

## CHAPTER 17- FROM GENE TO PROTEIN

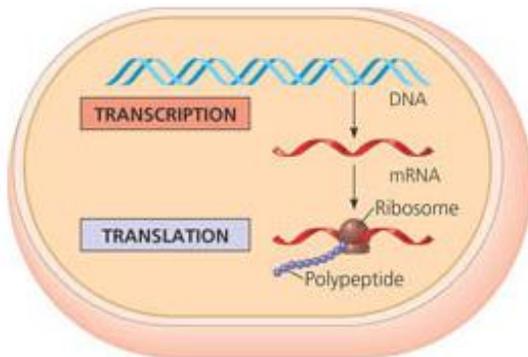
### Central Dogma of Molecular Biology

(Flow of information in cells)

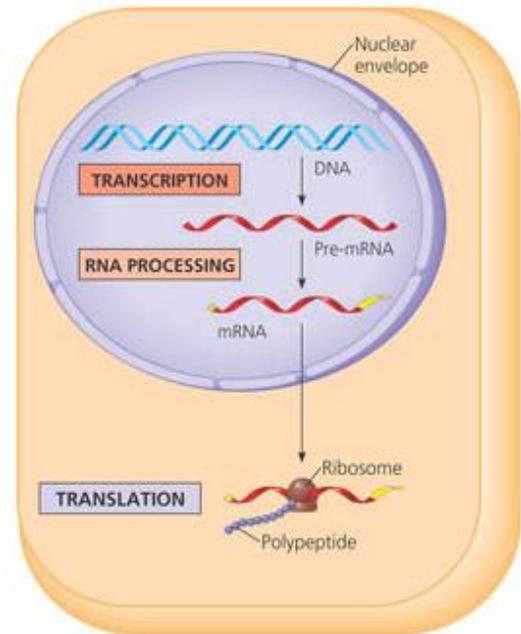
DNA → RNA → PROTEINS

DNA → DNA = REPLICATION  
 DNA → RNA = TRANSCRIPTION  
 RNA → PROTEINS = TRANSLATION

- **GENE** = sequence of DNA with a specific function (final product = polypeptide OR RNA)
- RNA's = intermediates between DNA code and proteins that determine phenotype
- For each gene only one of the two strands is transcribed into an RNA (template strand)
- For some genes one strand may be used; for other genes the complementary strand is used



(a) Prokaryotic cell. In a cell lacking a nucleus, mRNA produced by transcription is immediately translated without additional processing.



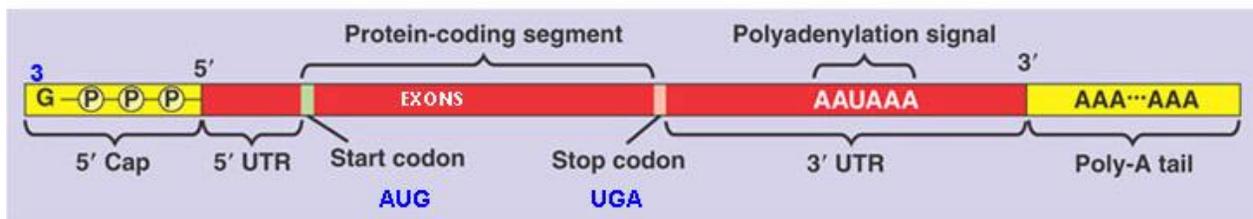
(b) Eukaryotic cell. The nucleus provides a separate compartment for transcription. The original RNA transcript, called pre-mRNA, is processed in various ways before leaving the nucleus as mRNA.

### 3 KINDS OF RNA

- Messenger RNA (mRNA)
- Transfer RNA (tRNA)
- Ribosomal RNA (rRNA)

### MESSENGER RNA

- carries DNA message from nucleus to cytoplasm; mMessage is read in "triplets" called **CODONS**
- 64 different codons code for 20 different amino acids; AUG = START codon; UAA, UAG, UGA are STOP codons;
- **REDUNDANCY OR "WOBBLE"** - codons for same amino acid can differ in 3<sup>rd</sup> base
- Code = universal to all life (found in all organisms) = evidence for common ancestry
- Prokaryotes~ m-RNA functional as soon as transcribed
- Eukaryotes~ m-RNA must be processed before use
  - **GTP "cap"** = METHYLATED GUANINE added to 5' end; for stability; prevents degradation used to bind mRNA to ribosome
  - **PolyA "tail"** added to 3' end (AAA)- stability; helps passage through nuclear membrane



