Watson & Crick's Model

(Structure of B-DNA)

The Watson- Crick structure of B-DNA has the following major features:

- It consists of two polynucleotide strands that wind about a common axis with a right handed twist to form a 20 A^0 in diameter double helix. The two strands are antiparallel (run in opposite direction) and wrap around each other such that they cannot be separated without unwinding the helix (a phenomenon known as **plectonemic coiling**). The base occupies the core of the helix while its sugar – phosphate chains are coiled about its periphery thereby minimizing the repulsions between charged phosphate groups.
- The planes of the bases are nearly perpendicular to the helix axis. Each base is hydrogen bonded to a base on the opposite strand to form a planar base pair. It is the hydrogen bonding interactions, a phenomenon known as complementary base pairing that result in the specific association of the two chains of the double helix.
- The ideal B-DNA helix has 10.4 base pairs per turn. The vertical rise per base pair is 3.4^0A. The helix pitch i.e. the helix in B-DNA moves a total distance 3.4x10.4 or $35.36A^0$. The value of rotation per base pair is 360/10.4 or 34.61^0 (recall that during one turn, the helix rotates by an angle 360^0).

Char gaff's rule: The base composition of DNA from a number of sources has been worked out by a number of investigators. The important conclusion drawn are :

- The sum of purines is equal to the sum of pyrimidines ,i.e. Pu/Py = 1. In other words, A+G=T+C.
- The ratio of adenine to thymine is also one, i.e. A/T=1.
- The ratio of guanine to cytosine is alo one ,i.e. G/C=1.

- Bases with 6-aminogroups are equal to bases with 6-keto groups, i.e. A+C=G+T.
- 5. The ratio of A+T/G+C, known as dissymmetry ratio, varies greatly from one species of DNA to the other and is characteristic of that species. When the dissymmetry ratio exceeds one, such a DNA is called AT type; when the value is less than one , the DNA is designated as GC type.

Chargaff's rule suggests that A is always paired with T and G is always paired with C.

How base complementarity of the poly nucleotide is maintained? An important feature of the double helix is the specificity of the pairing of bases. Pairing is always occurs between adenine and thymine and between guanine and cytosine. Base pairing is due to the following two factors:

- ***Steric factors*** : The steric restriction is imposed by the regular helical nature of the sugar phosphate backbone of each polynucleotide chain. The geometry of the base pair has some special consequences in that the distances between the glycosidic bonds are the same for both the base pairs and also because the bone angle between the glycosidic bond direction and the line joining the C1 atoms is the same in each pair. With the result the glycosidic bonds of all nucleotides are arranged in an identical manner in relation to the axis of the helix, despite the differences of the bases. The glycosidic bonds that are attached to a base pair are always 10.85 A0 apart. A purine pyrimidine base pair fits perfectly in this space. In contrary to this, there is insufficient space for two purines, whereas there is more than enough space for two pyrimidines so that would be far apart to form hydrogen bonding. Hence one member of a base pair in a DNA helix must invariably be a purine and the other a complementary pyrimidine because of steric reason.

- ***Hydrogen bonding factor*** : The base pairing is further restricted by hydrogen bonding requirements. The hydrogen atoms in purine and pyrimidine bases have well defined positions. Adenine can not pair with cytosine because there would be two hydrogen atoms near one of the bonding position but none at the other. Similarly, guanine cannot pair with thymine. In contrast adenine forms two hydrogen bond with thymine whereas guanine forms three with cytosine. The G-C bond is stronger by 50% than the A-T bond.

NUCLEOSIDES : The nucleoside are compounds in which nitrogenous bases (purines and pyrimidines) are conjugated to the pentose sugar (ribose or deoxyribose) by a β-glycosidic linkage. The β – glycosidic linkage involves the C-1' of sugar and the hydrogen atom of N9 (in case of purine) or n-1 (in the case of pyrimidines), thus eliminating a molecule of water. Therefore purine nucleosides are n-9 glycosides and the pyrimidine nucleosides are N-1 glycoside. Purine nucleosides are readily hydrolysed by acids whereas pyrimidine nucleosides are hydrolysed only after prolonged treatment with concentrated acid. The nucleosides are generally named for the particular purine or pyrimidine present. Nucleoside containing ribose are called ribonucleosides, while those possessing deoxyribose as deoxyribosnucleosides**.**

Pseudouridine, an unusual nucleoside, is present as a constituents of the transfer RNAs. In it the β-glycoside linkage occurs between the C1 of ribose and C5 or uracil. Recently nucleoside analogues 3'-azidodeoxythymidine (AZT) and 2',3'-dideoxycytidine (DDC), have been therapeutically used for AIDs patients.

NUCLEOTIDES : Nucleotides are the phosphoric acid ester derivatives of nucleosides. These occur either in the free from or as subunits in nucleic acids. The phosphate is esterified with sugar moiety.

In the ribose moiety of a ribonucleoside, the phosphorylation is possible only at three positions (C2',C3',C5') since C1' and C4' are involved in the furanose ring formation. In other word, phosphate group could be esterified only at these places. On the contrary, in the deoxyribose component of a 2-deoxyribonucleoside, only two positions (C3',C5') are available for phosphorylation, since in this sugar C1' and C4' are involved in the furanose ring formation and C2' does not bear any hydroxyl group. Accordingly, hydrolysis of the two nucleic acids, RNA and DNA, by various methods and under different set of conditions gives rise to isomeric nucleotide of 3 types and 2 types respectively. Names of nucleotides are generally derived from the corresponding bases. The base corresponding to the nucleoside called inosin (and the derived nucleotides) is called hypoxanthin.

Z- DNA : Z-DNA is the more radical departure from B-DNA and is characterized by a left handed helical rotation. It is discovered by Rich, Nordheim, and Wang in 1984. They found that a hexanucleotide, CGCGCG, forms a duplex of antiparallel strands held together by Watson Crick base pairing as expected. Surprisingly they found that this double helix was left-handed and the phosphate in the DNA backbone were in zigzag manner; hence, they termed this new from as Z- DNA. Another remarkable characteristic of Z-DNA is that in it the adjacent sugar residues have alternating orientation and it is because of this reason that in Z- DNA, the repeating unit is dinucleotide as against the B-DNA, where the adjacent sugar residues have same orientation so that the repeating unit in B- DNA is a mononucleotide. Z- DNA contains only one deep helical groove. There are 12 base pairs (six repeating dinuclotide units) per helical turn, with an axial rise 3.8A per base pair; the bases are inclined at 9 with the axis of the helix. Because 12 base pairs are accommodated in one helix, the angle of twist per repeating unit is 360/12x2 or 60 as against 34.61 per nucleotide in B-DNA. One complete helix is 45,60A in length in contrast to 35.36 in B-DNA. Since the bases get more length to spread out in Z- DNA and since the angle of tilt is 60 , they are more

closer to the axis; hence the diameter of Z-DNA molecule is 18.4A , whereas it is 23.7 A in B-DNA**.**