

Virtual Genetics Lab (VGL)

Experimental Objective

I. 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. This simulates a real lab in that there is no way to see if you've got the answer right. You will have to convince yourselves when you've done enough experiments to be sure.

II. To use your knowledge of genetics to design and interpret crosses to figure out the inheritance of very complex characters (these can include: sex-linkage, and incomplete dominance). This should bring together all parts of the genetics portion of the course.

Description

VGL is a computer simulation of genetics. 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.

Please note

VGL was developed recently by a group of Computer Science graduate students at UMB. It is a new program and, although it was extensively tested, it may contain bugs. In addition, it may run slowly and be a little 'touchy'. Therefore, please be patient and let the computer work for you. If you are impatient and click rapidly all over the screen when nothing seems to be happening, the program will likely crash. So please treat it gently and report all bugs to your TA or Brian White so they can be fixed.

The Genetic Models found in VGL

All the problems in VGL involve genetic models with one gene that has two alleles. Based on this, there are several features that can vary:

The interaction between the alleles; this can be either:

Simple Dominance: (Models 1, 3, & 5 below) The heterozygote has the same phenotype as the dominant homozygote. That is, with two alleles A and a:

- AA = tall
- Aa = tall
- aa = short

Incomplete Dominance: (Models 2, 4, & 6 below) The heterozygote has a different phenotype than either homozygote. In nature, this is usually intermediate; in VGL it need not be.

- AA = tall
- Aa = medium
- aa = short

VGL can also model more complex patterns of inheritance, such as sex linked, but today we will only attack problems involving simple dominance or incomplete dominance. The relevant genetic models are:

Model 1: Simple Dominance; Autosomal. For example:

<u>Genotype</u>	<u>Phenotype</u>
Green; Green	Green Body
Green; Red	Green Body
Red; Red	Red Body

Model 2: Incomplete Dominance; Autosomal. For example:

<u>Genotype</u>	<u>Phenotype</u>
Green; Green	Green Body
Green; Red	Purple Body
Red; Red	Red Body

The task:

To solve two different problems generated by VGL. A solution is a genetic model that accounts for all your data. Models will involve only one gene but may include incomplete dominance and/or sex-linkage (either XX/XY or ZZ/ZW).

Starting up VGL:

- 1) You will work in groups of three people per computer. You may want to take turns using the computer. It is easy to fill the screen with cages of creatures and get totally confused so you should work slowly and deliberately and keep careful notes about the experiments you do and the contents of each cage. If you get very confused, you can quit the program and start fresh with a new problem.
- 2) The program runs on two kinds of computers in the lab: the iMacs (one-piece blue computers in W-2-030) and the PCs (two-piece tan computers around the sides of W-2-031); it does not run on the Macs on the center tables in W-2-031.

You can also download the program and run it from your home computer; go to <http://v-g-l.sourceforge.net/index.html>.

- 3) To run the VGL program: follow the directions on the welcome page that appears on the screen; you either single-click (on the PCs) or double-click (on the iMacs) the VGL icon.
- 4) If you want to read the manual, click on the VGL Help bookmark at the top of the Welcome page. Note that the manual describes some features present in the version of VGL that you will not be using until later on in Bio 111.



- 5) Click on "New Problem" to begin. Each time you start a new problem, the computer will choose a new set of traits and characters as well as the underlying genetic model. Note that a character with the same name may have different properties in a different problem.

Once you click "New Problem", a window will appear for you to select the problem you will work on. Double-click on the "Problems" folder and select "Level 1".

- 6) You will then see a window that asks if you want to show the model and genotypes or not. Select the "Show model and genotypes" option and click "OK".
- 7) A cage will appear holding the "Field Population". It will look something like this:

Individual Animals	Number	Bodycolor	Phenotype
♂♂♂♂♂ ♀♀♀♀♀	5 ♂	green	
	5 ♀	green	
♂♂♂♂♂♂♂♂♂ ♀♀	9 ♂	blue	
	2 ♀	blue	

In your case, the phenotypes involved will likely be different. Your task is to figure out which is dominant and which is recessive. You will determine this by designing crosses and analyzing the resulting offspring.

