

# Introns, Exons and Splicing hn RNA

nds.u.edu/pubweb/~mcclean/plsc731/transcript/transcript4.htm

## Transcription

### Introduction RNA Polymerases and the Transcription Event

Introns are a common eukaryotic event. Several features of interrupted genes are:

- The sequence order is the same as in the mRNA
- The structure of an interrupted gene is identical in all tissues.
- Introns of nuclear genes have termination codons in all three reading frames.

### Transcription Products

### Introns, Exons, and Splicing hn RNA

**Exon** - RNA sequences in the primary transcript that are found in the mRNA  
**Intron** - RNA sequences between exons that are removed by splicing

Introns have been found in eukaryotic mRNA, tRNA and rRNA, as well as chloroplast, mitochondrial and a phage of *E. coli*. Eubacteria are the only species in which introns have not been found. In general, genes that are related by evolution have related organizations with conservation of the position at least some introns. Furthermore, conservation of introns is also detected between genes in related species.

### Alternate Splicing of Exons

The amount and size of introns varies greatly. The mammalian DHFR has 6 exons that total about 2000 bases, yet the gene is 31,000 bases. Likewise, the alpha-collagen has 50 exons that range from 45-249 bases and the gene is about 40,000 bases. Clearly two genes of the same size can have different number of introns, and introns that vary in size.

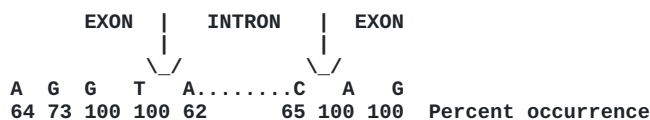
### Course Topics

Some species will have an intron in a gene, but another species may not have an intron in the same gene. An example is the cytochrome oxidase subunit II gene of plant mitochondria where some plant species have an intron in this gene and others do not.

### Course Home Page

## Features of Nuclear Splicing Junctions

1. No extensive homology exists between the ends of an intron.
2. The intron/exon junctions, though, do have well-conserved short sequences.



## Splicing of hnRNAs

1. The left exon is cleaved to produce a linear molecule and a right intron/exon molecule.
2. The left end of the right intron/exon molecule forms a 5'-2' linkage to the adenosine in the sequence 5'-CUGAC-3'. This sequence is about 30 bases upstream of the right exon junction. This produces a **lariat** structure.
3. The right junction is cut, the lariat becomes single-stranded and is degraded, and the exons are spliced.

Splicing appears to involve a complex called the **spliceosome**. This complex consists of RNA and protein, and appears to be composed of a group of **small nuclear ribonucleoprotein particles** or **snRNPs**. These snRNPs each seem to have a role in the splicing process. We will talk about just one snRNP, U1. U1 binds to the 5' splice site. The RNA is complementary to 4-6 nucleotides of the 5' end, but RNA cannot bind alone, it requires the proteins constituent of the particle. An important question is whether U1 is required. If the sequence of the splice site is mutated, binding to

the left junction will not occur. But if the U1 RNA is altered to be complimentary to the mutation in the left junction, binding is restored.

Other snRNPs recognized other regions of RNA involved in splicing. The following is a summary table.

snRNP	Splice Target	Abundance
U1	5' junction	Many
U2	branch	1
U5	3' junction	1
U4	?	1
U6	?	1

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