



Name: _____

Date: _____

Student Exploration: Fast Plants[®] 2 – Mystery Parent

Note to teachers and students: The Fast Plants[®] Gizmo was created in collaboration with Wisconsin Fast Plants. The Fast Plants 2 – Mystery Parent lesson was designed as a follow-up to the Fast Plants 1 – Growth and Genetics lesson.

Vocabulary: chi-squared test, degrees of freedom, deviation, dihybrid Punnett square, rosette-dwarf

Prior Knowledge Questions (Do these BEFORE using the Gizmo.)

In the *Fast Plants 1* lesson you learned about two alleles for stem color. *ANL* is the dominant allele for purple stems, and *anl* is the recessive allele for non-purple (green) stems.

1. Two *ANL/anl* plants are crossed. What percentage of the offspring plants will have purple stems? _____

2. An *ANL/anl* plant is crossed with an *anl/anl* plant. What is the percentage of purple-stem offspring now? _____

		Parent A	
		<i>ANL</i>	<i>anl</i>
Parent B	<i>ANL</i>		
	<i>anl</i>		

		Parent A	
		<i>ANL</i>	<i>anl</i>
Parent B	<i>anl</i>		
	<i>anl</i>		

Gizmo Warm-up


It is intern Mark's first day at the Fast Plants laboratory, and he is eager to impress. He gathers pollen from a set of plants on one side of the room and carefully pollinates a set of plants on the other side. Then he goes out to lunch. When he returns, his supervisor Pam compliments Mark on the great job he did pollinating the flowers. "So, where did the pollen come from?" Mark scratches his head in confusion. He knows it came from somewhere over there, but which plants? He has no idea. "No problem," says Pam. "We can figure it out from the offspring."



In the *Fast Plants 2 – Mystery Parent* Gizmo, you will use genetics to determine the identity of the unknown parent plant. To begin, select the **Mystery parent** mode. Drag seed packet **P1**, the "mother" plants, to container 1 and **F1**, the offspring plants, to container 2. Click **Play** (▶), and then **Pause** (⏸) after 10 simulated days.

What are the traits of the P1 and F1 plants? _____



Activity A: Creating a hypothesis	<u>Get the Gizmo ready:</u> <ul style="list-style-type: none"> • On the Mystery parent mode, click Reset (↺). • Turn on Auto grow and Show hints. 	
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Introduction: In this lesson you will look at the stem color and leaf color of Fast Plants®. Recall that the stem color is controlled by two alleles: *ANL* (purple) and *anl* (green). The leaf color is controlled by the alleles *YGR* (green) and *ygr* (yellow-green, which we will refer to as “yellow”). The *ANL* and *YGR* alleles are dominant, while the *anl* and *ygr* alleles are recessive.

Question: What do the P1 and F1 phenotypes tell you about the P2 “father” plants?

1. **Grow:** Plant the **P1** seeds in container 1 and the **F1** seeds in container 2. The F1 seeds are the offspring of the P1 mother plants and the mysterious P2 “father” plants. Click **Play**, and wait for the simulation to pause on day 9.

A. View the plants with the **magnifying glass**. Then, turn on the **clipboard**. Observe the results, then turn on **Add class data** to see simulated data from 1,000 plants.

Are all the P1 plants the same? _____ Are all the F1 plants the same? _____

B. What is the stem and leaf color of the P1 plants? _____

C. What is the stem and leaf color of the F1 plants? _____

2. **Form a hypothesis:** Click the **Develop hypothesis** button. This opens up a window that will allow you to create a hypothesis about the P1, F1, and P2 plants.

A. Drag the correct **Phenotypes** into the **P1 phenotype** and **F1 phenotype** boxes.

B. Under **P1 possible genotypes**, drag labels from the **Possible genotypes** area into the spaces for stem and leaf genotypes, then do the same for the F1 genotypes. What are the possible genotypes for the P1 and F1 plants?

P1 possible genotypes: _____ or _____

F1 possible genotypes: _____ or _____

3. **Predict:** Based on the P1 and F1 phenotypes and possible genotypes, you can make predictions about the phenotype and genotype of the “father” P2 plants. Fill in the **P2 possible phenotypes** and **P2 possible genotypes** areas, then list them below.

P2 possible phenotypes: _____

P2 possible genotypes: _____

Explain: _____

(Activity A continued on next page)



Activity A (continued from previous page)

4. Analyze: Look over your possible genotypes.

A. How do you know which stem alleles the P1 plants have? _____

B. How do you know which stem alleles the F1 plants have? _____

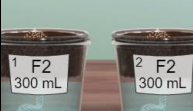
C. How do you know which stem alleles the P2 plants have? _____

D. What do you know about the leaf alleles for the P1, F1, and P2 plants? _____

5. Harvest: Click the **X** button to close the hypothesis window. Grab **container 1** and drag it over the waste hole to remove the P1 plants, they will not be needed for the remainder of this activity. Click **Play**, pollinate the F1 plants with the **bee stick**, and then click **Play** again. After 44 days, use the **tweezers** to harvest a seedpod and drop it into the **F2** bag.

