Dihybrid cross punnett square practice answers

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Punnett Squares

Dihybrid Crosses

Name Date

1. In horses, the coat color black is dominant (B) over chestnut (b). The trotting gait is dominant (T) over the pacing gait (t). If a homozygous black pacer is mated to a homozygous chestnut, heterozygous trotter, what will be the probabilities for genotype and phenotype of the F1 generation?

2. In rabbits, the coat color black dominant (B) over brown (b). Short hair is dominant (S) over long (s). In a cross between a homozygous black short-haired male and a brown homozygous long haired female, what would be the probabilities for genotype and phenotype of the F1 generation?

3. Imagine that a couple is planning to have children. The male is heterozygous for tongue rolling and homozygous dominant for unattached earlobes. The female is homozygous recessive for tongue rolling and heterozygous for unattached earlobes. The couple is curious about the possibility and probability of their offspring inheriting these traits. The ability to roll ones tongue is dominant (R) over the "non-rolling" condition (r.) Unattached earlobes (U) are dominant over attached earlobes (u) Complete a Punnett square for this cross and record the probabilities for genotypes and phenotypes of the offspring as ratios!

2. Tall tomato plants, D, is dominant to dwarf tomato plants, d. Hairy stems, H, are dominant to hairless stems, h. What are the genotypic and phenotypic ratios when you cross a heterozygous tall, hairless plant with a plant that is heterozygous for both tall and hairy stems?

_____ x _____

Genotypic ratio Phenotypic ratio

3. In fruit flies, red eyes, R, is dominant to magenta eyes, r. Long wings, L, is dominant to short wings, l. A heterozygous red-eyed, short-winged male is bred to a magenta-eyed, heterozygous long-winged female. What percentage of their offspring should have magenta eyes and short wings?

3

Dihybrid Punnett Square Practice Problems

Directions: Answer the questions that follow in your science notebook.

1. For a particular plant, the **allele for tall (T) is dominant** over the allele for short (t). For the same plant, the allele for **colored flowers (C)** is dominant over white flowers (c). A farmer crossbreeds the **hybrid plants as shown** in the Punnett square below. **What**

Parent 1: TtCc

	TC	Tc	tC	tc
TC	TTCC	TTCc	TtCC	TtCc
Tc	TTCc	TTcc	TtCc	Ttcc
tC	TtCC	TtCc	ttCC	ttCc
tc	TtCc	Ttcc	ttCc	ttcc

Parent 2: TtCc

2. For a particular rodent, **black fur (B)** is dominant over brown fur (b), and a long tail (L) is dominant over a short tail (l). **Create a Punnett square that shows the genotypes** of all the possible offspring that could result from the breeding of two of the rodents that are heterozygous for both traits.

Genotype for the cross

_____ **x** _____

Key
B-
b-

L-
l-

a. What ratio of genotypes would result? Show your work.
b. What ratio of phenotypes would result? Show your work.

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Name: _____

Bikini Bottom Genetics
Worksheet #1: Understanding Vocabulary & Punnett Squares

Complete the following practice activities…

1. **For each genotype below, indicate whether it is a heterozygous (He) OR homozygous (Ho).**

TT _____ Bb _____ DD _____ Ff _____ tt _____ dd _____
Dd _____ ff _____ Tt _____ bb _____ BB _____ FF _____

Which of the genotypes in #1 would be considered **purebred**?_____
Which of the genotypes in #1 would be **hybrids**?_____

2. **Determine the phenotype for each genotype using the information provided about SpongeBob.**

