

## Solutions to Practice Problems for Genetics, Session 2: Linkage and Recombination, Genetic Maps

### Question 1

You are doing a genetics experiment with the fruit fly. In the "P" generation, you cross two true-breeding flies. The female parent is brown and wingless and the male parent is black with normal wings. All of the flies in the F1 generation are brown and have normal wings.

Indicate the alleles associated with dominant phenotypes by uppercase letters and alleles associated with recessive phenotypes by lowercase letters. Assume the genes are not found on a sex chromosome. Indicate the color alleles as "B" and "b" the wing alleles by the letters "N" and "n".

a) The genotypes of the flies in the P generation are:

BBnn female and bbNN male.

b) The genotype of the flies in the F1 generation is: BbNn

c) You now take an F1 female and cross her to a true-breeding black, wingless male.

This male's genotype is: bbnn.

d) You count 1600 offspring in the F2 generation. If the wing and the color traits were linked and no recombination occurred, you would expect to count:

0 # of brown, winged flies (of the genotype BbNn)  
800 # of black, winged flies (of the genotype Bbnn)  
800 # of brown, wingless flies (of the genotype bbNn)  
0 # of black, wingless flies (of the genotype bbnn)

e) When you count the F2 generation, you really get:

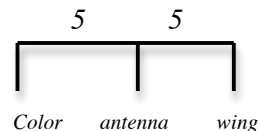
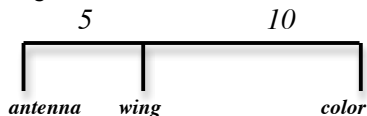
85 brown winged flies  
 728 black winged flies  
 712 brown wingless flies  
 75 black wingless flies

What is the genetic distance between the color and wing genes?

*Recombination frequency = # recombinants/total (100) = 85 + 75 / 85 + 75 + 728 + 712 = 0.1(100) = 10%*

f) A series of fruit fly matings shows that the recombination frequency between the gene for wing size and the gene for antenna length is 5% (i.e. the genetic distance between them is 5 centimorgans). List all possible recombination frequencies between the gene for color and the gene for antenna length.

*The genetic distance is either 5 cM or 15 cM*



## Question 2

You are working with a hypothetical fly and have found color and wing mutants. Preliminary work indicates that the mutant traits are recessive and the associated genes are not sex-linked, but beyond that you have no information. You first look at 2 genes, each with two alleles: "B or b" for body color and "W or w" for wing surface. The red body phenotype is dominant to the yellow body phenotype and smooth wings are dominant to crinkled wings.

a) You cross a true-breeding yellow-bodied, smooth-winged female with a true-breeding red-bodied, crinkle-winged male. What will be the phenotype(s) of the F1 progeny?

$RRaa \times rrAA = RrAa$  Thus the F1 fly has a red body and smooth wings.

b) You cross several pairs of F1 siblings.

i) What ratio of phenotypes do you expect in the offspring?

$\frac{9}{red\ smooth} : \frac{3}{red\ crinkled} : \frac{3}{yellow\ smooth} : \frac{1}{yellow\ crinkled}$

ii) The actually data is shown below. Does this date match your expectation? If not, explain why there is a difference in the expected and actual numbers.

body	wing surface	Number
red	smooth	310
yellow	smooth	142
red	crinkled	131
yellow	crinkled	23

*It is hard to tell, although this ratio does not match the 9:3:3:1 expected, but it is not terribly far off. You would suspect that these two genes may be linked, but doing a test cross (back cross) will give much clearer results.*

c) To determine the recombination frequency between these two genes, you perform several crosses where you cross an F1 from part (a) with a yellow-bodied, crinkle-winged fly. You get the following results. What is the distance between the genes for body color and wing surface in map units?

body	wing surface	Number
red	crinkled	396
red	smooth	102
yellow	crinkled	98
yellow	smooth	404

$$(102+98)/(396+102+98+404) * 100 = 20\ cM$$

You decide to turn your attention to a different gene, one that controls wing length. This gene has two alleles, "L or l" where long wings are dominant to short wings. Remember that the red body phenotype is dominant to the yellow body phenotype. You again mate two true-breeding lines:

red-bodied, short wing male      X      yellow-bodied, long wing female

↓

F1:      All red-bodied, long wing

d) To determine the recombination frequency between these two genes, you perform several crosses where you cross an F1 from part (d) with a yellow-bodied, short-winged fly. You get the following results. What is the distance between the genes for body color and wing length in map units?

body	wing length	Number
red	long	45
red	short	460
yellow	long	440
yellow	short	55

$$(45+55)/(45+460+440+55) * 100 = 10\ cM$$

**Question 2, continued**

e) Given your answers to parts (c) and (d), what can you say about the relationship between the gene for wing length and the gene for wing surface?

*You would expect the gene for wing length and the gene for wing surface to be linked and the distance is expected to be either approximately 10 cM or approximately 30 cM apart.*

f) Based on the preceding, what are the two possible arrangements of the three genes? Indicate the map distance between genes for each arrangement.



g) In a final mapping experiment, you cross a true-breeding red-bodied, short and crinkle-winged male with a true-breeding yellow-bodied, long and smooth-winged female. List the expected genotypes of the F1 progeny. What are the associated phenotypes?

*P: RRllaa x rrLLAA*

*F1: RrLlAa red-bodied, long and smooth-winged*

**Question 3**

While working with a type of beetle that is normally smooth, large, and white, you discover three mutations that lead to the recessive phenotypes bumpy, small, and grey, respectively. You cross true-breeding smooth white beetles to true-breeding bumpy grey beetles and get all smooth white F1 beetles. Then you cross the F1 beetles to true-breeding bumpy grey beetles and, after analyzing 800 F2s, calculate a map distance of 5 cM between the smoothness and color loci.

a) What are the four phenotypic classes you got in the F2, and about how many of each did you get?

- For the body type (i.e., smooth or bumpy) use B or b to designate the alleles.
- For the color (i.e., white or grey) use G or g to designate the alleles.
- For the size (i.e., large or small) use L or l to designate the alleles.

\*In each case, use the uppercase letter for the associated with the dominant phenotype and the lower case letter for the allele associated with the recessive phenotype.

<i>Genotypic class</i>	<i>Phenotypic class</i>	<i>How many of this phenotype</i>
<i>Bbgg</i>	<i>Smooth White</i>	<i>380</i>
<i>bbGg</i>	<i>Bumpy Grey</i>	<i>380</i>
<i>bbGb</i>	<i>Smooth Grey</i>	<i>20</i>
<i>bbgg</i>	<i>Bumpy White</i>	<i>20</i>

b) You cross two true-breeding parents to get all F1 beetles that are large and smooth. You cross the F1 to true-breeding small, bumpy beetles and get: 228 large and smooth, 19 small and smooth, 16 large and bumpy, 237 small and bumpy. What were the genotypes and phenotypes of the two parental beetles (P generation)?

	<i>genotype</i>	<i>phenotype</i>
<i>Parent 1</i>	<i>LLBB</i>	<i>Large Smooth</i>
<i>Parent 2</i>	<i>llbb</i>	<i>Small bumpy</i>

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