

Learning Objectives

Upon completing the exercise, each student should be able:

- to define the following terms: gene, allele, genotype, phenotype, homozygous, heterozygous, dominant, recessive, monohybrid cross, dihybrid cross, epistasis;
- to explain how to set up a monohybrid cross and a dihybrid cross;
- to determine expected genotypic and phenotypic frequencies in monohybrid and dihybrid crosses;
- to determine expected genotypic and phenotypic frequencies in crosses involving epistasis;
- to test hypotheses based on expected frequencies using the chi-square test.
- to write a formal laboratory report based on this laboratory exercise.

Background

Gregor Mendel discovered the laws of random segregation and independent assortment by performing crosses in the pea plant. In this exercise, you will learn about these principles by analyzing results from crosses in the maize plant.

In the maize plant, the male gametes (pollen) are formed in organs called anthers located at the tops of the maize stalks. The female gametes (ovules) are formed on the maize ears located along the sides of the stalks. When a pollen grain fertilizes an ovule, the fertilized ovule develops into a kernel that contains an embryonic maize plant. There are several genetic traits in the kernels that can be easily observed, including the kernel color and shape.

A. Random Segregation

Mendel's law of random segregation: Diploid germ-line cells of sexually reproducing species contain two copies of almost every chromosomal gene. The two copies are located on members of a homologous chromosome pair. During meiosis, the two copies separate, so that a gamete receives only one copy of each gene.

Random segregation can be demonstrated by a monohybrid cross. In a monohybrid cross, a parental cross is made between two individuals that differ in the genotype of one gene. The offspring of the parental generation is called the F₁ (first filial) generation. The F₁ generation can be allowed to interbreed or self-fertilize (inter se cross, or "selfing") to produce the F₂ (second filial) generation.

For example, consider a monohybrid cross involving kernel color in maize. There are several genes that control seed color in maize. One gene for seed color is designated by the letter R and has two alleles.

Seed color gene with two alleles:

- R = purple (or red) allele (dominant allele)
- r = yellow (or white) allele (recessive allele)

Possible genotypes and phenotypes:

- R R = purple phenotype
- R r = purple phenotype
- r r = yellow phenotype

Using these probabilities, we can predict the phenotypic ratio we should see in the F₂ generation.

Probability of F ₁ pollen	x	Probability of F ₁ ovule	=	Probability of F ₂ genotype
$\frac{1}{2}$ R		$\frac{1}{2}$ R		$\frac{1}{4}$ RR
$\frac{1}{2}$ R		$\frac{1}{2}$ r		$\frac{1}{4}$ Rr
$\frac{1}{2}$ r		$\frac{1}{2}$ R		$\frac{1}{4}$ Rr
$\frac{1}{2}$ r		$\frac{1}{2}$ r		$\frac{1}{4}$ rr

