HELICATE · A-LEVEL BIOLOGY · TOPIC BANK

3.7.3 Evolution may lead to speciation

Mark scheme

Version 2 · 17 October 2026

TOTAL MARKS	QUESTIONS
57	8

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.

Variation and natural selection 3.7.3

Question	Marking guidance	Mark	Comments
01.1	39.4 (%);	**1** (1 × AO2)	Working: (142 − 86) ÷ 142 × 100 = 39.44 **Accept** 39 or 39.44 **Reject** 65.1 (increase calculated from group Q)

Question	Marking guidance	Mark	Comments
01.2	1. The plants in P and Q have the same genotype, so the difference in mean leaf length (142 mm and 86 mm) is caused by the environment (eg temperature/altitude/exposure); 2. Variation within group P (118–165 mm) OR within one group is also caused by the environment (eg differences in light/water/soil within the site);	**2** (2 × AO3)	1. **Accept** 'genetically identical/clones' for same genotype 1. Must link the difference between the groups to environment, not only state 'environment affects phenotype' 2. **Accept** 'the range in each group must be environmental because there is no genetic variation' **Reject** 'mutation' as the cause of either difference

Question	Marking guidance	Mark	Comments
01.3	1. Plants in R are genetically different from each other but plants in P are genetically identical, so R varies because of genetic and environmental factors (P only environmental); 2. The 40 parent plants (of group R) carry different alleles, which arose by mutation; 3. Crossing over (in meiosis) produces new combinations of alleles; 4. Independent segregation of homologous chromosomes (in meiosis) produces new combinations of alleles; 5. Random fertilisation of gametes;	**3 max** (2 × AO1) (1 × AO2)	**Max 2** if point 1 is not given 3. **Accept** recombination for crossing over 4. **Accept** independent assortment or random assortment 3 and 4. **Accept** 'meiosis' for one of these points if neither is given 5. **Accept** random mating or random fusion of gametes; do not accept 'fertilisation is random' without reference to gametes **Accept** epigenetic differences for one mark **Ignore** natural selection, genetic drift, isolation or speciation given as causes of variation Two versions of the same point gain one mark only Penalise 'gene' for 'allele' once

Question	Marking guidance	Mark	Comments
02.1	The frequency of allele R at site A increased;	**1** (1 × AO2)	Evolution is a change in allele frequency in a population; the other options do not describe a change in allele frequency.

Question	Marking guidance	Mark	Comments
02.2	1. Frequency of R increased at site A (0.12 to 0.34) but stayed about the same at site B, so the change is linked to DFTD (as a selection pressure); 2. Devils with allele R are more likely to survive DFTD/infection (because tumours grow more slowly); 3. (So devils with R are) more likely to reproduce OR have more offspring (before they die); 4. Pass on allele R to their offspring/the next generation; 5. So the frequency of allele R increases over (several) generations;	**4 max** (2 × AO1) (1 × AO2) (1 × AO3)	**Max 3** if Table 2 is not used 2 and 3. Must be in the context of DFTD or allele R 'Pass on allele R to offspring' = points 3 and 4 5. **Reject** 'more alleles' or 'the number of R alleles increases' for an increase in frequency **Reject** devils become immune/develop resistance during their lifetime **Reject** mutation caused by DFTD Penalise 'gene' for 'allele' once

Question	Marking guidance	Mark	Comments
02.3	Correct answer for 2 marks: (+)0.055 (per generation);; Accept for 1 mark: 0.22 ÷ 4 **OR** 0.0275 (change per year)	**2** (2 × AO2)	**Accept** 5.5×10^{-2} or 0.06 for 2 marks Working: 0.34 − 0.12 = 0.22; 8 ÷ 2 = 4 generations; 0.22 ÷ 4 = 0.055

Question	Marking guidance	Mark	Comments
02.4	1. (Random) mutation (of the gene/DNA) OR a change in the base sequence (before DFTD arrived); 2. Before DFTD, allele R gave no (selective) advantage OR was not selected for (so its frequency did not increase);	**2** (1 × AO1) (1 × AO2)	1. **Reject** mutation caused by DFTD/the disease, or mutation 'in order to' survive/adapt 2. **Accept** 'allele R may have been slightly disadvantageous' 2. **Accept** 'no selection pressure for R' Penalise 'gene' for 'allele' once

Types of selection 3.7.3

Question	Marking guidance	Mark	Comments
03.1	Disruptive selection, because birds with bills at both extremes of width were more likely to survive;	**1** (1 × AO2)	Percentage survival was highest in the narrowest (71%) and widest (83%) classes and lowest in the 13.0–13.4 mm class (14%).

