



AB7D Genetics, Populations, Evolution and Ecosystems: Depth and Exam Drill

AQA 7402 · Calculator allowed · about 140 minutes

Total Marks

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Name: _____ Date: ____ / ____ / ____

Answer ALL questions. Show all your working.

- 1** This question tests basic genetic definitions and understanding of DNA structure and gene expression.
- (a) State the meaning of the term locus in genetics. (1)
 - (b) Give one difference between DNA and mRNA in terms of sugar and one-nucleotide base. (2)
 - (c) Describe briefly how a point mutation in a coding region could lead to a nonfunctional protein. (3)
 - (d) Name the two main stages of gene expression and give the location in a eukaryotic cell where each occurs. (2)

(Total for Question 1 is 8 marks)

- 2** A sample of a diploid plant species shows two alleles at a locus for petal colour: A (dominant red) and a (recessive white). In a randomly mating large population, the frequency of the recessive phenotype (white) is measured as 4.0%.
- (a) Assuming Hardy-Weinberg equilibrium, calculate the allele frequencies of a and A. (b) Calculate the expected percentage of heterozygotes in the population. (c) In a sample of 500 plants, 28 are white. Use a chi-squared test at 5% significance to determine whether the population is in Hardy-Weinberg equilibrium for this locus. Use 1 degree of freedom and state your conclusion.
- (a) Calculate the allele frequency q for a and p for A given that the recessive phenotype frequency is 4.0%. Show working and give frequencies to 3 significant figures. (4)
 - (b) Calculate the expected percentage of heterozygotes (Aa) in the population. Give your answer to 3 significant figures. (3)
 - (c) Use a chi-squared test with the sample of 500 plants (observed white = 28) to test HWE at 5% significance. Show your calculations and conclude whether the population is in equilibrium. Use expected frequencies from (a) and (b). (7)

(Total for Question 2 is 14 marks)

- 3** Genetic drift is being investigated in a small island population of a bird species. At a neutral locus there are two alleles, B and b. In generation 0 the frequency of B is 0.60. A biologist samples 25 breeding pairs and counts 50 gametes effectively sampled; in one replicate she observes 38 copies of B among these gametes.
- (a) Calculate the sample allele frequency of B. (b) Calculate the standard error for the allele frequency sampling in this sample and use it to give a 95% approximate confidence interval for the true allele frequency. (c) Comment briefly whether the observed sample provides evidence for change from the original frequency 0.60 at the 95% level.
- (a) Calculate the sample allele frequency of B from the observation of 38 copies of B in 50 sampled gametes. Give your answer to 3 significant figures. (2)
- (b) Calculate the standard error for the allele frequency sampling using $SE = \sqrt{p(1-p)/n}$, where p is the sample frequency and n is number of gametes sampled. Then give a 95% approximate confidence interval using $p \pm 1.96 SE$. Give interval limits to 3 significant figures. (6)
- (c) Comment briefly whether the observed sample provides evidence for change from the original frequency 0.60 at the 95% level. (4)

(Total for Question 3 is 12 marks)

- 4** A herbivore population is exposed to a new plant toxin. Individuals with genotype TT have survival 90%, Tt have survival 60% and tt have survival 30% to reproductive age. Before exposure, genotype frequencies were 0.25 TT, 0.50 Tt and 0.25 tt in a large randomly mating population. Assume random mating after selection and discrete non-overlapping generations.
- (a) Calculate the mean fitness of the population after selection. (b) Calculate the frequency of allele T in the surviving adults (after selection). Give answers to 3 significant figures. (c) Explain briefly how directional selection at this locus affects allele frequency over generations.
- (a) Calculate the mean fitness w_{bar} of the population using genotype frequencies and fitnesses given. (6)
- (b) Calculate the frequency of allele T among surviving adults after selection. Show working and give final frequency to 3 significant figures. (8)
- (c) Explain briefly how directional selection at this locus affects allele frequency over generations, referencing the results above. (4)

(Total for Question 4 is 18 marks)

- 5** Levels question (6 marks). Discuss the evidence and mechanisms by which human activity can drive rapid evolutionary change in wild populations. Your answer should include specific mechanisms, at least one quantitative example or calculation, and a judgement on the likely reversibility of such changes.

