EXPLORATIONS

Activity 5

Objectives

- To differentiate between homozygosity and heterozygosity
- To differentiate between dominant and recessive
- To generate random numbers on the TI-83 Plus
- To produce a histogram and analyze it with respect to genetic probability
- To compare actual and expected results of genetic crosses

Call it…Dominant or Recessive

In this activity you will

- make predictions about genetic crosses.
- simulate a Punnett square.

Introduction

At the start of a football game, who will kick off and who will get the ball first Is usually decided by flipping a coin. When a coin is flipped into the air, what is the chance that it will land with heads showing? What is the chance that it will land with tails showing? How many possible outcomes are there when a coin is flipped? When the captain of the football team calls heads, what is the chance that he will be correct and be the first hero of the game? If the referee secretly had a coin that had heads on both sides, and the captain called heads, what is the chance that the captain will call it correctly? If the captain called tails, what would be his chance of success? If you know the answers to all of these questions, you are on your way to understanding what basic genetics is all about. Another word for *chance* is *probability*, and in this activity you will come to understand that genetics is due, in large part, to probability.

Just two genes determine many of your individual traits. You got one of the genes from your mother and the other from your father at the moment of fertilization. Genes usually come in two varieties: dominant and recessive. For many of your traits, you have either two dominant genes (homozygous dominant), two recessive genes (homozygous recessive), or one of each (heterozygous). Traditionally, letters have been assigned to represent genes. For example, **A** is often used to represent the dominant gene for a particular trait, while **a** is used to represent the recessive gene for the same trait. If you were homozygous dominant for the trait, your genes would be **AA**. Homozygous recessive individuals would be indicated by **aa**, and heterozygous individuals would be **Aa**.

Before babies can be formed, gametes (sperm or eggs) need to be produced, join together to form a zygote, and start to develop. When an organism forms gametes, the pair of genes for a trait gets split up and each gamete gets only one gene from the pair. As you read earlier, for each trait an individual has, only one gene was given by the father and only one by the mother. This way, when fertilization occurs, the new baby will have two genes for each trait, just as its parents do.

Problem

If you are heterozygous for a trait (**Aa**) and only one gene from the pair can go into each gamete you produce, what is the probability that a gamete will inherit the **A** gene? (Think of the coin toss example). What is the probability that a gamete will inherit the **a** gene? If you are homozygous dominant for a trait (**AA**), now what is the probability that a gamete will inherit the **A** gene? The **a** gene? What is the probability of each if you are homozygous recessive?

Since the TI-83 Plus deals with numbers more effectively than letters, in this activity you will use the number **1** to represent **A**, and the number **2** to represent **a**. Using this system, you can develop the following scheme:

Homozygous dominant (**AA**) = **1** + **1**, for a total of **2**. All gametes produced will have **1**.

Heterozygous (**Aa** or **aA**) = **1** + **2**, for a total of **3**. Half of gametes = **1**, half = **2**.

Homozygous recessive (**aa**) = **2** + **2**, for a total of **4**. All gametes = **2**.

A model of a cross between two heterozygous individuals would look like this table, called a Punnett square.

Gametes	**A (or 1)**	**a (or 2)**
A (or 1)	AA (or 2)	Aa (or 3)
a (or 2)	Aa (or 3)	aa (or 4)

Offspring (predicted outcomes)
(¼ homozygous dominant, ½ heterozygous, ¼ homozygous recessive)
(¾ show dominant trait, ¼ show recessive trait)

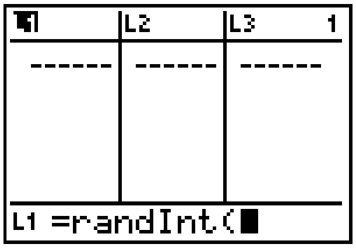
✐ *Complete questions 1 through 18 on the Data Collection and Analysis page.*

Procedure

Simulate a cross between two heterozygous individuals (**Aa** x **Aa**).

1. Press [STAT] [ENTER].
2. Clear **L1** of all data. Press [▲] to move to the heading **L1**. Press [CLEAR] [ENTER].
3. Go back to **L1** and make sure **L1** is highlighted.

