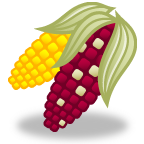
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 Corn Genetics Lab[[1]](#footnote-1) C:\Users\tcurry\AppData\Local\Microsoft\Windows\Temporary Internet Files\Content.IE5\DDP6K8H1\MC900348429[1].wmf

**Introduction:**

This lab will test Mendel’s laws by making predictions about the **phenotypes** of the kernels of Indian corn and then doing actual counts of the kernels. Each corn kernel is the product (child) of two parnet corn plants. This makes corn an exellent model organism for studying genetics because we can see a large number of offspring all at once on a single ear of corn! This allows us to count a large number of individuals very easily.

The corn we will use in this lab was specially prouduced in a controled lab where the pollen from only one plant was used to pollinate each ear. Therefore, each ear demonstrates all of the possible phenotypes from the mating of two individuals.

**Background:**

**Gametes** are brought together to form a new individual during sexual reproduction. Each parent produces gametes by the process of **meiosis**. Meiosis is special cell division during which chromosomes are replicated and sorted into like (**homologous**) pairs, with one member from each homologous pair ending up in each gamete. Male parents usually produce large amounts of small, motile gametes; female parents produce a low number of large gametes. Male gametes (**sperm**, or pollen) travel to the female gametes (**ova**, or seeds), each carrying a set of instructions for the new life. During fertilization, the nuclei of the sperm and egg fuse, resulting in a **zygote**, whose nucleus contains all of the genetic instructions from both gametes. The zygote now contains all of the genetic information needed for the growth and development of a new individual.

In the mid 1800s, a monk named Gregor Mendel developed 4 postulates (laws of inheritance) that govern the inheritance of traits. His postulates were based on his observations from his experiments in breeding pea plants.

Mendel’s First Three Postulates:

1. For each trait, organisms inherit 2 alleles, one from each parent.
2. **The Principle of Dominance** - If the 2 inherited alleles differ, then the dominant allele is expressed and the recessive allele is not.
3. **The Law of Segregation** – two alleles of a given gene segregate (separate) from each other during gamete production (meiosis). The result of that gamete **randomly** receives one allele of each gene.

**Activity 1: Monohybrid Cross**

In corn plants, seed traits for color and texture demonstrate Mendel’s postulates. The trait studied in this activity is seed color. Seed color is controlled by a gene that has two **alleles** (forms of a trait). The **dominant** allele causes the production of **purple** pigment in the seed coat. The **recessive** allele results in the production of no pigment causing the seed coat to appear **white**.

The ears of corn you will use are from the **F2 generation** of corn. What does this mean?

The P generation of this corn was created by crossing a true breeding purple corn plant with a true breeding white corn plant. Perform the cross by doing the Punnett square below to determine the phenotype and genotype of the F1 generation.

Genotype of F1 generation:\_\_\_\_\_

Phenotype of F1 generation:\_\_\_\_\_\_\_\_

**Prediction:**

Punnett squares are a neat trick but what is there actual use? Their use is they make predictions, or hypothesis in genetics. Since we cannont see the genes but we can see the phenotypes we must figure out genotypes from ratios of phenotypes. We will now make a prediction about the F1 corn that you do not have by predicting ratios of the F2 corn that you will count. F2 is the prodcut of the mating of two F1 individuals.

What is the genotype of the parent corn used to produce the F2 corn?

Perform the Punnett square for the F1 cross:

What percentage of F2 kernels should be purple? \_\_\_\_\_\_\_\_

White? \_\_\_\_\_\_\_

**Procedure:**

1. Use an ear of corn labeled “A”
2. Place a rubber band around a specimen so that it separates the corn into two equal halves.
3. Count the kernels that have one phenotype on one half of the ear and then the other half. Record your counts on the data table below.
4. Count the kernels of the other phenotype on one half of the ear and then the other half. Record your counts on the data table below.
5. Caculate the percentage of each phenotype by dividing the number of kernels for a phenotype on an ear by the total number of kernels on the ear.

