The basic informational macromolecules biology essay

Nucleic acids are the basic informational macromolecules that contributes to the most essential characteristic properties of living system, reproduction and genetic conttrols. Lower and higher molecular weight of nucleic acids are utilized in metabolic and catalytic reactions respectively.

DNA(deoxyribonucleic acid) and RNA(ribonucleic acid) are nucleic acid of polymers composed of nitrogenous base either a double ring of purines and single ring of pyrimidine which is further connected to the phosphorylated sugar to make up the nucleotides. The sugar attached with base without phosphate group is called nucleoside. The DNA molecule has sugar 2′-deoxyribose and RNA molecule has ribose and every backbone of DNA or RNA chain are linked by covalent phosphodiester bond between 5'and 3'carbons of two sugars either from 5′—> 3′ or 3′—> 5′ directions.

Phosphate groups are attached at the end of the sugar at 5′-carbon and at the 3'end , the hydroxyl group is added. Most probably all natural DNA or RNA polymer extend in a direction of 5'to 3'end direction. The structures that join the nulceotides together in DNA and RNA are called phosphodiester bonds due the presence of phosphoric acid linkage between the two sugars(fig. 1)

Fig. 1 RNA nucleotides linked by phosphodiester bonds between 3′-OH and 5′-C.

(RNA structure, n. d)

Structures of DNA

DNA(deoxyrinucleic acid)is the linear of nucleic acids which is composed of four different building blocks of nucleotides and is lack of one oxygen atom at carbon2′(fig. 2) and as a result it is named as deoxyribose sugar.

Fig. 2 Structure of DNA.

(DNA Structure, n. d)

DNA is commonly found in nucleous and scientist called Erwin Chargaff found that DNA has four nucleotide bases namely pyrimidine(cytosine and thymine)and purine(adenine and guanine) (fig. 3)

Purines: a)

Adenine A Guanine G

Pyrimidines: b)

Thymine T Cytosine C

Fig. 3. Structure of DNA bases.

(DNA and RNA Structures, n. d)

The total amount of pyrimidine nucleotide bases thymine+cytosine is always equal to the total amount of purine nucleotide bases adenine+guanine. The amount of thymine is always equal to the amount of adenine(A= T)and the amount of cytosine is always equal to the amount of guanine(GºC). But the amount of adenine +thymine is not necessarily equal to the amount of guanine+cytosine.

(Gupta , P. K., 2000)

The Double Helix Structure

By the study of x-ray diffration, Rosalind Franklin and Maurice Wilkens suggested that DNA has a helical structure with a diameter of 20A and 34A distance in the helix(fig. 4a). DNA consists of two helix which the two chains are coiled around the same axis to form a right-handed helix and they can be separated from one another only by uncoiling.

The backbone of altertnating deoxyribose and phosphate groups are placed outside the helix facing the surrounding water(hydrophilic) whereas the bases are inside the helix(hydrophobic) and are set in a plane at right angle to the long axis. The right-handed DNA forms are called B-DNA having 3. 4A distance between the two base pairs and it has 10 base pairs in each turn. DNA can also exist as left-handed and since left-handed DNA follow a zig-zag way, it is called as Z-DNA. The main difference between Z-DNA and B-DNA is that in Z-DNA, one complete helix has 12 base pairs per turn whereas B-DNA has only 10 base pairs per turn.

(Gupta, P. K., 2000)

Fig. 4)a) Structure of double helix, b) DNA structure showing parallel and anti-parallel, c) double helix showing minor and major grooves.

(DNA Structures, n. d)

In double helix, the two strands of DNA runs opposite in direction ie, 5′—> 3’and 3′—> 5′ which means the two strands should be parallel or anti-parallel to make the stabilized structure and hold the two polynucleotides together. There is an interaction of base-pair between the adenine on one strand and a thymine on the other(A= T) and similarly between cytosine and guanine (GºC (fig. 4b) with hydrogen bond two and three rrespectively. These pairing of this two strands creates minor and major grooves on the surfaces of double helix(fig. 4c) .

