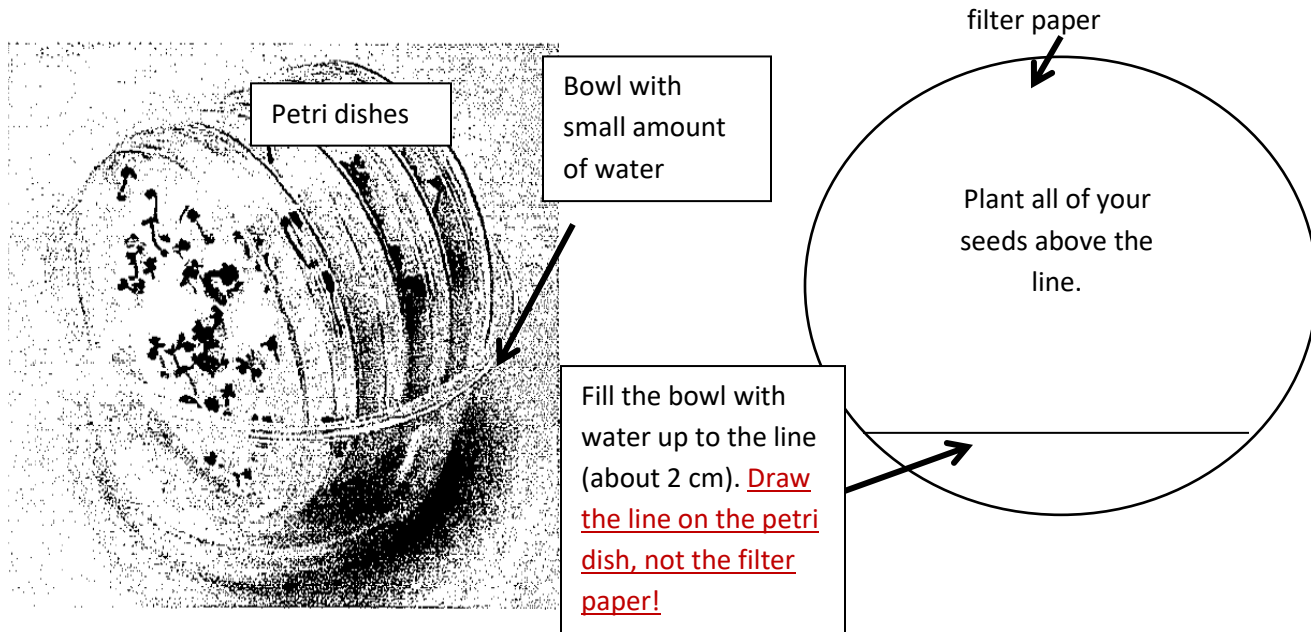


## Wisconsin Fast Plant Genetics®

**Scientific Question:** (Write this heading and the questions into your notebooks) Which trait is dominant and how is it inherited? What will the phenotypic ratios of the  $F_2$  generation be?

**Background:** The Wisconsin Fast Plants® we are working with are radishes. There are 2 alleles for stem color. The coloration is the result of a protein that is produced or not produced in the plant. Remember, it is the DNA that gives instructions for proteins to be made. So these phenotypes are a direct result of what is found on the chromosomes.

The seeds must be moist and warm in order to germinate. These are called “72 hour” plants because they grow very rapidly and the phenotypes can be seen in only a few days. It is not necessary to sow the seeds in soil. You can set up a growth plate in this way:



The seeds will stick to wet filter paper. Be sure your seeds are stuck before you turn your Petri dishes sideways! We will practice growing the Parent seeds before we grow our offspring.

**Procedure: Day 1** – you will be given about 12 seeds from one of the 2 parents to sow into petri dishes. You will then be given about 12 of the  $F_1$  and  $F_2$  generation seeds. Plant as shown above and give to the teacher to put under the grow light.

