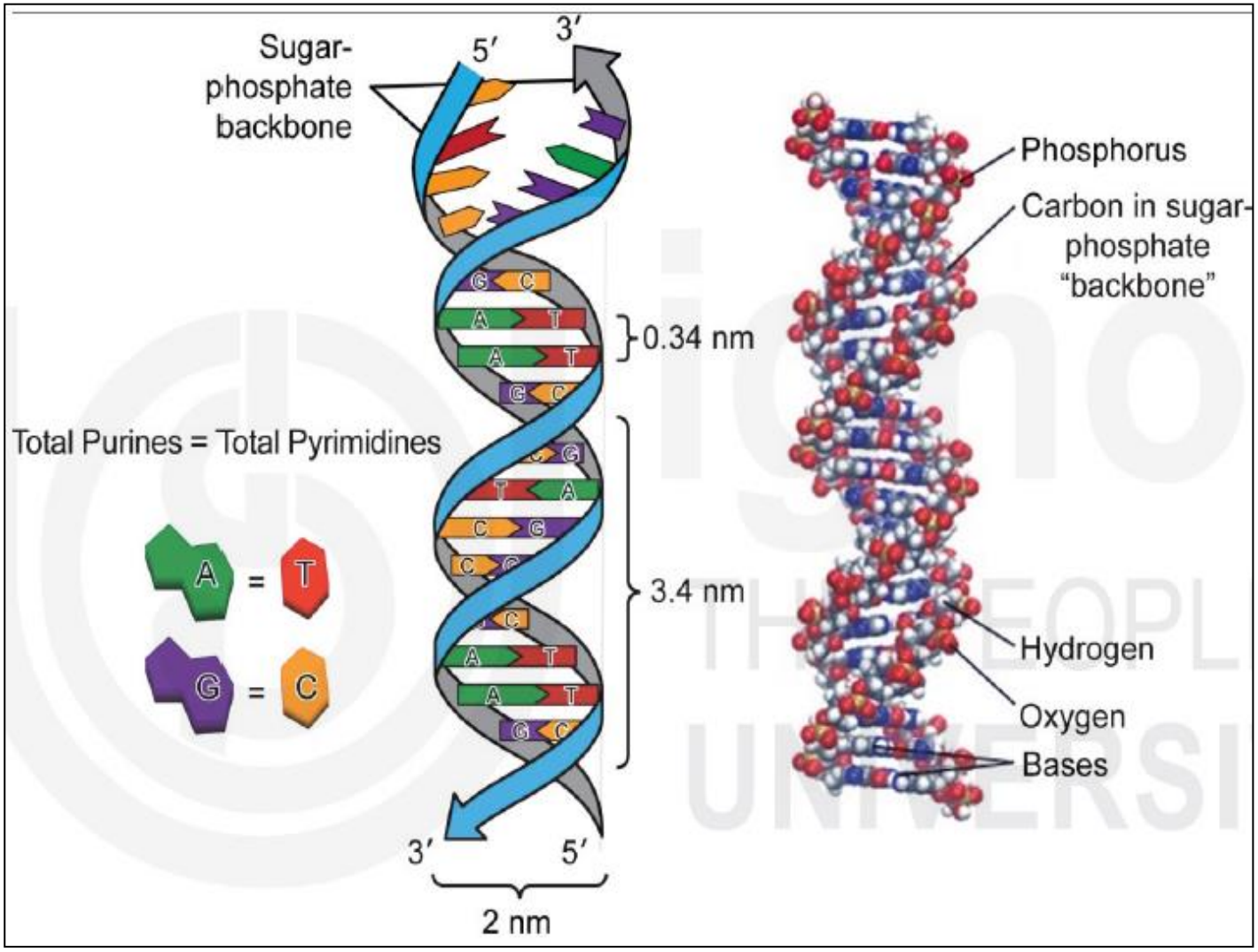