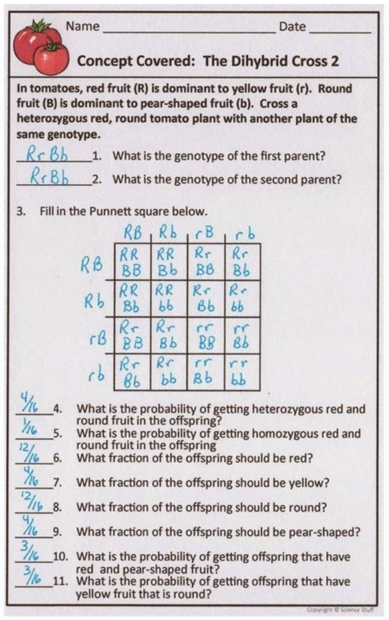
Yellow body color is dominant to blue.
YY _____ Yy _____ yy _____

3. **For each phenotype, give the genotypes that are possible for Patrick.**

A tall head (T) is dominant to short (t).
Tall = _____ Short = _____

Match each term with its meaning…

1.	**Allele**	**A**	Cell with one of each kind of chromosome
2.	**Dominant**	**B**	Outward appearance of an organism, regardless of its genes
3.	**Gamete**	**C**	Characteristic that is inherited; can be either dominant or recessive
4.	**Genotype**	**D**	Trait of an organism that can be masked by the dominant form of a trait
5.	**Haploid**	**E**	Observed trait of an organism that mask the recessive form of a trait
6.	**Heredity**	**F**	Transfer of male pollen grains to the pistil of a flower
7.	**Heterozygous**	**G**	Alternative forms of a gene for each variation of a trait of an organism
8.	**Homozygous**	**H**	Passing on of characteristics from parents to offspring
9.	**Phenotype**	**I**	Combination of genes in an organism
10.	**Pollination**	**J**	When there are two different alleles for a trait
11.	**Recessive**	**K**	When there are two identical alleles for a trait
12.	**Trait**	**L**	Male and female sex cells, sperm and eggs



Name _____ Date _____

Concept Covered: The Dihybrid Cross 2

In tomatoes, red fruit (R) is dominant to yellow fruit (r). Round fruit (B) is dominant to pear-shaped fruit (b). Cross a heterozygous red, round tomato plant with another plant of the same genotype.

RrBb 1. What is the genotype of the first parent?

RrBb 2. What is the genotype of the second parent?

3. Fill in the Punnett square below.

	RB	Rb	rB	rb
RB	RR BB	RR Bb	Rr BB	Rr Bb
Rb	RR Bb	RR bb	Rr Bb	Rr bb
rB	Rr BB	Rr Bb	rr BB	rr Bb
rb	Rr Bb	Rr bb	rr Bb	rr bb

4/16 4. What is the probability of getting heterozygous red and round fruit in the offspring?

1/16 5. What is the probability of getting homozygous red and round fruit in the offspring

12/16 6. What fraction of the offspring should be red?

4/16 7. What fraction of the offspring should be yellow?

12/16 8. What fraction of the offspring should be round?

4/16 9. What fraction of the offspring should be pear-shaped?

3/16 10. What is the probability of getting offspring that have red and pear-shaped fruit?

3/16 11. What is the probability of getting offspring that have yellow fruit that is round?

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How to cross a dihybrid punnett square. How to use a punnett square dihybrid cross. Dihybrid cross punnett square practice problems with answers.

