

**Computer Flies 3:**

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

Again, we'll look at two loci at a time. 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: 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 F<sub>1</sub> 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 2: 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 F<sub>1</sub> 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				

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

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

**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 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?

What might be an explanation for the unexpected results?

4) Figure out the linkage distance between these two genes. F<sub>2</sub> 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)

**Now choose any 2 loci that you like – Write your lab report about these**

1) You should be able to make one cross to determine whether each mutation is dominant or recessive. Remember, things could get tricky if one trait (or both traits) is sex linked or lethal.

- a) Describe what cross you made:
- b) Is *trait 1* \_\_\_\_\_ dominant or recessive?
- c) Is *trait 2* \_\_\_\_\_ 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 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?

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) If the two genes are linked, calculate the linkage distance (cM) between these two genes: (linkage distance is  $r = (\# \text{ recombinants} / \text{total offspring}) \times 100$ )

(Show your math)