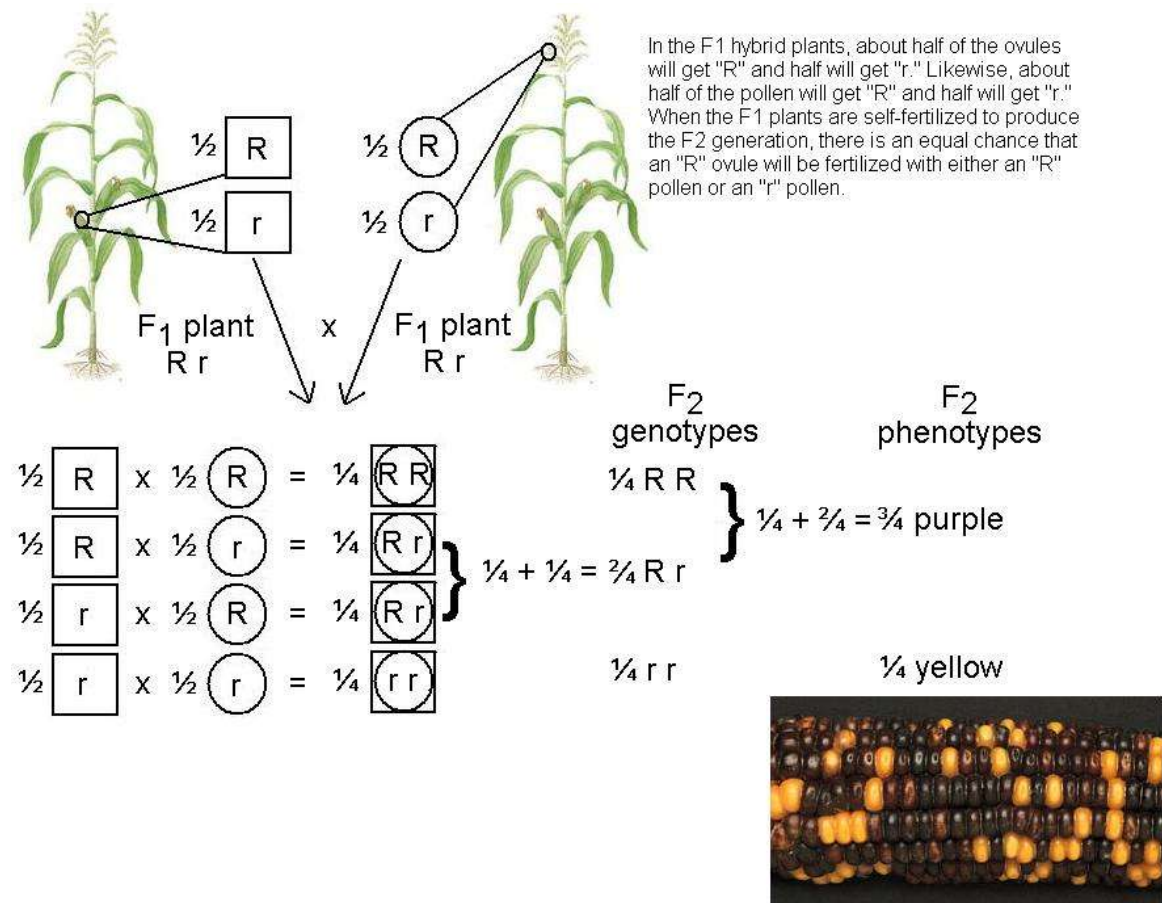
Note that there are two ways of producing “Rr” in the F₂ generation. We can add these together to get a probability of $\frac{2}{4}$ or $\frac{1}{2}$ for Rr.

Therefore, the F₂ generation should have the following genotypes and phenotypes.

F₂ generation: $\frac{1}{4}$ RR $\frac{1}{2}$ Rr $\frac{1}{4}$ rr

$\frac{1}{4} + \frac{1}{2} = \frac{3}{4}$ Purple $\frac{1}{4}$ Yellow

We expect a 3:1 ratio of dominant:recessive in the F₂ generation. The F₁ x F₁ to produce the F₂ generation is summarized in the following diagram.



Another way to analyze the outcome of a monohybrid cross is the Punnett square. The Punnett square method uses a simple grid to match all of the possible combinations of gametes in a cross. The gamete genotypes of one parent are listed along the top of the grid, and the gamete genotypes of the other parent are listed along the side of the grid. By filling in each square with the alleles from the top with the alleles from the side, the different possible combinations of genotypes in the offspring are found in the grid. The following diagram shows a Punnett square analysis for the monohybrid cross that we just covered.

Parental (P) generation: $RR \text{ ♀}$ x $rr \text{ ♂}$
 Purple Yellow

Punnett square analysis for the parental cross:

♂ ♀	R	R
r	Rr	Rr
r	Rr	Rr

Expected F_1 genotype: All Rr
 Expected F_1 phenotype: All purple

The F_1 plants are allowed to self-fertilized

$Rr \text{ ♀}$ x $Rr \text{ ♂}$

Punnett square analysis for the F_1 cross:

♂ ♀	R	r
R	RR	Rr
r	Rr	rr

Expected F_2 genotypic frequencies: $\frac{1}{4} RR, \frac{1}{4} + \frac{1}{4} = \frac{1}{2} Rr, \frac{1}{4} rr$
 Expected F_2 genotypic ratio: 1:2:1 RR: Rr: rr
 Expected F_2 phenotypic frequencies: $\frac{1}{4} + \frac{1}{4} + \frac{1}{4} = \frac{3}{4}$ purple, $\frac{1}{4}$ yellow
 Expected F_2 phenotypic ratio: 3:1 purple: yellow

B. Independent Assortment

Mendel's Law of Independent Assortment: When the alleles of two different genes separate during meiosis, they do so independently of one another unless the genes are located on the same chromosome (linked). This is the principle of independent assortment. Mendel discovered independent assortment by performing dihybrid crosses in the pea plant. We will examine dihybrid crosses in maize.