8) 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" button at the top of the VGL window. A cage will appear with the resulting offspring. A typical result is shown here:

Individual Animals	Number	Bodycolor	Phenotype
♂♂♂♂♂♂♂♂♂♂ ♀♀♀♀♀♀♀♀♀	10 ♂ 7 ♀	green	
♂♂ ♀	2 ♂ 1 ♀	blue	

Parent ♂ (2) green ♀ (2) green

The information in this vial could also be presented in words:

“A male with a green body from Cage 2 (this is a translation of: “♂ (2) green”) was crossed with a female with a green body from Cage 2 (this is a translation of: “♀ (2) green”) This cross resulted in 20 (= 10+ 7 + 2 + 1) offspring:

- 10 males with green wings
- 7 females with green wings
- 2 males with blue wings
- 1 female with blue wings”

9) Continue crossing as needed; the objective is to make a genetic model to explain the inheritance of the traits you are studying. You decide whether you’re convinced or not; if not, keep crossing until you are. A complete model would look like:

“The color of the body is controlled by one gene with two alleles:

<u>allele</u>	<u>contribution to phenotype</u>
G	green body (dominant)
g	blue body (recessive)

10) Once you and your partner are convinced of your model, you can check to see if you are right. Click on Cage 1 to bring it to the front of the screen. Click on the button marked “Show Model and Genotypes”. The window will expand to show the genetic model underlying the trait you are studying.

11) When you are done with this problem, click the “Close Work” button at the top of the VGL window. When it asks if you want to save your work, click “Don’t save”.



12) Click the “New Problem” button and choose “**Level 2**”. You should solve this problem with your partner as you did before. However, this time you will not be able to see the correct answer; you must decide for yourselves when you have it right. At this point, you will then present it to another pair of lab partners, called the **reviewers**. The reviewers will then perform a cross with your creatures to test your model. The final step is to have your TA check off that the reviewers’ cross results agree with the prediction.

13) Choose a second Level 2 problem to solve which will be the focus of your lab report. For practice, you can choose other odd numbered levels, which will allow you to see the underlying genetic model and the genotype of each fly (to see the genotypes, just leave the cursor over a creature’s symbol and a window will pop up that shows its genotype).

14) Finish by cleaning up the computer screen. Quit VGL by clicking the box in the upper right corner of the window; you do not need to save your work. Please leave the welcome page up on the browser window.

Virtual Genetics Lab Report

This report will not be a traditional “Introduction, Materials and Methods, Results and Discussion” style report (like the Planarians and Fermentation reports). You will report the results of your investigations into the inheritance of a particular character using the VGL simulation software. Although you have performed these experiments as a group, each member of the group must turn in an individual lab report. For your selected character you must:

- 1) Provide your model of the inheritance of a particular character.
- 2) Give the results of one cross which are consistent with your model (phenotypes).
- 3) Show the genotypes of all the individuals involved.

- 4) Provide a Punnett Square and a brief explanation showing that these are the expected results.
- 5) Provide a Punnett Square and explanation showing that **the alternative model is inconsistent with the data**. When a given parent could have more than one genotype, you must list all the possibilities and show that they do not match the data.

See the following example for clarification of what your report should contain:

- 1) Your model of the inheritance of a particular character. For example:

The shape of the thorax is controlled by one gene with two alleles:

T - tetraltera (dominant)

t - grooveless (recessive)

- 2) The results of one cross which are consistent with your model. For example:

Cross 27: Male Tetraltera X Female Grooveless gave these offspring:

41 Tetraltera

- 3) The genotypes of all the individuals involved. For example:

Parents: Male Tetraltera (TT) X female grooveless (tt) gave offspring:

41 tetraltera (Tt)

- 4) A Punnett Square and a brief explanation showing that these are the expected results. For example:

	T	T
t	Tt	Tt
t	Tt	Tt

All the offspring should be Tt - tetraltera as was observed.

- 5) A Punnett Square and explanation showing that **the alternative model is inconsistent with the data**. When a given parent could have more than one genotype, you must list all the possibilities and show that they do not match the data. For example:

The only alternative model is:

G - grooveless (dominant)

g - tetraltera (recessive)

If this were so, then the male tetraltera would have to be gg. The female grooveless could be GG or Gg. This leads to 2 possible cases:

Case 1: tetraltera male (gg) X grooveless female (GG)

	G	G
g	Gg	Gg
g	Gg	Gg

All the offspring should be Gg - grooveless. No grooveless offspring were observed, so this is not consistent with the data.

Case 2: tetraltera male (gg) X grooveless female (Gg)

	G	g
g	Gg	gg
g	Gg	gg

Half the offspring should be Gg - grooveless. No grooveless offspring were observed, so this is not consistent with the data.

