The structure of dna

DNA (deoxyribonucleic acid) and RNA (ribonucleic acid) are genetic materials. They are chemically similar but their 3 dimensional structures are different. DNA is informational molecule carrying genetic information in the exact sequences of its nucleotides but RNA is a catalytic molecule. DNA and RNA have three different conformations each, with distinct structure which are variously suited for their functions. (Freifelder et al. 1998) So, after reading this booklet, one can know about the different forms of DNA and RNA, how their different structural plans are ideally suited for their functions?

1. 2: STRUCTURE OF DNA:

The correct structure of DNA was first obtained by J. D. Watson and F. H. C. Crick of Cambridge University in the year 1953. Their double-helix model of DNA structure was based on the E. Chargaff's base composition rule. According to Chargaff, the concentration of thymine (T) was always equal to that of adenine (A) and the concentration of guanine (G) was always equal to that of cytosine(C). It was only true within the same species but was found different in the organism of different species. (Hartl et al. 2000)

DNA has no oxygen atom at the 2′ carbon. Nitrogenous bases are attached at the 1'carbon and phosphate group to the 5′ carbon of the pentose sugar. DNA double-helix contains two polynucleotide chains coiled one another in a spiral manner. Each polynucleotide chains consist of sequence of nucleotides joined together by the phosphodiester bonds. The two chains are linked together by H-bonds to give a helical configuration. H-bonds are formed between the purines (Adenine & Guanine) and the pyrimidines (Thymidine & Cytosine). Bases in DNA are specifically paired. Adenine (A) of one strand is linked with Thymine (T) of other strand through two H-bonds and Guanine

(G) with Cytosine (C) through three H-bonds. Thus, base sequences of other strand are known through the base pairing of one strand (specific base pairing). Such condition is called “ complementary base pairing”. Two strands runs antiparallel, with one strand in the 3′-5′ and other in the 5′-3′ direction (opposite chemical polarity). (Gardner et al. 2005)

In DNA double-helix, base pairs are stacked one upon another like a pile of papers with a 3. 4Çº gap between consecutive base pairs. (Hartl et al. 2000) Bases are hidden towards inner side forming hydrophobic core and they are perpendicular to the axis of the helix. Bases are moving in the spiral manner around the helical axis and each turn has ten base pairs. Each base pair is rotated through 36Ëš around the helical axis relative to the next base pair. Therefore, ten base pairs make the complete turn of 360Ëš. The twisting of two complementary strands in DNA double-helix forms a minor groove (12Çº) and a major groove (22Çº). (Nelson et al. 2000)

- (B)

Fig1. 1: (A) & (B): Double Helical Structure of DNA. (n. d)

(C)

Fig1. 2: (C): Complementary base pairing in DNA. Sugar phosphate backbone is on outside. (n. d)

1. 3: Various forms of DNA:

- B-form:

The standard model of DNA and is right handed. This conformation is shown by the DNA in the aqueous solution of low salt concentration. It has exactly 10. 4 nucleotide pairs per turn. Each base is twisted to 36Ëš and has a diameter of 2nm. The base plane is tilted to 6Ëš and length of each turn measures 3. 4nm. (Freifelder et al. 1998)

- A-form:

It is the conformation shown by DNA in the high salt concentration solution or dehydrated state. It has wider and flatter helix. Helix has minor and major grooves. It has 11 nucleotides per turn and each turn twisted to 33Ëš. (Gardner et al. 2005) Each turn is 3. 1nm in length. Base plane is tilted to the helix at 20Ëš. (Freifelder et al. 1998)

- Z-form: (Z- zigzagged path of the sugar phosphate backbone of the structure)

Twist in the left handed direction. It has 12 base pairs per turn and the length of turn is 4. 5nm. Diameter of each turn is 1. 8nm and the base plane is tilted to 7Ëš. (Freifelder et al. 1998) B-form change to the Z-form and vice versa with the help of certain regulatory protein.