Consider the genes for kernel color and kernel composition in maize.

Seed color gene	Seed composition gene
R allele, dominant, for purple kernels	Su allele, dominant for smooth (starchy) kernels
r allele, for yellow kernels	su allele, for wrinkled (sweet) kernels

In the P generation, a homozygous plant with purple, smooth kernels was crossed with a plant having yellow wrinkled kernels. The F₁ plants were allowed to fertilize themselves. What genotypes and phenotypes are expected in the F₂, and in what frequencies or ratio? To answer this question, you should begin by outlining the P and F₁.

P: R R Su Su ♀ x r r su su ♂

F₁: All R r Su su, heterozygous purple smooth kernels
 R r Su su ♀ x R r Su su ♂

According to the principle of independent assortment, the color gene and the seed shape gene should not affect one another; that is, they should behave independently. This means that there are four possible classes of pollen and ovules, in equal frequencies.

F ₁ pollen	F ₁ ovules
$\frac{1}{4}$ R Su	$\frac{1}{4}$ R Su
$\frac{1}{4}$ R su	$\frac{1}{4}$ R su
$\frac{1}{4}$ r Su	$\frac{1}{4}$ r Su
$\frac{1}{4}$ r su	$\frac{1}{4}$ r su

From this, we can calculate the probability of each genotype in the F₂ generation, as shown in the table on the next page.

F₂ genotype	Probability	Phenotype
R R Su Su	$\frac{1}{4} \times \frac{1}{4} = \frac{1}{16}$	Purple Smooth
R r Su Su	$(\frac{1}{4} \times \frac{1}{4}) + (\frac{1}{4} \times \frac{1}{4}) = \frac{2}{16} = \frac{1}{8}$	Purple Smooth
R R Su su	$(\frac{1}{4} \times \frac{1}{4}) + (\frac{1}{4} \times \frac{1}{4}) = \frac{2}{16} = \frac{1}{8}$	Purple Smooth
R r Su su	$(\frac{1}{4} \times \frac{1}{4}) + (\frac{1}{4} \times \frac{1}{4}) + (\frac{1}{4} \times \frac{1}{4}) + (\frac{1}{4} \times \frac{1}{4}) = \frac{4}{16} = \frac{1}{4}$	Purple Smooth
R R su su	$\frac{1}{4} \times \frac{1}{4} = \frac{1}{16}$	Purple Wrinkled
R r su su	$(\frac{1}{4} \times \frac{1}{4}) + (\frac{1}{4} \times \frac{1}{4}) = \frac{2}{16} = \frac{1}{8}$	Purple Wrinkled
r r Su Su	$\frac{1}{4} \times \frac{1}{4} = \frac{1}{16}$	Yellow Smooth
r r Su su	$(\frac{1}{4} \times \frac{1}{4}) + (\frac{1}{4} \times \frac{1}{4}) = \frac{2}{16} = \frac{1}{8}$	Yellow Smooth
r r su su	$\frac{1}{4} \times \frac{1}{4} = \frac{1}{16}$	Yellow Wrinkled

The genotypes tell us that expected phenotypic ratio of the F₂ generation is 9:3:3:1.

$$\text{Purple Smooth} = \frac{1}{16} + \frac{2}{16} + \frac{2}{16} + \frac{4}{16} = \frac{9}{16}$$

$$\text{Purple Wrinkled} = \frac{1}{16} + \frac{2}{16} = \frac{3}{16}$$

$$\text{Yellow Smooth} = \frac{1}{16} + \frac{2}{16} = \frac{3}{16}$$

$$\text{Yellow Wrinkled} = \frac{1}{16}$$



It is also possible to analyze the dihybrid cross with a Punnett square. For a dihybrid cross, we'll need a 4 x 4 grid because there are four genotypes in the F₁ gametes. Here is the Punnett square analysis of the F₁ cross from the above example.