Question	Marking guidance	Mark	Comments
03.2	Correct answer for 2 marks: 6.0;; Accept for 1 mark: 83.3(%) **and** 13.8(%) OR 10/12 ÷ 8/58 **OR** a correct answer not to 2 significant figures, eg 6.04	**2** (2 × AO2)	Plotted values: 14.5–14.9 mm: 12 juveniles, 10 survived; 13.0–13.4 mm: 58 juveniles, 8 survived 6 = 1 mark (not to 2 significant figures)

Question	Marking guidance	Mark	Comments
03.3	1. Birds with wide bills can crack/feed on the large, hard seeds OR birds with narrow bills feed (more efficiently) on the small, soft seeds; 2. Birds with intermediate bill widths are less efficient at feeding on either type of seed, so they get less food OR are outcompeted; 3. So birds with the narrowest and widest bills are more likely to survive and reproduce; 4. And pass on their alleles for narrow or wide bills (to offspring); 5. Frequency of alleles for extreme bill widths increases OR frequency of alleles for intermediate widths decreases; 6. (Over generations) two peaks/a bimodal distribution OR fewer birds with intermediate bill widths;	**4 max** (1 × AO1) (2 × AO2) (1 × AO3)	3. **Accept** 'selection for both extremes' OR 'selection against the middle/intermediate widths' for the idea of extreme birds surviving; 'disruptive selection' named alone gains no mark 2. **Accept** 'less competitive for food' **Max 3** if there is no reference to later generations (point 5 or 6) 5. **Reject** 'more alleles' for an increase in frequency **Reject** birds change their bills to suit the seeds Penalise 'gene' for 'allele' once

Genetic drift 3.7.3

Question	Marking guidance	Mark	Comments
04.1	1. Genetic drift; 2. (By) chance/randomly, which individuals reproduce OR which alleles are passed on (to the next generation) OR random sampling of alleles in each generation;	**2** (1 × AO1) (1 × AO2)	2. Must include the idea of chance or random **Accept** 'alleles passed on are not a perfect sample of the parents' alleles' for point 2 **Reject** natural selection, mutation or migration as the cause (excluded by the model)

Question	Marking guidance	Mark	Comments
04.2	1. In the population of 20, the frequency of A changed greatly/fell to 0 (by generation 40) **but** in the population of 2000 it stayed close to 0.5 (between 0.49 and 0.53); 2. In a small population, each individual/gamete carries a large proportion of the gene pool, so chance events have a large effect on allele frequency; 3. In a large population, chance effects tend to cancel out OR the alleles passed on are a large sample, so allele frequency changes little; 4. Loss or fixation of alleles by chance reduces genetic diversity/the number of different alleles in small populations;	**3 max** (1 × AO2) (2 × AO3)	**Max 2** if Figure 2 is not used 1. **Accept** readings for the population of 2000 between 0.47 and 0.55, or 'about 0.5' 1. **Accept** the population of 200 as an intermediate (change to about 0.6), or as still relatively small 4. Requires reduced genetic diversity; do not award point 4 for the same observation of allele A falling to 0 already credited in point 1 **Reject** natural selection as the cause of the changes

Question	Marking guidance	Mark	Comments
04.3	Allele A was lost (from the gene pool) OR allele a was fixed OR all individuals were aa, so there was no variation for drift to act on;	**1** (1 × AO2)	**Accept** 'frequency of A is 0, and there is no mutation/immigration in the model to bring it back' **Ignore** 'no mutation/immigration' unless the loss of allele A is also stated **Reject** 'the population reached a stable size'

Question	Marking guidance	Mark	Comments
04.4	1. Genetic drift is random/due to chance, so another run could give a different result, eg allele A fixed (frequency 1) or still present; 2. Only one run (for each population size) OR the model needs to be run many times (to find the proportion of runs in which A is lost); 3. Real populations may have selection/mutation/migration (which the model leaves out);	**2 max** (2 × AO3)	**Ignore** 'more repeats' unless linked to runs of the model **Ignore** 'it is only a model' unqualified

Question	Marking guidance	Mark	Comments
05	1. Fill a bag with a known proportion of red and white beads, eg 50 of each (allele frequency 0.5), with the same starting frequency for each population size; 2. Mix/shake the bag and take beads without looking (so sampling is random); 3. Take two beads for each individual in the population, using at least two population sizes, eg 10 beads for 5 individuals and 100 beads for 50 individuals; 4. Return each bead before taking the next OR use a very large number of beads in the bag, so the frequency in the bag stays the same during sampling; 5. Calculate the frequency of red beads in the sample and set up a new bag with this frequency for the next generation; 6. Repeat for a set number of generations, eg 20; 7. Repeat the whole simulation several times for each population size; 8. Plot allele frequency against generation for each population size OR compare the (mean) change in allele frequency / number of runs in which one colour is lost for each population size;	**6 max** (1 × AO1) (2 × AO2) (3 × AO3)	**Max 4** if the results are not analysed (point 8) **Max 4** if population size is not varied 3. **Accept** 'number of beads drawn represents population size' 5. **Accept** a calculation of percentage or proportion of red beads **Ignore** references to natural selection or to adding beads of a new colour

Allopatric and sympatric speciation 3.7.3

Question	Marking guidance	Mark	Comments
06.1	Correct answer for 2 marks: 10.3;; Accept for 1 mark: 77.5(%) **and** 7.5(%) **OR** (31/40) ÷ (6/80)	**2** (2 × AO2)	**Accept** 10, 10.33 or 10⅓ for 2 marks **Reject** 5.2 (numbers of pairs not converted to percentages) = 0 marks