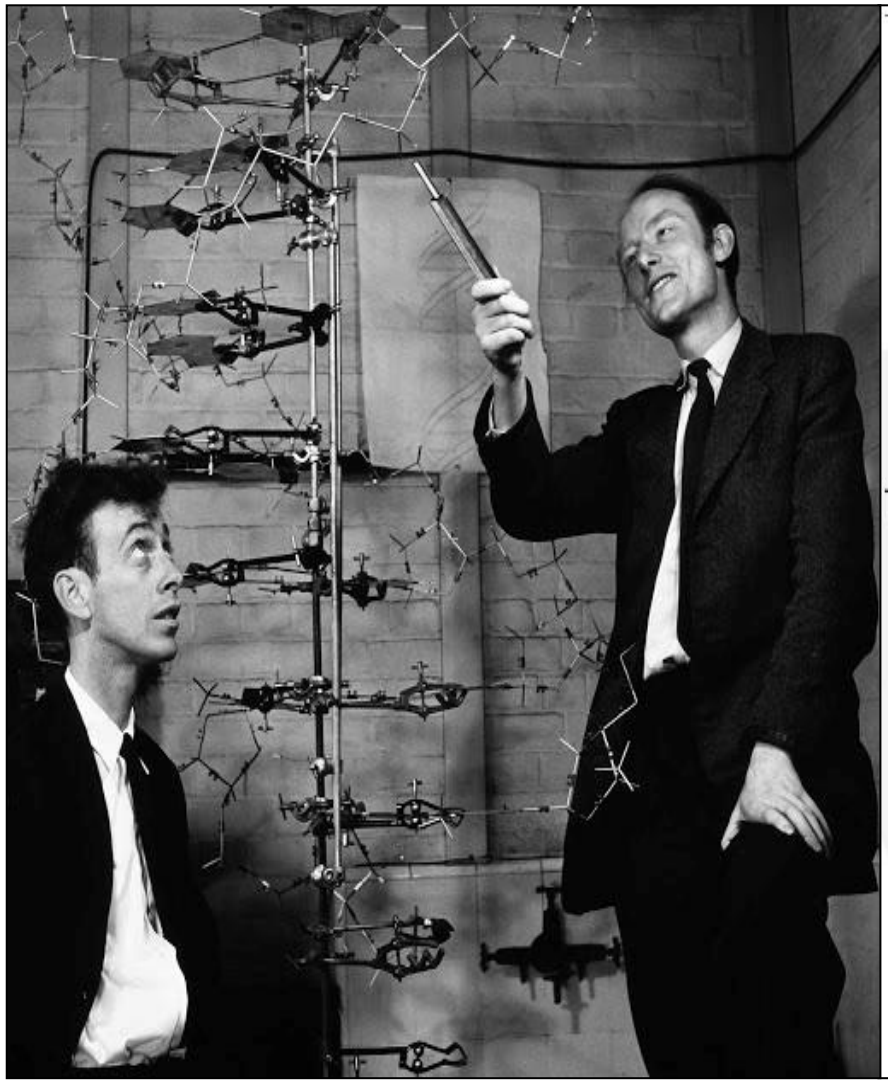
WATSON AND CRICK MODEL OF DNA



Dr. R. Prasad, Department of Zoology, Eastern Karbi Anglong College, Sarihajan

WATSON AND CRICK MODEL OF DNA



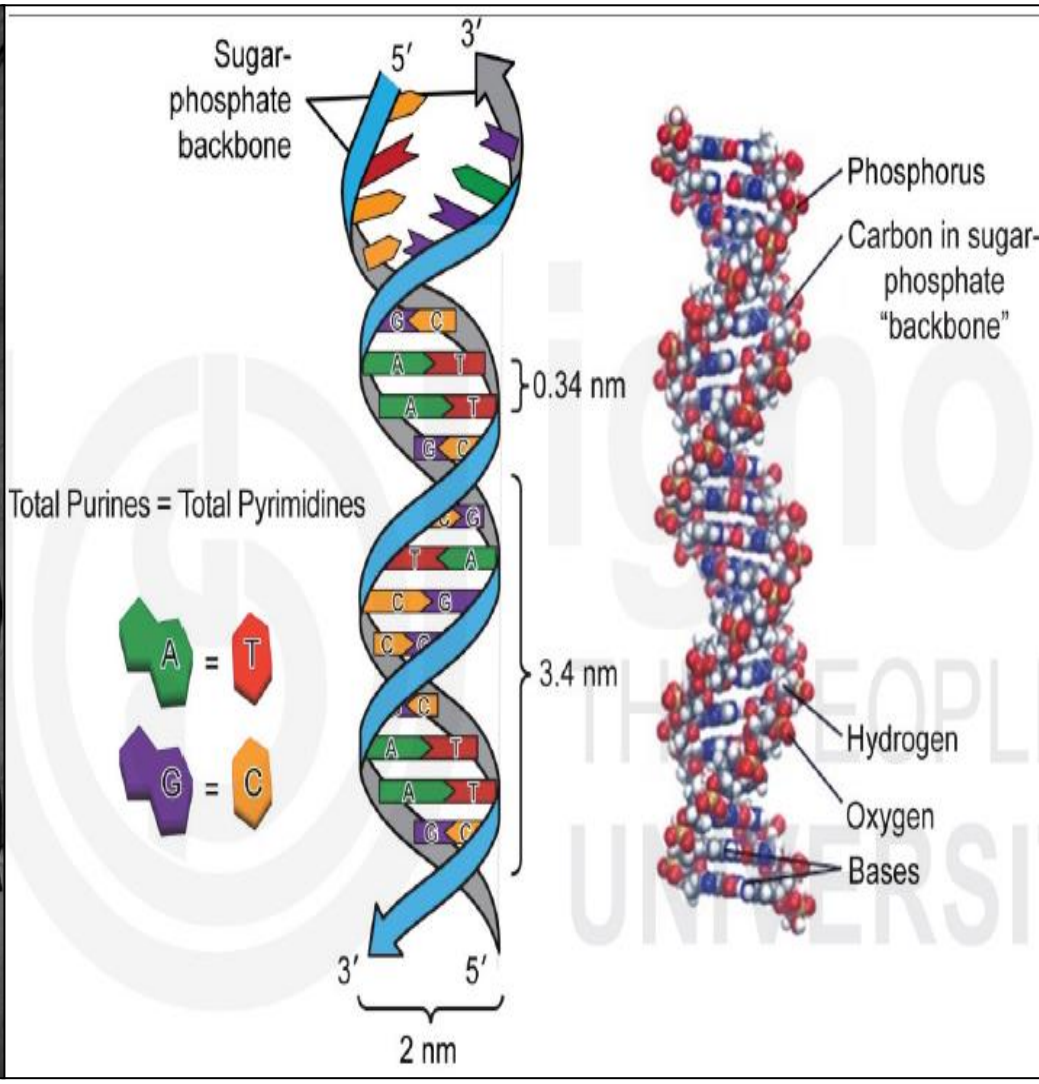
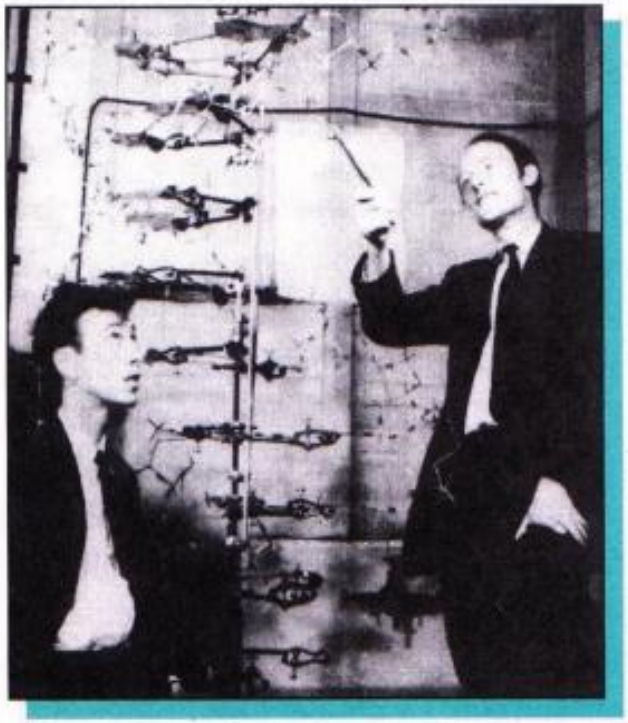
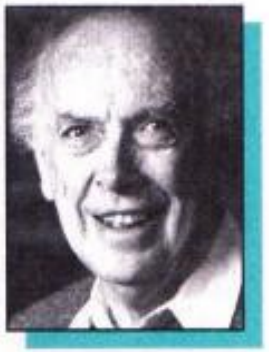


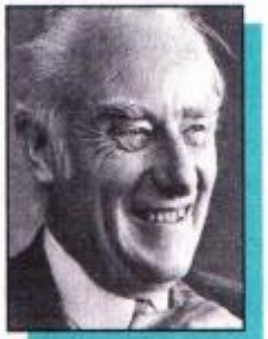
Fig.: A double helix model of DNA as proposed by Watson and Crick.

Discovery of DNA structure by X-ray Diffraction Technology



(a)

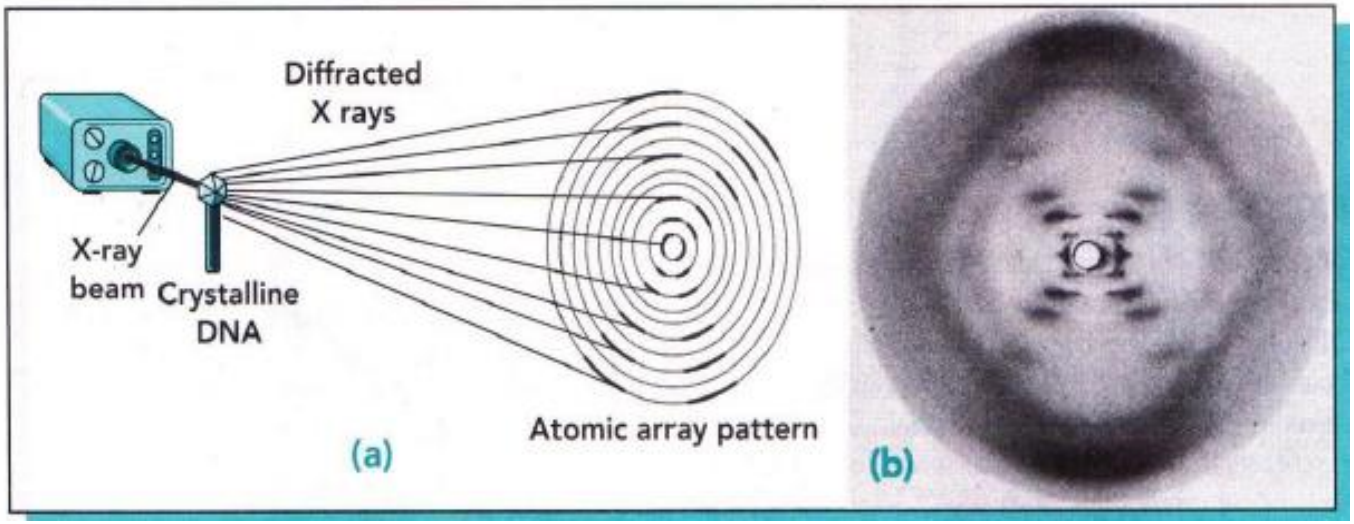




(b)

FIGURE 2.5

James D. Watson and Francis H. C. Crick, the American graduate student and the British biochemist, who correctly explained the structure of DNA. (a) The scientists as they appeared in 1952, when the structure of DNA was formulated. (b) Photographs of more recent vintage.



Landmark Publication

NATURE

No. 4356 April 25, 1953

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A structure for Deoxyribose Nucleic Acid

We wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate—sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3′, 5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed gelices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the *z*-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical *z*-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrmidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data[5,6] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on inter-atomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at King's College, London. One of us (J. D. W.) has been aided by a fellowship from the National Foundation for Infantile Paralysis.

J. D. Watson
F. H. C. Crick

Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems, Cavendish Laboratory, Cambridge.
April 2.

[1]Pauling, L., and Corey, R. B., *Nature*, 171, 346 (1953); *Proc. U.S. Nat. Acad. Sci.*, 39, 84 (1953).
[2]Furberg, S., *Acta Chem. Scand.*, 6, 634 (1952).
[3]Chargaff, E., for references see Zamenhof, S., Brawerman, G., and Chargaff, E., *Biochim. et Biophys. Acta*, 9, 402 (1952).
[4]Wyatt, G. R., *J. Gen. Physiol.*, 36, 201 (1952).
[5]Astbury, W. T., Symp. Soc. Exp. Biol. 1, Nucleic Acid, 66 (Camb. Univ. Press, 1947).
[6]Wilkins, M. H. F., and Randall, J. T., *Biochim. et Biophys. Acta*, 10, 192 (1953).

- **DNA is the genetic material found in nucleus of the cell.**
- **It is a double helical structure made up of two polynucleotide chains coiled around one another.**
- **Each strand of DNA has a backbone made of sugar (deoxyribose) and phosphate groups.**
- **The two strands are held together by bonds between the bases.**
- **Each base is attached to a sugar molecule and a phosphate molecule. This pairing between the bases of two strands leads to formation of base pairs.**
- **The structure formed by joining together of base, sugar and phosphate together is called a nucleotide.**
- **In a double helix, the base pairs are present in the middle while sugar and phosphate molecules are present towards the outer side.**

Watson and Crick Double Helix Model

- DNA is made up of nucleotides which possess three parts: a deoxyribose (5- carbon sugar), a phosphate group, and a nitrogenous base. The nitrogenous bases in DNA are of four types -adenine (A), guanine (G) which are double-ringed purines, and cytosine (C), thymine (T) which are small single-ringed pyrimidines. The phosphate group of one nucleotide bonds covalently with the sugar molecule of the next nucleotide. This results in formation of long chain of nucleotides.
- The sugar–phosphate groups form the backbone of each strand of DNA. The sugar-phosphate bonds in this backbone are called **phosphodiester bonds**. The base pairs are held together by specific hydrogen bonds.

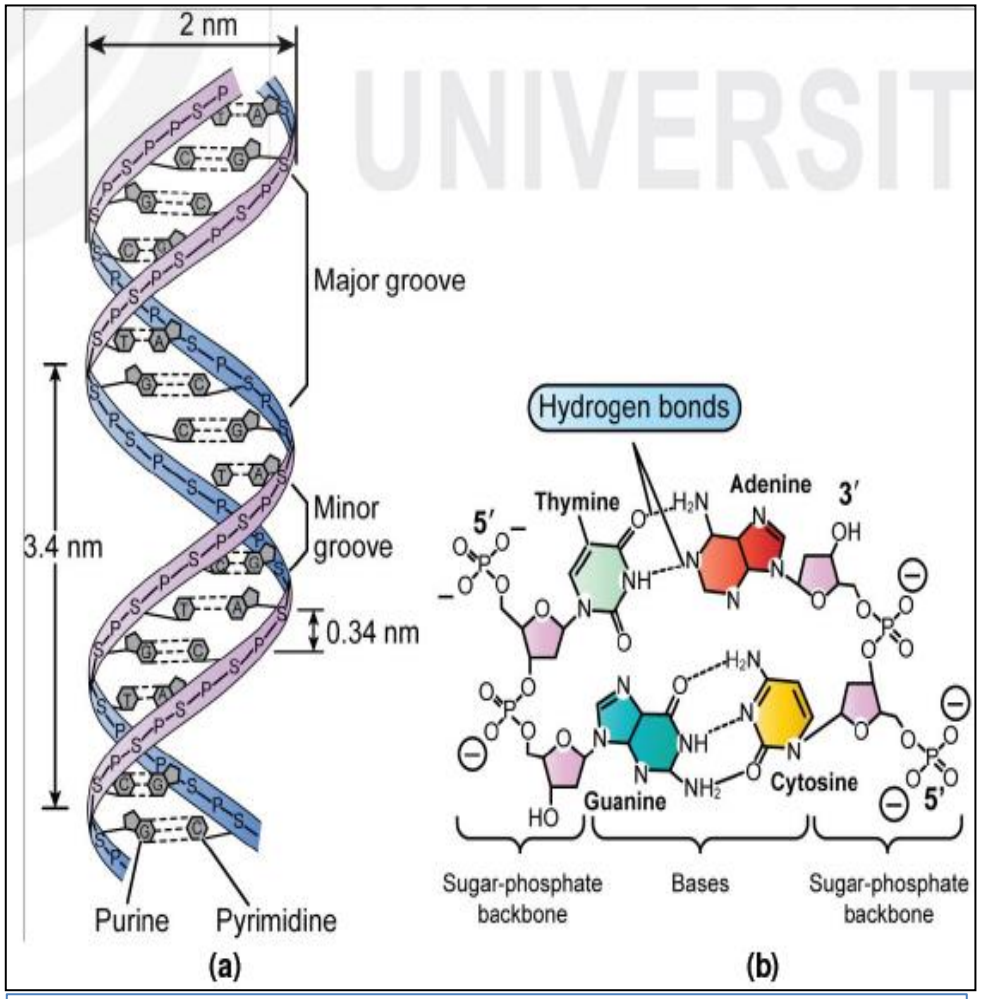


Fig.: Diagrammatic representation of (a) DNA double helix; and (b) sugar phosphate backbone formed in nucleotide.

- **The phosphate group is attached to the 5 carbon of one nucleotide and the 3 carbon of the next nucleotide. Hydrogen bonds formed between the bases assist in holding together the two strands in a DNA molecule. The two strands of DNA are twisted around each other to form a right-handed helix, called a double helix.**
- **Pairing takes place between purine and pyrimidine bases. Adenine pairs with thymine and guanine pairs with cytosine. Adenine and thymine are complementary base pairs. Similarly cytosine and guanine are also complementary base pairs. This feature of DNA is known as complementarity. The quantity of adenine is equal to thymine and quantity of guanine is equal to cytosine in a DNA molecule. Adenine and thymine are connected by two hydrogen bonds, and cytosine and guanine are connected by three hydrogen bonds. The base sequence of one polynucleotide chain determines the base sequence of the opposite chain. The two chains are therefore considered to be complementary to each other.**
- **These two strands are anti-parallel in nature. One strand has 3 carbon of the sugar in the upward position, whereas the other strand will have the 5 carbon in the upward position. The diameter of the DNA double helix remains uniform throughout the structure because a purine base always pairs with a pyrimidine base.**

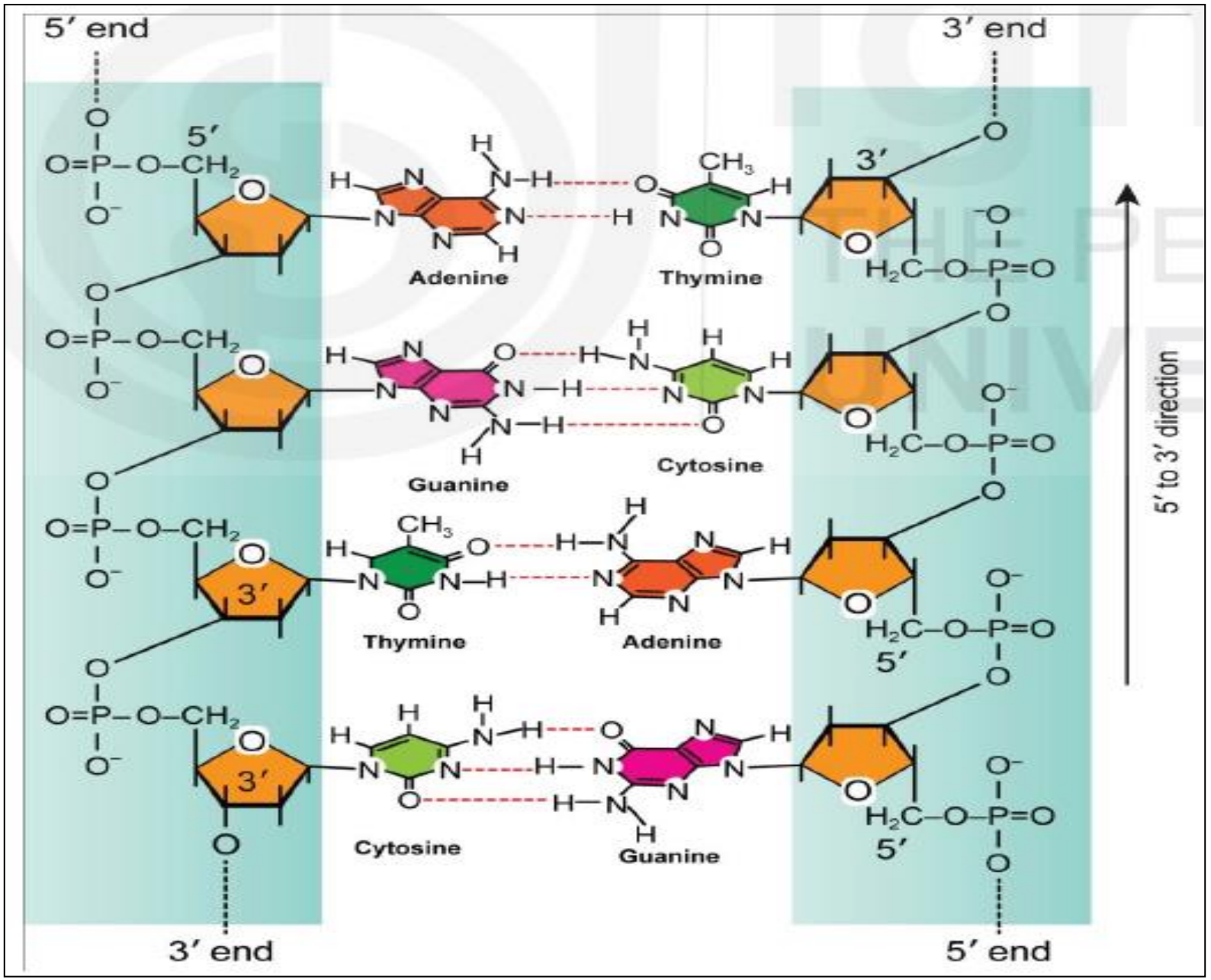


Fig.: Diagram showing bonding between the bases, sugar and phosphate groups present in DNA nucleotide strand.

The main features of the Watson -Crick Model of DNA can be summarize as:

i) Two polynucleotide chains are coiled around a common axis. Both the nucleotide chains run in opposite directions. One end of a DNA strand has a 5′ phosphate and the other end has a 3′ hydroxyl group. The two strands are antiparallel.

ii) The sugar-phosphate backbones are present outside, while the purine and pyrimidine bases lie on the inside of the helix.

iii) In a helix, the bases are separated by distance of 3.4 Å. Ten bases have been found per turn (360°) of helix helical structure. The base pairs are stacked about 0.34 nm apart.

iv) The diameter of the helix is 20 Å.

Chargaff's rule

Erwin Chargaff, an Austrian biochemist, expanded Levene's work and found additional information of the structure of DNA. Chargaff found that nucleotid composition of DNA varies among species. He concluded that almost all DNA, no matter what **organism** or tissue type it comes from but maintains certain properties; even as its composition varies.

Using paper chromatography, he found that the amount of adenine (A) is usually similar to the amount of thymine (T), and the amount of guanine (G) usually approximates the amount of cytosine (C). In other words, the total amount of purines (A + G) equals the total amount of pyrimidines (C + T) (known as "**Chargaff's rule**"). All DNA follow Chargaff's Rule that states that the total number of purines in a DNA molecule is equal to the total number of pyrimidines.

A+T=G+C

The analysis of DNA obtained from different organs of body of the same individual or from different individuals belonging to the same species showed no differences in the relative composition of different bases. The studies suggested that:

- Number of adenine molecules is equal to number of thymine molecules.
- Number of cytosine molecules is equal to number of guanine molecules.

