

## BIOLOGY CAPSULE 2 – GENETIC CODE AND PROTEIN SYNTHESIS

### GENETIC CODE

- 1. AMBER CODON** – Codon that causes termination of protein synthesis. *Amber codon is UAA*
- 2. OCHRE CODON** *UAG*
- 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

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

### PEPTIDYL SYNTHETASE

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

### TRANLOCATION

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.

#### EUKARYOTIC 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.