In **EUKARYOTES** mRNA is made as **pre-mRNA** containing:

- **INTRONS**- noncoding DNA segments  
may provide cross over places without interrupting code  
may facilitate evolution of new proteins by *exon shuffling*
- **EXONS** - coding DNA segments; code for different **DOMAINS**  
=structural/functional regions

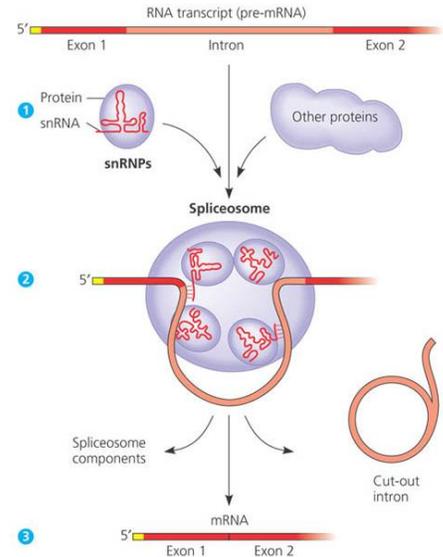
**snRNPs** (small nuclear ribonucleoproteins)

- Made of proteins and RNA
- Part of **SPLICEOSOME** (complex that edits pre-mRNA  
cuts out the introns and reattaches the remaining mRNA)

### ALTERNATIVE RNA SPLICING-

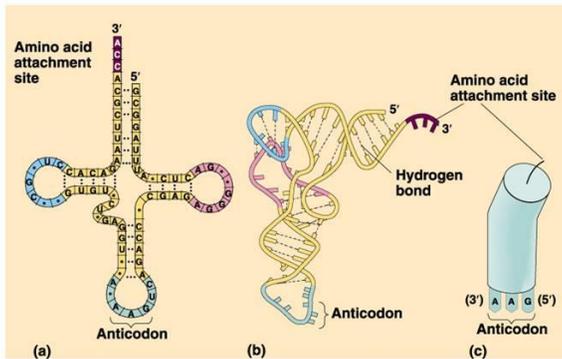
can produce different proteins by editing mRNA in different ways

EX: Immunoglobulins (antibodies) that match new antigens



**RIBOZYMES** = RNA molecules that function as enzymes

EX: Some preRNA's can self edit own introns;



### TRANSFER RNA (tRNA)

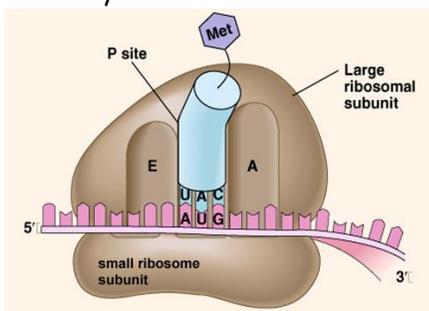
- cloverleaf-like secondary structure folds into L shape
- brings amino acids to ribosome
- attaches amino acids in proper place
- **ANTICODON** region matches codon on mRNA

**AMINOACYL-tRNA SYNTHETASE** enzyme

attaches a specific amino acid using energy from ATP

### RIBOSOMES (=RIBOZYMES RNA that functions as an enzyme)

- Made up of **rRNA** (2/3) and **PROTEINS** (1/3) ;
- rRNA **made in NUCLEOLUS** in eukaryotes and assembled with proteins imported from cytoplasm
- **Large and small subunits** join to form functional ribosome only when attach to mRNA;
- Ribosomes not making proteins exist as separate subunits
- Ribosomes making proteins for membranes/export: proteins are "tagged" so can be attached to rough ER;
- Cytoplasmic proteins made on "free" ribosomes
- Prokaryotic and eukaryotic subunits are different sizes = evidence for Endosymbiotic theory  
(**PROKARYOTIC RIBOSOMES**: 30S + 50S = 70S; **EUKARYOTIC RIBOSOMES**: 40S + 60S = 80S)
- Subunit size is medically significant  
~ Certain antibiotics work by inhibiting prokaryotic ribosomes without affecting ribosomes of the eukaryotic host cell



