



**Grade Level:** 9-12

**Essential Skills:** 3, 4, 5

**NGSS:** HS-LS3-3

**Math:** HS.MP.1, S.IC.6

**Time:** 60 minutes

**Materials:**

- Barley Punnett Squares Lab Packet
- *Crossing Buck and Lightning* video
- Chi-Square calculator

**[AITC Library Resources:](#)**

**More Lessons:**

A Recipe for Genetics:  
Selective Breeding and  
Transgenics  
Apple Genetics: A Tasty  
Phenomena  
Applying Heredity Concepts

## Lesson to Grow

# The F2 Generation of Buck and Lightning

**Description:**

Students will explore the use of Punnett squares and rudimentary statistical math through the lens of a real-life barley breeding scenario. Students will be introduced to the genetics of two barley varieties and will work towards an objective using Punnett squares and reasoning. In this activity, students will cross the *Buck* and *Lightning* varieties to create an F1, then cross two F1s to create an F2, to satisfy the objective. Finally, they will use a Chi-square calculator to evaluate a set of real-life data in comparison to their results. *This lab assumes that students have already had a basic introduction to Punnett squares, their uses, and how to complete them. It is designed as a potential culmination of, and not a replacement for a genetics and Punnett square unit.*

**Background:**

Barley is an important and ancient cereal crop grown worldwide. Barley breeders around the world work to develop barleys that are most useful for the varying purposes of farmers and consumers. A variety of breeding techniques are used to target desired traits in barley. While many aspects of barley genetics are more complex than can be understood with Punnett squares, there are other aspects that can be analyzed using Mendelian genetics, such as shown in this lesson. Whether a barley is 2-row or 6-row is controlled by a single gene, and the same goes for whether it is naked or covered. While the 2-row allele is dominant, the naked allele is recessive. Therefore, breeding for these two traits together poses an interesting challenge for students, as they will have to work through multiple generations of crossing to meet the objective.

**Directions:**

**Part 1: Buck x Lightning (F1) Cross**

1. Provide each student with a copy of the *Barley Punnett Squares Lab* packet.
2. Discuss the background lab and the professions of breeding and genetics of the lab as a class.
3. Begin by discussing key vocabulary. Have students develop definitions and record them in their lab packet using prior knowledge and class notes as reference.
4. Watch the [Crossing Buck and Lightning](#) video as a class.
5. Instruct students to fill in the key information section of their lab packet while watching.
6. After watching, go over the bullet points as a class or have students check with a partner to ensure they got all the information and understand the scenario and objective.
7. Explain to students that the first step in breeding will be to cross the *Buck* and *Lightning* barley varieties.
8. Instruct students to complete the Punnett square crossing *Buck* and *Lightning* and answer the ratio questions listed below on their worksheet. *Depending on the math level of your class, you may want to then walk students through the process of multiplying the Punnett square ratios together to predict the ratios of both traits together.*
9. Review the answers to each of the Punnett Squares and ratio calculations as a class.
10. Introduce students to a 4x4 Punnett square if they haven't seen one before. Provide students about 5 minutes to work the one on their worksheet and record the quantities for each allele combination.
11. After, discuss with the following questions as a class:
  - a. Why do the numbers from the big Punnett square match the numbers from multiplying the small ones together?
  - b. Did we meet the breeding objective with this cross? Why not?
  - c. What should we do next to get closer to the objective?