**Day 3** – View the  $P_1$  and  $F_1$  seedlings, write the numbers of each seedling’s stem color into a data table. Predict what color you think the other parent ( $P_2$ ) is, and think about how you will determine that based on the results you have seen so far.

**Hypothesis and prediction:** Below is one hypothesis regarding the inheritance of color in the radishes. This will be the “working hypothesis” guiding your experiments. (However, it will be the null hypothesis I will give you later that you will be using in your conclusion/discussion.) Fill in the blank for hypothesis 1 and fill in what you observed today in the experiment that makes this hypothesis correct. Then complete H<sub>2</sub>.

Hyp. 1 – \_\_\_\_\_ is the dominant color for radish plants.

How I know H<sub>1</sub> is correct:

Hypothesis 2 – If your hypothesis is correct and \_\_\_\_\_ is the dominant color and \_\_\_\_\_ is the recessive color, then a ratio of \_\_\_\_\_ will be seen in the F<sub>2</sub> generation seedlings.

**Also on Day 3** –view the missing parent (P<sub>2</sub>) and F<sub>2</sub> generation seedling stems. Count and record your data in your lab notebook. Enter the F<sub>2</sub> data only into the google spreadsheet emailed to you. Complete the Chi-Square data analysis described below.

### Data:

Construct a data table to describe the results of the Day 1 planting. Give it a descriptive title.

**Data Analysis:** An important question to answer in any genetic experiment is “how can we decide if our data fits any of the Mendelian ratios we have discussed”. A statistical test that can test our ratios is the Chi-Square or Goodness of Fit test.

This test allows you to determine whether your results could have happened by chance alone. Write the Bold-Faced sentences from the box below into your BILL..

In our experiment, the null hypothesis would be **“There is no statistical difference between the observed and expected counts.”** The observed ratio of \_\_\_\_\_ is not due to chance. In other words, any differences that exist between observed and expected are totally random and occurred by chance alone. We are not trying to prove that differences are due to Mendel’s Laws of Dominance and Segregation. We are merely ruling out that it is chance causing our results.

The general equation for the chi-square value is:

$$\chi_c^2 = \sum \frac{(O_i - E_i)^2}{E_i}$$

1. You will need two tables that look like this in your data analysis section. One will be your own group's data and the other will be for the entire data set including our class and the past 4 years. Don't forget to give each table a title.

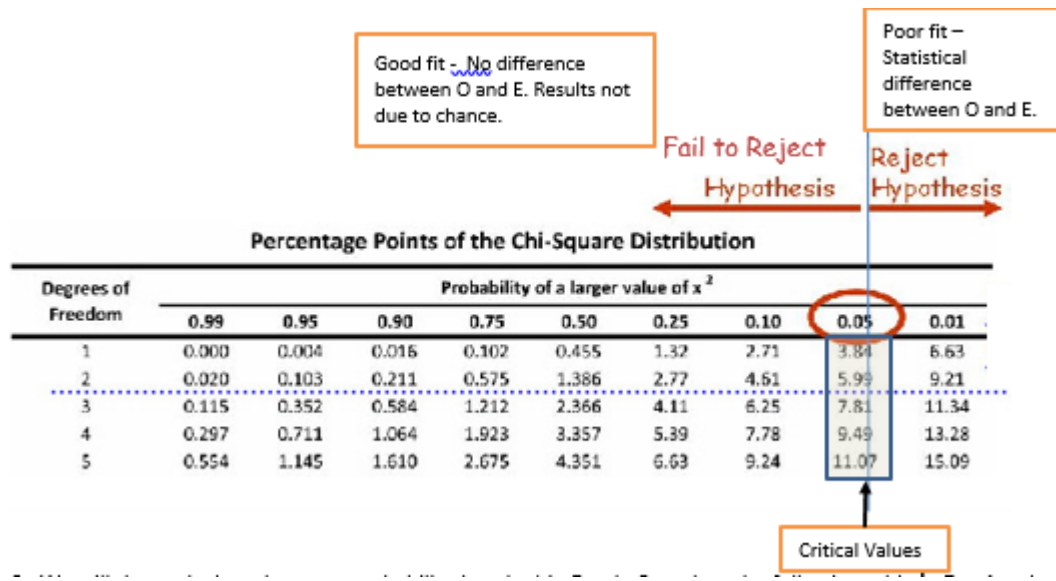
	Phenotypes		
	Purple	Green	Total
Observed (O)			
Expected (E)			
Difference (O-E)			
Difference Squared (O-E) <sup>2</sup>			
(O-E) <sup>2</sup> /E			
$\chi^2 = \sum (O-E)^2 / E$			

