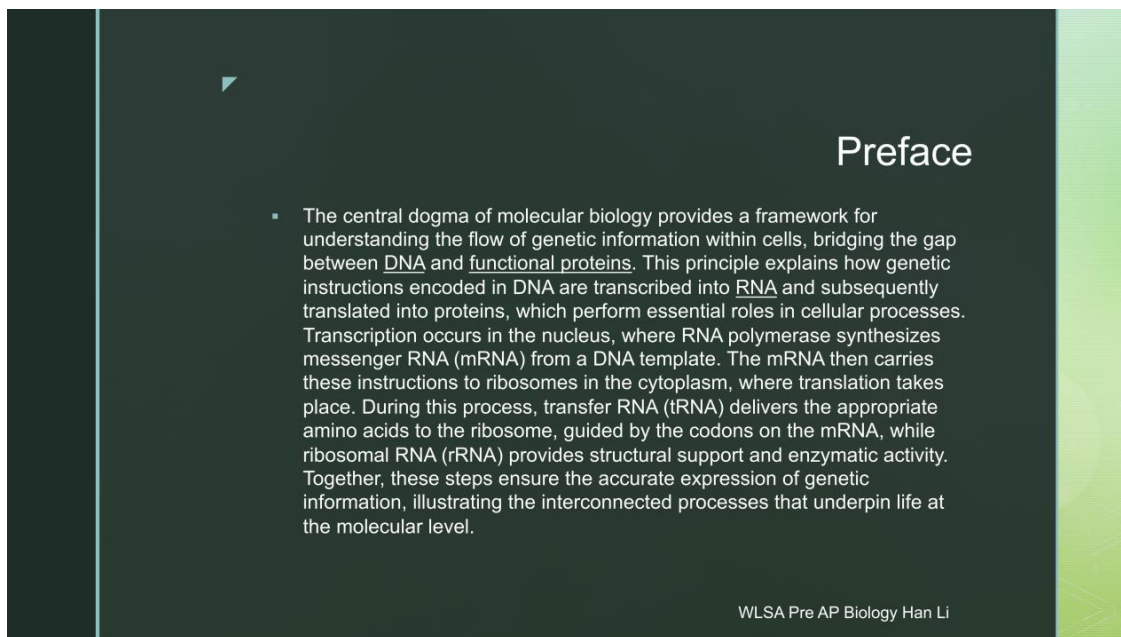


Central dogma

# Nucleic acid

WLSA Pre AP Biology Han Li



### Preface

- The central dogma of molecular biology provides a framework for understanding the flow of genetic information within cells, bridging the gap between DNA and functional proteins. This principle explains how genetic instructions encoded in DNA are transcribed into RNA and subsequently translated into proteins, which perform essential roles in cellular processes. Transcription occurs in the nucleus, where RNA polymerase synthesizes messenger RNA (mRNA) from a DNA template. The mRNA then carries these instructions to ribosomes in the cytoplasm, where translation takes place. During this process, transfer RNA (tRNA) delivers the appropriate amino acids to the ribosome, guided by the codons on the mRNA, while ribosomal RNA (rRNA) provides structural support and enzymatic activity. Together, these steps ensure the accurate expression of genetic information, illustrating the interconnected processes that underpin life at the molecular level.

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### Page 2 Annotation

**Title:** Preface

**Clear Explanation:**

The Central Dogma is the basic framework that explains how genetic information moves from DNA to functional proteins inside cells. DNA stores the instructions.

Transcription turns a section of DNA into messenger RNA (mRNA).

Translation reads the mRNA and assembles amino acids into proteins.

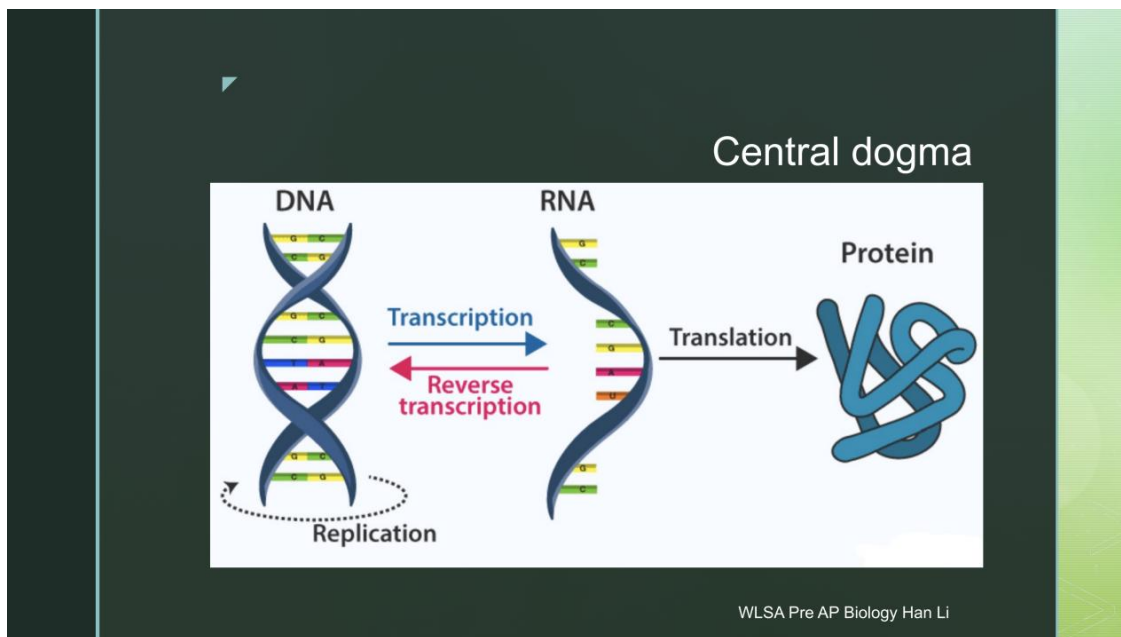
Proteins then perform almost all the important jobs in the cell (structure, enzymes, transport, signaling, etc.).

**Key Points:**

- DNA → RNA (Transcription)
- RNA → Protein (Translation)
- Transcription happens in the nucleus
- Translation happens in the cytoplasm at ribosomes
- tRNA brings amino acids
- rRNA helps form the ribosome structure

**Why It Matters:**

This is the core “information flow” rule of molecular biology. Almost every topic in genetics and biotechnology connects back to these steps.



### Page 3 Annotation

**Title:** Central Dogma (Diagram)

**Clear Explanation:**

This diagram shows the complete Central Dogma flow:

- **DNA** can make copies of itself (**Replication**)
- DNA is transcribed into **RNA** (Transcription)
- RNA can also be reverse-transcribed back into DNA (Reverse Transcription – important in viruses like HIV)
- RNA is translated into **Protein** (Translation)

**Key Points:**

- Arrows show the direction of information flow
- Replication = DNA → DNA
- Transcription = DNA → RNA
- Translation = RNA → Protein

**Why It Matters:**

The diagram gives you a visual “roadmap” of how genetic information is used. Most questions in this unit will ask you to identify or explain one of these arrows.

### Central dogma

- The central dogma was first proposed by Francis Crick in 1958, about five years after the discovery of DNA's double-helix structure.
- The central dogma explains the flow of genetic information and the interactions between different molecular components within a cell.
- The central dogma begins with DNA replication, the process by which an organism ensures its genetic information is accurately passed to its offspring. Transcription follows, during which specific sections of DNA are transcribed into RNA as needed. Finally, during translation, this RNA serves as a template to guide the synthesis of proteins, which act as essential tools for the cell's structure and function.

