**Punnett squares dihybrid crosses worksheet**

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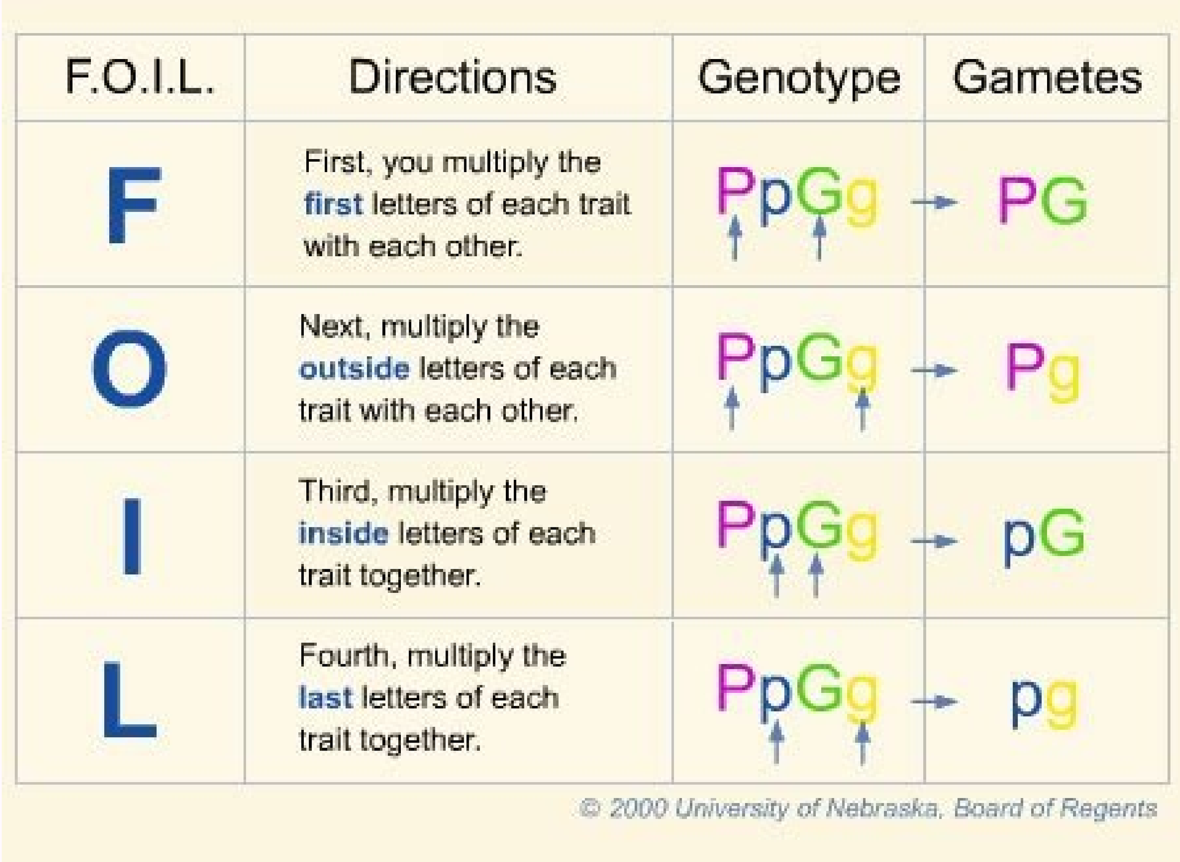

| F.O.I.L. | Directions | Genotype | Gametes |
| --- | --- | --- | --- |
| F | First, you multiply the **first** letters of each trait with each other. | PpGg | PG |
| O | Next, multiply the **outside** letters of each trait with each other. | PpGg | Pg |
| I | Third, multiply the **inside** letters of each trait together. | PpGg | pG |
| L | Fourth, multiply the **last** letters of each trait together. | PpGg | pg |