Chargaff's rule may be represented as follow:

A=T: G=C; A+T= G+C

A+G=T+C

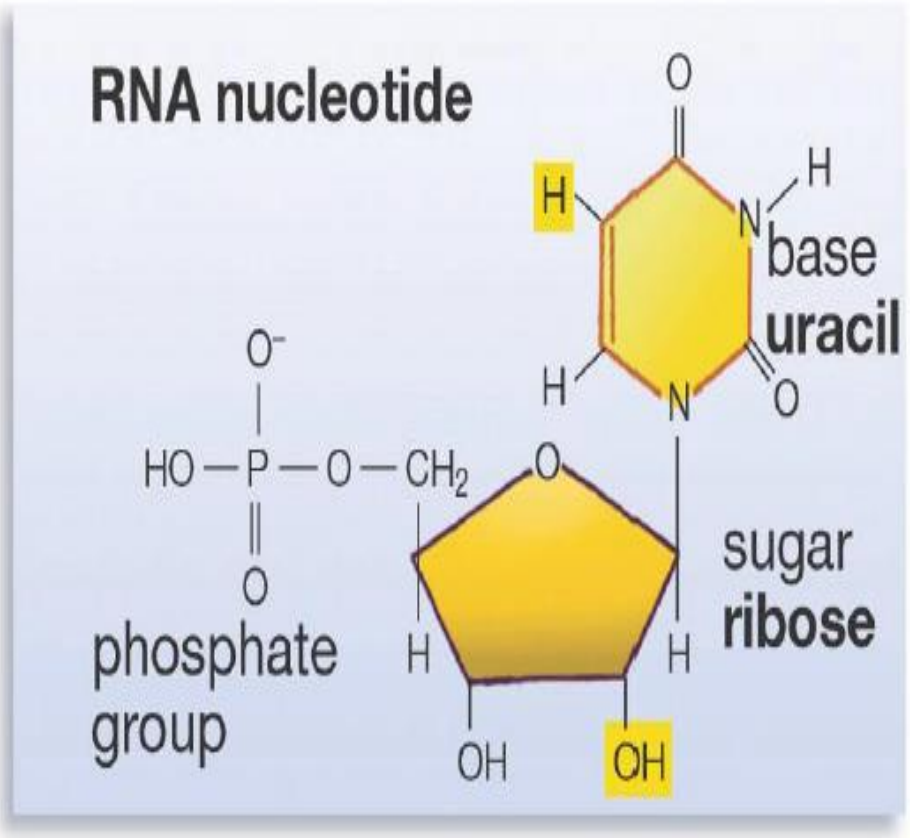
A+G/T+C=1; But

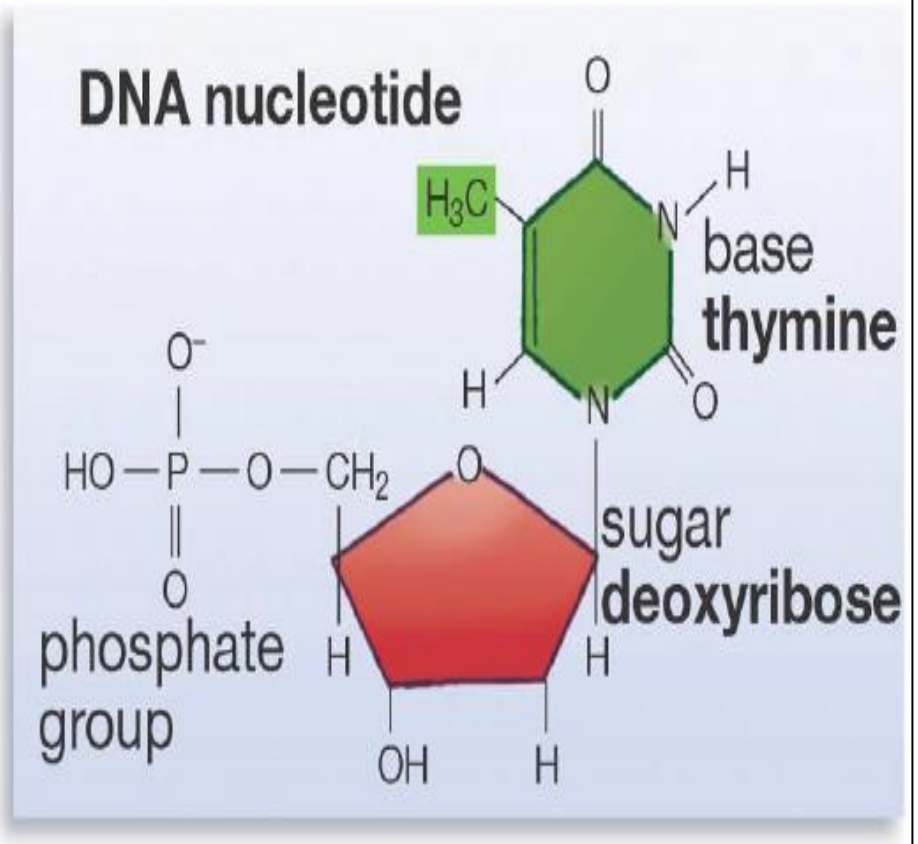
A+T ≠ G+C

i.e., A=T/G+C = constant

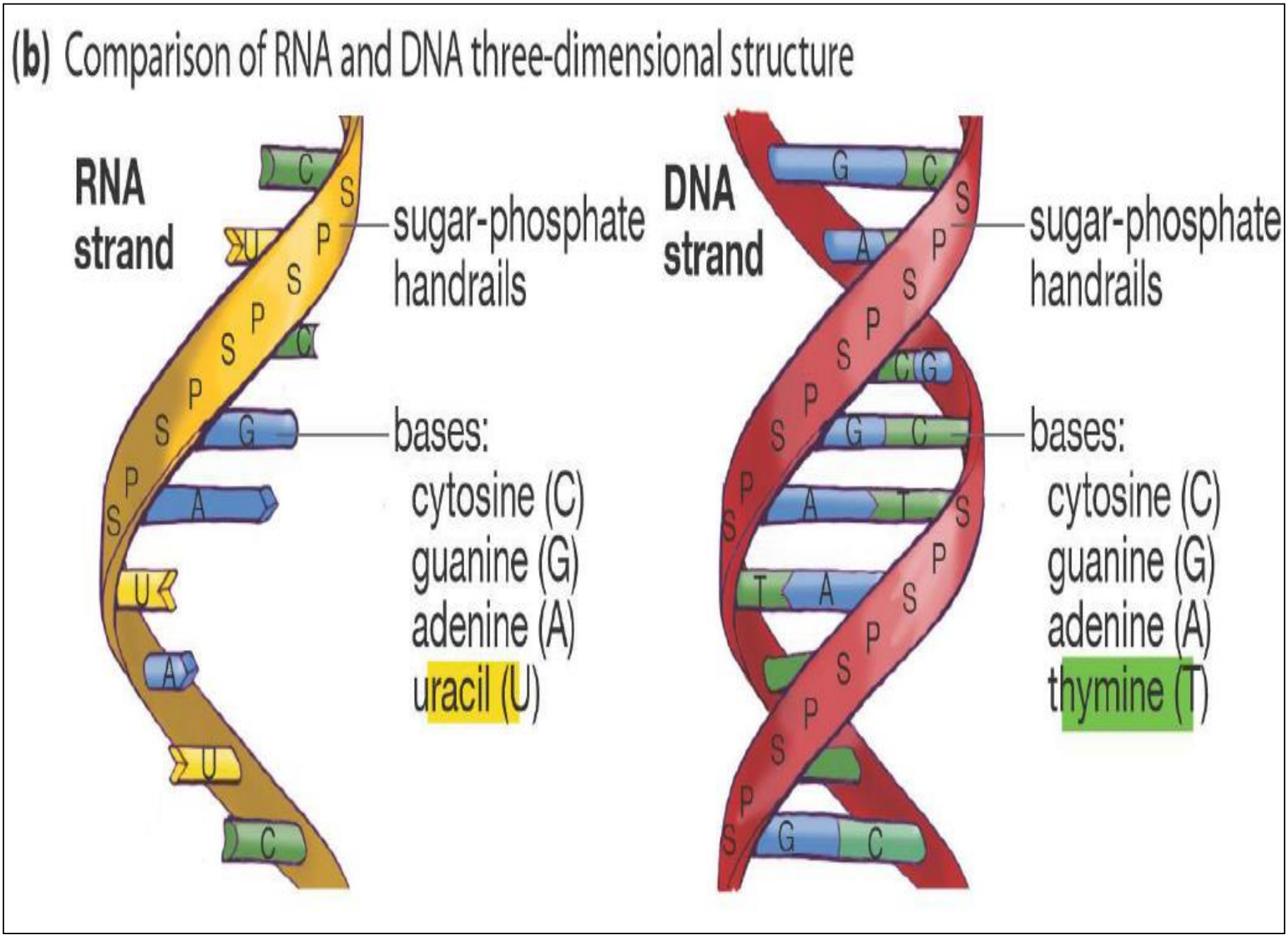
For example, this ratio is 0.4 for *Bacillus* whereas human DNA has the A:G ratio of 1.56

(a) Comparison of RNA and DNA nucleotides





RNA is a nucleic acid polymer that uses a slightly different sugar than DNA and the base uracil (U) in place of thymine (T).


(b) Comparison of RNA and DNA three-dimensional structure
RNA strand
sugar-phosphate handrails
bases:
cytosine (C)
guanine (G)
adenine (A)
uracil (U)
DNA strand
sugar-phosphate handrails
bases:
cytosine (C)
guanine (G)
adenine (A)
thymine (T)