

Monohybrid Crosses and the Punnett Square

Names _____ Date _____ Period ____

Introduction: Scientists use a grid-like tool (Punnett Square) to make predictions about various genetic problems. The Punnett Square shows only the probability of what might occur and not the actual results. Probability is the chance of something occurring.

For example: If one wants to flip a coin 100 times, since there are 2 sides to the coin, he would expect 50 heads and 50 tails. If he flips the coin 100 times, he may actually get 60 heads and 40 tails.

Prediction is one thing, and actually getting the predicted results is another. The Punnett square only shows **the chances** of what might occur each time the event is under taken.

Objective: In this investigation you will use a Punnett square to predict the possible genotypes and phenotypes and their ratios from a monohybrid cross and compare the predicted results to actual experimental outcome.

Materials:

- 2 paper bags (one bag of male gametes and the other of female gametes)
- Red beads represent the dominant allele (ex: red coloration)
- White beads represent the recessive allele (ex: white coloration).

Procedure:

You and your partner will each impersonate a potential “parent” with paper bags containing beads to represent your gametes. Each “gamete” contains an allele for **coloration**, red or white. Check the contents of your bag. It should contain 15 red beads and 15 white beads.

1. Judging by the contents of your bag, are you (circle one):
 - a. homozygous dominant
 - b. heterozygous
 - c. homozygous recessive
2. If you are to be judged by the contents of your bag, write your genotype: _____
3. What color (phenotype) are you? _____

EXPECTED RESULTS

4. Complete the Punnett square, using the genotypes of you and your partner as “parents”, based on your answers to #2, above.

5. Summarize the expected **genotypes** in **ratio form** of your potential F₁ offspring:

6. Express your (above) answer as a **percentage**.

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7. What are the expected **phenotypes**, in **ratio form** of your potential F₁ offspring?
8. Express the phenotypes (above) as a **percentage**:

LAB EXERCISE:

Pull one bead out of each bag. Record the genotype and phenotype of the resulting "offspring". *Return the beads back into their bag* after each "fertilization" and conduct the same process 29 more times.

Data Table

Trial Number	Offspring Genotype	Offspring phenotype	Trial Number	Offspring Genotype	Offspring phenotype
1			16		
2			17		
3			18		
4			19		
5			20		
6			21		
7			22		
8			23		
9			24		
10			25		
11			26		
12			27		
13			28		
14			29		
15			30		

Next, Tally up the total # of each type of offspring you produced in your 30 matings:

Genotypes: _____ RR _____ Rr _____ rr

Phenotypes: _____ red _____ white

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If you weren't told on page 1 which was the dominant and which was the recessive allele, could you tell what the dominant trait is by looking at the phenotypes of the offspring? Explain.

YOUR ACTUAL LAB RESULTS: do this *after* pulling beads from bags

1. What is the genotypic ratio you found in the F₁ generation?
2. Express your (above) answer as a percentage:
3. What is the phenotypic ratio you found in the F₁ generation?
4. Express the phenotypic outcome (above) as a percentage:
5. **Calculate** the differences (in *phenotype percentages*) between the *expected result* and the *actual result* you found when you did your crosses (actual - expected, for both red and white).

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ANALYSIS

1. In your opinion, how did your actual finding compare to the expected results? How can you explain any differences? Why do you think the exact ratios don't always come about?
2. When you did your 30 test crosses, why was it important to replace your beads into the bags before each successive cross?
3. Had you performed 100 (or 1000) "matings" instead of only 30, do you expect that your results would have been closer to your expected result? Why or why not? Does the # of test trials matter, statistically?
 - This lab can be performed by tossing two coins if red and white beads are not available. Designate each "head" as a R (red) outcome and each "tail" as a r (white) outcome.