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undergo polymerization under low oxygen tension causing change in shape of the RBC from biconcave to sickle like structure.

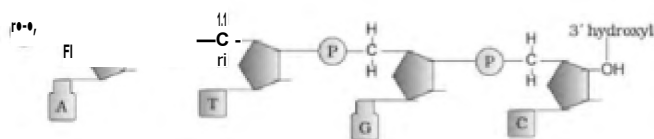
- c. **Phenylketonuria** - inborn error of metabolism inherited as autosomal recessive trait. The affected individual lacks an enzyme that converts the amino acid phenylalanine to tyrosine that results into mental retardation.

Chromosomal Disorders-Failure of segregation of chromatids during cell division results in loss or gain of chromosome called aneuploidy. The failure of cytokinesis leads to two sets of chromosome called polyploidy,

- a. **Down's Syndrome** - is due to presence of additional copy of the chromosome number 21. The affected individual is short statured with small rounded head, furrowed tongue and partially open mouth. Mental development is retarded.
- b. **Klinefelter's Syndrome** - due to presence of an additional copy of X-chromosome (XXY). Such persons have overall masculine development. They are sterile.
- c. **Turner's Syndrome** - caused due to the absence of one of the X-chromosomes. In such females are sterile as ovaries are rudimentary. They lack secondary sexual characters.

Cytosine is common for both DNA and RNA and Thymine is present in DNA. Uracil is present in RNA at the place of Thymine.

5' 131uHs1h.Lic



nitrogenous base is linked to pentose sugar with N-glycosidic linkage to form a nucleoside. When phosphate group is linked 5' OH of a nucleoside through phosphoester linkage nucleotide is formed. Two nucleotides are linked through 3'-5' phosphodiester linkage to form dinucleotide. More nucleotide joins together to form polynucleotide.

In RNA, nucleotide residue has additional —OH group present at 2' position in base and uracil is found at the place of Thymine.

Double helix model for structure of DNA - James Watson and Francis Crick. based on X-ray diffraction data produced by Wilkin and Rosalind proposed this model of DNA.

The salient features of this model are-

- DNA is made of two polynucleotide chains in which backbone is made up of sugar-phosphate and bases projected inside it.
- Two chains have anti-parallel polarity.
- The bases in two strands are paired through H-bonds. Adenine and Thymine forms double hydrogen bond and Guanine and Cytosine forms triple hydrogen bonds.
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- Two chains are coiled in right handed fashion. The pitch of helix is 3.4 nm and roughly 10 bp in each turn.
- The plane of one base pair stacks over the other in double helix to confer stability.

Packaging of DNA helix-

- In prokaryotes, well defined nucleus is absent and negatively charged DNA is combined with some positively charged proteins called nucleoids.
- In eukaryotes, histones, positively charged protein organized to form subunit called histone octamer. Negatively charged DNA is wrapped around the nucleosome to form nucleosome. A single nucleosome contains about 200 base pairs. Chromatin is the repeating unit of nucleosome.

Replication of DNA

Watson and Crick suggested that two strands of DNA, separate from each other and act as template for synthesis of new complementary strands. After the completion of replication each DNA molecule would have one parental and one newly synthesised strand, this method is called semiconservative replication.

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Messelson and Stahl's shows experiment!! evidence of semiconservative replication. Using radioactive Nitrogen

Replication of DNA require Enzyme DNA polymerase that catalyse the polymerisation in one strand 5' to 3' only, So. replication **in one strand** is continuous and other strand it is discontinuous due to the synthesized fragments that are joined together by enzyme DNA ligase.

repliment

transcription

mRNA

transcription

protein.

Central dogma.

Transcription is the process of copying genetic information from one strand of DNA into RNA. In transcription **only one strand of DNA is copied and only one strand is copied in RNA. The Adenosine forms** be pair with thymine. Lead of thymine.

