

Test (UAS) Outline

Learning Objectives	Items	Important aspect of answer key	Scoring rubric
<p>The students be able to solve the problem of genetics involving the polygenic inheritance</p>	<p>1. An inbred strain of plants has a mean height of 24 cm. A second strain of the same species from a different country also has a mean height of 24cm. The F1 plants from a cross between these two strains are also 24 cm high. However, the F2 generation shows a wide range of heights; the majority are like the P1 and F1 plants, but approximately 4 of 1000 are only 12 cm high, and 4 of 1000 are 36 cm high.</p> <p>(a) What mode of inheritance is occurring here? (b) How many gene pairs are involved? (c) How much does each gene contribute to the plant height? (d) Indicate one possible set of genotypes of the P1 and F1 plants that could explain their heights. (e) Indicate one possible set of genotypes to account for F2 plants that are 18 cm or 33 cm high</p>	<p>(a) Quantitative inheritance (b) The frequency of either extreme phenotype gives us n, the number of gene pairs-- Frequency of one extreme phenotype = $(1/4)^n = 1/250$ of gene pairs = $\log(250) / \log(4) = 4$. (c) The maximum contribution of additive alleles = $36 - 12 = 24$ cm. Since 8 additive alleles (4 genes) contribute 24 cm, each additive allele contributes 3 cm. (d) Each parent has 4 additive alleles; since the F1 also have 4 additive alleles, the parents must be each be homozygous; the additive alleles of one parent are not present in the other. For example, the genotypes could be AABbCCdd x aabbCCDD (or other genotypes following that pattern). (e) An 18 cm plant has 2 additive alleles; any genotype such as AAbbCCdd or aaBBCCdd would work. A 33 cm plant has 7 additive alleles; any genotype such as AABbCCDd or AaBBCCDD would work.</p>	<p>There are five important aspects, one aspect is true got 1/5 x 100 score</p>
<p>The students be able to solve the problem of genetics involving the sex linkage</p>	<p>2. Marian's father is colorblind, as is her maternal grandfather (her mother's father). Marian herself has normal color vision. Marian and her husband, Martin, who is also colorblind, have just had their first child, a son they have named Mickey. Please answer the following questions about this small family.</p> <p>a. What is the probability that this child will be colorblind? b. Three sources of the colorblindness allele are mentioned in this family. If Mickey is colorblind, from which of these</p>	<ul style="list-style-type: none"> Marian is a heterozygote, because she herself is not colorblind, but her father was. For Marian, her maternal grandfather's colorblindness is immaterial. The X she inherited from her mother must carry the dominant normal color vision allele. Martin, Marian's husband, had the colorblindness allele on his only X chromosome. <p>a. The probability that Mickey will be colorblind is 0.5 (50%). A son inherits his X chromosome from his mother, and Marian has one with the C allele and one with the c allele. He has an</p>	<p>There are three important aspects. One aspect is true, got 1/3 x 100 score</p>

	<p>three men (Marian's grandfather, Marian's father, or Martin) did he inherit the allele?</p>	<p>equivalent chance of receiving either one. b.Mickey's colorblindness allele came from Marian's father (via Marian herself, of course. Mickey's direct source of the allele was Marion. Mickey didn't get it from Martin, his father, because he had to get his Y chromosome from Martin, and the Y chromosome has no allele for this gene on it.</p>																			
<p>The students be able to solve the problem of genetics involving the linkage genes</p>	<p>3. An individual is heterozygous for four genes, named a, b, c and d. The mutations are recessive. This individual is test-crossed with another individual who is homozygous recessive for all 4 traits. 1,000 progeny are found as follows:</p> <table border="1" data-bbox="324 608 1115 967"> <thead> <tr> <th>phenotype</th> <th># of progeny</th> </tr> </thead> <tbody> <tr> <td>ab⁺c⁺d⁺</td> <td>42</td> </tr> <tr> <td>a⁺bcd</td> <td>43</td> </tr> <tr> <td>a⁺b⁺c⁺d</td> <td>140</td> </tr> <tr> <td>abcd⁺</td> <td>145</td> </tr> <tr> <td>ab⁺cd⁺</td> <td>6</td> </tr> <tr> <td>a⁺bc⁺d</td> <td>9</td> </tr> <tr> <td>a⁺b⁺cd</td> <td>305</td> </tr> <tr> <td>abc⁺d⁺</td> <td>310</td> </tr> </tbody> </table> <p>Which genes, if any, are linked?</p>	phenotype	# of progeny	ab ⁺ c ⁺ d ⁺	42	a ⁺ bcd	43	a ⁺ b ⁺ c ⁺ d	140	abcd ⁺	145	ab ⁺ cd ⁺	6	a ⁺ bc ⁺ d	9	a ⁺ b ⁺ cd	305	abc ⁺ d ⁺	310	<ul style="list-style-type: none"> The a and b loci should be 1:1:1:1 if they assort independently (1/2 X 1/2 for each of the 4 phenotypes) and If not then they must not assort independently For phenotype a = 42 + 145 + 6 + 310 = 503 a⁺ = 43 + 140 + 9 + 305 = 497 b = 43 + 145 + 9 + 310 = 507 b⁺ = 42 + 140 + 6 + 305 = 493 c = 43 + 145 + 6 + 305 = 499 c⁺ = 42 + 140 + 9 + 310 = 501 d = 43 + 140 + 9 + 305 = 497 d⁺ = 42 + 145 + 6 + 310 = 503 In all cases the a 1:1 which implies a heterozygous individual crossed with homozygous recessive. If they assort independently we would expect to find a 1:1:1:1 for ab, ab⁺, a+b, a+b⁺. calculation : ab = 145 + 310 = 455, ab⁺ = 42 + 6 = 48, a+b = 43 + 9 = 52, a+b⁺ = 140 + 305 = 445. They don't see a 1:1:1:1 and instead see ab as one parental chromosome and a+b⁺ as the other. Map distance = 100/1,000. 10 map units between a & b It would then look at bc. b+c⁺ = 42 + 140 = 182, bc = 43 + 145 = 188, b+c = 6 + 305 = 311, bc⁺ = 9 + 310 = 319. Map distance = 370/1,000 = 37 map units between b and c. Check c and d. c+d⁺ = 42 + 310 = 352, cd = 43 + 305 = 348, c+d = 140 + 9 = 149, cd⁺ = 145 + 6 = 151. Map distance = 300/1,000 = 30 map units between c and d. Check a and c. a c⁺ = 42 + 310 = 352, a⁺ c = 43 + 305 = 	<p>There are ten important aspect. One aspect is true got 1/10 x 100 score</p>
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		<p>348, $a^+ c^+ = 140 + 9 = 149$, $a c = 145 + 6 = 151$. $300/1,000 = 30$ map units between a and c.</p> <ul style="list-style-type: none">• Gene order is c a d b. The a and d alleles are actually very close to one another.• The parental chromosomes are $c^+ a^+ d^+ b^- / c^- a^- d^- b^+$.• In each case they do not show independent assortment – thus all 4 are genetically linked	
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