino acids (aspartate, glycine, and glutamine), carbon dioxide (CO_2), and N10-formyltetrahydrofolate (N10-formyl-THF), as shown in Figure. The purine ring is constructed primarily in the liver by a series of reactions that add the donated carbons and nitrogens to a pre-formed ribose 5-phosphate.

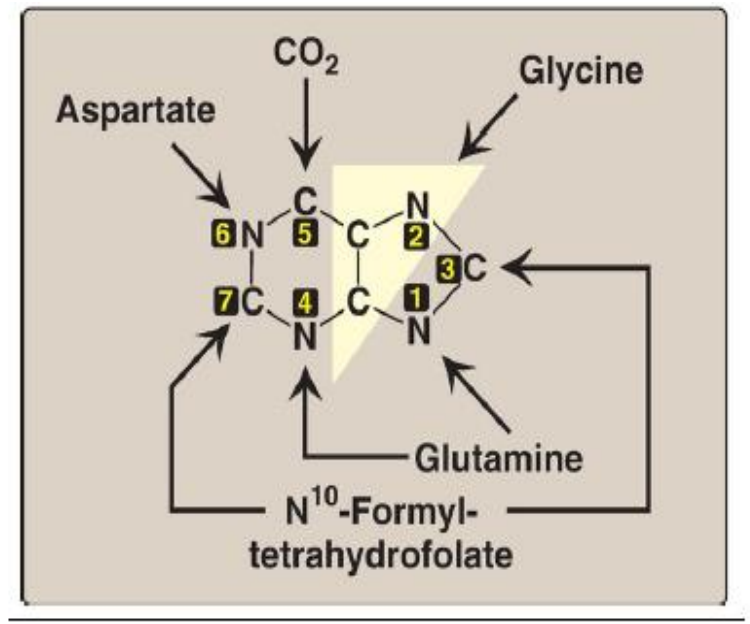

Fig: Sources of the individual atoms in the purine ring. The order in which the atoms are added is shown by the numbers in the black boxes. CO_2 = carbon dioxide.

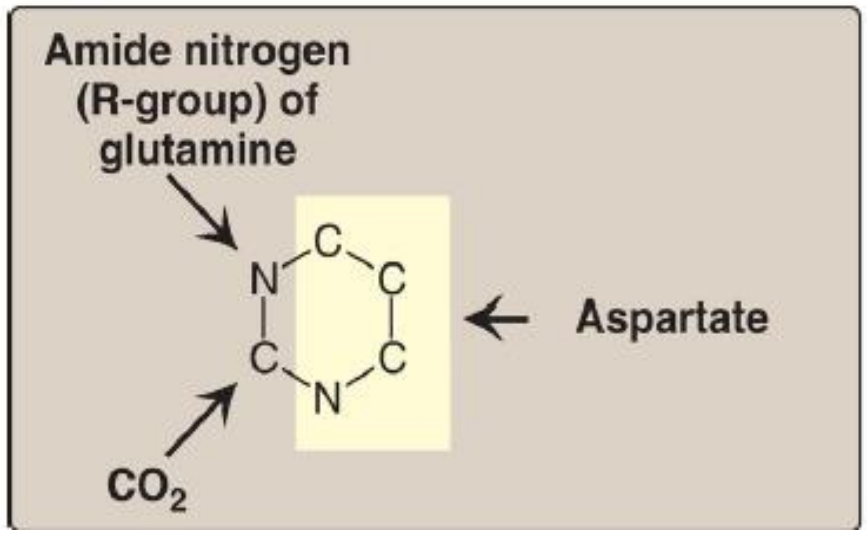

Fig: Sources of the individual atoms in the pyrimidine ring. CO_2 =carbon dioxide.

