

GENETICS

The first part of this lab will allow you to relive some of Gregor Mendel's findings on inheritance. The second part of the lab explores the consequences of natural selection against certain alleles.

I. GENETIC ANALYSIS IN CORN

In 1865 when Gregor Mendel presented his findings on inheritance in garden peas (*Pisum sativum*) to the Natural History Society of Brunn, he laid the first brick in the foundation of genetics. The combination of his abilities in experimental design, record keeping and mathematical analysis were key to his success. In this lab you will repeat his basic investigations, but use corn (*Zea mays*) instead of peas.

Although corn is a distant relative of the garden pea, it can provide much of the same genetic information as Mendel's peas. Each kernel is the result of a separate fertilization event and the kernels on an ear of corn represent the next generation of plants derived from the pollen and ova from the parent plant or plants. Assuming random access to the fertilization tubes (corn silk), the kernels of one ear are no more closely related to each other than to kernels on any other ear from the same plant.

You will treat the kernels on an ear of corn as individuals of a generation from a specific cross.

PROCEDURE

1. Study Figure 1 to determine the parentage of the F₂ ears of corn used in this exercise.
2. Count all of the kernels on your ear, keeping track of the phenotype of each (Purple Starchy; Purple Sweet; Yellow Starchy; Yellow Sweet). Use the push pins to mark off counted rows of kernels, and keep a tally in Table 1.
3. Obtain the counts your partner made on her/his ear and also record those totals in Table 1. Complete Table 2 by combining the appropriate counts, e.g. the total number of purple kernels is the sum of purple starchy and purple sweet. Also calculate the appropriate percents and ratios.
4. Complete Table 3 in the same way. Remember, the data are the same in Tables 2 & 3, just examined in a different way.

Purple Starchy	Purple Sweet
Yellow Starchy	Yellow Sweet

ANALYSIS

A monohybrid cross is a controlled cross where only one trait is being analyzed at a time. Your results in Table 3 are the results of two monohybrid crosses. A dihybrid cross is one where two traits are analyzed simultaneously as in Table 2. Keep in mind that the data and the cross is the same in Tables 2&3, but analyzed in a different way in each. Both types of crosses are instructive and exemplify Mendel's First and Second Principles.

Examine the ratios you obtained in Table 2. The ratio of Purple to Yellow kernels should be close to 3:1, as should the ratio of Starchy to Sweet. This is said to be a simple Mendelian ratio for an F₂ generation in a monohybrid cross.