(Total for Question 5 is 6 marks)

6 Experimental ecologists measured nitrate concentration (micromol per litre) and species richness of aquatic invertebrates at 8 ponds to investigate the effect of nutrient pollution. Data collected: Pond A 12.4, 22; B 8.7, 29; C 15.2, 18; D 5.6, 34; E 20.1, 15; F 9.3, 27; G 3.8, 38; H 16.5, 20. Each nitrate concentration measurement has an uncertainty of ± 0.2 micromol per litre. (a) Calculate the mean nitrate concentration and its standard deviation. (b) Calculate the mean species richness and its standard deviation. (c) Compute the Pearson correlation coefficient r between nitrate concentration and species richness and test whether the correlation is significantly different from zero at the 5% level using $t = r \sqrt{(n-2)/(1-r^2)}$, with $n = 8$. Use two significant figures for r and give your conclusion. (d) Briefly suggest one plausible ecological explanation for the observed relationship and one improvement to the experiment to reduce uncertainty.

(a) Calculate the mean nitrate concentration (micromol per litre) and its sample standard deviation for the eight ponds. Give mean to 3 s.f. and SD to 2 s.f. **(4)**

(b) Calculate the mean species richness and its sample standard deviation for the eight ponds. Give mean to 3 s.f. and SD to 2 s.f. **(4)**

(c) Compute the Pearson correlation coefficient r between nitrate concentration and species richness and test whether the correlation is significantly different from zero at the 5% level using $t = r \sqrt{(n-2)/(1-r^2)}$, with $n = 8$. Use two significant figures for r and give your conclusion. **(6)**

(d) Briefly suggest one plausible ecological explanation for the observed relationship and one improvement to the experiment to reduce uncertainty. (2 marks) **(2)**

(Total for Question 6 is 16 marks)

Mark scheme · AB7D Genetics, Populations, Evolution and Ecosystems: Depth and Exam Drill

Question 1

- (a) **B1** position of a gene on a chromosome or specific location on DNA
- (a) **Answer: Position of a gene on a chromosome.**
- (b) **B1** DNA contains deoxyribose, mRNA contains ribose
- (b) **B1** DNA has thymine, mRNA has uracil
- (b) **Answer: DNA has deoxyribose and thymine; mRNA has ribose and uracil.**
- (c) **M1** mutation changes a codon in mRNA, altering one amino acid or creating a premature stop codon
- (c) **M1** change alters the primary sequence leading to incorrect folding or a truncated polypeptide
- (c) **A1** nonfunctional protein results due to lost active site, instability or truncation, cao
- (c) **Answer: A point mutation alters a codon so one amino acid is changed or a premature stop codon is produced; this can change the primary sequence and so disrupt folding or produce a truncated polypeptide, preventing normal function.**
- (d) **B1** transcription - nucleus
- (d) **B1** translation - cytoplasm (on ribosomes)
- (d) **Answer: Transcription in the nucleus; translation in the cytoplasm on ribosomes.**

Question 2

- (a) **M1** use $q^2 = 0.04$ or equivalent
- (a) **M1** $q = \sqrt{0.04} = 0.200$
- (a) **M1** $p = 1 - q = 0.800$
- (a) **A1** final frequencies $q = 0.200$ and $p = 0.800$ to 3 s.f., cao
- (a) **Answer: $q = 0.200$, $p = 0.800$**
- (b) **M1** substitute p and q into $2pq = 2 \times 0.800 \times 0.200$
- (b) **M1** evaluate $2 \times 0.800 \times 0.200 = 0.320$
- (b) **A1** $2pq = 0.320 = 32.0\%$ to 3 s.f., cao
- (b) **Answer: 32.0%**
- (c) **M1** calculate expected numbers: expected white = $q^2 \times 500 = 0.04 \times 500 = 20$; expected non-white = 480
- (c) **M1** set up chi-squared for two categories: $\text{sum } (\text{observed} - \text{expected})^2 / \text{expected}$
- (c) **M1** compute contribution for white: $(28 - 20)^2 / 20 = 64/20 = 3.20$
- (c) **M1** compute contribution for non-white: $(472 - 480)^2 / 480 = 64/480 = 0.1333$
- (c) **M1** sum contributions = 3.3333 and compare with critical value 3.84 at 1 d.f., oe
- (c) **M1** state conclusion: chi-sq 3.33 < 3.84 so do not reject H_0 ; population not significantly different from HWE at 5% significance
- (c) **A1** clear statement of conclusion with comparison to critical value, cao
- (c) **Answer: Chi-squared = 3.33; since 3.33 < 3.84 at 1 d.f., do not reject HWE; the sample is consistent with Hardy-Weinberg equilibrium at 5% significance.**