*Lesson developed by Barleyworld, Oregon State University, [barleyworld.org/main/education](http://barleyworld.org/main/education)*

## Part 2: The F2 Generation

1. Students will now use two F1 barleys to cross to continue trying to meet the objective. Provide students about 10 minutes to complete the next two small Punnett squares and phenotype quantities.
2. After, discuss with the following questions as a class:
  - a. Did we meet the breeding objective? How do we know?
  - b. Is it enough to make a decision based on phenotype alone?
3. Explain to students that a selfing plant (self-fertilization) does not cross-pollinate with other plants, it makes seed by pollinating itself (meaning the offspring has genetic material from the one parent). Barley is a selfing plant unless intentionally crossed by scientists or breeders. When breeding for a new barley with specific alleles, breeders use plants that are homozygous for the desired traits. If a heterozygous plant is used for a certain allele, it would produce offspring (seed) with any possible combination of the dominant and recessive alleles. To ensure the seed maintains the same traits as the parent plant, homozygosity is needed. After discussing, give students 2 minutes to write this answer in their own words on their worksheet.
4. Explain to students that with barley being a selfing plant, we know that we want to use a heterozygous plant, next we will complete a 4x4 Punnett square to determine the proportion of plants produced from this cross with the desired allele.
5. Instruct students to complete the 4x4 Punnett square and answer the questions.

## Part 3: Chi-Square Test

1. Explain to students that they will use a Chi-square test to analyze their results.
2. Discuss the following questions with students:
  - a. What does statistical significance mean, and why does it matter?
  - b. Why would we want to check our predicted results against what actually happened?
3. Instruct students to complete the chart on their worksheet to determine the expected percent of their data. Give students about 15 minutes to calculate their percentages and use this [Chi-square calculator](#) to check and note the viability of their results.
4. Debrief as a class about the process:
  - a. What did they think of it?
  - b. Was it difficult? Why or why not?
  - c. How could these statistical tools be used in other ways?
  - d. Would a breeding/genetics career be interesting to anyone? Why or why not?
5. Give students time to reflect and answer the final question.



## Barley Punnett Squares Lab

Student Name: \_\_\_\_\_

Barley is an important and ancient cereal grain grown around the world for food. Barley geneticists and breeders are always trying to breed barleys for combinations of **alleles** and **phenotypes** that are desirable for farmers and consumers. Some examples of traits that can be selected (bred for) are those determining grain color, grain size and shape, disease resistance, absence or presence of awns (hair-like things that extend from the seed heads), 2-row or 6-row, and nakedness (absence or presence of a hull, a papery covering around the grain). In this lab, you'll use a Punnett square to predict the outcome of crossing plants to select for certain **alleles**.

Fill in the definitions for each vocabulary word in the chart below.

Word	Definition
Gene	
Allele	
Locus	
Selfing	
Phenotype	
Genotype	
Homozygous	
Heterozygous	
Chi-square test	

**Your task:**

After watching the introduction video presented by your teacher, complete the sentences below with information for the task presented by the video.

My objective is to breed a barley that is...

•  
Nakedness is a \_\_\_\_\_ phenotype. The opposite of naked is covered, which is a \_\_\_\_\_ trait.

•  
2-row is a \_\_\_\_\_ phenotype. The opposite of 2-row is 6-row, which is a \_\_\_\_\_ allele.

•  
I am starting off with two barleys called \_\_\_\_\_ and \_\_\_\_\_.

•  
Buck is \_\_\_\_\_ for covered and \_\_\_\_\_ for 2-row.

•  
Lightning is \_\_\_\_\_ for covered and \_\_\_\_\_ for 2-row.

•  
You heard right! Your job will be to use your knowledge of genetics and Punnett squares to meet the objective given in the video.

