Unit 7 · Genetic Material

STUDY NOTES

WHAT NEB'S GRADE 12 EXAM ASKS

- **CDC's grid (2078):** Genetics (Units 7–10 together): 12 of 75 marks; 1 short question (4 marks: understanding 1, application 2, higher ability 1) and 1 long question (8 marks: understanding 2, application 3, higher ability 3)
- **The paper:** Botany 37 + Zoology 38; each part: MCQs × 1 (5 Botany, 6 Zoology) · 4 short × 4 · 2 long × 8; one OR in each short and long group; 3 hours; 1 mark per expected point
- **CDC's model paper:** short: what genetic material is; the structure and functions of RNA (1 + 2 + 1)
- **MCQ (1 mark)**
  - uracil only in RNA; phosphodiester bond
  - A–T, C–G; 3 bases a codon; code universal
  - helicase unwinds; polymerase only $5' \rightarrow 3'$
  - conservative, semi-conservative, dispersive from a figure
  - 2000 bp $\approx$ 680 nm; stronger H-bonds hit replication and transcription
- **Short and long (in parts)**
  - heredity, variation; parts of a nucleotide; purine vs pyrimidine
  - DNA structure, function with a diagram; RNA, its three types
  - genetic code and its characteristics
  - semi-conservative replication with a diagram; leading vs lagging
  - RNA on template TACGGA; uracil + ribose $\rightarrow$ RNA (viruses)
  - a replication fork from a figure: label, enzyme, Okazaki fragment

Key terms

Heredity: passing of characters from one generation to the next.

Variation: differences between individuals of a species; inherited or from surroundings.

Genetics (Bateson, 1905): the study of heredity and variation.

Genetic material: substance carrying the instructions and passing them to offspring; **DNA** (RNA in some viruses).

Nucleotide: pentose sugar + nitrogenous base + phosphate.

Purines: two rings: A, G; **pyrimidines**: one ring: C, T (DNA), U (RNA).

Phosphodiester bond: phosphate joining C-3′ of one sugar to C-5′ of the next.

Antiparallel: strands run $5' \rightarrow 3'$ and $3' \rightarrow 5'$.

Complementary: A pairs with T (U), G with C.

Central dogma (Crick, 1958): DNA $\rightarrow$ RNA $\rightarrow$ protein.

Replication: one DNA $\rightarrow$ two identical DNAs (S phase).

Semi-conservative: each copy has one old strand, one new.

Okazaki fragments: short pieces of the lagging strand.

Codon: three mRNA bases for one amino acid or stop; **anticodon**: the matching three on tRNA.

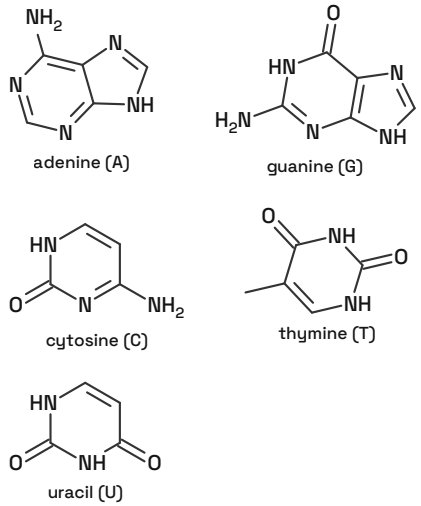
Genetic code: rules turning mRNA base order into amino-acid order.

$\frac{A+G}{T+C} = 1$	A = T, G = C (double-stranded DNA) **Use:** Chargaff's rule (1950)
$L = n \times 0.34$ nm	L length, n base pairs **Use:** length of DNA
turns $= n \div 10 = L \div 3.4$ nm	10 bp per turn **Use:** turns of the helix
$4^3 = 64$	4 bases, 3 per codon **Use:** codons (61 for amino acids, 3 stop)

Nucleic acids

- **pentose**: **ribose** (RNA); **deoxyribose** (DNA): H, not –OH, on C-2′
- **purines** (2 rings): adenine, guanine (DNA and RNA)

- **pyrimidines** (1 ring): cytosine (both), **thymine** (DNA), **uracil** (RNA)
- **phosphoric acid** H_3PO_4 → phosphate; **phosphodiester bonds** make the strand
- ribose + guanine + phosphate = GMP (RNA unit); with deoxyribose → DNA unit: the **sugar** decides



Purines and pyrimidines.

