Lecture Series 10

The Eukaryotic Genome and Its Expression

The Eukaryotic Genome and Its Expression

A. The Eukaryotic Genome

B. Repetitive Sequences

C. The Structures of Protein-Coding Genes

D. RNA Processing

E. Transcriptional Control

F. Posttranscriptional and Posttranslational Control

A. The Eukaryotic Genome

- Although eukaryotes have more DNA in their genomes than prokaryotes, in some cases there is NO apparent relationship between genome size and organism complexity.

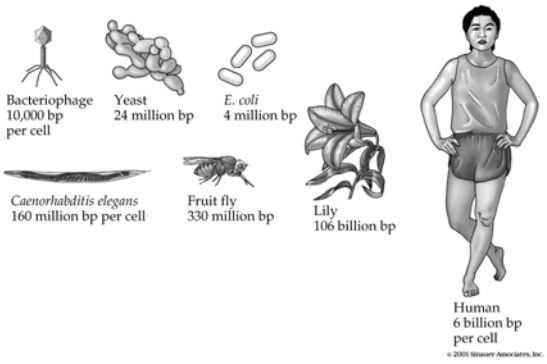
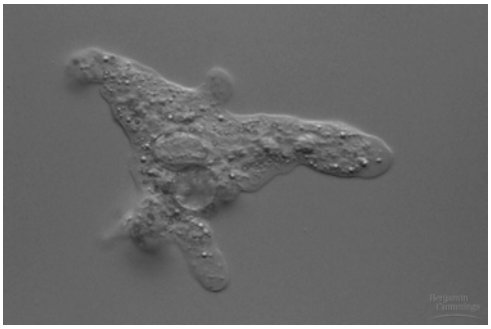


Figure 14.1



Amoeba dubia is the big winner at **670 Billion** base pairs per cell and an uncertain phylogeny!

14.1 A Comparison of Prokaryotic and Eukaryotic Genes and Genomes

CHARACTERISTIC	PROKARYOTES	EUKARYOTES
Genome size (base pairs)	10^4–10^7	10^8–10^{11}
Repeated sequences	Few	Many
Noncoding DNA within coding sequences	Rare	Common
Transcription and translation separated in cell	No	Yes
DNA segregated within a nucleus	No	Yes
DNA bound to proteins	Some	Extensive
Promoter	Yes	Yes
Enhancer/silencer	Rare	Common
Capping and tailing of mRNA	No	Yes
RNA splicing required	Rare	Common
Number of chromosomes in genome	One	Many

A. The Eukaryotic Genome

- Unlike prokaryotic DNA, eukaryotic DNA is separated from the cytoplasm by being contained within a nucleus. The initial mRNA transcript of the DNA may be modified before it is exported from the cytoplasm.

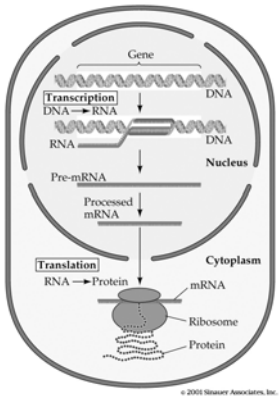


Figure 14.2

A. The Eukaryotic Genome

- The genome of the single-celled budding yeast contains genes for the same metabolic machinery as bacteria, as well as genes for protein targeting in the cell.

14.2 Comparison of the Genomes of E. coli and Yeast

	E. COLI	YEAST
Genome length (base pairs)	4,640,000	12,068,000
Number of proteins	4,300	6,200
Proteins with roles in:		
Metabolism	650	650
Energy production/storage	240	175
Membrane transporters	280	250
DNA replication/repair/ recombination	120	175
Transcription	230	400
Translation	180	350
Protein targeting/secretion	35	430
Cell structure	180	250

Table 14.2

A. The Eukaryotic Genome

- The genome of the multicellular roundworm *Caenorhabditis elegans* contains genes required for intercellular interactions.
- The genome of the fruit fly has fewer genes than that of the roundworm. Many of its sequences are homologs of sequences on roundworm and mammalian genes.

14.3 C. elegans Genes Essential to Multicellularity

FUNCTION	PROTEIN/DOMAIN	GENES
Transcription control	Zinc finger; homeobox	540
RNA processing	RNA binding domains	100
Nerve impulse transmission	Gated ion channels	80
Tissue formation	Collagens	170
Cell interactions	Extracellular domains; glycotransferases	330
Cell–cell signaling	G protein-linked receptors; protein kinases; protein phosphatases	1,290

Table 14.3

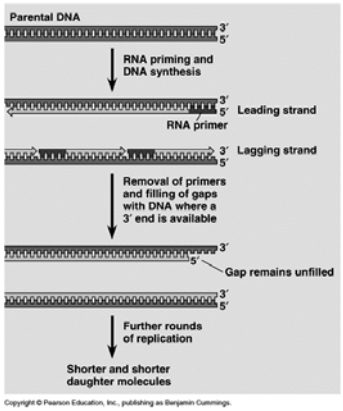
B. Repetitive Sequences

- Highly repetitive DNA is present in up to millions of copies of short sequences. It is not transcribed. Its role is unknown.

