

Dihybrid Practice Problems Answer Key

Dihybrid Cross Problems:

Use Punnett Squares to solve these problems. You **MUST** show your work!

B = bark b = silent S = Standing ears s = droopy ears

1. Some dogs bark when trailing, others are silent. The barking trait is due to a dominant gene. Standing ears are dominant to drooping ears. Show the cross between a heterozygous standing-eared barker and a homozygous droopy eared silent trailer.

$SsBb \times ssbb$

	SB	Sb	sB	sb
sB	SsBb	Ssbb	ssBb	ssbb
sb	SsBb	Ssbb	ssBb	ssbb
sB	SsBb	Ssbb	ssBb	ssbb
sb	SsBb	Ssbb	ssBb	ssbb

a. What is the phenotypic ratio?

1 Standing Eared Barker:
1 Standing Eared Silent:
1 droopy eared Barker:
1 droopy eared Silent.

b. What is the genotypic ratio?

1 SsBb:
1 Ssbb:
1 ssBb:
1 ssbb

2. In guinea pigs, rough coat is dominant to smooth coat; and short hair is dominant over long hair. Cross a guinea pig homozygous for a rough and short coat with a guinea pig with a smooth long hair. After doing the cross, write the expected phenotypic and genotypic ratios of the offspring.

$RRSS \times rrss$

	RS	RS	RS	RS
rS	RrSs	RrSs	RrSs	RrSs
rS	RrSs	RrSs	RrSs	RrSs
rs	RrSs	RrSs	RrSs	RrSs
rs	RrSs	RrSs	RrSs	RrSs

c. Summarize the Phenotypes:

1 Rough, Short Coat : 0

b. Summarize the Genotypes:

1 RrSs : 0

Dihybrid Practice Problems: Answer Key and Mastering Mendelian Genetics

Understanding Mendelian genetics, particularly dihybrid crosses, can be challenging. But mastering these concepts is crucial for success in biology. This comprehensive guide provides a wealth of dihybrid practice problems, complete with detailed answer keys, to help you solidify your understanding. We'll walk through the principles, offer strategies for solving problems, and provide a series of practice questions to test your knowledge. By the end, you'll confidently tackle any dihybrid cross problem thrown your way!

Understanding Dihybrid Crosses: A Quick Refresher

Before diving into the practice problems, let's briefly revisit the fundamentals of dihybrid crosses. A dihybrid cross involves tracking the inheritance of two different traits, each controlled by a separate gene. These traits are passed down independently of each other, a principle known as Mendel's Law of Independent Assortment.

Key Terminology:

Allele: A variant form of a gene. For example, the gene for flower color in pea plants might have alleles for purple (P) and white (p).

Homozygous: Having two identical alleles for a particular gene (e.g., PP or pp).

Heterozygous: Having two different alleles for a particular gene (e.g., Pp).

Genotype: The genetic makeup of an organism (e.g., PP, Pp, pp).

Phenotype: The observable characteristics of an organism (e.g., purple flowers, white flowers).

Punnett Square: A diagram used to predict the genotypes and phenotypes of offspring from a cross.

The Dihybrid Punnett Square: A Step-by-Step Approach

A dihybrid Punnett Square is larger than a monohybrid square (used for single traits) because it accounts for all possible combinations of alleles from both parents. Here's a simplified approach:

1. **Identify the parental genotypes:** Determine the genotypes of the parents for both traits. For example, a parent heterozygous for both traits (e.g., RrYy) would contribute RY, Ry, rY, or ry gametes.
2. **Construct the Punnett Square:** Create a 4x4 grid to represent all possible combinations of gametes from both parents.
3. **Determine the offspring genotypes and phenotypes:** Fill in the Punnett Square by combining the alleles from each parent's gametes. This will reveal the genotypes and phenotypes of the offspring.
4. **Calculate probabilities:** Determine the probability of each genotype and phenotype by dividing the number of occurrences of each by the total number of offspring.

Dihybrid Practice Problems: Answer Key Included

Now let's move on to the practice problems. Each problem will be followed by a detailed solution.

Problem 1:

In pea plants, round seeds (R) are dominant to wrinkled seeds (r), and yellow seeds (Y) are dominant to green seeds (y). Cross two heterozygous plants (RrYy x RrYy). What are the phenotypic ratios of the offspring?

Answer Key Problem 1:

Using a 4x4 Punnett Square, we find the following phenotypic ratios:

9/16 Round, Yellow
3/16 Round, Green
3/16 Wrinkled, Yellow
1/16 Wrinkled, Green

This demonstrates the classic 9:3:3:1 phenotypic ratio expected in a dihybrid cross of heterozygotes.

Problem 2:

A homozygous dominant black, long-haired cat (BBLL) is crossed with a homozygous recessive white, short-haired cat (bbll). What are the genotypes and phenotypes of the F1 generation? What would be the phenotypic ratio of the F2 generation if two F1 cats were crossed? (Assume black (B) and long hair (L) are dominant traits).