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### Page 4 Annotation

**Title:** Central Dogma (Detailed Explanation)

**Clear Explanation:**

The Central Dogma was first proposed by Francis Crick in 1958. It describes the normal flow of genetic information in cells:

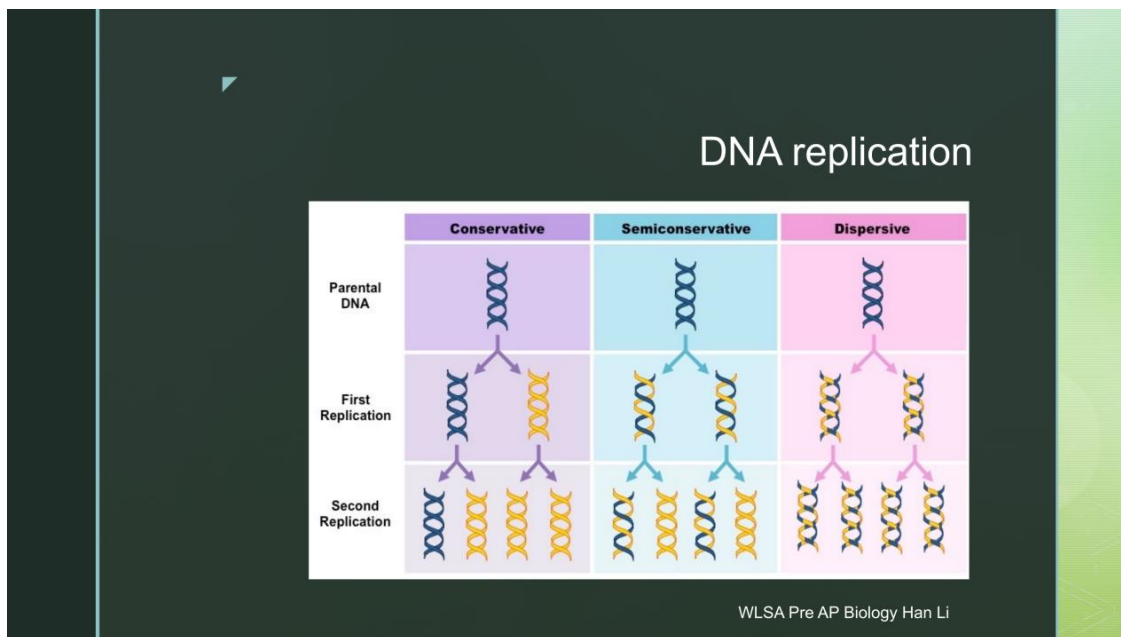
1. **Replication:** DNA makes an exact copy of itself so it can be passed to daughter cells.
2. **Transcription:** Specific genes are copied from DNA into mRNA when the cell needs that protein.
3. **Translation:** The mRNA is read by ribosomes and used to build proteins.

**Key Points:**

- Proposed by Francis Crick (1958)
- DNA replication ensures genetic information is passed to offspring
- Transcription and translation allow cells to make the proteins they need

**Why It Matters:**

This principle connects genes (DNA) to actual cell function (proteins). It is the foundation of modern molecular biology and biotechnology.



## Page 5 Annotation

**Title:** DNA Replication (Three Models)

**Clear Explanation:**

Scientists once debated how DNA replicates. There were three main theories:

- **Conservative:** The original double helix stays together and a completely new copy is made.
- **Semiconservative:** Each new DNA molecule has one old strand and one new strand.
- **Dispersive:** The DNA is broken into pieces and new pieces are mixed in randomly.

The diagram shows what each model would look like after one and two rounds of replication.

**Key Points:**

- Conservative: Parental strands stay together
- Semiconservative: Each daughter DNA has 1 parental + 1 new strand
- Dispersive: Strands are mixed old and new pieces

**Why It Matters:**

The correct model (semiconservative) was proven by the Meselson-Stahl experiment. This is one of the most famous experiments in biology.

### Types of DNA replication

- There was a controversy about how DNA replicates. Some believed that DNA replication produces entirely new DNA molecules, while others thought it was a chaotic, mosaic-like process in which DNA strands are broken and randomly rejoined. A third group proposed that DNA replication is semi-conservative, where each new DNA molecule retains one original strand. To resolve this debate, Meselson and Stahl conducted their groundbreaking investigation.

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### Page 6 Annotation

**Title:** Types of DNA Replication

**Clear Explanation:**

Early scientists had different ideas about DNA replication. Some thought it made entirely new DNA, others thought it was messy and random, and a third group proposed the **semiconservative** model (each new DNA keeps one original strand).

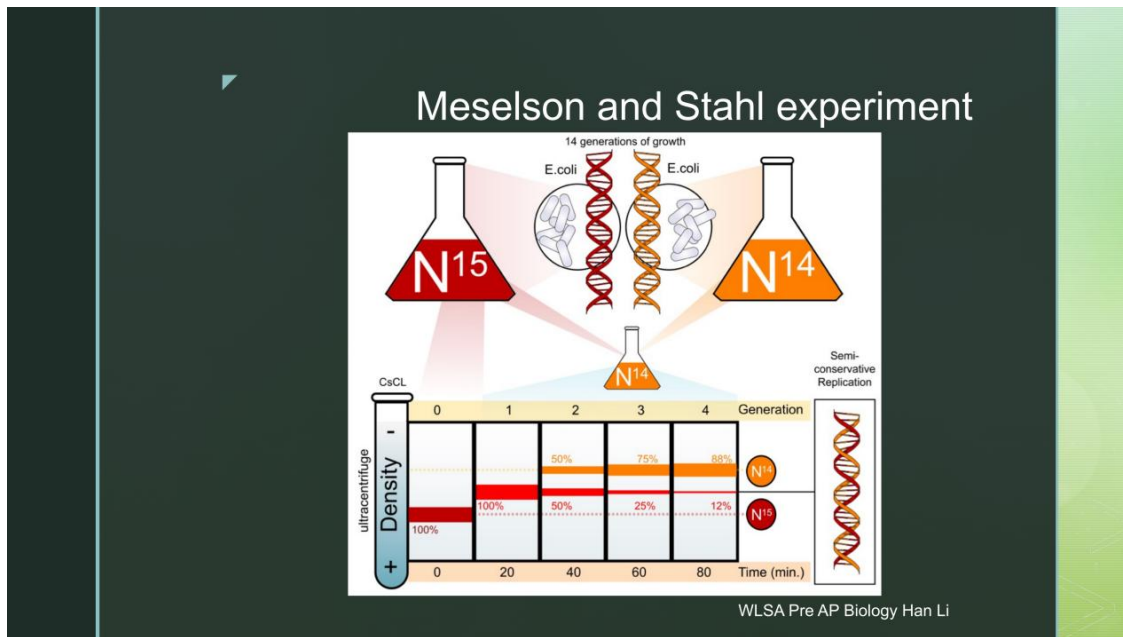
To settle the debate, Meselson and Stahl designed a famous experiment using heavy and light nitrogen isotopes to track old and new DNA strands.

**Key Points:**

- There was a scientific controversy in the 1950s
- Meselson and Stahl's experiment (1958) proved the semiconservative model is correct

**Why It Matters:**

This example shows how science works: hypotheses are tested with experiments. The semiconservative model is now accepted as the universal mechanism of DNA replication in living cells.



## Page 7 Annotation

**Title:** Meselson and Stahl Experiment

**Clear Explanation:**

This diagram shows the famous Meselson and Stahl experiment (1958) that proved DNA replication is **semiconservative**.