1. 4: STRUCTURE OF RNA:

RNA: ribonucleic acid has the same structure as that of DNA but not identical, RNA has ribose sugar instead of deoxyribose. It is not duplex but single stranded. Uracil (U) is present in the place of thymine (T). The

backbone in RNA is an alternating polymer of ribose and phosphate with phosphodiester bonds between 3′ and 5′ atoms from consecutive ribose.

RNA form comparatively shorter double strand on itself, thereby forming hairpin, stem and loop structures. Hairpins are formed by base pairing 5-10 nucleotides of each other. Stem-loops are formed by pairing of those bases which are separated more than ten to several hundreds nucleotides. When these simple folding comes together, they make up a more complex structure termed as ‘ pseudo knot’. (Lodish et al. 2009) Double helix formed between DNA & RNA or RNA & RNA has the conformation same to that of A-form DNA. Such RNA is called A-RNA or RNA-II. Double helix of A-RNA contains 11bp per turn and each turn measuring to 3nm in length. (Lodish et al. 2009)

1. 5: Bases of RNA. (Uracil instead of thymine):

Purines:

Adenine (A). Guanine (G).

Pyrimidines:

Uracil (U). Cytosine (C).

Fig1. 3: Bases of RNA. (n. d)

1. 6: Structure of RNA:

RNA molecule consists of four components: ribose, five carbon sugar, phosphate & family of four heterocyclic bases.

Fig1. 4: RNA structure. (n. d)

1. 7: Various forms of RNA based on their function in the protein synthesis:

- Ribosomal RNA (rRNA),

- Messenger RNA (mRNA) and

- Transfer RNA (tRNA).

i. rRNA:

It is a single, continuous strand H-bonded back on itself, with a 5′ at the start and 3′ at the end. It contains a complex pattern of short double stranded stems, interspersed with unpaired single-stranded loops and bubbles.

Fig1. 5: Secondary structure of rRNA. (Steven 2009)

ii. mRNA:

The mRNA constitutes 3-5% of total cellular RNA. (n. d). It is always single stranded. Some of the common bases found in the mRNA are A, G, C and U. Certain amount of random coiling occurs in it but base pairing never happen in it, as it will destroy its biological properties. Its base sequences are complementary to the segment of DNA from which it is transcribed. Its size is at least 100×3= 300nts. (n. d).

Cap is formed at 5′ end by the condensation of guanylate residue in most eukaryotes and animal viruses. Cap is thus a blocked methylated structure, m7GppNmp Np; where m7G=

7methyl guanosine cap, N= any of the 4 nucleotides & Nmp= 20 methyl ribose. (n. d). It has behind its cap a non-coding region 1 (NC1) composed of

10-100 nucleotides. This region is rich in A and G residues. It does not translate protein. Then, it has initiation codon containing AUG in both prokaryotes and eukaryotes. It also consists of coding region containing 1500 nucleotides and it can translate protein. (n. d).

Fig: mRNA.

Fig1. 6: Structure of mRNA. (n. d)

iii: tRNA:

It is smallest of all RNA species. It contains sequence of 60-95 bases, mostly 76. It has a molecular weight of 18-20kd. Secondary structure is ‘ cloverleaf’ shaped with four constant arms (D-arm, T-arm, anti-codon arm and variable arm); additional arm is present in case of larger tRNAs. (n. d) 5′ terminus tRNA is always phosphorylated. Seven base pair stem has non-Watson and Crick pairing like G pairing with U. Stem 3-4 and loop of D-arm contains dihyuridine (D) base. Anti-codon triplet (anti-codon arm) and TYC sequence, pseudouradine (T-arm) are present at 5bp stem. Between anti-codon and T-arm is ‘ variable arm’ measuring 3-21 nucleotides in length.

This 3-D structure is formed in the solution. When ester linkage between 2′ or 3’OH group of adenylic acid at the end of acceptor arm and COOH group of the amino acid, it gives charged aminoacyl-tRNA. (Lodish et al. 2009) L-shaped tertiary structure formed from the cloverleaf has the acceptor arm at one end and anticodon arm at the other end.

