Mark scheme

Question			Answer/Indicative content	Marks	Guidance
1		i	double peaks / they , are heterozygous / have different alleles ✓ single peaks , are homozygous / have the same allele ✓	2 (AO 2.2)	**IGNORE** genes / coding **ALLOW** VNTR length as AW for allele *If no other mark awarded* **ALLOW** 1 mark for using the terms 'homozygous' and 'heterozygous' (not linked to peaks) **Examiner's Comments** This was a challenging question in which only around 1 in 10 responses scored any marks. Candidates were required to understand the context provided and use key terms correctly to express their ideas. Some responses had the right idea, but they confused key terms such as gene with allele, homologous with homozygous (and their hetero-equivalents), and polygenic with polymorphic. Autosomal linkage was often seen as an incorrect answer.
		ii	*claim is supported because…* 1 (DNA profiles) are identical / match / AW ✓ 2 probability / chance , of 2 people having identical profiles is <u>very</u> low / AW ✓ however… 3 (6 is) a low number of , loci / peaks ✓ 4 … so they could have been , <u>closely</u> related / AW ✓ 5 could be identical twins ✓	3 max	*Assume correct context unless answer contradicts it* **1 ALLOW** are the same **1 IGNORE** similar / same number of base pairs **2 ALLOW** <u>very</u> low <u>likelihood</u> / near impossibility , that 2 people would have matching profiles **2 IGNORE** so they probably come from the same person **3 ALLOW** only 6 genes were tested **3 ALLOW** 17 loci are needed in court **3 IGNORE** small sample **4 ALLOW** only if mp 3 has been **AWARDED** **Examiner's Comments**

<table>
<tr><td></td><td></td><td></td><td></td><td></td><td>Most candidates gained the first marking point but then filled the rest of their answer space with examples to illustrate this point. An explanation of how strong support is requires some consideration of what might make the support weak, and few responses attempted to do this. A minority of candidates suggested that S might have belonged to the suspects twin, but many omitted the important detail about twin being identical (or monozygotic). Other marking points were seen, but rarely. Some answers went beyond the claim in the question and discussed whether the suspect was guilty.</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>5</td><td></td></tr>
<tr><td>2</td><td></td><td>i</td><td>FIRST CHECK ON ANSWER LINE
If answer = 16.8 award 3 marks

<table><tr><th></th><th>O</th><th>E</th><th>O-E</th><th>(O-E)^2</th><th>(O-E)^2/E</th></tr><tr><td>A</td><td>44</td><td>40</td><td>4</td><td>16</td><td>0.4</td></tr><tr><td>O</td><td>56</td><td>40</td><td>16</td><td>256</td><td>6.4</td></tr><tr><td>S</td><td>20</td><td>40</td><td>20</td><td>400</td><td>10</td></tr><tr><td></td><td></td><td>✓</td><td></td><td></td><td>✓</td></tr></table>
ΣU(O.E)^2/E = 16.8 / 16.80 ✓</td><td>3
(AO 2.4)</td><td>CREDIT working marks seen anywhere

ALLOW 1 mark for correct summation of candidate’s ‘(O-E)2/E’ column

ALLOW 2 marks for…

• 17 / 16.800

ALLOW 2 marks for common errors with Expected numbers (IGNORE s.f.)

• 165.6 (E = 120)
• 16.4 (E = 44)
• 25.7 (E = 56)

<u>Examiner’s Comments</u>

Around half of candidates scored all 3 marks and many of those that didn’t gain some credit for summing (O-E)^2/E, calculating the expected values, or both. Miscalculation of the expected values was the most common repeated error.</td></tr>
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					OCR support The maths skills handbook and the guidance on statistics for biologists offer further support on the use of statistical tests. Additional support on all the maths skills can be found on 'Maths for Biology' resources on 'Teach Cambridge'.
		ii	differences (between observed and expected) are significant ✓ (less than) 5% chance that (difference is) due to chance ✓ reject , null hypothesis / H_0 ✓ there is an association between tree species and wood sorrel population / AW ✓	3 max (AO 3.1)	**ALLOW ora** if candidate answer in (i) is below 5.991 **ALLOW** (>) 95% confident that (the difference is) not due to chance **ALLOW** tree species affects wood sorrel **ALLOW** wood sorrel less likely to grow near sycamore **ora** **Examiner's Comments** This question differentiated well, and all marking points were regularly seen. Candidates seemed better at discussing statistical significance correctly than in previous years. There were, for example, fewer responses that ascribed significance to 'results' or 'data', rather than to a 'difference'. Candidates who had miscalculated the chi-squared value in part (i) were able to access all of the available marks.
		iii	age / size / height , of tree ✓ gradient (of ground) ✓ density / AW , of surrounding trees ✓ *idea of* direction of sunlight ✓	2 max (AO 3.3)	**ALLOW** shading from adjacent trees **IGNORE** light intensity unqualified **ALLOW** e.g., whether they are all on the same side of a hill **IGNORE** presence of other species **IGNORE** all other variables **Examiner's Comments** Unusually for a 'identify some control variables' question, the usual answers common to a range of laboratory-based investigations did not apply to this environmental