F₁: All R r Su su, heterozygous purple smooth kernels
 R r Su su ♀ x R r Su su ♂

Punnett square analysis for the F₁ cross:

♀ \ ♂	R Su	R su	r Su	r su
R Su	RR SuSu	RR Su su	Rr SuSu	Rr Su su
R su	RR Su su	RR su su	Rr Su su	Rr su su
r Su	Rr SuSu	Rr Su su	rr SuSu	rr Su su
r su	Rr Su su	Rr su su	rr Su su	rr su su

From the Punnett square, you can obtain the same genotypic and phenotypic frequencies as shown in the table on page 6.

C. A Short-cut to Genetic Ratios

There is a fast way to determine genetic ratios based on independent assortment. Since the genes behave independently, the probability of a genotype amounts to independent events occurring together. Therefore, we can consider each trait separately and then multiply the probabilities. This method will allow you to solve most of the complex heredity problems you will face on tests, so you need to learn it and learn it well.

In the same dihybrid cross outlined above with the seed shape and composition in maize, we expect a 3:1 ratio for each trait in the F_2 .

F_2 generation:	Seed color	Seed composition
	$\frac{3}{4}$ Purple	$\frac{3}{4}$ Smooth
	$\frac{1}{4}$ Yellow	$\frac{1}{4}$ Wrinkled

Combining the phenotypes for color and composition, we obtain the following.

$$\begin{aligned}\frac{3}{4} \times \frac{3}{4} &= \frac{9}{16} \text{ Purple Smooth} \\ \frac{3}{4} \times \frac{1}{4} &= \frac{3}{16} \text{ Purple Wrinkled} \\ \frac{1}{4} \times \frac{3}{4} &= \frac{3}{16} \text{ Yellow Smooth} \\ \frac{1}{4} \times \frac{1}{4} &= \frac{1}{16} \text{ Yellow Wrinkled}\end{aligned}$$

Note that this method could work just as easily for determining the genotypic ratio. Starting out with the F_2 genotypic frequencies for each individual gene, see if you can figure out the F_2 genotypic frequencies combined.

F_2 generation:	Seed color	Seed composition
	$\frac{1}{4}$ R R	$\frac{1}{4}$ Su Su
	$\frac{2}{4}$ R r	$\frac{2}{4}$ Su su
	$\frac{1}{4}$ r r	$\frac{1}{4}$ su su

Combining the genotypes for color and composition, we obtain the following.

????????????????

Work it out for yourself.

In your formal report for this laboratory, you will determine expected genotypic and phenotypic frequencies by both the Punnett square method and the probability computation method (“short-cut” method). However, you should note that the short-cut method is much quicker on exams. Punnett squares should be avoided on exams. **Mastery of the short-cut method is one of the single greatest factors determining how well students succeed on heredity problems.**

D. Epistasis

Most phenotypic traits are influenced by the action of several genes. For example, the synthesis of a pigment might require an enzymatic pathway with multiple steps. Each step is catalyzed by its own enzyme, and each enzyme is encoded by a different gene. If an individual is lacking the functional enzyme for any step in the pathway (for example, in a homozygous recessive mutant that lacks an allele to encode the functional enzyme) then the pathway is blocked and the pigment will not be produced, **regardless of the genotype of any other genes in the individual.**

Epistasis: Epistasis occurs when the genotype of one gene hides or “masks” the phenotypic effect of a second gene, regardless of the genotype of the second gene. Do not say that the first gene is “dominant” over the second gene; say that the first gene “epistatically masks” the second gene. Genes can interact epistatically if each encodes a different enzyme in a multi-step pathway. They can also interact epistatically if one gene encodes a regulatory protein that regulates the transcription of the other gene.

The purple color in the maize kernels is due to the presence of a pigment called anthocyanin. There are several genes that encode proteins to regulate anthocyanin production. Each of the genes has a large number of known alleles. The genes interact epistatically with each other, depending on the genotype of the individual. We need to consider two of these genes.

The “R” gene.

This gene has two major alleles:

- R** The presence of at least one copy of R (homozygous R R or heterozygous R r) is required for purple kernels. The allele “R” is dominant to “r.”
- r** The genotype “r r” gives yellow kernels, regardless of the genotype of any other genes. The allele “r” is recessive to “R.” The genotype “r r” epistatically masks the genotypes of other kernel genes and gives a yellow phenotype.

The “C” gene.