Bacteria were first grown in heavy nitrogen ( $^{15}\text{N}$ ) so all DNA was heavy. Then they were switched to light nitrogen ( $^{14}\text{N}$ ). After each generation, scientists used centrifugation to see how heavy or light the DNA was.

The results showed that after one generation, all DNA was “hybrid” (one heavy strand + one light strand). After two generations, half was hybrid and half was completely light.

**Key Points:**

- Used heavy ( $^{15}\text{N}$ ) and light ( $^{14}\text{N}$ ) nitrogen to label DNA
- After 1 generation → only hybrid DNA
- After 2 generations → hybrid + light DNA
- This matches the semiconservative model

**Why It Matters:**

This experiment ended the debate and confirmed that each new DNA molecule keeps one original (parental) strand — the foundation of modern genetics.

### Evidences Supporting Semi-Conservative Replication

- The Meselson and Stahl experiment demonstrated that DNA replication follows a semi-conservative model.
- After the first round of replication, no completely old DNA molecules or randomly disrupted DNA strands were observed.
- DNA molecules appeared in only three distinct bands during the experiment.

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### Page 8 Annotation

**Title:** Evidences Supporting Semi-Conservative Replication

**Clear Explanation:**

The Meselson and Stahl experiment provided strong evidence that DNA replication follows the **semiconservative model**.

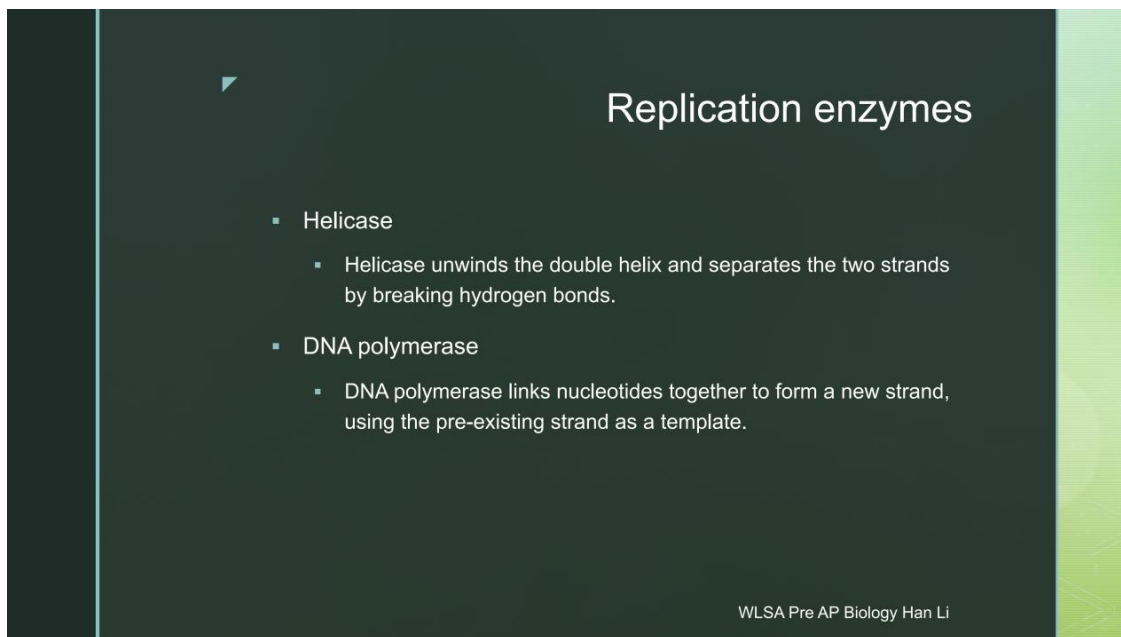
After the first round of replication, scientists did not see any completely old DNA or randomly mixed DNA. Instead, they saw only three clear bands in the centrifuge, which perfectly matched the prediction of the semiconservative model.

**Key Points:**

- No fully old DNA after first replication
- No randomly broken and rejoined strands
- Only three distinct density bands appeared

**Why It Matters:**

This is a classic example of how a well-designed experiment can definitively prove one scientific hypothesis over others.



### Replication enzymes

- Helicase
  - Helicase unwinds the double helix and separates the two strands by breaking hydrogen bonds.
- DNA polymerase
  - DNA polymerase links nucleotides together to form a new strand, using the pre-existing strand as a template.

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### Page 9 Annotation

**Title:** Replication Enzymes

**Clear Explanation:**

Two key enzymes are essential for DNA replication:

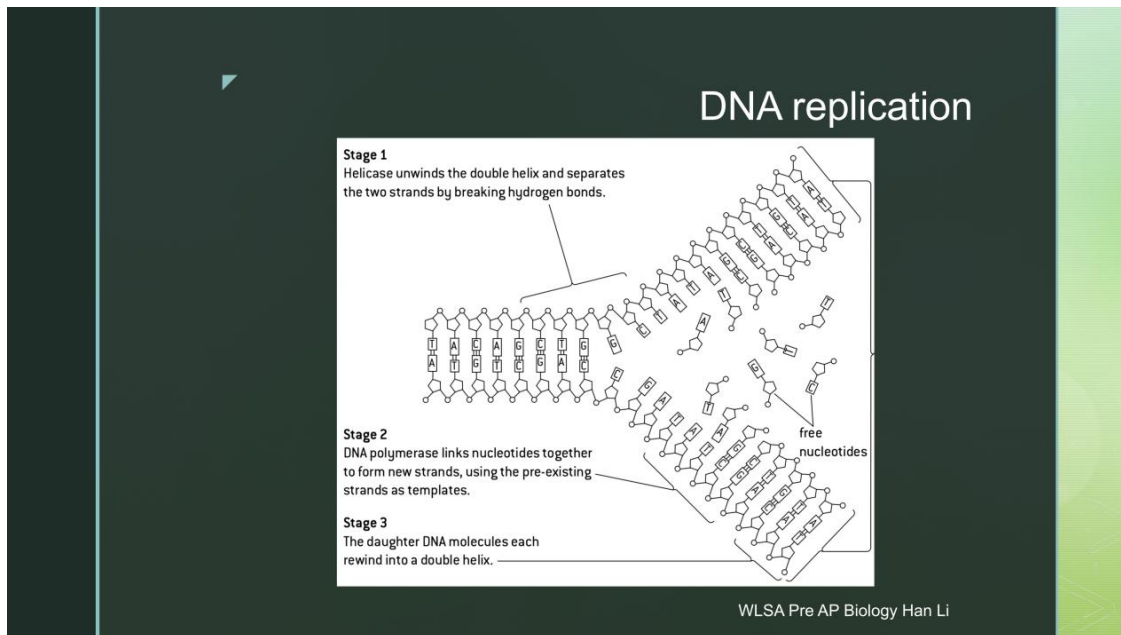
- **Helicase:** Unwinds the double helix by breaking the hydrogen bonds between base pairs, separating the two DNA strands.
- **DNA Polymerase:** Reads the template strand and adds complementary nucleotides to build the new strand.

**Key Points:**

- Helicase = “unzipper” of DNA
- DNA polymerase = “builder” of new strand
- Both work together during replication

**Why It Matters:**

These enzymes make the complicated process of copying 3 billion base pairs fast and accurate.



