

**Computer Flies 2:**

Name: \_\_\_\_\_

This time, we'll look at two loci at a time. You'll need to figure out expected phenotype ratios from your crosses.

**Please fill in these tables before coming to lab so you can refer to them during lab.**

**Table 1: Unlinked genes.** The genetics of many cat traits is well understood. We know that short hair (L) is dominant to long hair (l), and the albino allele (c) is recessive to fully colored fur (C). If these genes are on separate chromosomes, what phenotype frequencies do you expect from the following crosses?

Cross	Phenotype frequency			
	Short, colored	Short, white	Long, colored	Long, white
LLCC x LLCC				
LLCC x LICC				
LLCC x lICC				
LICC x LICC				
LICC x lICC				
lICC x lICC				
LLCC x LLCc				
LLCC x LLcc				
LLCc x LLCc				
LLCc x LLcc				
LLcc x LLcc				
LlCc x LlCc				
LlCc x Llcc				
Llcc x Llcc				
LLCc x lICc				
LlCc x lICc				
lICc x lICc				
LlCc x llcc				
lICc x llcc				
llcc x llcc				

**Table 2: Epistasis.** Lots of genes are known to interact to influence a cat's coat color. In some cases, one allele can mask the effects of alleles in another gene. For instance, the black gene determines if a cat will be black (B) or chocolate (b). However, if a cat has two albino alleles (cc), no color will be produced, and the cat will be white, regardless of the genotype at other coat color genes. The black gene can only influence coat color if the cat has at least one color allele (CC or Cc). This is called epistasis. In the following crosses, what phenotype ratios do you expect, assuming that the two genes are on separate chromosomes?

Cross	Phenotype frequency		
	Black	Chocolate	White
BBCC x BBCC			
BBCC x BbCC			
BBCC x BbCc			
BbCC x BbCC			
BbCC x BbCc			
BbCc x BbCc			
BbCc x bbCc			
BbCc x bbcc			
Bbcc x bbcc			
bbCc x bbcc			
bbcc x bbcc			

**You can do the rest at home before or wait until lab.**

Write your lab report on any 1 of the three pairs of traits below

<http://ScienceCourseware.org/vcise/drosophila/>

**2 loci: black body and radius incompletus**

Let's look at the mutations *black body* and *radius incompletus* (called "incomplete" under "wing vein").

1) You should be able to make one cross to determine whether each mutation is dominant or recessive.

- Describe what cross you made:
- Is *black body* dominant or recessive?
- Is *radius incompletus* dominant or recessive?
- How did you reach this conclusion?

2) Is either mutation sex-linked? \_\_\_\_\_ How do you know?

3) Now, use these F1s to produce F2s.

- What were the phenotypes of the flies you crossed to make F2s?
- Is either mutation lethal? \_\_\_\_\_ How do you know?

c) Use a chi square test to compare your F<sub>2</sub> data to what you would expect if the two loci are unlinked, given your above conclusions about dominance and sex-linkage.

Phenotype	Observed Num	Expected ratio

Chi square test statistic ( $\chi^2$ ): \_\_\_\_\_

Degrees of Freedom (d.f.): \_\_\_\_\_

Level of significance (P-value): \_\_\_\_\_

Does this indicate that you should reject your null hypothesis? Why or why not?

Based on the results of your chi square test, describe the genetic basis of these two traits (dominant, recessive, sex-linked, lethal), and whether the genes appear to be on separate chromosomes

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**2 loci: *sepia eye* and *eyeless*:**

5) Now you are dealing with two mutations that both influence the eyes.

a) Can an individual express both sepia colored eyes and eyelessness at the same time? \_\_\_\_\_

b) Can an individual carry mutations for sepia eyes and eyelessness at the same time? \_\_\_\_\_

c) Think about how this might influence the results of your crosses. Do you think that one mutation might mask the other? \_\_\_\_\_ What is this called? \_\_\_\_\_

6) You should be able to make one cross to determine whether each mutation is dominant or recessive.

a) Describe what cross you made:

b) Is *sepia eye* dominant or recessive?

c) Is *eyeless* dominant or recessive?

- d) How did you reach this conclusion?
- 7) Is either mutation sex-linked? \_\_\_\_\_ How do you know?
- 8) Now, use these F<sub>1</sub>s to produce F<sub>2</sub>s.
- a) What were the phenotypes of the flies you crossed to make F<sub>2</sub>s?
- b) Use a chi square test to compare your F<sub>2</sub> data to what you would expect if the two loci are unlinked, and exhibit masking, given your above conclusions about dominance and sex-linkage.

Phenotype	Observed Num	Expected ratio

Chi square test statistic ( $\chi^2$ ): \_\_\_\_\_

Degrees of Freedom (d.f.): \_\_\_\_\_

Level of significance (P-value): \_\_\_\_\_

Does this indicate that you should reject your null hypothesis? Why or why not?

- c) Based on the results of your chi square test, describe the genetic basis of these two traits (dominant, recessive, sex-linked), and whether the genes exhibit masking:

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**2 loci: purple eyes and yellow body**

**Extra Credit**

- 1) You should be able to make one cross to determine whether each mutation is dominant or recessive.

- a) Describe what cross you made:  
 b) Is *yellow body* dominant or recessive?  
 c) Is *purple body* dominant or recessive?  
 d) How did you reach this conclusion?
- 2) Is either mutation sex-linked? \_\_\_\_\_ How do you know?
- 3) Now, use these F1s to produce F2s.  
 What were the phenotypes **AND GENOTYPES** of the flies you crossed to make F2s?
- b) Use a punnet square or probabilities to predict the offspring ratio in the F2 generation.
- c) Use a chi square test to compare your F<sub>2</sub> data to what you would expect if the two loci are unlinked, given your above conclusions about dominance and sex-linkage.

Phenotype	Observed Num	Expected ratio

Chi square test statistic ( $\chi^2$ ): \_\_\_\_\_

Degrees of Freedom (d.f.): \_\_\_\_\_

Level of significance (P-value): \_\_\_\_\_

Does this indicate that you should reject your null hypothesis? Why or why not?

Based on the results of your chi square test, describe the genetic basis of these two traits (dominant, recessive, sex-linked, lethal), and whether the genes appear to be on separate chromosomes