This gene has three major alleles:

- C** The presence of at least one copy of C (homozygous C C or heterozygous C c) is required for purple kernels. The allele “C” is dominant to “c.” The allele “C” is recessive to “C’.”
- c** The genotype “c c” gives yellow kernels, regardless of the genotype of any other genes. The allele “c” is recessive to “C.” The genotype “c c” epistatically masks the genotypes of other kernel genes and gives a yellow phenotype.
- C’** C’ is called the “dominant color inhibitor allele” of the C gene. The presence of at least one copy of C’ (homozygous C’ C’, heterozygous C’ C, or heterozygous C’ c) inhibits the production of purple pigment and causes the yellow phenotype. The allele “C’” is dominant to “C” and “c.” Genotypes “C’ C’,” “C’ C,” or “C’ c” epistatically mask the genotypes of other kernel genes and gives a yellow phenotype.

The R and C genes are located on different chromosomes, so they assort independently of each other. Consider each of the following parental crosses. In each case, what outcome do you expect to see in the F₁ and F₂ generations?

Parental cross "a"	R R C C	x	r r C C
Parental cross "b"	R R C' C'	x	R R C C
Parental cross "c"	r r C C	x	R R c c
Parental cross "d"	R R C' C'	x	r r C C

Here is the analysis of cross "a."

P:	R R C C	x	r r C C	
F ₁ :	All R r C C			
	R r C C	x	R r C C	
F ₂	Expected "R" genotype <u>frequencies:</u>	Expected "C" genotype <u>frequencies:</u>	<u>Combined</u>	F ₂ <u>Phenotypes</u>
	$\frac{1}{4}$ R R	All C C	$\frac{1}{4}$ R R C C	$\frac{3}{4}$ Purple
	$\frac{2}{4}$ R r		$\frac{2}{4}$ R r C C	
	$\frac{1}{4}$ r r		$\frac{1}{4}$ r r C C	$\frac{1}{4}$ Yellow

On the worksheet, you will complete a similar analysis for the other crosses. You will receive a numbered "unknown" ear of maize representing the F₂ generation from one of these four possible crosses. You will use the χ^2 test to determine which cross your ear represents.

E. References

<http://www.iita.org/crop/maize.htm>
<http://www.maizegdb.org/>

Definitions	
Gene	Classical definition: A unit of inheritance; a factor transmitted during reproduction and responsible for the appearance of a given trait. Contemporary understanding: A segment on a DNA molecule, usually at a specific location (locus) on a chromosome, characterized by its nucleotide sequence. Genes play three notable roles: to encode the amino acid sequences of proteins, to encode the nucleotide sequences of tRNA or rRNA, and to regulate the expression of other genes.
Allele	Variant forms of a gene found within a population. Alleles of a gene usually have small differences in their nucleotide sequences. The differences can affect the trait for which the gene is responsible. Most genes have more than one allele.
Genotype	The genetic makeup of an individual with reference to one or more specific traits. A genotype is designated by using symbols to represent the alleles of the gene.
Phenotype	The appearance or discernible characteristics of a trait in an individual. Phenotypes can be determined by a combination of genetic and environmental factors.
Homozygous and Heterozygous	In a diploid species, each individual carries two copies of each gene (with some exceptions). The two copies are located on different members of a homologous chromosome pair. If the two copies of the gene are identical alleles, then the individual is homozygous for the gene. If the two copies are different, then the individual is heterozygous.
Dominant and Recessive	A dominant allele is expressed over a recessive allele in a heterozygous individual. This means that a heterozygous individual and a homozygous dominant individual have identical phenotypes. Often, a dominant allele encodes a functional protein, such as an enzyme. The recessive allele is a mutation that no longer has the information for the correct amino acid sequence; therefore, its protein product is nonfunctional. In the heterozygote, the dominant allele encodes sufficient production of the protein to produce the dominant phenotype. This is also called complete dominance.
Codominance	Two alleles are codominant if each encodes a different but functional protein product. In the heterozygote, the presence of two different functional proteins means that the phenotype of the heterozygote is different from either homozygous dominant or homozygous recessive.
Incomplete Dominance	An incompletely dominant allele produces a functional protein product. However, in the heterozygote, there is insufficient protein production from the allele to produce the same phenotype as homozygous dominant. Therefore, the phenotype of the heterozygote is different from either homozygous dominant or homozygous recessive.
Epistasis	Most phenotypic traits are formed by the interactions of several genes. Epistasis is one type of gene interaction. In epistasis, the genotype of one gene masks the expression of the genotype of another gene.
Sex chromosome and Autosome	Many species that exhibit sexual dimorphism have a sex chromosome system to determine the sex of an individual. In mammalian species, <i>Drosophila</i> , and certain other species, the sex chromosomes are designated as X and Y. Females in these species have two X chromosomes, and males have one X and one Y chromosome. Chromosomes other than sex chromosomes are called autosomes.
X-linkage	When a gene is located on the X chromosome, it is X-linked. Since males have only one X chromosome, they have only one copy of each X-linked gene. Instead of homozygous or heterozygous, males are hemizygous for X-linked traits.

