

Hello students.

Course title is molecular biology.

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Today I'm going to help you

understand and gain knowledge

about the concept of genetic code,

its properties, Wobble Hypothesis,

codon and anticodon,

start and stop codon.

This topic deals with the

concept of genetic code,

The relationship between

genes and proteins,

and properties of the genetic code.

From this presentation,

the students will be able to explain

how DNA encodes genetic information

and the role of mRNA and tRNA.

and also be able to understand and describe

the properties of the genetic code.

What is the relationship

between genes and proteins?

DNA is read in segments called genes.

A gene is a particular sequence of

nucleotides that code for a protein.

The sequence of bases determines what

sequence the amino acids are in.

which in turn determines

the protein functions.

The relationship between genes and

proteins can be stated as follows.

All metabolic reactions are

catalyzed by specific enzymes.

Enzyme function depends on sequence

of amino acids constituting it.

The one gene-

one enzyme hypothesis of Beadle and Tatum

states that the synthesis of enzyme

is controlled by a particular gene.

A gene transcribes mRNA strand,

which in turn translates a protein.

Thus, mRNA conveys information from

sequence of nucleotides in the DNA to

the sequence of amino acids in a protein.

This was known as the sequence hypothesis.

Each amino acid is specified by a sequence

of three bases called codon on mRNA.

Each tRNA molecule has a sequence

of three bases called anticodon,

which reads a codon on mRNA.

tRNA molecules thus serve as adapters

in protein synthesis by reading

the mRNA codons in a sequence.

This was known as Crick's adapter hypothesis.

The relationship between the sequence

of bases in DNA or RNA and the sequence

of amino acids in a polypeptide

chain is called the genetic code.

The code indicates which codons

specify which amino acids,

Properties of the genetic code.

The first property: amino acids are

involved in protein synthesis.

Of the 150 amino acids found in nature,
only 20 are specified by the genetic
code and take part in protein synthesis.

The genes of a cell direct the
arrangement of these 20 amino acids
into polypeptide chains of a protein.

Polypeptide chain typically contains
100 to 300 amino acids and is
formed by specific arrangement of
the twenty types of amino acids.

The genetic code is a triplet code.

A triplet code or three letter
code was first suggested by
the physicist Gamov in 1954.

Three bases specify one amino acid.

Thus 64 distinct triplets of purine

And/or pyrimidine bases determine
the 20 amino acids.

These triplets are called codons.

Of the 64 codons,

61 code for individual amino acids.

The other three are nonsense or stop codons.

The code is non overlapping.

In a non overlapping code.

As seen in the example shown below,

6 nucleotides would code for two amino acids.

In overlapping code, however,

up to four amino acids could be coded.

Mutational changes in one letter would

affect only one word in non-overlapping code,

while it would affect 3

words in overlapping code.

Studies on gene mutation show

that the code is non-overlapping.

The code is comma less.

There is no demarcating

signal between codons.

When one amino acid is coded,

the next amino acid will be automatically

coded by the next 3 letters

and no letters are wasted

as punctuation marks.

The code has polarity.

The code is always read in five

prime to three prime direction.

If the code is read in opposite directions,

it would specify two different

proteins since the codons would

have reversed base sequences.

Codons and anticodons.

The polarity of DNA codes is 3

prime to five prime direction.

And mRNA is 5 prime to three

prime direction.

Three bases

forming the anticodon of tRNA run in three

prime to five prime direction.

Three bases of anticodon pair

with the mRNA on the ribosomes

during protein synthesis,

which proceeds from the N

to the C direction.

Initiation codons: In most organisms,

AUG codon is the initiating codon

coding for methionine in eukaryotes.

Or N-formyl methionine in prokaryotes.

In rare cases,

GUG also serves as the initiating codon,

for example, in bacterial protein synthesis.

Normally GUG codes for valine,

but when normal AUG codon

is lost by deletion,

only then GUG acts as initiating

codon. Termination codons:

Three of the 64 codons do not

code for any of the amino acids

and therefore, are called nonsense codons.

These are UAA,

UGA and UAG.

They bring about termination and release

of polypeptide chain synthesis and are

therefore, called termination codons.

Termination codons are not read

by any tRNA molecules but by

proteins called release factors.

There are three of them in prokaryotes

designated RF-1, RF-2 and RF-3.

While in eukaryotes there is

a single release factor,

The code is degenerate:

There are 64 codons of which

61 specify amino acids.

Since only 20 amino acids take

part in protein synthesis,

there are many more codons

than there are amino acids.

More than one codon may specify

the same amino acid,

and this was called degeneracy of the code.

The table shows the number of codons

that code for a single amino acid.

For example,

Alanine can be coded for by 4 codons.

The code is non-ambiguous:

A non-ambiguous code means that

a particular codon will always

code for the same amino acid.

However, an exception is a AUG & GUG,

which may code for methionine

as initiating codon,

although GUG codes for valine.

The code is universal:

The genetic code is valid for all organisms,

ranging from bacteria to man

and the same for all organisms

and therefore said to be universal.

Colinearity of gene structure

and its polypeptide product:

The gene is an unbranched

structure consisting of linear

sequence of nucleotide pairs.

The polypeptide chain is also

unbranched and consists of a linear

series of amino acid residues.

The Wobble hypothesis: was proposed

by Crick in 1966 to explain the

degeneracy of the triplet code.

When one amino acid is specified by different codons, the difference between them usually lies at the third base position.

Although there are 61 codons specifying amino acids, the cell contains less than 61 tRNA molecules.

Crick's wobble hypothesis allows some tRNA molecules to recognize more than one codon.

Wobble hypothesis is a set of four relationships.

The first relationship states that the first two bases of an mRNA codon always form strong Watson-Crick base pairs with the corresponding bases of the tRNA anticodon and confer most of the coding specificity.

The second relationship states that

the first base of the anticodon pairs

with the third base of the codon

and determines the number of

codons recognized by tRNA:

When the first base of

the anticodon is C or A,

base pairing is specific and only one

codon can be recognized by that tRNA.

However, when the first base is U or G,

the binding is less specific and

two different codons may be read.

When inosine is the first

nucleotide of an anticodon,

three different codons can be recognized,

the maximum number for any tRNA molecule.

The third relationship states that

when an amino acid is specified

by several different codons,

the codons that differ in either

of the first two bases require

different tRNA molecules.

The 4th relationship states that a minimum of 32 tRNA molecules are required to translate all 61 codons, that is 31 to encode the amino acids and one for initiation.

The references.