- 1. Explain the contribution that Beadle and Tatum made to understanding the role of DNA.
- 2. Compare and contrast DNA to RNA.
- 3. What is the difference between replication, transcription and translation?

### Ch. 14 Warm-Up

- 1. What are similarities between DNA and RNA?
- 2. What are differences between DNA and RNA?
- 3. What is a ribozyme?
- 4. How many different codons (3-letter RNA nucleotide combinations) are possible?
- 5. If there are all of the possibilities (in #4) , how come there are only 20 amino acids?

#### Ch. 14 Warm-Up

1. Describe the steps in transcription.

- 2. Contrast transcription in prokaryotes vs. eukaryotes.
- 3. What is the minimum # of nucleotides needed in an mRNA molecule to code for a protein with 200 amino acids?

1. How does mRNA differ from pre-mRNA?

- 2. What is the difference between introns and exons?
- 3. Describe how spliceosomes modify mRNA.
- An original hypothesis was One Gene = One Protein.
  But how is it possible to have 22,000 genes but over 100,000+ different proteins??

1. Describe the steps of translation.

- 1. If the DNA sequence is: 3' TACGATCAG 5'
  - the cDNA would be:
  - the mRNA is:
  - the tRNA is:
  - the amino acid sequence is:
- 2. How does the cell determine the ultimate destination of a polypeptide being synthesized?

- 1. What are some examples of point mutations?
- 2. Contrast a missense vs. nonsense mutation.



- 3. What is a frameshift mutation? How can it impact protein synthesis?
- 4. What kind of cell is shown below? Provide3 pieces of evidence to support your claim.

Refer to page 296. Fill in the chart comparing prokaryotic and eukaryotic gene expression:

Prokaryotes	Eukaryotes



# Gene Expression: From Gene to Protein

Chapter 14

#### **CONCEPT 14.1:** GENES SPECIFY PROTEINS VIA TRANSCRIPTION AND TRANSLATION

# Gene Expression: process by which DNA directs the synthesis of proteins (or RNAS)

Old idea: one gene-one enzyme hypothesis

- Proposed by Beadle & Tatum mutant mold experiments
- Function of a gene = dictate production of specific enzyme
- Newer idea: one gene-one polypeptide hypothesis
- Most accurate: one gene-one RNA molecule (which may or may not be translated into a polypeptide)



- Central Dogma: DNA → RNA → protein
  Transcription: DNA → RNA
  Translation: RNA → protein
- Ribosome = site of translation

Flow of Genetic Information in Prokaryotes vs. Eukaryotes





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(b) Eukaryotic cell

#### One gene = One RNA molecule

#### DNA

- Nucleic acid composed of nucleotides
- Double-stranded
- Deoxyribose=sugar
- Thymine
- Template for individual

 Nucleic acid composed of nucleotides

RNA

- Single-stranded
- Ribose=sugar
- Uracil
- Many different roles!





## RNA plays many roles in the cell

- 1. pre-mRNA=precursor to mRNA, newly transcribed and not edited
- 2. mRNA= edited version; carries the code from DNA that specifies amino acids
- tRNA= carries a specific amino acid to ribosome based on its anticodon to mRNA codon
- 4. **rRNA**= makes up 60% of the ribosome; site of protein synthesis
- 5. snRNA=small nuclear RNA; part of a spliceosome; structural and catalytic roles
- 6. **srpRNA**= signal recognition particle that binds to signal peptides
- 7. **RNAi**= interference RNA; a regulatory molecule
- 8. miRNA/siRNA= micro/small interfering RNA; binds to mRNA or DNA to block it, regulate gene expression, or cut it up
- **9. ribozyme**= RNA that functions as an enzyme

The Genetic Code

- For each gene, one DNA strand  $(3' \rightarrow 5')$  is the **template strand** (aka: noncoding, minus or antisense strand)
- mRNA  $(5' \rightarrow 3')$ complementary to template
- mRNA triplets
  (codons) code for amino acids in polypeptide chain



DNA

molecule

Gene

Gene 2

The Genetic Code

- 64 different codon combinations
- **Redundancy**: 1+ codons code for each of 20 AAs
- Reading frame: groups of 3 must be read in correct groupings
- This code is universal: all life forms use the same code.