Table of χ^2 values

P value = Probability that the Difference is due to Chance and is Not Significant							
df	0.95	0.80	0.50	0.20	0.10	0.05	0.01
1	0.00393	0.0642	0.455	1.642	2.706	3.841	6.635
2	0.103	0.446	1.386	3.129	4.605	5.991	9.210
3	0.352	1.005	2.366	4.642	6.251	7.815	11.34
4	0.711	1.649	3.357	5.989	7.779	9.488	13.277
5	1.145	2.343	4.351	7.289	9.236	11.070	15.086
6	1.635	3.070	5.348	8.558	10.645	12.592	16.812
7	2.167	3.822	6.346	9.803	12.017	14.067	18.475
8	2.733	4.594	7.344	11.030	13.362	15.507	20.090
9	3.325	5.380	8.343	12.242	14.684	16.919	21.666
10	3.940	6.179	9.342	13.442	15.987	18.307	23.209

**Patterns of Inheritance in Maize
Laboratory Report Sheet**

Name _____
Lab Partners _____

For your grade on the maize lab, you will write a formal lab report that summarizes the principles, methods, analysis, results, and conclusion that you reached. Details on the format for the lab report are given at the end of the worksheet section. Completing the worksheet will help you to write your laboratory report. You should pay careful attention to collecting complete and accurate counts of the maize kernels in order to do well on your results, analysis, and conclusion.

A. Random segregation and independent assortment.

Your group will receive an ear of maize representing the F₂ generation of the following cross.

P: R R Su Su x r r su su

F₁: All R r Su su
 R r Su su x R r Su su

F₂: Your ear of maize

1. Consider the following hypothesis:

The “R” and “r” alleles of maize segregate randomly during meiosis.

Based on this hypothesis, what genotypic and phenotypic frequencies for the R gene and kernel color do you expect in the F₂ ear?

2. Considering kernel color only, count the purple and yellow kernels on the ear and use the χ^2 method to test the hypothesis that the R and r alleles segregate randomly. You should count at least 500 kernels to get a valid statistical sample.

F ₂ Phenotype	# obtained (O)	# expected (E)	O – E	(O – E) ²	$\frac{(O - E)^2}{E}$
Purple					
Yellow					
Total:					$\chi^2 =$

df = _____

_____ < χ^2 < _____

_____ > P > _____

P _____ 0.05
(< or >)

At a 5% level of significance, the deviation is _____. (significant or not significant)
Therefore, the data _____ (support or do not support) the hypothesis.

3. Consider the following hypothesis:

The “Su” and “su” alleles of maize segregate randomly during meiosis.

Based on this hypothesis, what genotypic and phenotypic frequencies for the Su gene and kernel shape do you expect in the F₂ ear?

4. Considering kernel shape only, count the number of smooth and wrinkled seeds. Use the χ^2 method to test the hypothesis that the Su and su alleles segregate randomly. You should count at least 500 kernels to get a valid statistical sample.

F ₂ Phenotype	# obtained (O)	# expected (E)	O – E	(O – E) ²	$\frac{(O - E)^2}{E}$
Smooth					
Wrinkled					
Total:					$\chi^2 =$

df = _____

_____ < χ^2 < _____

_____ > P > _____

P _____ 0.05
(< or >)

At a 5% level of significance, the deviation is _____. (significant or not significant)
Therefore, the data _____ (support or do not support) the hypothesis.

5. Consider the following hypothesis:

The “R” and “Su” genes of maize assort independently during meiosis.

Based on this hypothesis, what genotypic and phenotypic frequencies for these genes do you expect in the F₂ ear?

6. Consider kernel color and kernel shape. Count the number of purple smooth, purple wrinkled, yellow smooth, and yellow wrinkled kernels. You should count at least 500 kernels to get a valid statistical sample. Use the χ^2 method to test the hypothesis that the genes for kernel color and shape assort independently.