What phenotype or phenotypes do you expect to see when you grow the F2 plants? Explain.



Activity B: Identifying the father	<u>Get the Gizmo ready:</u> <ul style="list-style-type: none"> Click Reset. Check that Auto-grow is still selected. 	
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Introduction: At this point, you have identified the phenotypes of the P1 (mother) and F1 (offspring) plants. To determine the genotypes of the P1, F1, and P2 (father) plants it is necessary to look at the “grandchildren” F2 plants, the offspring of F1.

Question: What is the genotype of the P1, F1, and P2 (father) plants?

1. Predict: Select **Develop hypothesis**. What are the two possible F1 genotypes? For each of these genotypes, predict what the F2 plants would look like, given that the F1 seeds are the offspring of the F1 plants. (Note: Assume all of the F1 plants have the same genotype.)

Possible genotype 1: _____ Offspring phenotypes: _____

Possible genotype 2: _____ Offspring phenotypes: _____

2. Observe: Plant the **F2** seeds in container 1 *and* container 2. Click **Play**, then wait for the simulation to pause after 9 days. Observe the resulting plants with the **Magnifying glass**.

What phenotypes do you see? _____

3. Collect data: Select the **clipboard** to see the results. Fill in the first row of the table. Then, turn on the **Add class data** checkbox to see simulated results of 1,000 plants. Use this data to fill in the second row of the table.

Data source	Purple stem, green leaf	Purple stem, yellow leaf	Green stem, green leaf	Green stem, yellow leaf	Total
Single trial					
Class data					

4. Infer: Click **Develop hypothesis**. Based on the phenotypes of the F2 plants, what do you think is the genotype of the F1 plants? Explain your reasoning.

(Activity B continued on next page)

Activity B (continued from previous page)

5. **Model:** The possible allele combinations for two traits is shown by a **dihybrid Punnett square**. Based on the inferred F1 genotype, fill in the Punnett square below.

Parent 1: _____

Parent 2:				

6. **Analyze:** Based on the Punnett square, count the number of boxes that represent each phenotype combination. Then, predict the percentages of each combination. Fill in the bottom row with the observed percentages based on the F2 results in the Gizmo. (Hint: You can divide each of the class results by 10 to find the percentages.)

Data source	Purple stem, green leaf	Purple stem, yellow leaf	Green stem, green leaf	Green stem, yellow leaf
Number of boxes				
Predicted F2 percentages				
Observed F2 percentages				

Are the actual results close to the predicted percentages? _____

If not, adjust your F1 genotype and repeat steps 5 and 6. Show your work on another page.

7. **Infer:** Now that you know the F1 genotype, you can determine the P1 and P2 genotypes. On the hypothesis window, make any necessary adjustments to the alleles, and then select the correct **P1 genotype**, **F1 genotype**, and **P2 genotype**. If needed, drag the correct phenotype into the **P2 phenotype** box. Click **Check**. If necessary, make adjustments.


What is the P1 phenotype and genotype? _____

What is the F1 phenotype and genotype? _____

What is the P2 phenotype and genotype? _____

Explain how you know the P2 genotype: _____



Activity C: Designing offspring	<u>Get the Gizmo ready:</u> <ul style="list-style-type: none"> • On the Mode menu, select Design offspring. • Check that Auto-grow is selected. 	
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Question: How can you breed Fast Plants® to have any combination of traits?

1. Observe: In the **Design offspring** mode, you will see two seed packets, **C** and **D**. Plant the **C** seeds in container 1 and the **D** seeds in container 2. Click **Play** and wait for day 9.

A. Move the magnifier over the C plants. What is the phenotype of these plants?

B. Observe the D plants with the magnifier. What is the phenotype of these plants?

C. Click **Play** and wait for day 15. How else do the D plants differ from the C plants?

The D plants exhibit a new trait, called **rosette-dwarf**. These plants are shorter than normal plants and have leaves that grow closer to the base of the stem than normal leaves.

2. Pollinate: Use the **bee stick** to pollinate only the C plants, then return the bee stick to the bottom area. Use a clean bee stick to pollinate only the D plants. Click **Fastplay** (▶▶).

When the seeds have matured, harvest a C plant seedpod and place it in a bag. Label this bag "C1." Then harvest a D plant seedpod and label the bag "D1."

What do you think the phenotypes of the C1 and D1 seeds will be? _____

3. Observe: Click **Reset**. Plant the C1 and D1 seeds in containers 1 and 2. Click **Play**. What are the phenotypes of the offspring plants?

C1 plants: _____

D1 plants: _____

4. Infer: Are the C and D seeds homozygous for each trait? _____ How do you know?

(Activity C continued on next page)

Activity C (continued from previous page)

5. Pollinate: Click **Play**. When the simulation pauses, move the **bee stick** over the D1 plants and then over the C1 plants. Click **Fastplay**, then harvest a seedpod. Label the bag "F1."

What do you think will be the phenotype of the F1 plants? _____

6. Test: Click **Reset**. Plant and grow the F1 seeds.

A. What is the phenotype of the F1 plants? _____

B. Which three traits are dominant? _____

C. Which traits are recessive? _____

D. The rosette-dwarf trait is controlled by two alleles: *ROS* for the normal phenotype, and *ros* for the rosette-dwarf phenotype. Given this, what are the genotypes of the C plants, the D plants, and the F1 plants?