Question	Marking guidance	Mark	Comments
06.2	1. Temperature affects mating/egg production/hatching OR temperature is a control variable that would affect the results; 2. So differences between the types of pair are due to the origin/(genetic) differences of the shrimp, not to temperature;	**2** (2 × AO3)	**Ignore** 'fair test' unqualified 1. **Accept** a named effect, eg on activity of enzymes/rate of development of eggs

Question	Marking guidance	Mark	Comments
06.3	1. Geographical isolation (of the two populations) by the isthmus OR allopatric speciation; 2. (From when the isthmus formed) no gene flow OR gene pools separate OR reproductive isolation between the Pacific and Caribbean populations; 3. Different selection pressures OR different environmental conditions on each coast, eg water temperature/amount of food/size of tides; 4. (Variation due to) (different) mutations in each population; 5. Different advantageous alleles selected/passed on OR change in allele frequencies (in each population); 6. Eventually (the populations) cannot interbreed to produce fertile offspring, eg only 6 of 80 mixed pairs produced eggs / only 1 clutch hatched;	**5 max** (3 × AO1) (2 × AO2)	1. Requires 'geographical isolation' or 'geographically isolated'; a description such as 'separated by land' alone does not gain the point 1. **Accept** allopatric speciation only if linked to the populations being separated by the isthmus 2. Must be at the start of the process; reproductive isolation given only as the end result does not gain point 2 2. **Accept** 'no interbreeding' only as a separate idea from point 6. Reject 'no inbreeding' 3. Must be in context; 'different environment' unqualified is not enough 4. **Reject** mutations caused by the environment or 'in order to adapt' 5. **Accept** increase or decrease for change 6. Both 'interbreed' and 'fertile offspring' are needed. Reject 'inbreeding' **Ignore** sympatric **Ignore** 'two species at the start' Penalise 'gene' for 'allele' once

Question	Marking guidance	Mark	Comments
07.1	A new species arises from a population that is not geographically isolated from the rest of its species;	**1** (1 × AO1)	In sympatric speciation, populations living in the same area become reproductively isolated.

Question	Marking guidance	Mark	Comments
07.2	1. Flies from apple trees emerge (about 22 days/3 weeks) earlier than flies from hawthorn (16 July compared with 7 August) OR emergence matches the ripening of their host fruit; 2. (And) flies mate on their own host fruit OR most flies choose their own host fruit (86% and 81%); 3. So most matings are between flies from the same type of tree OR few flies from apple trees mate with flies from hawthorn; 4. So there is little gene flow OR the gene pools are (largely) separate;	**3 max** (1 × AO1) (2 × AO2)	**Max 2** if no data from Table 4 are used 4. **Accept** 'reduced interbreeding' for little gene flow **Reject** geographical isolation **Ignore** allopatric

Question	Marking guidance	Mark	Comments
07.3	1. The frequency of allele E is different in the two groups (0.62 in flies from apple trees and 0.35 in flies from hawthorn), even though they live in the same area; 2. If the flies interbred freely, the allele frequencies would be (about) the same OR the difference shows there is little gene flow between the groups; 3. Different selection pressures OR allele E is selected for in flies from apple trees, because apples ripen earlier (so faster development is an advantage);	**2 max** (2 × AO3)	**Max 1** if point 2 is not given 1. Must use the data **Accept** 'E is more common in apple flies' with figures for point 1 **Reject** gene frequency for allele frequency

Extended response: the diversity of species 3.7.3

Question	Marking guidance	Mark	Comments
08	1. Birds colonised different islands, so populations were geographically isolated OR allopatric speciation; 2. No gene flow OR gene pools separate OR reproductive isolation between the populations; 3. Mutation produced new alleles/variation in each population; 4. Different selection pressures on each island/in each habitat, eg different food sources such as seeds, nectar or insects; 5. Birds with beaks suited to the available food were more likely to survive and reproduce, passing on their alleles; 6. Allele frequencies changed differently in each population; 7. Genetic drift changed allele frequencies by chance in small populations (eg the first birds to reach a new island); 8. Eventually populations could not interbreed to produce fertile offspring, so they became new species; 9. Repeated many times over millions of years/many generations, with each new species able to split again (giving many species); 10. Sympatric speciation within one island, eg disruptive selection for different beak types with reproductive isolation, could also produce new species;	**6 max** (5 × AO1) (1 × AO2)	**Max 5** if the answer is not linked to the islands or to beak shape and food 2. Must be at the start of the process (eg populations on different islands); reproductive isolation given only as the end result does not gain point 2 1. Requires 'geographical isolation' or 'geographically isolated', or allopatric speciation linked to different islands 3. **Reject** mutation caused by the environment or 'in order to adapt' 7. **Accept** founder effect OR genetic bottleneck 8. Both 'interbreed' and 'fertile offspring' are needed. Reject 'inbreeding' 10. Must refer to the same island/area or no geographical isolation **Reject** birds changed their beaks to suit the food Penalise 'gene' for 'allele' once

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