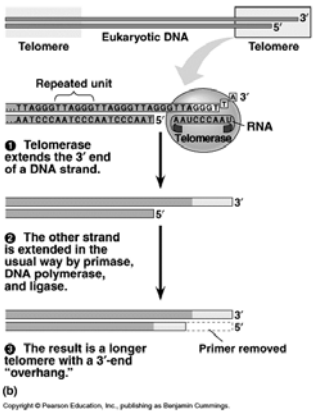
B. Repetitive Sequences

- Some moderately repetitive DNA sequences, such as telomeric DNA is found at the ends of chromosomes. Some may be lost during each DNA replication, leading to chromosome instability and cell death.
- Telomerase catalyzes the restoration of lost telomeric DNA.
- Most somatic cells lack telomerase and thus have limited life spans.

The end-replication problem



Telomeres and telomerase



B. Repetitive Sequences

- Some moderately repetitive DNA sequences, such as those coding for ribosomal RNA's, are transcribed.
- Three rRNAs result, two go to the large subunit and one goes to the small subunit.

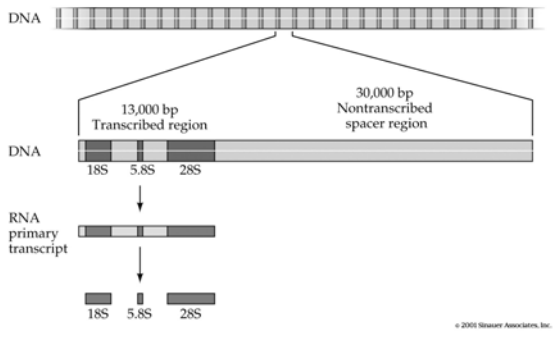


Figure 14.4

B. Repetitive Sequences

- Some moderately repetitive DNA sequences are transposable, or able to move about the genome. These are known as Transposons.

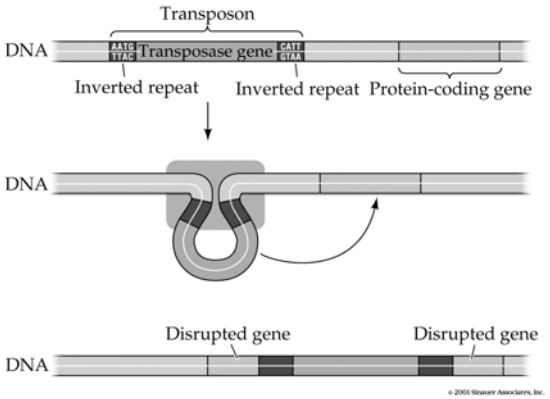


Figure 14.5

C. The Structures of Protein-Coding Genes

- A typical protein-coding gene has noncoding internal sequences (introns) as well as flanking sequences that are involved in the machinery of transcription and translation in addition to its exons or coding regions.
- These are usually single copy genes.

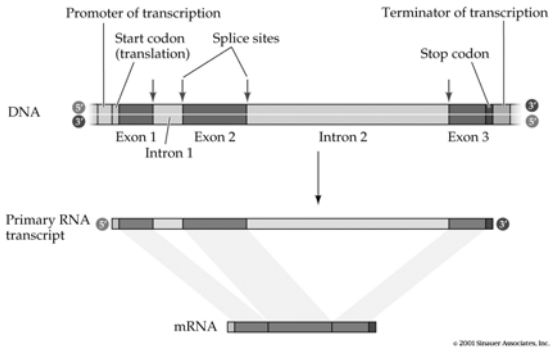


Figure 14.6

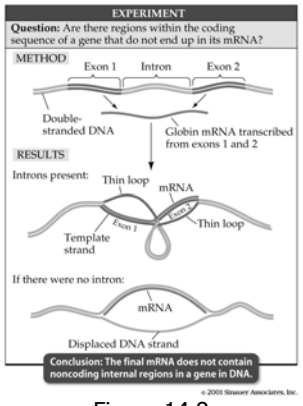


Figure 14.8

C. The Structures of Protein-Coding Genes

- Some eukaryotic genes form families of related genes that have similar sequences and code for similar proteins. These related proteins may be made at different times and in different tissues.
- Some sequences in gene families are pseudogenes, which code for nonfunctional mRNA's or proteins.

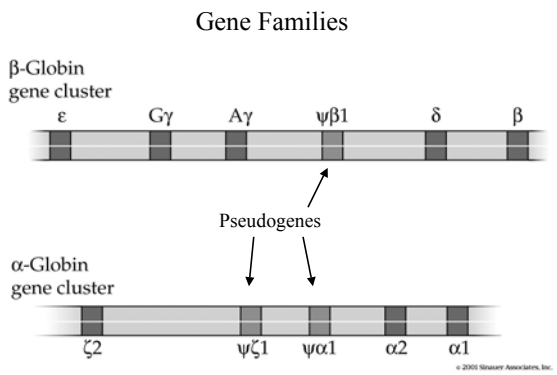


Figure 14.9

C. The Structures of Protein-Coding Genes

- Differential expression of different genes in the β-globin family ensures important physiological changes during human development.

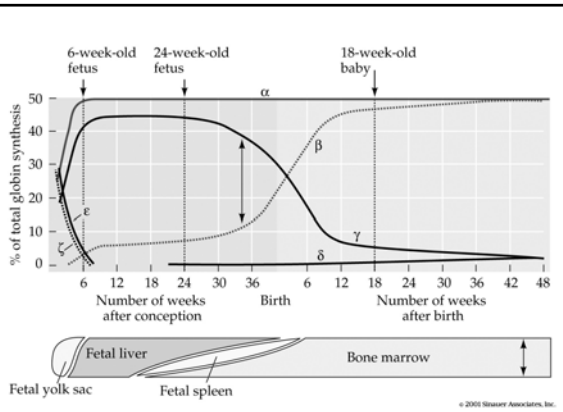
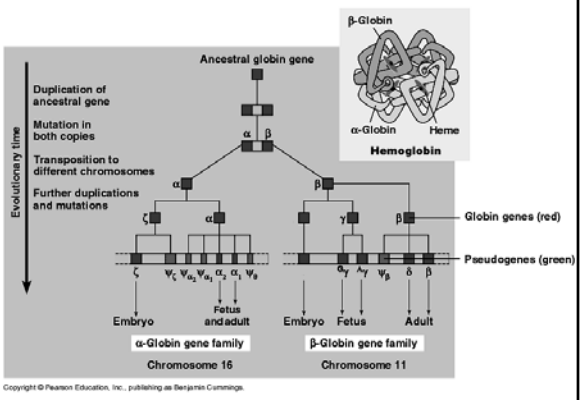


Figure 14.10

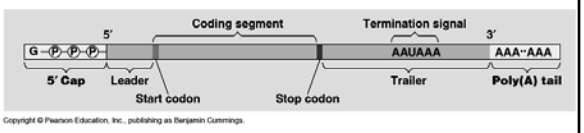
The evolution of human α-globin and β-globin gene families



D. RNA Processing

- After transcription, the pre-mRNA is altered by the addition of a G cap at the 5′ end and a poly A tail at the 3′ end.

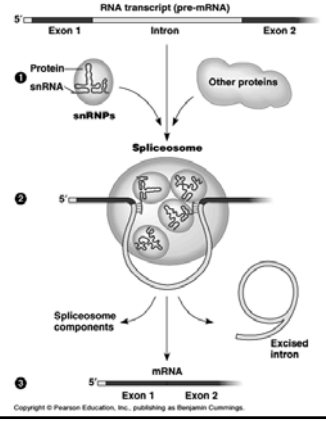
RNA processing; addition of the 5′ cap and poly(A) tail



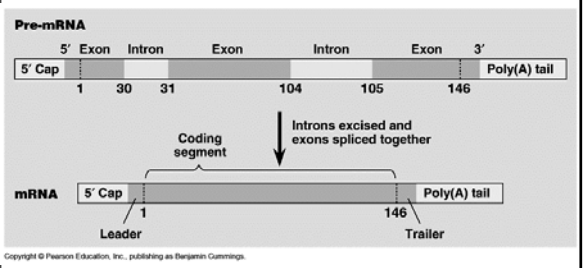
D. RNA Processing

- The introns are removed from the mRNA precursor by the spliceosome, a complex of RNA's and proteins.
- These RNA's are snRNP RNA which are ~300 bases long.

The roles of snRNPs and spliceosomes in mRNA splicing



RNA processing: RNA splicing



E. Transcriptional Control

- Eukaryotic gene expression can be controlled at the transcriptional, posttranscriptional, translational, and posttranslational levels.

