

Genetics Introduction

We will work through the following problems while waiting for different parts of the GFP lab to complete.

We will start with some pencil-and-paper problems to introduce a systematic way to approach genetics problems and then use jsVGL (Virtual Genetics Lab) as another way to explore these issues.

First: Notebook Review

To be sure that you have all the information you need for this lab, with your lab partners, go over the notes you took while doing the SPOC and from lecture and be sure you have the information listed below. You should fill in any gaps in your notes so everyone in your group has all they need. You can check these items off as you go.

- How do you define allele symbols so they show dominant and recessive clearly?
- What is the difference between an allele with a dominant phenotype and one with a recessive phenotype?
- How can you tell from the results of a cross if a trait is dominant or recessive? (Hint: “recessive can hide in dominant”)

You will then discuss these with your TA as a class to clarify any issues that remain.

(1) For each of the following sets of data, give a genetic model that explains all the data. A genetic model contains the following:

- the number of genes and alleles involved, e.g., “tooth shape is controlled by one gene with two alleles.”
- a statement of which phenotype is dominant and which is recessive.
- symbols denoting each allele such that uppercase letters are associated with the dominant phenotype and lowercase letters are associated with the recessive phenotype.
- the genotypes of all the individuals involved.

a) Cross 1: Red-eyed mouse X white-eyed mouse

gives F₁: all red-eyed

Cross 2: Red-eyed F₁ X red-eyed F₁

gives F₂: 36 red-eyed
13 white-eyed

allele contribution to phenotype

b) Cross 1: Long-eared mouse X short-eared mouse

gives F₁: 12 long-eared
 10 short-eared

Cross 2: Long-eared F₁ X long-eared F₁

gives F₂: 34 long-eared
 14 short-eared

allele contribution to phenotype

(2) The Virtual Genetics Lab (jsVGL)

The goal of jsVGL is to use your knowledge of genetics to design and interpret crosses to figure out which allele of a gene has a dominant phenotype and which has a recessive phenotype. In later problems, we will expand this to include more complex models.

jsVGL is a computer simulation of the genetics of an imaginary insect. The computer randomly picks a character with two traits. It then randomly chooses which form of the character will be dominant and which will be recessive. That way, each time you start the program, you get a different problem (also, every group will get a different problem). Finally, it creates a population of insects with random genotypes called the Field Population.

As in a real genetics lab, the insects are kept in cages; Cage 1 contains the Field Population. You can select any two insects (one must be male and the other female) and cross them; the computer automatically puts their offspring in a new cage. You can cross any male and female from any cage as you work to determine how the traits involved are inherited.

As a warm-up, we'll all start working on the same problem with the same traits, inherited in the same way. Later on, as you sharpen your skills, we'll work on individual problems.

jsVGL works best on Chrome; it does not work well on Safari or Firefox (on those browsers, you cannot load a saved work file).

Go to the OLLM and click on the “jsVGL exercises for lab” link for this lab. You should see something like this:

jsVGL Problems for Lab

The screenshot shows the jsVGL interface with several callout boxes:

- File Menu** – lets you save and load your work (points to the File button).
- Sample Problems** – click these to load a known problem (points to the Sample problems for lab section).
- Click here to get a new random problem where you **can** see the correct answer. (points to the New Practice Problem button).
- Click here to get a new random problem where you **cannot** see the correct answer. (points to the New Graded Problem button).
- Click here to see some instructions for using jsVGL. (points to the Instructions tab).
- Click here to enter the genetic model you have found (in Graded mode) or see the correct answer (in Practice Mode). (points to the Genetic Model tab).

To start, click the “Blue & Yellow Wings” button and scroll down until you see something like this:

The screenshot shows the "Cages with Organisms for crossing" interface. The "Field Population" cage contains the following data:

Wing	Organisms	Counts
Blue	♂♂♂♂♂♂♀♀	06 ♂ 02 ♀
Yellow	♂♂♂♂♂♂♂♂♂♂♂♀	11 ♂ 11 ♀

The cage shown is called the “Field Population” and it simulates a random collection of organisms you collected in the wild. At this point, you don’t know which trait is dominant and which is recessive. Your task is to design, carry out, and interpret the results of a series of crosses to determine which is dominant and which is recessive.

Begin your experiments. Select a male and a female fly to be the parents: click on one parent then click on the other parent. One parent must be male and the other female but they may come from different cages. Note that you can cross a given fly more than once.

To cross (also known as “mate”) the selected flies, click the "Cross Two" button just above the collection of cages. A cage will appear below the last cage made with the resulting offspring. A typical result is shown below. Take a little time to look at it carefully; it contains a lot of useful information:

The screenshot shows a window titled "Cage 2" with a "Minimize" button. Below the title bar, there are two sections: "Parents" and "Offspring".

The "Parents" section shows a male fly (♂) labeled "(Cage 1) Blue-Wing" crossed with a female fly (♀) labeled "(Cage 1) Yellow-Wing".

The "Offspring" section contains a table with three columns: "Wing", "Organisms", and "Counts".

Wing	Organisms	Counts
Blue	♂♂♂♂♂♂♂♂♀	07 ♂
	♀♀♀	04 ♀
Yellow	♂♂♂♂♂♂♂♂♀	07 ♂
	♀♀♀♀♀♀♀♀	08 ♀

Four callout boxes provide additional information:

- "This is the unique serial number for each cage." (points to "Cage 2")
- "This gives information about the parents." (points to the "Parents" section)
- "These show the total number of each phenotype present among the offspring." (points to the "Counts" column)
- "These are the offspring. You can select any of these for further crosses." (points to the "Organisms" column)

Working with your classmates and your TA, conduct a series of crosses to develop a genetic model that explains the cross results you have observed.

allele contribution to phenotype

If you would like further practice, the problem “5 & 6 Legs” also involves a non-sex-linked trait where one form is dominant and the other recessive.

Finally, if you click the OLLM link to “Extra Practice with Simple Dominance”, you can practice with randomly-generated problems like these.