**RIBOSOME BINDS mRNA**

Has 3 tRNA **BINDING SITES**:

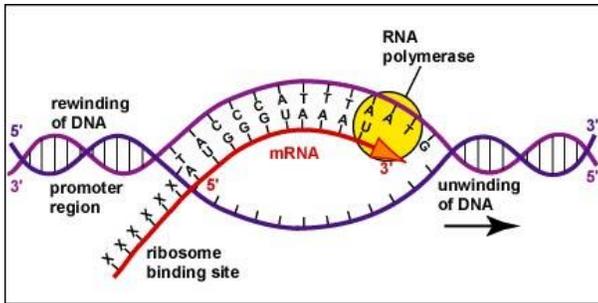
**A (AMINOACYL-tRNA site)**- tRNA with new amino acid attaches

**P (PEPTIDYL-tRNA site)** - peptide bond forms

holds tRNA carrying growing polypeptide chain;

**E (EXIT site)** - empty tRNA exits

## TRANSCRIPTION = DNA → RNA (Occurs in the NUCLEUS)



### 1. INITIATION

- **RNA POLYMERASE** binds to DNA at region called **PROMOTER**
  - LIKE **DNA POLYMERASE**: can only attach nucleotides in 5' → 3' direction;
  - UNLIKE **DNA POLYMERASE**: can start a chain from scratch; no primer needed
- In eukaryotes: **TRANSCRIPTION FACTORS & TATA BOXES** help position/bind to correct spot
- **RNA POLYMERASE** separates the DNA strands to begin transcription

### 2. ELONGATION

- RNA chain **grows in the 5' → 3' direction** nucleotides base pair with template strand; nucleotides **added to the 3' end of preceding nucleotide** (60 nucleotides/sec)
- the non-coding strand of DNA reforms a DNA double helix by pairing with the coding strand

### 3. TERMINATION

- transcription proceeds until RNA polymerases reaches a **TERMINATOR** site on the DNA;
- RNA molecule is then released
- Segment of DNA transcribed into one RNA = **TRANSCRIPTION UNIT**

\* \* \* \* \*

## TRANSLATION = RNA → PROTEINS (Occurs on RIBOSOMES in CYTOPLASM)

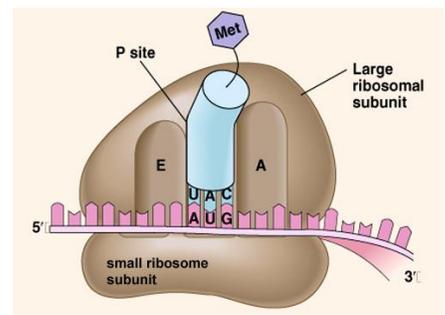
Specific **AMINO ACYL tRNA SYNTHETASES** added amino acids to correct tRNA's

### 1. INITIATION

- **Small ribosomal subunit** attaches to the **5' end** of the mRNA ('start' codon - **AUG**)
- **energy comes from GTP** (guanosine triphosphate)
- tRNA carries **1<sup>st</sup> amino acid (METHIONINE)** to the mRNA
- **large ribosomal subunit** attaches to the mRNA

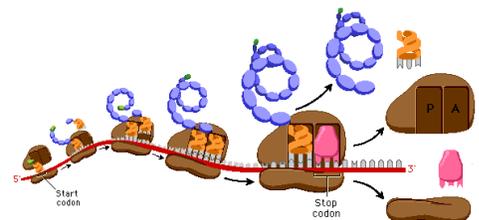
### 2. ELONGATION

- Ribosome moves along mRNA matching **tRNA ANTICODONS** with **mRNA CODONS**
- tRNA with new amino acid **attaches at A site**
- tRNA at A site moves to P site and receives growing chain
- tRNA at P site moves to E site and exits
- Released tRNA can recycle and bring in a new amino acid
- a new tRNA enters the A site and repeats the process increasing the polypeptide chain length



### 3. TERMINATION

- occurs when the ribosome encounters a 'stop' codon
- ribosome subunits detach; polypeptide is released
- mRNA can be reread multiple time
- **POLYSOMES**- = strings of ribosomes can work on same mRNA at same time