Second mRNA base											
		U	U		С		Α		G		
(5' end of codon)	U	ບບບ-	Phe	່ມດກ_		UAU <sup>-</sup>	Tyr	ี่ บดบ -		U	
		ບບເ		UCC	Ser	UAC		UGC	Cys	С	
		UUA <sup>-</sup>	Leu	UCA		UAA	Stop	UGA	Stop	A	
		UUG_		UCG _		UAG	Stop	UGG	Trp	G	
	с	CUU	Leu	ccu -	Pro	CAU	His	CGU	Arg	U	nopo
		CUC		ccc		CAC		CGC		С	of co
		CUA		CCA		CAA	GIn	CGA		A	pu
		CUG_				CAG		CGG _		G	(3,
First mRNA base	A	AUU	lle			AAU	Asn	AGU	Ser	U	ase
		AUC		ACC	The			AGC		С	d A b
		AUA _		ACA	Inr		Lys		Arg	A	n BN
		AUG 🖁	Met or start	ACG _	ļ			AGG _		G	hird 1
	G	GUU		GCU	Ala	GAU	Asp	GGU	Gly	U	È
		GUC		GCC		GAC		GGC		С	
		GUA	vai	GCA		GAA	Glu	GGA		Α	
		GUG_		GCG_		GAG _		GGG_		G	
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#### CONCEPT 14.2: TRANSCRIPTION IS THE DNA-DIRECTED SYNTHESIS OF RNA



### Transcription

Transcription unit: stretch of DNA that codes for a polypeptide or RNA (eg. tRNA, rRNA)

#### <u>RNA polymerase</u>:

- Separates DNA strands and transcribes mRNA
- mRNA elongates in 5'  $\rightarrow$  3' direction
- Uracil (U) replaces thymine (T) when pairing to adenine (A)
- Attaches to <u>promoter</u> (start of gene) and stops at <u>terminator</u> (end of gene)



Source: G. Bradley Schaefer, James N. Thompson, Jr.: Medical Genetics: An Integrated Approach Copyright © McGraw-Hill Education. All rights reserved.

## 1. Initiation

# Bacteria: RNA polymerase binds directly to promoter in DNA



# 1. Initiation

<u>Eukaryotes:</u> **TATA box** = DNA sequence (TATAAAA) in promoter region

*upstream* from transcription start site

**Transcription factors** 

must recognize TATA box before RNA polymerase can bind to DNA promoter

Transcription Factors + RNA Polymerase =





## 2. Elongation



As RNA polymerase moves, it <u>untwists</u> DNA, then <u>rewinds</u> it after mRNA is made

3. Termination

RNA polymerase transcribes a **terminator** sequence (prok) or **polyadenylation signal** sequence (euk), then mRNA and polymerase detach.

It is now called **pre-mRNA** for <u>eukaryotes</u>.

<u>Prokaryotes</u> = mRNA ready for use



Flow of Genetic Information in Prokaryotes vs. Eukaryotes





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Concept 14.3: Eukaryotic cells modify RNA after transcription Additions to pre-mRNA:

#### <u>5' cap</u> (modified guanine) and 3' <u>poly-A tail</u> (50-250 A's) are added



#### **Functions:** I. Export from nucleus

D

2. Protect mRNA from enzyme degradation3. Attach mRNA to ribosomes in cytoplasm

RNA Splicing

Pre-mRNA



- Pre-mRNA has introns (noncoding sequences) and exons (codes for amino acids)
- Splicing = introns cut out, exons joined together

RNA Splicing



- small nuclear ribonucleoproteins = snRNPs
  - snRNP = snRNA + protein
  - Pronounced "snurps"
  - Recognize splice sites
- snRNPs join with other proteins to form a <u>spliceosome</u>

- Spliceosomes catalyze the process of removing introns and joining exons
- Ribozyme = RNA acts as enzyme (catalytic role)

## why have introns?

- Some regulate gene activity
- Alternative RNA Splicing: produce different combinations of exons
  - One gene can make more than one polypeptide!
  - > 20,000 genes  $\rightarrow$  100,000 polypeptides



Concept 14.4: Translation is the RNAdirected synthesis of a polypeptide

### Components of Translation

- I. <u>mRNA</u> = message
- 2. <u>tRNA</u> = interpreter
- 3. **<u>Ribosome</u>** = site of translation



# Summary of Translation



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### FRNA

- Transcribed in nucleus
- Specific to each amino acid
- Transfer AA to ribosomes
- Anticodon: pairs with complementary mRNA <u>codon</u>
- Base-pairing rules between 3<sup>rd</sup> base of codon & anticodon are not as strict. This is called wobble.