### Page 10 Annotation

**Title:** DNA Replication (Stages)

**Clear Explanation:**

This diagram illustrates the three main stages of DNA replication:

- **Stage 1:** Helicase unwinds the double helix and separates the two strands.
- **Stage 2:** DNA polymerase adds free nucleotides to form new complementary strands.
- **Stage 3:** The two new double helices rewind and separate into two daughter molecules.

**Key Points:**

- Helicase opens the helix
- DNA polymerase synthesizes new strands
- Each daughter DNA has one old and one new strand

**Why It Matters:**

This shows the actual molecular mechanism behind semiconservative replication.

### Significance of DNA Replication

- With semi-conservative DNA replication, organisms or cells can faithfully pass their genetic information to the next generation, ensuring the continuity and expansion of their genetic material. The high fidelity of this process minimizes the risk of severe errors or mutations, allowing organisms to thrive and adapt over time.



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### Page 11 Annotation

**Title:** Significance of DNA Replication

**Clear Explanation:**

Because DNA replication is semiconservative and extremely accurate, organisms can reliably pass their genetic information to the next generation.

The high fidelity (accuracy) of this process greatly reduces dangerous mutations, allowing life to continue and evolve over billions of years.

**Key Points:**

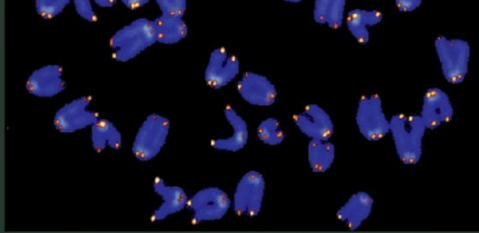
- Faithful copying of genetic information
- Minimizes harmful mutations
- Essential for growth, reproduction, and evolution

**Why It Matters:**

Without accurate DNA replication, life as we know it could not exist.

### Telomeres

- Repetitive nucleotide sequences at the ends of chromosomes that protect them from damage and maintain genomic stability. They shorten with each cell division, influencing aging and disease processes like cancer.



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### Page 12 Annotation

**Title:** Telomeres

**Clear Explanation:**

Telomeres are repetitive DNA sequences (like TTAGGG repeated many times) located at the very ends of chromosomes. They act like protective “caps” that prevent chromosomes from breaking or sticking together.

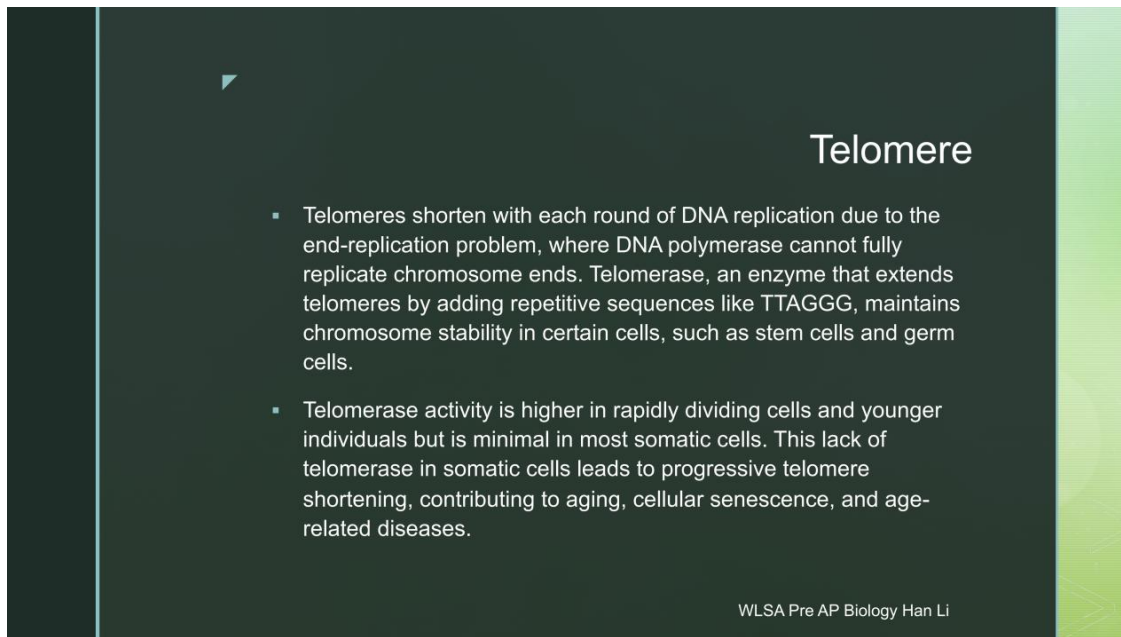
With each cell division, telomeres naturally get a little shorter.

**Key Points:**

- Protective caps at chromosome ends
- Shorten with every cell division
- Related to aging and cancer

**Why It Matters:**

Telomere shortening is one of the reasons cells eventually stop dividing (senescence), which is linked to aging and some diseases.



**Telomere**

- Telomeres shorten with each round of DNA replication due to the end-replication problem, where DNA polymerase cannot fully replicate chromosome ends. Telomerase, an enzyme that extends telomeres by adding repetitive sequences like TTAGGG, maintains chromosome stability in certain cells, such as stem cells and germ cells.
- Telomerase activity is higher in rapidly dividing cells and younger individuals but is minimal in most somatic cells. This lack of telomerase in somatic cells leads to progressive telomere shortening, contributing to aging, cellular senescence, and age-related diseases.

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### Page 13 Annotation

**Title:** Telomere (Continued)

**Clear Explanation:**

Telomeres shorten because DNA polymerase cannot fully copy the very end of the linear chromosome (the “end-replication problem”). The enzyme **telomerase** can add extra TTAGGG repeats to the ends, but it is only active in stem cells, germ cells, and cancer cells. In normal body (somatic) cells, telomerase is turned off, so telomeres keep shortening.

**Key Points:**

- End-replication problem → telomeres shorten
- Telomerase adds repeats (active in certain cells)
- Short telomeres → aging and disease

**Why It Matters:**

Understanding telomeres helps explain why we age and why cancer cells can divide forever.

### Short tandem repeats

- Short tandem repeats (STRs) are highly variable sequences found in non-coding regions of the genome and are widely used for DNA fingerprinting due to their variability among individuals. Unlike the conserved telomeric repeats that serve a protective role at chromosome ends, STRs are ideal for genetic identification because of their high variability.
- Using PCR, STR regions can be amplified by targeting them with specific primers, even from very small DNA samples. The number of repeats in STRs, which differs between individuals, is determined by analyzing the PCR products. This variability makes STR analysis a powerful tool for DNA fingerprinting, paternity testing, and forensic investigations.

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### Page 14 Annotation

**Title:** Short Tandem Repeats (STRs)

**Clear Explanation:**

Short tandem repeats (STRs) are short DNA sequences that repeat many times in non-coding regions of the genome. The number of repeats varies greatly between individuals.

