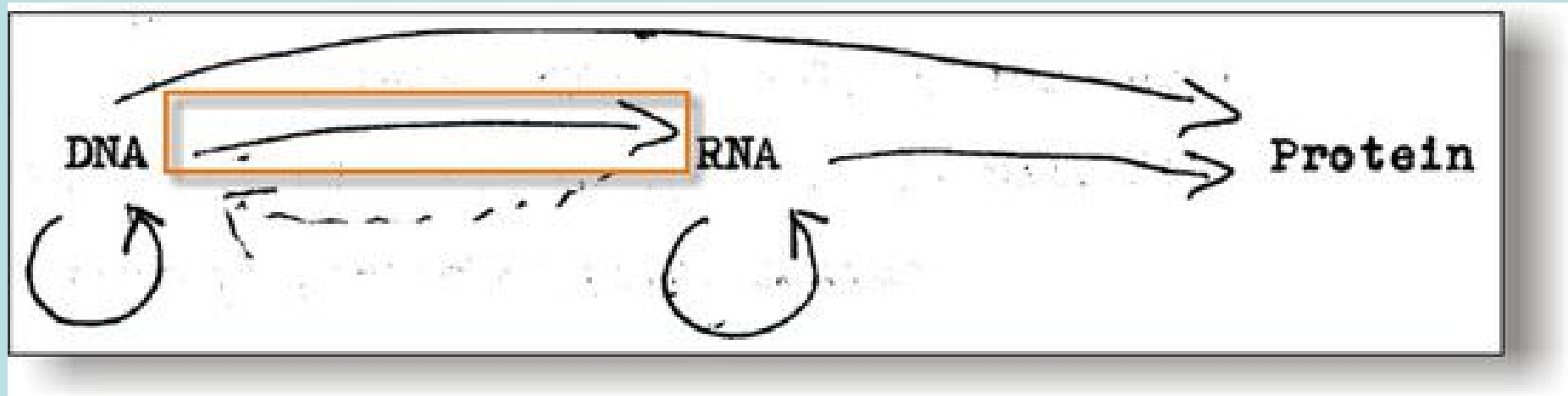
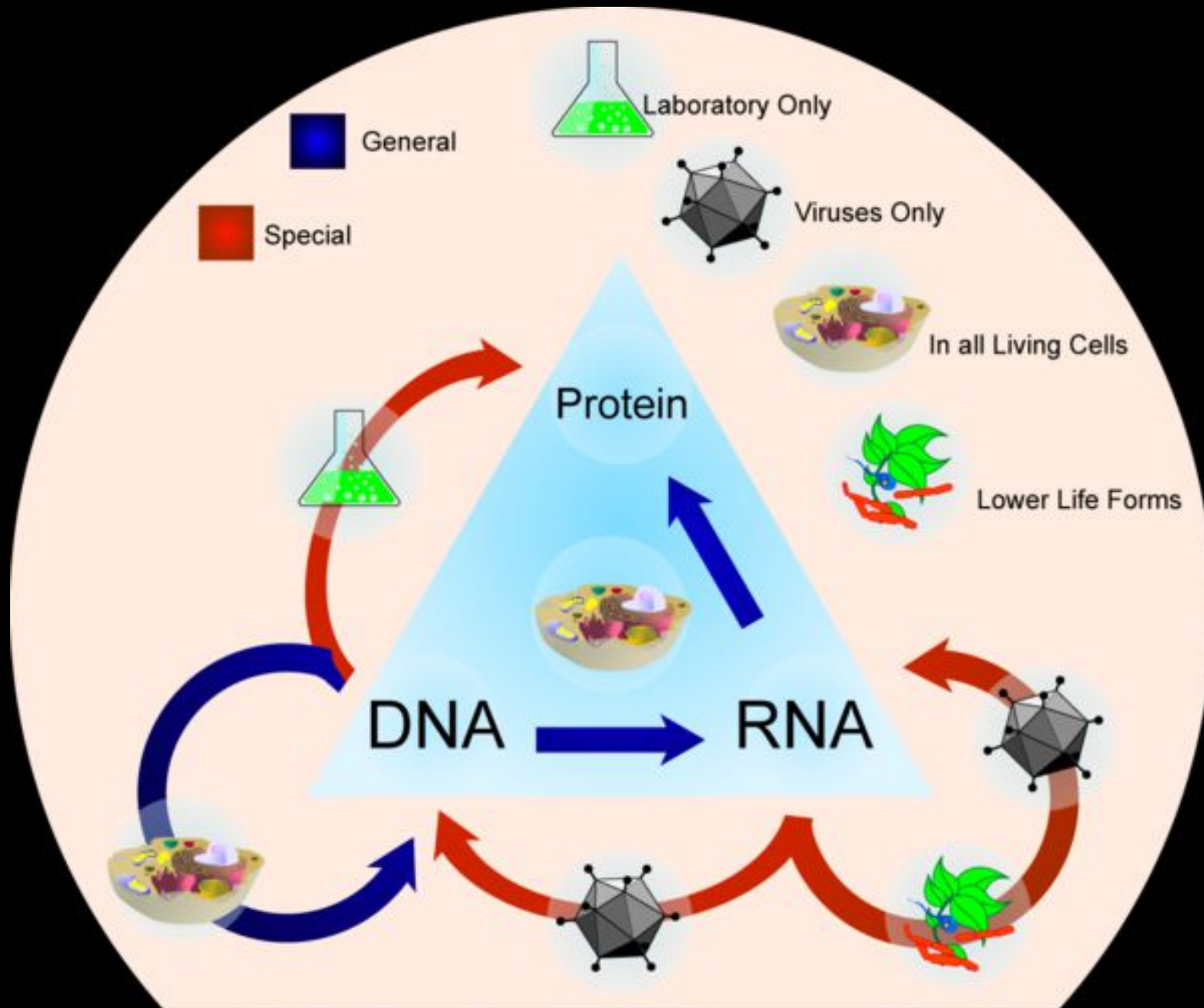


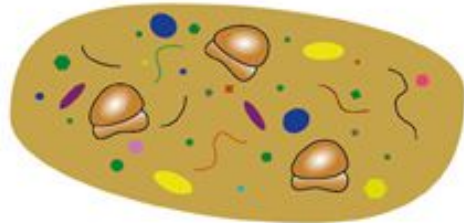
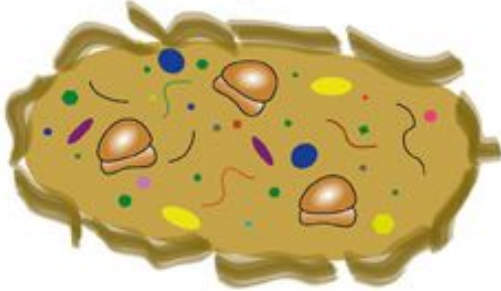
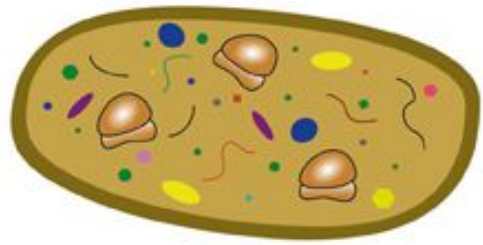
FIGURE 1.2 A gene encodes an RNA, which may encode a polypeptide.

The Central Dogma of Molecular Biology by Francis H. C. Crick 'On Protein Synthesis', Manuscript 1956.





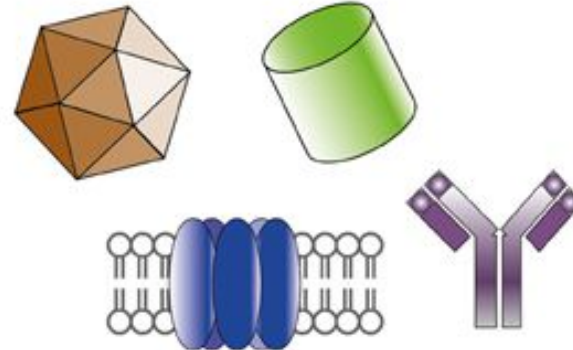
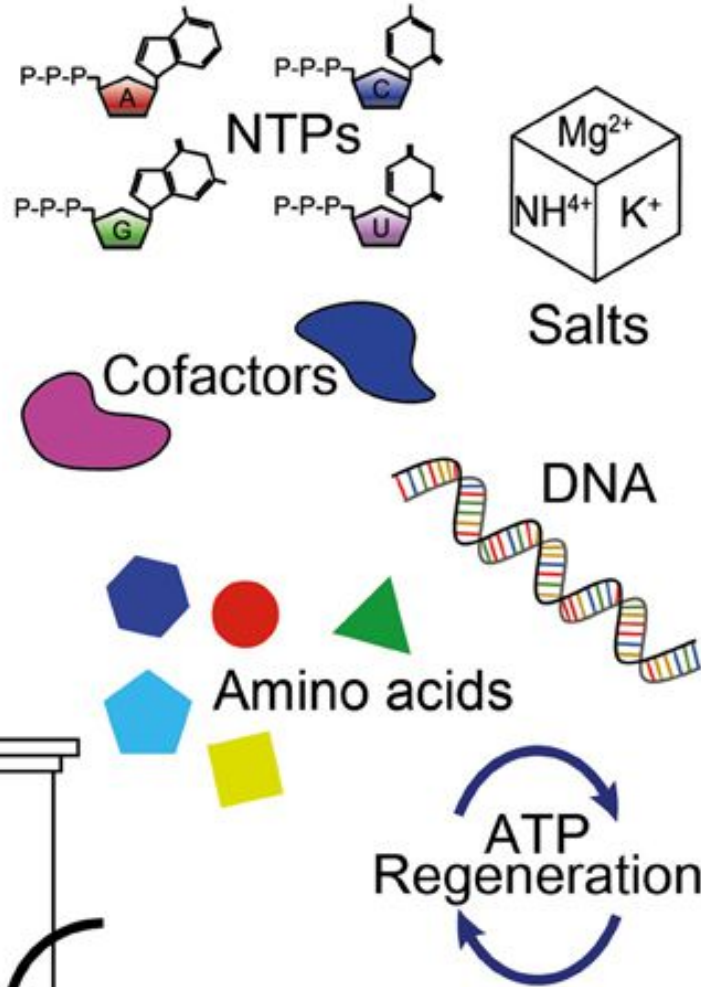
Biological Information Flow



