

Nucleic acids and protein synthesis

A-Level Biology 9700 · Topic 6 revision notes

Everything from the 4 lessons of this topic on a few pages: the key idea of each lesson, the diagram to remember, the points to learn and the traps examiners set. Read it, cover it, test yourself.

1. The structure of nucleic acids

3. Transcription and translation

2. Semi-conservative replication of DNA

4. Gene mutations

1 The structure of nucleic acids

Syllabus 6.1

A **nucleotide** is a **phosphate group**, a **pentose sugar** (deoxyribose in DNA, ribose in RNA) and a **nitrogen-containing base**. **Adenine** and **guanine** are **purines** with a double ring; **cytosine**, **thymine** and **uracil** are **pyrimidines** with a single ring. **ATP** is a phosphorylated nucleotide: adenine, ribose and three phosphates. Nucleotides are joined into a polynucleotide by **phosphodiester bonds** (condensation reactions) between the phosphate of one and the sugar of the next. **DNA** is a **double helix** of two **antiparallel** strands, one running 5' to 3' and the other 3' to 5', held together by **hydrogen bonds** between **complementary bases**: A with T (two hydrogen bonds) and C with G (three). **mRNA** is a single, short, unpaired polynucleotide with ribose and uracil in place of deoxyribose and thymine.

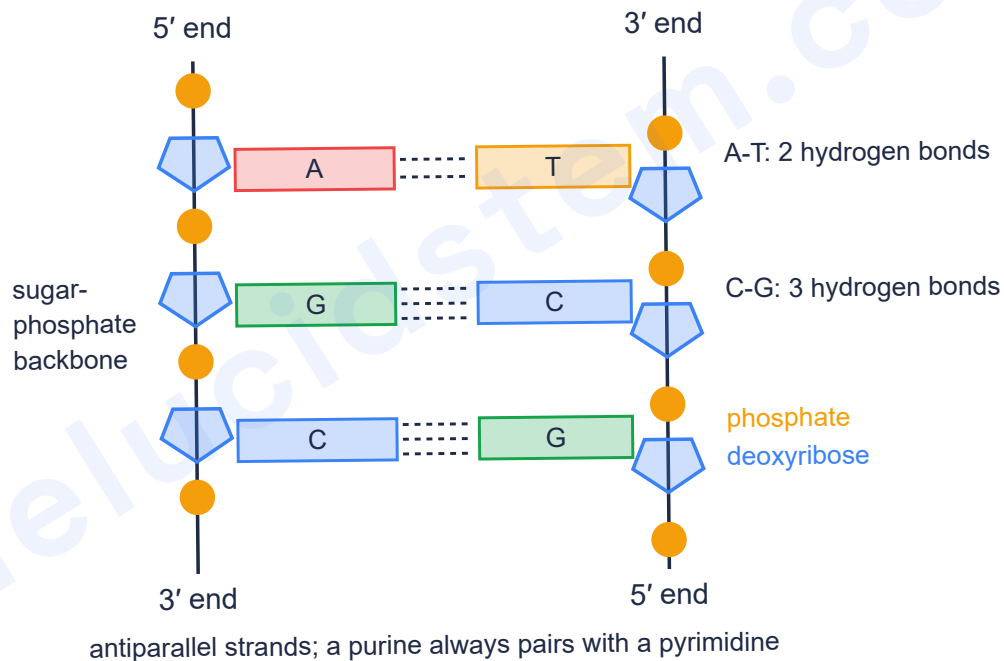


Fig. 1: a short length of DNA, untwisted; the two sugar-phosphate backbones run in opposite directions and the bases pair inside

Sugar, base, bond.

- ✓ **Purines** (A, G) double ring; **pyrimidines** (C, T, U) single ring.
- ✓ **Phosphodiester bonds** within a strand; **hydrogen bonds** between strands.
- ✓ **A-T: 2** hydrogen bonds; **C-G: 3**.
- ✓ **Antiparallel:** 5' to 3' alongside 3' to 5'.

Watch out!

Do not say thymine is a purine because it pairs with adenine.

Pairing tells you nothing about the class: every pair is one of each.

Learn the ring count instead (memory aid: *pure As Gold*): adenine and guanine are the double-ringed **purines**; C, T and U are single-ringed **pyrimidines**.

Antiparallel does not just mean the strands are side by side. It means they run in **opposite directions**: where one strand has its 5' end, the other has its 3' end.