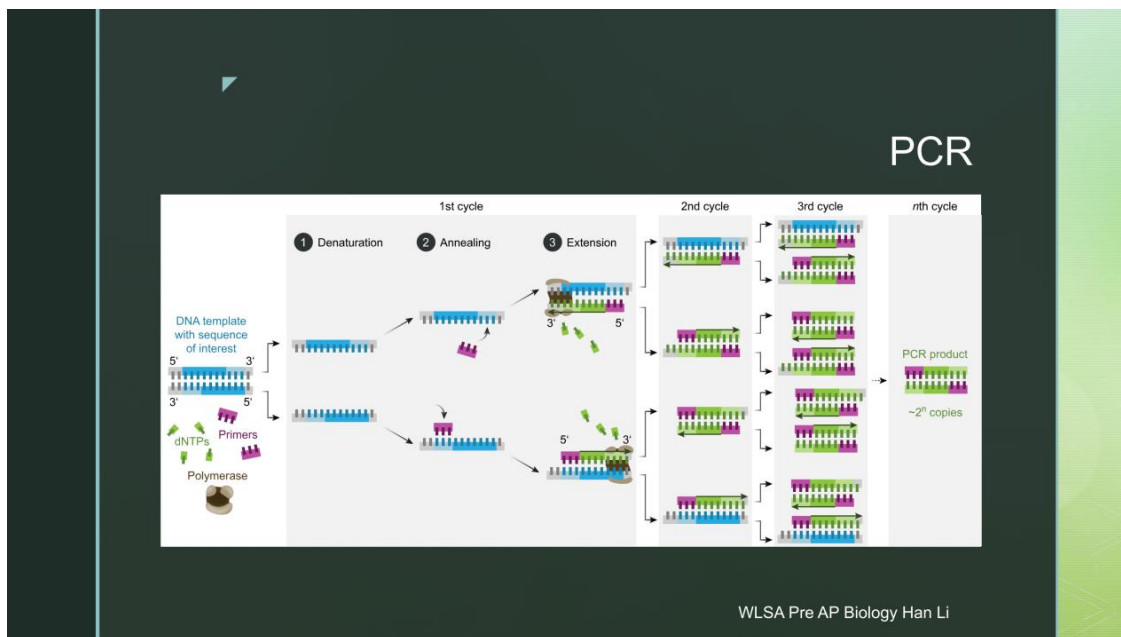
Because they are so variable, STRs are the main tool used in **DNA fingerprinting** for forensics, paternity tests, and crime scene investigations.

**Key Points:**

- Highly variable between people
- Used in DNA fingerprinting
- Amplified using PCR

**Why It Matters:**

STR analysis allows scientists to identify individuals with extremely high accuracy from tiny amounts of DNA.



## Page 15 Annotation

**Title:** PCR (Polymerase Chain Reaction) – Diagram

**Clear Explanation:**

This diagram shows how PCR works to make millions of copies of a specific DNA segment.

It repeats three steps in a cycle:

4. **Denaturation** — heat separates the DNA strands
5. **Annealing** — primers bind to the target sequence
6. **Extension** — Taq polymerase builds new DNA strands

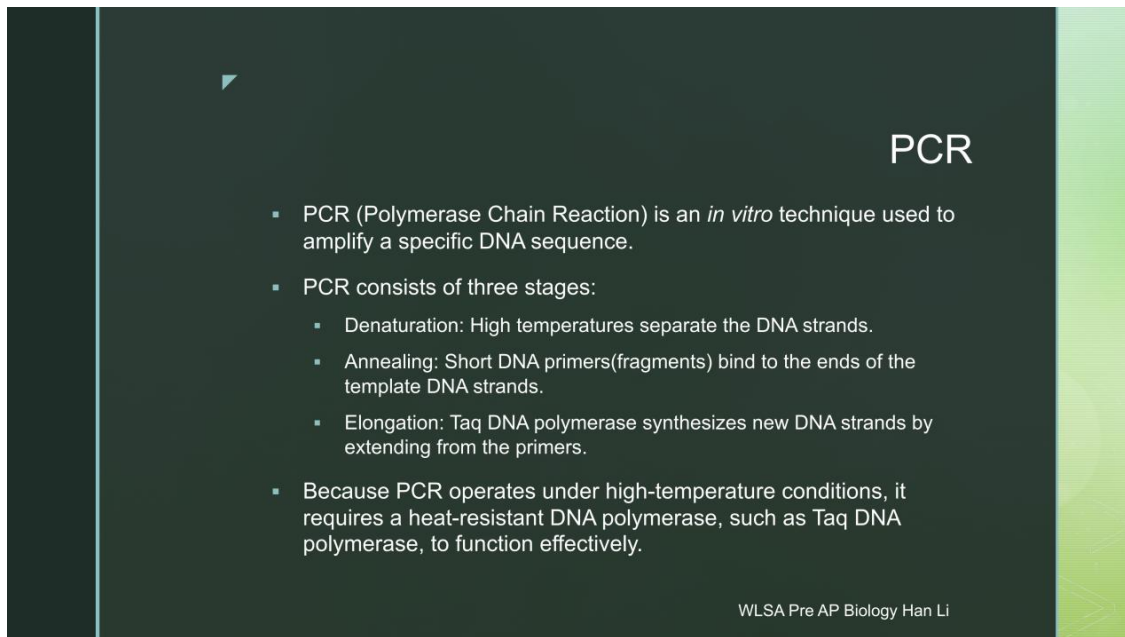
After many cycles, you get billions of copies of the target DNA.

**Key Points:**

- In vitro (test-tube) DNA amplification
- Three steps per cycle: Denature → Anneal → Extend
- Uses heat-stable Taq polymerase

**Why It Matters:**

PCR is one of the most important techniques in modern biology and medicine.



PCR

- PCR (Polymerase Chain Reaction) is an *in vitro* technique used to amplify a specific DNA sequence.
- PCR consists of three stages:
  - Denaturation: High temperatures separate the DNA strands.
  - Annealing: Short DNA primers (fragments) bind to the ends of the template DNA strands.
  - Elongation: Taq DNA polymerase synthesizes new DNA strands by extending from the primers.
- Because PCR operates under high-temperature conditions, it requires a heat-resistant DNA polymerase, such as Taq DNA polymerase, to function effectively.

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### Page 16 Annotation

**Title:** PCR (Summary)

**Clear Explanation:**

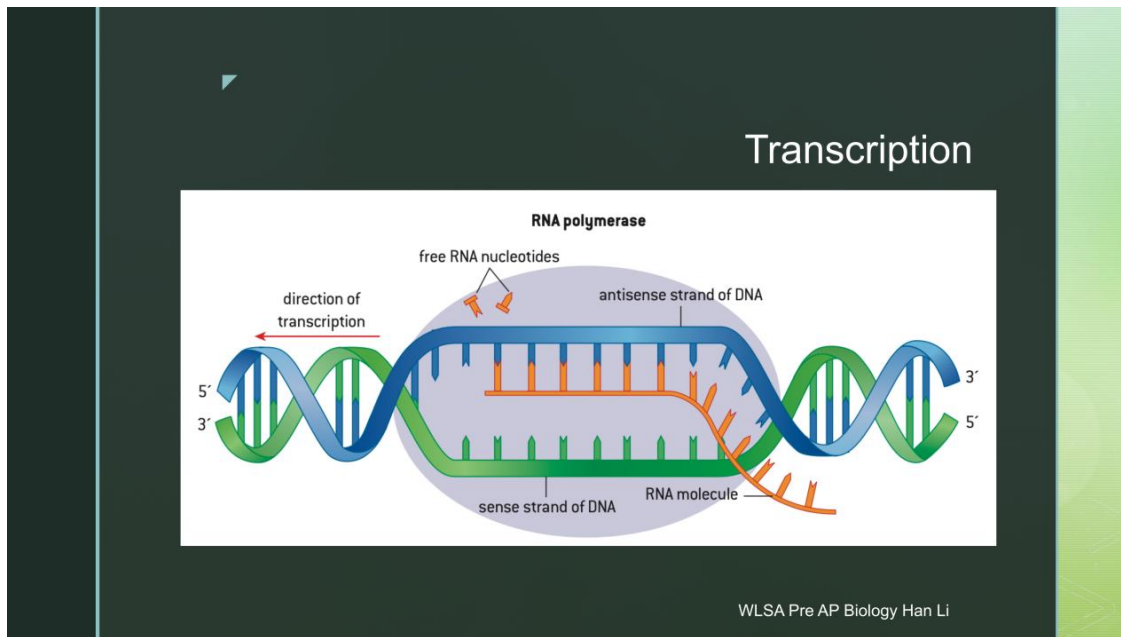
PCR (Polymerase Chain Reaction) is a laboratory technique used to make millions or billions of copies of a specific piece of DNA. It has three repeated steps and requires a special heat-resistant enzyme called Taq DNA polymerase.