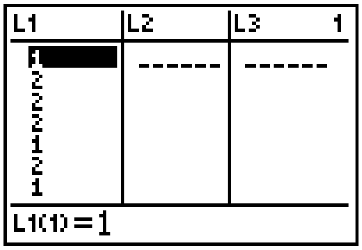
4. Press [MATH] [◄]. Highlight **5:randInt(** . Your TI-83 Plus screen should look like the screen at the right.



```
L1     |L2     |L3     1
------ |------ |------
L1 =randInt(
```

5. Enter the following arguments after **randInt(: 1** [,] **2** [,] **2 0 0** [)] [ENTER].

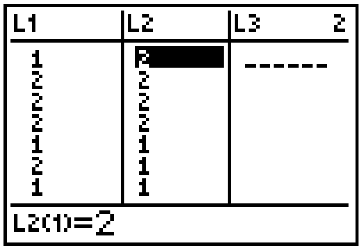
   You just told the TI-83 Plus to generate 200 random integers between 1 and 2, inclusive. In other words, the only integers it has to choose from are 1 and 2. After you press [ENTER], your screen will look like the one at the right. Although the numbers in **L1** may be different, all of them should be 1's and 2's. Remember that a **1** represents **A** and a **2** represents **a**. You typed in **200** because you are going to generate 200 offspring from the cross **Aa** x **Aa**. **L1** represents the gene that is in each gamete of one of the parents.



```
L1     |L2     |L3     1
 1     |------ |------
 2     |       |
 2     |       |
 2     |       |
 1     |       |
 2     |       |
 1     |       |
L1(1)=1
```

Generate the gametes for the other parent and place them in **L2**.

6. Highlight the heading **L2.** Repeat the procedure described above to generate 200 **1**'s (**A**'s) and **2**'s (**a**'s) in **L2**. These numbers represent the genes in the gametes of the second parent. Again, your screen might not have the same numbers in **L1** and **L2**. That's OK!

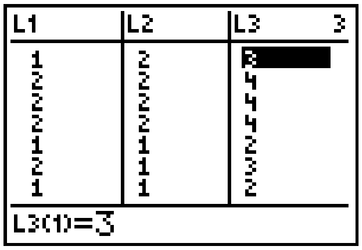


```
L1     |L2     |L3     2
 1     | 2     |------
 2     | 2     |
 2     | 2     |
 2     | 2     |
 1     | 1     |
 2     | 1     |
 1     | 1     |
L2(1)=2
```

Join these gametes in **L1** and **L2** to produce 200 offspring in **L3**.

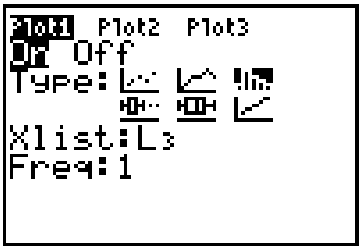
7. Highlight the heading **L3.** Enter the following: [2nd] [L1] [+] [2nd] [L2] [ENTER]. You have now produced 200 offspring!

   Refer to the Punnett square (page 42) to see what the numbers in **L3** represent.



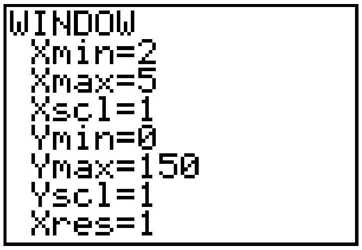
```
L1     |L2     |L3     3
 1     | 2     | 3
 2     | 2     | 4
 2     | 2     | 4
 2     | 2     | 4
 1     | 1     | 2
 2     | 1     | 3
 1     | 1     | 2
L3(1)=3
```

Graphically represent the distribution of the different types of offspring using a histogram.



```
Plot1 Plot2 Plot3
On Off
Type:
Xlist:L3
Freq:1
```

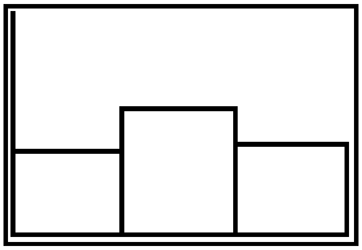
8. Press [2nd] [STAT PLOT]. Press [ENTER] to select **1:Plot1**. Set your TI-83 Plus as shown at the right.



```
WINDOW
 Xmin=2
 Xmax=5
 Xscl=1
 Ymin=0
 Ymax=150
 Yscl=1
 Xres=1
```

9. Press [WINDOW] and set your screen as shown at the right.

✐ *Go to question 19 on the Data Collection and Analysis page. Enter your predictions in the **Expected Number** column.*



10. Press [GRAPH]. You have produced a histogram of the data in **L3**. Your TI-83 Plus screen should look similar to the screen at the right.