Name	Alternate name	Abbreviation
Adenosine monophosphate	Adenylic acid	AMP
Deoxy adenosine monophosphate	Deoxyadenylic acid	dAMP
Guanosine monophosphate	Guanylic acid	GMP
Deoxy guanosine monophosphate	Deoxy guanylic acid	dGMP
Cytidine monophosphate	Cytidylic acid	CMP
Deoxy cytidine monophosphate	Deoxy cytidylic acid	dCMP
Deoxy thymidine monophosphate	Deoxy thymidylic acid	dTMP
Uridine monophosphate	Uridylic acid	UMP
Inosine monophosphate	Inosinic acid	IMP
Orotidine monophospahate	Orotidylic acid	OMP

Table: Nomenclature of nucleotides

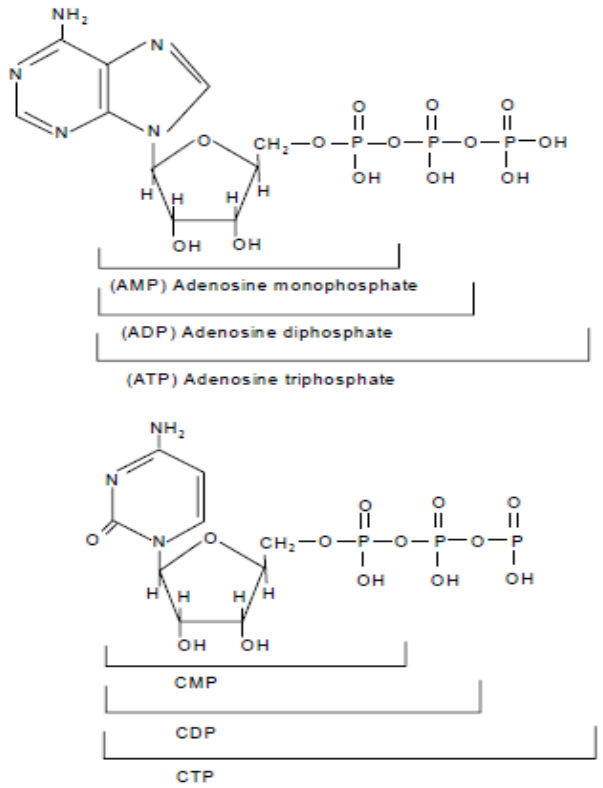

Fig: Structures of nucleoside mono, di and triphosphate of adenine and cytosine

Nucleoside (di and triphosphates)

- They are nucleosides in which two or three phosphate groups are attached to C-5 or C-3 of ribose. Since they are phosphorylated nucleosides, they are nucleotides also. For example, adenosine with two phosphates attached to ribose is called as adenosine diphosphate (ADP) (Fig). Likewise adenosine triphosphate (ATP) (Fig.). Names and abbreviations of some nucleoside di and tri phosphates are given in Table.

Phosphates are in acid anhydride forms.

Name of diphosphate	Abbreviation	Name of triphosphate	Abbreviation
Adenosine diphosphate	ADP	Adenosine triphosphate	ATP
Deoxy Adenosine diphosphate	dADP	Deoxy Adenosine triphosphate	dATP
Guanosine diphosphate	GDP	Guanosine triphosphate	GTP

(Contd.)

Table: Some nucleoside di and triphosphates

Deoxy Guanosine diphosphate	dGDP	Deoxy Guanosine triphosphate	dGTP
Cytidine diphosphate	CDP	Cytidine triphosphate	CTP
Deoxy Cytidine diphosphate	dCDP	Deoxy Cytidine triphosphate	dCTP
Thymidine diphosphate	TDP	Thymidine triphosphate	TTP
Deoxy Thymidine diphosphate	dTDP	Deoxy Thymidine triphosphate	dTTP
Uridine diphosphate	UDP	Uridine triphosphate	UTP

Table: Some nucleoside di and triphosphates

Dinucleotides

They consist of two nucleotides. They are joined together by phosphodiester linkage. 3'-OH of first nucleotide is linked to 5'-OH of second nucleotide through the phosphodiester linkage.

- Two co-enzymes, which are dinucleotides are NAD^+ ($NADP^+$) and FAD. But in these dinucleotides, nucleotides are held together through anhydride linkage formed between phosphate of first nucleotide and phosphate of second nucleotide. Further in FAD the glycosidic linkage between sugar and base is absent.