**Let's begin by taking a look at barley!**



**2-Row Barley**  
One row of kernels on each side of the seed head.



**6-Row Barley**  
Kernels are all around the seed head.



**Covered Barley**  
A papery-looking wrapper (called a hull) around the seed.



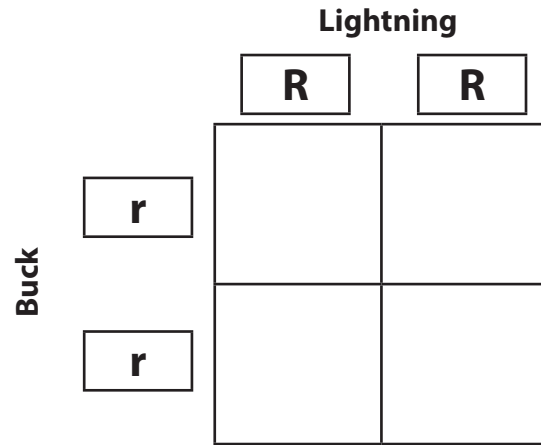
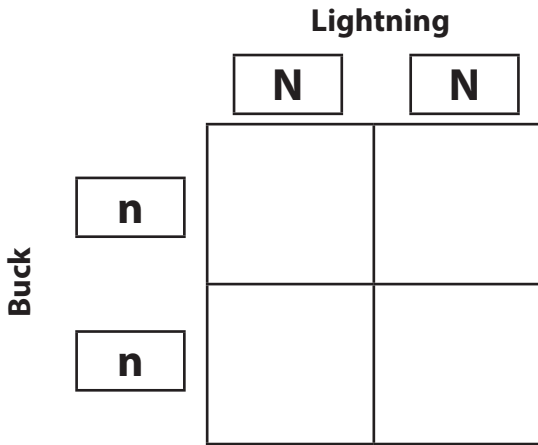
**Naked Barley**  
Seed is smooth, without a wrapping (hull).

### Part 1: Buck x Lightning (F1) Cross

Based on background information, complete the Punnett square for the initial cross (F1) between *Buck* and *Lightning* for nakedness and row count.

Naked/Covered  
 N is dominant (covered)  
 n is recessive (naked)

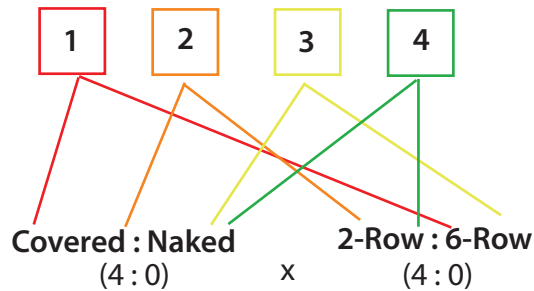
2-Row/6-Row  
 R is dominant (2-row)  
 r is recessive (6-row)



Based on these Punnett squares, what will be the ratio of covered:naked offspring?

Based on these Punnett squares, what will be the ratio of 2-row:6-row offspring?

Punnett squares are like multiplying two inputs to get an outcome. We can multiply the ratios from the squares, using the distributive property to predict what the ratios would be if we crossed for both traits. Fill in the colored boxes in the drawing to predict the amount of offspring with each phenotype (set of observable traits):



- |    |         |   |                      |
|----|---------|---|----------------------|
| 1. | 4 x 0 = | <div style="border: 1px solid red; width: 30px; height: 30px; display: inline-block;"></div>    | <b>Covered 6-Row</b> |
| 2. | 4 x 4 = | <div style="border: 1px solid orange; width: 30px; height: 30px; display: inline-block;"></div> | <b>Covered 2-Row</b> |
| 3. | 0 x 0 = | <div style="border: 1px solid yellow; width: 30px; height: 30px; display: inline-block;"></div> | <b>Naked 6-Row</b>   |
| 4. | 0 x 4 = | <div style="border: 1px solid green; width: 30px; height: 30px; display: inline-block;"></div>  | <b>Naked 2-Row</b>   |

4x4 Punnett squares allow you to check for two traits at once. This 4x4 Punnett square shows the exact same information as the two little ones but in one place with no extra math required. Fill in the square to check your math from the previous page, then record the amounts for each **phenotype** in the boxes to the right of the Punnett square.

