HELICATE · A-LEVEL BIOLOGY · TOPIC BANK

# 3.7.2 Populations

Mark scheme

Version 1 · 16 October 2026

| TOTAL MARKS | QUESTIONS |
|---|---|
| 45 | 5 |

## 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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## Populations and gene pools 3.7.2

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **01.1** | All the common toads breeding in one pond in one spring; | **1**<br>(1 × AO1) | A population is one species in a particular space at a particular time that can (potentially) interbreed. Option 1 has two species, option 3 has no particular time and option 4 cannot interbreed. |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **01.2** | 1. A population is (a group of organisms of) one species in a particular space/area at a particular time OR the toads at one pond (in one spring) occupy one particular space at one time;<br>2. Toads at one pond (can) interbreed with each other, but rarely/do not interbreed with toads at other ponds (because they return to their own pond/the ponds are far apart); | **2**<br>(1 × AO1)<br>(1 × AO2) | 1. **Accept** habitat/area/place for space<br>1. Time must be included for the mark<br>2. **Accept** '(potentially) produce fertile offspring with each other' for interbreed<br>**Ignore** 'community' unless described as more than one species, in which case reject<br>**Reject** answers that say toads at different ponds are different species |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **01.3** | All the alleles of all the genes in a population (at one time); | **1**<br>(1 × AO1) | **Accept** 'all the alleles in a population'<br>**Reject** 'all the genes in a population' (alleles needed)<br>**Reject** 'all the alleles in an organism/individual'<br>**Ignore** 'in a species' if a population is also described |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **01.4** | 1. Allele frequencies (in the population) do not change/stay constant from generation to generation;<br>2. Large population OR no genetic drift;<br>3. Random mating;<br>4. No mutation;<br>5. No migration OR no immigration/emigration OR population is isolated (eg no toads joining from other ponds);<br>6. No selection (for or against any allele/phenotype); | **3 max**<br>(3 × AO1) | **Max 2** if point 1 is not given<br>Penalise 'gene frequency' for 'allele frequency' once<br>**Ignore** 'no births/deaths' and 'random fertilisation'<br>**Reject** 'no change in phenotypes' for point 1 |

