HELICATE · AS AND A-LEVEL BIOLOGY · TOPIC BANK

3.4.7 Investigating diversity

Mark scheme

Version 2 · 15 October 2026

TOTAL MARKS	QUESTIONS
53	6

How to use this mark scheme

;	Separates marking points. Each semicolon marks the end of one creditable point, and each point is worth one mark.
;;	Two marks for this answer (used for calculations).
/	Alternative words or phrases that are credited for the same point.
OR	An alternative answer for the same mark.
( )	Words in brackets are not needed to gain the mark.
max	More marking points are listed than marks available. Award up to the number of marks shown.
Accept	An alternative answer that gains credit.
Reject	A wrong answer. It does not gain credit and cancels a correct point it contradicts.
Ignore	Neither credited nor penalised. Mark the rest of the answer.
ECF	Error carried forward: credit correct working that uses an earlier wrong answer.
AO	Assessment objective: AO1 knowledge and understanding; AO2 applying knowledge; AO3 analysing, interpreting and evaluating.

Where an answer is correct but not listed, credit it if it is biologically accurate and answers the question at the depth the marks require. Right + wrong = wrong: a contradiction cancels a correct point.

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Ways of comparing genetic diversity 3.4.7

Question	Marking guidance	Mark	Comments
01.1	Comparing the number of different species in the habitat of each population;	**1** (1 × AO1)	

Question	Marking guidance	Mark	Comments
01.2	Correct answer for 2 marks: 54 (%);; Accept for 1 mark: 57.5 (%) **and** 3.5 (%)	**2** (2 × AO2)	**Accept** 'percentage points' as the unit **Reject** 85 (difference in numbers of fish) for 2 marks

Question	Marking guidance	Mark	Comments
01.3	1. (The) base sequence of DNA; 2. (The) base sequence of mRNA; 3. (The) amino acid sequence of (the same/named) proteins/polypeptides;	**2 max** (2 × AO1)	1. and 2. 'Base' must be given; penalise a missing 'base' once only 1. and 2. Accept nucleotide sequence for base sequence 3. The protein/polypeptide must be named or implied; 'amino acid sequence' alone is not enough **Accept** DNA hybridisation or immunological comparison of proteins, but neither is required **Reject** 'comparing the DNA', 'genes' or 'the genetic code' unqualified **Ignore** other observable/measurable characteristics

Question	Marking guidance	Mark	Comments
01.4	1. (Before gene technology) differences in DNA were inferred from (the frequency of) measurable/observable characteristics, eg plate form; 2. (Now) DNA base sequences are investigated/compared directly OR DNA/genome sequencing is used; 3. So (more) differences in DNA can be detected, including those that do not affect observable characteristics;	**2 max** (2 × AO1)	2. **Accept** mRNA (base) sequencing or amino acid sequencing **Ignore** 'better/more advanced technology' unqualified **Ignore** details of how DNA is sequenced (not required) **Reject** electron microscopy as the change

Question	Marking guidance	Mark	Comments
01.5	1. Plate form may (also) be affected by the environment, so differences in plate form may not be (only) genetic; 2. Plate form shows differences in only one/a few gene(s), but DNA sequencing can compare many genes/the genome; 3. Different base sequences/alleles can give the same plate form, eg recessive alleles are hidden, (base) changes in non-coding DNA/introns, degenerate code;	**2 max** (2 × AO2)	2. **Accept** 'plate form is only one characteristic' 3. **Accept** 'some differences in DNA have no effect on plate form' **Ignore** 'DNA sequencing is more accurate/reliable/modern' unqualified

Using sequence data to suggest relationships 3.4.7

Question	Marking guidance	Mark	Comments
02.1	Correct answer for 2 marks: 85 (%);; Accept for 1 mark: 6 (positions) differ OR 34 (positions) are the same	**2** (2 × AO2)	**Reject** 25 (%) (only the 8 listed positions used) for 2 marks; award 1 mark if 6 differences are shown **Reject** 15 (%) (percentage that differ) for 2 marks; award 1 mark

Question	Marking guidance	Mark	Comments
02.2	Species **T**;	**1** (1 × AO2)	Differences from S: P 6, Q 4, R 4, T 2

Question	Marking guidance	Mark	Comments
02.3	1. (Genetic) code is degenerate OR more than one triplet codes for the same amino acid; 2. So a different base/a (base) substitution can give a (different) triplet that codes for the same amino acid; 3. Differences may be in introns, which are non-coding/removed (so do not affect the amino acid sequence);	**2 max** (2 × AO2)	1. and 2. Accept codon for triplet 2. **Reject** 'the same amino acid is produced' unless linked to the triplet coding for it 3. **Reject** 'introns code for amino acids'