10. Press [TRACE] and observe where the blinking cursor is located. The values at the bottom of the screen reflect the *x*-value, *y*-value, or number represented by the position of the cursor.

11. Press [◀] and [▶] to move from bar to bar in the histogram, recording the **n=** values. These represent the number of individuals having each gene combination. The first bar represents the **AA**, the second bar is **Aa**, and the third bar is **aa**.

✐ *Complete the rest of the table under question 19 of the Data Collection and Analysis page.*

Since **AA** and **Aa** both have at least one dominant gene, they would both show the dominant form of the trait. In other words, both **AA** and **Aa** would have the same *phenotype* (physical expression of the genes), even though they have different *genotypes* (type of genes inherited). For example, if the 200 offspring in **L3** are baby fish, and having spots is dominant while being spotless is recessive, then in your histogram, the only bar representing the number of spotless fish is the third bar (**aa**, or the 4's). The first two bars would represent fish with the same phenotype (spotted), even though they have different *genotypes* (**AA** and **Aa**).

✐ *Complete the table under question 20 of the Data Collection and Analysis page.*

12. Collect the data from the entire class.

✐ *Complete the tables under question 21 of the Data Collection and Analysis page.*

Data Collection and Analysis

Name ___________________________

Date ___________________________

Activity 5: Call it…Dominant or Recessive

Data Collection

1. If a homozygous dominant organism is crossed with another homozygous dominant organism, according to your numerical system (**A**=1, **a**=2), what will be the numerical value of all of the gametes produced?

   What will be the numerical value for all the offspring of this cross?

2. If a homozygous dominant organism is crossed with a homozygous recessive organism, what will be the possible numerical values for the gametes of each?

   Homozygous dominant:

   Homozygous recessive:

3. What will be the possible numerical values for the offspring?

4. If a homozygous dominant is crossed with a heterozygous organism, what will be the possible numerical values for the gametes of each?

   Homozygous dominant:

   Heterozygous:

   What will be the possible numerical values of the offspring?

5. If two homozygous recessives are crossed, what will be the possible numerical values?

Gamete value:

Offspring value:

6. If two heterozygotes are crossed, what will be the possible numerical values?

Gamete values of one individual:

Gamete values of the other:

Possible values for the offspring:

7. If two homozygous dominants are crossed, what is the probability that an offspring will be homozygous dominant? Express your answer both as a percentage and as a decimal.

8. If two homozygous recessives are crossed, what is the probability that an offspring will be homozygous recessive?

9. If a homozygous dominant is crossed with a heterozygote, what is the probability that an offspring will be homozygous recessive?

10. If two heterozygotes are crossed, what is the probability that an offspring will be homozygous recessive?

Homozygous dominant?

Heterozygous?

11. Any time a dominant gene shows up in the offspring, that offspring shows the dominant trait. In other words, individuals who are homozygous dominant (**AA** or 1+1) and those who are heterozygous (**Aa** or 1+2) both show the dominant trait. Only those individuals who are **aa** (or 2+2) show the recessive trait. Knowing this, if two heterozygotes are crossed, what is the probability that an offspring will show the dominant trait?

What is the probability that an offspring will show the recessive trait?

12. Refer to the Punnett square on page 42. If two heterozygous fish are crossed and 200 baby fish are produced, predict how many of each of the following you would expect. Remember that these are the PREDICTED (or theoretical, or expected) number of offspring based on probability. The ACTUAL (or experimental) numbers of offspring are likely to be somewhat different from the predicted. However, the more offspring that are produced, the closer you should get to the predicted numbers.

Homozygous dominant fish:

Homozygous recessive fish:

Heterozygous fish:

Fish showing the dominant trait:

Fish showing the recessive trait:

13. In a cross between two spotless fish, what would be the probability of obtaining a spotted fish?

14. In the same cross, what would be the probability of obtaining a spotless fish?

15. Imagine that a heterozygous (spotted) fish is crossed with a homozygous recessive (spotless) fish and 300 babies are produced. In the blank graph below, draw a histogram of the babies that you would expect to be produced. Include labels on the bars, and the number associated with each bar.

16. If two heterozygous fish (**Aa**) were crossed and 500 babies were produced, how many of the babies would you expect to be homozygous dominant?

Homozygous recessive?

Heterozygous?

17. If two heterozygous fish were crossed and 50 babies were produced, how many of the babies would you expect to be homozygous dominant?

