Quadrant II – Transcript and Related Materials

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Unit: II Transcription, Post transcriptional modification, and processing of Eukaryotic RNA

Module Name: TRANSCRIPTION UNIT

Module No: 12

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Notes

Transcription is the process of syntheses of mRNA from the DNA double helix. The mRNA is synthesized with the help of **RNA polymerase** which catalyses formation of complementary base pairs from the template strand.

Transcription unit is the part of DNA that is involved in transcription. The product of transcription is called a **primary transcript (mRNA)**.

It carries information of the genes to be transcribed into **mRNA** which is translated into protein during the process of translation.

In eukaryotes the transcription unit carries information of 1 gene so this is called the monocistronic transcription unit.

Polycistronic transcription mostly seen in prokaryotes carries information of a set of genes which is transcribed in 1 transcription unit

The eukaryotic transcription unit may be simple/complex i.e.it can produce a single mRNA encoding a single protein. In complex transcription units the primary transcript can be processed in more than one way to produce more than one polypeptide.

Transcription unit consists of:

- 1. Promoter
- 2. Gene coding sequence
- 3. Terminator

PROMOTER

It is the first part of the transcription unit so it is important for initiation of transcription. It contains the **core promoter** and certain **regulatory promoter elements**

CORE PROMOTER

It initiates transcription by allowing binding of RNA polymerase and transcription factors. Transcription factors are proteins that will help in regulation and synthesis of mRNA. There are general transcription factors and specific transcription factors.

REGULATORY PROMOTER ELEMENTS

They are located upstream of core promoter i.e. ahead of the core promoter. They help regulate the process of transcription. Regulation is basically controlling the process of transcription by activating / initiating it or by stopping / repressing.

Core promoter consists of 2 segments:

- 1. **-30 or TATA box** (consensus 5'-TATAXAX-3' where, X is A or T)
- 2. **Initiator (Inr) sequence** located around nucleotide +1. It is a consensus sequence 5'-Py₂ CAPy₅- 3'. Initiators are rich in pyrimidine residues.

These two regions serve as binding site for the general transcription factors and other regulatory elements.

TATA- BOX

- Since this is present upstream of the gene the nucleotides will be labelled as 10 and so on based on the position.
- It is the binding site for the general transcription factors, cis-acting regulatory promoter sequences and RNA polymerase.
- It shows the start site of transcription. Start site is from where the coding gene will begin.

• Regulatory elements – CAAT box and GGGCGG.

GENE CODING SEQUENCE

- Located downstream of promoter i.e. after the promoter. The nucleotides heer will be labelled as +1 and so on
- It contains the information for synthesizing mRNA by RNA polymerase II
- One strand of DNA is transcribed i.e. **template strand.** This strand will be complementary to the **mRNA**
- The transcript is identical to the **coding strand** so it is complementary to the template strand. It has the same nucleotides as the mRNA.
- Contains coding and non coding sequences (exons and introns)

TERMINATOR

- Last component of the transcription unit
- RNA polymerase detaches from the DNA template
- In eukaryotes it is coupled with RNA processing i.e. 3' end of nascent mRNA undergoes splicing
- Other modifications during termination are addition of 5'capping i.e. methylguanosine residue on 5' end and addition of a poly A tail on the 3' end.