Question	Marking guidance	Mark	Comments
02.4	1. S and T differ at only 2 positions, fewer than either differs from P, Q or R (so the data support the conclusion); 2. Only a (short) section/40 amino acids of one protein was compared; 3. Only one beetle of each species was used OR variation within each species is not known; 4. Amino acid sequences do not show all differences in base sequence (as shown by Q and R); 5. Should compare (base sequences of) more genes/proteins OR the whole protein/gene;	**3 max** (3 × AO3)	1. **Accept** a correct pair of counts from the table, eg 'S and T differ at 2 but S and Q at 4' 1. **Accept** 'more recent common ancestor' for more closely related 3. **Ignore** 'sample size too small' unqualified 5. **Reject** using a species shown in the table as an improvement

Question	Marking guidance	Mark	Comments
03.1	33.6;	**1** (1 × AO2)	**Accept** 34

Question	Marking guidance	Mark	Comments
03.2	To avoid bias OR so the sample is representative (of the population);	**1** (1 × AO1)	**Accept** 'so results are reliable' only if linked to the population/representative **Ignore** 'fair test'

Question	Marking guidance	Mark	Comments
03.3	1. To find the (genetic) variation within a population/species; 2. So they can tell whether differences between populations are greater than differences within a population OR whether differences between populations are significant/not (likely to be) due to chance;	**2** (2 × AO2)	2. **Reject** 'to see if the results are significant'

Question	Marking guidance	Mark	Comments
03.4	1. Mainland with mainland 0.3–1.5 **and** mainland with island A 0.5–1.7; 2. Ranges overlap, so the difference is not significant OR the difference is (likely to be) due to chance;	**2** (2 × AO2)	1. **Accept** ranges using 1.96 standard deviations: 0.31–1.49 and 0.51–1.69 2. **Accept** SD for standard deviation 2. **Reject** 'the results are not significant' or 'the results are due to chance' 2. **Accept** ECF for a correct conclusion from incorrect ranges

Question	Marking guidance	Mark	Comments
03.5	1. Mainland and island A lizards differ by 1.1% but mainland and island B lizards differ by 4.2%; 2. Mainland with island A (0.5–1.7) overlaps the within-population ranges (mainland/island A/island B), so there is no significant difference between them OR the difference is (likely) due to chance; 3. Mainland with island B (3.4–5.0) does not overlap with any within-population range OR with mainland with island A, so there is a significant difference OR the difference is (probably) not due to chance; 4. So island A lizards (probably) share a more recent common ancestor with mainland lizards (than island B lizards do); 5. Only one (section of one) gene/800 bases compared; 6. Only 15 lizards (from each population) sampled; 7. Mitochondrial DNA (only) compared, not nuclear DNA;	**4 max** (1 × AO2) (3 × AO3)	**Max 3** if no limitation (points 5–7) is given 2. and 3. Accept answers using standard deviations without doubling, if overlap is judged correctly 2. **Credit** comparison with any one of the within-population ranges 3. **Reject** 'results are significant' 6. **Ignore** 'sample size too small' unless the number of lizards is referred to

Investigating variation within a species 3.4.7

Question	Marking guidance	Mark	Comments
04.1	1. Choosing the largest flower heads is biased, so the mean would be too high/an overestimate; 2. Flower heads near the path may differ from the rest of the lawn (eg trampled) OR are not representative of the whole lawn; 3. Divide the lawn into a grid OR lay out two (long) tape measures at right angles (along two edges); 4. Use random numbers/a random number generator/calculator/computer/table to give coordinates; 5. Measure the flower head (of the daisy) nearest to each coordinate; 6. Random selection gives every flower head (on the lawn) an equal chance of being chosen, so there is no (selection) bias;	**5 max** (4 × AO1) (1 × AO3)	**Max 1** from points 1 and 2; max 4 from points 3–6 6. **Accept** 'so the sample is representative (of the whole lawn)' 1. **Accept** 'not representative because only large flower heads are chosen' **Reject** throwing quadrats (over the shoulder/at random) for point 4 **Reject** choosing sites at random for point 5 unless an individual flower head is then chosen at each coordinate **Ignore** 'repeat' or 'take more measurements' unqualified

Question	Marking guidance	Mark	Comments
04.2	1. Yes, because the running mean levels off/changes very little after about 20 flower heads; 2. So measuring more flower heads would not change the mean much OR the mean (of 15.3 mm) is reliable/representative;	**2** (2 × AO3)	1. **Accept** any number from 15 to 28 at which the running mean is described as levelling off 1. **Reject** numbers below 15 (the running mean is still falling) 1. **Accept** 'the running mean stays at about 15.3–15.5 mm after 20 flower heads'

