A-LEVEL BIOLOGY • EXERCISE SHEET

6.2 Protein synthesis

Name: _____ Class: _____ Date: _____ **Total: 17 marks**

KEY WORDS gene 基因 • triplet 三联体 • mutation 突变 • intron 内含子 • translation 翻译

Objective

Build the skills to answer exam questions on **protein synthesis** — the **genetic code** 遗传密码, **transcription** 转录 and **translation** 翻译, splicing, and **gene mutations** 基因突变.

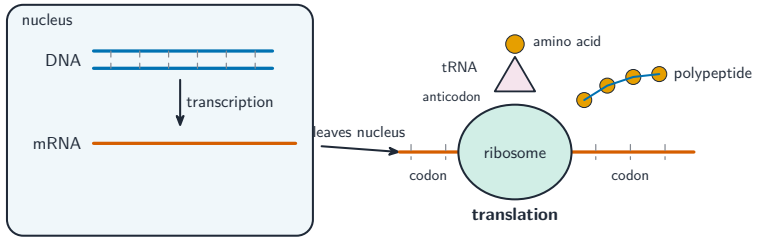
You must be able to:

- describe the universal triplet code and the roles of RNA polymerase, mRNA, codons, tRNA, anticodons and ribosomes
- work out an mRNA sequence and amino acids from a DNA template
- explain splicing (introns/exons) and the effects of substitution, deletion and insertion mutations

1 Worked examples

The genetic code and protein synthesis

A **gene** 基因 is a DNA sequence coding for one **polypeptide** 多肽. The code is read in **triplets** 三联体 (three bases): each codes one amino acid or a start/stop signal. It is **universal**.



Transcription (nucleus) → mRNA → translation (ribosome) → polypeptide

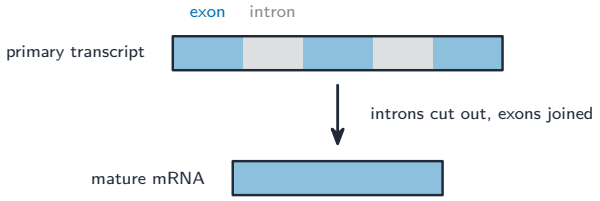
- **transcription** — **RNA polymerase** copies the DNA **template strand** 模板链 into mRNA (uracil pairs with adenine).
- **translation** — at the **ribosome** 核糖体, mRNA is read in **codons** 密码子; **tRNA** 转运 RNA brings amino acids whose **anticodon** 反密码子 pairs with the codon; amino acids join by peptide bonds.

Reading the code from a DNA template

To find the amino acids, copy the template into mRNA (A→U, T→A, C→G, G→C), then read the mRNA codons. Example: DNA template `TAC` → mRNA codon `AUG` (the start codon, methionine); the tRNA anticodon is `UAC`.

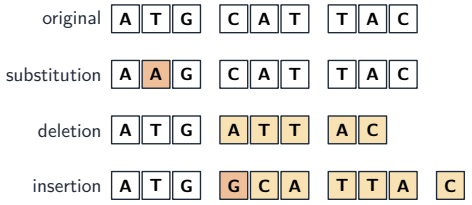
Splicing

In eukaryotes the **primary transcript** 初级转录本 has coding **exons** 外显子 and non-coding **introns** 内含子. The introns are removed and exons joined to make the finished mRNA.



Splicing removes introns and joins exons

Mutations



red = changed base; shaded = shifted by a frameshift (deletion or insertion)

A substitution changes one triplet; a deletion or insertion shifts every later triplet (a frameshift)

- **substitution** 替换 — one base swapped; changes at most one amino acid (sometimes none).
- **deletion** 缺失 / **insertion** 插入 — shifts how every later triplet is read (a **frameshift**), usually changing many amino acids.

2 Practice

2.1 Name the molecule that (a) carries the code from the nucleus to the ribosome, and (b) brings amino acids to the ribosome. [2]

2.2 Complete the table for this DNA template strand. [3]

DNA template	mRNA codon	tRNA anticodon
T A C		
C G A		

3 Exam-style questions

3.1 What is a codon? [1]

- **A** a triplet of DNA bases on the template strand
- **B** a triplet of mRNA bases coding for one amino acid
- **C** a tRNA molecule
- **D** an enzyme that builds mRNA

3.2 Which type of mutation is most likely to change **every** amino acid after the point of mutation? [1]

- **A** a substitution
- **B** a deletion of one base
- **C** no mutation changes later amino acids
- **D** a substitution at the start codon

3.3 (a) Describe what happens during transcription. [3]

(b) Explain the roles of tRNA and the ribosome during translation. [3]

3.4 (a) Explain why a substitution mutation sometimes has no effect on the polypeptide. [2]

(b) Explain why removing introns is necessary before translation. [2]

Solutions

2.1 (a) messenger RNA (mRNA); (b) transfer RNA (tRNA).

2.2 `TAC` → mRNA `AUG` → anticodon `UAC`; `CGA` → mRNA `GCU` → anticodon `CGA`.

3.1 B. A codon is a triplet of mRNA bases coding for one amino acid (or stop).

3.2 B. A deletion causes a frameshift, changing every later triplet.

3.3 (a) RNA polymerase binds and the DNA unwinds at the gene; free RNA nucleotides pair with the template strand (A with U); they are joined into mRNA, which leaves the nucleus.
(b) each tRNA brings a specific amino acid and its anticodon pairs with the matching mRNA codon; the ribosome moves along the mRNA and joins the amino acids by peptide bonds in order.

3.4 (a) most amino acids are coded by more than one triplet, so the changed triplet may still code for the same amino acid.
(b) introns are non-coding; if left in they would be translated into wrong/extra amino acids, giving a faulty polypeptide.