In DNA double helix, one strand act as parent strand and the other new strand as template which

synthesize complementary daughter strands(fig. 5). The double helix is hold together by H-bonding between complementary base pairs and base stacking interaction. (Voet, D. Et al

Fig. 5 DNA replication. Each strand of a parental DNA acts as a template for the synthesis of a complementary daughter strand.

(Voet, D. et al, 2006)

Structure of RNA

RNA(ribonucleic acid) is the second type of nucleic acid found in throuhtout the cell. In case of RNA , it has a sugar and an -OH group at 2′ carbon atom(fig. 6).

Fig. 6 Structure of ribose.

(RNA Structure, n. d)

Similarly, RNA has also four nucleotide bases as purine and pyrimidine(fig. 7) except the thymine is replaced by uracil in pyrimidine.

Purines:

Adenine A Guanine G

Pyrimidines:

Uracil U Cytosine C

Fig. 7 Structures of RNA bases.

(RNA and DNA Structures, n. d)

Though RNA is single -stranded structure , when RNA fold back on itself , by chance or

occasional base pairing and hydrogen bonding , it forms some of a paired helical structure (fig. 8) which results in three dimensional structure and they are copmplex and unique. They form intra-strand base pairs from self complementary region along the chain.

Fig. 8 Base pairing within a single strand of RNA showing a possible folded structure.

(RNA Structure, n. d)

The information from RNA determines the protein synthesis through the series of translation which involves three types of RNA molecules to perform different functions:

1)Messenger RNA(mRNA)Structure

Messenger RNA(mRNA) is a linear sequence of amino acid in polypeptide chain and has longer chain than the reading frame that has to be translated. To begin and end translation , specific start and stop codons are required. Mostly mRNAs has start (initiator) codons AUG that can be served as methionine codon at 5'carbon.. Occasionally GUG and CUG can alsobe used as initiator codon in some of the bacterial and eukaryotic mRNA respectively. GUG codes for valine and CUG for leucine to initiate a protein chain. The stop codon are UAA, UGA and UAG and do not code for any amino acid. The stop codon indicates that translation is to be terminated and the ribosome has to be released polypeptide product. The sequence of start and stop codon are called a reading frame. Codon having overlapping information, mRNA can be translated to different reading frames and formed different polypeptides(fig. 9). Each genetic code specifies different amino acids and rarely unusual coding occurs.

(Lodish, etal , 1986)

Frame 1

5'â”€â”€ GCU UGU UUA CGA AUU A â”€ mRNA

â”€â”€â”€ Ala Cys Leu Arg Ile â”€â”€â”€ polypeptide 1

Frame 2

5'â”€â”€ G CUU GUU UAC GAA UUA â”€â”€ mRNA

â”€â”€â”€ Leu Val Tyr Glu Leu â”€â”€â”€â”€ polypeptide 2

Figure 9; Multiple reading frames in an mRNA sequence

(Lodish , etal , 1986)

2)Transfer RNA(tRNA) Structure

Transfer RNA(tRNA) is an adaptor molecule that serve as a bridge between mRNA and the amino acids leading to the Polypeptide chain. tRNA exists in primary, secondary and tertiary structure. A tRNA molecule is chemically linked to amino acids through a bond forming an aminoacyl-tRNA. The general structure of tRNA is represented by Cloverleaf model(fig. 10). The anticodon at the bottom is complementary to the mRNA codon with the pairing of base to it. Due to the presence of mRNA codon and tRNA anticodon, base-pairing is in anti-parallel directions. Amino acids are attached to the acceptor stem at the 3′ terminus having sequence CCA and protrudes beyond the 5′ end. The dihydrouracil loop(D loop)contained always uracil base and TCG loop has invariant sequence of bases. Variable loop has variation in both nucleotides composition and in length. (Lodish, et al, 1986)

Fig. 10. Structure of tRNA.