Transcription of DNA includes a promoter, the structural gene and a terminator. The strands that has polarity **3' act as template and called template strand and other strand is called coding strand.**

- Promoter is located at 5' end and that binds the enzyme RNA polymerase to start transcription. The terminator is located at the end of coding strand and usually defines the end of transcription.
 - Exons are those sequences that appear in mature and processed RNA. Exons are interrupted by introns. Introns do not appear in mature and processed RNA.
- In bacteria there are three types of RNA's - mRNA, t-RNA and r-RNA. All these are needed for synthesis of protein in the cells.
- The mRNA provides the template. t-RNA brings the amino acids and reads the genetic code, the r-RNA plays structural and catalytic role during translation.
 - The primary transcript contains both exon and intron and is non-functional. It undergoes the process of splicing in which introns are removed and exons are joined in a defined order.
 - The hnRNA (heterogeneous nuclear RNA) undergoes additional processing called as capping and tailing. In capping, an unusual nucleotide (7-methylguanosine triphosphate) is added to the 5' end of hnRNA. In tailing, a poly-A tail is added at the 3' end in a template-independent manner.

Genetic Code is the relationship of amino acid sequence in a polypeptide and nucleotide/base sequence in mRNA. It directs the sequence of amino acids during synthesis of proteins.

Salient features of Genetic Code are-

- The code is triplet. 61 codons code for amino acids and 3 codons do not code for any amino acids called stop codons.
- Codon is unambiguous and specific, code for one amino acid.
- The code is degenerate. Some amino acids are coded by more than one codon.
- The codon is read in mRNA in a contiguous fashion without any punctuation.
- The codon is nearly universal. AUG has dual functions. It codes for methionine and also acts as initiator co-don.

Mutations and Genetic code

- A change of single base pair (point mutation) in the chain of Beta globin chain that results in the change of amino acid residue glutamate to valine. These results into a diseased condition called Sickle cell anaemia.
- Insertion and deletion of three or its multiple bases insert or delete one or multiple codons hence one or more amino acids and reading frame remain unaltered from that point onwards. Such mutations are called frame-shift insertion or deletion mutations.

The t-RNA called as adaptor molecules. It has an anticodon loop that has bases complementary to code and also has an amino acid acceptor to which amino acid binds. t-RNA is specific for each amino acid. It also contains another specific t-RNA referred as initiator t-RNA. The secondary structure of t-RNA is depicted as clover-leaf. In actual structure, the t-RNA is a compact molecule which looks like an inverted L.

- Translation is the process of polymerisation of amino acids to form a polypeptide. The order and sequence of amino acids are defined by the sequence of bases in the mRNA. Amino acids are joined by peptide bonds. It involved following steps-
 - a) Charging of tRNA.
 - b) Formation of peptide bonds between two charged tRNA.
- The start codon is AUG. An mRNA has some additional sequence that are not translated called untranslated region.
- For initiation ribosome binds to mRNA at the start codon. Ribosome moves from codon to codon along mRNA for elongation of protein chain. At the end release factors bind to the stop codon, terminating the translation and release of polypeptide from ribosome.

The Lac Operon

- Lac operon consists of one regulatory gene (i^+) and three structural genes ($lacZ$, $lacY$ and $lacA$). Gene i codes for the repressor of the lac operon. The $lacZ$ gene codes for beta-galactosidase, that is responsible for hydrolysis of disaccharide, lactose into monomeric units, galactose and glucose. Gene $lacY$ codes for permease, which increases permeability of the cell. Gene $lacA$ encodes for transacetylase.
- Lactose is the substrate for enzyme beta-galactosidase and it regulates switching on and off of the operon, so it is called inducer.
- Regulation of Lac operon is done by repressor referred as negative regulation. Operation of Lac operon is also under the control of positive regulation.

Human Genome Project was launched in 1991 to find out the complete DNA sequence of human genome using genetic engineering technique to isolate and clone the DNA segment for determining DNA sequence.

DNA fingerprinting is a very quick way to compare the DNA sequence of any two individuals. It includes identifying differences in some specific region in DNA sequence called as repetitive DNA because in this region, a small stretch of DNA is repeated many times.

Depending upon the base composition, length of segment and number of repetitive units satellite DNA is classified into many categories.

Polymorphism in DNA sequence is the basis for genetic mapping of human genome as well as fingerprinting.

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- The technique of fingerprinting was initially developed by Alec Jeffrey. He used a satellite DNA as probe for which so high polymorphism was called Variable Number of Tandem Repeats (VNTR).