D

# Aminoacyl-tRNA-synthetase: enzyme that binds tRNA to specific amino acid



#### Ribosomes

- Ribosome = rRNA + proteins
- made in nucleolus
- 2 subunits



(a) Computer model of functioning ribosome

Ribosomes

#### Active sites:

- A site: holds AA to be added
- P site: holds growing polypeptide chain
- **E site: e**xit site for tRNA



### Translation: 1. Initiation



- Small subunit binds to start codon (AUG) on mRNA
- tRNA carrying Met attaches to P site
- Large subunit attaches



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2. Elongation



2. Elongation



## 3. Termination

- Stop codon reached and translation stops
- Release factor binds to stop codon; polypeptide is released
- Ribosomal subunits dissociate



# Protein Folding

- During synthesis, polypeptide chain coils and folds spontaneously
- Chaperonin: protein that helps polypeptide fold correctly



### Post-Translational Modifications

- > Attach sugars, lipids, phosphate groups, etc.
- Remove amino acids from ends
- Cut into several pieces
- Subunits come together



#### Insulin Production



## Types of Ribosomes

- Free ribosomes: synthesize proteins that stay in cytosol and function there
- Bound ribosomes (to ER): make proteins of endomembrane system (nuclear envelope, ER, Golgi, lysosomes, vacuoles, plasma membrane) & proteins for secretion
  - Uses signal peptide to target location

# Cellular "Zip Codes"

- <u>Signal peptide</u>: 20 AA at leading end of polypeptide determines destination
- Signal-recognition particle (SRP): brings ribosome to ER



### Polyribosomes

 A single mRNA can be translated by several ribosomes at the same time



#### Prokaryotes can transcribe + translate



Concept 14.5: Mutations of one or a few nucleotides can affect protein structure and function

#### The Central Dogma



Mutations = changes in the genetic material of a cell

- <u>Chromosomal</u>: large-scale; always causes disorders or death (eg. nondisjunction, translocation, inversions, duplications, large deletions)
- Point Mutations: change single nucleotide pair of a gene
  - I. **Substitution** replace I with another
    - Silent: same amino acid
    - Missense: different amino acid
    - Nonsense: stop codon, not amino acid
  - Frameshift (insertion/deletion) mRNA read incorrectly; nonfunctional proteins

# Mutagens: substances of forces that cause mutations in DNA



Substitution = Silent (no effect)

#### Wild type



Nucleotide-pair substitution: silent



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Substitution = Missense

#### Wild type



Nucleotide-pair substitution: missense



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Substitution = Nonsense (STOP)

#### Wild type



Nucleotide-pair substitution: nonsense



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#### Frameshift Mutation = Insertion/Deletion Wild type



Nucleotide-pair insertion: frameshift causing immediate nonsense



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Nucleotide-pair deletion: frameshift causing extensive missense



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3-Nucleotide-Pair Deletion/Insertion Wild type 3' 🚺 DNA template strand С G 5 С C 5' A G G 3 С G G mRNA 5' Protein Phe Glv Met LVS Stop Amino end

3 nucleotide-pair deletion: no frameshift, but one amino acid missing



Carboxyl end

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#### Sickle Cell Disease

Symptoms Anemia Pain Frequent infections Delayed growth Stroke Pulmonary hypertension Organ damage Blindness Jaundice gallstones



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Caused by a genetic defect

Carried by 5% of humans

Carried by up to 25% in some regions of Africa

Life expectancy 42 in males 48 in females

#### Sickle-Cell Disease = Point Mutation





#### Sickle cell hemoglobin forms long, inflexible chains







#### Coevolution of Genes and Culture: <u>Got Lactase?</u>

#### Comparison: Prokaryotes vs. Eukaryotes

#### Prokaryote vs. Eukaryote



#### Prokaryotes vs. Eukaryotes

#### **Prokaryotes**

- Transcription and translation both in cytoplasm
- DNA/RNA in cytoplasm
- RNA poly binds directly to promoter
- Transcription makes mRNA (not processed)
- No introns

#### **Eukaryotes**

- Transcription in nucleus; translation in cytoplasm
- DNA in nucleus, RNA travels in/out nucleus
- RNA poly binds to TATA box & transcription factors
- Transcription makes premRNA → RNA processing → final mRNA
- Exons, introns (cut out)

A Summary of Protein Synthesis (p. 297)

#### Most current definition for a GENE:

A region of DNA that can be expressed to produced a final product that is either a polypeptide or an RNA molecule