Oligonucleotides

They consist of less than ten nucleotides but more than two nucleotides. Nucleotides are joined by phosphodiester linkage.

Example: Oligo adenylate.

Naturally occurring nucleotides

Cells contain several free nucleotides. Several biological processes depend on free nucleotides.

Adenine nucleotides and their functions

1. ATP is energy currency of the cell. In mammalian cells, its concentration is about 1 mM/L.
2. Oxidative phosphorylation of respiratory chain requires ADP. ADP is a high energy compound.
3. ATP, ADP and AMP are allosteric effectors of several enzymes.
4. Several hormones exert their action through cyclic AMP or cAMP.
5. Phosphoadenosine phosphosulfate (PAPS) is the donor of sulfate groups in many biosynthetic reactions (Fig.)
6. Adenine nucleotides are constituents of FAD and NAD+, NADP+ (Fig), coenzyme A and vitamin B12 co-enzyme.
7. Diadenosine triphosphate and diadenosine poly phosphate are neurotransmitters and affect platelet aggregation and blood pressure.
8. Oligoadenylate is mediator for interferon action.
9. ATP is required for protein biosynthesis

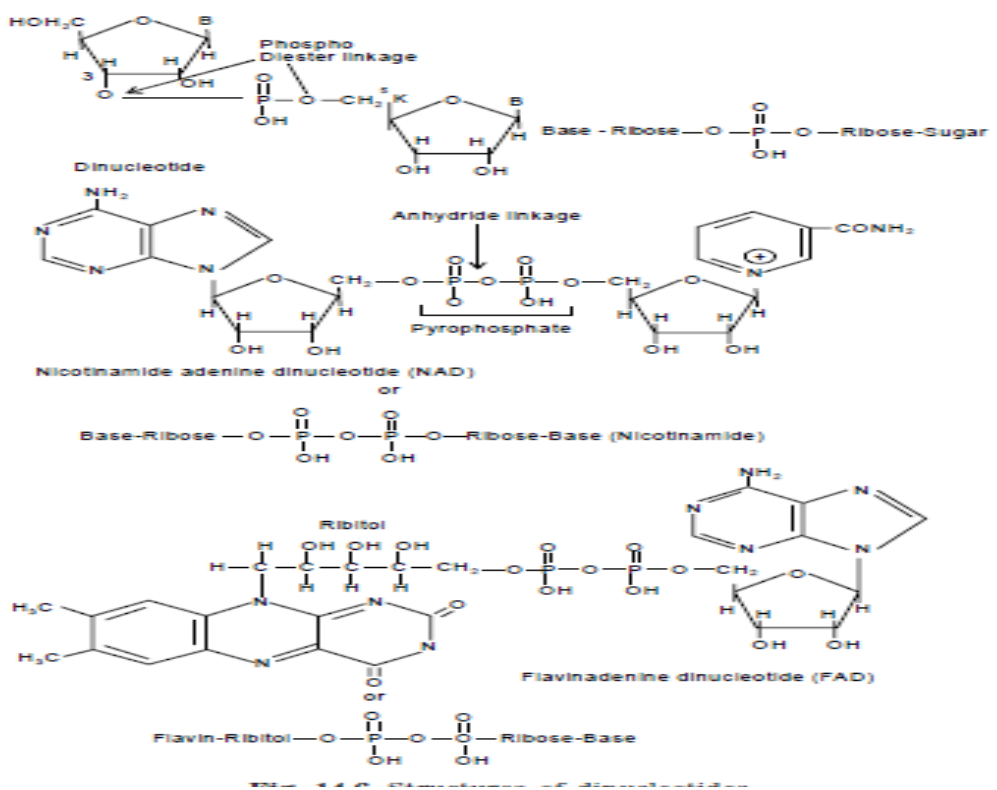

Fig: Structure dinucleotides

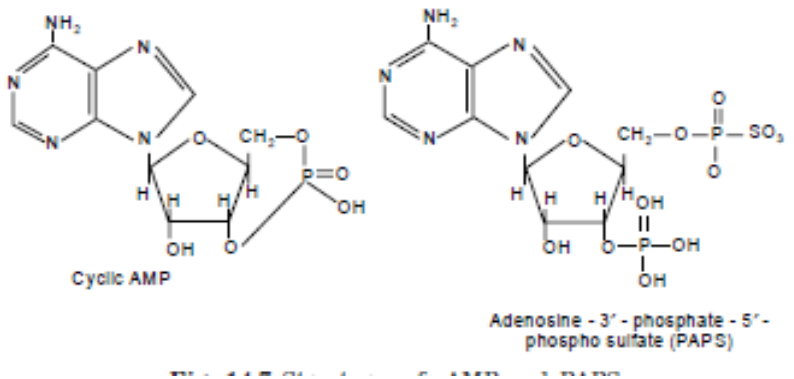

Fig: Structures of cAMP and PAPS

Guanine nucleotides and their functions

1. GTP and GDP are high energy compounds. They participate in energy-dependent reactions.

2. GTP is required for protein biosynthesis.

3. Many hormones mediate their action though cyclic GMP or cGMP. cGMP is involved in vasodilation and smooth muscle relaxation.

4. G-proteins, which require GTP and GDP are involved in signal transduction of several biological processes like vision, taste, metabolic regulation, olfaction, and cancer.

5. RNA is catalytically active in presence of GMP or Ribozyme action depends on GMP.

6. GDP is carrier of activated sugars in biosynthesis of mucopolysaccharides

Hypoxanthine nucleotides

1. IDP and IMP are high energy compounds.

2. IMP is intermediate in purine ribonucleotide synthesis.

Uracil nucleotides

1. UTP and UDP are high energy compounds.

2. UDP is carrier of activated sugars and amino sugars needed for the synthesis of glycogen, glycoprotein, gangliosides etc.

