



## AP<sup>®</sup> Biology 2003 Sample Student Responses

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## Critical Values of the Chi-Squared Distribution

Probability (p)	Degrees of Freedom (df)				
	1	2	3	4	5
0.05	3.84	5.99	7.82	9.49	11.1

The formula for Chi-squared is:

$$\chi^2 = \sum \left[ \frac{(o-e)^2}{e} \right]$$

where o = observed number of individuals

e = expected number of individuals

$\Sigma$  = the sum of the values (in this case, the differences, squared, divided by the number expected)

a) The genotypes of the original parents ~~are~~ <sup>are</sup>  $X^e X^e$  for the female and  $X^E Y$  for the male. The trait is sex-linked, only carried on the X chromosome. The female is homozygous recessive for white eyes while the male has a single dominant gene. The validity of these genotypes can be seen with a Punnett square:

	$X^E$	$Y$
$X^e$	$X^E X^e$	$X^e Y$
$X^e$	$X^E X^e$	$X^e Y$

In the F<sub>1</sub> generation, half of the offspring are females heterozygous for wild-type eyes while the other half are males with <sup>only</sup> white-eye genes.

GO ON TO THE NEXT PAGE.

## ADDITIONAL PAGE FOR ANSWERING QUESTION 1

b) The expected genotypes for generation  $F_2$  are shown in a Punnett square:

	$x^e$	$Y$
$X^E$	$X^E x^e$	$X^E Y$
$x^e$	$x^e x^e$	$x^e Y$

Wild-type females <sup>( $X^E x^e$ )</sup>, white-eyed females ( $x^e x^e$ ), wild-type males ( $X^E Y$ ), and white-eyed males ( $x^e Y$ ) should all show up in equal proportions (1:1:1:1). Thus, it is expected <sup>(null hypothesis)</sup> that for the 100 individuals of generation  $F_2$ , 25 individuals should show each phenotype <sup>(not brown-eyed)</sup>. This would be the expected count for each term in the  $\chi^2$  test.

$$\chi^2 = \frac{(23-25)^2}{25} + \frac{(31-25)^2}{25} + \frac{(22-25)^2}{25} + \frac{(24-25)^2}{25}$$

$$= \frac{4+36+9+1}{25} = \frac{50}{25} = 2$$

$$df = (\text{rows}-1)(\text{cols}-1) = (1)(3) = 3$$

The critical value for the  $\chi^2$  test statistic at the  $\alpha=0.05$  significance level is  $\chi^2 = 7.82$ . Since the observed  $\chi^2$  statistic ( $\chi^2 = 2$ ) is less than this value, ~~it~~ can be concluded the observed phenotypes do not vary statistically significantly from the expected <sup>counts</sup> ~~ratios~~ of each phenotype. The proposed genotypes for each generation and the proposed pattern of inheritance (sex-linked) are statistically affirmed to be true.

GO ON TO THE NEXT PAGE.

## ADDITIONAL PAGE FOR ANSWERING QUESTION 1

c) A mutation is the change in the ~~genetic~~ <sup>genotype</sup> or DNA of an individual. A mutation, depending on what type it is, may or may not be reflected in the phenotype of the individual. In this case, a mutation was reflected in the brown-eyed phenotype of 1 individual in generation F<sub>1</sub>. This could have been the result of a base pair substitution or an inversion. A base pair substitution would have occurred the DNA replication of the individual in which a single wrong base pair would have been substituted for a correct one. For example, opposite a guanine, an adenine may have been placed in the complementary strand instead of cytosine. In this case, the substitution would have changed a single codon (3 consecutive base pairs) so that it began to code for a single different amino acid, which would have changed the resulting protein the amino acid is incorporated into for eye color. Thus, the eye color would have changed. In an inversion, a sequence of base pairs would have been inverted in the DNA sequence. For example GCAATTG may have been changed to GCTTAG. This inversion would have led to the change in one or more codons, resulting in the production

GO ON TO THE NEXT PAGE.