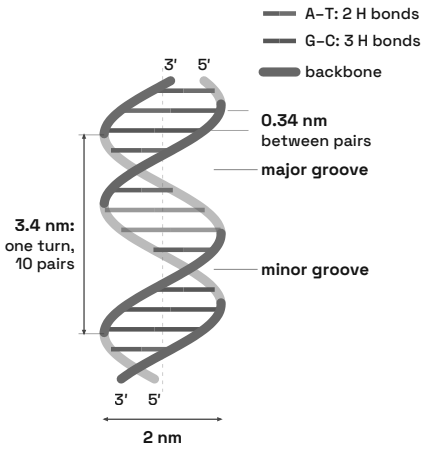
	Purines	Pyrimidines
rings	two (6 + 5)	one (6)
bases	A, G	C, T, U
size	larger	smaller
pairs with	a pyrimidine	a purine

DNA

- prokaryotes: **cytoplasm** (nucleoid, **plasmids**); eukaryotes: **nucleus**, a little in mitochondria, plastids
- deoxyribonucleotides (A, G, C, T)

Watson and Crick model (1953; X-rays of Franklin, Wilkins; Chargaff's data)

1. **two strands**, **double helix**, **right-handed**
2. **antiparallel**
3. diameter **2 nm**
4. **major** and **minor grooves**; one of each = one turn
5. one turn = **3.4 nm** (pitch)
6. **sugar–phosphate backbone** outside, **bases inside**, stacked
7. **H-bonds**: **A=T (2)**, **G≡C (3)**; purine with pyrimidine → constant width
8. base pairs **0.34 nm** apart → **10 bp per turn**
9. A = T, G = C → **Chargaff's rule**



The double helix.

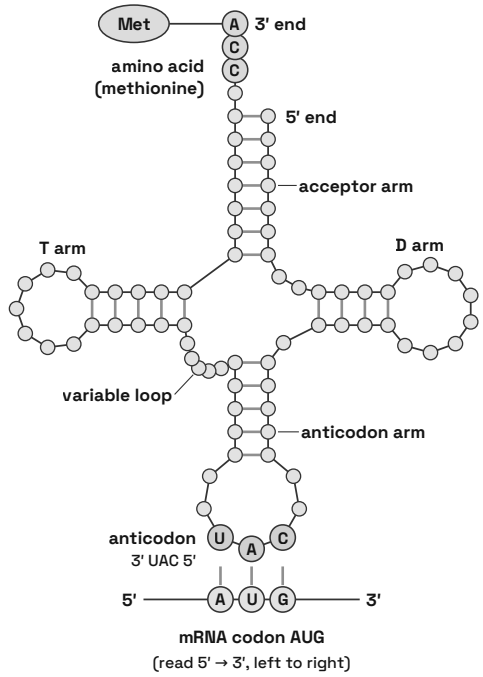
- (A + T) ÷ (G + C) ≠ 1, differs by species (~1.5 human); rule holds only for double-stranded DNA
- 22% T → A 22%, G = C = 28%
- 5000 bp → 1700 nm, 500 turns; human cell 6.4×10^9 bp ≈ 2.2 m (wound on histones)

Functions

1. carries hereditary characters as base sequence
2. **replicates** → copies to each cell, generation
3. **crossing over** → recombination
4. **mutations** → variation → new species
5. **transcribed** into RNAs
6. controls metabolism through RNA, proteins (central dogma)

RNA

- in every cell; made in the nucleus; nucleus, nucleolus, cytoplasm, ribosomes, mitochondria, plastids
- ribonucleotides: ribose + phosphate + A, G, C, **U**
- usually **single-stranded**; folds where bases pair (A–U, G–C): hairpins, loops (**pseudohelix**)
- 5′ and 3′ ends; complementary to its DNA **template**: template 3′-CAATGA-5′ → RNA 5′-GUUACU-3′; template TACGGA → AUGCCU

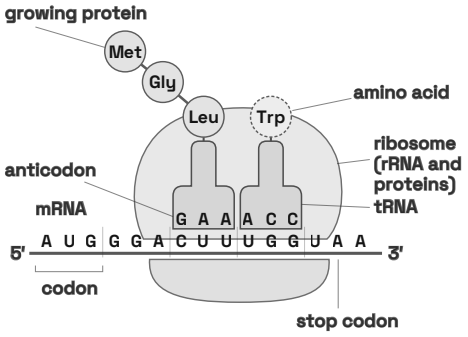


tRNA, the clover leaf.

Type	Share	Job
mRNA	3–5%, short-lived	copy of a gene, DNA → ribosomes
rRNA	~80%, stable	ribosomes; holds mRNA, joins amino acids
tRNA	~15%, 75–90 nucleotides	**adapter**: carries one amino acid; **anticodon** pairs with codon

Functions

- mRNA carries information for protein synthesis
- tRNA brings amino acids in codon order
- rRNA in ribosomes; itself forms peptide bonds
- **genetic material** of some viruses: influenza, measles, polio, rabies, HIV, COVID-19, TMV
- **ribozymes**: RNA enzymes, cut other RNAs

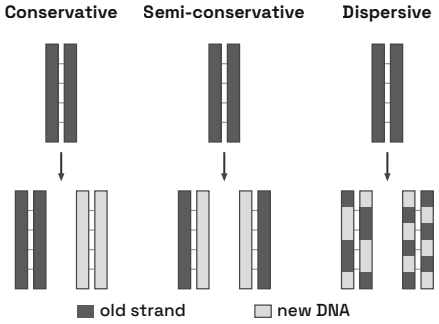


mRNA, tRNA and rRNA at work.