	<b>NR</b>	<b>NR</b>	<b>NR</b>	<b>NR</b>	
<b>nr</b>					<p><b>Naked/Covered</b> N is dominant (covered) n is recessive (naked)</p> <p><b>2-row/6-row</b> R is dominant (2-row) r is recessive (6-row)</p> <p><span style="border: 1px solid red; display: inline-block; width: 20px; height: 20px; vertical-align: middle;"></span> <b>Covered 6-Row</b></p> <p><span style="border: 1px solid orange; display: inline-block; width: 20px; height: 20px; vertical-align: middle;"></span> <b>Covered 2-Row</b></p> <p><span style="border: 1px solid yellow; display: inline-block; width: 20px; height: 20px; vertical-align: middle;"></span> <b>Naked 6-Row</b></p> <p><span style="border: 1px solid green; display: inline-block; width: 20px; height: 20px; vertical-align: middle;"></span> <b>Naked 2-Row</b></p>
<b>nr</b>					
<b>nr</b>					
<b>nr</b>					

See? It works! You get the same numbers either way.

So, you made your first cross, resulting in the F1 (Filial 1) generation. F1 is the first generation resulting from crossing two plants.

Did we meet our objective with the F1 generation?

## Part 2: The F2 Generation

Since nakedness is a recessive phenotype, it's a little harder to isolate. The first cross did help us take a step in the right direction! By crossing two varieties that were homozygous, we got a heterozygous result. This gives us more possibilities for the F2 generation (the second generation) if we cross two of the offspring with each other. So let's do it! We'll start with small squares for the individual traits again.

Complete the Punnett squares for a cross of two F1 plants from the *Buck* x *Lightning* cross.

	<b>N</b>	<b>n</b>
<b>N</b>		
<b>n</b>		

	<b>R</b>	<b>r</b>
<b>R</b>		
<b>r</b>		

**Naked/Covered**  
N is dominant (covered)  
n is recessive (naked)

**2-row/6-row**  
R is dominant (2-row)  
r is recessive (6-row)

What will be the ratio of covered:naked barleys?

What will be the ratio of 2-row:6-row barleys?

Now, you can calculate the phenotype outcomes by multiplying the two ratios together, just like last time. This time, fill in your own ratios and numbers to be multiplied:

	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>
<b>Covered : Naked</b>				
(_:_)				
		<b>x</b>		
			<b>2-Row : 6-Row</b>	
			(_:_)	
<b>1.</b>	_ x _ =	<input type="text"/>		<b>Covered 6-Row</b>
<b>2.</b>	_ x _ =	<input type="text"/>		<b>Covered 2-Row</b>
<b>3.</b>	_ x _ =	<input type="text"/>		<b>Naked 6-Row</b>
<b>4.</b>	_ x _ =	<input type="text"/>		<b>Naked 2-Row</b>

This gives us predicted phenotypes for the F2, or second generation (the generation that comes from crossing F1s with the same parents). However, in breeding, the genotype is also important to produce seeds with the desired traits. Barley is a crop that usually produces seed by selfing, meaning that one plant produces seed with only the genes it has. Because of this, barley geneticists want plants that are homozygous for a desired trait.

Why would plant breeders use seeds that are homozygous from selfing plants to select for desired alleles rather than seeds that are heterozygous?

So, if we want plants that are only homozygous for our two traits (naked and 2-row), we could predict the genotypes using the same ratio math, but it would be more complicated because now we would have to use the genotypic ratio, which involves more numbers. It's quicker to do a 4x4 Punnett square for both traits so that we can easily see the odds of getting our desired genotype. In this Punnett square, include the **genotype and the phenotype** for each offspring.

	NR	nR	Nr	nr
NR				
nR				
Nr				
nr				

**Covered 6-Row**



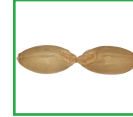
**Covered 2-Row**



**Naked 6-Row**



**Naked 2-Row**



**Naked/Covered**

N is dominant (covered)  
n is recessive (naked)

**2-row/6-row**

R is dominant (2-row)  
r is recessive (6-row)

**From the results above, answer the following questions:**

Which genotypes will give us the desired phenotype?

Which is homozygous for both the naked and 2-row alleles?

What proportion of the offspring will result in the phenotype and homozygous genotype that we want?

