

AS Level Biology

Topic 6: Genetic Information, Variation and Biodiversity

AQA Biology (7401)

Mark Scheme

100 marks

Instructions

- Answer **all** questions.
- In calculations show your working and give your answer to an appropriate number of significant figures.
- In extended-response questions you should write in clear, well-organised continuous prose.
- There are 18 questions in this paper. The total mark is **100**.

1. This question is about genes and the genetic code.

- (a) Define the term *gene*. (2)
- ✓ a sequence of (DNA) bases / nucleotides (1)
- ✓ that codes for the (amino acid sequence of a) polypeptide / a functional RNA (1)
- (b) State what is meant by a *codon*. (1)
- ✓ a sequence of three (DNA/mRNA) bases that codes for one amino acid (1)
- (c) The genetic code is described as degenerate. Explain what this means. (1)
- ✓ most amino acids are coded for by more than one (triplet/codon) (1)
- (d) The genetic code is also described as non-overlapping and universal. Explain what each term means. (2)
- ✓ non-overlapping: each base is part of only one triplet/codon (read in sequence) (1)
- ✓ universal: the same triplet codes for the same amino acid in (almost) all organisms (1)

2. This question is about the structure of a gene and a chromosome.

- (a) State what is meant by an *allele*. (1)
- ✓ a different version/form of a gene (1)
- (b) In eukaryotes, a gene contains coding and non-coding sequences. Name the parts that code for the polypeptide and the parts that do not. (2)
- ✓ exons code for the polypeptide (1)
- ✓ introns are non-coding (1)
- (c) State what is meant by the term *genome*. (1)
- ✓ the complete set of genes / all the DNA in a cell (of an organism) (1)
- (d) State what is meant by the term *proteome*. (1)
- ✓ the full range of proteins that a cell (or organism) is able to produce (1)

3. This question is about transcription, the first stage of protein synthesis.

(a) State where in a eukaryotic cell transcription takes place. (1)

✓ (in) the nucleus (1)

(b) Describe the process of transcription to produce pre-mRNA. (4)

✓ DNA helicase / the enzyme breaks the hydrogen bonds and the two strands of DNA separate (1)

✓ one strand acts as a template (1)

✓ free RNA nucleotides line up by complementary base pairing with the template strand (1)

✓ RNA polymerase joins the RNA nucleotides together to form pre-mRNA (1)

(c) In eukaryotes, the pre-mRNA is modified before leaving the nucleus. Describe this process of splicing. (2)

✓ the introns (non-coding sections) are removed (1)

✓ the exons (coding sections) are joined together to form mature mRNA (1)

4. This question is about translation, the second stage of protein synthesis.

(a) State where in the cell translation takes place. (1)

✓ (at the) ribosomes (1)

(b) Describe the role of transfer RNA (tRNA) in translation. (3)

✓ each tRNA carries a specific amino acid (1)

✓ the anticodon on the tRNA is complementary to / pairs with a codon on the mRNA (1)

✓ this brings the amino acids together in the correct order / sequence (1)

(c) Describe how a polypeptide is assembled during translation. (3)

✓ the ribosome moves along the mRNA, reading the codons (1)

✓ tRNA molecules bring amino acids that pair (by anticodon-codon) to the ribosome (1)

✓ peptide bonds form between adjacent amino acids (using ATP) to build the polypeptide (1)

5. A short section of the template (antisense) strand of DNA has the base sequence: TAC GGA TTC.

(a) Write the base sequence of the mRNA transcribed from this template strand. (2)

✓ AUG CCU AAG (1)

✓ (correct use of U instead of T and correct complementary bases) (1)

(b) State the anticodon of the tRNA molecule that would pair with the first mRNA codon (AUG). (1)

✓ UAC (1)

(c) State how many amino acids would be coded for by this section of mRNA. (1)

✓ 3 (one per codon/triplet) (1)

6. This question is about gene mutation.

(a) State what is meant by a *gene mutation*. (1)

✓ a change in the (sequence of) bases / nucleotides (in DNA) (1)

(b) A substitution mutation changes one base for another. Explain why a substitution mutation may have no effect on the polypeptide produced. (2)

✓ the genetic code is degenerate / more than one triplet codes for the same amino acid (1)

✓ so the new triplet may still code for the same amino acid (1)

(c) Explain why a deletion mutation usually has a greater effect on the polypeptide than a substitution mutation. (3)

✓ a deletion causes a frame shift (all the triplets after it are read differently) (1)

✓ so many/all of the amino acids after the mutation are changed (1)