F ₂ Phenotype	# obtained (O)	# expected (E)	O - E	(O - E) ²	$\frac{(O - E)^2}{E}$
Purple Smooth					
Purple Wrinkled					
Yellow Smooth					
Yellow Wrinkled					
	Total:				$\chi^2 =$

df = _____

_____ < χ^2 < _____

_____ > P > _____

P _____ 0.05
(< or >)

At a 5% level of significance, the deviation is _____. (significant or not significant)
Therefore, the data _____ (support or do not support) the hypothesis.

B. Epistasis

You will receive a numbered “unknown” ear of maize representing the F₂ generation from a cross involving one or more seed color genes. Four possible parental genotypes for the cross are given below. For each cross, determine the expected phenotypic frequency in the F₂ generation. Count the number of purple and yellow kernels on your unknown ear (you should count at least 800 kernels, or as many kernels as there are on your ear, to get a valid statistical sample). Then, use the χ^2 method to determine which cross your ear represents.

Cross “a”

P: RR CC x rr CC
 Phenotype _____ Phenotype _____

F₁: Genotype _____
 Phenotype _____

F₂: List the expected genotypes and phenotypes and their frequencies.

Data and analysis:

F ₂ Phenotype	# obtained (O)	# expected (E)	O – E	(O – E) ²	$\frac{(O - E)^2}{E}$
Purple					
Yellow					
Total:					$\chi^2 =$

$$df = \underline{\quad}$$

$$\underline{\quad} < \chi^2 < \underline{\quad}$$

$$\underline{\quad} > P > \underline{\quad}$$

$$P \underline{\quad} 0.05$$

(< or >)

At a 5% level of significance, the deviation is _____. (significant or not significant)
 Therefore, the data _____ (support or do not support) the hypothesis that the
 unknown ear is the F₂ progeny of cross (a).

Cross "b"

P: RR C' C' x RR C C
 Phenotype _____ Phenotype _____

F₁: Genotype _____
 Phenotype _____

F₂: List the expected genotypes and phenotypes and their frequencies.

Data and analysis:

F ₂ Phenotype	# obtained (O)	# expected (E)	O - E	(O - E) ²	$\frac{(O - E)^2}{E}$
Purple					
Yellow					
Total:					$\chi^2 =$

df = _____

_____ < χ^2 < _____

_____ > P > _____

P _____ 0.05
 (< or >)

At a 5% level of significance, the deviation is _____. (significant or not significant)
 Therefore, the data _____ (support or do not support) the hypothesis that the
 unknown ear is the F₂ progeny of cross (b).

Cross “c”

P: r r C C x R R c c
 Phenotype _____ Phenotype _____

F₁: Genotype _____
 Phenotype _____

F₂: List the expected genotypes and phenotypes and their frequencies.

Data and analysis:

F ₂ Phenotype	# obtained (O)	# expected (E)	O - E	(O - E) ²	$\frac{(O - E)^2}{E}$
Purple					
Yellow					
Total:					$\chi^2 =$

df = _____

_____ < χ^2 < _____

_____ > P > _____

P _____ 0.05
 (< or >)

At a 5% level of significance, the deviation is _____. (significant or not significant)
 Therefore, the data _____ (support or do not support) the hypothesis that the
 unknown ear is the F₂ progeny of cross (c).

Cross “d”

P: RR C' C' x rr CC
 Phenotype _____ Phenotype _____

F₁: Genotype _____
 Phenotype _____

F₂: List the expected genotypes and phenotypes and their frequencies.

Data and analysis:

F ₂ Phenotype	# obtained (O)	# expected (E)	O - E	(O - E) ²	$\frac{(O - E)^2}{E}$
Purple					
Yellow					
Total:					$\chi^2 =$

df = _____

_____ < χ^2 < _____

_____ > P > _____

P _____ 0.05
 (< or >)

At a 5% level of significance, the deviation is _____. (significant or not significant)
 Therefore, the data _____ (support or do not support) the hypothesis that the
 unknown ear is the F₂ progeny of cross (d).

Conclusion

1. List the number of your unknown. _____
2. On the basis of your analysis, write a short paragraph explaining the genetic basis of the kernel color in your unknown ear. In writing your conclusion, you should clearly summarize your statistical analysis, and you should explain how epistasis has played a role in determining the kernel color in your unknown ear.