A chi-square (X2) goodness of fit test is a type of Pearson’s chi-square test. You can use it to test whether the observed distribution of a categorical variable differs from your expectations. Example: Chi-square goodness of fit testYou’re hired by a dog food company to help them test three new dog food flavors. You recruit a random sample of 75 dogs and offer each dog a choice between the three flavors by placing bowls in front of them. You expect that the flavors will be equally popular among the dogs, with about 25 dogs choosing each flavor. Once you have your experimental results, you plan to use a chi-square goodness of fit test to figure out whether the distribution of the dogs’ flavor choices is significantly different from your expectations. The chi-square goodness of fit test tells you how well a statistical model fits a set of observations. It’s often used to analyze genetic crosses. What is the chi-square goodness of fit test? A chi-square (X2) goodness of fit test is a goodness of fit test for a categorical variable. Goodness of fit is a measure of how well a statistical model fits a set of observations. When goodness of fit is high, the values expected based on the model are close to the observed values. When goodness of fit is low, the values expected based on the model are far from the observed values. The statistical models that are analyzed by chi-square goodness of fit tests are distributions. They can be any distribution, from as simple as equal probability for all groups, to as complex as a probability distribution with many parameters. Hypothesis testing The chi-square goodness of fit test is a hypothesis test. It allows you to draw conclusions about the distribution of a population based on a sample. Using the chi-square goodness of fit test, you can test whether the goodness of fit is “good enough” to conclude that the population follows the distribution. With the chi-square goodness of fit test, you can ask questions such as: Was this sample drawn from a population that has… Equal proportions of male and female turtles? Equal proportions of red, blue, yellow, green, and purple jelly beans? 90% right-handed and 10% left-handed people? Offspring with an equal probability of inheriting all possible genotypic combinations (i.e., unlinked genes)? A Poisson distribution of floods per year? A normal distribution of bread prices? Example: Observed and expected frequenciesAfter weeks of hard work, your dog food experiment is complete and you compile your data in a table: Observed and expected frequencies of dogs’ flavor choices Flavor Observed Expected Garlic Blast 22 25 Blueberry Delight 30 25 Minty Munch 23 25 To help visualize the differences between your observed and expected frequencies, you also create a bar graph: The president of the dog food company looks at your graph and declares that they should eliminate the Garlic Blast and Minty Munch flavors to focus on Blueberry Delight. “Not so fast!” you tell him. You explain that your observations were a bit different from what you expected, but the differences aren’t dramatic. They could be the result of a real flavor preference or they could be due to chance. To put it another way: You have a sample of 75 dogs, but what you really want to understand is the population of all dogs. Was this sample drawn from a population of dogs that choose the three flavors equally often? Chi-square goodness of fit test hypotheses Like all hypothesis tests, a chi-square goodness of fit test evaluates two hypotheses: the null and alternative hypotheses. They’re two competing answers to the question “Was the sample drawn from a population that follows the specified distribution?” These are general hypotheses that apply to all chi-square goodness of fit tests. You should make your hypotheses more specific by describing the “specified distribution.” You can name the probability distribution (e.g., Poisson distribution) or give the expected proportions of each group. Example: Null and alternative hypothesis Null hypothesis (H0): The dog population chooses the three flavors in equal proportions (p1 = p2 = p3). Alternative hypothesis (Ha): The dog population does not choose the three flavors in equal proportions. When to use the chi-square goodness of fit test The following conditions are necessary if you want to perform a chi-square goodness of fit test: You want to test a hypothesis about the distribution of one categorical variable. If your variable is continuous, you can convert it to a categorical variable by separating the observations into intervals. This process is known as data binning. The sample was randomly selected from the population. There are a minimum of five observations expected in each group. Example: Chi-square goodness of fit test conditionsYou can use a chi-square goodness of fit test to analyze the dog