**Key Points:**

- Denaturation (high temperature)
- Annealing (primers bind)
- Elongation (polymerase builds new strands)

**Why It Matters:**

PCR allows scientists to study tiny amounts of DNA — essential for forensics, disease diagnosis, and genetic research.



## Page 17 Annotation

**Title:** Transcription (Diagram)

**Clear Explanation:**

Transcription is the process of copying a gene from DNA into messenger RNA (mRNA).

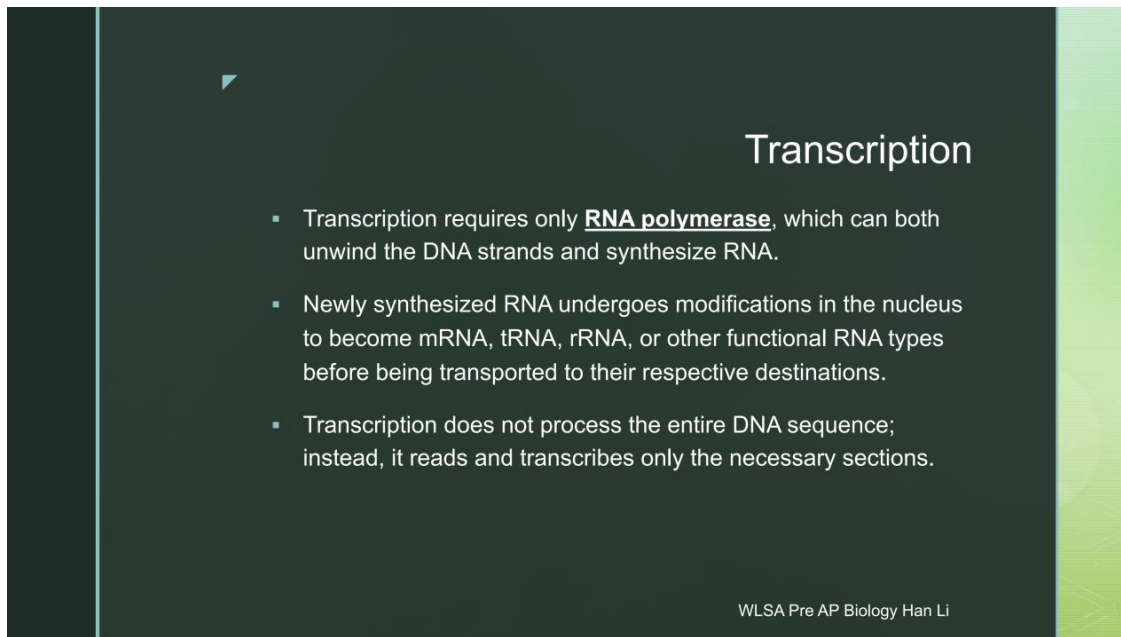
RNA polymerase moves along the DNA template strand, reading it and building a complementary RNA molecule. Only one DNA strand (the template or antisense strand) is transcribed.

**Key Points:**

- RNA polymerase does both unwinding and synthesis
- Direction of transcription is 5' → 3' on RNA
- Only specific genes are transcribed when needed

**Why It Matters:**

Transcription turns the genetic code in DNA into a usable message (mRNA) that can leave the nucleus.



### Transcription

- Transcription requires only **RNA polymerase**, which can both unwind the DNA strands and synthesize RNA.
- Newly synthesized RNA undergoes modifications in the nucleus to become mRNA, tRNA, rRNA, or other functional RNA types before being transported to their respective destinations.
- Transcription does not process the entire DNA sequence; instead, it reads and transcribes only the necessary sections.

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### Page 18 Annotation

**Title:** Transcription (Summary)

**Clear Explanation:**

Transcription uses only RNA polymerase. It does not copy the entire DNA — only the sections (genes) that the cell currently needs. The newly made RNA is then processed and modified in the nucleus before becoming mature mRNA, tRNA, or rRNA.

**Key Points:**

- RNA polymerase unwinds DNA and builds RNA
- Newly made RNA is modified in the nucleus
- Only necessary genes are transcribed

**Why It Matters:**

This allows cells to control which proteins are made at any given time.

The diagram illustrates the flow of genetic information. At the top, a DNA molecule contains three genes. A specific DNA template strand is shown with the sequence 3'-A C C A A A C G A G T-5'. Through the process of transcription, an mRNA strand is synthesized with the complementary sequence 5'-M G G U U M G G C U C A-3'. The mRNA is then translated into a protein chain. Each three-nucleotide sequence (codon) on the mRNA corresponds to a specific amino acid: MGG codes for Trp, UUM for Phe, GGC for Gly, and UCA for Ser.

## The Genetic Code

- For each gene, one DNA strand is the template strand
- mRNA (5' → 3') complementary to template
- mRNA triplets (**codons**) code for amino acids in polypeptide chain

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## Page 19 Annotation

**Title:** The Genetic Code

**Clear Explanation:**

The genetic code is the set of rules by which information in mRNA is translated into proteins.

- Each gene has a **template strand** of DNA
- mRNA is complementary to the template (but uses U instead of T)
- mRNA is read in groups of three nucleotides called **codons**
- There are 64 possible codons ( $4^3$ ) that code for 20 amino acids + 3 stop signals

**Key Points:**

- 64 codons total
- Redundancy: most amino acids have more than one codon
- Reading frame must be correct
- The code is **universal** — almost all living things use the same code

**Why It Matters:**

The genetic code is the “language” that connects genes to proteins.

## The Genetic Code

		Second mRNA base				Third mRNA base (3' end of codon)
		U	C	A	G	
First mRNA base (5' end of codon)	U	UUU Phe	UCU	UAU Tyr	UGU Cys	U C A G
	UUC	UCC	UAC	UGC		
	UUA	UCA Ser	UAA Stop	UGA Stop		
	UUG	UCG	UAG Stop	UGG Trp		
C	CUU	CCU	CAU His	CGU	U C A G	
CUC	CCC Pro	CAC	CGC			
CUA	CCA	CAA Gln	CGA			
CUG	CCG	CAG	CGG			
A	AUU	ACU	AAU Asn	AGU Ser	U C A G	
AUC	ACC	AAC	AGC			
AUA	ACA Thr	AAA Lys	AGA Arg			
AUG Met or start	ACG	AAG	AGG			
G	GUU	GCU	GAU Asp	GGU	U C A G	
GUC	GCC	GAC	GGC			
GUA	GCA Ala	GAA Glu	GGA			
GUG	GCG	GAG	GGG			

- 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.

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## Page 20 Annotation

**Title:** The Genetic Code

**Clear Explanation:**

The genetic code is the set of rules by which information in mRNA is translated into proteins.