	DNA	RNA
strands	two, double helix	usually one
sugar	deoxyribose	ribose
bases	A, G, C, **T**	A, G, C, **U**
pairing	A=T, G≡C between strands	A–U, G–C within its strand
Chargaff's rule	holds	doesn't
where	nucleus; mitochondria, plastids	made in nucleus; works in cytoplasm
kinds	one	mRNA, rRNA, tRNA
size	millions of bp	tens to thousands
stability	stable	less stable
copying	replicates	transcribed from DNA
job	stores information	uses it; genome of some viruses

DNA replication

- before division, in the **S phase**; each daughter cell gets one copy
- **conservative**: one copy both old, other both new
- **semi-conservative**: each copy one old + one new
- **dispersive**: every strand a patchwork



Three possible modes of replication.

Meselson and Stahl (1958, Caltech)

- *E. coli* on ^{15}**N** (heavy) → moved to ^{14}**N**; DNA spun in **cesium chloride**
- 1 generation: **one band, halfway** → not conservative
- 2 generations: **halfway + light**, equal → not dispersive
- → **semi-conservative**

1. Initiation

- **origins (ori)**: one in bacteria, many in eukaryotes

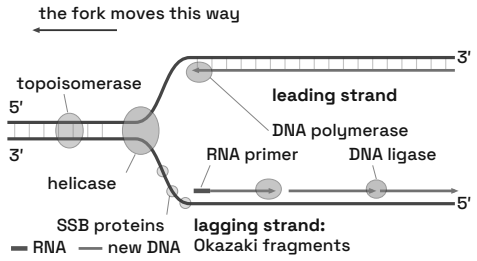
- **helicase** breaks H-bonds → strands separate → templates
- **replication fork** (Y); two forks from each origin → bubble
- **SSB proteins** keep strands apart; **topoisomerase** (gyrase) relieves twisting
- **primase** makes an **RNA primer** (~10 nucleotides): polymerase can't start a strand

2. Elongation

- **DNA polymerase III** adds nucleotides to the **3′ end**: new strand grows **5′ → 3′**
- **leading strand**: towards the fork, **continuous**, one primer
- **lagging strand**: away from the fork, in **Okazaki fragments** (1000–2000 nt bacteria, 100–200 eukaryotes), a primer each
- primers removed (DNA polymerase I), gaps filled
- **DNA ligase** seals fragments (phosphodiester bond)
- → **semi-discontinuous**

3. Termination

- forks meet (circle in bacteria; neighboring origins in eukaryotes); telomeres finished
- two DNAs, each one old, one new strand; each winds into a helix
- **proofreading**: ~1 mistake per billion bases



The replication fork.

	Leading strand	Lagging strand
grows	towards the fork	away from the fork
made	continuously	in Okazaki fragments
primers	one	many
ligase	hardly needed	joins fragments
speed	ahead	lags behind

Genetic code

- 20 amino acids; $4^1 = 4$, $4^2 = 16$ too few; $\mathbf{4^3 = 64}$ → **triplet**
- written for **mRNA**; coding strand same with T; template complementary
- read a codon: row of the first two bases, column of the third (GGA → glycine)

Characteristics

1. **triplet**: AUG = methionine
2. **non-overlapping**: ACUAAG → ACU, AAG
3. **commaless**: read continuously; one base added or lost → **frameshift**
4. **universal** (few exceptions: human mitochondria UGA = Trp)
5. **degenerate**: 61 codons for 20 amino acids; glycine GGU, GGC, GGA, GGG; only Met (AUG), Trp (UGG) one each; third base often doesn't matter
6. **unambiguous**: one codon → one amino acid
7. **stop codons**: **UAA, UAG, UGA** (nonsense)
8. **start codon**: **AUG** (Met); GUG, rarely UUG in some bacteria
9. **colinearity**: codon order = amino-acid order

	Sequence
coding strand	5′- ATG GGA CTT -3′
template strand	3′- TAC CCT GAA -5′
mRNA	5′- AUG GGA CUU -3′
protein	Met – Gly – Leu

- GGU → GGC: still glycine; sickle cell: one letter, one disease

COMMON MISTAKES

✗ Thymine in RNA
✓ **uracil**; T only in DNA.

✗ A pairs with G
✓ A with **T** (2 H-bonds), G with **C** (3).

✗ Strands run parallel
✓ **antiparallel**.

✗ $(A + T) \div (G + C) = 1$
✓ $\mathbf{(A + G) \div (T + C)} = 1$.

✗ Each copy is all old or all new
✓ **one old, one new** (semi-conservative).

✗ Polymerase builds 3′ → 5′
✓ new strand grows **5′ → 3′**.

✗ Lagging strand made continuously
✓ in **Okazaki fragments**, joined by ligase.

✗ Degenerate means one codon, many amino acids
✓ one amino acid, **many codons**; one codon, one amino acid is unambiguous.

✗ AUG is a stop codon
✓ **start** (Met); stops are UAA, UAG, UGA.