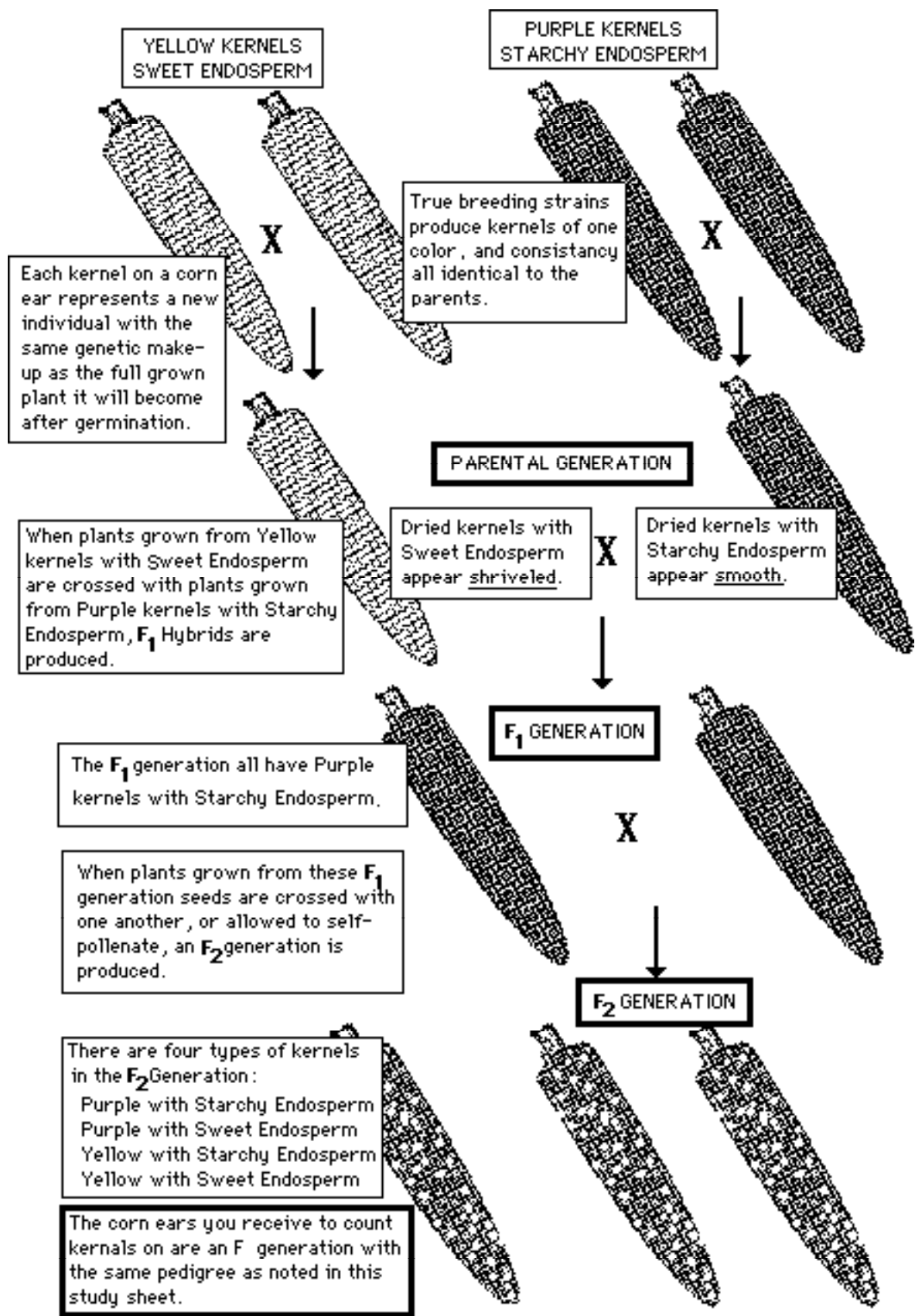


FIGURE 1. Corn ear pedigree.

The 3:1 ratio demonstrates Mendel's First Principle of Segregation. One would expect such ratios if each individual carries two factors governing each trait, and the factors segregate such that each gamete carries only one of the factors. Another requirement to achieve this ratio is that when the individual carries two different factors for a trait, one of the factor masks or dominates the other.

The ratios may also be used to express probabilities as well. Since the ratio of Starchy to Sweet is 3:1, one expects to encounter a Starchy kernel 3 out of four times. This means that the probability of an F2 kernel being Starchy is 3/4 (which of course is the same as 0.75).

	Purple	Yellow
Team Total		
Observed Ratio		1
Expected Ratio	3	1
	Starchy	Sweet
Team Total		
Observed Ratio		1
Expected Ratio	3	1

The rules of probability state that the probability of two independent events occurring simultaneously is the product of their individual probabilities. In other words, if the inheritance of Starchy or Sweet endosperm is independent of the inheritance of Purple or Yellow color, then the probability of obtaining Purple Starchy kernels should be:

$$\begin{array}{ccccc} \text{PURPLE} & & \text{STARCHY} & & \text{PURPLE STARCHY} \\ 3/4 & \times & 3/4 & = & 9/16 \end{array}$$

Likewise, the probability of obtaining Purple Sweet kernels should be:

$$\begin{array}{ccccc} \text{PURPLE} & & \text{SWEET} & & \text{PURPLE SWEET} \\ 3/4 & \times & 1/4 & = & 3/16 \end{array}$$

Using the same reasoning (that the traits are inherited independently of each other), calculate the probabilities for the various phenotypes from a dihybrid cross noted in Table 4 using the idealized 3:1 ratio.