2 Semi-conservative replication of DNA

Syllabus 6.1

DNA is copied during the **S phase** of the cell cycle. The hydrogen bonds between bases break and the double helix unwinds, so each strand is exposed as a **template**. Free DNA nucleotides pair with the exposed bases by **complementary base pairing** (A with T, C with G). **DNA polymerase** joins the new nucleotides by forming **phosphodiester bonds**, but it can add nucleotides **only to the 3' end** of a growing strand, so new DNA is always built in the **5' to 3' direction**. On one template the new strand grows towards the replication fork **continuously** (the **leading strand**); on the other it must grow away from the fork, in **short fragments** (the **lagging strand**), which **DNA ligase** joins with phosphodiester bonds. Each daughter molecule has one original and one new strand: replication is **semi-conservative**.

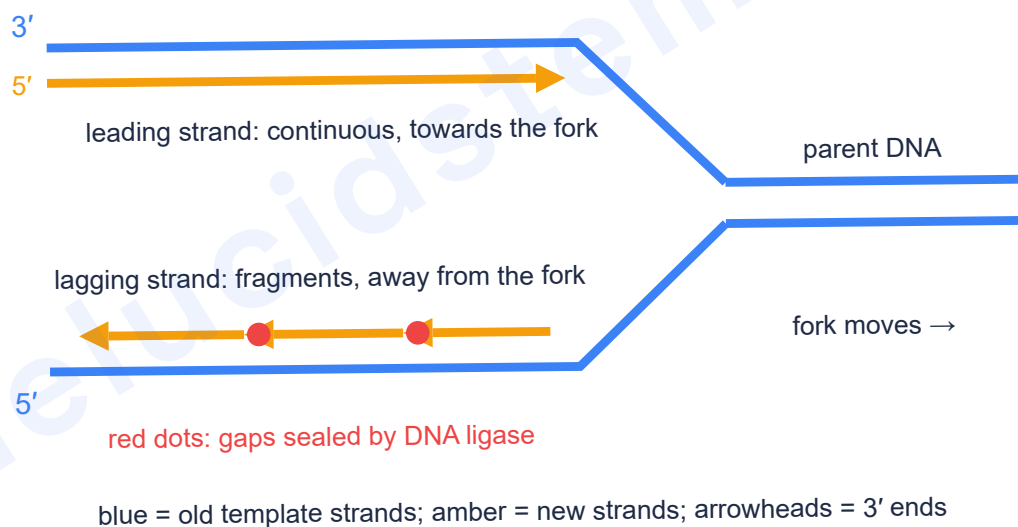


Fig. 1: a replication fork; new DNA grows only 5' to 3', so one new strand is continuous and the other is made in fragments

Template, polymerase, ligase.

- ✓ **Semi-conservative:** each new molecule = one old strand + one new.
- ✓ **DNA polymerase** builds new strands 5' to 3' only.
- ✓ **Leading:** continuous. **Lagging:** fragments joined by **DNA ligase**.
- ✓ **Both enzymes** make phosphodiester bonds; hydrogen bonds form by pairing.

Watch out!

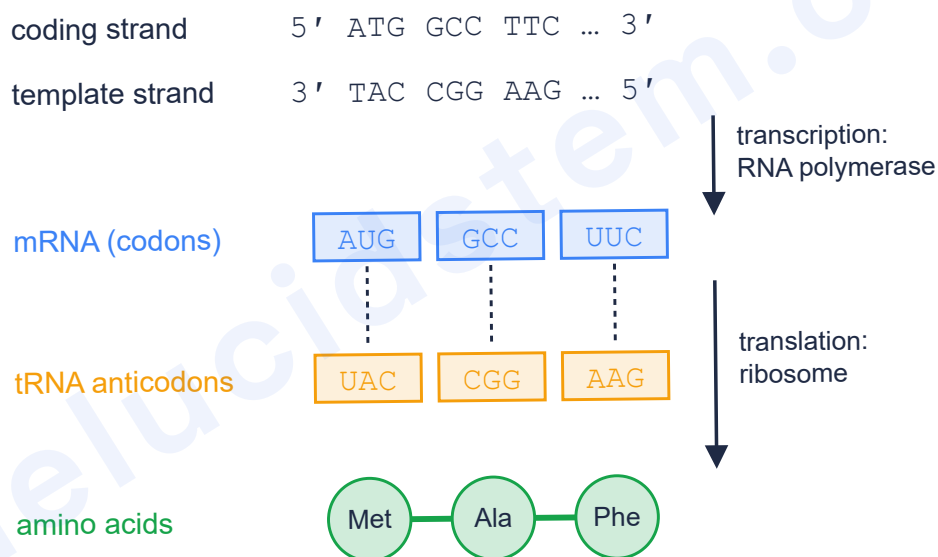
Do not say DNA polymerase builds the lagging strand 3' to 5'. It **never** does: both new strands are made 5' to 3'. The lagging strand is in fragments precisely because its 5' to 3' direction points away from the fork.