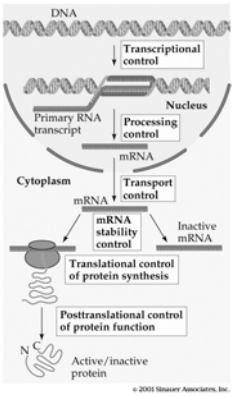


Figure 14.13

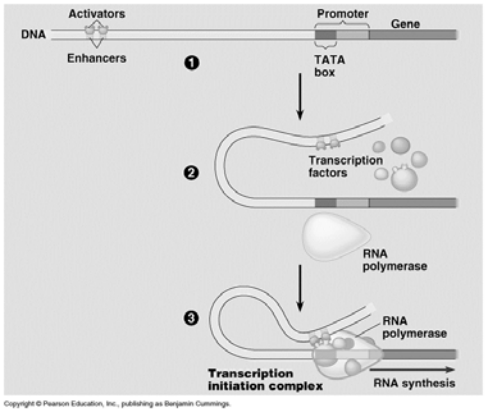
E. Transcriptional Control

- The major method of control of eukaryotic gene expression is selective transcription, which results from specific proteins binding to regulatory regions on DNA.

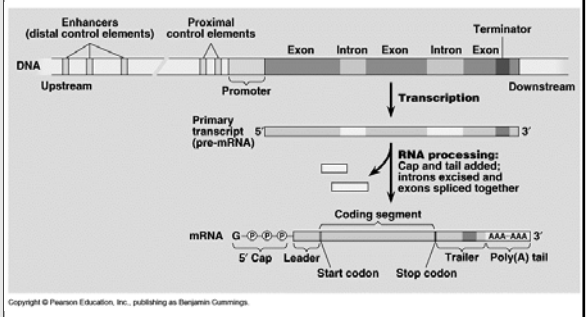
E. Transcriptional Control

- A series of transcription factors must bind to the promoter before RNA polymerase can bind.
- Whether RNA polymerase will initiate transcription also depends on the binding of regulatory proteins, activator proteins, and repressor proteins.

A model for enhancer action



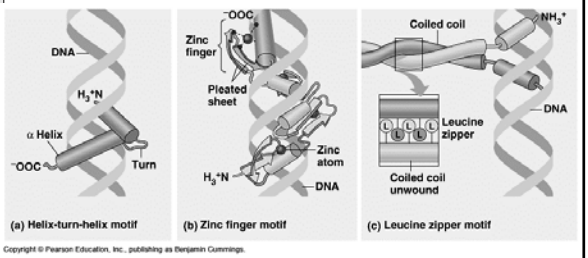
A eukaryotic gene and its transcript



E. Transcriptional Control

- The DNA-binding domains of most DNA-binding proteins have one of four structural motifs: helix-turn-helix, zinc finger, leucine zipper, or helix-loop-helix.

Three of the major types of DNA-binding domains in transcription factors



E. Transcriptional Control

- Local remodeling of chromatin occurs during transcription causing the disaggregation of the nucleosome.

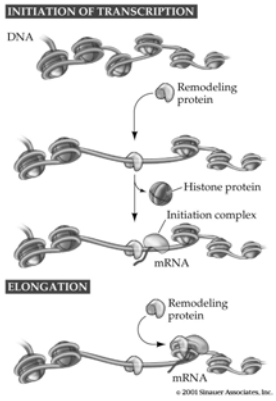
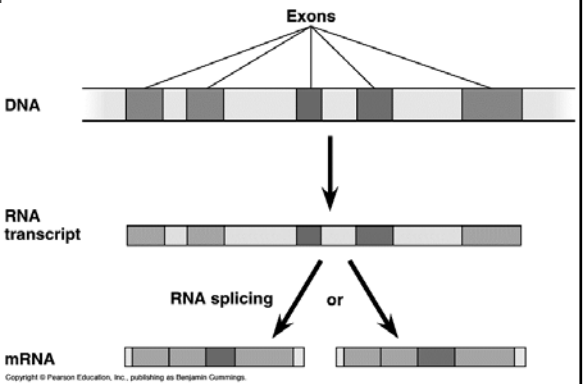


Figure 14.17

F. Posttranscriptional Control

- Because eukaryotic genes have several exons, alterative mRNAs can be generated from the same RNA transcript.
- This alternate splicing can be used to produce different proteins.
- The stability of mRNA in the cytoplasm can be regulated by the binding of proteins.

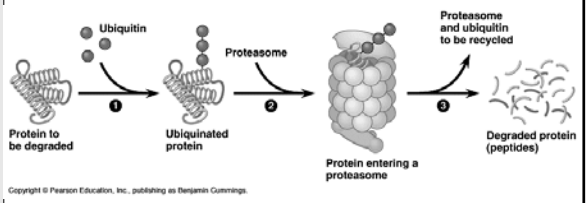
Alternative RNA splicing



F. Posttranslational Control

- Proteasomes degrade proteins targeted for breakdown.

Degradation of a protein by a proteasome



Proteasomes