- Each gene has a **template strand** of DNA
- mRNA is complementary to the template (but uses U instead of T)
- mRNA is read in groups of three nucleotides called **codons**
- There are 64 possible codons ( $4^3$ ) that code for 20 amino acids + 3 stop signals

**Key Points:**

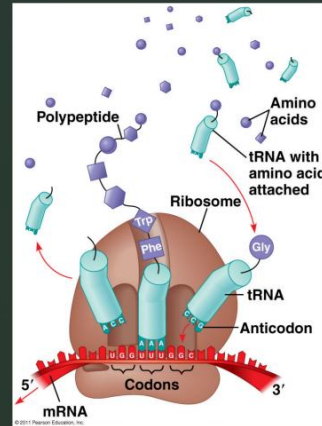
- 64 codons total
- Redundancy: most amino acids have more than one codon
- Reading frame must be correct
- The code is **universal** — almost all living things use the same code

**Why It Matters:**

The genetic code is the “language” that connects genes to proteins.

## Components of Translation

- **mRNA** = message
- **tRNA** = interpreter
- **Ribosome** = site of translation



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## Page 21 Annotation

**Title:** Components of Translation

**Clear Explanation:**

Translation is the process of building a protein using mRNA as the instructions.

Three main components:

- **mRNA** = the message (carries the code)
- **tRNA** = the interpreter (brings the correct amino acid)
- **Ribosome** = the factory where translation happens

**Key Points:**

- mRNA = message
- tRNA = brings amino acids
- Ribosome = site of protein synthesis

**Why It Matters:**

These three work together like a factory assembly line to turn the genetic code into real proteins.

The diagram illustrates the structure of tRNA. Part (a) shows the two-dimensional structure as a cloverleaf, with an amino acid attachment site at the 3' end (A-C-C-A) and an anticodon at the 3' end (A-A-G). Hydrogen bonds are shown between complementary bases. Part (b) shows the three-dimensional structure as a compact L-shape. Part (c) shows the anticodon symbol (AAG) used in the book.

### tRNA

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

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### Page 22 Annotation

**Title:** tRNA

**Clear Explanation:**

Transfer RNA (tRNA) is a small RNA molecule that acts like a translator. Each tRNA carries one specific amino acid and has an **anticodon** that matches a codon on the mRNA.

The third base of the codon and anticodon can “wobble” (not follow strict base-pairing rules), allowing fewer tRNAs to cover all 61 codons.

**Key Points:**

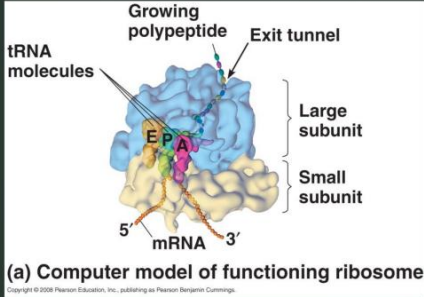
- Specific to one amino acid
- Has anticodon that pairs with mRNA codon
- Third-base wobble

**Why It Matters:**

tRNA is the bridge between the nucleic acid language (codons) and the protein language (amino acids).

### Ribosomes

- Ribosome = rRNA + proteins
- made in nucleolus
- 2 subunits
  - 30S+50S in 70S
  - 40S+60S in 80S



(a) Computer model of functioning ribosome

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### Page 23 Annotation

**Title:** Ribosomes

**Clear Explanation:**

Ribosomes are the cellular machines that build proteins. They are made of ribosomal RNA (rRNA) and proteins.

A ribosome has two subunits (small and large) and three important sites:

- **A site:** holds the incoming tRNA with the next amino acid
- **P site:** holds the tRNA with the growing polypeptide chain
- **E site:** exit site for empty tRNA

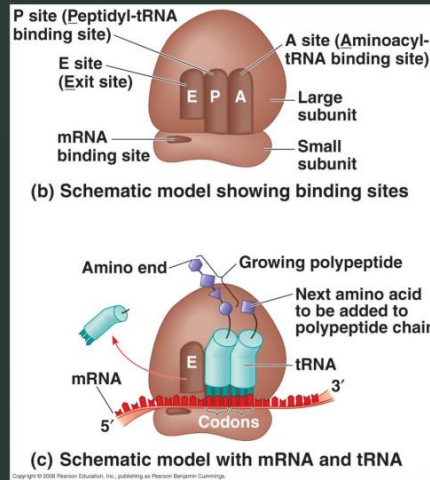
**Key Points:**

- Made in the nucleolus
- Two subunits (prokaryotes 70S, eukaryotes 80S)
- Three binding sites: A, P, E

**Why It Matters:**

The ribosome is where translation actually happens — turning mRNA instructions into a chain of amino acids.

## Ribosomes



- Active sites:
  - A site: holds AA to be added
  - P site: holds growing polypeptide chain
  - E site: exit site for tRNA

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## Page 24 Annotation

**Title:** Ribosomes

**Clear Explanation:**

Ribosomes are the cellular machines that build proteins. They are made of ribosomal RNA (rRNA) and proteins.

A ribosome has two subunits (small and large) and three important sites:

- **A site:** holds the incoming tRNA with the next amino acid
- **P site:** holds the tRNA with the growing polypeptide chain
- **E site:** exit site for empty tRNA

**Key Points:**

- Made in the nucleolus
- Two subunits (prokaryotes 70S, eukaryotes 80S)
- Three binding sites: A, P, E

**Why It Matters:**

The ribosome is where translation actually happens — turning mRNA instructions into a chain of amino acids.

### Translation: Initiation

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

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## Page 25 Annotation

**Title:** Translation: Initiation

**Clear Explanation:**

Translation begins (initiation) when:

7. The small ribosomal subunit binds to the start codon (AUG) on mRNA.
8. The initiator tRNA carrying methionine (Met) attaches to the P site.
9. The large subunit joins to form the complete ribosome.

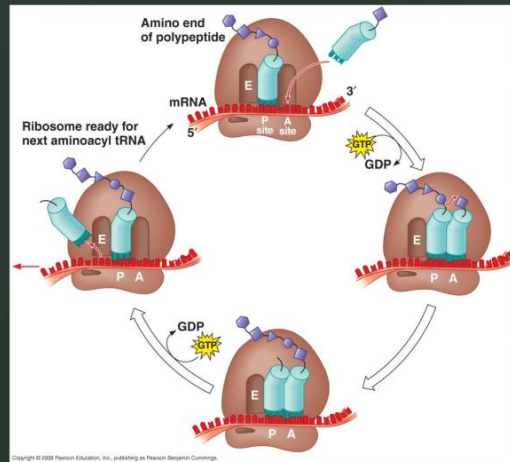
**Key Points:**

- Starts at AUG (methionine)
- Forms the translation initiation complex

**Why It Matters:**

Correct initiation ensures the protein starts at the right place and in the right reading frame.

Translation:  
Elongation



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Page 26 Annotation

**Title:** Translation: Elongation

**Clear Explanation:**

During elongation, the ribosome moves along the mRNA one codon at a time.

- A new tRNA with the next amino acid enters the A site
- A peptide bond forms between the growing chain and the new amino acid
- The ribosome shifts (translocates), moving the empty tRNA to the E site and the growing chain to the P site

This cycle repeats, making the polypeptide longer.

**Key Points:**

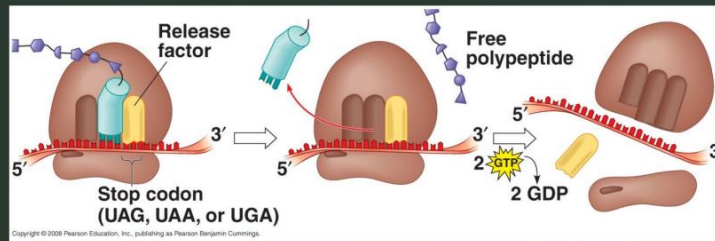
- Incoming amino acid enters A site
- Peptide bond formation
- Ribosome translocates

**Why It Matters:**

Elongation is the main phase where the protein chain is actually built.