Question 3

- (a) **M1** use frequency = number of B / total = 38/50
- (a) **A1** frequency = 0.760 to 3 s.f., cao
- (a) **Answer: 0.760**
- (b) **M1** substitute $p = 0.76$ and $n = 50$ into $SE = \sqrt{p(1-p)/n}$
- (b) **M1** compute $SE = \sqrt{0.76 \times 0.24 / 50}$
- (b) **M1** evaluate $SE = \sqrt{0.1824 / 50} = \sqrt{0.003648} = 0.0604$ (ft)
- (b) **M1** compute 95% interval $p \pm 1.96 SE$ using $p = 0.76$
- (b) **M1** evaluate limits: lower = $0.76 - 1.96 \times 0.0604 = 0.76 - 0.1184 = 0.6416$; upper = $0.76 + 0.1184 = 0.8784$
- (b) **A1** state interval = 0.642 to 0.878 (3 s.f.), cao
- (b) **Answer: SE = 0.0604; 95 % CI = 0.642 to 0.878**
- (c) **M1** compare original $p_0 = 0.60$ with 95% CI 0.642 to 0.878
- (c) **M1** note that 0.60 is below the lower limit 0.642
- (c) **M1** conclude that the sample provides evidence at the 95% level that the allele frequency differs from 0.60
- (c) **A1** clear concluding statement: sample suggests a higher frequency than 0.60 at 95% confidence, cao
- (c) **Answer: 0.60 lies outside the 95 % CI (0.642 to 0.878), so the sample provides evidence at the 95 % level that the allele frequency has increased relative to the original 0.60.**

Question 4

- (a) **M1** use $w_{\text{bar}} = \text{sum}(\text{frequency_genotype} \times \text{fitness_genotype}) = 0.25 \times 0.90 + 0.50 \times 0.60 + 0.25 \times 0.30$
- (a) **M1** substitute numbers: $0.225 + 0.30 + 0.075$
- (a) **M1** evaluate sum = 0.600
- (a) **M1** state $w_{\text{bar}} = 0.600$ with appropriate units (dimensionless)
- (a) **M1** round to 3 s.f. if required
- (a) **A1** final 0.600 cao
- (a) **Answer: 0.600**
- (b) **M1** compute contribution of T alleles from each genotype among survivors: from TT all alleles are T; from Tt half are T
- (b) **M1** calculate weighted surviving genotype frequencies before normalisation: $TT_{\text{survive}} = 0.25 \times 0.90 = 0.225$;
 $Tt_{\text{survive}} = 0.50 \times 0.60 = 0.300$; $tt_{\text{survive}} = 0.25 \times 0.30 = 0.075$
- (b) **M1** compute total T alleles in survivors per initial population: $2 \times TT_{\text{survive}} + 1 \times Tt_{\text{survive}} = 2 \times 0.225 + 0.300 = 0.450 + 0.300 = 0.750$
- (b) **M1** compute total alleles in survivors per initial population: $2 \times (TT_{\text{survive}} + Tt_{\text{survive}} + tt_{\text{survive}}) = 2 \times w_{\text{bar}} = 2 \times 0.600 = 1.200$
- (b) **M1** compute $p_{\text{after}} = \text{total T alleles} / \text{total alleles} = 0.750 / 1.200$
- (b) **M1** evaluate $p_{\text{after}} = 0.625$
- (b) **M1** give final answer to 3 s.f.: 0.625
- (b) **A1** final frequency $p = 0.625$ cao
- (b) **Answer: 0.625**
- (c) **M1** state that allele T has higher fitness on average and increases in frequency after selection (example: p increases from 0.500 initial to 0.625 among survivors if starting allele freq implied by genotype frequencies)
- (c) **M1** explain that repeated differential survival will increase T frequency over generations
- (c) **M1** note that if selection continues strong T may approach fixation while genetic variation at the locus decreases
- (c) **A1** clear consequence given: directional selection shifts the mean allele frequency toward the favoured allele, reducing diversity, cao
- (c) **Answer: Because individuals carrying T have higher survival, the frequency of T among survivors is higher (0.625 here), so repeated selection will increase T over generations, potentially leading to fixation and reduced genetic variation at this locus.**