✓ the polypeptide produced has a very different primary structure / shape, so may not function (1)

7. This question is about meiosis and genetic variation.

(a) State the type of cells produced by meiosis and their chromosome number compared to the parent cell. (2)

✓ gametes / sex cells (1)

✓ haploid / half the number of chromosomes of the parent cell (1)

(b) Describe how independent segregation of homologous chromosomes during meiosis produces genetic variation. (3)

✓ homologous chromosomes (pairs) line up randomly at the equator (1)

✓ either chromosome of a pair can go to either pole / different combinations are possible (1)

✓ this produces gametes with different combinations of (maternal and paternal) chromosomes/alleles (1)

(c) Describe how crossing over during meiosis increases genetic variation. (2)

✓ sections of (non-sister) chromatids are exchanged between homologous chromosomes (1)

✓ producing new combinations of alleles (on the chromosomes) (1)

8. A diploid organism has a diploid number of 8 (4 homologous pairs).

(a) Calculate the number of different combinations of chromosomes possible in the gametes due to independent segregation alone. Show your working. (2)

✓ number of combinations = 2^n where n = number of homologous pairs = 4 (1)

✓ $2^4 = 16$ (1)

(b) State two further sources of genetic variation in sexually reproducing organisms, in addition to independent segregation. (2)

✓ crossing over (during meiosis) (1)

✓ random fertilisation (random fusion of gametes) (1)

9. This question is about variation within and between species.

(a) Explain how genetic factors can cause variation within a species. (2)

- ✓ individuals have different alleles (genes) (1)
- ✓ arising from mutation / meiosis / random fertilisation (sexual reproduction) (1)

(b) Explain how the environment can cause variation within a species. (1)

- ✓ environmental conditions (e.g. diet, light, temperature) affect characteristics / how genes are expressed (1)

(c) A student wanted to investigate the variation in leaf length of a species of plant in a field. (3)

Explain why the student should take a large, random sample.

- ✓ a random sample avoids bias (so the sample represents the population) (1)
- ✓ a large sample reduces the effect of chance / anomalies (1)
- ✓ so the mean is more reliable / a statistical test can be used (1)

10. This question is about the principles of classification.

(a) State what is meant by a *species*. (2)

- ✓ a group of (similar) organisms able to breed together (1)
- ✓ to produce fertile offspring (1)

(b) Name the system of naming species using two names, and state what the two names represent. (2)

- ✓ the binomial system (1)
- ✓ the first name is the genus and the second name is the species (1)

(c) List the eight taxonomic groups (taxa) used in classification, in order from the largest to the smallest. (2)

- ✓ domain, kingdom, phylum, class (1)
- ✓ order, family, genus, species (1)

11. This question is about how scientists classify organisms and clarify evolutionary relationships.

(a) Explain what is meant by a *phylogenetic* classification. (2)

- ✓ it classifies organisms according to their evolutionary relationships / common ancestry (1)
- ✓ groups are arranged into a hierarchy reflecting how recently they shared a common ancestor (1)

(b) Scientists now compare the DNA base sequences and amino acid sequences of different species to study their evolutionary relationships. Explain how comparing DNA base sequences can show how closely related two species are. (3)

- ✓ the more similar the DNA base sequences, the more closely related the species (1)
- ✓ because the species share a more recent common ancestor (1)
- ✓ differences/mutations accumulate over time, so more differences indicate a longer time since they diverged (1)

(c) Suggest why comparing amino acid sequences of a protein can also be used to investigate evolutionary relationships. (2)

- ✓ the amino acid sequence is determined by the DNA base sequence (1)
- ✓ so more similar amino acid sequences indicate more similar DNA / a closer relationship (1)

12. This question is about biodiversity and species diversity.

(a) State what is meant by the term *biodiversity*. (1)

✓ the variety/range of living organisms (in an area) / genes / habitats (1)

(b) Explain why species diversity is a better measure of biodiversity than simply counting the number of species present. (2)

✓ species diversity takes into account the number of individuals of each species (as well as the number of species) (1)

✓ so it shows how evenly the organisms are distributed / not just species richness (1)

(c) Explain why an ecosystem with a higher species diversity is generally more stable. (2)

✓ there are more food sources / more complex food webs (1)

✓ so the ecosystem is less affected if one species is lost / changes occur (1)

13. The index of diversity (d) can be calculated using the formula $d = N(N - 1) / \sum n(n - 1)$, where N is the total number of organisms of all species and n is the number of organisms of each species.