### Part 3: Chi-Square Test

Now, we know the expected results of creating these crosses. However, expected and observed results do not always match perfectly. One statistical tool that scientists can use to test predicted results against observed results is called a chi-square test. If our observed results are confirmed by the chi-square test, even if the numbers don't perfectly match what we predicted, we can be confident that our cross was successful.

Why would we want to check our predicted results against what actually happened?



The observed F1 populations for both traits were consistent with the expected results. Out of 100 seeds planted of the F1, 100% plants produced covered and 2-row seed heads. Great! The F2 population is where it got more interesting. Fill in the table below with your expected results for 100 plants, using percentages from your calculations on the previous pages(the colored boxes).

<b>Traits</b>	<b>Observed Percent</b>	<b>Expected Ratio (Colored boxes above)</b>	<b>Expected Percent (Calculate by Multiplying the ratio number by 100 then dividing by 16.)</b>
<b>Covered 6-Row</b>	22		
<b>Covered 2-Row</b>	22		
<b>Naked 6-Row</b>	8		
<b>Naked 2-Row</b>	18		

1. Go to the the following chi-square calculator: <https://www.graphpad.com/quickcalcs/chisquared1.cfm>
2. Enter the traits, observed percent and the expected percent that you calculated from the table above.
3. If it says the difference is statistically significant, something happened when we crossed the plants so that we didn't get the desired results (maybe a few of the seeds self-fertilized). If it says that the difference is not statistically significant, we're in the clear! This means that our results were close enough to what should have happened that we can safely assume that the crossing went right.

Was the difference statistically significant?

Congratulations! You are on the way to becoming a successful barley breeder! The next steps in the breeding process are to plant the seeds from the plants that produced naked 2-row seeds, observe the results to see which ones are homozygous and produce all the same offspring, and use the seeds from those plants to keep growing your naked 2-row barleys.

As you can see, breeding barley isn't easy. Punnett squares are a useful tool that real plant breeders and geneticists use to make simple predictions. This was an example of a real-life genetics cross done by OSU researchers. However, Punnett squares are just a small component of plant breeding. Plant breeders and geneticists also spend time crossing plants in the field and in the lab, working with farmers to determine useful traits to breed for and to help farmers choose crop varieties right for them, analyzing plant genomes to connect traits to genes, designing studies to find out more about crops and their traits, growing crops and analyzing their data for those studies, and thinking about new ways that genetics can be used to work towards better crops and better food products.

Would you ever consider a career in plant breeding and/or genetics? Why or why not? What components of a plant breeder/geneticist's job sound interesting to you?



# Activity Page - Answer Key

## Barley Punnett Squares Lab

Student Name: \_\_\_\_\_

Barley is an important and ancient cereal grain grown around the world for food. Barley geneticists and breeders are always trying to breed barleys for combinations of **alleles** and **phenotypes** that are desirable for farmers and consumers. Some examples of traits that can be selected (bred for) are those determining grain color, grain size and shape, disease resistance, absence or presence of awns (hair-like things that extend from the seed heads), 2-row or 6-row, and nakedness (absence or presence of a hull, a papery covering around the grain). In this lab, you'll use a Punnett square to predict the outcome of crossing plants to select for certain **alleles**.

Fill in the definitions for each vocabulary word in the chart below.

Word	Definition
Gene	A unit of heredity responsible for one trait that is passed from parent to offspring
Allele	Alternative forms of the same gene
Locus	The location of a gene on a chromosome
Selfing	Self-pollinating
Phenotype	The observable expression of a gene
Genotype	The allelic makeup of a gene, which controls the phenotype
Homozygous	Having two of the same alleles for a particular gene
Heterozygous	Having two different alleles for a particular gene
Chi-square test	A statistical method used to determine whether the difference between an observed outcome and an expected outcome is significant

## Your task:

After watching the introduction video presented by your teacher, complete the sentences below with information for the task presented by the video.

My objective is to breed a barley that is...