	Purple Starchy	Purple Sweet	Yellow Starchy	Yellow Sweet
Team Total				
Observed Ratio				
Expected Ratio				

Phenotype	Independent Probability				Expected
	Purple	Yellow	Starchy	Sweet	
Purple Starchy					
Purple Sweet					
Yellow Starchy					
Yellow Sweet					

If the ratios obtained experimentally from a dihybrid cross, match those predicted on the basis of each event being independent of the other, then one could safely say that the inheritance of each trait is independent of the other. This is precisely what Mendel figured out and verified experimentally in his research. It is often referred to as Mendel's Second Principle of Independent Assortment.

Phenotype	Expected Ratio	Observed Ratio
Purple Starchy		
Purple Sweet		
Yellow Starchy		
Yellow Sweet		

Complete Table 5 by filling in the expected ratios calculated in Table 4, and the observed ratios from Table 3. What does close alignment of these values indicate?

II. NATURAL SELECTION AND ALLELE FREQUENCIES

Allele frequency refers to how often a particular allele appears in a population. Evolution can be defined as a change in the frequency of alleles over time. The allele frequency for a given trait changes over time in response to changes in the environment. At the beginning of the quarter you saw how natural selection influenced changes in the frequency of a particular phenotype. This exercise will illustrate how natural selection influences genotype.

A. How To Calculate Allele Frequency

Think of a population as a pool of genes instead of individuals, as though each of the individuals pulled out his or her genes and threw them in a big pot.

Suppose we have a population of 100 individuals:

- 25 of which are "AA"
- 50 of which are "Aa"
- 25 of which are "aa"

This population contains 200 total alleles, because 100 individuals with 2 alleles each = 200 alleles total.

Counting up all the "A's" in the population, we find there are 100 because:

$$\begin{array}{r} 2 \times 25 = 50 \text{ "AA"} \\ + 1 \times 50 = 50 \text{ "Aa"} \\ \hline 100 \text{ "A" genes} \end{array}$$

Allele frequency of "A" is $100/200 = 0.5$ (or 50%). Similarly, the allele frequency for "a" in this population is 0.5 (or 50%).

B. Selection against the aa genotype

We have just seen how two alleles of the same gene can be passed on if both genes have an equal chance of surviving. Now we will demonstrate what happens to allele frequency when there is a **selective disadvantage** to a particular genotype. In particular, genotype "aa" causes a fatal disease which results in death during childhood.

1. Everyone will begin with a heterozygous genotype. (Everyone is healthy, but carries a recessive gene for the disease.) Record your initial genotype on the first line of Table 6.
2. Instead of mating with your lab partner, roam around the room and find another person in the class AT RANDOM (without respect to charm, appearance, or even gender) to mate with. Mate twice. These two offspring will replace you and your partner in the next generation. If one offspring has the genotype is "aa", it dies. One of you cannot reproduce again. If both offspring are "aa", then neither of you can reproduce again. Record your offspring's genotype in Table 6.

Stop at this point until everyone in the class has finished mating.
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3. You will now assume the identity of your offspring and take on its genotype. Remember, if you were aa, you cannot mate again. If you are "AA" or "Aa", replace your beads with the appropriate colors.

4. **Find a new partner** to mate with and produce two offspring. Record the genotypes. Again, if you produce an "aa" offspring, you cannot mate in the next generation.
5. Repeat the mating four more until a total of **six generations** have been completed.
6. Report your results to the class and record the class results in Table 7. Calculate the allele frequencies for each generation based on the class results.

Table 6: Your Individual Genotypes

	Your Genotype
Original Genotype	
Genotype of 1st Generation	
Genotype of 2nd Generation	
Genotype of 3rd Generation	
Genotype of 4th Generation	
Genotype of 5th Generation	
Genotype of 6th Generation	

Table 7: Class Genotypes

	# of People with genotypes:			# of Individual Alleles		Allele Frequency	
	AA	Aa	aa	A	a	A	a
Original genotype							
Genotype of 1st Generation							
Genotype of 2nd Generation							
Genotype of 3rd Generation							
Genotype of 4th Generation							
Genotype of 5th Generation							
Genotype of 6th Generation							

Discussion: How did allele frequencies change? What was the affect of natural selection? Why does the "a" allele never disappear completely?