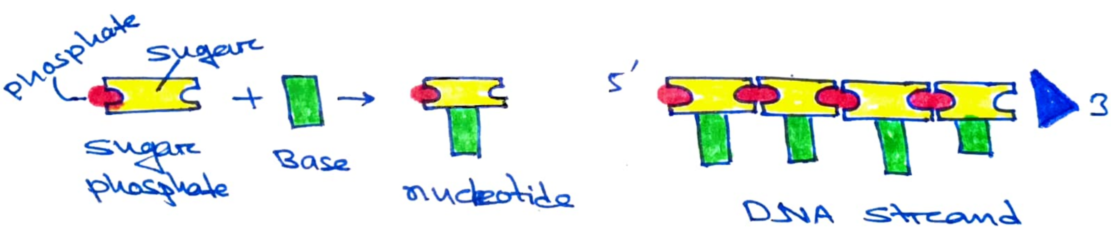
Structure of DNA →

(X-ray diffraction analysis)

- A DNA molecule consists of two long polynucleotide chains composed of 4 types of nucleotide subunits. Each of these chains are known as a DNA chain, or a DNA strand. H-bonds betn the base portions of the nucleotides hold the two chains together.

- Nucleotides are composed of a five-carbon sugar to which are attached one or more phosphate groups and a N containing base. In case of nucleotides in DNA, the sugar is deoxyribose attached to a single phosphate group and the base may be either adenine (A), cytosine (C), guanine (G) or thymine (T).

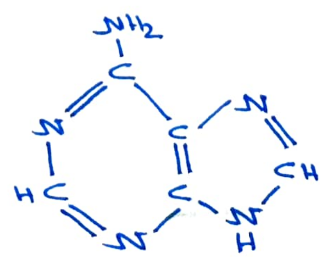


(sugar + nitrogenous base → nucleoside)

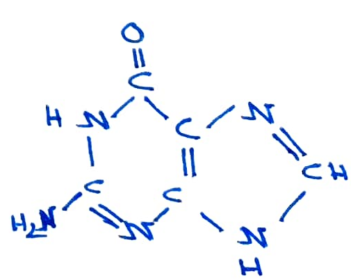
- Nitrogenous bases are of two types-

→ Fused 5 and 6 membered rings (heterocyclic) called as purines e.g. Adenine (A) and Guanine (G)

