Virtual Genetics Lab (VGL) II

Exercise 2[1]

Objective

To use your knowledge of genetics to design and interpret crosses to figure out

1) which allele of a gene has a dominant phenotype and which has a recessive phenotype;

2) whether a gene exhibits simple dominance or incomplete dominance;

3) whether a gene is autosomal or sex-linked.

You will first be given the opportunity to practice crosses involving each of these modes of inheritance. Then, you will conduct a cross that exhibits simple dominance, but there will be no way to see if you've got the answer right. This simulates a real lab in which you will have to convince yourselves when you've done enough experiments to be sure.

Description

VGL II 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.

The task:

You will need to solve a genetics problem slightly more complex than those in the last lab period and write a lab report. 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

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BEFORE starting this problem. You will need to choose a cross that 'supports 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).

Starting up VGLII:

1) You will work in groups of two 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 Internet at http://intro.bio.umb.edu/VGL/index.htm. Click the "DOWNLOAD" link on the left hand side of the page.

3) To run the VGLII program: double-click the VGLII icon.

4) If you want to read the manual, click on the "Help" bookmark at the top of the Welcome page. Note that the manual describes some features present in VGLII that you will not be using for this week's lab exercise.

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 "OneGene" folder and select "OneGene05.pr2".

6) A cage will appear holding the "Field Population". It will look something like this, with minor changes in the updated version of the software:

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.

7) 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 VGLII window. A cage will appear with the resulting offspring. A typical result is shown below:

Cage 3 ✕

Individual Animals	Number	Bodycolor Phenotype
♂♂♂♂♂♂♂♂♂♂♀♀♀♀♀♀♀ *These are the offspring of the*	10♂ 7♀	green
♂♂♀ *parents selected in Cage 2.*	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: "♂ (Cage 2) Green")

was crossed with

a female with a green body from Cage 2 (this is a translation of: "♀ (Cage 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"

8) 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 convinced. An example of a complete model is shown below:

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

allele	contribution to phenotype
G	green body (dominant)
g	blue body (recessive)

Lab report:

It is very important that you follow **all** of the directions for preparing your lab report in order to receive full credit. Feel free to contact your instructor in advance of the due date if you have any questions.

Overall notes

- Your lab report is due at the end of the week in the ANGEL dropbox. It will not be accepted late.

- Although you and your group members worked on the same problem, your lab report must be in your own words.

- Your lab report must be typed; handwritten lab reports will not be accepted.

Special note for this lab

- The lab report **must be in the format described below** including titles for each section (Abstract, etc.). Lab reports that are not in this format will receive an automatic deduction of 5 points.

Parts of the Lab Report

An important thing to keep in mind is that a scientific paper is not the story of what you did. It is a logical argument in a prescribed format designed to convince your reader that your conclusions are correct. The most crucial issue is making a clear and logical argument that is supported by data. This means that, in most cases, you will not present your data in the order that you got it; you should present it in a way that makes the clearest case for your interpretation.

These are the remaining parts of the lab report. *Descriptions in italics indicate their role in the argument you are developing.*

- (2 points) **Abstract** A 1-3 sentence description of the genetic model that explains the inheritance of your trait. *This introduces your reader to the model you are going to be arguing for.*

- (2 points) **Introduction** A short paragraph that explains the research question being addressed (the inheritance of your trait) and why the methodology being used (crossing individual organisms and looking at the offspring) is believed to be able to answer that question. *This introduces the background behind your studies and why they are worth reading about.*

- (2 points) **Materials and Methods** A short paragraph that explains what you did. **Do not** give the details of **all** the crosses you did. All you need here is a few sentence summary of: how many crosses you did; roughly how many of those were necessary to figure out the model; and any strategies you used in choosing what to cross (just describe these in general **do not** talk about each and every cross in detail). *This tells the reader the details of the techniques you used.*

- (8 points) **Results and Discussion** *This is the most important part of the paper. It is where you make the argument for your interpretation of the data.* Start by introducing the genetic model you have found and defining appropriate symbols (2 points). Then go point-by-point to show the evidence for your model. This is not a narrative or a history, it is a logical argument supported by data. Do not present all your crosses in the order you did them; present them in the order that makes the clearest argument for the model you described in the Abstract.

It is probably best to break this down into parts. For each part of your model, give the evidence for that part. For example, if you want to argue that red eyes are sex-linked dominant, you would have separate arguments to show that it is (1) sex-linked and (2) dominant.

In addition to the 2 points for defining the symbols, we will grade this part using the following rubric:

- *All parts of model are supported* (0 - 3 points). All parts of the model you presented are specifically supported by one or more pieces of data. Less than full credit will be given for answers that do not support all parts of your model. That is, if you say it is "sex-linked simple dominance", you have to show data that it is sex-linked and simple dominant.

- *Data rule out all possible alternative models* (0 - 2 points). You present data that specifically exclude all relevant alternative models. Less than full credit if other interpretations are possible. That is, if you choose the above model, you would have to show that it cannot be autosomal, incomplete dominance, etc.

- *Only relevant data are presented* (0 - 2 points). All pieces of data presented are part of an explicit argument that supports the selected model or rules out other models. Less than full credit for data presented that are not part of your argument.