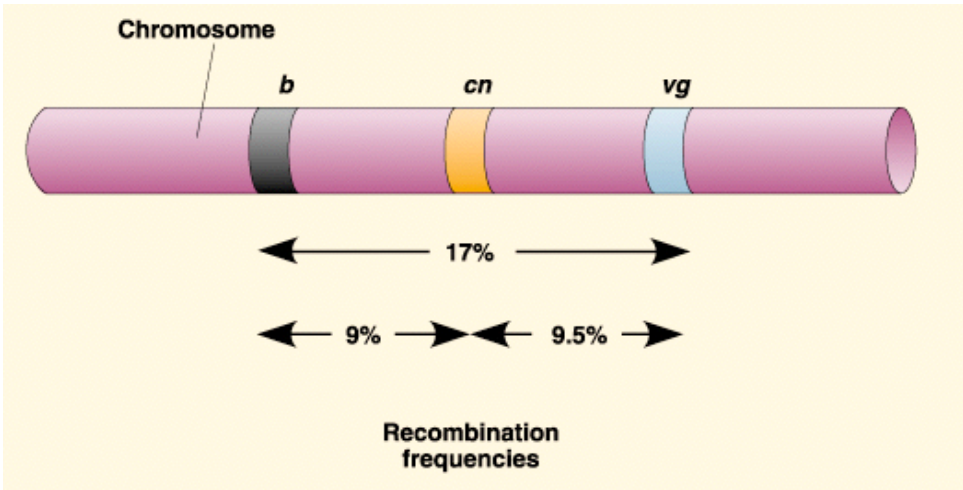
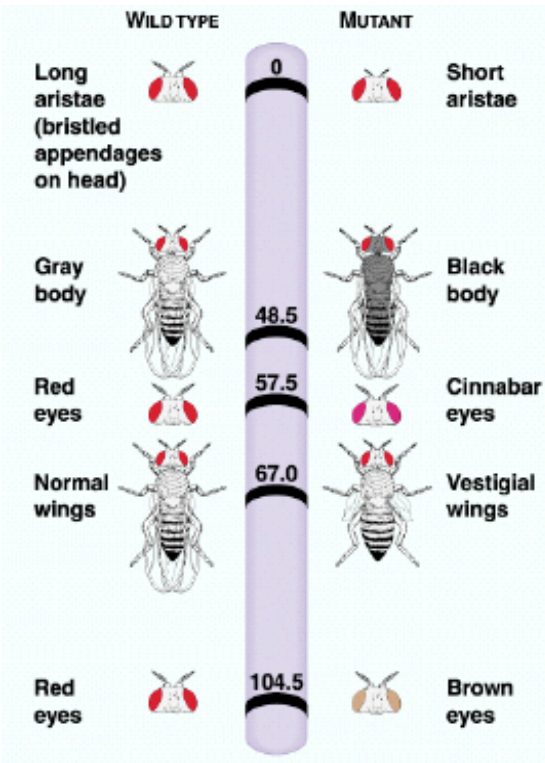


# Gene Mapping

## Principles of Gene Mapping & Practice Problems

See Freeman 2e pp. 285-287; or Campbell 7e pp. 277-281.



The central idea of gene mapping, as first developed by Sturtevant, is that the frequency of recombination between two genes can be used as a measure of the actual distance between them on a chromosome.

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# Gene Mapping - an Example

Assignment: Construct a genetic map using the following data:

A line of drosophila has been constructed with three recessive mutations:  
*sc* = loss of thorax bristles ("scute")  
*ec* = roughened eye surface ("echinus")  
*vg* = vestigial wings

The dominant, wild-type version of each allele could be written as *vg+* or *ec+*, but we will write them just as "+" for simplicity.

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**P:** we cross homozygous recessive flies (*sc ec vg / sc ec vg*) with homozygous dominant (wild-type) flies (*+++ / +++*).

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**F1:** All of the flies produced by the parental cross have the dominant (wild-type) phenotype. Genetically, these flies are:  
*(sc ec vg / +++)*

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**F2:** we produce an F2 generation by mating the F1 flies with homozygous recessive flies (*sc ec vg / sc ec vg*). This cross produces an F2 generation with 6 different phenotypes:

<i>sc</i>	<i>ec</i>	<i>vg</i>	417	<i>(parental combination of alleles)</i>
+	+	+	430	<i>(parental combination of alleles)</i>
<i>sc</i>	+	+	25	
+	<i>ec</i>	<i>vg</i>	29	
<i>sc</i>	<i>ec</i>	+	44	
+	+	<i>vg</i>	37	
<i>sc</i>	+	<i>vg</i>	4	
+	<i>ec</i>	+	5	

*total flies in F2:*            991

Assignment:

From this genetic data determine the recombination frequencies between each pair of genes (there are 3 pairs: *sc/ec ec/vg sc/vg* ). After you have calculated the recombination frequencies for each gene pair you should be able to construct a genetic map:

## Solution to gene mapping problem

<u>Data:</u>	sc	ec	vg	417	(parental combination of alleles)
	+	+	+	430	(parental combination of alleles)
	sc	+	+	25	
	+	ec	vg	29	
	sc	ec	+	44	
	+	+	vg	37	
	sc	+	vg	4	
	+	ec	+	5	
	total flies in F2:			991	

• First, we figure out the degree of recombination between each of the 3 possible gene pairs. The key to getting this right is a correct identification of which phenotypes are "parental" and which are "recombinant." In this cross, this is pretty easy to do. Any combinations that include only sc, ec, or vg are parental. So are those with only  $\pm$  alleles. All others are recombinant:

**Recombination between sc & vg:**  
 "recombinants" = 25+29+44+37 = 135  
 $\% \text{ recombination} = \frac{135}{991} = 13.6\%$

**between sc & ec**  
 "recombinants" = 25+29+4+5 = 63  
 $\% \text{ recombination} = \frac{63}{991} = 6.4\%$

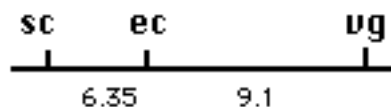
**between ec & vg**  
 "recombinants" = 44+37+4+5 = 90  
 $\% \text{ recombination} = \frac{90}{991} = 9.1\%$

• The three recombination frequencies give us enough data to construct the map:

1) Most distant?? *sc* & *vg*  
 (total map distance = 13.6)



2) The intermediate gene is *ec*. It is closer to *sc*. So we locate it like this:



*The genetic map is complete!*

NOTE: The two rarest recombinant phenotypes are shown here:

sc	+	vg	4
+	ec	+	5

- These two recombinants are much rarer than the other types. Why???
- From one look at these data, could you position the *ec* gene immediately?
- Why or why not?

## A few practice Gene Mapping problems

1. Genetic analysis has shown that the recessive genes *an* ("Anther ear"), *br* ("brachytic") and *f* ("fine stripe") are all found on chromosome #1 of maize (corn). When a plant that is heterozygous<sup>1</sup> for each of these markers is test-crossed with a homozygous recessive plant, the following results are obtained:

Test Cross Progeny	Numbers
wild type	98
<i>fine</i>	26
<i>brachytic</i>	2
<i>brachytic fine</i>	379
<i>anther</i>	385
<i>anther fine</i>	3
<i>anther brachytic</i>	20
<i>anther brachytic fine</i>	87
Total Offspring:	1000

Analyze this data in two steps:

- a) Calculate recombination frequencies between each of these three pairs of genes.  
*and*  
 b) Draw a genetic map for the location of these 3 genes on chromosome #1 of maize. