

Structure of DNA

In 1953, the American biologist James D. Watson and the British physicist Francis H. C. Crick proposed the double strand helix structure of DNA.

The structure of nucleic acid studied at two different levels

- 1) Primary structure
- 2) Secondary structure.

Primary structure of DNA -

Nucleic acids are polynucleotide, i.e., they are formed by the condensation of thousands of molecules of nucleotides with the elimination of water molecules. During this polymerisation the $5'\text{CH}_2\text{-OH}$ hydroxyl group of the sugar residue of one nucleotide combines with one of the -OH groups of the phosphoric acid group present at the $3'$ of the other nucleotide to form a long polynucleotide chain. Thus the backbone of nucleic acids consists of alternating sugar-phosphate residues; each sugar on this backbone is further connected to one of the four nitrogenous bases (A, G, C and T in DNA). Thus, the sequence in which the four nitrogen bases are attached to the sugar phosphate backbone of nucleotide chain is called primary structure of nucleic acid.

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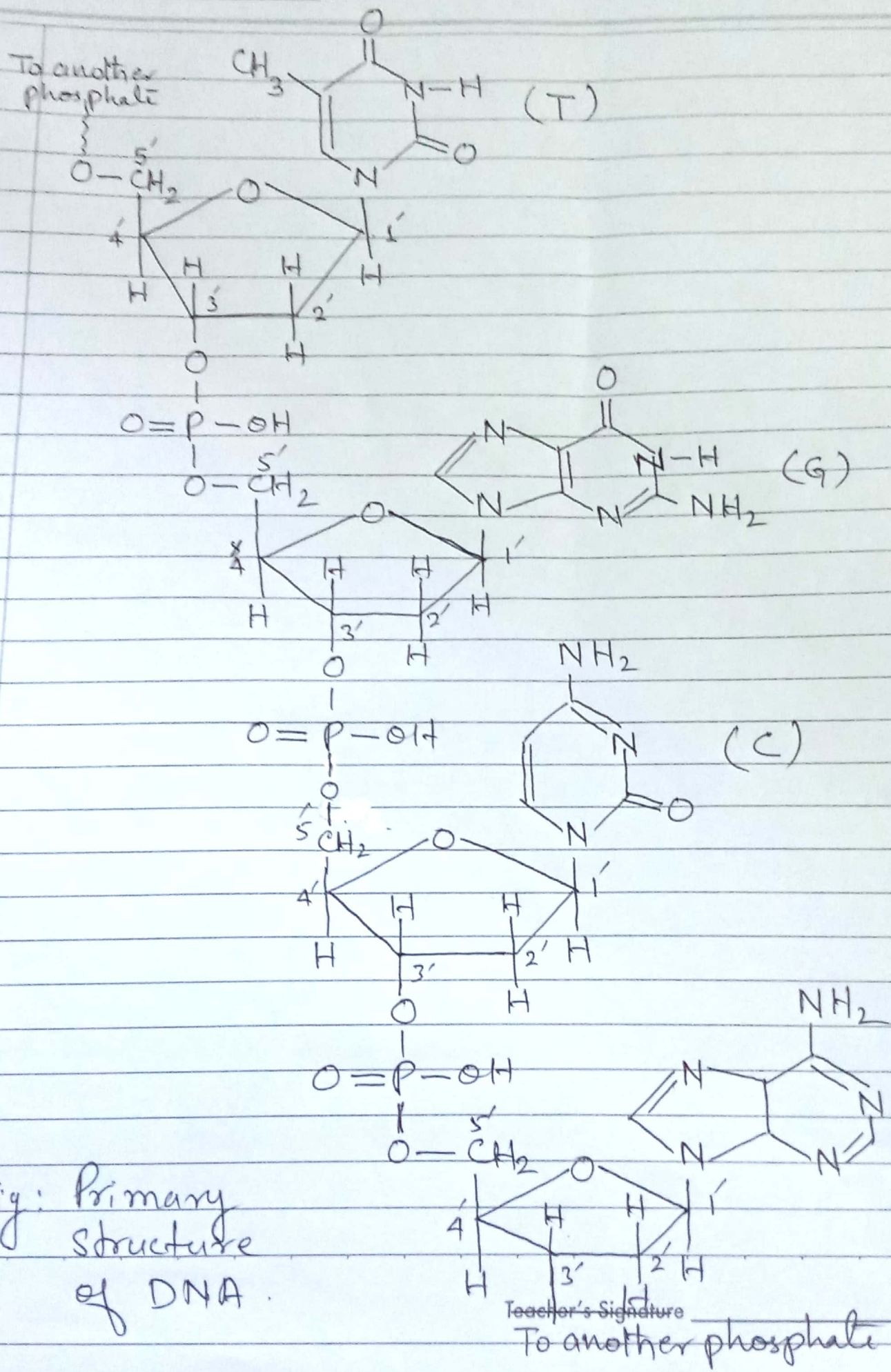


Fig: Primary
Structure
of DNA.

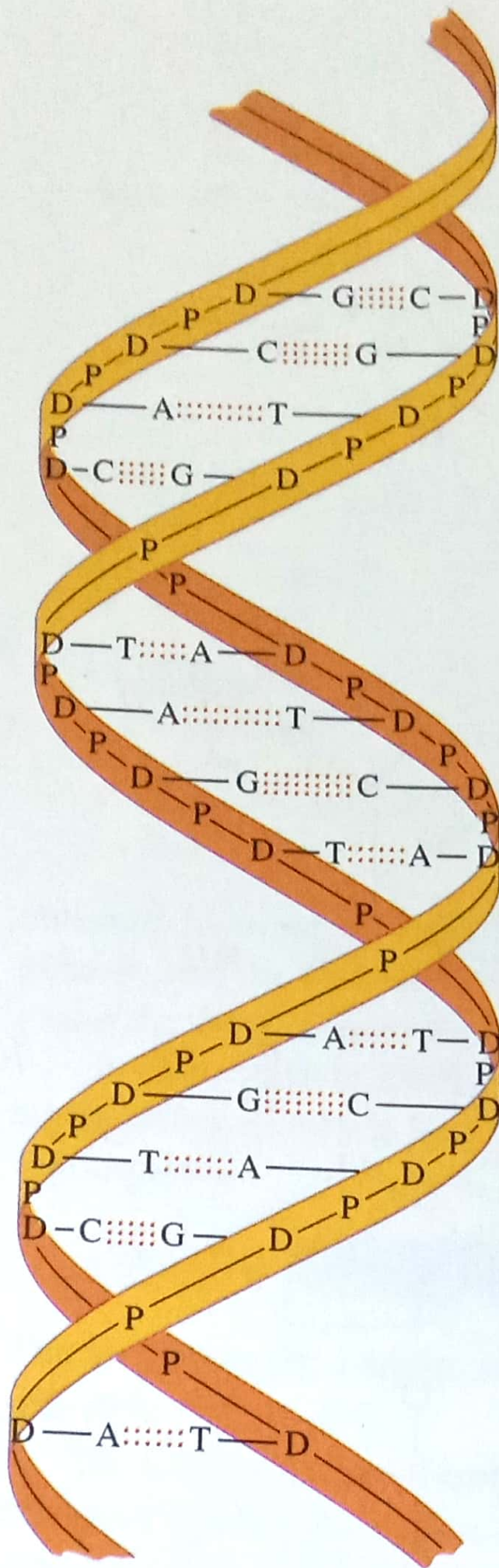
(2) Secondary structure of DNA

It consists of two strands of polynucleotide around each other in the form of double helix; the backbone of each strand consists of sugar-phosphate units and the base units of each strand are pointed into the interior of the helix and are linked together through H-bonds. Guanine (G) and Cytosine (C) are held by three H-bonds. Adenine (A) and Thymine (T) are held by two H-bonds.

The structure of DNA has been compared to a ladder twisted into a double helix with the rungs of the ladder perpendicular to the twisted railings. The phosphate and deoxyribose units alternating along the two railings of the ladder and two nitrogen bases form each rung of the ladder.

The two strands of double helix are complementary and not identical since the base sequence of the two strands automatically fixes that of the other due to base pairing principle. (The amount of adenine is equal to the amount of thymine ($A=T$) and that of cytosine is equal to guanine ($C=G$)). Thus from the base sequence of one chain of DNA, the base sequence of the other complementary chain can easily be predicted. For example if base sequence on one chain is $-TATCGGCA-$ that in the other chain will be $-ATAGCCGT-$.

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P = Phosphate
 D = Deoxyribose
 A = Adenine
 T = Thymine
 C = Cytosine
 G = Guanine