## The Hardy-Weinberg principle and equation 3.7.2

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **02.1** | 0.98; | **1**<br>(1 × AO2) | Frequency of white foxes ($q^2$) = 2401 ÷ 2500 = 0.9604; q = $\sqrt{0.9604}$ = 0.98 |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **02.2** | 1. A heterozygote can form in two ways: **B** from the father and **b** from the mother, OR **b** from the father and **B** from the mother;<br>2. The probability of each way is $p \times q$, so the total is $pq + pq = 2pq$; | **2**<br>(1 × AO1)<br>(1 × AO2) | 1. **Accept** 'from either gamete/parent' or 'egg **B** and sperm **b**, or egg **b** and sperm **B**'<br>2. **Accept** a Punnett square with *p* and *q* showing two *pq* boxes for both points<br>Penalise 'gene' for 'allele' once |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **02.3** | Correct answer for 3 marks: 99.0 (%);;;<br>Accept for 2 marks:<br>2*pq* = 0.0392 OR 3.92% OR 98 heterozygous foxes<br>OR $p^2$ = 0.0004 used with the frequency of blue foxes, 0.0396 (eg 1 − 0.0004 ÷ 0.0396)<br>Accept for 1 mark:<br>$q^2$ = 0.9604 OR 96.04% (white foxes) shown and used, OR *q* = 0.98 OR *p* = 0.02 | **3**<br>(3 × AO2) | **Accept** 99% or 98.99% for 3 marks<br>Working: $q^2$ = 0.9604, q = 0.98, p = 0.02; 2pq = 2 × 0.02 × 0.98 = 0.0392; 0.0392 ÷ 0.0396 × 100 = 99.0%<br>A correct decimal (0.99) when a percentage was asked = 1 mark max<br>3.92% as the final answer (heterozygotes as a percentage of all foxes) = 2 marks<br>**Reject** *pq* (0.0196) for 2*pq*; 2pq ÷ 2 gains 1 mark only if *q* or *p* is correct |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **02.4** | 1. (Almost) all/99% of blue foxes are heterozygous/**Bb**/carry the **b** allele, so most blue × blue matings are **Bb** × **Bb**;<br>2. Each cub has a 1 in 4/0.25/25% chance of being **bb**/white, so in a litter of five or more, some are likely to be white; | **2**<br>(1 × AO2)<br>(1 × AO3) | **Accept** ECF from the answer to 02.3 if it shows that most blue foxes are heterozygous<br>2. **Accept** a genetic diagram showing **Bb** × **Bb** giving 1 **bb** in 4<br>**Reject** 'white is dominant'<br>Penalise 'gene' for 'allele' once |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **03.1** | Foxes of both coat colours dying of old age at the same rate; | **1**<br>(1 × AO2) | Option 1 is non-random mating, option 2 is immigration and option 3 is selection. Deaths that are equally likely for every genotype do not change allele frequencies. |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **03.2** | 1. 2000: 0.43;<br>2. 2020: 0.54; | **2**<br>(2 × AO2) | Working: 2000 (2 × 30 + 78) ÷ (2 × 160) = 138 ÷ 320 = 0.43125; 2020 (2 × 50 + 90) ÷ (2 × 175) = 190 ÷ 350 = 0.54286<br>**Accept** correct answers not given to two decimal places for 1 mark in total, eg 0.431 and 0.543<br>**Reject** 0.55 or 0.53 for 2020 (the Hardy-Weinberg equation was used instead of the genotype numbers)<br>2000: 0.43 gains credit only if obtained by counting alleles (working shown); the Hardy-Weinberg equation also gives 0.43 for 2000, which gains no credit<br>Frequencies of **b** (0.57 and 0.46) = 0 marks<br>**Accept** 43% and 54% for 2 marks |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **03.3** | 1. Frequency of **B** rose (from 0.43 to 0.54) OR frequency of **b** fell (from 0.57 to 0.46);<br>2. White/**bb** foxes fell from 32.5% to 20% (of those tested) OR blue foxes rose from 67.5% to 80%;<br>3. Allele frequency changed between generations, so the Hardy-Weinberg conditions are not met/the principle does not apply (to this population);<br>4. Selection for blue/**B** OR against white/**b**, because with less snow (on dark ground) white foxes are more visible/blue foxes are better camouflaged;<br>5. Foxes from the mainland are mostly white/carry **b**, so immigrants (across the sea ice) bring **b** alleles;<br>6. Sea freezes in fewer winters, so fewer (white) foxes/**b** alleles immigrate (so the frequency of **B** rises); | **5 max**<br>(1 × AO1)<br>(2 × AO2)<br>(2 × AO3) | **Max 4** if selection (point 4) or migration (points 5–6) is not discussed<br>4. **Accept** 'blue foxes more likely to survive and reproduce/pass on **B**' as alternative wording for selection, if linked to snow or dark ground; this gains point 4 only<br>**Reject** 'no selection' or 'no migration' as explanations (converse of the conditions)<br>**Ignore** births and deaths unless linked to coat colour<br>**Ignore** 'small population' and genetic drift (the population is large)<br>**Ignore** mutation<br>Penalise 'gene' for 'allele' once |

