1.11 DNA, replication and the genetic code

Name: _____ Class: _____ Date: _____ **Total: 22 marks**

KEY WORDS mononucleotide • phosphodiester bond • semi-conservative • triplet code • degenerate

Objective

Practise statements 2.9–2.12: nucleotide structure, the double helix, semi-conservative replication with its Meselson–Stahl evidence, genes and the triplet code.

1 Key knowledge and worked examples

■ From nucleotide to double helix

A **mononucleotide** = pentose sugar (deoxyribose in DNA, ribose in RNA) + phosphate + nitrogenous base. Condensation between phosphate and sugar of neighbours makes a strand of **phosphodiester bonds**. DNA: two **antiparallel** strands, A=T (two hydrogen bonds) and G≡C (three), twisted into a double helix 2 nm wide, 0.34 nm per base pair.

■ Semi-conservative replication

Helicase breaks the hydrogen bonds and unzips; each old strand is a template; **DNA polymerase** DNA links free nucleotides in the 5'→3' direction; each new double helix is half old, half new.

■ Meselson and Stahl in one line each

After one generation in ^{14}N: all DNA one intermediate band (rules out conservative – that would keep a heavy band). After two: half intermediate, half light (rules out dispersive – that would give only intermediate). Semi-conservative is the survivor.

■ The code

A gene is a sequence of bases coding for one polypeptide's amino-acid sequence. The code is a **triplet code** (3 bases = 1 amino acid), **non-overlapping**, **degenerate** (most amino acids have several codons), read from a start codon to a stop codon.

■ **Worked example: base counting**

A DNA molecule is 15 % adenine. A=T, so T = 15 %; A+T = 30 %, so G+C = 70 %, and G = C = 35 %. If a protein has 120 amino acids, the coding region (with stop) is $121 \times 3 = 363$ base pairs.

2 Practice

2.1 Name the three components of a mononucleotide and the bond joining nucleotides in a strand. [2]

2.2 Explain why the two strands of DNA are described as antiparallel and complementary. [2]

2.3 State what is meant by a degenerate code and one consequence of degeneracy. [2]

3 Exam-style questions

3.1 DNA from bacteria grown for many generations in ^{15}N is mixed into a centrifuge tube with DNA from bacteria grown in ^{14}N only, alongside DNA from bacteria shifted to ^{14}N for exactly one and exactly two rounds of division. State how many bands appear in each sample and where each lies (heavy, intermediate, light), and explain which replication models each result excludes. [6]

3.2 A section of a coding (sense) DNA strand reads ATG GGT TTA CCG. Write the sequence of the template strand, the mRNA transcribed from it, and the first two anticodons that pair with that mRNA. [5]

3.3 A mutation changes the sixth base of a gene from C to A. Explain why this substitution may have no effect on the protein, and contrast this with the likely effect of deleting the sixth base entirely. [5]

Solutions

Original-task marking: M1 method, A1 accuracy, B1 reasoning.

2.1 Pentose sugar, phosphate group, nitrogenous base; phosphodiester bonds between sugar and phosphate of adjacent nucleotides.

2.2 The sugar-phosphate backbones run in opposite directions (one 5'→3', the other 3'→5') – antiparallel; each strand's base sequence determines the other's exactly (A with T, G with C) – complementary.

2.3 Most amino acids are coded for by more than one triplet; many base substitutions change nothing because the new triplet still codes for the same amino acid.

3.1 ^{15}N-only: one heavy band; ^{14}N-only: one light band. One round: a single intermediate band – excludes conservative replication, which would give heavy plus light bands. Two rounds: half intermediate and half light – excludes dispersive replication, which would give only intermediate.

3.2 Template: TAC CCA AAT GGC. mRNA (from template): AUG GGU UUA CCG. First two anticodons pair with AUG and GGU: UAC and CCA.

3.3 Degeneracy: the new triplet may still code for the same amino acid, or for one with similar chemistry, leaving the protein functional. Deleting a base shifts the reading frame: every triplet from that point on is read differently, usually producing a completely different – and often prematurely stopped – amino-acid sequence.