(A) (B)

Fig1. 7: (A) structure of tRNA and (C) cloverleaf structure of tRNA (n. d).

1. 8: Comparative functions of DNA and RNA as per their structural plan:

Functions of DNA:

Due to the formation of minor and major groove in DNA, edge atoms of individual bases inside the grooves are made reachable from outside the helix. Thus, DNA binding proteins can read the base sequences of duplex DNA by coming in contact with atoms either in minor or major groove. (Hartl et al. 2000)

H-bonds are not parallel to the axis of DNA unlike alpha helix in proteins. This property enables DNA to bend in order to form a complex with binding proteins. Protein-DNA complex occurs as nuclear DNA in eukaryotic cells. This bending property of DNA allows it to get densely packed in the chromatin.

In DNA, H-atom at 2'position of deoxyribose sugar (OH in RNA) accounts for comparatively greater stability of the molecule. It allows DNA molecule to store genetic information for the longer duration. Whereas, in RNA 2′-OH group undergoes alkaline hydrolysis of phosphodiester bond at neutral pH catalyzed by OH anion. It does not takes place in DNA.

The presence of Thymine (T) instead of Uracil (U) also enables DNA for the long term stability because of Thymine's function in DNA repair. (Lodish et al. 2009) Complementary base pairing in DNA (A= T, G= C) form the basis for exact duplication. This allows precise replication process to occur so, that the information stored in them is replicated correctly and successfully inherited by the daughter cells

. Group of three bases in DNA molecule constitute genetic code which specifies amino acid sequence in proteins. All information contained in the genetic code plays a major role in directing the cell organization and cell metabolic functions. Sometimes bases are mispaired in DNA. This leads to the occasional mutations. An occasional mutation allows slow accumulation of favorable mutations, which as a whole leads to the evolution of variety of organisms. (Nelson et al. 2000) Certain bases are methylated in DNA molecule. Adenine & cytosine are more methylated then guanine & thymine. Presence of methylated base (like thymine) suppresses the migration of segment of DNA called transposons. Methylation of cytidine posses' structural importance as it increases the tendency of that segment of DNA to take the Z-form. (Nelson et al 2000)

Functions of RNA and its different forms:

RNA is a catalytic molecule. It plays a wide range of roles in the living cells.

Functions of rRNA:

It has folded structure like that of Î±-helices & Î² strands of proteins but they has catalytic properties. Thus, it catalyses the splicing process during the formation of majority of functional mRNA in multicellular & unicellular (yeast, bacteria etc.) eukaryotes. rRNA has the catalytic role in the formation of peptide bonds during protein synthesis. rRNA serves as the central component of the ribosome protein manufacturing machinery. (Hartl et al. 2000)

Functions of tRNA:

It functions as adaptor molecules that decode the genetic code. (n. d) The anti-codon end of tRNA has nucleotide sequence complementary to the codon representing its amino acid. The anticodon enables tRNA to recognize the codon through complementary base pairing. Amino-acyl tRNA-synthase proteins formed by the reaction between 3'OH group of adenylic acid at acceptor arm & COOH group of amino acid, is the true translator of genetic code into amino acid sequence. If it fails to acetylate RNA properly then it will lead to amino acid mutation. RNA has three different species viz. mRNA, tRNA & rRNA. The mRNA carries coding information from the DNA to the site of protein synthesis (the ribosome), tRNA helps in the recognition of the codons & provides corresponding amino acid. (Nelson et al. 2000)

Functions of mRNA:

It is used as the template for protein synthesis. The presence of cap at 5′ end of mRNA plays vital role in recognition of ribosome and also in protection of RNAses. After polyadenylation, poly-A tail is attached to the 3′ end of mRNA. It is the binding site of proteins. These proteins shield mRNA from degradation by exonucleases. The process of polyadenylation is also vital for termination of transcription, export of mRNA from the nucleus & translation. (n. d)

1. 9: References:

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