Homozygous recessive?

Heterozygous?

18. Would you predict that the actual numbers of babies of each genotype would more closely compare with the fish that had 500 babies, or the fish that had 50 babies? Explain.

19. After working through the steps under **Procedure**, enter your predictions in the **Expected Number** column below, and then complete the table after you graph the histogram.

Gene Combination	Actual Number: Number from Graph (n=)	Expected Number	Difference between Actual and Expected
AA (first bar)			
Aa (second bar)			
aa (third bar)			
TOTAL	200	200	

20. Enter the required information in the table below.

Phenotype	Actual Number: Number from Graph	Expected Number	Difference between Actual and Expected
Spotted (1st & 2nd bars)			
Spotless (3rd bar)			
TOTAL	200	200	

21. Enter the data from the entire class in the tables below.

Gene Combination	Actual Number: Number from Graph (n=)	Expected Number	Difference between Actual and Expected
AA (first bar)			
Aa (second bar)			
aa (third bar)			
TOTAL			

Phenotype	Actual Number: Number from Graph	Expected Number	Difference between Actual and Expected
Spotted (1st & 2nd bars)			
Spotless (3rd bar)			
TOTAL			

Extensions

- Go back to the procedure for producing babies on the TI-83 Plus and produce 20 babies, rather than 200. After you have done this, produce a histogram and record your data in the data table below.

Phenotype	Actual Number: Number from Graph	Expected Number	Difference between Actual and Expected
Spotted (1st & 2nd bars)			
Spotless (3rd bar)			
TOTAL	20	20	

- What is the relationship between genetics and probability?

Teacher Notes

Activity 5

Call it...Dominant or Recessive

Objectives

- To differentiate between homozygosity and heterozygosity
- To differentiate between dominant and recessive
- To generate random numbers on the TI-83 Plus
- To produce a histogram and analyze it with respect to genetic probability
- To compare actual and expected results of genetic crosses

Concepts

- Basic probability
- Mendelian genetics
- Single-variable data

Data Collection - Answer Key

1. The numerical value of all of the gametes produced = 1. The numerical value for all the offspring of this cross = 2.

2. Homozygous dominant: 1.

Homozygous recessive: 2.

3. The possible numerical values for the offspring = 3.

4. Homozygous dominant: 1.

Heterozygous: 1 or 2.

The possible numerical values of the offspring: 2 or 3.

5. Gamete value: 2.

Offspring value: 4.

6. Gamete values of one individual: 1 or 2.

Gamete values of the other: 1 or 2.

Possible values for the offspring: 2, 3, or 4.

7. If two homozygous dominants are crossed, the probability that an offspring will be homozygous dominant is 100% or 1.00.

8. If two homozygous recessives are crossed, the probability that an offspring will be homozygous recessive is 100% or 1.00.

9. If a homozygous dominant is crossed with a heterozygote, the probability that an offspring will be homozygous recessive is 0%.

10. If two heterozygotes are crossed, the probability that an offspring will be homozygous recessive is 25% or 0.25.

Homozygous dominant: 25% or 0.25.

Heterozygous: 50% or 0.50.

11. If two heterozygotes are crossed, the probability that an offspring will show the dominant trait is 75% or 0.75.

The probability that an offspring will show the recessive trait is 25% or 0.25.

12. Homozygous dominant fish: 50.

Homozygous recessive fish: 50.

Heterozygous fish: 100.

Fish showing the dominant trait: 150.

Fish showing the recessive trait: 50.

13. In a cross between two spotless fish, the probability of obtaining a spotted fish is 0%.

14. In the same cross, the probability of obtaining a spotless fish is 100%.

15. Both histogram bars should be the same height, with 150 fish of each phenotype.

16. Number of babies expected to be homozygous dominant: 125.

Homozygous recessive: 125.

Heterozygous: 250.

17. If two heterozygous fish were crossed and 50 babies were produced, the number of babies expected to be homozygous dominant: 12 or 13.

Homozygous recessive: 12 or 13.

Heterozygous: 25.

18. The actual number of babies should more closely compare with the fish who had 500 babies, because an increase in sample size should more closely reflect the expected ratios.

19. All numbers will vary.

20. All numbers will vary.

21. All numbers will vary.

Extensions – Answer Key

- All numbers will vary.
- Genetics is all about probability. Which alleles make it into each gamete is largely a matter of chance. Because of this, we can use probability to make predictions about genetic outcomes.