3. UDP-glucuronate serves as a donor of glucuronide in conjugation reactions. For example, formation of bilirubin diglucuronide and detoxification reactions.

Cytosine nucleotides

1. CTP and CDP are high energy compounds.

2. CDP-choline serves as a donor of choline in biosynthesis of phospholipids.

3. CMP-NANA is donor of NANA in biosynthesis of gangliosides.

4. Cyclic CMP also exists in cells.

Adenine nucleoside

S-adenosyl methionine is an adenine nucleoside. It is the donor of methyl groups in biosynthesis reactions.

Unusual nucleosides

1. Pseudouridine

In this unusual nucleoside, ribose is attached to C-5 of uracil instead of N-1, which is not common. Hence in pseudouridine —C—C— linkage is present between uracil and ribose instead of —C—N linkage. It is present in RNA

2. Ribothymidine

This unusual nucleoside of thymine contains ribose and it is present in RNA, which is not common.

Purine and pyrimidine analogs

Several synthetic analogs of purines and pyrimidines are used as anti-cancer agents.

Purine analogs

1. Mercaptopurine
2. Thioguanine
3. 2-Aminopurine
4. Allopurinol
5. Azathiopurine. A modified mercaptopurine. It is an immune suppressive agent.

Pyrimidine analogs

1. 5-Flurouracil

Nucleoside analogs

Nucleoside analogs containing modified bases or sugars are used as anti-cancer agents, anti-viral agents and mutagens.

1. **Deazauridine** It is nucleoside with unnatural base. It is anti-cancer drug.
2. **6-Azauridine** Another nucleoside with unnatural base. An anti-cancer agent.
3. **Adenine arabinoside (Ara-A)** It is a nucleoside with abnormal pentose. It acts as anti-cancer agent as well as anti-viral agent.
4. **Arabinosyl cytosine (Ara-C)** It is a cytosine arabinoside used in cancer treatment.
5. **AZT (3'-azido-3'-deoxy thymidine) or Azido thymidine** It is used in treatment of AIDS. It can prevent progression of the disease if given at an early stage.
6. **Dideoxy cytidine** It is used in viral infections.
7. **Bromodeoxy uridine** It is a mutagen.
8. **Iododeoxy uridine** It is an anti-viral agent.
9. **Fluorodeoxy uridine** It is anti-cancer agent.

