Transcription in Prokaryotes

1.What is wobble hypothesis? [Crick (1966) proposed this hypothesis]

According to this hypothesis, the base in first position of anti-codon on tRNA is usually an abnormal base like inosine, pseudouridine, tyrosine etc. These abnormal bases are able to pair with more than one type of nitrogenous base in the third position of the codon on mRNA.Example- Inosine (I) can pair with A, C or U, this base is called Wobble base or fluctuating base. Wobble occurs at position 1 of the anticodon and position 3 of the codon.

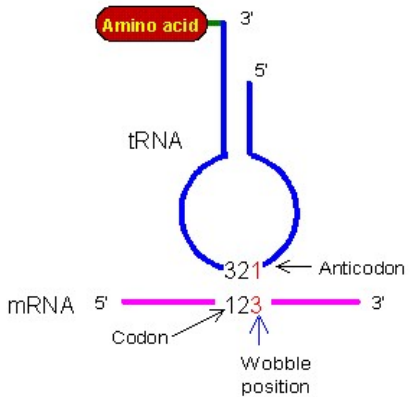

Figure1. Association of mRNA and t-RNA to justify wobble hypothesis

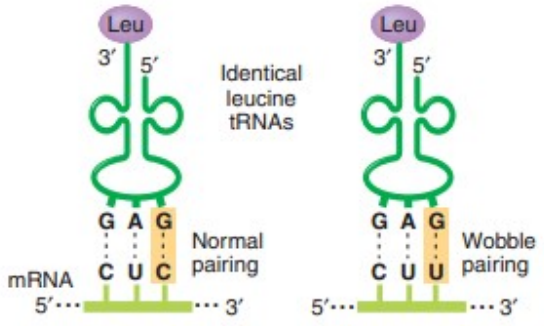

Figure1. Two different leucine codons (CUC , CUU) can be read by the same leucine tRNA molecule, con-trary to regular base-pairing rules

What do you mean by degeneracy of amino acid?

This phenomenon gives rise to: multiple codes for a given amino acid (degeneracy), possible suppression of point mutation in the 3rd base of the codon, Easilt removed deacylated t-RNA during protein synthesis.

There are three amino acids encoded by six different codons: serine, leucine, and arginine. Only two amino acids are specified by a single codon. One of these is the amino-acid methionine, specified by the codon AUG, which also specifies the start of translation; the other is tryptophan, specified by the codon UGG.

2.What is Shine- Dalgarno sequence?

The Shine-Dalgarno sequence is a specific, purine rich arrangement of nucleotides in prokaryotic mRNA that targets the RNA to a small ribosomal subunit for translation. This sequence is required for ribosomal binding and protein synthesis to occur in prokaryotic cells. It is also known as the ribosome binding site.

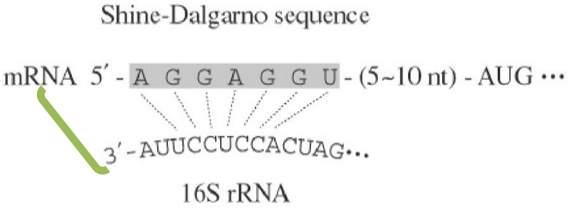

Figure 2. Base-pairing between the Shine—Dalgarno sequence of mRNA and the 16S rRNA 3′ tail.

3.Mention the function of aminoacyl-tRNA synthetase (aaRS). (Figure 3, 4)

$$\mathbf{aa + ATP} \xrightleftharpoons[\mathbf{Mg^{++}}]{\text{aa-tRNA synthetase(E)}} \mathbf{E\text{-}aa\text{-}AMP + P\sim P}$$

This enzyme attaches the appropriate amino acid onto its tRNA. It does so by catalyzing the esterification of a specific cognate amino acid or its precursor to one of all its compatible cognate tRNAs to form an aminoacyl-tRNA. The synthetase first binds ATP and the corresponding amino acid (or its precursor) to form an aminoacyl-adenylate, releasing inorganic pyrophosphate (PPi). The adenylate-aaRS complex then binds the appropriate tRNA molecule's D