ADDITIONAL PAGE FOR ANSWERING QUESTION 1

of a different amino acid than normal, resulting in a protein for brown eye color rather than the typical wild-type or white.

GO ON TO THE NEXT PAGE.

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a) The original parents had the genotype  $EY$  and  $ee$ . The trait must be sex-linked because in the  $F_1$  generation each phenotype occurred in either females or males, but not both. The ratio of Wild-type to White-eyed is approximately 1:1, and by crossing  $EY$  and  $ee$  (where  $EY$  is the father,  $ee$  is the mother), a 1:1 ratio of phenotypes is produced so that all females are one type, all males are another:

	$E$	$Y$	
$e$	$Ee$	$eY$	$Ee$ = Wild Type females
$e$	$Ee$	$eY$	$eY$ = White-eyed males

In this cross, the allele for wild-type eyes is dominant and for white-eyes is recessive.

GO ON TO THE NEXT PAGE.

b)

	e	Y
E	Ee	EY
e	ee	eY

ADDITIONAL PAGE FOR ANSWERING QUESTION 1

100 individuals were tested, and since the ratios of male to female and wild to white are both predicted to be 1:1, each gender phenotype would have an expected number of 25 individuals

$$\chi^2 = \sum \left( \frac{(O - E)^2}{E} \right)$$

Wild Male  $23 - 25 = (-2)^2 = \frac{4}{25}$

Wild Female  $31 - 25 = (6)^2 = \frac{36}{25}$

White Male  $22 - 25 = (-3)^2 = \frac{9}{25}$

White Female  $24 - 25 = (-1)^2 = \frac{1}{25}$

$$\frac{4}{25} + \frac{36}{25} + \frac{9}{25} + \frac{1}{25} = \frac{50}{25} = 2$$

$$2 = 5.99$$

This is the Chi-squared value

c) A mutation is any random spontaneous change in the genotype of an individual. It can be as small as the change in one base pair, or the relocation of an entire codon.

GO ON TO THE NEXT PAGE.

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- a) The genotype of the original female fruit fly is:  $X^E X^E$ , and the genotype of the original male fruit fly is:  $X^E Y$ . This is known because besides the 1 brown-eyed female in the F1 generation, all the rest of the F1 females are wild-type, and all the F1 males are white-eyed. Because there are only white-eyed males in F1, each male has to have gotten the recessive "e" allele from his mother. Because no F1 males show they received a dominant "E" allele from his mother, one can conclude that both of the mother's alleles were the recessive "e's". One can then also conclude that the original male carried the dominant allele. This is the only way all the females in the F1 generation can be wild type. If the original male carried the recessive allele, that allele combined with the recessive allele from the mother would produce all white-eyed females in the F1 generation.  $\longrightarrow$

GO ON TO THE NEXT PAGE.



ADDITIONAL PAGE FOR ANSWERING QUESTION 1

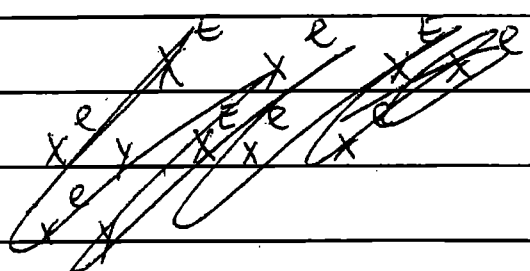
The punnett square for the original cross would be:

	$X^E$	$X^e$
$X^E$	$X^E X^E$	$X^E X^e$
$X^e$	$X^E X^e$	$X^e X^e$
$Y$	$X^E Y$	$X^e Y$

as the punnett square shows, all the females are heterozygous dominant (wild-type) and all the males are recessive (white-eyed)