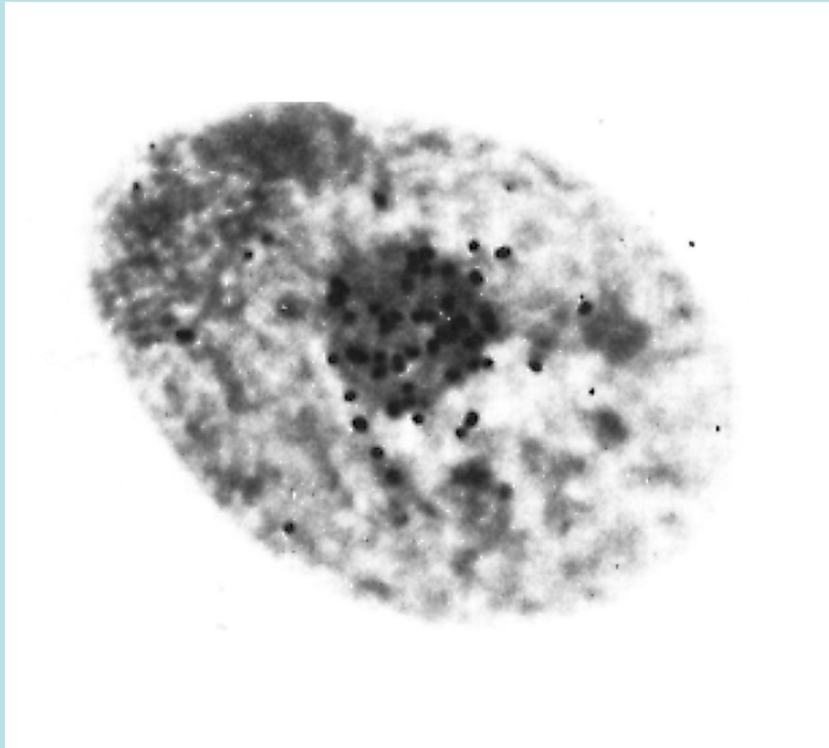
Cell extract

- Grow and lyse cells
- Prepare crude extract
- Add substrates and salts
- Add template
- Incubate

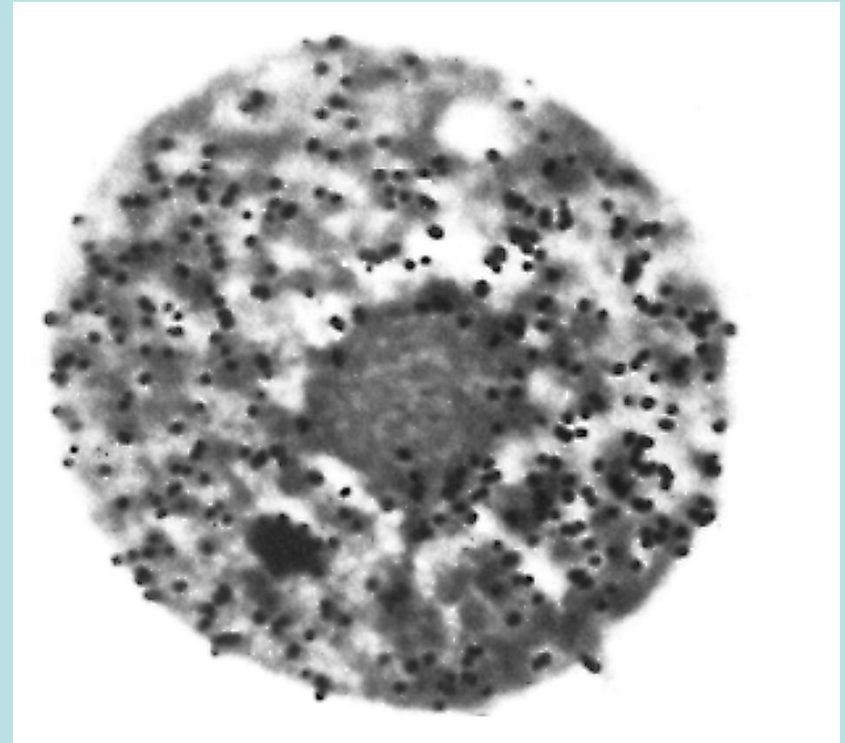
CFPS



RNA is the intermediate between DNA and proteins



Autoradiography of a cell exposed to radioactive uridine for 15 min




Autoradiography of a cell exposed to radioactive uridine for 15 min and subsequently to non-radioactive uridine for 80 min

DNA consists of two base-paired strands

top strand
5' ATGCCGTTAGACCGTTAGCGGACCTGAC
3' TACGGCAATCTGGCAATCGCCTGGACTG
bottom strand

RNA
synthesis



5' AUGCCGUUAGACCGUUAGCGGACCUGAC 3'

RNA has same sequence as DNA top strand:
is complementary to DNA bottom strand

FIGURE 2.13 RNA is synthesized by using one strand of DNA as a template for complementary base pairing.

RNA

- **Messenger → mRNA**
- **Ribosomal → rRNA**
- **Transport → tRNA**

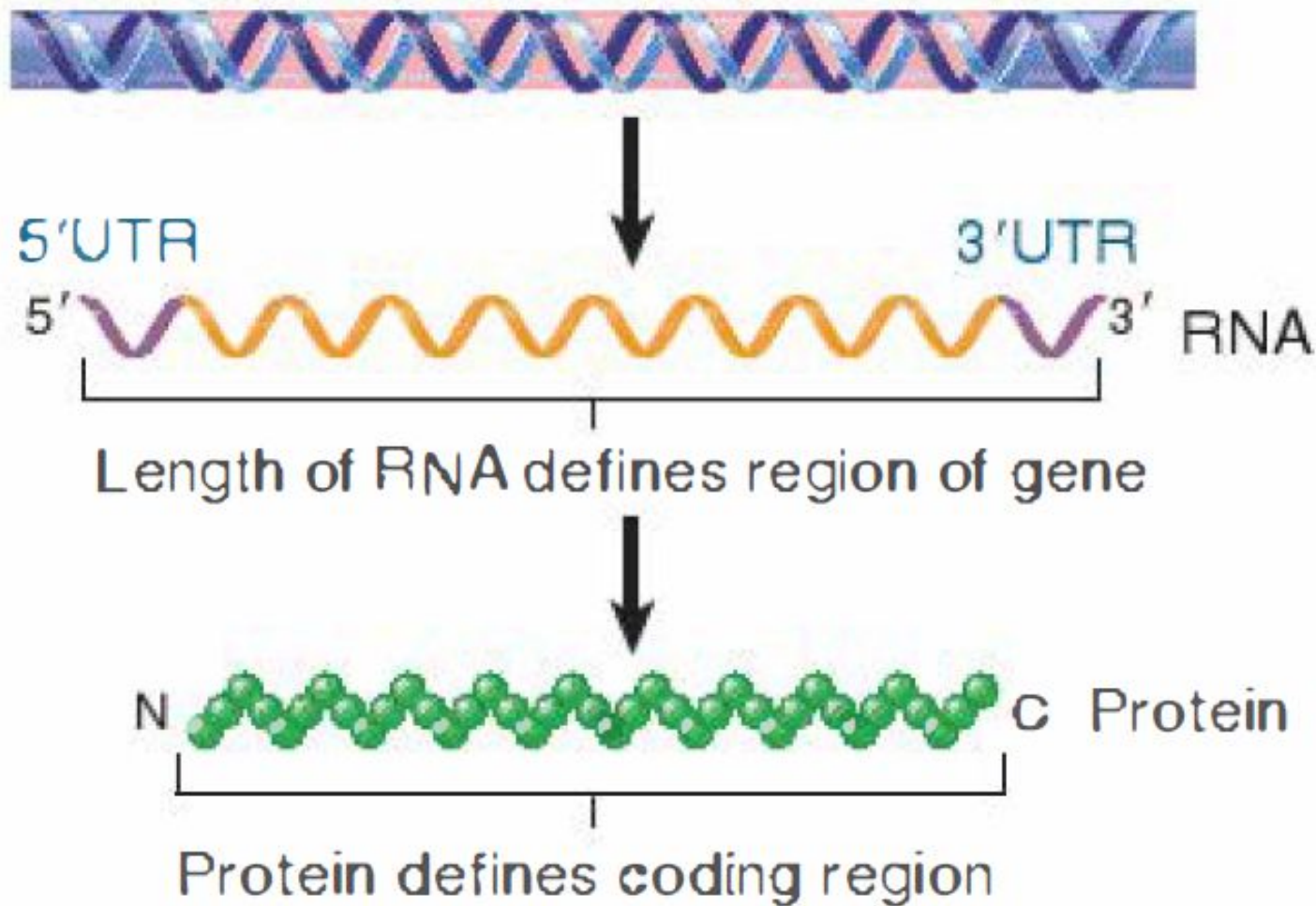
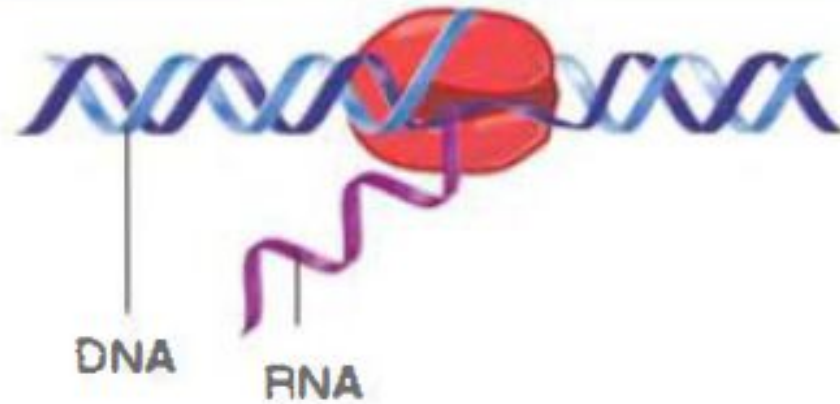


FIGURE 2.14 The gene is usually longer than the sequence encoding the polypeptide.

Transcription



Translation

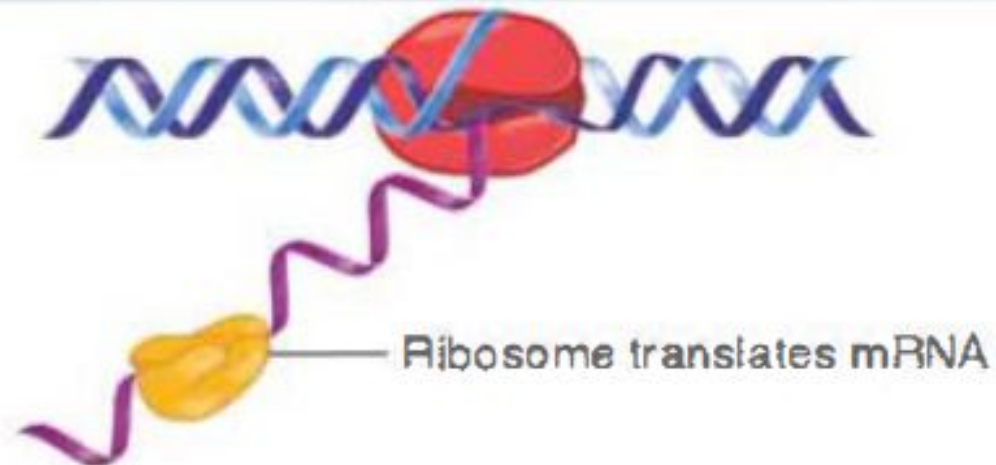


FIGURE 2.15 Transcription and translation take place in the same compartment in bacteria.