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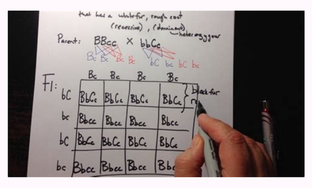
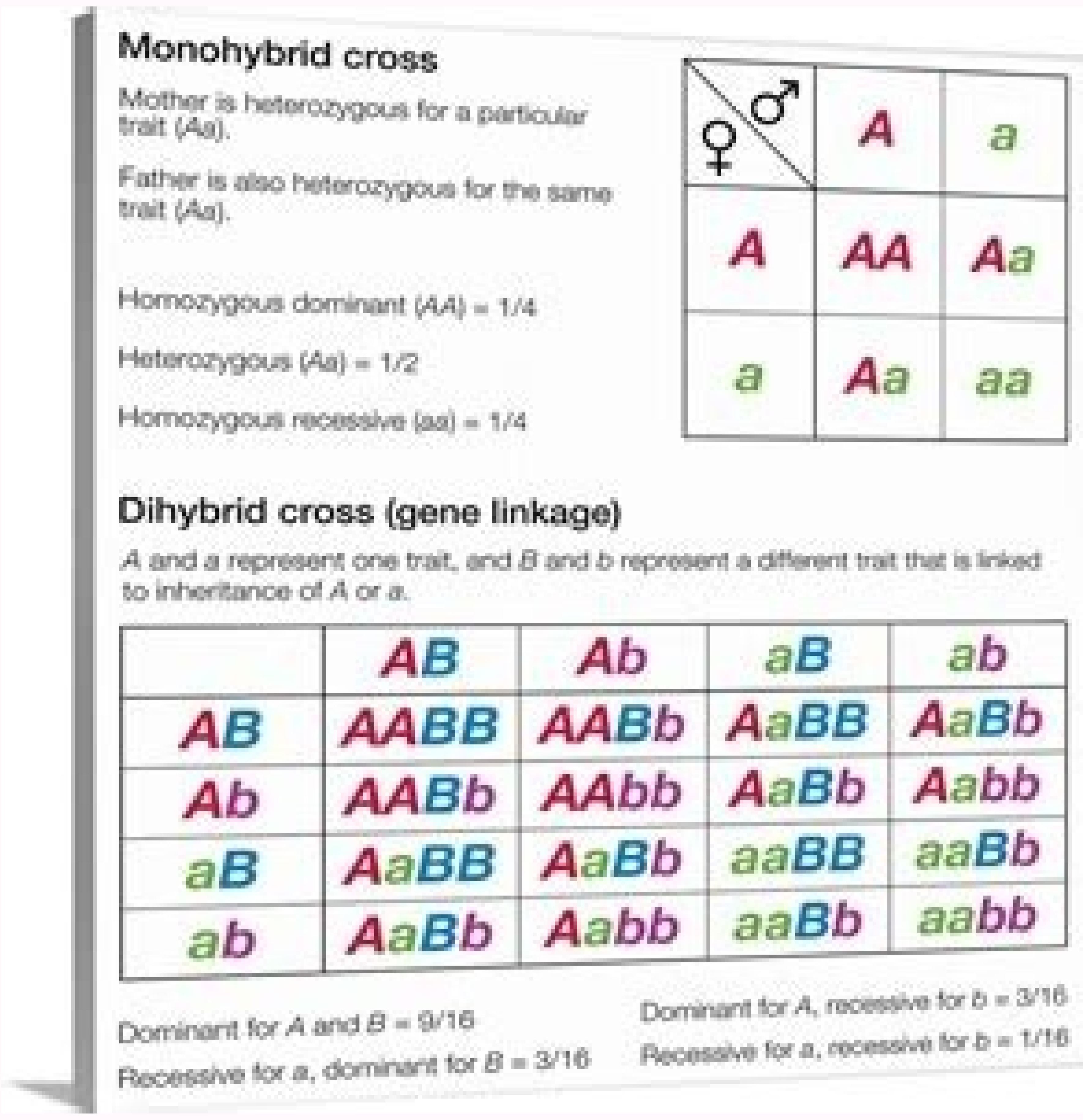




**Monohybrid cross**

Mother is heterozygous for a particular trait (*Aa*).