Occurrence

Nucleotides are present in all types of cells.

MEDICAL AND BIOLOGICAL IMPORTANCE

- Nucleotides are high energy compounds.
- Nucleotides are required for formation of co-enzymes of some members of vitamin B complex group.
- Some nucleotides are called as ‘second messengers’ because many hormones exert their action through them.
- Some nucleotides act as carrier or donor of activated sugars, sulphates and nitrogenous compounds.
- Some nucleotides are involved in signal transduction.
- Some nucleotides are involved in regulation of metabolic pathways.
- Nucleotides act as alarmones. They regulate cell metabolism and alarms cell when all is not well in cell.

MEDICAL AND BIOLOGICAL IMPORTANCE (continued)

- Synthetic analogs of nucleosides and nitrogenous bases are anticancer and antiviral agents.
- Some nitrogenous bases are CNS stimulants
- Some bases act as anti-oxidants.
- Some nucleotide analogs are mutagens
- Nucleosides also act as carriers of groups or compounds.

MEDICAL AND BIOLOGICAL IMPORTANCE

- Nucleotides are building blocks of nucleic acids.
- Purines play major role in cardiovascular biology in normal and pathological conditions.
- They are involved in cardiac aging, angiogenesis, hypertension etc. Purino receptors are identified in cardiovascular system.
- Cyclic nucleotide cAMP is involved in regeneration of nervous tissues that are injured.
- Some nucleotides are involved in regulation of ion channel activity. For example, ATP sensitive K^+ channel couple cell metabolism to either cell excitability or potassium secretion.
- Purine nucleotides support rotation of γ-subunit of ATP synthase of electron transport chain. Extra ring in purines is indispensable for the operation of molecular motor.

SUMMARY

A nucleotide consists of a nitrogenous base (purine or pyrimidine), a pentose sugar, and one or more phosphate groups. Nucleic acids are polymers of nucleotides, joined together by phosphodiester linkages between the 5- hydroxyl group of one pentose and the 3-hydroxyl group of the next.

Two types of nucleic acids: RNA and DNA. The nucleotides in RNA contain ribose, and the common pyrimidine bases are uracil and cytosine. In DNA, the nucleotides contain 2-deoxyribose, and the common pyrimidine bases are **thymine** and cytosine. The primary purines are **adenine** and **guanine** in **both** RNA and DNA.

Nucleic Acid Structure

Discovery of the structure of DNA by **Watson and Crick** in 1953 was a momentous event in science, an event that gave rise to entirely new disciplines and influenced the course of many established ones. Present understanding of the storage and utilization of a cell's genetic information is based on work made possible by this discovery and an outline of how genetic information is processed by the cell is now a prerequisite for the discussion of any area of biochemistry.

Concern: Experiments that led to its discovery and more recent refinements in our understanding.

As in the case of protein structure, it is sometimes useful to describe nucleic acid structure in terms of hierarchical levels of complexity (**primary, secondary, tertiary**). The primary structure of a nucleic acid is its covalent structure and nucleotide sequence.

Any regular, stable structure taken up by some or all of the nucleotides in a nucleic acid can be referred to as secondary structure. All structures considered in the remainder fall under the heading of secondary structure. The complex folding of large chromosomes within eukaryotic chromatin and bacterial nucleoids is generally considered tertiary structure

DNA Molecules Have Distinctive Base Compositions

A most important clue to the structure of DNA came from the work of Erwin Chargaff and his colleagues in the late 1940s. They found that the four nucleotide bases of DNA occur in different ratios in the DNAs of different organisms and that the amounts of certain bases are closely related. These data, collected from DNAs of a great many different species, led Chargaff to the following conclusions:

- The base composition of DNA generally varies from one species to another.
- DNA specimens isolated from different tissues of the same species have the same base composition.