Purine

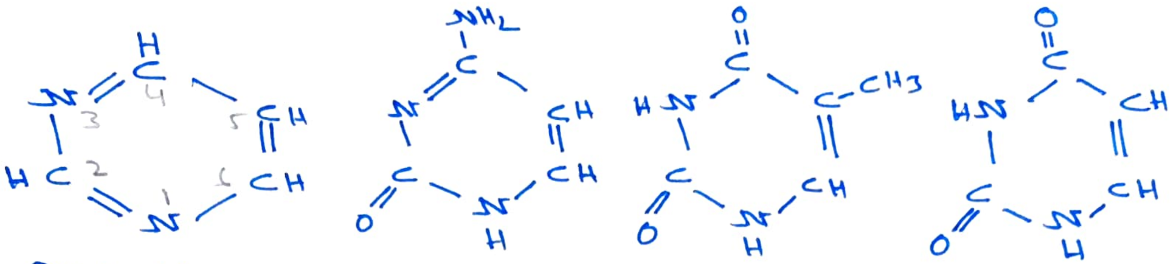


Adenine



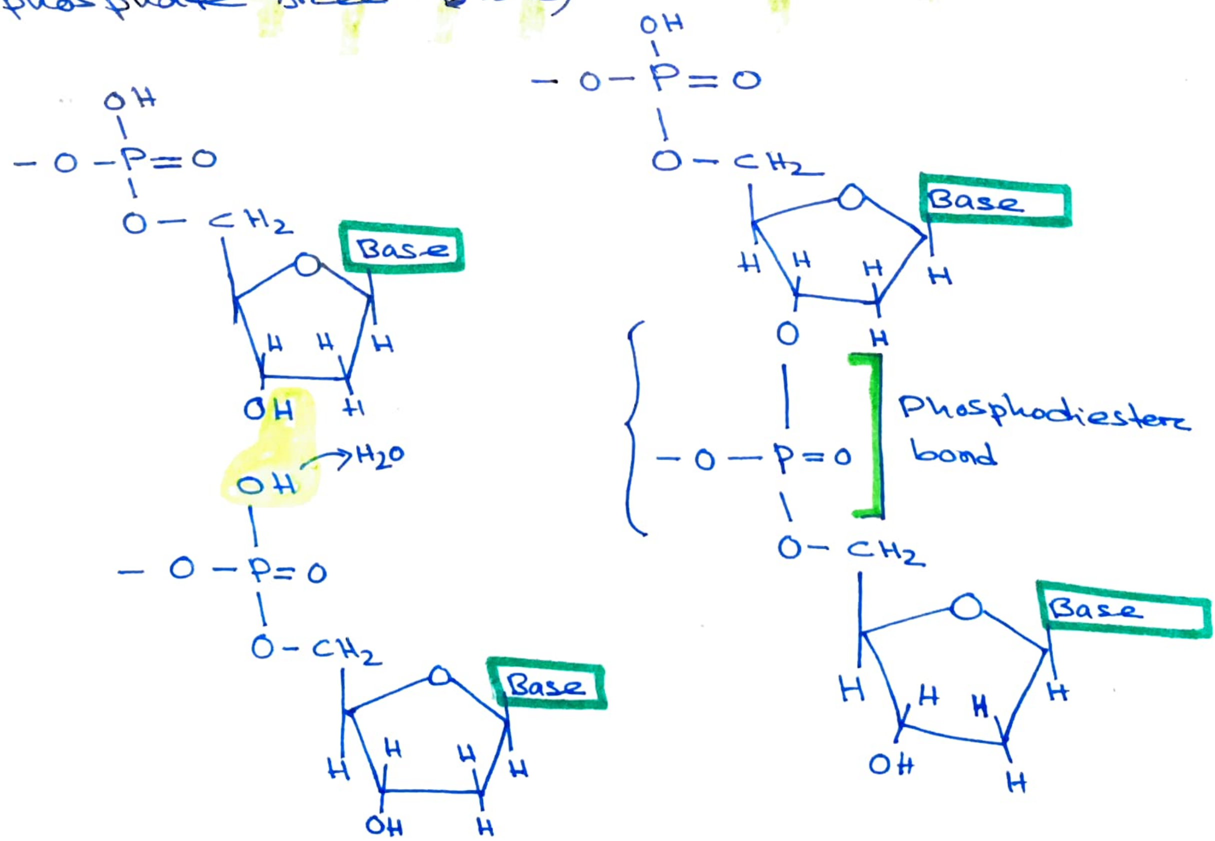
Guanine

→ Six membered rings called are the pyrimidines eg- Thymine(T), Cytosine (c) and Uracil(U)



Pyrimidine   Cytosine   Thiamine (DNA)   Uracil (RNA)

• In a nucleotide the base is joined to 1′ carbon of pentose by an N-β-glycosyl bond and a phosphate is esterified to 5′ carbon. Phosphate of 5′ carbon reacts with -OH group attached to 3′ ribose sugar carbon. During this bond formation a water molecule is removed. This process is continued to make a polynucleotide with one end 3′ sugar carbon attached -OH free (called 3′ end) and other end 5′ sugar carbon attached phosphate free (5′ end)



- Pentose sugar + N. base → Nucleoside.

- adenine → deoxyadenosine
- guanine → deoxyguanosine
- cytosine → deoxycytidine
- Thymine → deoxythymidine.

- Nucleoside + Phosphate → nucleotide

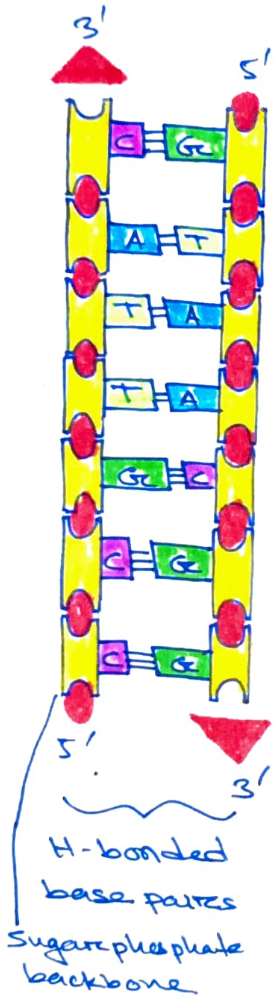
bond betn N. base & sugar →	N-ribosidic or glucosidic bond
bond betn sugar & phosphate →	ester bond