Father is also heterozygous for the same trait (*Aa*).

Homozygous dominant (*AA*) = 1/4

Heterozygous (*Aa*) = 1/2

Homozygous recessive (*aa*) = 1/4

| ♀ \ ♂ | A | a |
| --- | --- | --- |
| A | AA | Aa |
| a | Aa | aa |

**Dihybrid cross (gene linkage)**

*A* and *a* represent one trait, and *B* and *b* represent a different trait that is linked to inheritance of *A* or *a*.

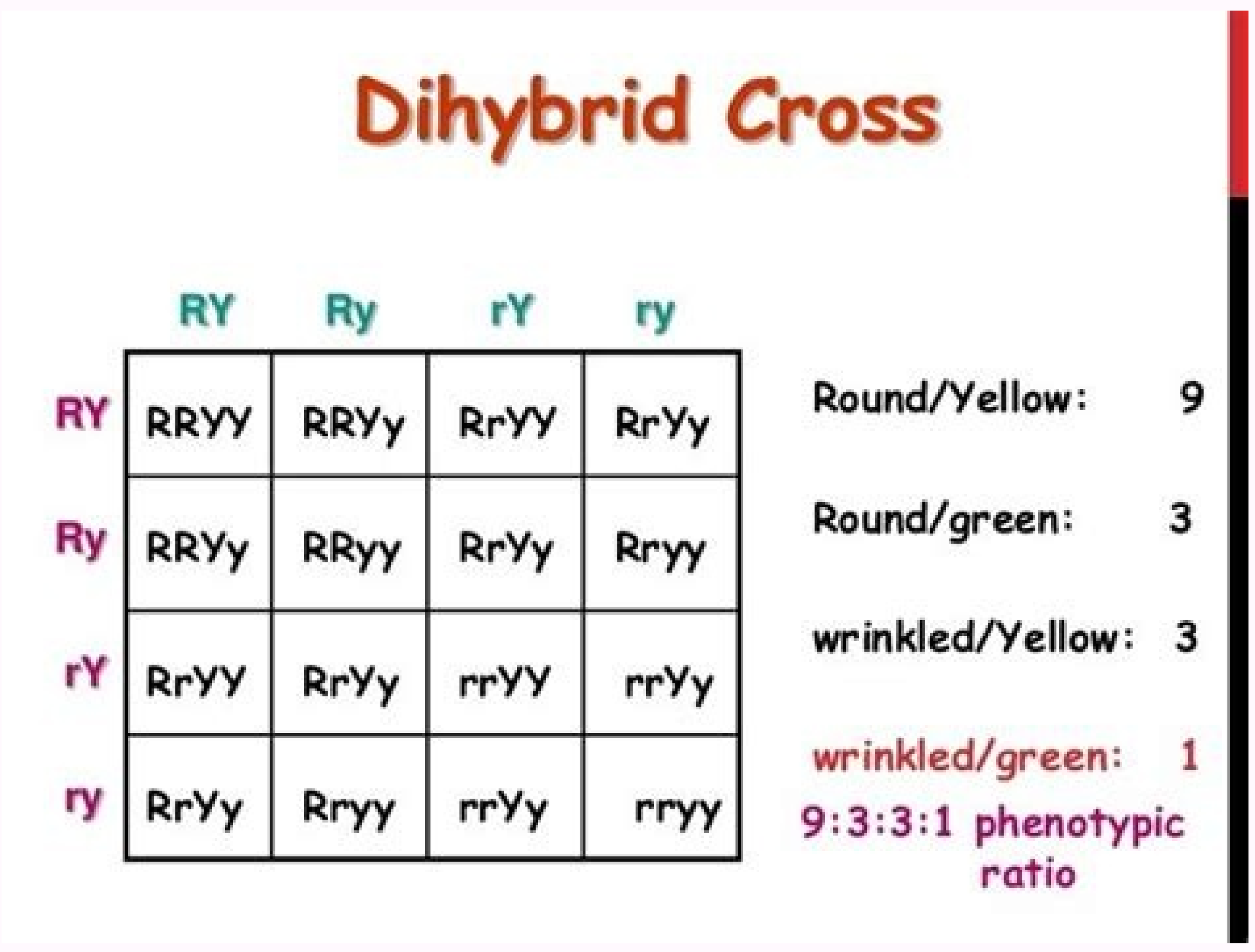
| | AB | Ab | aB | ab |
| --- | --- | --- | --- | --- |
| AB | AABB | AABb | AaBB | AaBb |
| Ab | AABb | AAbb | AaBb | Aabb |
| aB | AaBB | AaBb | aaBB | aaBb |
| ab | AaBb | Aabb | aaBb | aabb |