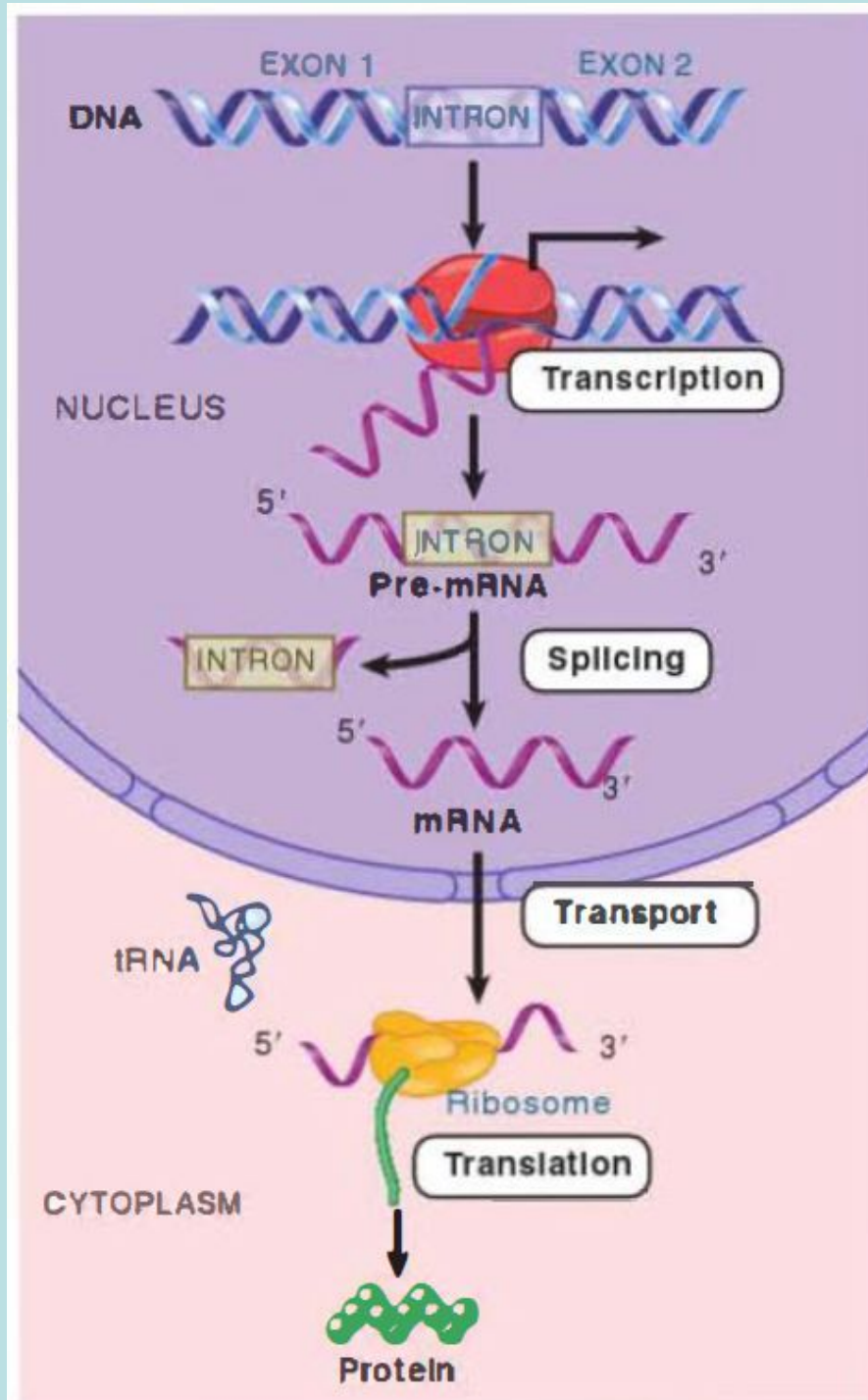
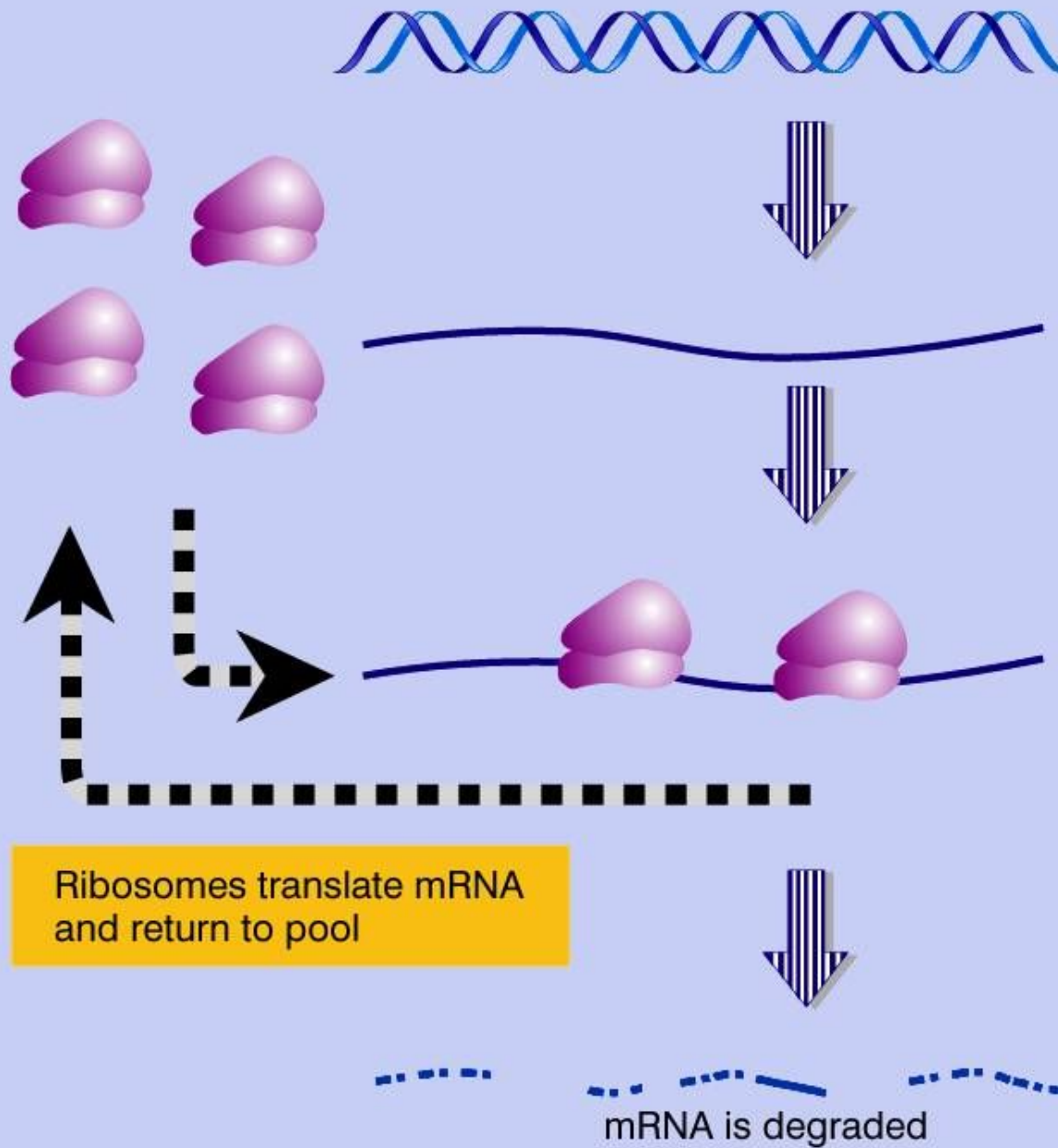


FIGURE 2.16 In eukaryotes, transcription occurs in the nucleus and translation occurs in the cytoplasm.

Figure 5.10 Messenger RNA is translated by ribosomes that cycle through a pool.



