Gummy Bear Genetics

Brightly colored candy is an appealing tool for teaching genetics lessons

FOR YEARS WE SOUGHT A SIMPLE BUT meaningful way to teach the complex principles of genetics and were inspired by others who designed laboratory exercises based on candy or simulated organisms (Bonsangue and Pagni, 1996; Burns, 1996). Our goal was to design a lab that was quick to prepare, motivating, and interesting; we wanted to promote both content mastery and critical thinking through discovery. With these ideas in mind, we developed an investigative laboratory exercise using gummy bears.

THE BEAR FACTS

Because gummy bears are available in a variety of different colors, they are excellent for simulating cross breeding. We prepare for this laboratory by placing gummy

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bears in numbered paper bags, making sure to include predetermined numbers of different colored bears to represent Mendelian and non-Mendelian ratios. Examples of the numbers we use are shown in Figure 1. It is important to remember to vary the numbers of bears slightly from ideal ratios to be somewhat realistic. For example, we use 31:9 or 29:11 (instead of 30:10) to simulate a 3:1 ratio. As always, we remind students that they cannot eat or drink anything in the lab.

Students can work individually or in small groups depending on class size. Each student or group selects a numbered paper bag, and we tell them that the bears in each bag are the result of a different cross-breeding experiment (part of our captive-breeding program). Students begin by sorting bears based on phenotypes that can be easily observed and quantified. Each student or group then completes a worksheet (see ''Bear Breeding'' on page 26) listing their bears' cross numbers, the phenotypic characteristic they quantified, the alternate

BEAR BREEDING

Purposes:
1. To discover and study basic principles of genetics.
2. To propose and test hypotheses to explain Mendelian and non-Mendelian genetic patterns.
3. To graph data in a way that organizes the results.

Materials needed:
> One bag of gummy bears (per group)
> Graph paper
> Chi-squared table (optional)
> Colored pencils

Procedure:
1. Working with a lab partner, obtain a bag of gummy bears, and record the total number of bears here: _____.
    These bears represent the F_1 generation of a cross-breeding experiment.

2. Empty the contents of the bag onto the table and sort the gummy bears into groups based on phenotypic differences that can be easily observed and quantified.

3. What is the phenotypic characteristic you used to sort the bears? Why?

4. 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 forms	Number	Ratio

5. Write your data on the chalkboard. Compare your results with the results of the other teams in the class.

6. Which type of inheritance in exhibited by your sample of bears?

7. Select gene symbols to represent the alleles for the characteristic you studied.
    a. Based on the evidence, what are the probable genotypes for each phenotype you observed?

    b. What were the probable genotypes of the original parental cross?

    c. What were the phenotypes of these parent individuals?

8. Now with the gene symbols chosen, show a Punnett square that will test your hypothesis (i.e. show the predicted outcome of the parental cross that led to the gummy bears in your bag).
    a. You have already obtained a ratio based on your data. How closely do the data approximate the ratio predicted by your Punnett square?

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

9. Based on the evidence, determine the probable modes of inheritance for each bear phenotype observed in class. Select gene symbols to represent the alleles for each phenotype. Gene symbols chosen to represent the alleles for each phenotype must be consistent. Be able to identify each mode of inheritance.

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

FIGURE 1.

Sample student data for seven genetic crosses.

Cross number	Phenotypic frequency	Ratio	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

forms of the characteristic they observed, and the number and ratio of each alternative form.

After filling out their worksheets, students write their data on the chalkboard and the class selects symbols to represent the alleles for each phenotype. Students then work in groups again and use the available evidence to describe the probable genotype for each phenotype observed. Next, they describe the probable genotypes and phenotypes of the original parental cross that led to the various types of bears and use the gene symbols they selected to show a Punnett square that confirms their hypothesis. We encourage students to interact so that learning results from discovery and collaboration.

Once we have covered genotypes and phenotypes, the class determines the probable modes of inheritance for each bear phenotype. Each student completes a chart listing phenotypes, genotypes, modes of inheritance, and parental genotypes for each phenotype. Students must obtain clues from each other's results to solve some of the crosses, so the gene symbols chosen to represent the alleles for each phenotype must be consistent.

Student data for seven sample genetic crosses are listed in Figure 1. 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.

BEYOND THE BASICS

Detailed explanations of the concepts of Mendelian and non-Mendelian inheritance can be found in a variety of textbooks (Weaver and Hedrick, 1992). During this laboratory, it is especially important to point out to students that there are differences between ideal ratios and the real ratios obtained from an actual cross-breeding experiment. This exercise can be adapted to demonstrate the

chi-squared method of judging whether data is consistent with a given genetic hypothesis.

To assess student understanding, we discuss the experimental results using open-ended questions that allow application of key concepts. For example, if the data does not support a hypothesis, students must offer an explanation for the results. Next, students apply what they have learned to predict how coat color is inherited in common animals. Students also use a reference book or the Internet to learn about human characteristics and their inheritance.

Students generally enjoy exploring the basic principles of Mendelian and non-Mendelian inheritance in this colorful way. One student noted on a questionnaire following the lab that "mixing the colors to figure the offspring" made it "very easy to see and understand the process." This lab is not a replacement for actual crosses of organisms such as fungi, Drosophila, or Brassica (often performed in advanced genetics courses), but it does provide an effective alternative when the time and labor involved in crossing live organisms is prohibitive. ✧

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