

BIOLOGY CAPSULE – 2 DNA STRUCTURE AND DNA SEQUENCES

RECON

Cross over unit of DNA. *Unit of recombination.*
Minimum 2 pairs of nucleotides are present.

MUTON

Unit of mutation. Only one nitrogen base is sufficient

CISTRON

Unit of transcription. Contain many nucleotide pairs.

ALU FAMILY

A set of dispersed related sequence of DNA each 300 bp long. Present in human genome.

BLUNT – END LIGATION

Reaction that joints two DNA directly at their ends.

CAAT BOX

A part of Conserved sequence of DNA located in the start point of Eukaryotic transcription unit.

c-DNA

Single stranded DNA complementary to RNA produced during Reverse transcription.

CRUCIFORM

Structure produced at inverted repeats of DNA if the repeated sequence pairs with its complement on the same strand.

CRYPTIC SATELLITE

Satellite DNA sequence not identified as such by a separate peak on density gradient

Ct DNA

It is the chloroplast DNA

FINGER PRINT OF DNA

Polymorphic restriction fragments of DNA

FOLD BACK DNA

Inverted repeats that have re natured by intra strand re association of denatured DNA.

HETERODUPLEX DNA

Hybrid DNA generated by base pairing between complementary single strands.

HIGHLY REPETITIVE DNA

First component to re associate and is equated with Satellite DNA.

Kb Abbreviation of 1000 base pairs of DNA or RNA

LINKER DNA

Part of DNA in the Nucleosome contain *146 bp.*

MAR – Matrix Attachment Region

Also called **SAR** (Scaffold Attachment Region).
Region of DNA that attaches to the Nuclear Matrix.

MARKER DNA

Fragment of known size used to calibrate an Electrophoretic gel.

MELTING OF DNA

DNA denaturation is called melting.

OKASAKI FRAGMENTS

Short DNA with 1000 – 2000 bases. Produced during discontinuous DNA synthesis. Later joined by covalent bonds.

ORIGIN – ori

It is a sequence of DNA at which replication starts.

OVER WINDING OF DNA

It is caused by Positive Super Coiling.

PALINDROME SEQUENCE

Sequence of DNA that is same when one strand is read left to right or the other is read right to left.

Consists of adjacent inverted repeats.

PARANEMIC JOINT

Region of DNA in which two complementary sequences are associated side by side.

PLECTONEMIC WINDING

Inter twining of the two DNA strands in the classical double helix DNA.

PROMOTER REGION

Region of DNA involved in the binding of RNA polymerase to initiate transcription. **TATAATG** in bacteria.

R-LOOP

Structure formed when RNA strand hybridize with its complementary DNA strand.

REPETITIVE DNA

It behaves in a re association reaction, although many sequences are present in a component allowing any pair of complementary sequences to re associate.

SALTATORY REPLICATION

Sudden lateral amplification to produce a large number of copies of some sequence.

SATELLITE DNA

Many tandem repeats (identical) of a short basic repeating unit.

STAGGERED CUT

DNA strands are cut at different points near each other.

SUPER COILING

Coiling of a closed duplex of DNA in space so that it crosses over its axis.

TANDEM REPEATS

Multiple copies of the same sequence lying in series.

TATA BOX

Conserved A-T rich Septamer found about 25 bp before the start point in each Eukaryotic RNA Polymerase II transcription unit. Involved in positioning the enzyme for correct initiation.

BIOLOGY CAPSULE – GENETIC CODE AND PROTEIN SYNTHESIS

GENETIC CODE

1. **AMBER CODON** – Codon that causes termination of protein synthesis. *Amber codon is UAA*
2. **OCHRE CODON** *UAA*
3. **NON SENSE CODONS** – Codons that will not represent any amino acids. They are also called Stop codons or Terminator codons because the protein synthesis will be terminated on reaching these codons.
4. **DEGENERACY** Lack of an effect of many changes in the third base of the codon on the amino acid that is represented. That is one amino acid is represented by more than one genetic code.
5. **OPEN READING FRAME – ORF** Series of triplets coding for amino acid without termination codon.
6. **PROOF READING** Mechanism for correcting errors in protein or Nucleic acid synthesis.
7. **START POINT** Position on DNA corresponding to the first base to be incorporated in to the RNA.
8. **AUG** Starting or Initiation codon

TRANSLATION

1. Key players of protein synthesis are m-RNA, t-RNA, Ribosomes AND amino acids.
2. 20 Amino acids are present in nature.
3. Combination of t- RNA with its Amino acid is called Charging.
4. Amino acyl synthetase enzyme helps to bind Amino acid with t- RNA in the presence of ATP.
5. Activated Amino acid is called Amino acyl adenylic acid.
6. **INITIATION COMPLEX** – Starts translation. It includes Small ribosome sub unit, m-RNA, Charged t-RNA, UTP, Mg ions.
7. The Initiation complex in Prokaryotes is IF and that of Eukaryotes is eIF
8. AUG is the Initiation codon. In prokaryotes it represents Formyl methionine (Formylmet) and in Eukaryotes AUG represents Methionine.
9. t-RNA binds with the P site (Peptidyl site) on the ribosome.
10. Triplet codon of m-RNA binds with the A site (Amino acyl site).
11. Amino acids are transferred to the A site.
12. Peptidyl transferase forms bond between amino acids.
13. Dipeptide is then transferred to the P site.

PEPTIDYL SYNTHETASE

Enzyme that links two amino acids transferred to the **A site**.

TRANSLLOCATION

Placing of codons in the A site. Translocation is carried out by Elongation Factors with the use of energy from **GTP**.

ELONGATION FACTORS

In Prokaryote the *Efs are EF-Tu, EF-Ts, EF-G*.

GTP DEPENDANT RELEASE FACTOR

RF1, RF2, RF3. These cleave the polypeptide from the last t- RNA.

RIBOSOMES

PROKARYOTIC RIBOSOME 70 S

Large sub unit – 50S – small sub unit 30S

Large sub unit has 23S r-RNA, 5S r- RNA, 32 proteins.

Small sub unit has 16S r-RNA, 21 proteins.

EUKARYPTIC RIBOSOME 80 S

Large sub unit – 60S and Small sub unit 40S

Large sub unit has 28 r-RNA, 5S r- RNA, 5.8S r- RNA, 50 Proteins.

Small sub unit has 18S r-RNA and 32 Proteins.

TRANSFER RNA

CLOVER LEAF MODEL

Proposed by **R.W Holley in 1965**.

t- RNA has Amino acid site at the 3' end, Enzyme binding site, Anticodon site, D – Loop, and a Hump.

WOBBLE HYPOTHESIS

Ability of t-RNA to recognize more than one codon by unused (Non-G – C, A – T) pairing with the third base of a codon.

