

## **Quadrant II – Transcript and Related Materials**

**Programme: Bachelor of Science (Third Year)**

**Subject: Botany**

**Course Code: BOC 109**

**Course Title: Molecular Biology and Genetic Engineering**

**Unit: VI**

**Module Name: Gene Organisation in Eukaryotes**

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### **Notes**

#### **Eukaryotic genome organization**

Eukaryotes have much more DNA than prokaryotes. For example, an *E. coli* bacteria contains roughly 3 million base pairs of DNA, while a human contains roughly 3 *billion*.

Eukaryotes contain multiple linear chromosomes, each eukaryotic chromosome is made by a single linear DNA molecule.

The cell can have one single copy (haploid), two (diploid) or multiple (polyploid) copies of each chromosome, in a membrane-bound nucleus.

Extrachromosomal plasmids are not commonly present in eukaryotes.

Eukaryotes contain large amounts of noncoding and repetitive DNA.

In eukaryotic cells, the DNA is associated with proteins to form chromatin which then gets organised into compact structures the chromosomes . DNA helix is wrapped around core proteins, the histones which are basic in nature.

The core is composed of 2 molecules of histones ( H2A, H2B, H3 and H4). Each core with two turns of DNA wrapped round it (approx. with 150 bp) it is termed as nucleosome, the basic unit of chromatin.

Nucleosomes are separated by spacer DNA, to which histone H1 is attached. This continuous string of nucleosomes, representing beads –on- a string form of chromatin is termed as 10nm fiber. The length of DNA is considerably reduced by formation of 10-nm fiber, which is further coiled to produce 30- nm fiber. These 30-nm fibers are further organised into loops by anchoring the fiber at A/T regions namely scaffold-associated regions (SARS) to a protein scaffold. During the course of mitosis, the loops are further coiled, chromosomes condense and become visible.

### **Salient features of genes**

In eukaryotes, transcription occurs in the nucleus, and translation occurs in the cytoplasm.

Eukaryotic genes are not grouped into operons as are prokaryotic genes.

Each eukaryotic gene is transcribed separately, with separate transcriptional controls on each gene.

Prokaryotes have one type of RNA polymerase for all types of RNA, eukaryotes have a separate RNA polymerase for each type of RNA.

Number of genes in each organism is more than the number of chromosomes, hence several genes are located on each chromosome.

### **Eukaryotic gene structure**

Eukaryotic genes have more complex structure as compared to prokaryotes.

Exons & Introns

Promoter sequences

Upstream region

Downstream region

Terminator sequences

Enhancers and silencers

Signals ( Upstream and downstream sequence signal)

Exons & Introns

In typical eukaryotes, the region of the DNA coding for a protein is usually not continuous. This region is composed of alternating stretches of *exons* and *introns*.

Exons

Coding sequence, transcribed and translated. Codes for amino acids in the polypeptide chain. vary in number, sequence and length. A gene starts and ends in Exons (5' to 3' ).

### Introns

Coding sequences are separated by non coding sequences called introns. During transcription, both exons and introns are transcribed onto the RNA, in their linear order. Process called *splicing* takes place, in which, the intron sequences are excised when the primary transcript is processed to give the mature RNA sequence. All introns share the base sequence GT in the 5' end and AG in the 3' end.

### Promoters

Regulatory regions of DNA located upstream controlling gene expression. Composed of core promoter sequence and proximal promoter sequence. Core promoter marks the start site (-34) for transcription by binding RNA polymerase and other proteins necessary for copying DNA to RNA. Proximal promoter contain primary regulatory element and transcription factor binding sites. TATA box or hogness box (-30 to -80) and CAAT (upstream TATA) are two distinct sequences.

Together responsible for binding of RNA polymerase II, for transcription.

### Upstream region (5' end)

5' untranslated region (5' UTR) is the non coding region which has several functions. mRNA transport and initiation of translation. Signal for addition of cap (7 methyl guanosine) to the 5' end of mRNA. Cap facilitates the initiation of translation. Stabilization of mRNA.

### Downstream region (3' end)

3' untranslated region (3' UTR) is also the non coding region, which serves to add mRNA. Provides stability and attachment site for poly – A tail. AAUAA sequence signal for addition of poly A tail. Termination codon TAA for translation.

### **Enhancers and silencers**

Enhancers and silencers may be distantly located from the gene, Upstream or downstream, many thousands of base pairs away. Enhancers enhances the transcription of a gene upto few thousands base pairs upstream. Silencers reduce or shut down the expression of a near by gene.

### **Terminator**

Recognised by RNA polymerase as a signal to stop transcription.