Virtual Genetics Lab (VGL) I

Objective

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.

Description

VGL 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.

Warm-up

As a warm-up to this lab, you will work through Problem 1.1.2 from the Genetics chapter of *A Problems Approach to Introductory Biology (APAIB).*

The task:

To solve two different problems generated by VGL. A solution is a genetic model that accounts for all your data. This will be your first introduction to hypothesis testing. Here, the hypotheses are your genetic models, the experiments are the crosses you do, the results are the offspring the crosses generate, and the conclusions are the model you finally choose as the correct one.

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 <u>keep careful notes about the experiments you do and the contents of each cage</u>. If you get very confused, you can quit the program and start fresh with a new problem.

2) The program runs all of the computers in the lab. You can run the program on your home computer (Mac or PC); it can be found on the CD-ROM that came with the APAIB textbook.

3) To run the VGL program: double-click the VGL icon in the dock at the bottom of the screen. The icon looks like a little fly.

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:

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 on the next page:

Cage 3   ✕

Individual Animals	Number	Bodycolor	Phenotype
♂♂♂♂♂♂♂♂♂♂♀♀♀♀♀♀♀ *These are the offspring of the parents selected in Cage 2.*	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 body
7 females with green body
2 males with blue body
1 female with blue body"

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 "Level2". 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 **<u>reviewers</u>**. 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) You will need to solve one more problem for your lab report. This must also be a Level2 problem. For this problem, you should take careful notes about which flies were

crossed and what the results were. You will need these results for your lab report (see later). You should read over the instructions for the lab report BEFORE starting this problem. You will need to choose a cross that 'proves your model'; that is, one that gives results that are consistent with one model and inconsistent with the alternative (where the other character is dominant).

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.

Lab report:
• Must be typed; handwritten reports will <u>not</u> be accepted.
• Due next week at the start of the lab session you are currently in. This is a <u>firm</u> deadline.
• Although you will perform these experiments as a group, each member of the group must turn   in an <u>individual</u> lab report.
Your lab report <u>must</u> include:

1) Your model of the inheritance of a particular trait. You must include tables of gene/allele/dominant/recessive like those shown below. Note that, in these problems, there are only two alternatives:
    For example, suppose that the shape of the thorax is controlled by one gene with two alleles:
        there are two possible models; only one can be correct:

        <u>Model 1:</u> "Tetraltera is dominant"
                <u>allele</u>   <u>contribution to phenotype</u>
                  T   tetraltera (dominant)
                  t   grooveless (recessive)

        <u>Model 2:</u> "Grooveless is dominant"
                <u>allele</u>   <u>contribution to phenotype</u>
                  G   grooveless (dominant)
                  g   tetraltera (recessive)

        In your report, you should give **both models** and **indicate clearly** which you think is correct. If you thought that model 1 was correct, you'd say something like, "I feel that model 1 is correct".

2) The results of one cross that 'prove your model'; that is, results that are consistent with model 1 and inconsistent with model 2. 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. **You must use the SAME cross as you used in part (2)**. 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.