A Level Biology A

H420/02 Biological Diversity

Question Set 2

1   The sweet pea plant has been used to study inheritance since the nineteenth century. The seedsof the sweet pea can vary in colour and shape.

The gene that controls colour has two alleles:
- **Y** is dominant and produces yellow seeds.
- **y** is recessive and produces green seeds.

The gene that controls shape has two alleles:
- **R** is dominant and produces round seeds.
- **r** is recessive and produces wrinkled seeds.

(a)   In the nineteenth century, Gregor Mendel crossed a pea plant that was heterozygous for bothseed colour and shape with a pea plant that had green and wrinkled seeds.

(i)   List the gametes that would be produced by a sweet pea plant that was heterozygous forboth seed colour and shape.

YR, Yr, yR, yr

[1]

(ii)   List the genotypes of the offspring that were produced from Mendel's cross and state the corresponding phenotypes.

genotypes......YyRr., Yyrr., yyRr, yyrr...

phenotypes...yellow round., yellow wrinkled, green round....
and green wrinkled

[2]

(b)   When Mendel crossed two pea plants that were heterozygous for both seed colour andshape, the ratio of phenotypes in the offspring was:
- 9 yellow round
- 3 green round
- 3 yellow wrinkled
- 1 green wrinkled.

Some students tried to recreate this investigation using a modern variety of plant that showedthe same phenotypic variation in seed colour and shape.

The students crossed two of the modern plants that were heterozygous for both seed colourand shape. The results of this cross were:
- 58 yellow and round
- 31 green and round
- 21 yellow and wrinkled
- 2 green and wrinkled

The students used the chi-squared test to compare their data to the expected 9:3:3:1 ratio.

(i)

Use the chi-squared formula $\chi^2 = \sum \dfrac{(O-E)^2}{E}$ to calculate the χ^2 value for these data.

You may use the table below for working out.

O	E	O−E	$(O-E)^2$	$\dfrac{(O-E)^2}{E}$	
58	63	−5	25	0.40	
31	21	10	100	4.76	
21	21	0	0	0	
2	7	−5	25	3.57	

$\chi^2 =$ ......**8.73**...... **[3]**

Table 17 shows a χ^2 probability table.

Degrees of freedom	Probability (p)					
	0.95	0.90	0.10	0.05	0.025	0.01
1	0.00	0.02	2.71	3.84	5.02	6.64
2	0.10	0.21	4.61	5.99	7.38	9.21
3	0.35	0.58	6.25	7.82	9.35	11.34
4	0.71	1.06	7.78	9.49	11.14	13.28
5	1.15	1.61	9.24	11.07	12.83	15.09
6	1.64	2.20	10.64	12.59	14.45	16.81
7	2.17	2.83	12.02	14.07	16.01	18.48

Table 17

(ii) After analysing the results, the students stated that the inheritance of the seed colour and shape in their investigation was different from that in Mendel's investigation.

Using Table 17, discuss whether the results of the investigation and the chi-squared test support the students' statement. **[3]**

4 expected outcomes so df = 4−1 = 3
For the difference to be significant p needs to be less than 0.05 so the χ^2 needs to be greater than 7.82.
Since 8.73 is greater than 7.82, the Chi squared test and the observation do support the student's statement.
p is less than 0.05 thus the difference is significant. The probability that the difference is due to chance is about less than 5% and more than 2.5%.

(iii) A ratio that is different from the expected 9:3:3:1, in a cross such as this, can be the result of epistasis.

Suggest and explain one reason, **other** than epistasis, why the phenotype ratio might not be 9:3:3:1.

[3]

Both alleles may occur on the same chromosome so no independent assortment may occur. Hence the alleles would inherit together in the same gamete unless chiasma is formed between gene loci.

(c) The yellow colour in peas is the result of an enzyme that breaks down chlorophyll, which is green.

- The **Y** allele codes for the production of an enzyme that breaks down chlorophyll.
- The **y** allele is the result of a mutation in the **Y** allele.
- The **y** allele codes for an inactive form of this enzyme.

(i)* Outline how the **Y** allele codes for the production of this enzyme **and** explain why the **y** allele codes for an enzyme with a different primary structure.

[6]

DNA base sequence codes for amino acid sequence using mRNA. The base triplet on mRNA codes for one amino acid. The code is degenerate thus substitution at the 3rd base could result in same amino acid. During transcription, complementary base pairing occurs (A with U / T with A / C with G / G with C) to form a strand of mRNA that is complementary to the DNA strand. This process is catalysed by RNA polymerase. After transcription of mRNA, translation occurs in the ribosomes where mRNA is translated into chain of amino acids. mRNA binds to the ribosome then tRNA brings specific amino acid and binds to mRNA. This process repeats across the whole mRNA resulting production of polypeptide.

Y allele may result in a different primary structure due to base substitution or deletion (leading to frame-shift). Both affects the base sequence of DNA resulting in different mRNA codon and different amino acid. Hence the amino acid sequence (the primary structure) is different.

(ii) With reference to the proteins coded for by the seed colour gene, explain why the **y** allele is recessive.

2 y alleles are required to prevent the functional enzymes [1] from being synthesized.

Total Marks for Question Set 2: 19