Question 5

- **Level 3** (5-6): Detailed, well-structured answer. Explains multiple mechanisms (selection, gene flow, genetic drift, mutation) with clear examples or a short calculation showing rate of change; evaluates reversibility and provides a supported judgement.
- **Level 2** (3-4): Clear explanation of one or two mechanisms with an example and some quantitative element; limited evaluation of reversibility.
- **Level 1** (1-2): Basic statements about human-caused selection or habitat change with little or no quantitative support and minimal evaluation.
- **Indicative content:**
 - Mechanisms: directional selection from harvesting, pesticides, antibiotics; altered gene flow due to habitat fragmentation; founder effects and bottlenecks; mutation rates.
 - Quantitative example: show simple selection response calculation or allele frequency change e.g. p increasing from 0.40 to 0.55 in X generations or use selection differential and heritability in words; use numbers to illustrate rapid change over a few generations.
 - Evidence: documented cases like insecticide resistance evolving in tens of generations, fish maturing earlier in heavily fished populations, urban adaptation to pollutants.
 - Reversibility: depends on selection pressure removal, genetic architecture, pleiotropy and gene flow; can be partially reversible but may be constrained by loss of genetic variation or linked deleterious alleles.
 - Judgement: weigh likelihood of reversal case by case, consider management implications.

Question 6

- (a) **M1** list data and compute mean = $\text{sum}(\text{concentrations})/8$
- (a) **M1** compute individual deviations squared and sum for variance
- (a) **M1** evaluate sample standard deviation using $\sqrt{\text{sum}(x - \text{mean})^2/(n-1)}$
- (a) **A1** state mean and SD to required s.f., cao
- **(a) Answer: Mean nitrate = 11.5 micromol per litre; SD = 5.6 micromol per litre**
- (b) **M1** compute mean richness = $\text{sum}(\text{richness})/8$
- (b) **M1** compute deviations squared and sum
- (b) **M1** compute sample SD = $\sqrt{\text{sum dev}^2/(n-1)}$
- (b) **A1** state mean and SD to required s.f., cao
- **(b) Answer: Mean richness = 25.4 species; SD = 8.0 species**
- (c) **M1** compute covariance and standard deviations or use formula for r ; show substitution
- (c) **M1** evaluate r value correctly to 2 s.f.
- (c) **M1** compute $t = r \sqrt{(n-2)/(1-r^2)}$ with $n = 8$
- (c) **M1** compare t with critical value t_{crit} for $df = 6$ at 5% two-tailed ~ 2.447
- (c) **M1** state whether correlation is significant
- (c) **A1** clear conclusion with numerical r and decision, cao
- **(c) Answer: $r = -0.98$ (2 s.f.); t approx -11.3; $|t| > 2.447$ so correlation is significant at 5% (strong negative correlation).**
- (d) **M1** plausible ecological explanation: e.g. higher nitrate leads to algal blooms reducing oxygen or habitat complexity reducing invertebrate richness
- (d) **M1** improvement: increase number of ponds sampled, measure nitrate multiple times per pond and average to reduce measurement uncertainty, or control for pond area
- **(d) Answer: Higher nitrate likely causes eutrophication, favouring tolerant taxa and reducing overall species richness; improve the experiment by sampling more ponds and taking repeated nitrate measurements per pond to reduce uncertainty and allow estimation of within-pond variability.**