

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. Some mutations will be linked to each other on the same chromosome. Others will be on separate chromosomes. Some will be on the same chromosome, but far enough apart that they are effectively unlinked. You'll first need to figure out whether each mutation is dominant/recessive/lethal/sex-linked. Then you can figure out whether the two loci are linked, and if so, how far apart.

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: Completely linked genes. If the L and C genes described above are actually on the same chromosome, **0 cM apart**, how will your phenotype ratios change? In the following F₁ and testcross progeny, what phenotype ratios do you expect?

Cross	Phenotype frequency			
	Short, colored	Short, white	Long, colored	Long, white
LLCC x llcc				
Above offspring x llcc				
LLcc x llCC				
Above offspring x llcc				

Table 3: Closely linked genes. If the L and C genes described above are actually on the same chromosome, **10 cM apart**, how will your phenotype ratios change? In the following F₁ and testcross progeny, what phenotype ratios do you expect?

Cross	Phenotype frequency			
	Short, colored	Short, white	Long, colored	Long, white
LLCC x llcc				
Above offspring x llcc				
LLcc x llCC				
Above offspring x llcc				

Table 4: 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 unlinked?

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 or wait until lab.

<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.

- a) Describe what cross you made:
- b) Is *black body* dominant or recessive?
- c) Is *radius incompletus* 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.

- a) What were the phenotypes of the flies you crossed to make F2s?
- b) Is either mutation lethal? _____ How do you know?

c) Use a chi square test to compare your F₂ 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 (χ^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 are linked or not:

2 loci: spineless bristles and ebony body

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 *spineless bristles* dominant or recessive?
- c) Is *ebony 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.

a) What were the phenotypes of the flies you crossed to make F2s?

b) Use a chi square test to compare your F₂ 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 (χ^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?

What might be an explanation for the unexpected results?

4) Figure out the linkage distance between these two genes. F2 crosses are not very good for calculating linkage distance, so you may need to go back and make different crosses. If needed, you can go back to the store to order new flies to cross with your existing F1s.

a) What types of crosses did we use in class to determine linkage distance?

b) Remember, **there is no recombination in *Drosophila* males**, only females, so make sure you are measuring recombination in females. How does this influence your crossing design?

c) Describe your crosses used to determine linkage distance between these two genes. Make sure you indicate the sex of the crossing parents.

d) Describe your results. Indicate whether individuals in each phenotypic class represent recombinants (R) or non-recombinants (NR):

Phenotype	Observed Num	Recombinant or not?

Total num (T): _____

e) Calculate the linkage distance (cM) between these two genes:
 (linkage distance is $r = (\# \text{ recombinants} / \text{total offspring}) \times 100$)
 (Show your math)

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 F₁s to produce F₂s.

a) What were the phenotypes of the flies you crossed to make F₂s?

b) Use a chi square test to compare your F₂ 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 (χ^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: