

Quadrant II – Transcript and Related Materials

Programme: Bachelor of Science (Second Year)

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Paper Title: Molecular Biology

Unit: 4: Translation

Module Name: Process of Translation: Part 1 (Ribosomes as sites of protein biosynthesis)

Module No: 22

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Notes:

Introduction

In the process of translation, a cell reads information from a molecule called a messenger RNA (mRNA) and uses this information to build a protein. Translation occurs constantly in a normal bacterial cell, just like it is in most of the cells of our body.

The Process of Translation

Translation involves “decoding” a messenger RNA (mRNA) and using its information to build a polypeptide protein, or chain of amino acids.

Requirements

mRNA, Ribosomes, tRNA, Translation Factors

mRNA

mRNA carries the genetic information copied from DNA in the form of a series of triplet codons. Each codon specifies a particular amino acid as described in the genetic code table. Based on the number of genes represented on a mRNA, they are classified as

Monocistronic and Polycistronic. A cistron is a functional unit of a gene. It is a sequence of nucleotides in a gene that determines the order of amino acid monomers in a polypeptide or protein.

Monocistronic mRNA: mRNA which represent only a **single gene** is called as monocistronic mRNA. Suppose, a cell has 10 genes, 10 separate mRNAs will be found in that cell. Monocistronic mRNAs are found in eukaryotes.

Polycistronic mRNA: mRNA which represents **more than one gene** is called Polycistronic mRNA. Suppose, a cell has 10 genes, a single mRNA will carry the information of all the 10 genes. Polycistronic mRNAs are found in prokaryotes.

Structure of mRNA:

mRNA is more than just a sequence of codons. It is always longer, as it has additional sequences along with codon sequences.

All mRNAs contain two types of region,

1. Coding or translatable region
2. Non-coding or non-translatable region.

The **coding region** consists of series of codons starting with an initiation codon and ending with a stop codon. But mRNAs are always longer than the coding region. Extra regions are always present on both the sides of the coding region which are called as non-coding or non-translatable region.

Non-Coding region is non-translatable. It does not code for any amino acid or protein. Different non-coding sequences are present on both the sides of a protein coding region. If a non-coding region is present before the protein coding region, it is said to be upstream. If a non-coding region is present after the protein coding region, it is said to be downstream.

Different non-coding regions in an mRNA are

1. **5'-UTR or Leader Sequence:** is found upstream (before) of initiation codon.
2. **3'-UTR or Trailer Sequence:** is found downstream (after) of stop codon.
3. **Intercistronic Spacer Sequence:** separates cistrons in polycistronic mRNA.

4. **Ribosome Binding Site:** Multiple in prokaryotic and single in eukaryotic mRNA.

UTR stands for Un-Translated Region.

Below are the diagrams of prokaryotic and eukaryotic mRNA. Coding region is represented in yellow colour and non-coding region is represented in grey colour. Each yellow region represents information of one gene.

Prokaryotic mRNA is polycistronic. Information of more than one gene will be present on it. Eukaryotic mRNA is monocistronic. Information of only one gene will be present on it.

Prokaryotic mRNA

5'-PPP-UTR	AUG	Gene A	UAA	Intercistronic Space	AUG	Gene B	UAA	UTR-AAA-3'
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Eukaryotic mRNA

5'-PPP-UTR	AUG	Gene A	UAA	UTR-AAA-3'
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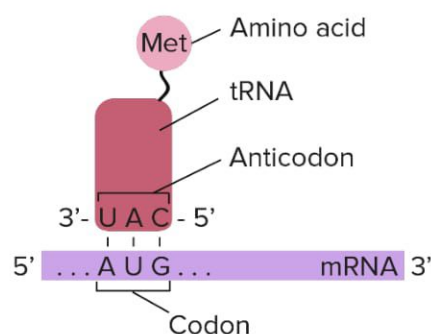
tRNA/Transfer RNA/ Adaptor RNA

It is referred to as **adaptor** as it acts as a connection to translate nucleic acid code on mRNA into amino acid code on proteins. It acts as the key to decode the code in mRNA.

It is a single RNA chain of 73 to 93 nucleotides. This single stranded tRNA folds into a secondary structure which is cloverleaf-like. This cloverleaf-like secondary structure has well defined arms which have stems and loops.

tRNA has 5 different arms as described below,

1. **D loop:** has 3 – 4 base pairs in the stem and 5 – 7 unpaired nucleotides in the loop. **D**ihydrouridine is an unusual nucleotide found in this arm. Remember the letter D.
2. **Anticodon Arm:** has 5 base pairs in the stem and 5 – 7 unpaired nucleotides in the loop. A three nucleotide long anticodon sequence in this arm is responsible for recognizing the codon on mRNA by complementary base pairing. Anticodon is complementary to codon. The anticodon sequence is always read in 5' to 3' direction.