Dominant for *A* and *B* = 9/16

Recessive for *a*, dominant for *B* = 3/16

Dominant for *A*, recessive for *b* = 3/16

Recessive for *a*, recessive for *b* = 1/16



## Dihybrid Cross

| | RY | Ry | rY | ry |
| --- | --- | --- | --- | --- |
| RY | RRYY | RRYy | RrYY | RrYy |
| Ry | RRYy | RRyy | RrYy | Rryy |
| rY | RrYY | RrYy | rrYY | rrYy |
| ry | RrYy | Rryy | rrYy | rryy |

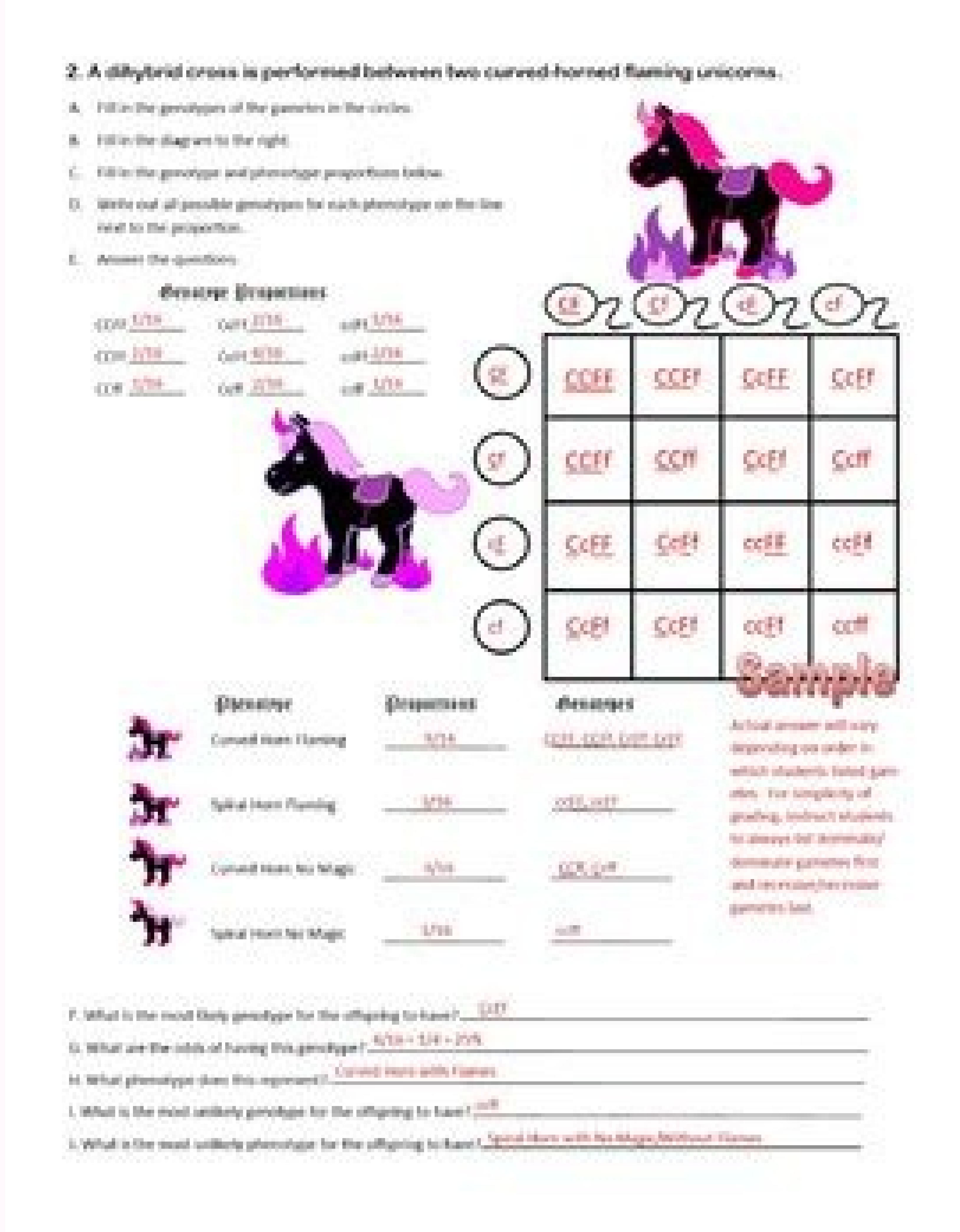
Round/Yellow: 9

Round/green: 3

wrinkled/Yellow: 3

wrinkled/green: 1

9:3:3:1 phenotypic ratio




These type of crosses can be challenging to set up, and the square you create will be 4x4. This simple guide will walk you through the steps of solving a typical dihybrid cross common in genetics. The method can also work for any cross that involves two traits. Consider this cross A pea plant that is heterozygous for round, yellow seeds is self fertilized, what are the phenotypic ratios of the resulting offspring? Step 1: Determine the parental genotypes from the text above, the word "heteroyzous" is the most important clue, and you would also need to understand that self fertilized means you just cross it with itself. RrYy x RrYy Step 2: Determine the gametes. This might feel a little like the FOIL method you learned in math class. Combine the R's and Ys of each parent to represent sperm and egg. Do this for both parents Gametes after "FOIL" RY, Ry, rY, ry (parent 1) and RY, Ry, rY, ry (parent 2) Step 3: Set up a large 4x4 Punnet square, place one gamete set from the parent on the top, and the other on the side Step 4: Write the genotypes of the offspring in each box and determine how many of each phenotype you have. In this case, you will have 9 round, yellow; 3 round, green; 3 wrinkled, yellow; and 1 wrinkled green Some Shortcuts In any case where the parents are heterozygous for both traits (AaBb x AaBb) you will always get a 9:3:3:1 ratio. 9 is the number for the two dominant traits, 3 is the number for a dominant/recessive combination, and only 1 individual will display both recessive traits. Another way to determine the ratios is to do it mathematically 3/4 of all the offspring will have round seeds 3/4 of all the offspring will have yellow seeds 3/4 x 3/4 = 9/16 will have round, yellow seeds. Crosses that Involve 2 Traits Consider: RrYy x rryy The square is set up as shown You might notice that all four rows have the same genotype. In this case, you really only need to fill out the top row, because 1/4 is the same thing as 4/16 Loading... If you're seeing this message, it means we're having trouble loading external resources on our website. If you're behind a web filter, please make sure that the domains *.kastatic.org and *.kasandbox.org are unblocked. We will start with the genotypic ratio. We can either count the combinations in the Punnett square, or use the dihybrid cross calculator to compute it for us. In the example presented to us in the section above the task is really easy: 50% of the Punnet square is taken by the Aabb combination, and the other half is aabb. It's easy to calculate that the genotypic ratio is 0.5:0.5, which is equal to 1:1. What is the phenotypic ratio? Phenotype for Aabb = Ab Phenotype for aabb = ab Now we know that that the phenotypic ratio is equal to the genotypic ratio = 1:1. In conclusion, 50% of the couple's children will be born with alleles Ab - that is curly, blond hair. The other half will be born with alleles ab - they will inherit straight, blond hair. ♀ Our dihybrid cross calculator will provide you with the percentages for the different sets of alleles. To receive the genotypic ratio, you need to divide all those numbers by the smallest percentage received, which gives you the lowest possible integer. Look at the example below: 6.25 : 12.5 : 6.25 : 12.5 : 25 : 12.5 : 6.25 : 12.5 : 6.25 6.25 is the smallest number, so we need to divide everything by 6.25: 1 : 2 : 1 : 2 : 4 : 2 : 1 : 2 : 1 Voila! Your genotypic ratio is ready. If you need any help with those calculations, check out our Greatest Common Factor tool! A Punnett Square* shows the genotype*s two individuals can produce when crossed. To draw a square, write all possible allele* combinations one parent can contribute to its gametes across the top of a box and all possible allele combinations from the other parent down the left side. The allele combinations along the top and sides become labels for rows and columns within the square. Complete the genotypes in the square by filling it in with the alleles from each parent. Since all allele combinations are equally likely to occur, a Punnett Square predicts the probability of a cross producing each genotype. A single trait Punnett Square tracks two alleles for each parent. The square has two rows and two columns. Adding more traits increases the size of the Punnett Square. Assuming that all traits exhibit independent assortment, the number of allele combinations an individual can produce is two raised to the power of the number of traits. For two traits, an individual can produce 4 allele combinations (2^2). Three traits produce 8 combinations (2^3). Independent assortment typically means the genes are on different chromosome*s. If the genes for the two traits are on the same chromosome, alleles for each trait will always appear in the same combinations (ignoring recombination). With one row or column for each allele combination, the