

AP Biology Virtual Genetics Lab (VGL)II:
Identifying Different Modes of Inheritance Through Breeding of Insects with Two Genes
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Objective

To use your knowledge of genetics to design and interpret crosses and 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. You will submit your answer digitally through the program as well as create a CER poster; this will help you to understand hypothesis testing and the process of presenting scientific data. You will have a lab period and an additional class period to work on collecting the data for the lab (126 total class minutes). We will assess if more time is needed the following day.

Description

VGLII is a computer simulation of genetics. The computer randomly picks one or more characters with one or more traits. It then randomly chooses how each trait is inherited. 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 creatures with random genotypes called the Field Population (your parent generation). As in a real lab, the creatures are kept in cages; Cage 1 contains the Field Population. You can select any two creatures (one must be male and the other female) and cross them; the computer automatically puts their progeny (next generation) in a new cage. Make sure you take **VERY** detailed notes of which organisms (ex: F₁ green male, F₂ brown female) you are crossing, this will help keep your data organized. You can also take screen shots of your data charts!

The Task:

To solve one different problems generated by VGLII. A solution is a genetic model that accounts for all your data. There are many possible genetic models. Based on this, there are several features that can vary:

- The number of alleles; this can be either:
 - Two alleles. Given this, there are two possible **interactions between the alleles**:
 - Simple Dominance: The heterozygote has the same phenotype as the dominant homozygote. That is, with two alleles A and a:
 - Incomplete Dominance: The heterozygote has a different phenotype than either homozygote. In nature, this is usually intermediate; in VGL it need not be.
 - Three Alleles. Given this, there are two possible **interactions between alleles**:
 - Hierarchical Dominance: A is dominant to all; A' is dominant to A'' and recessive to A; A'' is recessive to all (A > A' > A'').
 - Circular Dominance: B is dominant to B'; B' is dominant to B''; B'' is dominant to B.
- Whether the trait is sex-linked or not; this can be either:
 - Autosomal- the gene for the character is carried on an autosome so it is inherited identically in both sexes.
 - Sex-linked- the gene for the trait is located on a sex-chromosome so it is inherited differently in different sexes. **This can be either**:
 - XX/XY Females are XX; males are XY. Here, Y carries no genes except those needed to make the organism male.
 - ZZ/ZW Females are ZW; males are ZZ. Here, W carries no genes except those needed to make the organism female.

Your instructor will tell you which level problem you should work for this lab. Your problem is TWO GENES, PROBLEM 01.

Your task is to find the genetic mode of inheritance that best fits your data. You should know that, since VGLII selects traits randomly, the particular traits do not necessarily indicate the dominance relationships. That is, although you might expect otherwise, having no antennae may be dominant to having antennae. Similarly, having 4 legs may not be the heterozygote of 2-legs and 6-legs.

Procedure:

Go to the following website: <http://vgl.umb.edu/> click on the right hand side in red where it says DOWNLOADS and Lab Manuals. Scroll down to where it says Download Links. Click on the link for [VGLII](#) for Mac OS X. Click on the first link "[Grading" VGLII for Mac OS](#)". This will automatically download the program to your computer.

1. You will work pairs and use one 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**. You can click on UTILITIES and show/hide cages if you need to clear some view space, your cages are still there, you can bring them back at any time.
2. To run the VGLII program, click on the VGLII icon.
3. You will be assigned a problem at the level that your instructor has specified.
4. The objective is to make a genetic model to explain the inheritance of the traits you are studying. There is no way to find the "right answer"; you decide whether you're convinced or not. A complete model would look like:

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

T - tetraltera (dominant)

t - grooveless (recessive)

or:

In this creature, XX are female; XY are male. The color of the eyes is controlled by one gene, located on the X-chromosome with 2 alleles:

X^B - black (dominant)

X^b - blue (recessive)

Y - no contribution to phenotype

5. Once you and your partners are convinced of your model, you will then present it to another group for **peer review**. Your friends will then perform a cross with your information and with your creatures from your problem set to test your model and verify it.
6. I **strongly** advise you to work through this problem in class rather than at home. In class I can help you to make sure that you have worked it through completely. You can run VGLII at home however there is no guarantee that this will work and excuses will not be accepted.
7. You should also take careful notes of your results or print your data if you have a printer available (Choose "Print Work" from the "File" menu).

Two ways you will be graded:

1. Submitting your work in VGLII (10 points)
2. CER Poster (40 points)

Submitting your work to VGLII (10 points):



When using VGLII, you will enter the details of your genetic model as you determine them by using the Model Builder which is shown on the left. The Model Builder is customized to show only the options available in a particular Problem file; thus, for simpler problems, fewer options are shown.

Because the correct answer to the problem is saved with your work this will allow me to grade your model. **This is a required aspect of the lab and must be completed before you log out of your program.**

Don't forget that each group gets a different problem at the same level of difficulty.

How do you submit your final work to VGLII?

1. You were assigned a particular problem file.
2. You will work through the problem. Along the way, you can save your work as .wr2 files for further crossing, etc.
3. When you and your group has finished a problem and entered your answer into the Model Builder, you will then use the **Save For Grading...** option in the **File** menu. This saves your work in an encrypted format suitable for grading; these files have a .gr2 extension.
4. You will submit your .gr2 files to me via **e-mail and** you will also upload it to the **classroom** incase your email does not come through.

CER Presentation (40 total points):

It is very important that you follow **all** of the directions for preparing your lab report in order to receive full credit. You will have a week from the day we do the lab to create your CER poster. You must have your data present in the lab and when you present you will be defending your hypothesis of your chosen mode of inheritance.

Parts of the CER Poster:

This will be structured like a scientific presentation to your peers, and me, on your data. The most important thing to keep in mind is that a scientific poster 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 parts of the CER poster. Descriptions *in italics* indicate their role in the argument you are developing.

Left Side of the Poster:

- (5 points) **Purpose and Hypothesis:** 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.*
- (5 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.*
- (5 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
 - 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.*

Center of the Poster:

- (5 points) **Results:** *This is where you present your data in the form of charts, graphs, crosses, whatever you feel is necessary to support your claim.*

Right Side of the Poster:

- (20 points) **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 (5 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 Purpose.

For each part of your model, give the evidence for that part. For example, if you want to argue that red eyes are XX/XY sex-linked dominant, you would have separate arguments to show that it is (1) XX/XY sex-linked and (2) dominant.

In addition to the 5 points for defining the symbols, I will grade the discussion using the following rubric:

- *All parts of model are supported (0 - 5 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 “ZZ/ZW sex-linked incomplete dominant”, you have to show data that it is ZZ/ZW, sex-linked, and incomplete dominant.
- *Data rules out all possible alternative models (0 - 5 points).* You presented 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, XX/XY sex-linked, circular dominance, etc. By “relevant alternative models”, I mean that, (for example) if you have shown that it must be 3 alleles, you only need to distinguish between incomplete, circular, and hierarchical dominance.
- *Only relevant data are presented (0 - 5 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.