Using 1 degree of freedom, the p value from the chart below is: \_\_\_\_\_

2. Show everything in a completely labeled manner. You will complete all of the calculations first by hand and put into the data table.

The last ingredient needed for the test is the "degrees of freedom" (df), which is calculated at the number of different phenotypes minus one.


- A. Determine the total number of possible outcomes. In this case, it is 2: either purple stem or non-purple stem.
- B. Degrees of freedom = (number of possible outcomes) – 1. In our case: **degrees of freedom = (2-1) = 1**
- C. Use a chi-square distribution table to determine the probability that the deviation from the expected outcome (calculated using the chi-square formula) is due to chance. The table below is a portion of a  $\chi^2$  Distribution Table showing the probability that chance deviations led to the  $\chi^2_c$  value.



3. We will then calculate the exact probability (p value) in Excel. Complete the following table in Excel and enter your group's data:

	Purple	Green
Observed (O)		
Expected (E)		

Then follow these steps:

- Highlight any cell that is not part of your data table. Click on the function button - 
- Find the CHISQ.TEST option from the dropdown menu and click on OK.
- For "Actual Range" highlight the Observed values in your data table.
- For "Expected Range" highlight the Expected values from your data table. Then click OK. The decimal number shown will be your p value (NOT your Chi square value).

**In your notebook – write the “p value as calculated by Excel for my group is \_\_\_\_\_.”**

4. **Repeat** for the data that includes our class plus past years' data set.

**In your notebook – write the “p value as calculated by Excel for the entire data set from the past 4 years is \_\_\_\_\_.”**

Think about this:

**Determine if you should fail to reject or reject the null hypothesis for your lab group's data:**

- If the  $X^2$  value is **SMALLER** than the critical value (p value larger than 0.05), we **FAIL TO REJECT** the null hypothesis because our data are consistent with what we would expect – any slight difference is due to chance and our data are a good fit.
  - This would support Mendel's Laws of Dominance and Segregation.
- If the  $X^2$  value is **LARGER** than the critical value (p value smaller than 0.05), we **REJECT** the null hypothesis because our data are too different from what was expected to explain the differences by chance (our data are not a good fit) – there must be some other explanation.
  - This would not support Mendel's Laws of Dominance and Segregation.

**“If the p is low, reject the  $H_0$ .”      “ If the p is high, let the  $H_0$  fly”**

\*Why use 0.05/5%? 95% of our data should be due to Mendelian inheritance. Less than 5% should be poor data.

**Conclusion: (paragraph form)**

- When reporting chi square data use the following formula sentence....

With \_\_\_\_\_ degrees of freedom, my chi square value is \_\_\_\_\_, which gives me a p value of \_\_\_\_\_%, I therefore \_\_\_\_\_ (fail to reject/reject) my null hypothesis.

**(Report this for your group's data using the Excel p value. You will discuss class data p values in the following 2 questions.)**

- Contrast the two p values you obtained for the 2 data sets when you used Excel. How were they different?
- Explain the importance of the difference between the p values of the two data sets. Discuss sample size.
- Why would a scientist testing a new drug on people probably want to use a p value of 0.01 instead of 0.05?