## Testing Hardy-Weinberg predictions in the field 3.7.2

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **04.1** | There is no (significant) difference between the observed numbers and the numbers expected (from the Hardy-Weinberg equation with a $W^M$ frequency of 0.10); | **1** (1 × AO1) | **Accept** 'any difference between observed and expected numbers is due to chance'<br>**Reject** 'there is no difference' with no reference to observed and expected numbers |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **04.2** | Correct answer for 2 marks: 108;;<br>Accept for 1 mark:<br>$2pq = 2 \times 0.9 \times 0.1 = 0.18$ OR 18% | **2** (2 × AO2) | **Reject** 54 ($pq \times 600$) for any mark<br>**Reject** 80 (observed number) |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **04.3** | Correct answer for 3 marks: 10.74;;;<br>Accept for 2 marks:<br>all three values of $(O - E)^2 \div E$ correct: 1.98, 7.26, 1.50<br>Accept for 1 mark:<br>expected numbers 486 and 6 correct OR one correct value of $(O - E)^2 \div E$ | **3** (3 × AO2) | **Accept** 10.7 or 10.737 for 3 marks<br>**Accept** ECF for 2 and 3 marks from one incorrect expected number, including an incorrect answer to 04.2<br>**Accept** $\chi^2$ or Chi2 for chi-squared |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **04.4** | 1. 2 degrees of freedom so the critical value is 5.99;<br>2. Chi-squared/10.74 is greater than the critical value, so the probability that the difference is due to chance is less than 5%/0.05;<br>3. So reject the null hypothesis OR there is a significant difference between observed and expected numbers (so the $W^M$ allele frequency/genotype frequencies have probably changed since the survey); | **3** (3 × AO3) | **ECF**: allow points 2 and 3 for a correct conclusion from an incorrect value in 04.3<br>2. Must be 'less than' 5%; reject 0.05%<br>2. **Accept** 'more than 95% probability that the difference is not due to chance'; reject '95% probability that the difference is due to chance'<br>2. **Accept** P for probability<br>3. **Reject** 'proves the allele frequency has changed' |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **04.5** | Correct answer for 1 mark: 0.072; | **1**<br>(1 × AO2) | Working: (80 + 2 × 3) ÷ (2 × 600) = 86 ÷ 1200 = 0.0717<br>**Accept** 7.2%<br>**Reject** 0.071 (square root of the bimacula proportion) |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **04.6** | 1. For: frequency of $W^M$ fell (from 0.10 to 0.072) OR fewer medionigra/bimacula than expected (80 v 108, 3 v 6);<br>2. For: the difference is significant, so unlikely to be due to chance;<br>3. For: selection against moths with $W^M$ would reduce the frequency of $W^M$ (in the next generation);<br>4. Against: no data on predation/birds OR correlation not shown to be cause;<br>5. Against: another selection pressure could explain the fall (eg moths with $W^M$ less likely to be chosen as mates, disease, survival of caterpillars);<br>6. Against: moths with $W^M$ may have emigrated OR typical/$W^T$ moths may have immigrated (from another colony);<br>7. Against: one meadow on one day may not give a representative sample (of the colony) OR survey and students may have used different sampling methods; | **4 max**<br>(4 × AO3) | **Max 3** if only points for or only points against are given<br>6. **Accept** 'the colony may not be isolated' OR migration<br>**Ignore** non-random mating unless described as selection (eg mate choice against moths with $W^M$)<br>**Ignore** 'small population' (the colony is large)<br>Penalise 'gene' for 'allele' once |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **04.7** | 1. Sample at (several) random(ly chosen) locations/across the whole colony;<br>2. Sample on several days/at different times in the season;<br>3. Mark (and release) moths so the same moth is not counted twice (on later days);<br>4. Catch a larger sample (eg more than 600 moths); | **2 max**<br>(1 × AO1)<br>(1 × AO3) | **Ignore** 'repeat' unqualified<br>4. Must be linked to the whole colony or a named larger number<br>**Ignore** 'use a quadrat' |

| Question | Marking guidance | Mark | Comments |
|---|---|---|---|
| **05** | 1. Divide the area into a grid and use random numbers to choose coordinates OR random sampling method described;<br>2. At each coordinate, use a quadrat OR search a fixed area for a fixed time;<br>3. Use many sampling sites/a large sample of snails (eg at least 100);<br>4. Record/count the number of banded and unbanded snails;<br>5. Return snails where found OR mark shells so no snail is counted twice;<br>6. Proportion/frequency of banded snails = number banded ÷ total = $q^2$;<br>7. Frequency of the banded allele, $q$ = √(proportion of banded snails);<br>8. Assume the Hardy-Weinberg conditions apply, eg large population OR random mating OR no selection (for or against banding) OR no migration OR no mutation OR assume the sample is representative of the population OR assume banding is controlled only by this gene/not affected by the environment; | **6 max**<br>(4 × AO1)<br>(1 × AO2)<br>(1 × AO3) | **Max 4** if no calculation (points 6–7)<br>**Max 4** if no sampling method (points 1–3)<br>6. **Accept** 'frequency of homozygous recessive/banded snails' for $q^2$<br>7. **Reject** $q$ = proportion of banded snails (not square-rooted)<br>8. **Ignore** 'no births/deaths' OR 'population size stays the same'<br>**Reject** 'HW' for Hardy-Weinberg<br>8. Only one assumption is credited<br>Penalise 'gene' for 'allele' once |

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