- **Naked and 6-row**

Nakedness is a \_\_\_\_\_ phenotype. The opposite of naked is covered, which is a \_\_\_\_\_ trait.

- **Recessive, dominant**

2-row is a \_\_\_\_\_ phenotype. The opposite of 2-row is 6-row, which is a \_\_\_\_\_ allele.

- **Dominant, recessive**

I am starting off with two barleys called \_\_\_\_\_ and \_\_\_\_\_.

- **Buck, Lightning**

Buck is \_\_\_\_\_ for covered and \_\_\_\_\_ for 2-row.

- **Homozygous recessive, homozygous recessive**

Lightning is \_\_\_\_\_ for covered and \_\_\_\_\_ for 2-row.

- **Homozygous dominant, homozygous dominant**

You heard right! Your job will be to use your knowledge of genetics and Punnett squares to meet the objective given in the video.

## Let's begin by taking a look at barley!



**2-Row Barley**  
One row of kernels on each side of the seed head.



**6-Row Barley**  
Kernels are all around the seed head.



**Covered Barley**  
A papery-looking wrapper (called a hull) around the seed.



**Naked Barley**  
Seed is smooth, without a wrapping (hull).

## Part 1: Buck x Lightning (F1) Cross

Based on background information, complete the Punnett square for the initial cross (F1) between *Buck* and *Lightning* for nakedness and row count.

Naked/Covered

N is dominant (covered)

n is recessive (naked)

2-Row/6-Row

R is dominant (2-row)

r is recessive (6-row)

		Lightning	
		N	N
Buck	n	Nn	Nn
	n	Nn	Nn

		Lightning	
		R	R
Buck	r	Rr	Rr
	r	Rr	Rr

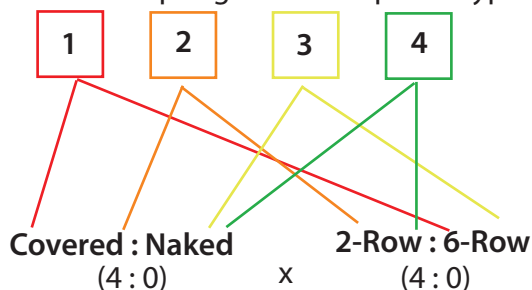
Based on these Punnett squares, what will be the ratio of covered:naked offspring?

**4 : 0**

Based on these Punnett squares, what will be the ratio of 2-row:6-row offspring?

**4 : 0**

Punnett squares are like multiplying two inputs to get an outcome. We can multiply the ratios from the squares, using the distributive property to predict what the ratios would be if we crossed for both traits. Fill in the colored boxes in the drawing to predict the amount of offspring with each phenotype (set of observable traits):



1.  $4 \times 0 =$  0 Covered 6-Row
2.  $4 \times 4 =$  16 Covered 2-Row
3.  $0 \times 0 =$  0 Naked 6-Row
4.  $0 \times 4 =$  0 Naked 2-Row

# Answer Key

4x4 Punnett squares allow you to check for two traits at once. This 4x4 Punnett square shows the exact same information as the two little ones but in one place with no extra math required. Fill in the square to check your math from the previous page, then record the amounts for each **phenotype** in the boxes to the right of the Punnett square.

	NR	NR	NR	NR
nr	NnRr	NnRr	NnRr	NnRr
nr	NnRr	NnRr	NnRr	NnRr
nr	NnRr	NnRr	NnRr	NnRr
nr	NnRr	NnRr	NnRr	NnRr

## Naked/Covered

N is dominant (covered)  
n is recessive (naked)

## 2-row/6-row

R is dominant (2-row)  
r is recessive (6-row)

**0** Covered 6-Row

**16** Covered 2-Row

**0** Naked 6-Row

**0** Naked 2-Row

See? It works! You get the same numbers either way.

So, you made your first cross, resulting in the F1 (Filial 1) generation. F1 is the first generation resulting from crossing two plants.

Did we meet our objective with the F1 generation?