## Translation: Termination

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



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## Page 27 Annotation

**Title:** Translation: Termination

**Clear Explanation:**

Translation stops when the ribosome reaches a **stop codon** (UAA, UAG, or UGA) on the mRNA. These codons do not code for any amino acid.

Instead of a tRNA, a special protein called **release factor** binds to the stop codon. This causes the ribosome to release the completed polypeptide chain. Finally, the two ribosomal subunits separate and can be reused for another round of translation.

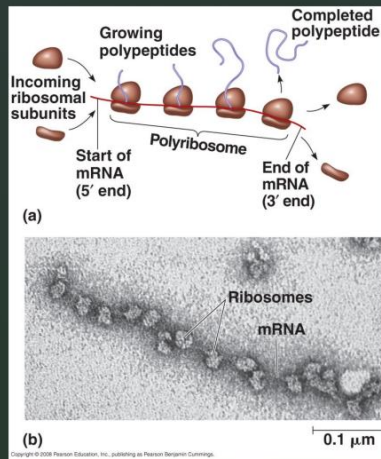
**Key Points:**

- Stop codons: UAA, UAG, UGA
- Release factor binds to stop codon
- Polypeptide (protein) is released
- Ribosomal subunits dissociate

**Why It Matters:**

Termination ensures the protein is finished at exactly the right length. Without proper termination, the cell could make incorrect or incomplete proteins.

## \*Polyribosomes



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

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## Page 28 Annotation

**Title:** Polyribosomes (Polysomes)

**Clear Explanation:**

A single mRNA molecule can be translated by **many ribosomes at the same time**. This structure is called a **polyribosome** (or polysome).

While one ribosome is moving along the mRNA making a protein, another ribosome can start right behind it. This allows the cell to produce many copies of the same protein very quickly from just one mRNA.

**Key Points:**

- One mRNA → multiple ribosomes
- Called polyribosome or polysome
- Increases efficiency of protein synthesis
- Visible in electron microscope images

**Why It Matters:**

Polyribosomes are an important way cells make large amounts of protein quickly (for example, when making antibodies or enzymes).

**Brief Overview**

- The central dogma of molecular biology explains how genetic information flows from DNA to RNA and finally to proteins, ensuring the accurate expression of genetic traits. DNA replication ensures the transmission of genetic material to the next generation, while transcription and translation convert the genetic code into functional proteins. Processes like PCR and the role of telomeres also illustrate the molecular mechanisms supporting genomic stability and cellular function.

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### Page 29 Annotation

**Title:** Brief Overview

**Clear Explanation:**

This slide gives a quick summary of the entire unit.

The **Central Dogma** explains how genetic information flows:

DNA → RNA (transcription) → Protein (translation).

DNA replication ensures genetic material is passed accurately to the next generation.

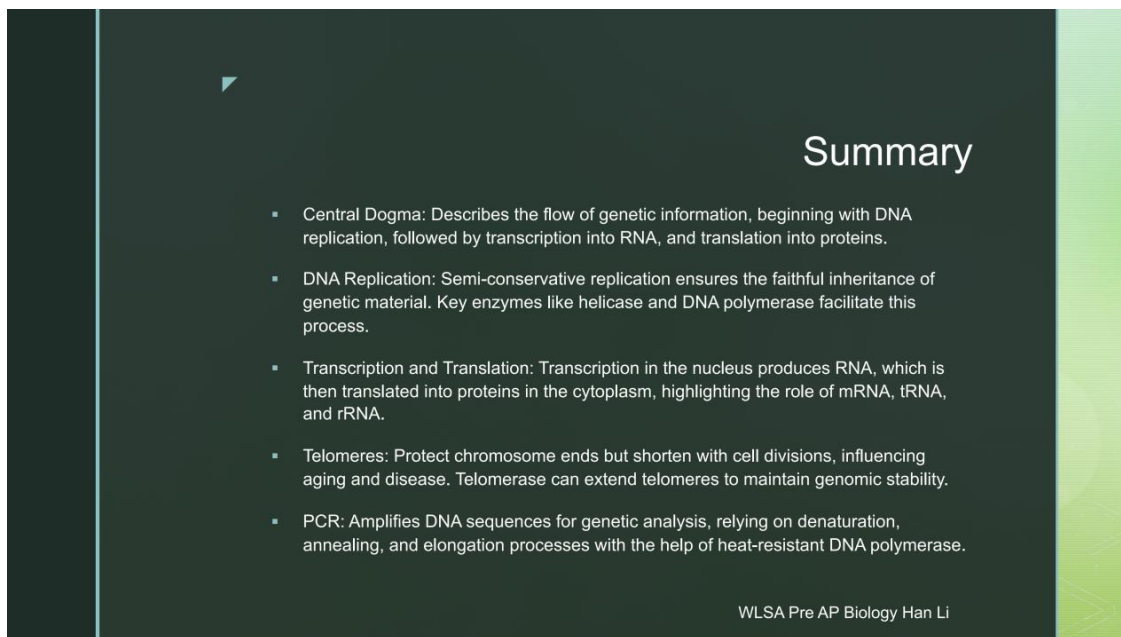
Other important topics include telomeres (which protect chromosome ends) and PCR (a technique to copy DNA in the lab).

**Key Points:**

- Central Dogma = DNA → RNA → Protein
- DNA replication = semiconservative
- Transcription + Translation = protein synthesis
- Telomeres and PCR are practical applications

**Why It Matters:**

This overview connects all the pieces you learned in the unit and shows how they work together in real biology.



### Summary

- Central Dogma: Describes the flow of genetic information, beginning with DNA replication, followed by transcription into RNA, and translation into proteins.
- DNA Replication: Semi-conservative replication ensures the faithful inheritance of genetic material. Key enzymes like helicase and DNA polymerase facilitate this process.
- Transcription and Translation: Transcription in the nucleus produces RNA, which is then translated into proteins in the cytoplasm, highlighting the role of mRNA, tRNA, and rRNA.
- Telomeres: Protect chromosome ends but shorten with cell divisions, influencing aging and disease. Telomerase can extend telomeres to maintain genomic stability.
- PCR: Amplifies DNA sequences for genetic analysis, relying on denaturation, annealing, and elongation processes with the help of heat-resistant DNA polymerase.

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### Page 30 Annotation

**Title:** Summary

**Clear Explanation:**

This is the final summary slide of the unit. It reviews the most important ideas:

- The **Central Dogma** describes the flow of genetic information (DNA replication → transcription → translation).
- DNA replication is **semiconservative** and uses enzymes like helicase and DNA polymerase.
- Transcription makes mRNA in the nucleus; translation makes proteins in the cytoplasm using mRNA, tRNA, and ribosomes.
- Telomeres protect chromosome ends but shorten with each cell division (related to aging).
- PCR is a lab technique that rapidly copies specific DNA segments using heat-resistant polymerase.

**Key Points:**

- Central Dogma flow
- Semiconservative replication
- Role of mRNA, tRNA, rRNA
- Telomeres and aging
- PCR technique

**Why It Matters:**

You should now understand the complete “information highway” of the cell — from DNA to functional proteins. This knowledge is the foundation for all future topics in genetics, biotechnology, and medicine.