C. Formal Lab Report for the Maize Lab

For your grade on the maize lab, you will write a formal lab report that summarizes the principles, methods, analysis, results, and conclusion that you reached. The report will be graded according to the rubric shown on the next page. The report should contain the following five sections: Introduction, Methods, Results, Analysis, and Conclusion. Basic instructions on the lab report format, as well as specific instructions for each section, are given below.

Basic Format

- **Each individual student must write his or her own individual laboratory report.**
- Any direct quotation from another work should be properly cited and referenced.
- The laboratory report should be typed (preferred) or neatly printed, with .
- All typographic conventions (Greek letters, special symbols, italics, mathematical formulas, superscripts and subscripts, etc.) must be correctly used.
- There should be no spelling or grammatical errors.
- Diagrams and Punnett squares should be neatly drawn.
- Each section of the laboratory report should be clearly indicated with a boldfaced label.

Introduction

The “Introduction” should consist of :

- a brief two or three paragraph background on the origin of Mendel’s Laws of Random Segregation and Independent Assortment;
- clear statements of each of the questions to be answered in this lab exercise;
- clear statements of each hypothesis to be tested (, with the hypotheses based on Mendel’s Laws.

Methods

The “Methods” section should:

- begin with an introductory paragraph stating that the hypotheses were tested by determining the phenotypes of kernels on F_2 maize ears produced by mating experiments;
- contain a detailed description of how the crosses were performed to obtain the F_2 ears counted in the exercise;
- contain mating diagrams showing the crosses to aid in the description of the crosses.

Results

The “Results” section should:

- begin with an introductory paragraph stating each set of data that was obtained in the experiment;
- have a separate table for the data from each kernel counting experiment;
- have each table clearly and accurately labeled.

Analysis

The “Analysis” section should:

- begin with an introductory paragraph stating that the results were compared with expected values determined from Mendel’s Laws, and compared using the χ^2 test;
- show the derivation of expected frequencies of genotypes and phenotypes for each hypothesis, using both the probability method (“short-cut” method) and the Punnett square method;
- list the expected genotypes and phenotypes both as frequencies (fractions) and as ratios;
- show the calculation and the evaluation of the χ^2 test for each hypothesis.

Conclusion

The “Conclusion” section should:

- begin with an introductory paragraph that briefly restates the questions that were answered in the lab exercise;
- summarize the essential data for each hypothesis tested and derive conclusions based on the data;
- clearly indicated how the statistical analysis (χ^2 test) was used to interpret whether the data supported or did not support a hypothesis;
- indicate how the results illustrate the genetics principles covered in the exercise;
- have an explanation of any sources of error, if there were any errors or discrepancies in the counts.

Lab Report Rubric for Lab I. Patterns of Inheritance in Maize (40 pts)

	Highest pts	Lower pts	pts	Professor I Evaluation	Professor II Evaluation
Introduction (section 1)	The questions to be answered during the lab are stated	One or more questions are missing	7		
	The hypothesis is stated based on Mendel's laws	Hypothesis is incorrect			
Methods (section 2)	A description of how the experiment was performed	Description is unclear	7		
	Mating diagrams are drawn to aid the description	Diagrams are drawn incorrectly			
Results (section 3)	Results and data are well organized in Tables	Wrong data entry	7		
	Tables are complete	Tables are incomplete			
Analysis (section 4)	Lists of genotypes and phenotypes are correct and complete	The lists are incorrect and incomplete	7		
	The genotype(s) with the highest ratio are listed first. The one with the lowest ratio is listed last.	Write the list randomly, or in the wrong order			
	X ² calculation is correct	Calculation is incorrect			
Conclusions (section 5)	Summarizes the essential data and derives conclusions based on the data	Conclusions are unclear	7		
	Conclusions are supported by the data	Data does not support the conclusions			
	Hypothesis is rejected or accepted based on the data	Wrong hypothesis is accepted			
	If there was an error, explain the possible source of the error	No explanations			
Format	Few spelling and grammar errors	Multiple spelling and grammar errors	5		
	Neat, with few smudges	Not neat, multiple smudges			
	Punnett square is well drawn as squares	Angles not 90°, lines not straight, sides of unequal length			
	Each section is clearly highlighted	Sections unclear			