total number of boxes in a Punnett Square equals the number of rows times the number of columns. Multi-trait Punnett Squares are large. A three trait square has 64 boxes. A four trait square has 256 boxes. The genotype in each box is equally likely to be produced from a cross. A two-trait Punnett Square has 16 boxes. The probability of a cross producing a genotype in any box is 1 in 16. If the same genotype is present in two boxes, its probability of occurring doubles to 1/8 (1/16 + 1/16). If one of the parents is a homozygote for one or more traits, the Punnett Square still contains the same number of boxes, but the total number of unique allele combinations is 2 raised to the power of the number of traits for which the parent is heterozygous. A commonly discussed Punnett Square is the dihybrid cross. A dihybrid cross tracks two traits. Both parents are heterozygous, and one allele for each trait exhibits complete dominance*. This means that both parents have recessive alleles, but exhibit the dominant phenotype. The phenotype ratio predicted for dihybrid cross is 9:3:3:1. Of the sixteen possible allele combinations: Nine combinations produce offspring with both dominant phenotypes. Three combinations each produce offspring with one dominant and one recessive phenotype. One combination produces a double recessive offspring. This pattern only occurs when both traits have a dominant allele. With no dominant alleles, more phenotypes are possible, and the phenotype probabilities match the genotype probabilities. A simpler pattern arises when one of the parents is homozygous for all traits. In this case, the alleles contributed by the heterozygous parent drives all of the variability. A two trait cross between a heterozygous and a homozygous individual generates four phenotypes, each of which are equally likely to occur. More complicated patterns can be examined. In an extreme case when more than two alleles exists for each trait and the parents do not possess same alleles, the total number of genotypes equals the number of boxes in the Punnett Square. It is possible to generate Punnett squares for more that two traits, but they are difficult to draw and interpret. A Punnett Square for a tetrahybrid cross contains 256 boxes with 16 phenotypes and 81 genotypes. A third allele for any one of the traits increases the number of genotypes from 81 to 108. Given this complexity, Punnett Squares are not the best method for calculating genotype and phenotype ratios for crosses involving more than one trait. Test your understanding with the Punnett Square Calculator Problem Set. Video Overview Related Content

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