food data because all three conditions have been met: You want to test a hypothesis about the distribution of one categorical variable. The categorical variable is the dog food flavors. You recruited a random sample of 75 dogs. There were a minimum of five observations expected in each group. For all three dog food flavors, you expected 25 observations of dogs choosing the flavor. How to calculate the test statistic (formula) The test statistic for the chi-square (X2) goodness of fit test is Pearson’s chi-square: Formula Explanation is the chi-square test statistic is the summation operator (it means “take the sum of”) is the observed frequency is the expected frequency The larger the difference between the observations and the expectations (O − E in the equation), the bigger the chi-square will be. To use the formula, follow these five steps: Step 1: Create a table Create a table with the observed and expected frequencies in two columns. Example: Step 1 Flavor Observed Expected Garlic Blast 22 25 Blueberry Delight 30 25 Minty Munch 23 25 Step 2: Calculate O − E Add a new column called “O − E”. Subtract the expected frequencies from the observed frequency. Example: Step 2 Flavor Observed Expected O − E Garlic Blast 22 25 22 − 25 = −3 Blueberry Delight 30 25 5 Minty Munch 23 25 −2 Step 3: Calculate (O − E)2 Add a new column called “(O − E)2”. Square the values in the previous column. Example: Step 3 Flavor Observed Expected O − E (O − E)2 Garlic Blast 22 25 −3 (−3)2 = 9 Blueberry Delight 30 25 5 25 Minty Munch 23 25 −2 4 Step 4: Calculate (O − E)2 / E Add a final column called “(O − E)² / E“. Divide the previous column by the expected frequencies. Example: Step 4 Flavor Observed Expected O − E (O − E)2 (O − E)² / E Garlic Blast 22 25 −3 9 9/25 = 0.36 Blueberry Delight 30 25 5 25 1 Minty Munch 23 25 −2 4 0.16 Step 5: Calculate X2 Add up the values of the previous column. This is the chi-square test statistic (X2). Example: Step 5 Flavor Observed Expected O − E (O − E)2 (O − E)2 / E Garlic Blast 22 25 −3 9 9/25 = 0.36 Blueberry Delight 30 25 5 25 1 Minty Munch 23 25 −2 4 0.16 X2 = 0.36 + 1 + 0.16 = 1.52 How to perform the chi-square goodness of fit test The chi-square statistic is a measure of goodness of fit, but on its own it doesn’t tell you much. For example, is X2 = 1.52 a low or high goodness of fit? To interpret the chi-square goodness of fit, you need to compare it to something. That’s what a chi-square test is: comparing the chi-square value to the appropriate chi-square distribution to decide whether to reject the null hypothesis. To perform a chi-square goodness of fit test, follow these five steps (the first two steps have already been completed for the dog food example): Step 1: Calculate the expected frequencies Sometimes, calculating the expected frequencies is the most difficult step. Think carefully about which expected values are most appropriate for your null hypothesis. In general, you’ll need to multiply each group’s expected proportion by the total number of observations to get the expected frequencies. Step 2: Calculate chi-square Calculate the chi-square value from your observed and expected frequencies using the chi-square formula. Step 3: Find the critical chi-square value Find the critical chi-square value in a chi-square critical value table or using statistical software. The critical value is calculated from a chi-square distribution. To find the critical chi-square value, you’ll need to know two things: Example: Finding the critical chi-square valueSince there are three groups (Garlic Blast, Blueberry Delight, and Minty Munch), there are two degrees of freedom. For a test of significance at α = .05 and df = 2, the X2 critical value is 5.99. Step 4: Compare the chi-square value to the critical value Compare the chi-square value to the critical value to determine which is larger. Example: Comparing the chi-square value to the critical valueX2 = 1.52 Critical value = 5.99 The X2 value is less than the critical value. Step 5: Decide whether the reject the null hypothesis If the X2 value is greater than the critical value, then the difference between the observed and expected distributions is statistically significant (p α). The data doesn’t allow you to reject the null hypothesis and doesn’t provide support for the alternative hypothesis. Example: Deciding whether to reject the null hypothesisThe X2 value is less than the critical value. Therefore, you should not reject the null hypothesis that the dog population chooses the three flavors in equal proportions. There is no significant difference between the observed and expected flavor choice distribution (p > .05). This suggests that the dog food flavors are equally popular in the dog population. You report your findings back to the dog food company president. He decides not to eliminate the Garlic Blast