Question	Marking guidance	Mark	Comments
04.3	The measurements are widely spread around the mean;	**1** (1 × AO1)	

Question	Marking guidance	Mark	Comments
04.4	1. Standard deviations/error bars do not overlap; 2. So the difference (in mean diameter) is significant OR the difference is not (likely to be) due to chance;	**2** (2 × AO2)	1. **Accept** SD for standard deviation 2. **Reject** 'the results are significant' or 'the results are not due to chance' 2. **Accept** 'meadow flower heads are significantly larger' **Ignore** comments on the size of the standard deviations **Accept** the same conclusion from mean ± 2 standard deviations (lawn 11.9–18.7, meadow 19.4–26.6; no overlap)

Question	Marking guidance	Mark	Comments
04.5	Correct answer for 2 marks: 50.3 (%);; Accept for 1 mark: (23.0 − 15.3) ÷ 15.3 × 100 **OR** 50.327 (not to three significant figures)	**2** (2 × AO2)	**Reject** 33.5 (%) (divided by the meadow mean) for 2 marks; award 1 mark only if the working is shown

Question	Marking guidance	Mark	Comments
04.6	1. The difference in mean diameter is significant/not due to chance (as standard deviations do not overlap); 2. But the difference may be caused by the environment, eg mowing/light/nutrients/trampling/competition, not by genes/alleles; 3. Diameter is only one (measurable/observable) characteristic; 4. Need to compare DNA base sequences OR grow (seeds from) both populations in the same conditions; 5. Only one lawn and one meadow were sampled; 6. The number of flower heads measured in the meadow is not given (so the meadow sample may be too small/unrepresentative);	**3 max** (3 × AO3)	1. **Reject** 'results are significant' 4. **Accept** compare base sequences of mRNA or amino acid sequences of proteins **Ignore** 'sample size too small' for the lawn (Figure 1 shows the running mean levelled off) 6. **Accept** 'the meadow sample may be too small'

Question	Marking guidance	Mark	Comments
05.1	1. Height: standard deviations overlap, so the difference is not significant/(probably) due to chance; 2. Root length (in zinc): standard deviations do not overlap, so the mine population has a significantly greater increase OR the difference is not due to chance; 3. Seed mass: standard deviations overlap, so the difference is not significant/(probably) due to chance;	**3** (3 × AO2)	Each point needs the overlap judgement **and** the conclusion about the difference **Accept** answers using mean ± 2 standard deviations; the conclusions are the same A single correct statement covering height **and** seed mass, eg 'for height and seed mass the standard deviations overlap, so these differences are not significant', gains points 1 and 3 **Reject** 'results are (not) significant' once only **Accept** SD for standard deviation

Question	Marking guidance	Mark	Comments
05.2	1. So differences in environment (eg soil/zinc/nutrients/light) do not affect the characteristics OR to control environmental variables; 2. So any (significant) difference between the populations is due to genetic differences/differences in alleles;	**2** (2 × AO3)	**Ignore** 'to make it a fair test' unqualified

Extended response: comparing two populations 3.4.7

Question	Marking guidance	Mark	Comments
06	1. Divide each woodland into a grid and use random numbers/a random number generator to give coordinates where beetles are collected; 2. Collect a large number (of beetles), eg 10 or more, from each population; 3. Random sampling avoids bias OR a large sample is representative/gives a reliable mean; 4. Find the base sequence of the same gene/section of DNA in each beetle; 5. Compare base sequences of beetles within each population **and** between the populations, eg percentage of bases that differ; 6. Calculate the mean (difference) and standard deviation (for each comparison); 7. If the standard deviations (of differences between populations and within populations) do not overlap, the difference is significant/not due to chance; 8. Compare more than one gene; 9. Use a non-lethal sample (eg a small tissue sample) and release the beetles, so the rare population is not reduced;	**6 max** (6 × AO1)	2. **Accept** many/multiple. Ignore 'several' 4. **Accept** comparing base sequences of mRNA or amino acid sequences of (named) proteins 7. **Accept** mean ± 2 standard deviations do not overlap **Max 5** if point 7 is not given (the question asks how significance is decided) 7. **Accept** use of a statistical test, eg Student's t-test, comparing the calculated value with the critical value at P = 0.05 7. **Reject** 'results are significant' **Accept** SD for standard deviation **Ignore** details of how DNA is extracted or sequenced **Reject** throwing quadrats for point 1

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