Transcription is specifically regulated

- **Cis-acting elements**
- **Trans-acting factors**

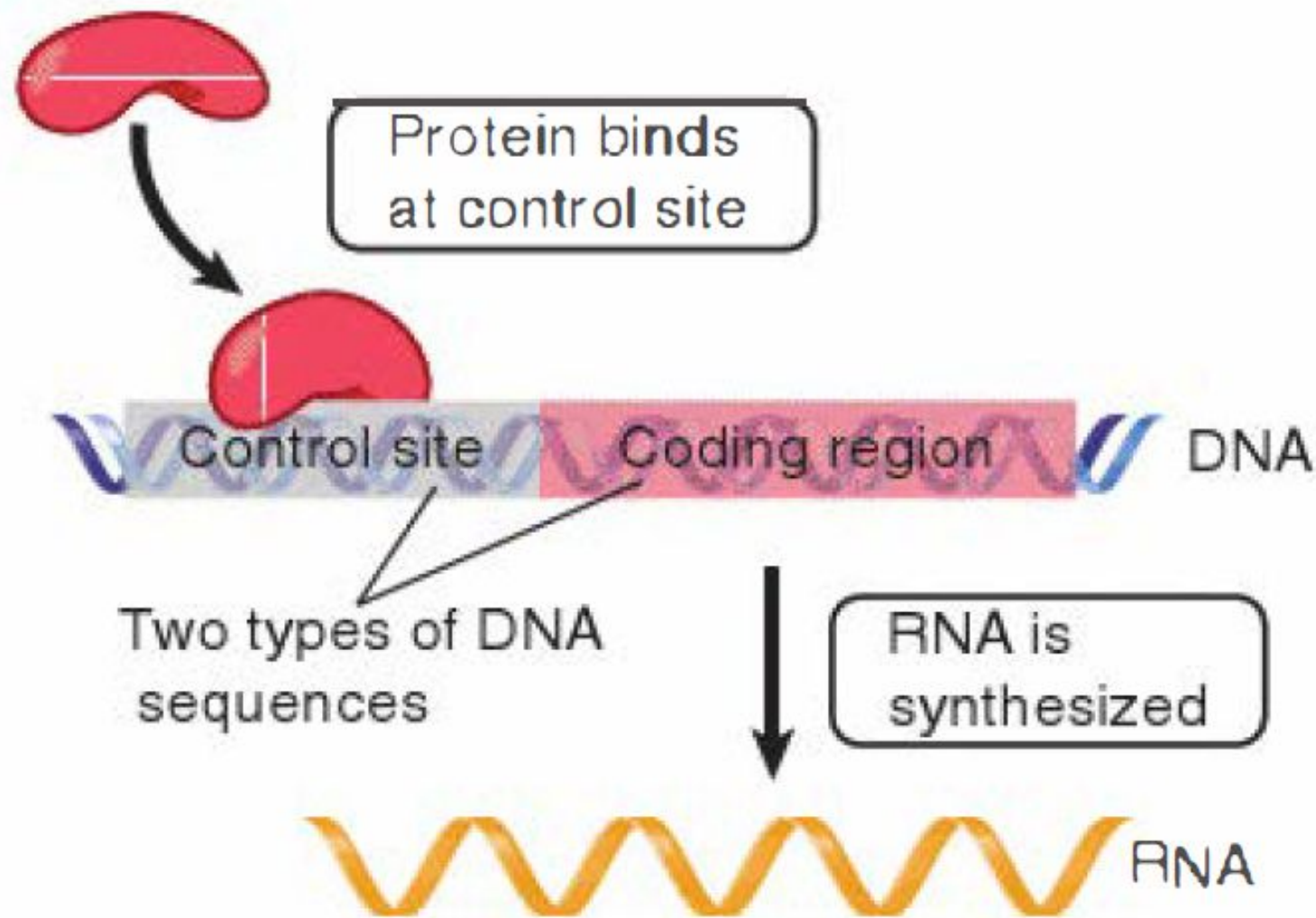
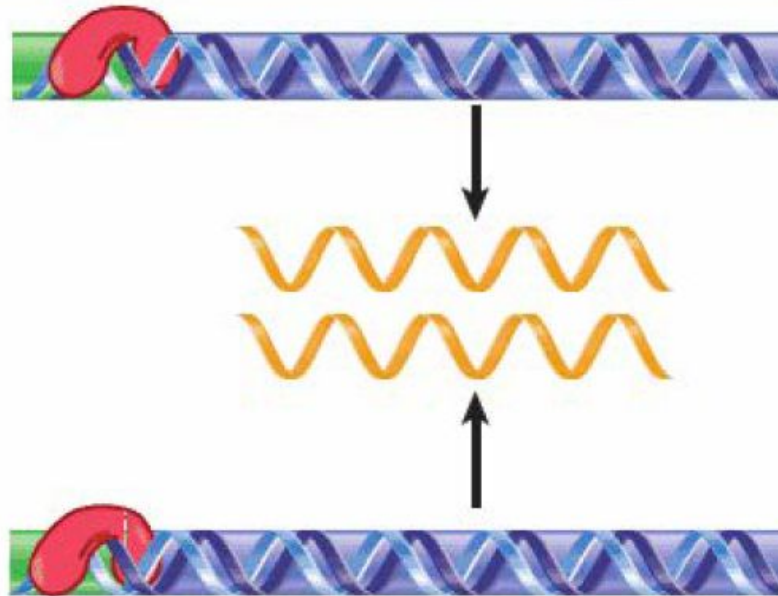


FIGURE 2.17 Control sites in DNA provide binding sites for proteins; coding regions are expressed via the synthesis of RNA.

Both alleles synthesize RNA in wild type



Control site mutation affects only contiguous DNA

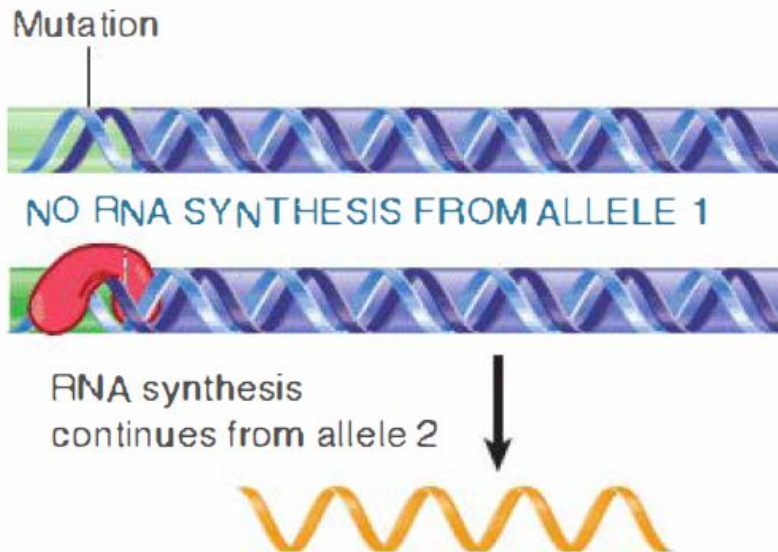


FIGURE 2.18 A *cis*-acting site controls expression of the adjacent DNA but does not influence the homologous allele.

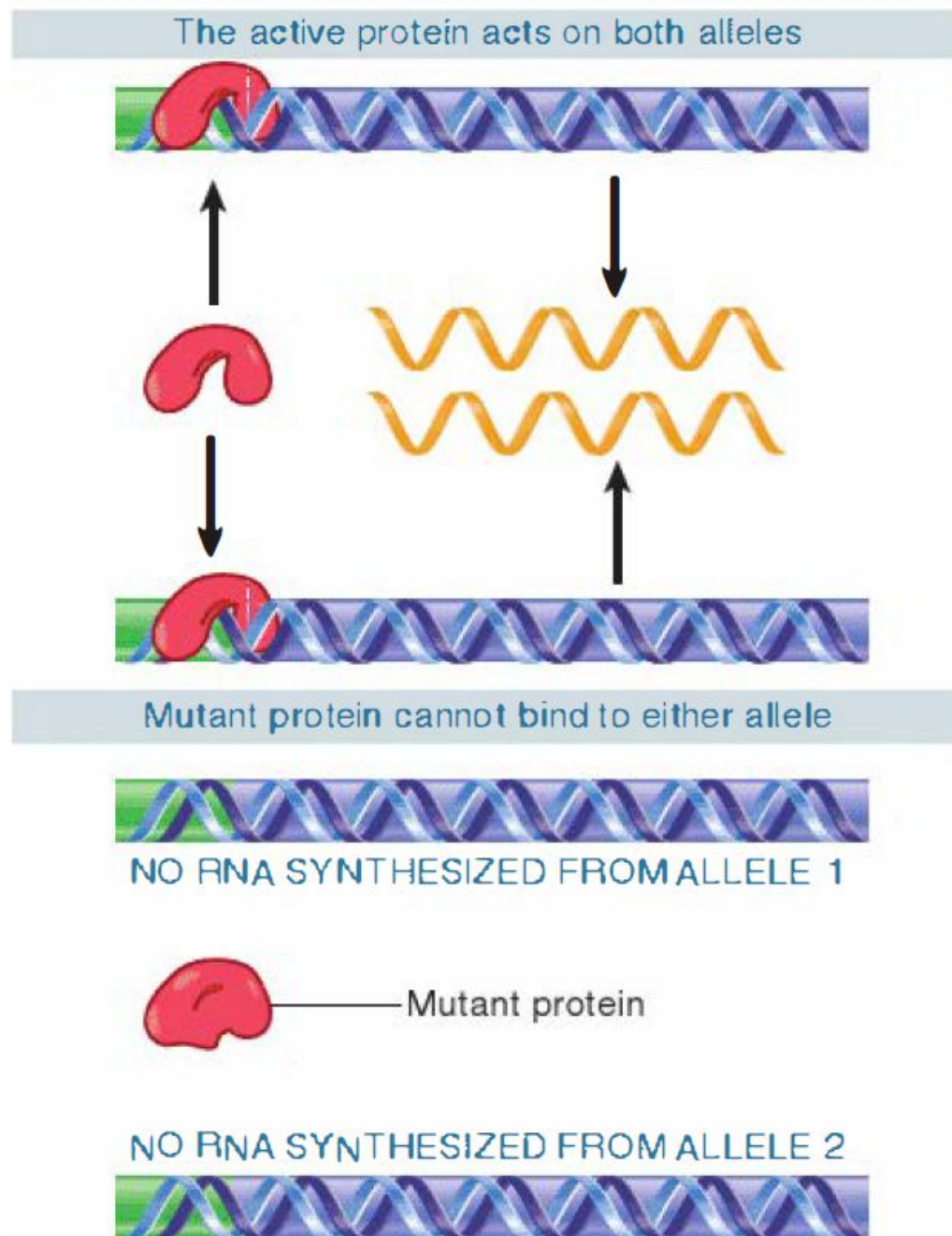


FIGURE 2.19 A *trans*-acting mutation in a gene for a regulatory protein affects both alleles of a gene that it controls.

GENOME ORGANIZATION

Definitions:

- **Genome** → in biology the **genome** of an organism is its whole hereditary information and is encoded in the DNA (or, for some viruses, RNA). This includes both the genes and the non-coding sequences of the DNA.
- **Transcriptome** → is the set of all messenger RNA (mRNA) molecules, or "transcripts," produced in one or a population of cells. The term can be applied to the total set of transcripts in a given organism, or to the specific subset of transcripts present in a particular cell type.
- **Proteome** → is the entire complement of proteins expressed by a genome, cell, tissue or organism. More specifically, it is the expressed proteins at a given time point under defined conditions.

