TRANSLATING THE GENETIC CODE

18. THE GENETIC CODE

Describe how the genetic code was deciphered
The logic goes like this: We know we have four nitrogenous bases (A, T, C, G), and we also know that these bases need to code for 20 amino acids.
If we look at the permutations 4 bases can undergo, we can work out how many "places"are needed to create 20 amino acids.

4^2 = 16 amino acids (insufficient)
4^3 = 64 amino acids (more than enough)

Thus, a triplet code was postulated as a theoretical basis.

The next curiousity was finding out whether the triplet code was read as ***overlapping*** or ***nonoverlapping***.
Whilst an overlapping code could be efficient for storing information, it would increase the severity of mutations within normal mutations. Instead of one substitute mutation affecting one codon, it would affect three. Thus, non-overlapping codons served as the theoretical basis, which turned out to be supported.

However, some bacteria have overlapping codes, giving them both efficient gene-storing capacity and high mutation rates.

The process of translation was very unclear. So Nirenberg and Matthaei in 1960's were able to synthesis mRNA sequences and study the amino acids that were synthesised.
They created mRNAs with repeating bases, which gave them repeating units of amino acids. But this didn't solve the overlapping vs non-overlapping curiosity.

To solve this, they used dinucleotides, and trinucleotides.
CACACACACA = thr-his-thr-his
CAC = thr
ACA = his

Through this method, they found all 64 codons, 3 of which are STOP codons, and 61 are amino acids.
Read 5' to 3'.
NOTE: AUG codes for both the START codon and Met amino acid.

Summarise the key features of the code
The code is a non-overlapping, triplet code that is read from 5' to 3'.
There are 64 combinations, 61 amino acids and 3 STOP codons.
The code is mainly unamigious, with the exception of AUG which codes for the START and Met amino acid.
The code is degenerate and ***virtually*** universal.

Understand the implications of the code being degenerate
The term "degenerate" means that 1 amino acid can be coded by multiple codons. This makes sense since there are 61 amino acid codes and only 20 amino acids that it can give rise to.

The value in degeneracy is that it decreases the chances of creating a STOP codon. The thing you have to understand is that mutations are happening all the time, and eventually the codon will mutate into a STOP codon, making the amino acid sequence redundant.

Thus, highly expressed genes are optimised for efficient translation.

In any given mRNA, there are three reading frames. Each reading frame will give a different sequence of codons, but only one will encode the correct sequence. This one is free of any intermediate STOP codons.

The rRNA will choose the reading frame with AUG, which indicate the start of the code.

We understand that DNA is universal, but the actual mRNA code is not universal. Codons in mitochondria will code for different amino acids compared with codons in the normal cell.

Understand how the structure of the tRNAs relates to their function
The general process of translation follows as:

1. Carrier molecules (tRNA) will bind a specific amino acid and a specific anticodon
2. A ribosome will bind the tRNA and mRNA, essentially acting as a polymerising machine.

tRNA are small, ***heavily-chemically modified RNAs***. They are chemically modified to allow for its unusual three dimensional shape. There have a characteristic tridimensional shape that is maintained via hydrogen bonds from internal base pairing.
tRNA have adaptor function connecting the amino acids, mRNA, and ribosome.

They recognise the mRNA through the anticodon, which sits on the anticodon loop, and the amino acid is attached to its 3' end.