- The base composition of DNA in a given species does not change with an organism's age, nutritional state, or changing environment.
- In *all* cellular DNAs, regardless of the species, the number of adenosine residues is equal to the number of thymidine residues (that is, A = T), and the number of guanosine residues is equal to the number of cytidine residues (G = C).
- From these relationships it follows that the sum of the purine residues equals the sum of the pyrimidine residues; that is, A + G=T + C.

These quantitative relationships, sometimes called "**Chargaff's rules**," were confirmed by many subsequent researchers. They were a key to establishing the three dimensional structure of DNA and yielded clues to how genetic information is encoded in DNA and passed from one generation to the next.

DNA Is a Double Helix

To shed more light on the structure of DNA, Rosalind Franklin and Maurice Wilkins used the powerful method of x-ray diffraction to analyze DNA fibers. They showed in the early 1950s that DNA produces a characteristic x-ray diffraction pattern.

From this pattern it was deduced that DNA molecules are helical with two periodicities along their long axis, a primary one of 3.4 Å and a secondary one of 34 Å. The problem then was to formulate a three-dimensional model of the DNA molecule that could account not only for the x-ray diffraction data but also for the specific A = T and G = C base equivalences discovered by Chargaff and for the other chemical properties of DNA.

In 1953 Watson and Crick postulated a three dimensional model of DNA structure that accounted for all the available data. It consists of two helical DNA chains wound around the same axis to form a right handed double helix.

The hydrophilic backbones of alternating deoxyribose and phosphate groups are on the outside of the double helix, facing the surrounding water. The furanose ring of each deoxyribose is in the C-2 end of conformation

The purine and pyrimidine bases of both strands are stacked inside the double helix, with their hydrophobic and nearly planar ring structures very close together and perpendicular to the long axis. The offset pairing of the two strands creates a **major groove** and **minor groove** on the surface of the duplex. Each nucleotide base of one strand is paired in the same plane with a base of the other strand. Watson and Crick found that the hydrogen-bonded base pairs, G with C and A with T, are those that fit best within the structure, providing a rationale for Chargaff's rule that in any DNA, G = C and A = T. It is important to note that three hydrogen bonds can form between G and C, symbolized GqC, but only two can form between A and T, symbolized AUT.

They found out that separation of paired DNA strands is more difficult the higher the ratio of GqC to AUT base pairs. Other pairings of bases tend (to varying degrees) to destabilize the double-helical structure.

When Watson and Crick constructed their model, they had to decide at the outset whether the strands of DNA should be **parallel** or **antiparallel**—whether their 5,3-phosphodiester bonds should run in the same or opposite directions. An antiparallel orientation produced the most convincing model, and later work with DNA polymerases provided experimental evidence that the strands are indeed antiparallel, a finding ultimately confirmed by x-ray analysis.

To account for the periodicities observed in the x-ray diffraction patterns of DNA fibers, Watson and Crick manipulated molecular models to arrive at a structure in which the vertically stacked bases inside the double helix would be 3.4 Å apart

The secondary repeat distance of about 34 Å was accounted for by the presence of 10 base pairs in each complete turn of the double helix. In aqueous solution the structure differs slightly from that in fibers, having 10.5 base pairs per helical turn.

The two antiparallel polynucleotide chains of double-helical DNA are not identical in either base sequence or composition. Instead they are **complementary** to each other. Wherever adenine occurs in one chain, thymine is found in the other; similarly, wherever guanine occurs in one chain, cytosine is found in the other.

The DNA double helix, or duplex, is held together by two forces, as described earlier: hydrogen bonding between complementary base pairs and base-stacking interactions. The complementarity between the DNA strands is attributable to the hydrogen bonding between base pairs. The base-stacking interactions, which are largely nonspecific with respect to the identity of the stacked bases, make the major contribution to the stability of the double helix.

The important features of the double-helical model of DNA structure are supported by much chemical and biological evidence.

Model immediately suggested a mechanism for the transmission of genetic information.