Characteristics of prokaryotic genome

- Smaller dimensions
- Collinearity between DNA and gene product
- Operons → polycistronic mRNA

Characteristics of eukaryotic genome

- monocistronic mRNA
- Interrupted genes (introns)
- Presence of repeated sequences and non-coding DNA (non-functional DNA)

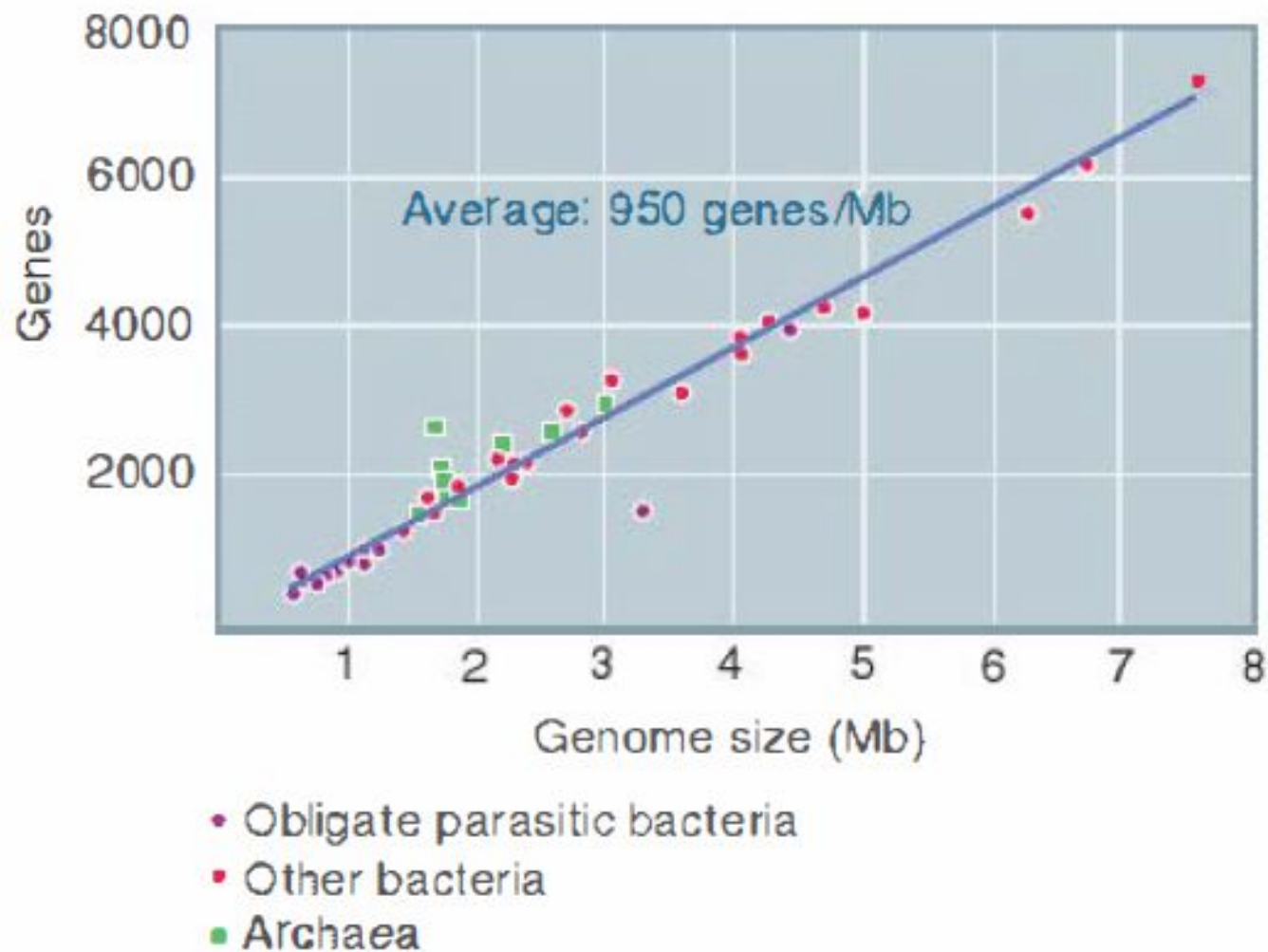


FIGURE 6.3 The number of genes in bacterial and archaeal genomes is proportional to genome size.

Phylum	Species	Genome (bp)
Algae	<i>Pyrenomas salina</i>	6.6×10^5
Mycoplasma	<i>M. pneumoniae</i>	1.0×10^6
Bacterium	<i>E. coli</i>	4.2×10^6
Yeast	<i>S. cerevisiae</i>	1.3×10^7
Slime mold	<i>D. discoideum</i>	5.4×10^7
Nematode	<i>C. elegans</i>	8.0×10^7
Insect	<i>D. melanogaster</i>	1.8×10^8
Bird	<i>G. domesticus</i>	1.2×10^9
Amphibian	<i>X. laevis</i>	3.1×10^9
Mammal	<i>H. sapiens</i>	3.3×10^9

FIGURE 8.15 The genome sizes of some commonly studied organisms.

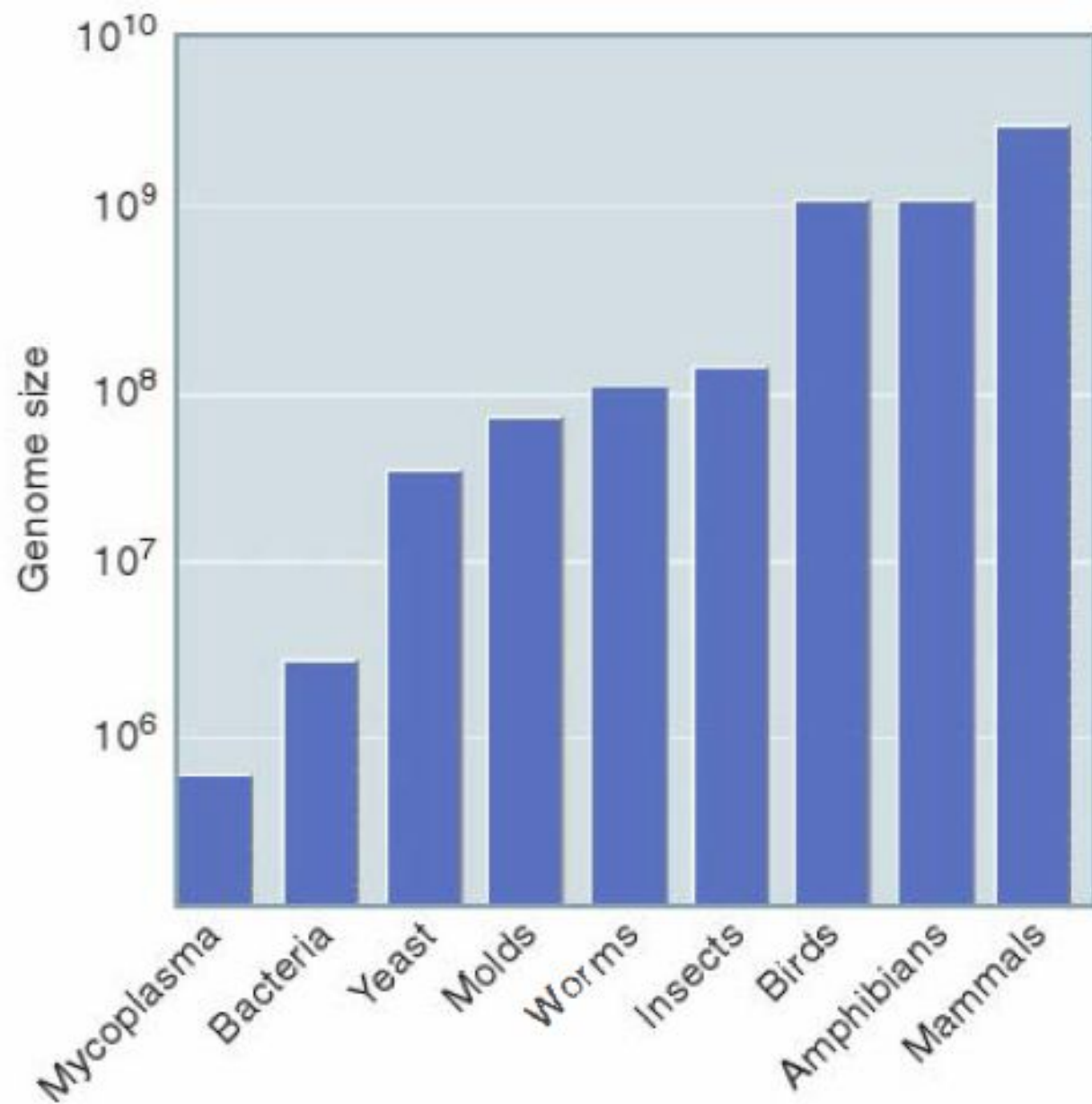


FIGURE 8.14 The minimum genome size found in each taxonomic group increases from prokaryotes to mammals.

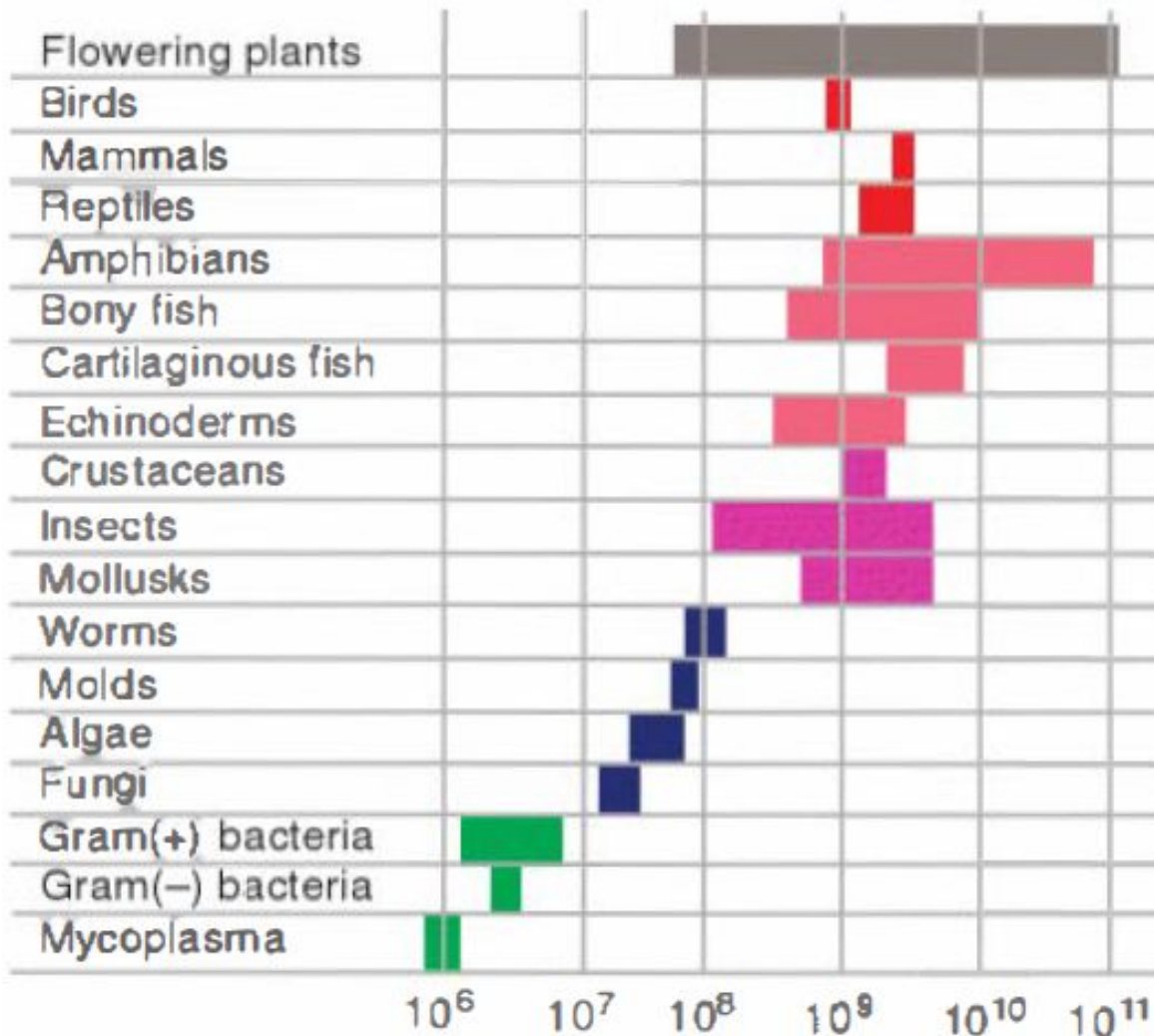
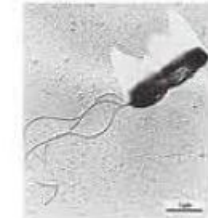


FIGURE 8.13 DNA content of the haploid genome increases with morphological complexity of lower eukaryotes, but varies extensively within some groups of animals and plants. The range of DNA values within each group is indicated by the shaded area.