and Minty Munch flavors based on your findings. The many dogs who love these flavors are very grateful! When to use a different test Whether you use the chi-square goodness of fit test or a related test depends on what hypothesis you want to test and what type of variable you have. When to use the chi-square test of independence There’s another type of chi-square test, called the chi-square test of independence. Use the chi-square goodness of fit test when you have one categorical variable and you want to test a hypothesis about its distribution. Use the chi-square test of independence when you have two categorical variables and you want to test a hypothesis about their relationship. When to use a different goodness of fit test The Anderson–Darling and Kolmogorov–Smirnov goodness of fit tests are two other common goodness of fit tests for distributions. Use the Anderson–Darling or the Kolmogorov–Smirnov goodness of fit test when you have a continuous variable (that you don’t want to bin). Use the chi-square goodness of fit test when you have a categorical variable (or a continuous variable that you want to bin). NoteThere are also goodness of fit tests for specific distributions. For example, the Shapiro–Wilk Test for normality is a goodness of fit test specifically to test for normal distributions. Specialized goodness of fit tests are usually more powerful, so they’re often the best choice when a specialized test is available for the distribution you’re interested in. Practice questions and examples Do you want to test your knowledge about the chi-square goodness of fit test? Download our practice questions and examples with the buttons below. Download Word doc Download Google doc Frequently asked questions about the chi-square goodness of fit test How do I perform a chi-square goodness of fit test for a genetic cross? Chi-square goodness of fit tests are often used in genetics. One common application is to check if two genes are linked (i.e., if the assortment is independent). When genes are linked, the allele inherited for one gene affects the allele inherited for another gene. Suppose that you want to know if the genes for pea texture (R = round, r = wrinkled) and color (Y = yellow, y = green) are linked. You perform a dihybrid cross between two heterozygous (RY / ry) pea plants. The hypotheses you’re testing with your experiment are: Null hypothesis (H0): The population of offspring have an equal probability of inheriting all possible genotypic combinations. This would suggest that the genes are unlinked. Alternative hypothesis (Ha): The population of offspring do not have an equal probability of inheriting all possible genotypic combinations. This would suggest that the genes are linked. You observe 100 peas: 78 round and yellow peas 6 round and green peas 4 wrinkled and yellow peas 12 wrinkled and green peas Step 1: Calculate the expected frequencies To calculate the expected values, you can make a Punnett square. If the two genes are unlinked, the probability of each genotypic combination is equal. RY ry Ry rY RY RRYY RrYy RRYy RrYY ry RrYy rryy Rryy rrYy Ry RRYy Rryy RRyy RrYy rY RrYY rrYy RrYy rrYY The expected phenotypic ratios are therefore 9 round and yellow: 3 round and green: 3 wrinkled and yellow: 1 wrinkled and green. From this, you can calculate the expected phenotypic frequencies for 100 peas: Phenotype Observed Expected Round and yellow 78 100 * (9/16) = 56.25 Round and green 6 100 * (3/16) = 18.75 Wrinkled and yellow 4 100 * (3/16) = 18.75 Wrinkled and green 12 100 * (1/16) = 6.21 Step 2: Calculate chi-square Phenotype Observed Expected O − E (O − E)2 (O − E)2 / E Round and yellow 78 56.25 21.75 473.06 8.41 Round and green 6 18.75 −12.75 162.56 8.67 Wrinkled and yellow 4 18.75 −14.75 217.56 11.6 Wrinkled and green 12 6.21 5.79 33.52 5.4 X2 = 8.41 + 8.67 + 11.6 + 5.4 = 34.08 Step 3: Find the critical chi-square value Since there are four groups (round and yellow, round and green, wrinkled and yellow, wrinkled and green), there are three degrees of freedom. For a test of significance at α = .05 and df = 3, the X2 critical value is 7.82. Step 4: Compare the chi-square value to the critical value X2 = 34.08 Critical value = 7.82 The X2 value is greater than the critical value. Step 5: Decide whether the reject the null hypothesis The X2 value is greater than the critical value, so we reject the null hypothesis that the population of offspring have an equal probability of inheriting all possible genotypic combinations. There is a significant difference between the observed and expected genotypic frequencies (p < .05). The data supports the alternative hypothesis that the offspring do not have an equal probability of inheriting all possible genotypic combinations, which suggests that the genes are linked

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