The F2 generation further proves the genotypes of the P generation. Wild-type males are present in the F2 generation in approximately the same amount as white-eyed males. This is because all the females in F1 are heterozygous, meaning they each have one dominant allele "E" and one recessive allele "e". This means that all the males have a 50% chance of receiving the dominant allele and a 50% chance of receiving the recessive allele. White-eyed females are also present in the F2 generation because like the males, they also have a 50% chance of receiving the recessive allele "e" from the heterozygous mother, and the F2 females always receive a recessive "e" from the father.

the punnett square for F1 x F1 is:



	$X^E$	$X^e$
$X^E$	$X^E X^E$	$X^E X^e$
$X^e$	$X^E X^e$	$X^e X^e$
$Y$	$X^E Y$	$X^e Y$

- 25 wild-type females
- 25 white-eye females
- 25 wild-type males
- 25 white-eye males

GO ON TO THE NEXT PAGE.

## ADDITIONAL PAGE FOR ANSWERING QUESTION 1

$$b) \quad \chi^2 = \sum \left[ \frac{(o-e)^2}{e} \right] \quad \text{total F}_2 = 23 + 31 + 22 + 24 = 100$$

$$\left[ \frac{(23-25)^2}{25} + \frac{(31-25)^2}{25} + \frac{(22-25)^2}{25} + \frac{(24-25)^2}{25} \right]$$

↑	↑	↑	↑
wild-type male	wild-type female	white-eyed male	white-eyed female

$$\frac{4}{25} + \frac{36}{25} + \frac{9}{25} + \frac{1}{25} = \frac{40}{25} \approx 1.6$$

The chi-squared test confirms the genotypes of the P generation. The actual and expected outcomes, as shown by the chi squared test are very similar (less than 2 degrees of freedom)

c) A mutation is a mistake that occurs when duplicating DNA, in this case before going through meiosis. Two mutations that could have occurred are an inversion or a repetition. The amino acid sequences determine the functions of a protein. So if this sequence is not exactly correct the gene for eye color (in this case) may be changed. If an inversion were to occur there would be extra amino acids inserted in the sequence. If a deletion were to occur some of the amino acids would be missing, and if a repetition were to occur there would appear to be extra amino acids. A difference in amino acid sequence completely changes a protein starting at primary structure, which would also alter secondary, tertiary, and quaternary structure. A protein does not perform the same function when its shape is altered.

GO ON TO THE NEXT PAGE.

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(a.) The original parents the mother was a homozygous recessive  $x^e x^e$  and the father was a dominant  $X^E Y$  in order to get their offspring white-eyes is a recessive trait and wild-type is dominant

		mom	
		$x^E$	$x^e$
dad	$x^E$	$X^E x^E$	$X^E x^e$
	$y$	$x^E y$	$x^e y$

(b.) Wild-type male " " female white male " " female

$$\Sigma = \left[ \frac{(23-25)^2}{25} \right] = 1.6 \quad \Sigma = \left[ \frac{(31-25)^2}{25} \right] = 1.44 \quad \Sigma = \left[ \frac{(22-25)^2}{25} \right] = 3.6 \quad \Sigma = \left[ \frac{(24-25)^2}{25} \right] = 0.4$$

(c.) A mutation is a change in the DNA sequence in an organism/cell in which the sequence is different from the original. Two types of mutations are deletion, where a part of the sequence is totally omitted in the copying process and thus a whole new sequence is made, (for example the original sequence AC<sub>6</sub> TAT CCT becomes AC<sub>6</sub> ATC CT<sub>-</sub>), and inversion, where a new amino acid or

GO ON TO THE NEXT PAGE.

ADDITIONAL PAGE FOR ANSWERING QUESTION 1

amino acid sequence is added to the sequence (for example ACG TAT CCT becomes ACG TAC <sup>added</sup> GGT CCT) these mutations could have produced the brown eyed mutation b/c they changed the entire sequence of ~~genes~~ nucleic acids in the DNA on a chromosome so that the sequence that coded for eyes was no longer white or wild-type but brown.

GO ON TO THE NEXT PAGE.