The essential feature of the model is the complementarity of the two DNA strands.

As Watson and Crick were able to see, well before confirmatory data became available, this structure could logically be replicated by (1) separating the two strands and (2) synthesizing a complementary strand for each. Because nucleotides in each new strand are joined in a sequence specified by the base-pairing rules stated above, each pre-existing strand functions as a template to guide the synthesis of one complementary strand. These expectations were experimentally confirmed, inaugurating a revolution in our understanding of biological inheritance.

DNA Can Occur in Different Three-Dimensional Forms

DNA is a remarkably flexible molecule. Considerable rotation is possible around a number of bonds in the sugar–phosphate (phosphodeoxyribose) backbone, and thermal fluctuation can produce bending, stretching, and unpairing (melting) of the strands. Many significant deviations from the Watson-Crick DNA structure are found in cellular DNA, some or all of which may play important roles in DNA metabolism. These structural variations generally do not affect the key properties of DNA defined by Watson and Crick: strand complementarity antiparallel strands, and the requirement for AUT and GqC base pairs.

Structural variation in DNA reflects three things:

The different possible conformations of the deoxyribose, rotation about the contiguous bonds that make up the phosphodeoxyribose backbone, and free rotation about the C-1–*N*-glycosyl bond.

Because of steric constraints, purines in purine nucleotides are restricted to two stable conformations with respect to deoxyribose, called syn and anti.

Pyrimidines are generally restricted to the anti conformation because of steric interference between the sugar and the carbonyl oxygen at C-2 of the pyrimidine.

The Watson-Crick structure is also referred to as **B form DNA,** or B-DNA. The B form is the most stable structure for a random-sequence DNA molecule under physiological conditions and is therefore the standard point of reference in any study of the properties of DNA. Two structural variants that have been well characterized in crystal structures are the **A** and **Z forms.**

The A form is favored in many solutions that are relatively devoid of water. The DNA is still arranged in a right-handed double helix, but the helix is wider and the number of base pairs per helical turn is 11, rather than 10.5 as in B-DNA.

The plane of the base pairs in A-DNA is tilted about 20 with respect to the helix axis. These structural changes deepen the major groove while making the minor groove shallower. The reagents used to promote crystallization of DNA tend to dehydrate it, and thus most short DNA molecules tend to crystallize in the A form.

Z-form DNA is a more radical departure from the B structure; the most obvious distinction is the left handed helical rotation. There are 12 base pairs per helical turn, and the structure appears more slender and elongated. The DNA backbone takes on a zigzag appearance.

Certain nucleotide sequences fold into left handed Z helices much more readily than others. Prominent examples are sequences in which pyrimidines alternate with purines, especially alternating C and G or 5-methyl-C and G residues. To form the left-handed helix in Z-DNA, the purine residues flip to the syn conformation, alternating with pyrimidines in the anti conformation. The major groove is barely apparent in Z-DNA, and the minor groove is narrow and deep.

Whether A-DNA occurs in cells is uncertain, but there is evidence for some short stretches (tracts) of Z-DNA in both prokaryotes and eukaryotes. These Z-DNA tracts may play a role (as yet undefined) in regulating the expression of some genes or in genetic recombination.

The bending observed with this and other sequences may be important in the binding of some proteins to DNA.

A rather common type of DNA sequence is a **palindrome.**

A palindrome is a word, phrase, or sentence that is spelt identically read either forward or backward; two examples are ROTATOR and NURSES RUN.

The term is applied to regions of DNA with **inverted repeats** of base sequence having twofold symmetry over two strands of DNA. Such sequences are self-complementary within each strand and therefore have the potential to form **hairpin** or **cruciform** (cross-shaped) structures. When the inverted repeat occurs within each individual strand of the DNA, the sequence is called a **mirror repeat.**

- Mirror repeats do not have complementary sequences within the same strand and cannot form hairpin or cruciform structures. Sequences of these types are found in virtually every large DNA molecule and can encompass a few base pairs or thousands.

Thank you very much