3. **Variable Arm:** contains 4 – 5 nucleotides but can go up to 24 nucleotides.
4. **T ψ C Arm:** has 5 base pairs in the stem and 5 – 7 unpaired nucleotides in the loop. Pseudouridine is an unusual nucleotide found in this arm.
5. **Acceptor Arm:** has 7 base pairs in the stem and 4 unpaired nucleotides. There is no loop in this arm. This arm contains a highly conserved sequence **5'-CCA-3'**. A specialized enzyme tRNA nucleotidyl transferase or CCA adding enzyme is responsible for adding 5'-CCA-3' sequence to all tRNAs. Amino acid is charged or is attached to this arm based on codon sequence.

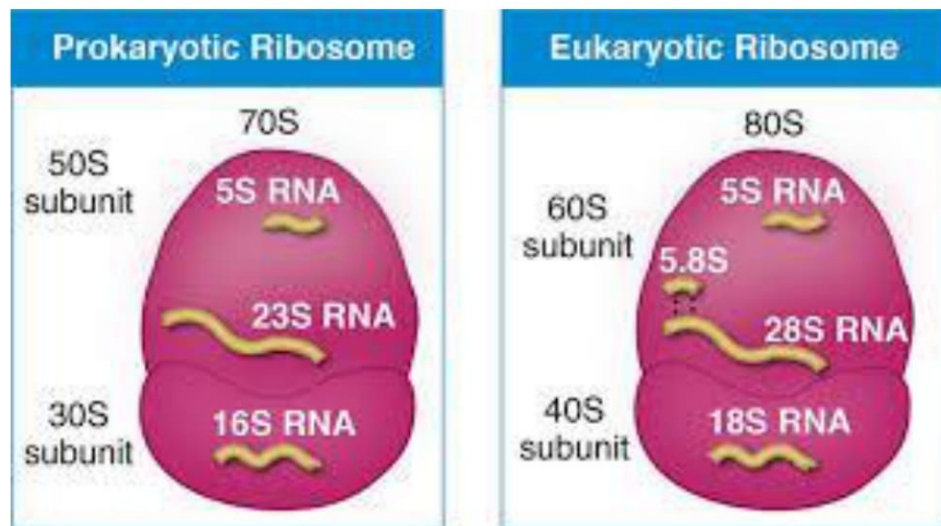
In the process of translation, tRNAs bind to mRNAs inside of a structure called the ribosome. To bind to an mRNA, anticodon arm plays an important role as contains a complementary base sequence to codon sequence in an mRNA.

Ribosome

The ribosome is made up of proteins and RNA. This organelle provides a place where mRNAs can interact with tRNAs bearing amino acids. Each ribosome has two

subunits, large subunit and small subunit. Both the subunits are made up of proteins and different rRNA molecules as described in the diagram below.

Prokaryotes have 70S and eukaryotes have 80S ribosomes. The 'S' refers to Svedberg coefficient.



There are three sites on the ribosome where tRNAs bind: The A site, P site, and E site.

1. **A** site: **accepts** an incoming tRNA bound to an amino acid. This site is also called as aminoacyl-tRNA binding site.
2. **P** site: holds a tRNA that carries a growing **polypeptide** chain. This site is also called as peptidyl-tRNA binding site.
3. **E** site: is the **exit** site where a tRNA goes after it is **empty**, meaning, that it has transferred its polypeptide chain to another tRNA (which now occupies the P site). In the diagram on page 1, the empty tRNA has already left the E site and is thus not shown.

Translation Factors

In addition to mRNA, tRNA, and Ribosomes, the process of translation requires several translation factors. These factors are basically proteins in nature. Their role is to aid in the process of translation by carrying out different functions in different steps.

Translation factors which take part in initiation, elongation, and termination step are called Initiation factors (IF), Elongation factors (EF), and Release factors (RF), respectively. Specific function of the translation factors will be discussed in the following notes.

Process	Prokaryotic TF	Eukaryotic TF
Initiation	IF-1, IF-2, IF-3	eIF1A, eIF2, eIF3, eIF5B, eIF4
Elongation	EF-Tu, EF-Ts, EF-G	eEF1 α , eEF1 β , eEF1 γ , eEF2 ^s
Termination	RF-1, RF-2, RF-3,	eRF-1, eRF-3

mRNA, Ribosomes, tRNA, and Translational factors are required to work together to carry out the process of translation.