500 genes
Intracellular (parasitic)
bacterium



1500 genes
Free-living bacterium



5000 genes
Unicellular eukaryote



13,000 genes
Multicellular eukaryote



25,000 genes
Higher plants

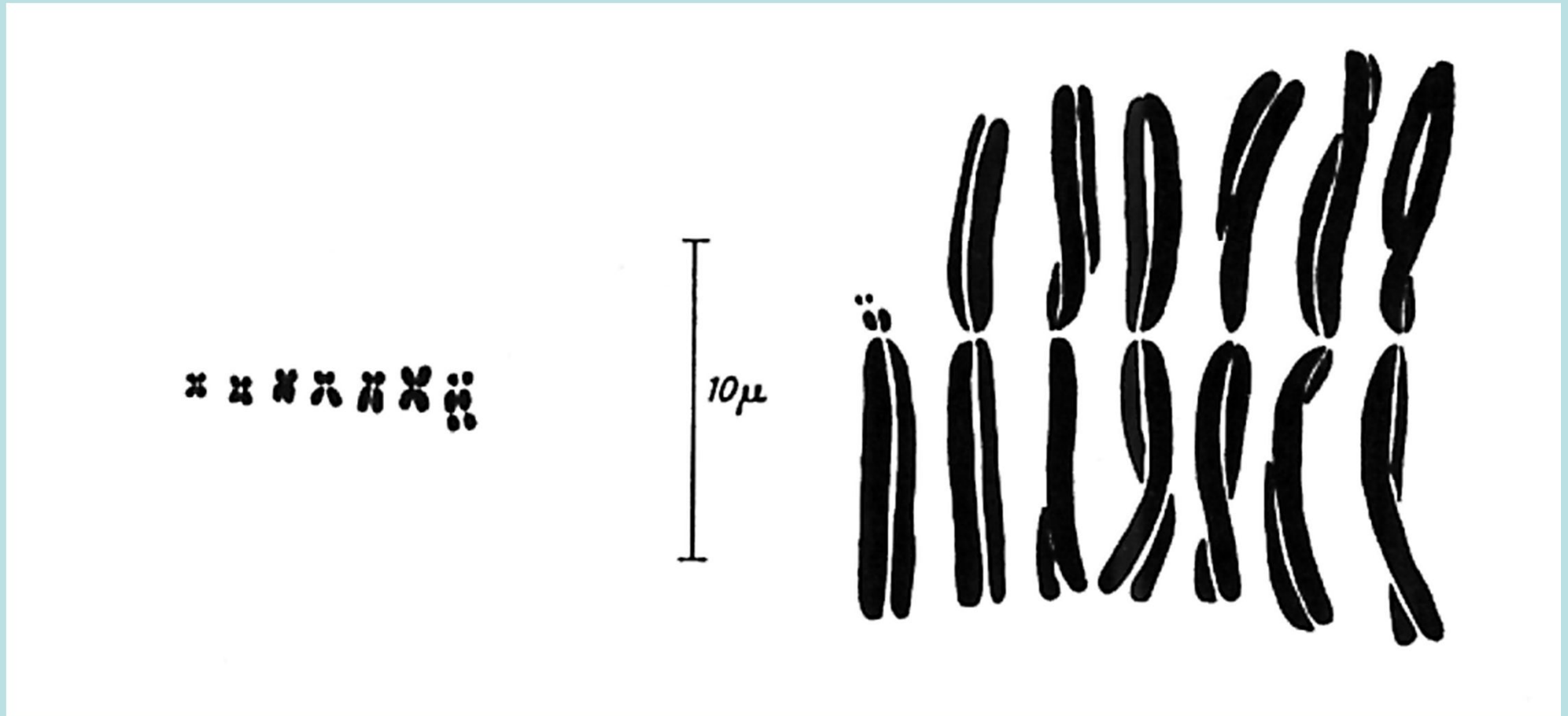


25,000 genes
Mammals



FIGURE 6.1 The minimum gene number required for any type of organism increases with its complexity.

Karyotype of two different species of Ranunculaceae



C Value → total amount of DNA in an haploid cell

C Value Paradox

- Excess of DNA if compared to organism complexity
- Variation of C value between organisms with similar complexity

Single sequences and repeated sequences in the eukaryotic genome

Single
(1-10 times)
50-70%

Most of genes

in tandem

Redundant genes
(rRNA, 5S RNA, tRNA, Histones, etc.)

Moderately repeated
(from hundred to
thousand times)
10-30%

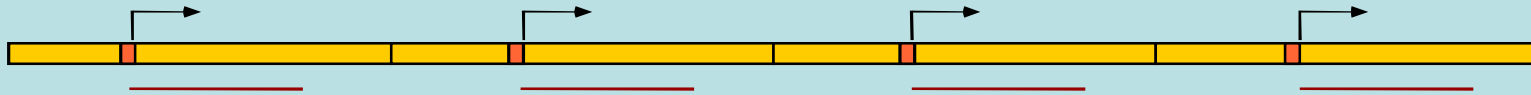
interspersed

Some regulative sequences
Mobile elements
Some sequences with special functions
(centromeres, origins, etc.)

Highly repeated
(from ten thousand
To million times)
5-25%

Satellite DNA
Simple sequences

GENOME REPEATED SEQUENCES



Genes for: rRNA (300)
tRNA (1300)
5S RNA (2000)
Histones(20)



- Interspersed repeated sequences
- Alu sequence family: 300 bp (> di 300.000 members) → ca 1.000.000 of total repeats
- DNA mobile elements



Simple sequences and satellites: 2-10 bp (x 2-100 tandem repeats x 1-100 interspersed blocks)

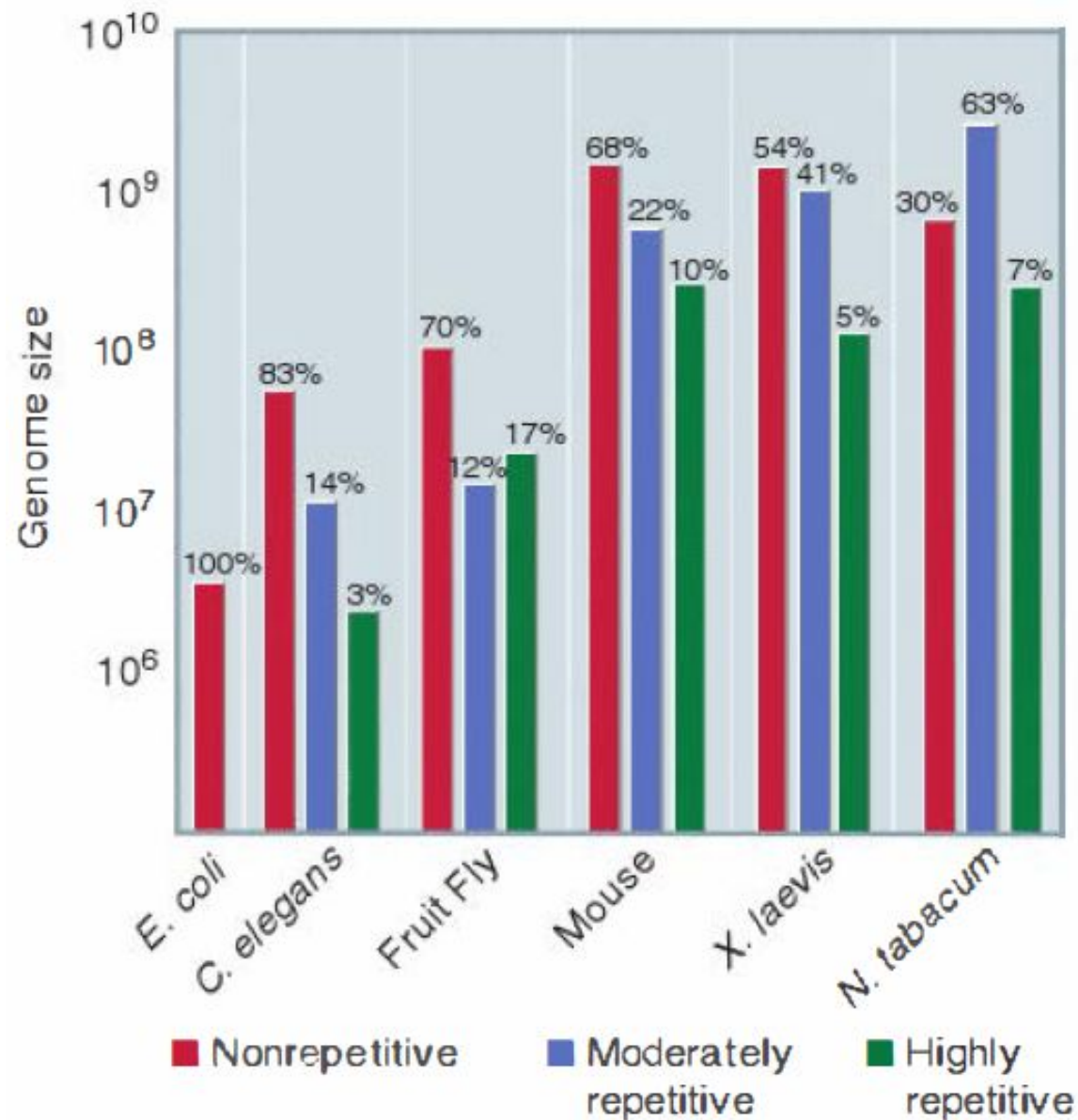
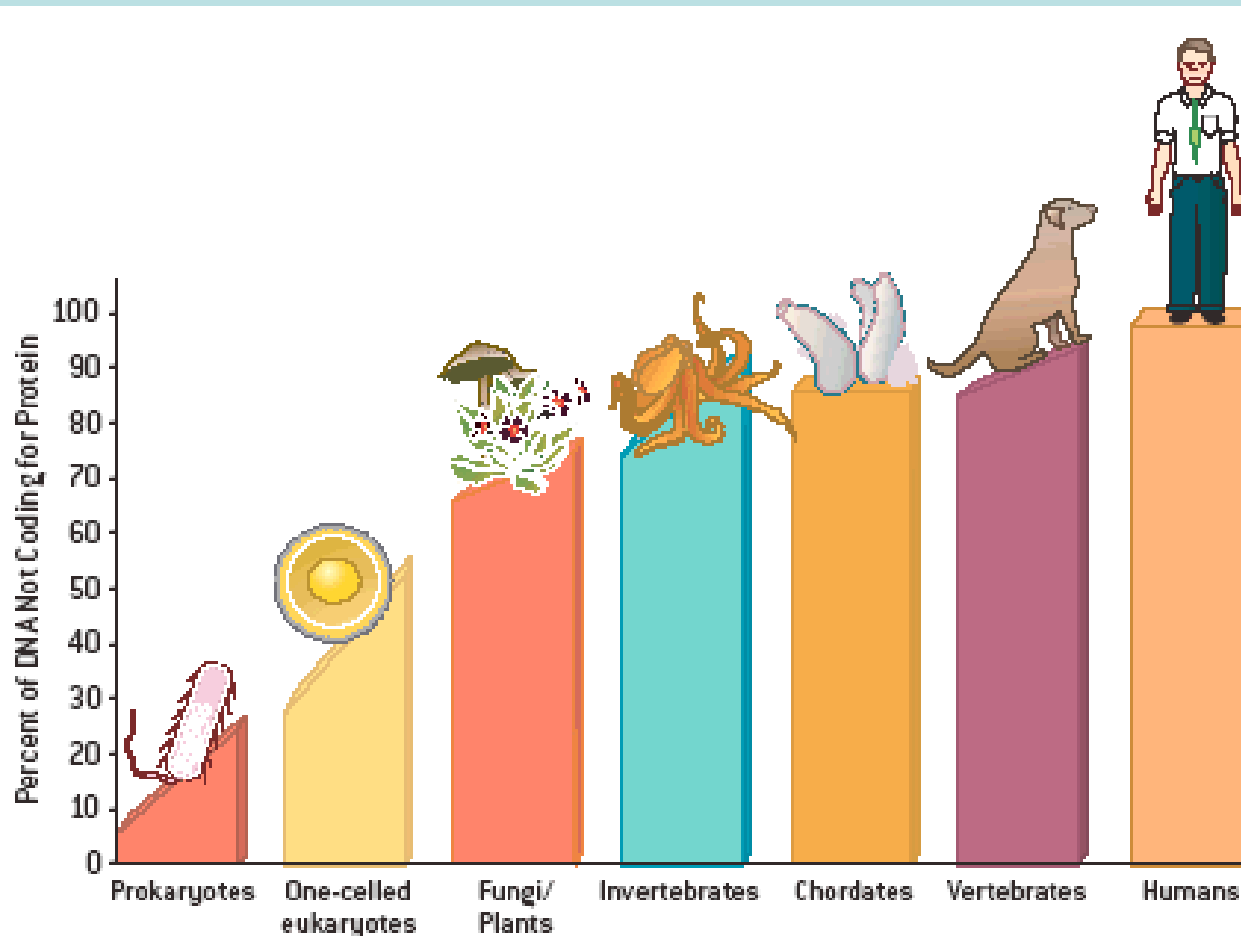


