

Activity: Gummy Bear Genetics

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Name: _____ Date: _____

You can work individually or in small groups. Select a numbered paper bag. The bears in each bag are the result of a different cross-breeding experiment (part of the captive breeding program). Sort the bears in your bag based on phenotypes that can be observed and quantified. Complete the worksheet on your station number.

Step 1:

Obtain a bag of gummy bears, and record the total number of bears here: _____. These bears represent the F1 generation of cross-breeding experiment.

Step 2:

Empty the bag and sort the gummy bears into groups based on phenotype differences that can be easily observed and quantified.

What is the phenotype characteristic you used to sort the bears? Why?

Step 3:

Count the number of individual bears for each of the alternate forms of this characteristic and fill in the table below.

Cross Number	Characteristic	Alternate Form	Number	Ratio

Write your data on the classroom chart. Compare your results with the results of the other teams in the class.

Which type of inheritance is displayed by your sample?

Step 4:

Select gene symbols to represent the alleles for the characteristic you studied.

Based on the evidence, what are the probable genotypes for each phenotype you observed?

What were the probable genotypes of the original parental cross?

What were the phenotypes of these parent individuals?

MOST*

HELPFUL TERMS

Allele

Cross-breeding

F1 generation

Genotype

Mendelian genetics

Phenotype

Punnett Square

MATERIALS NEEDED

1 bag of gummy bears

Graph paper

Colored pencils

Students should be able to:

Discover basic principles of genetics.

Test hypothesis to explain Mendelian and non – Mendelian genetic patterns.

Graph data in a way that organizes the results.

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New York State Standards

High School Living Environment

Standard 1:

Key idea 1.4a

Key idea 2.3a, 2.3b

Key idea 3.1, 3.3, 3.4c

Standard 4:

Key idea: 1.2a, 1.2e, 1.2f

Key idea 2: 2.1a, 2.1c, 2.1d, 2.1e, 2.1f, 2.1g, 2.1j

Key Idea 4:

Key Idea 5: 5.2j

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Step 5:

Now with the gene symbols chosen, show a Punnett square that will test your hypothesis (show the predicted outcome of the parental cross that led to the gummy bears in your bag).

You have already obtained a ratio based on your data. How closely does the data approximate the ratio predicted by the Punnett square?

Is your hypothesis confirmed by the evidence? If not, repeat steps 6-8. You must show all work to receive full credit.

Step 6:

Plot your data on a frequency graph. Title the graph and label both axes. Be prepared to present your graph during a class discussion.

Step 7:

Prepare a bag with gummy bears for another team to analyze. Know the phenotypes and genotypes of the parents that crossed to obtain the ratios in your bag of the F1 generation.

Information for the Teacher

Activity Prep

Before completing this module it would be helpful to complete the punnett square module and review mendelian and non-mendelian genetics.

Gummy bears are an inexpensive and effective way for simulating cross breeding to investigate Mendelian and non-Mendelian inheritance. Prepare the bags of gummy bears according to the chart provided below. The students will then prepare one of their own bags for another set of peers to analyze.

Bag Number	Phenotype	Ratios	Genotypes	Mode of Inheritance	Parental Cross
1	25 red	100%	RR or Rr	Mendelian	RR x RR or RR x Rr
2	24 colorless	100%	Rr	Mendelian	rr x rr
3	37 red/12 colorless	3:1	RR/rr	Mendelian	Rr x Rr
4	26 yellow	100%	YY	Co-dominance	YY x YY
5	30 orange	100%	RY	Co-dominance	RR x YY
6	11 red/20 orange/9 yellow	1:2:1	RR/RY/YY	Co-dominance	RY x RY
7	20 green/10 colorless	2:1	Gr/rr	Lethal allele	Gr x Gr

Students need to share information about their f1 generations so that the genotypes of the parents can be determined. Have student place their results on a large chart or chalkboard to share with the rest of the class. The class should determine the phenotypes and use these consistently between the groups. This will keep things from becoming too confusing.

The chart above shows 7 sample genetic crosses. For classes with more students, crosses may be duplicated using slightly different numbers to represent the variation that occurs in actual experiments. To further illustrate Mendelian versus non-Mendelian inheritance, students use colored pencils to plot data on a frequency graph. Students evaluate each other's work and resolve inconsistencies through interaction and class discussion.