C genotype: _____

D genotype: _____

F1 genotype: _____

7. Challenge: Turn on **Show challenge**. Now that you know the genotypes of the C and D plants, you can try creating custom combinations of traits in offspring plants. To solve each challenge, create a seed packet that contains seeds that meet the criteria of the challenge, and then click **Submit**.

Hint: If you have a variety of plants in a container, you can use the **tweezers** tool to remove unwanted plants and just keep the ones you want to use.

Each time you solve a challenge, take a screenshot of your successful seed packet with the "Congratulations" message. Paste these images into a document and hand it in with this worksheet.



Extension: The chi-squared test	<u>Get the Gizmo ready:</u>	Container	Purple stem, green leaf
	<ul style="list-style-type: none"> On the Mode menu, select Mystery parent. Click Start over. 	1,2	11

Introduction: In many experiments, it is not clear immediately if the evidence favors one theory or another. In these cases, statistical tests can be used to show how probable a given result will be. In this extension activity, you will learn about a test called the **chi-squared test**, or χ^2 test.

Question: How can you use a Chi-squared test to test a hypothesis?

- 1. Create a hypothesis:** Plant and grow the **P1** and **F1** seeds. Open the **Develop hypothesis** window and fill in all of the possible genotypes for P1, F1, and P2 as you did before. Suppose you started with the hypothesis that the P1 plants were *anl/anl, YGR/YGR* and the P2 plants were *ANL/ANL, ygr/ygr*.

If that were true, what would be the genotype of the F1 plants? _____

Parent 1: *ANL/anl, YGR/ygr*

- 2. Model:** As you did before, throw away the P1 plants and pollinate the F1 plants. Harvest the resulting seeds into the **F2** seed bag.

Suppose you had the hypothesis that the F1 plants were *ANL/anl, YGR/ygr*. Fill in the dihybrid Punnett square for this cross. If you want, color in the squares to show the corresponding stem and leaf colors.

Parent 2: *ANL/anl, YGR/ygr*

- 3. Predict:** Suppose you had a total of 16 offspring from this cross. How many of each phenotype would you expect? Fill in the table with the expected values. Then, predict the number of offspring of each phenotype if there were 1,000 offspring, and fill in the second row of the table. (Hint: Divide by 16 and multiply by 1,000.)

Number of offspring	Purple stem, green leaf	Purple stem, yellow leaf	Green stem, green leaf	Green stem, yellow leaf
16				
1,000				
Observed				

- 4. Grow:** Click **Reset**. Grow the F2 seeds in both containers. Open the **clipboard** and add the observed results of your trial to the table above. (Be sure **Add class data** is turned off.)

(Extension continued on next page)



Extension (continued from previous page)

5. **Calculate:** A chi-squared test poses the question: If a given hypothesis is true, how likely is it that the difference between the observed and expected results is due to chance? If the probability is very low then the hypothesis can be rejected. If the probability is high it doesn't mean the hypothesis is correct, just that it hasn't been proven to be incorrect.

To do a chi-squared test, first compare the observed results to the expected results. For each phenotype, list the observed value (*o*) and the expected value (*e*). Then, find the **deviation**, or $o - e$. Square the deviations, and then divide by the expected values. Fill in the table below for the "single trial" data.

Phenotype	Purple stem, green leaf	Purple stem, yellow leaf	Green stem, green leaf	Green stem, yellow leaf
Observed (o)				
Expected (e)				
Deviation (d) = o - e				
Deviation squared (d²)				
d²/e				

Sum all the d^2/e values to find the χ^2 value: _____

To find the **degrees of freedom**, subtract 1 from the number of possible phenotypes: _____

6. **Analyze:** The table below shows the χ^2 values, degrees of freedom, and the probability that the difference between the expected value and the observed value was just due to chance, rather than due to a flaw in the hypothesis. First, find the row of the table that corresponds to the degrees of freedom. Then, read across to find the χ^2 value closest to the one you calculated. Then, read up to estimate the probability of a chance occurrence.

Degrees of freedom	Probability that the deviation is due to chance								
	90%	80%	70%	50%	30%	20%	10%	5%	1%
1	0.016	0.064	0.148	0.455	1.074	1.642	2.706	3.841	6.635
2	0.211	0.446	0.713	1.386	2.408	3.219	4.605	5.991	9.210
3	0.584	1.005	1.424	2.366	3.665	4.642	6.251	7.815	11.341
4	1.064	1.649	2.195	3.357	4.878	5.989	7.779	9.488	13.277

What is the probability that the difference is due to chance? _____

Based on this test, should the hypothesis be rejected? _____

In general, the hypothesis is rejected if the probability that the deviation is due to chance is less than 5%. The chi-squared test cannot be used to accept a hypothesis, however.

7. **On your own:** Turn on **Add class data**. Using this data, repeat the chi-squared test, using the predictions you made in question 3. Describe your findings on an attached page.

