BIOCHEMISTRY- BP203T

UNIT: 4 Nucleic acid metabolism and genetic information transfer

CLASS:9

TOPIC: GENETIC CODE

GENETIC CODE:

- The three-nucleotide (triplet) base sequences in mRNA that act as code words for amino acids in protein constitute the genetic code or simply codons.
- The genetic code is regarded as a dictionary of nucleotide bases (A, G, C and U) that determines the sequence of amino acids in proteins.
- The codons consist of the four nucleotide bases, the purines—adenine (A) and guanine (G), and the pyrimidines—cytosine (C) and uracil (U).
- These four bases produce 64 different combinations (43) of three base codons.
- The nucleotide sequence of the codon on mRNA is written from the 5'- end to 3' end.
- Sixty one codons code for the 20 amino acids found in protein.
- The three codons UAA, UAG and UGA do not code for amino acids.
- They act as stop signals in protein synthesis.
- These three codons are collectively known as termination codons or non-sense codons.
- The codons UAG, UAA and UGA are often referred to, respectively, as amber, ochre and opal codons.
- The codons AUG—and, sometimes, GUG— are the chain initiating codons

Other characteristics of genetic code:

The genetic code is universal, specific, nonoverlapping and degenerate.

1. Universality:

The same codons are used to code for the same amino acids in all the living organisms.

Thus, the genetic code has been conserved during the course of evolution.

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Hence genetic code is appropriately regarded as universal.

There are, however, a few exceptions. For instance, AUA is the codon for methionine in mitochondria.

The same codon (AUA) codes for isoleucine in cytoplasm. With some exceptions noted, the genetic code is universal.

2. Specificity:

A particular codon always codes for the same amino acid, hence the genetic code is highly specific or unambiguous

e.g. UGG is the codon for tryptophan.

3. Non-overlapping:

The genetic code is read from a fixed point as a continuous base sequence.

It is non-overlapping without any punctuations.

For instance, UUUCUUAGAGGG is read as UUU/CUU/AGA/GGG.

Addition or deletion of one or two bases will radically change the message sequence in mRNA.

And the protein synthesized from such mRNA will be totally different.

This is encountered in frameshift mutations which cause an alteration in the reading frame of mRNA.

4. Degenerate:

Most of the amino acids have more than one codon.

The codon is degenerate or redundant, since there are 61 codons available to code for only 20 amino acids.

For instance, glycine has four codons.

The codons that designate the same amino acid are called synonyms.

Most of the synonyms differ only in the third (3c end) base of the codon. The Wobble hypothesis explains codon degeneracy.

Codon-anticodon recognition:

The codon of the mRNA is recognized by the anticodon of tRNA.

They pair with each other in an antiparallel direction (5c o 3c of mRNA with 3c o 5c of tRNA).

The usual conventional complementary base pairing (A U, C G) occurs between the first two bases of the codon and the last two bases of the anticodon.

The third base of the codon is rather lenient or flexible concerning the complementary base.

The anticodon region of tRNA consists of seven nucleotides and it recognizes the three-letter codon in mRNA.

Wobble hypothesis:

Wobble hypothesis, put forth by Crick, is the phenomenon in which a single tRNA can recognize more than one codon.

This is because the third base (3c-base) in the codon often fails to recognize the specific complementary base in the anticodon (5c-base).

Wobbling is attributed to the difference in the spatial arrangement of the 5c-end of the anticodon.

The possible pairing of 5c-end base of anticodon (of tRNA) with the 3c-end base of codon (mRNA) is given

Wobble hypothesis explains the degeneracy of the genetic code, i.e. existence of multiple codons for a single amino acid.

Although there are 61 codons for amino acids, the number of tRNAs is far less (around 40) which is due to wobbling.

Codon bias: Many amino acids have multiple codons. However, the organisms prefer to use one or two codons (not all of them), and this phenomenon is referred to as codon bias.

It is variable, depending the organism. As a result of codon bias, low amounts of tRNAs for the rarely used codons are made.

Mutations and genetic code:

Mutations result in the change of nucleotide sequences in the DNA, and consequently in the RNA.

The ultimate effect of mutations is on the translation through the alterations in codons.

Some of the mutations are harmful.

The occurrence of the disease sickle-cell anemia due to a single base alteration (CTC o CAC in DNA, and GAG o GUG in RNA) is a classical example of the seriousness of mutations.

The result is that glutamate at the 6th position of E-chain of hemoglobin is replaced by valine.

This happens since the altered codon GUG of mRNA codes for valine instead of glutamate (coded by GAG in normal people).

Frameshift mutations are caused by deletion or insertion of nucleotides in the DNA that generate altered mRNAs.

As the reading frame of mRNA is continuous, the codons are read in continuation, and amino acids are added.

This results in proteins that may contain several altered amino acids, or sometimes the protein synthesis may be terminated prematurely