## SIGNAL-RECOGNITION PARTICLE (SRP)

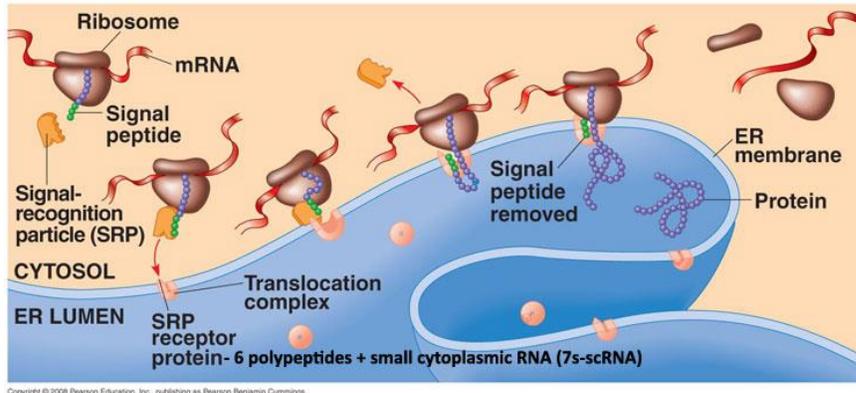
Protein synthesis begins on free ribosomes

Polypeptides that will become **MEMBRANE PROTEINS** or be **SECRETED** are marked

**SRP (SIGNAL RECOGNITION PARTICLE)** attaches to protein signal sequence and receptor on ER

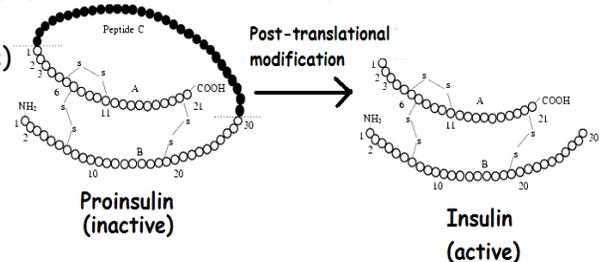
Growing protein chain is inserted into ER lumen

Complex disconnects



**POST TRANSLATIONAL MODIFICATION** - Changes to polypeptide chain to make it a protein

- **CHAPERONINS**-help wrap into 3D shape
- Some have groups added (sugars, lipids, phosphates, etc)  
EX: glycoproteins (protein + sugar)
- Some have segments removed  
EX: insulin made as one chain  
middle removed to become active



## MUTATIONS

• Not all harmful- can **PROVIDE GENETIC VARIABILITY**

~Foundation for **NATURAL SELECTION**

Can be:

- Spontaneous (errors in replication, repair, recombination)
- Caused by **MUTAGENS**  
EX: radiation, chemicals, cigarette smoke, etc  
= **CARCINOGENS** (can cause cancer)

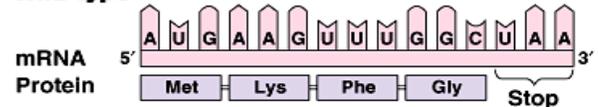
**HARMFUL MUTATIONS**- change protein function

- **POINT** mutation: change in one base pair of a gene  
Substitution- replace one base with another
- **SILENT**- change codes for same amino acid  
(due to redundancy)
- **MISSENSE**-codes for another amino acid  
Changes protein sequence and usually function  
Ex: sickle cell disease- T → A in hemoglobin
- **NONSENSE**-code changes to **STOP** codon  
makes **NONFUNCTIONAL** protein

## FRAMESHIFT

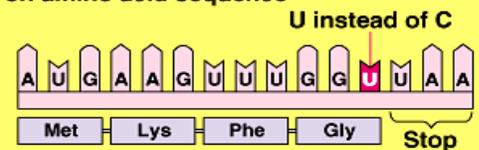
- All nucleotides downstream are grouped incorrectly;
- **INSERTION/DELETION**-causes **FRAMESHIFT**  
if not a multiple of 3
- Causes more damage at beginning of gene than at end  
EX: O blood type allele is deletion in A blood type code

**Wild type**

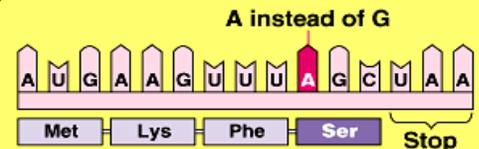


**Base-pair substitution**

**No effect on amino acid sequence**



**Missense**



**Nonsense**

**U instead of A**

