

Arabidopsis Mutants

Goals

- To learn about a plant used in biological research
- To have hands-on experience with genetics
- To relate offspring ratios, genetics, and molecular biology

Overview

A major goal of biologists is to discover the function of specific genes. Whether looking at a gene found in fruit flies, plants or humans it is important to understand how it works. One way that the function of a gene can be investigated is to study a mutant form of that gene. Mutants are extremely valuable tools for understanding the underlying metabolic pathways or molecular mechanisms of physiological processes. Indeed, much of what we know today about the biology of organisms has been obtained from characterizing mutants. By studying new characteristics caused by a gene mutation scientist can sometimes learn about the function of the gene.

In this lab you will be working with *Arabidopsis thaliana*, a plant that is related to radish and cabbage. *Arabidopsis* is an ideal model organism for this purpose due to its small size, short life cycle, and small genome. Hundreds of mutants of this plant have already been described.

You will do this project in two lab sessions. In the first, you will plant seeds. In the second, two to three weeks later, you will look at the plants that have grown. You will then observe the phenotypes present, count the numbers of each phenotype, and determine which phenotype is dominant, recessive, or incompletely dominant. You will then correlate this with the nature of the mutation.

Today, the *Arabidopsis* plants you will be working with have already been seeded and sown on a salt and sucrose agar. You will observe the phenotypes of the plants present, count the numbers of each phenotype, and determine which phenotype is dominant, recessive, or incompletely dominant. You will then correlate this with the nature of the mutation.

The history of these particular plants...

- There are two alleles associated with these *Arabidopsis* plants.
 - M = mutant allele
 - N = normal (wild type) allele
- The following crosses were performed to produce the plants seen on the agar plates in lab.

Cross 1	Parents:	MM x NN
		↓
	F₁:	100% MN
Cross 2	F₁:	MN x MN
		↓
	F₁:	25% MM
		50% MN
		25% NN

Predict the phenotype ratios resulting from Cross 2 if:

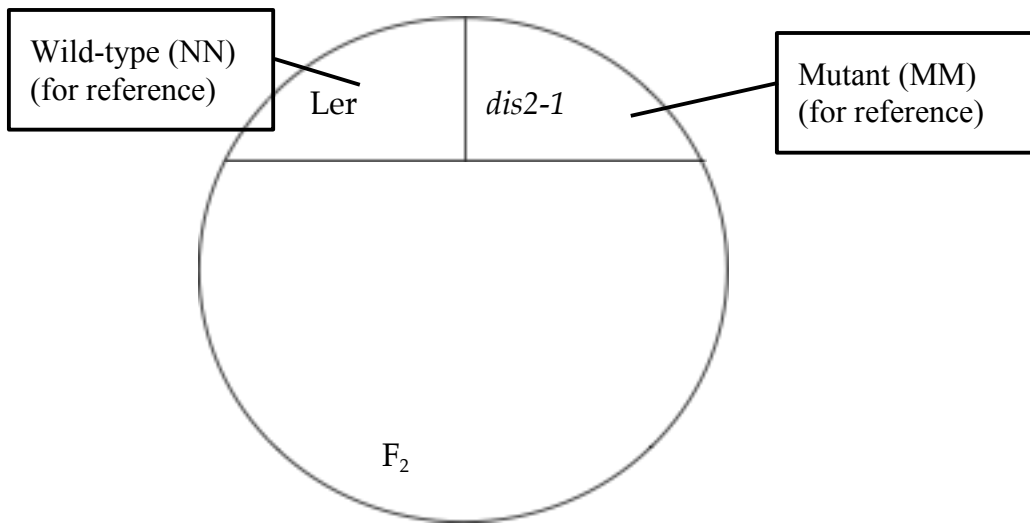
- M is dominant:

- N is dominant:

- Incomplete dominance between M and N:

Procedure

1) Your TA will give each group a pair of plates for your mutant. Write down the name of the mutant in your lab notebook. Your plate will look something like this:



2) Compare the phenotypes of MM (mutant) and NN (wild type – Col or Ler). Describe what the mutant phenotype looks like in your lab notebook.

3) Count all of the F₂ plants shown on your plate. Determine the number of those with wild type, mutant, or intermediate phenotypes (if present). Record your data in a table.

4) Use the data recorded in Step 3 to determine if the mutant is dominant, recessive, or incompletely dominant.

Lab Report (20 points)

1. Name the mutation and describe the mutant phenotype compared to the wild type phenotype.
2. Data table of counts of wild type, mutant, and intermediate (if present) phenotypes.
3. Conclusion
 - a. Give a genetic argument for what you would expect to see if mutant was dominant, recessive, or incompletely dominant. *Example: "There are F₂ offspring from crossing a mutant with a wild type plant. Therefore, we would expect to see X if the mutant is dominant, Y if the mutant is recessive, and Z if the mutant is incompletely dominant."*
 - b. Explain your argument based on your data seen in lab. *Example: "Since we saw 27 mutants out of 90 total F₂ plants, which is close to 25%, we can conclude that the mutant phenotype is recessive."*