(RNA-Ribonucleic acid, n. d)

3)Ribosome RNA(rRNA) Sructures

Ribosome RNA(rRNA) carries ribosome particles and consists of one small and one large subunit ribosome and protein. The rRNA is the largest structure among the RNAs. Each of the subunits composed of one to three rRNA s types and as many as protein components. Comparing to prokaryotes, eukaryotic cells are larger and more particles whereas the eukaryotes has 40s and 60s with 80s for complete ribosome.

Functions of DNA

• DNA serve as a storage materials for genetic information in all living cells.

• Due to the double helical structure, DNA provides more stability storing more genetic information since the double bond required more force to break up the structures .

• DNA is building block of the protein synthesis which takes by the process of Central Dogma relationship. Genetic information from the DNA is transcribed to mRNA carrying the genetic codon and later translated to the polypeptide chain.

• DNA provides for long term storage of genetic information due to the presence of deoxyribose sugar at 2'carbon, thus preventing the formation of cyclic phosphate ester since hydrogen cannot hydrolysis the phosphodiester bond, whereas 2'hydroxyl group in RNA act as a nucleophile attacking the phosphodiester bond and results in less efficiency of storing information.

(Lodish, ea al, 1986)

• DNA act as template or semiconservative. During the replication of double helix, DNA double strsnded DNA that consists of one old (template) strand and one new daughter strand. two ddaughter duced pronew daughter strand. This two new DNA molecules is identical to the parents molecule and this type of conservation of old template strand is called semiconservative.

• The major and minor grooves formed during the coiling or wounding of duoble strands provides the reading of protein binding DNA. s

(Lodish, etal, 1986)

Function of mRNAs:

• mRNA carries genetic information which is transcribed from DNA in a linear sequence of amino acid to a peptide chain.

• mRNA carries three codons for a specific amino acids. AUG act as start codon for a specified amino acids at 5′ and UAA, UAG and UGA as stop codon or termination of translation.

Function of tRNA:

• The main function of aminoacyl-tRNA is to recognise the specific codon for the activation of correct amino acids.

• tRNA make sure that the amino acid are placed in correct sequence to the growing peptide chain during the interaction of codon with the specific anticodon.

• Helps in Abinding the growing peptide chain to the ribosome during translation process.

(Conn, E. E., 1987)

Function of rRNA:

• rRNA could serve as template RNA .

• rRNA with ribosome particles provides shapes and structure during protein synthesis.

It also helps in speeding or catalysing the chemical reaction by enzyme called ribozymes.

The main difference between the DNA and RNA structures are that DNA has deoxyribose sugar and lack one oxygen at carbon 2′, wheraes in RNA has ribose sugar and one -OH group attached at carbon 2′. DNA is double stranded in nature , providing more stability than single stranded RNA. Again one big difference is that the presence of thymine in DNA and uracil in RNA srtucture.

The main difference in the function of DNA and RNA is that the DNA functions mainly for the storage of genetic informations and the RNA as transcription and translation of genetic informations.

Since the DNA is double helix that wound around the plane of the helix hiding the base -paired inside the helix that prevents from contacting with water(hydrophobic) this base pairing interaction provides more stability to the nucleic acids storing more genetic information. In both

DNA and RNA base pairing between GºC provides more stronger and stable bond than the A= T since it requires more force to break up the three H-bonding of GºC than the A= T.

In DNA , thymine is present and instead of thymine uracil is replaced in RNA . Since thymine contain methyl group , this base act as a protection and moreover methyl is strongly neutral. It is methylated group and methylation newly suppresses the migration of DNA segments. These all reasons provides that DNA is strongly stable than RNA nucleic acid. Again methylation can help in identifying the parental (template) strands from newly synthesized strands in DNA strands.

Each of the 3’end of the sugar are used to initiate the genetic exchange and this point act as primer for DNA replication.

The attachment of more ribosome on mRNA provides high sedimentation rate than the unattached ribosomes which means the polyribosome or polysome complexes are actively synthesizing protein than single ribosomes.

(Strickberger, M. W., 1976)