**Data:**

Give this table a title:

|  |  |  |
| --- | --- | --- |
| **Phenotype** | **Number Counted** | **Percentage** |
|  |  |  |
|  |  |  |

**Analysis:**

1. What is a dominant aleele? A recessive allele?
2. For each phenotype, compare the predicted percentages with the observed percentages in the data table. Are the results exactly the same?
3. Are the observed results close to the predicted results?
4. Why would you expect a descrepancy between predicted and observed results?
5. What would happen if alleles did not segregate in meiosis?

**Activity 2: Testcross**

Sometimes a person might want to figure out what types of alleles are present in an organism. To do this a **testcross** is performed. A testcross is when an individual of an unknown genotype is mated with a individual of a known genotype and then the results of the mating are examined to figure out the genotype of the parent. Usually the known organism is the recessive phenotype because *we always know the genotype of the recessive phenotype*. Why is this?

In this experiment a purple seed of an unknown genotype and a white seed were planted. When the resulting corn plants were sexually mature pollen from the purple plant was brushed onto the silk of the white plant. I bet you didn’t know that the ear of corn is a flower! Once again you will be making a prediction:

You have two possibilities with this cross so you will have to make a prediction (Punnett square) for both.

Possibility 1 : the purple plant is homozygous

Penotypic ratio of offspring:\_\_\_\_\_\_\_\_\_\_\_\_\_

Possibility 2: the purple plant is heterozygous

Phenotypic ratio of offspring:\_\_\_\_\_\_\_\_\_\_\_\_\_

**Procedure:**

1. Use an ear of corn labeled “B”
2. Place a rubber band around a specimen so that it separates the corn into two equal halves.
3. Count the kernels that have one phenotype on one half of the ear and then the other half. Record your counts on the data table below.
4. Count the kernels of the other phenotype on one half of the ear and then the other half. Record your counts on the data table below.
5. Caculate the percentage of each phenotype by dividing the number of kernels for a phenotype on an ear by the total number of kernels on the ear.

**Data:**

Give this table a title:

|  |  |  |
| --- | --- | --- |
| **Phenotype** | **Number Counted** | **Percentage** |
|  |  |  |
|  |  |  |

**Analysis:**

1. What was the genotype of the original purple kernel and how do you know?
2. How could this process be useful in a real-life situation?

**Activity 3: The Dihybrid Cross**

Corn specimen C is the result of a cross between two plants that are **heterozygous for both seed coat** **and seed texture**. Seed color was studied in Activities 1 & 2. You may want to look back at those activities to remind yourself of the genes involved in the control of purple and white seed coats.

Seed texture is the result of the way starch is stored within the seed. If the corn has at least one copy of the dominant allele for the seed texture gene, it produces an enzyme that causes sucrose to be converted to starch, which is more loosely packed than sucrose, causing a smooth seed. The presence of two recessive alleles results in less sucrose being converted. As the corn is dried, the seed coat collapses because there is less starch, giving the seed a wrinkled appearance.

This experiment will test to see if the corn is really the result of a heterozygous dihybrid cross. Make a prediction for the phenotypic ratios that should be seen from the result of the above cross.

Cross: \_\_\_\_\_\_\_\_\_\_x \_\_\_\_\_\_\_\_\_\_\_

Gametes:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Punnett square:

Predicted phenotypic ratio: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Procedure:**

1. Use an ear of corn labeled “B”
2. Place a rubber band around a specimen so that it separates the corn into two equal halves.
3. Count the kernels that have one phenotype on one half of the ear and then the other half. Record your counts on the data table below.
4. Count the kernels of the other phenotype on one half of the ear and then the other half. Record your counts on the data table below.
5. Caculate the percentage of each phenotype by dividing the number of kernels for a phenotype on an ear by the total number of kernels on the ear.

**Data:**

Give this table a title:

|  |  |  |
| --- | --- | --- |
| **Phenotype** | **Number Counted** | **Percentage** |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |

Phenotypic ratio: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Analysis:**

1. In your own words, explain independent assortment.
2. Did the phenotypic ratio you calculated for your corn match your dihybrid prediction? Was it close?
3. Was the genotype of the F1 corn (the corn that produced the corn you counted) heterozygous for both genes? How do you know?
4. If both genes were on the same chromosome what phenotype(s) would you see in the resulting generation?

1. Adapted from : *Corn Genetics Student Guide*, Carolina Biological Supply [↑](#footnote-ref-1)