We aren't able to reach the objective with this cross, because we got all covered 2-row plants and we want naked 2-row plants.

## Part 2: The F2 Generation

Since nakedness is a recessive phenotype, it's a little harder to isolate. The first cross did help us take a step in the right direction! By crossing two varieties that were homozygous, we got a heterozygous result. This gives us more possibilities for the F2 generation (the second generation) if we cross two of the offspring with each other. So let's do it! We'll start with small squares for the individual traits again.

Complete the Punnett squares for a cross of two F1 plants from the *Buck* x *Lightning* cross.

	<b>N</b>	<b>n</b>
<b>N</b>	<b>NN</b>	<b>Nn</b>
<b>n</b>	<b>Nn</b>	<b>nn</b>

	<b>R</b>	<b>r</b>
<b>R</b>	<b>RR</b>	<b>Rr</b>
<b>r</b>	<b>Rr</b>	<b>rr</b>

**Naked/Covered**  
N is dominant (covered)  
n is recessive (naked)

**2-row/6-row**  
R is dominant (2-row)  
r is recessive (6-row)

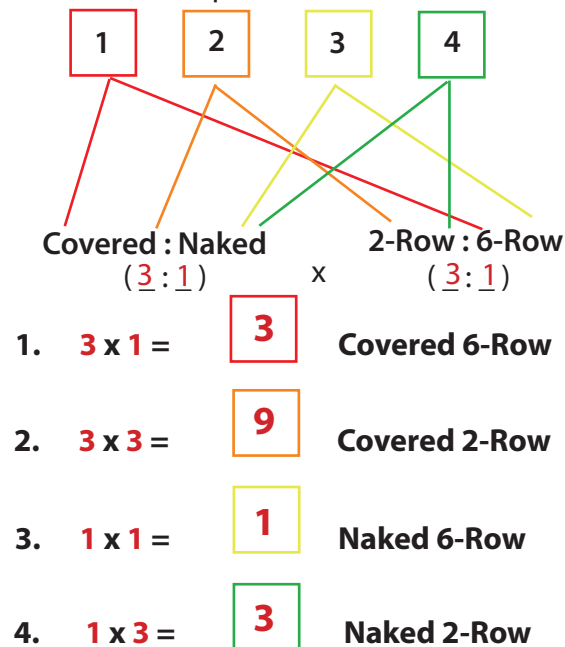
What will be the ratio of covered:naked barleys?

**3 : 1**

What will be the ratio of 2-row:6-row barleys?

**3 : 1**

Now, you can calculate the **phenotype** outcomes by multiplying the two ratios together, just like last time. This time, fill in your own ratios and numbers to be multiplied:



This gives us predicted phenotypes for the F2, or second generation (the generation that comes from crossing F1s with the same parents). However, in breeding, the genotype is also important to produce seeds with the desired traits. Barley is a crop that usually produces seed by selfing, meaning that one plant produces seed with only the genes it has. Because of this, barley geneticists want plants that are homozygous for a desired trait.

Why would plant breeders use seeds that are homozygous from selfing plants to select for desired alleles rather than seeds that are heterozygous?

Homozygous seed ensures that all seed produced from the plant will come out with the same desired traits because there will be no mixing and matching of alleles in the offspring as there would be with a heterozygous plant.

So, if we want plants that are only homozygous for our two traits (naked and 2-row), we could predict the genotypes using the same ratio math, but it would be more complicated because now we would have to use the genotypic ratio, which involves more numbers. It's quicker to do a 4x4 Punnett square for both traits so that we can easily see the odds of getting our desired genotype. In this Punnett square, include the **genotype and the phenotype** for each offspring.