Answer Key Problem 2:

F1 Generation: All F1 offspring will be heterozygous (BbLl) and exhibit the dominant phenotypes: black, long hair.

F2 Generation: A dihybrid cross of two F1 cats (BbLl x BbLl) will result in a phenotypic ratio of 9 black, long-haired : 3 black, short-haired : 3 white, long-haired : 1 white, short-haired.

Problem 3:

In tomatoes, red fruit (R) is dominant to yellow fruit (r), and tall plants (T) are dominant to short plants (t). A plant homozygous for red fruit and heterozygous for plant height (RR Tt) is crossed with a plant homozygous for yellow fruit and short height (rr tt). What are the expected genotypes and phenotypes of the offspring?

Answer Key Problem 3:

All offspring will be $RrTt$, resulting in a 100% red fruit, tall plant phenotype. This is because the dominant alleles (R and T) are present in every offspring genotype.

Conclusion

Mastering dihybrid crosses requires understanding the principles of Mendelian genetics and utilizing the Punnett Square effectively. By working through practice problems and carefully analyzing the results, you can build your confidence and expertise in this fundamental area of biology. Remember to practice regularly and consult additional resources if needed. The key is consistent effort and a clear understanding of the underlying concepts.

FAQs

Q1: Can I use a forked-line method instead of a Punnett Square for dihybrid crosses?

A1: Yes, the forked-line method (also known as the branch diagram) is an alternative method that can be equally effective, particularly for more complex crosses. It's often considered more efficient for larger crosses.

Q2: What if a gene shows incomplete dominance or codominance? How does this affect dihybrid crosses?

A2: In cases of incomplete dominance (blending of traits) or codominance (both alleles expressed equally), the phenotypic ratios will differ from the classic 9:3:3:1 ratio seen with complete dominance. You will need to adjust your phenotypic predictions to reflect the specific nature of the incomplete or codominant alleles.

Q3: Are there online tools or calculators that can help with dihybrid crosses?

A3: Yes, several online tools and calculators can assist you in solving dihybrid cross problems. These tools can automate the Punnett Square construction and calculations, saving you time and reducing the chance of errors.

Q4: How do linked genes affect dihybrid crosses?

A4: Linked genes, located close together on the same chromosome, do not assort independently as Mendel's Law suggests. Their inheritance is more complex and requires consideration of recombination frequencies to accurately predict offspring genotypes and phenotypes.

Q5: What are some real-world applications of understanding dihybrid crosses?

A5: Understanding dihybrid crosses has practical applications in various fields, including agriculture (plant breeding), animal husbandry, and genetic counseling. It's crucial for predicting traits in offspring and developing strategies for selective breeding.

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alone. That's why she enrolled at Columbia University to study Ecology, Evolution, and Environmental Biology. Her stories about being a middle-aged mom embedded in undergrad college life are spot-on and hilarious. But more profoundly, when Bone went back to school she learned that biology is a vast conspiracy of microbes. Microbes invented living and as a result they are part of every aspect of every living thing. This popular science book takes the layman on a broad survey of the role of microbes in nature and illustrates their importance to the existence of everything: atmosphere, soil, plants, and us.

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on the AP Test Development Committee, the Holtzclaws have designed their resource to help your students prepare for the AP Exam. Completely revised to match the new 8th edition of Biology by Campbell and Reece. New Must Know sections in each chapter focus student attention on major concepts. Study tips, information organization ideas and misconception warnings are interwoven throughout. New section reviewing the 12 required AP labs. Sample practice exams. The secret to success on the AP Biology exam is to understand what you must know and these experienced AP teachers will guide your students toward top scores!

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Example, Second Edition provides a wealth of information—from assumptions and design to computation, interpretation, and presentation of results—to help users save time, money, and frustration.

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molecular, quantitative, and population genetics, with a few more specialized areas. Whenever possible, the student is provided with the appropriate basic statistics necessary to make some the analyses. The book also builds on itself; that is, analytical methods learned in early parts of the book are subsequently revisited and used for later analyses. A deliberate attempt is made to make complex concepts simple, and sometimes to point out that apparently simple concepts are sometimes less so on further investigation. Any student taking a genetics course will find this an invaluable aid to achieving a good understanding of genetic principles and practice.

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from the basics through to genome expression and molecular phylogenetics, *Genomes 3* is the latest edition of this pioneering textbook. Updated to incorporate the recent major advances, *Genomes 3* is an invaluable companion for any undergraduate throughout their studies in molecular genetics. *Genomes 3* builds on the achievements of the previous two editions by putting genomes, rather than genes, at the centre of molecular genetics teaching. Recognizing that molecular biology research was being driven more by genome sequencing and functional analysis than by research into genes, this approach has gathered momentum in recent years.

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