					context. Hence only a minority of candidates scored at all, and it was very rare to award both marks. Most commonly candidates gained a mark for suggesting that size (age, height or girth) of trees should be controlled as far as possible. References to density of surrounding trees and slope were seen but much less frequently. Although ensuring that the mineral or water content of the soil were controlled might well have been beneficial, such levels of control in a field study context are impractical. Time of day was a regular incorrect response but taking readings at different times of day would not realistically affect the number of small herbaceous plants growing under a tree. **Assessment for learning** Although time and resource constraints can make field trips difficult, experience of conducting a study such as this one in a site larger than school grounds is a useful way to learn about the issues involved in carrying out a scientific investigation in an environmental context.
			Total	**8**	
3			C✓	1 (AO 1.1)	**Examiner's Comments** Around half of candidates knew that discontinuous variation could not be under the control of many genes on different chromosomes.
			Total	**1**	
4			**FIRST CHECK ON ANSWER LINE** **If answer = 1024 award 2 marks** number of combinations = 2^n ✓ 2^{10} = 1024 ✓	2 (AO2.2)	If answer is incorrect **ALLOW** 1 mark for 512 or 2048 or 1000 **Examiner's Comments**

					Most candidates found this question very challenging, either because they did not know, or could not work out that the number of gamete combinations would be 2^n. Less than 1 in 5 candidates got this right but, of those that did, almost all achieved both marks. The most common incorrect response was '40'.
			Total	**2**	
5	a		sequence genomes (of different varieties) ✓ (*use bioinformatics and computational biology to*) develop / use, (appropriate) software ✓ use , algorithms / statistical tests / (mathematical) models ✓ store , data / information (from different DNA sequences) ✓ analyse / identify, differences / similarities, in DNA (sequences) / alleles ✓	3 max (AO1.2) (AO2.5) (AO2.7)	**ALLOW** 'develop theoretical models' **ALLOW** 'use a database' / 'storing genomes (on a database)' **ALLOW** 'comparison of, differences / similarities, in their genes' **Examiner's Comments** This question was proven challenging for the candidates. Only a few candidates were confident with these processes and knew what a genome is. These candidates mentioned storing information on databases or using software or models to compare and identify similarities or differences between the DNA sequences of different varieties of maize. Lots of candidates included irrelevant descriptions of lab methods such as PCR, Southern Blotting, or referenced sequencing amino acids, rather than sequencing genomes. Some candidates went into detail about how sequencing is carried out, or just repeated the stem of the question and talked about 'comparing genomes'.
	b		(parental genotypes) AaBb and aaBb ✓	4 (AO2.6) (AO2.5)	If incorrect symbols used throughout = **max 3 ALLOW ECF** for mp2-4 if incorrect genotypes used

(gametes) AB Ab aB ab **and** aB ab ✓

purple & smooth : purple & wrinkled : yellow & smooth : yellow & wrinkled ✓

(ratio =) 3:1:3:1 ✓

ALLOW mp2 if gamete line is incomplete (e.g. only one parental genotype given - AB, Ab, aB, ab) **but** Punnett square is correct for both sets of gametes
If AA /aa / BB / bb / Aa / Bb given as gametes no further mp's awarded as incorrect biology

	AB	Ab	aB	ab
aB	AaBB purple & smooth	AaBb purple & smooth	aaBB yellow & smooth	aaBb yellow & smooth
ab	AaBb purple & smooth	Aabb purple & wrinkled	aaBb yellow & smooth	aabb yellow & wrinkled

ALLOW mp2 and mp3 from a Punnett square

all four phenotypes should be listed (in any order)

ALLOW ratio of 6:2:6:2

ALLOW phenotypes and ratio in a different order for mp3 and mp4, providing they correctly correspond.

Examiner's Comments

Relatively few candidates were able to work through this cross to deduce the correct offspring phenotypic ratio. Many candidates were prepared for a standard dihybrid cross with heterozygous parents, giving a 9:3:3:1 ratio. Most candidates were able to give the parental genotypes but couldn't identify how the gametes were derived from the genotype. A few candidates did not know what a phenotype is, and several candidates who did work through this cross correctly lost a mark for not matching up the correct

					phenotype with the phenotypic ratio.  **Assessment for learning** Candidates could be given a range of possible parental genotype combinations to work through hybrid cross, not just the standard dihybrid cross with two heterozygous parents. Placing gametes in circles might help candidates understand how the gametes are derived from the genotype.
			Total	**7**	
6			C ✓	1 (AO1.2)	Very few candidates selected the correct answer for this question, option **C**. A range of incorrect responses were seen**,** highlighting a misconception on how mutations are caused.  **Misconception** Mutations cannot be caused by selective breeding. Mutations occur randomly either due to random errors during DNA replication, exposure to mutagens or a viral infection.
			Total	**1**	
7			B ✓	1 (AO1.2)	**<u>Examiner's Comments</u>** Candidates found this question challenging, with only around a quarter selecting the correct response, **B**. Option **D** and, to a lesser extent, option **A** were common incorrect responses. Option **A** would increase the occurrence of genetic disorders. Option **D** is also incorrect because the wild ancestor of dogs (and wolves) no longer exists.
			Total	**1**	