FIGURE 5.5 The proportions of different sequence components vary in eukaryotic genomes. The absolute content of nonrepetitive DNA increases with genome size but reaches a plateau at $\sim 2 \times 10^9$ bp.

- Relative proportions among DNA components vary in different eukaryotic genomes.
- The absolute non-repetitive DNA content increases with genome dimension, but reaches a plateau at about 2×10^9 bp.

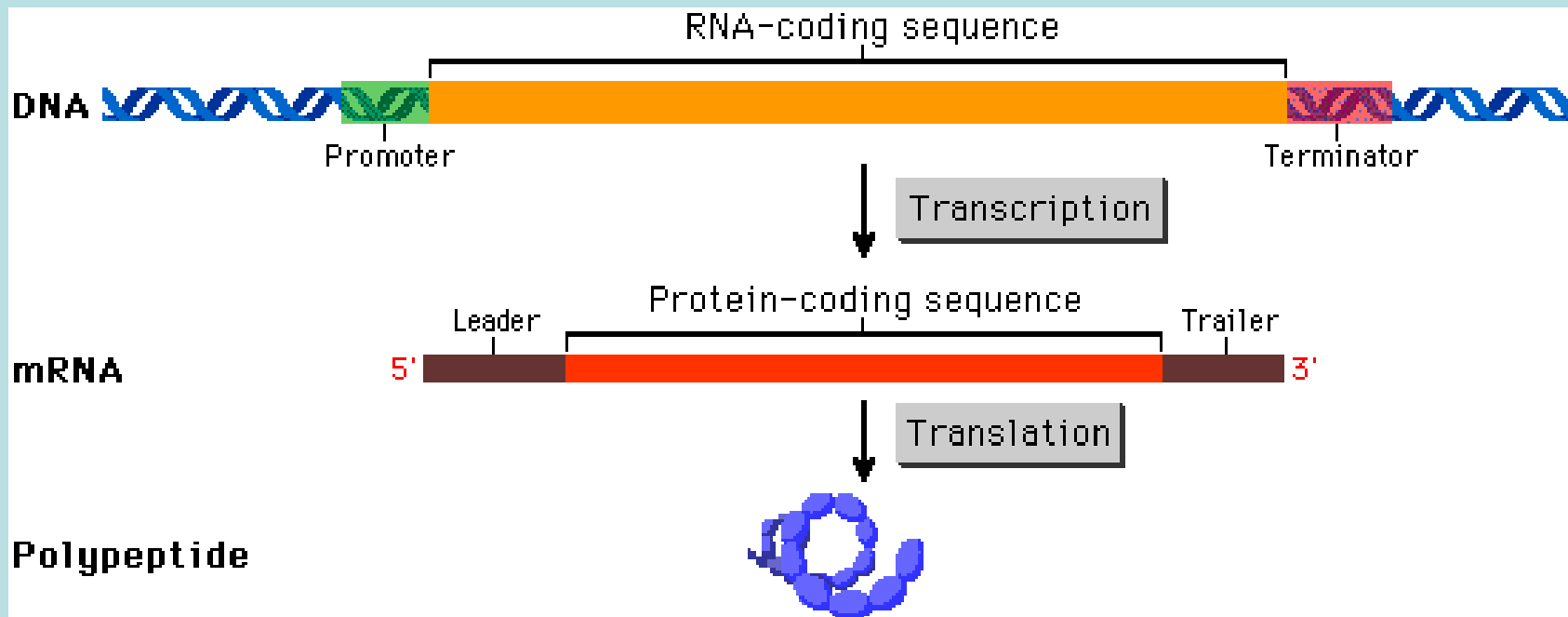
Non-repetitive DNA percentage drops with the increasing of genome size



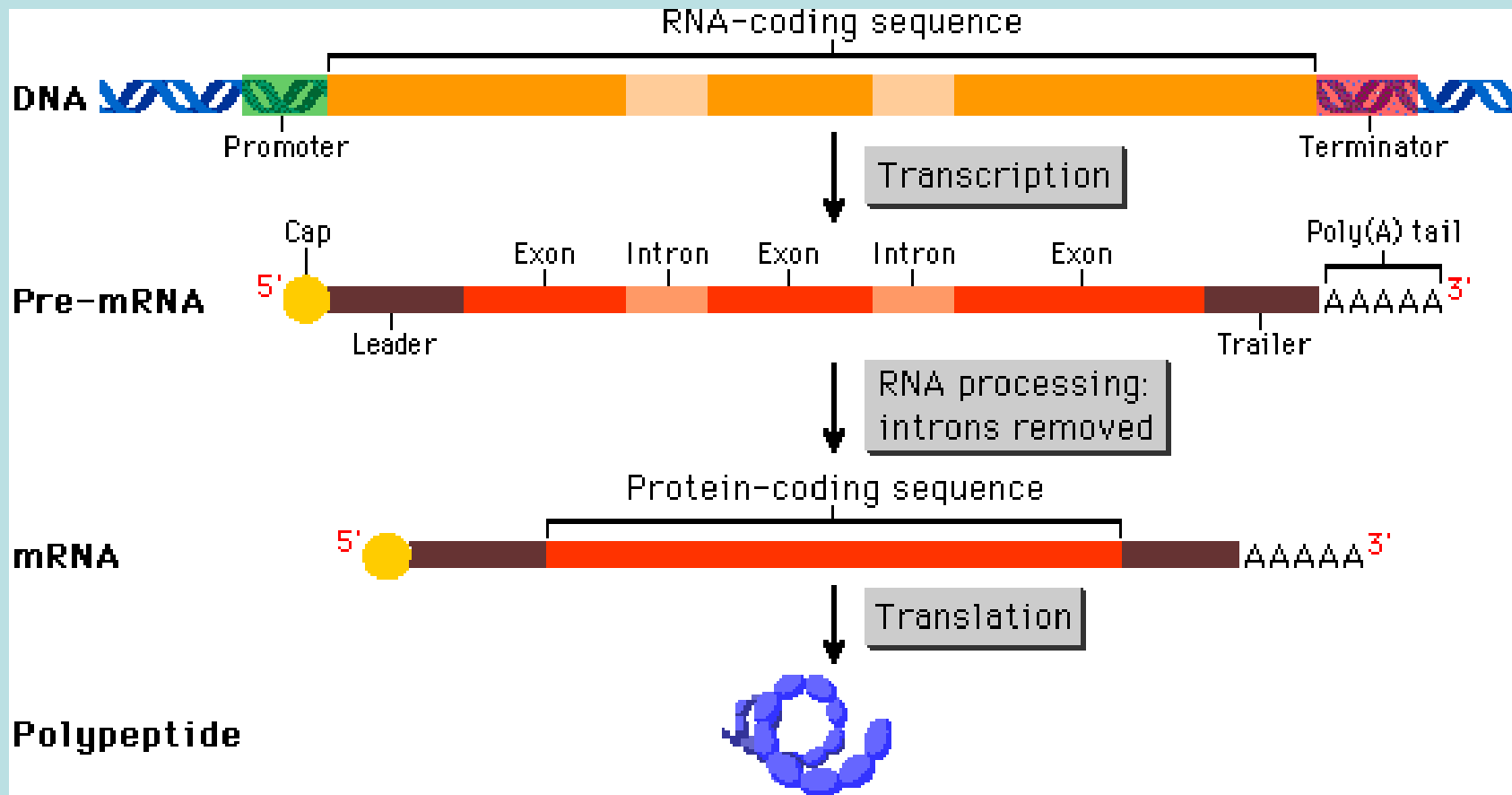
NONPROTEIN-CODING SEQUENCES make up only a small fraction of the DNA of prokaryotes. Among eukaryotes, as their complexity increases, generally so, too, does the proportion of their DNA that does not code for protein. The noncoding sequences have been considered junk, but perhaps it actually helps to explain organisms' complexity.