(a) In a sample, there are 3 species. Species A has 5 organisms, species B has 3 organisms and species C has 2 organisms. Calculate the total number of organisms, N . (1)

✓ $N = 5 + 3 + 2 = 10$ (1)

(b) Calculate the value of $\sum n(n - 1)$ for this sample. Show your working. (2)

✓ $(5 \times 4) + (3 \times 2) + (2 \times 1) = 20 + 6 + 2$ (1)

✓ $= 28$ (1)

(c) Hence calculate the index of diversity, d , for this sample. Give your answer to 2 decimal places. (2)

✓ $d = (10 \times 9) / 28 = 90 / 28$ (1)

✓ $= 3.21$ (1)

14. This question is about the effect of farming and human activity on biodiversity.

(a) Explain how clearing land to grow a single crop (monoculture) reduces biodiversity. (2)

✓ habitats are destroyed / a variety of plant species is replaced by one species (1)

✓ so fewer species (and food sources) are present, lowering the diversity (1)

(b) Suggest two farming practices that could help to conserve biodiversity. (2)

✓ maintain/plant hedgerows or woodland / leave field margins (1)

✓ reduce pesticide/herbicide use / use crop rotation / plant a variety of crops (any one) (1)

(c) Explain why there is often a conflict between conservation of biodiversity and the need to produce enough food. (2)

✓ conservation practices may reduce the area or efficiency of food production / lower crop yields (1)

✓ but high food production (e.g. monoculture, pesticides) reduces biodiversity (so a balance/compromise is needed) (1)

15. This question is about genetic diversity and natural selection.

(a) State what is meant by the term *genetic diversity*. (1)

✓ the number of different alleles (of genes) in a population (1)

(b) Explain how natural selection can lead to a change in the allele frequency in a population over time, using the example of antibiotic resistance in bacteria. (4)

✓ there is variation in the population due to (random) mutation, e.g. some bacteria have an allele for antibiotic resistance (1)

✓ when the antibiotic is present, the resistant bacteria survive (have a selective advantage) while non-resistant bacteria die (1)

✓ the surviving (resistant) bacteria reproduce and pass on the allele for resistance to their offspring (1)

✓ so over time the frequency of the resistance allele increases in the population (1)

(c) Explain why a population with a greater genetic diversity is more likely to survive a change in the environment. (2)

✓ there is a greater range of alleles, so a greater range of characteristics/phenotypes (1)

✓ so some individuals are more likely to have a (favourable) allele/characteristic allowing them to survive and reproduce (1)

16. This question is about types of natural selection.

(a) Describe the effect of *directional* selection on a characteristic in a population. (2)

✓ individuals with an extreme phenotype (one end of the range) are more likely to survive and reproduce (1)

✓ so the mean of the characteristic shifts in that direction over time (1)

(b) Describe the effect of *stabilising* selection on a characteristic in a population. (2)

✓ individuals with the modal/average phenotype are favoured (more likely to survive and reproduce) (1)

✓ extreme phenotypes are selected against, so variation is reduced (the mean stays the same) (1)

17. This question is about courtship behaviour as an adaptation.

(a) Explain how courtship behaviour increases the probability of successful mating and reproduction. (2)

✓ it allows individuals to recognise members of their own species (so mating produces fertile offspring) (1)

✓ it allows recognition of a mate of the opposite sex / that is sexually mature and receptive / forms a pair bond to synchronise mating (1)

(b) Adaptations of organisms can be anatomical, physiological or behavioural. State which type of adaptation courtship behaviour is, and give one example of a physiological adaptation. (2)

✓ courtship is a behavioural adaptation (1)

✓ example of a physiological adaptation: e.g. producing venom / a high concentration of an enzyme / hibernation involving metabolic change (any one suitable) (1)

18. A student used the mark-release-recapture method to estimate the population size of a species of beetle in a field. The estimate is given by: $\text{population} = (\text{number in first sample} \times \text{number in second sample}) / \text{number marked in second sample}$.

(a) In the first sample, 40 beetles were caught and marked. In the second sample, 50 beetles were caught, of which 8 were marked. Calculate the estimated population size. Show your working. **(2)**

✓ $\text{population} = (40 \times 50) / 8 = 2000 / 8$ (1)

✓ $= 250$ (1)

(b) State two assumptions that must be made for this estimate to be valid. **(2)**

✓ the marked individuals mix randomly / fully with the rest of the population (1)

✓ there is no significant migration, birth or death between the two samples / marking does not affect survival (any one) (1)