The intermediate band never disappears in later generations: the two original heavy strands are kept, so there are always exactly two hybrid molecules. Only their **proportion** halves each generation.

3 Transcription and translation

Syllabus 6.2

A **polypeptide** is coded for by a **gene**, a sequence of nucleotides forming part of a DNA molecule. The **genetic code** is a **triplet** code: each group of three bases codes for one amino acid, or acts as a **start** or **stop** signal, and it is **universal** (the same in almost all organisms). In **transcription**, in the nucleus, **RNA polymerase** separates the strands of the gene and builds **mRNA** complementary to the **template (transcribed) strand**; the other is the **non-transcribed strand**. In eukaryotes the **primary transcript** is modified: **introns** (non-coding) are removed and **exons** (coding) are joined. In **translation**, at a **ribosome** in the cytoplasm, each **tRNA** carries a specific amino acid and has an **anticodon** complementary to an mRNA **codon**. Starting at AUG, amino acids are joined by **peptide bonds** until a **stop codon** is reached.



mRNA = coding strand with U for T; one codon, one amino acid

Fig. 1: the first three codons of the gene in the lab, from DNA to mRNA to tRNA to amino acids

Template, codon, anticodon.

- ✓ **mRNA** = complement of the **template** strand = coding strand with U for T.
- ✓ **Anticodon** on tRNA is complementary to the **codon** on mRNA.
- ✓ **Start** AUG (Met); **stop** codons have no tRNA.
- ✓ **Introns** removed, **exons** joined, before mRNA leaves the nucleus.

Watch out!

mRNA is complementary to the **template** strand, not to the coding strand. So the mRNA reads the same as the coding (non-transcribed) strand, with U instead of T. If you are given the template strand, pair every base and swap T for U.

Remember which is which: **exons** are **expressed** (they stay in the mRNA); **introns** are **in the way** (they are removed). It is the RNA that is edited, not the DNA: the introns stay in the gene.

4 Gene mutations

Syllabus 6.2

A **gene mutation** is a change in the **sequence of base pairs** in a DNA molecule that **may** result in an altered polypeptide. In a **substitution** one base pair is replaced by another, so only **one codon** changes: because the code is **degenerate** it may still code for the same amino acid (no effect), it may code for a different amino acid (as in **sickle cell anaemia**, where glutamic acid becomes valine in β -globin), or it may become a **stop codon** (a shortened polypeptide). A **deletion** or **insertion** of one nucleotide causes a **frameshift**: every codon after the mutation is read differently, so many amino acids change and a stop codon often appears early. The polypeptide usually folds wrongly and cannot function.

original

AUG GUG CAC CUG ACU CCU
Met-Val-His-Leu-Thr-Pro

substitution

AUG GUG CAC CUG ACU **CAU**
Met-Val-His-Leu-Thr-His

deletion

AUG GUG CAC **CGA** CUC CUG
Met-Val-His-Arg-Leu-Leu

mRNA read in
triplets from AUG

one codon changed:
at most one amino acid

frameshift: every codon
after the deleted U changes

red = changed; an insertion also shifts the reading frame

Fig. 1: the start of the β -globin mRNA after a substitution and after a deletion; only the deletion shifts the reading frame

Codon, frame, function.

- ✓ **Gene mutation** = change in DNA base sequence; may alter the polypeptide.
- ✓ **Substitution** changes one codon: same, different or stop.
- ✓ **Deletion / insertion** of one base: frameshift.
- ✓ **Explain effects** via primary structure, folding and function.

Watch out!

Do not write that a mutation is a change in an amino acid or in a protein. A **gene mutation** is a change in the **DNA base sequence**; a changed polypeptide is a possible **consequence**.

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