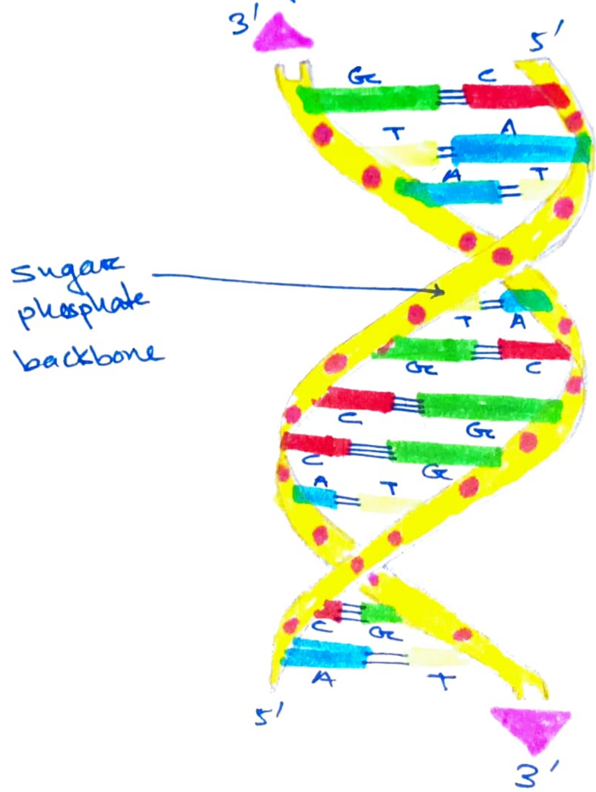
A → deoxyadenylic acid
G → deoxyguanylic acid
C → deoxycytidilic acid
T → deoxythymidilic acid
} nucleotide

- The nucleotides are covalently linked together in a chain through the sugars and phosphates, which thus form a "back bone" of alternating sugar-phosphate-sugar phosphate.

- The way in which the nucleotide subunits are linked together gives a DNA strand a chemical polarity. This polarity in a DNA chain is indicated by referring to one end 3′ end and the other as the 5′ end.

- The ~~three~~ dimensional str. of DNA - the double helix arises from the chemical and structural features of its 2 polynucleotide chains. Because these 2 chains are held together by hydrogen bonding between the bases on the different strand. All the bases are on the inside of the double helix and the sugar-phosphate backbones are on the outside. In each case, a bulkier two ring base (a purine) is paired with a single-ring (a pyrimidine); A with T and G with C always.





• In this arrangement, each base pair is of similar width, thus holding the sugar phosphate backbones an equal distance apart along the DNA molecule. To maximize the efficiency of base pair packing, the two sugar phosphate backbones wind around each other to form a double helix, with one complete turn every 10 base pairs.

• The members of each base pair can fit together within the double helix only if the two strands of the helix are anti parallel that is, only if the polarity of one strand is oriented opposite to that of the other strand.

- A consequence of these base pairing requirements is that each strand of a DNA molecule contains a sequence of nucleotides that is exactly complementary to the nucleotide sequence of its partner strand.

Watson and Crick structure of DNA (B-DNA) →

(i) It consists of 2 antiparallel polynucleotide strands that wind about a common axis with a right handed twist to form a double helix.

(ii) The diameter of a double helix will be 20 A°.

(iii) Each base is hydrogen bonded to a base on opposite strand (A with T & G with C) to form a planar base pair and the planes of these base pairs are nearly perpendicular to the helix axis. (A = T & G ≡ C)

(iv) The ideal B DNA helix has 10 base pairs per turn and the helix rotates 36° per base pair.

(v) The helix has a pitch (the distance raised by common axis in a complete turn) of 34 A°. So per base pair raise in common axis will be 3.4 A°.

(vi) The double helix has major and minor grooves.

Forms of DNA →

DNA may exist in other forms depending on the no. of nucleotides per turn and the distance between adjacent repeating units.

• **The 'A' form** is found in fibres of 75% relative humidity and requires the presence of Na^+, K^+ or Ca^{2+} as the counter ions. The bases donot lie flat, but are tilted 20° away from the perpendicular to the helical axis. A form is probably very close to the conformation of double stranded regions of RNA hybrid duplexes with one strand of DNA & one strand of RNA.

• Watson and Crick constructed the model of DNA in its **B lattice** configuration found in fibres of very high (92%) relative humidity and in solutions of low ionic strength. This B form of DNA having major and minor grooves is thought to prevail in the living cell.

• **The C form** occurs when DNA fibres are maintained in 66% relative humidity in presence of lithium ions. It does not occur in vivo. These 3 forms of DNA are available in all DNAs irrespective of sequence.

• **The 'D'** and **E forms** have the fewest base pairs per turn (only 8 & 7.5 respectively) and are lacking in guanine.

• **Z DNA** provides the most striking contrast with the classical structural families. It is a left handed double helical DNA containing about 12 residues per turn. The str. was proposed by Alexander Rich and his coworkers. The path of the sugar-phosphate backbone is zigzag in nature. For that reason it is known as Z-DNA. This str. is found in fibres having alternating purine pyrimidine sequences. It exists only at very high salt conc.

Helix type	Base pair/turn	Degree of rotation/bp	Vertical rise/bp	Helix dia.	conditions
A	11	+34.7	2.56 A°	23 A°	75% RH, Na, K, Ca
B	10	+36.0	3.4 A°	20 A°	92% RH, Na
C	9.33	+38.6	3.32 Å	19 Å	66% RH, Li ions
Z	12	-30.0	5.71 A°	18 Å	High salt conc. alternating purine & pyrimidine sequence.