	NR	nR	Nr	nr
NR	<b>NNRR</b> Covered 2-Row	<b>NnRR</b> Covered 2-Row	<b>NNRr</b> Covered 2-Row	<b>NnRr</b> Covered 2-Row
nR	<b>NnRR</b> Covered 2-Row	<b>nnRR</b> Naked 2-Row	<b>NnRr</b> Covered 2-Row	<b>nnRr</b> Naked 2-Row
Nr	<b>NNRr</b> Covered 2-Row	<b>NnRr</b> Covered 2-Row	<b>NNrr</b> Covered 6-Row	<b>Nnrr</b> Covered 6-Row
nr	<b>NnRr</b> Covered 2-Row	<b>nnRr</b> Naked 2-Row	<b>Nnrr</b> Covered 6-Row	<b>nnrr</b> Naked 6-Row

**Covered 6-Row**



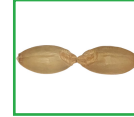
**Covered 2-Row**



**Naked 6-Row**



**Naked 2-Row**



**Naked/Covered**

N is dominant (covered)  
n is recessive (naked)

**2-row/6-row**

R is dominant (2-row)  
r is recessive (6-row)

**From the results above, answer the following questions:**

Which genotypes will give us the desired phenotype?

**Only nnrr**

Which is homozygous for both the naked and 2-row alleles?

**Only nnrr**

What proportion of the offspring will result in the phenotype and homozygous genotype that we want?

**1/16**

### Part 3: Chi-Square Test

Now, we know the expected results of creating these crosses. However, expected and observed results do not always match perfectly. One statistical tool that scientists can use to test predicted results against observed results is called a chi-square test. If our observed results are confirmed by the chi-square test, even if the numbers don't perfectly match what we predicted, we can be confident that our cross was successful.

Why would we want to check our predicted results against what actually happened?

To ensure that the cross was successful and that no mistakes or confounding events occurred in the cross.

The observed F1 populations for both traits were consistent with the expected results. Out of 100 seeds planted of the F1, 100% plants produced covered and 2-row seed heads. Great! The F2 population is where it got more interesting. Fill in the table below with your expected results for 100 plants, using percentages from your calculations on the previous pages(the colored boxes).

<b>Traits</b>	<b>Observed Percent</b>	<b>Expected Ratio (Colored boxes above)</b>	<b>Expected Percent (Calculate by Multiplying the ratio number by 100 then dividing by 16.)</b>
<b>Covered 6-Row</b>	22	3	18.75%
<b>Covered 2-Row</b>	52	9	56.25%
<b>Naked 6-Row</b>	8	1	6.25%
<b>Naked 2-Row</b>	18	3	18.75%

1. Go to the the following chi-square calculator: <https://www.graphpad.com/quickcalcs/chisquared1.cfm>
2. Enter the traits, observed percent and the expected percent that you calculated from the table above.
3. If it says the difference is statistically significant, something happened when we crossed the plants so that we didn't get the desired results (maybe a few of the seeds self-fertilized). If it says that the difference is not statistically significant, we're in the clear! This means that our results were close enough to what should have happened that we can safely assume that the crossing went right.

Was the difference statistically significant?

No, the expected and observed results did not have a statistically significant difference.

Congratulations! You are on the way to becoming a successful barley breeder! The next steps in the breeding process are to plant the seeds from the plants that produced naked 2-row seeds, observe the results to see which ones are homozygous and produce all the same offspring, and use the seeds from those plants to keep growing your naked 2-row barleys.

As you can see, breeding barley isn't easy. Punnett squares are a useful tool that real plant breeders and geneticists use to make simple predictions. This was an example of a real-life genetics cross done by OSU researchers. However, Punnett squares are just a small component of plant breeding. Plant breeders and geneticists also spend time crossing plants in the field and in the lab, working with farmers to determine useful traits to breed for and to help farmers choose crop varieties right for them, analyzing plant genomes to connect traits to genes, designing studies to find out more about crops and their traits, growing crops and analyzing their data for those studies, and thinking about new ways that genetics can be used to work towards better crops and better food products.

Would you ever consider a career in plant breeding and/or genetics? Why or why not? What components of a plant breeder/geneticist's job sound interesting to you?