8			A ✓	1 (AO2.7)	**Examiner's Comments** About half of candidates selected the correct response, **A**. The most common incorrect responses were **B** and **C.**
			Total	**1**	
9			**FIRST CHECK ON ANSWER LINE** **If answer = 150 award 2 marks** 150/600 = 0.25 (q2) square root of 0.25 = 0.5 (q) ✓ p = 1 − 0.5 = 0.5 p^2 = 0.5^2= 0.25 0.25 × 600 (= 150) ✓	2(AO2.2)	**ALLOW** 0.25 for 1 mark **ALLOW** 1 mark for any 2 correct steps of process Step 1 150/600 = 0.25 (q^2) **ALLOW ECF** for steps 2 −5 2. Find square root of q^2 (q) 3. Subtract figure(q) from 1 (p) 4. Multiply p × p (p^2) 5. (p2) × 600 **Examiner's Comments** Candidates who were able to calculate the allele frequency correctly (q^2=150/600=0.25) often later reached the correct answer of 150 for 2 marks, or gained a mark for their calculations, even if they didn't reach the correct answer. The most common error was to assume 150/600 was q rather than q^2.
			Total	**2**	
10			environmental ✓ stimuli ✓ apoptosis ✓ enzymes ✓ phagocytes / phagocytosis ✓	5(AO1.2)	**ALLOW** stress / factors **ALLOW** proteases / caspases **IGNORE** lysosomes **ALLOW** macrophages / endocytosis **Examiner's Comments** The majority of responses for the first three blank spaces were correct. Few responses were able to gain full marks. For each blank, the most common incorrect responses were 'hormonal' and 'conditions'. Nearly all candidates got this right, although spellings that were not phonetically similar were not given marks. Examples of these are: phagocytes, lysosomes and

					lysozyme, exocytosis, enzymes and vesicles.
			Total	**5**	
11		i	1 horizontal axis labelled 'body length (mm)' **AND** vertical axis labelled , 'frequency' / 'frequency density' (/100 mm) ✓ 2 linear scale on both axes **AND** at least 50% of grid covered by plotted area ✓ 3 histogram plotted with ruled lines and touching bars ✓ 4 first 5 bars plotted accurately ± 0.5 squares and equal width ✓ 5 6th bar twice the width and height 23 ✓	5(AO3.3)	*Points 1 and 2 can be awarded for a line graph*. **1 ALLOW** unit written as '/ mm' **1** Unit for frequency density can be omitted. **4** Correct numbers: 10, 48, 121, 130, 119 (or 0.10, 0.48. 1.21, 1.30, 1.19 if frequency density used) **5** Height 0.23 if axis labelled 'frequency density' **Examiner's Comments** The full range of marks was seen for this question in which candidates had to draw a histogram to represent the data they had been given. The vast majority achieved the first marking point with very few reversing the axes, neglecting to label the axes or omitting units for body length. The second marking point was given to most of the answers seen but often candidates used a categoric scale on the *x*-axis or, occasionally, used a *y*-axis scale that did not fill enough of the available space. Some candidates did not achieve the third marking point because they had drawn a bar chart (where the bars didn't touch) rather than a histogram but almost all knew to use a ruler. Of the candidates who drew bars, most drew them the correct height; however, a few, usually those who had chosen an unusual *y*-axis scale (e.g., going up in 15s), did not manage to find 121 or 119. Very few got the final marking point, suggesting not much practice of histograms in lessons. It was noted that those few candidates who achieved all 5 marks tended to plot

					frequency density. **OCR support** Presentation of practical results is regularly assessed in examinations. Help in development of these skills can be found in the OCR Biology Practical Skills Handbook: Biology Practical Skills Handbook (ocr.org.uk)
		ii	bell-shaped / normal distribution ✓ (data / variation) continuous ✓	2(AO2.2)(AO3.2)	**ALLOW** most frequent values in middle of range **ALLOW** e.g., most common length is between 400 and 500 **Examiner's Comments** Around half of responses achieved a mark here for stating either that the variation was continuous or describing the shape of the curve, but very few candidates did both and hence both marks were rarely given. The first marking point was often given for a description of a bell-shaped curve; however, some potentially creditworthy descriptions ended up as attempts to support hypotheses about selection pressures and so were not given marks. **Misconception** A number of responses stated that the graph did not show a normal distribution but the shape of the graph in this question is about as close to a normal distribution as is likely to be achieved with real data of this type.
			Total	**7**	