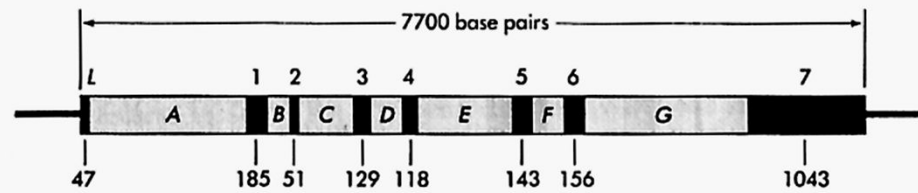
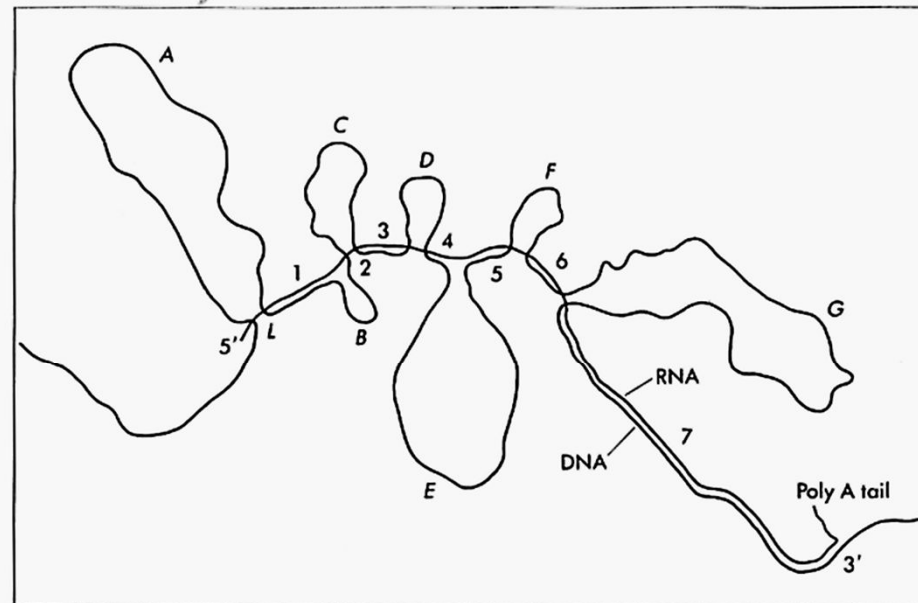
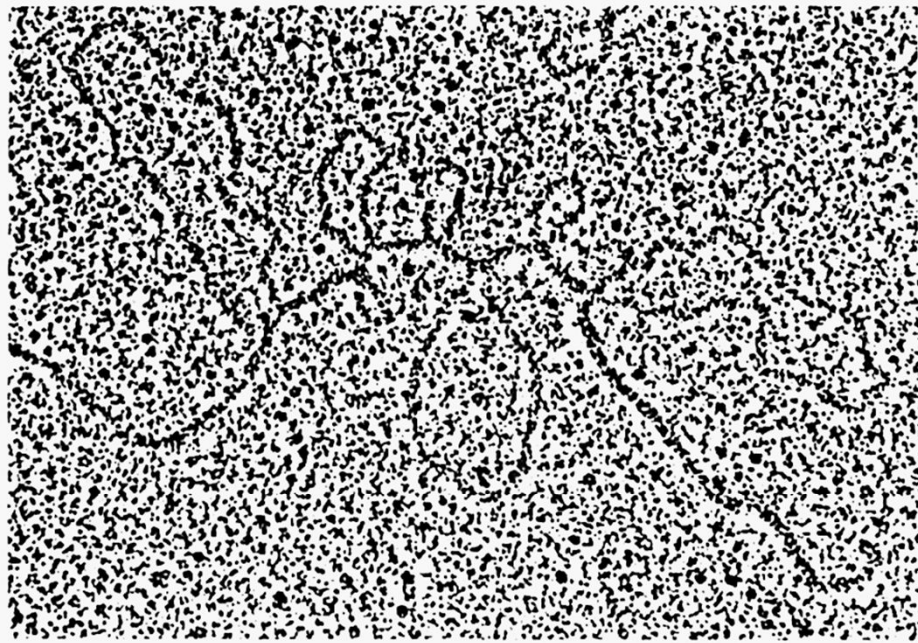
Interrupted genes

Prokaryotes: collinearity between genes and mRNAs

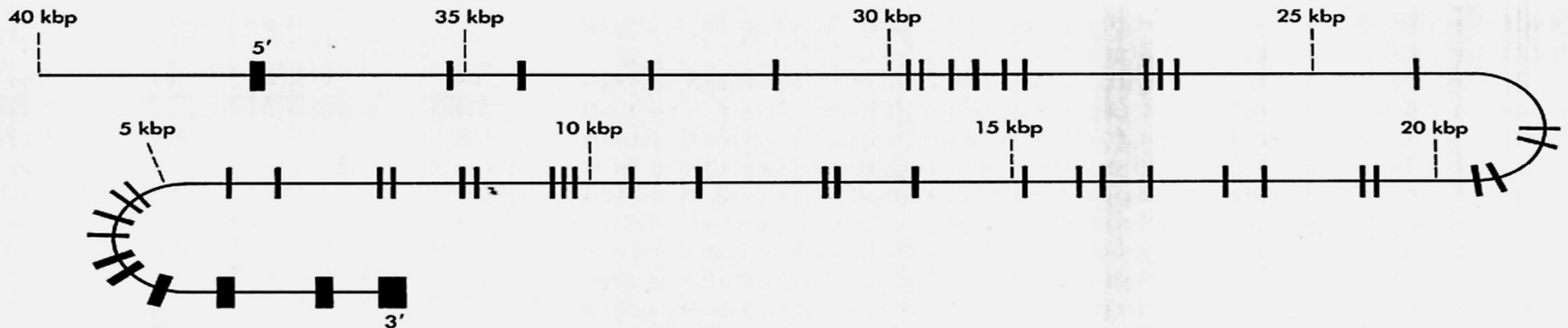
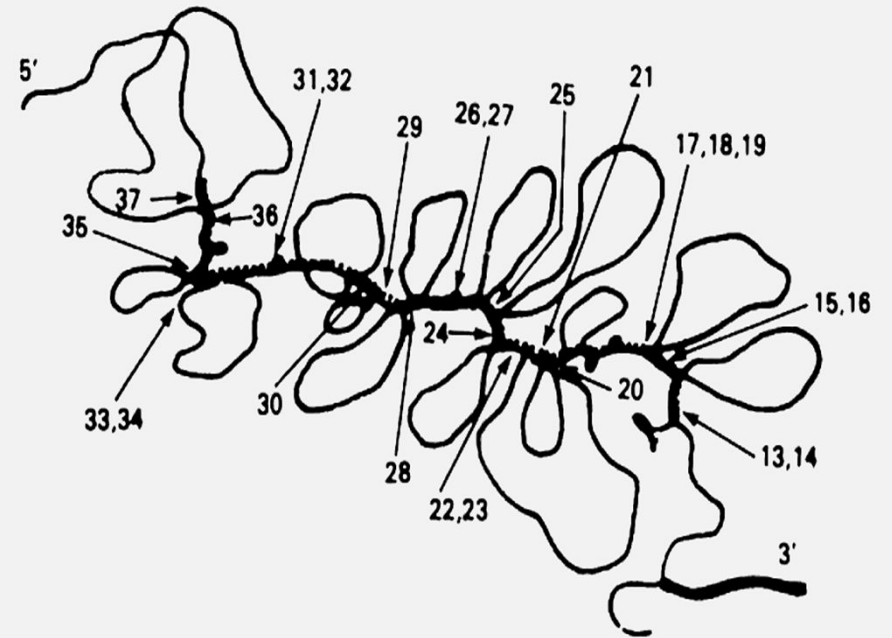
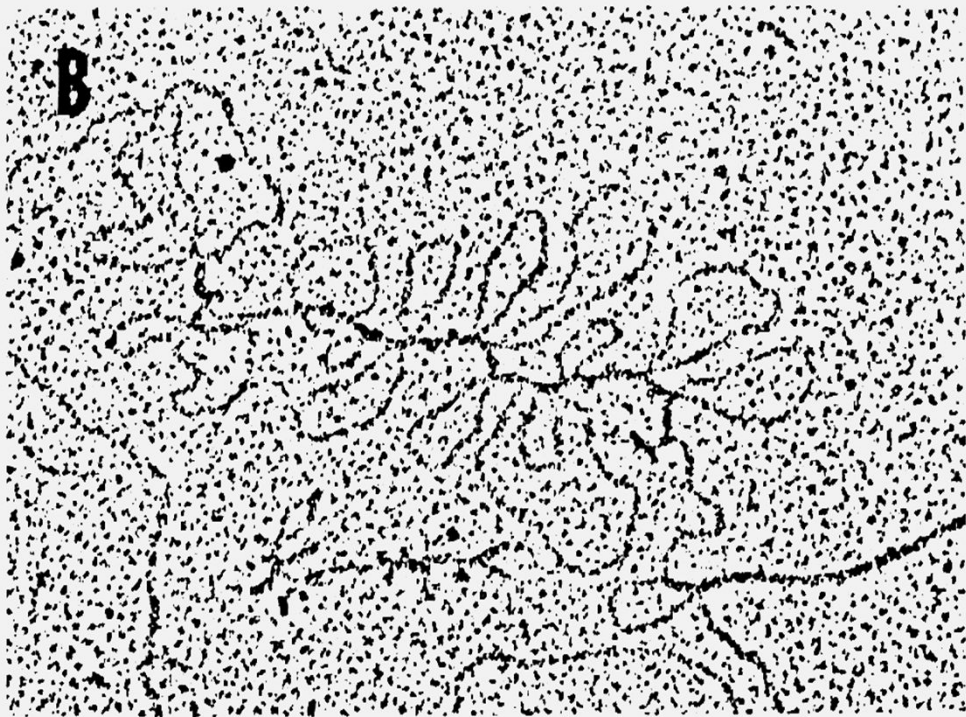


Eukaryotes: non-collinearity between genes and mRNAs





Chicken collagen 1 α 2 gene



- **Exons:** sequences found in mature RNA
- **Introns:** sequences removed from primary transcript (pre-mRNA)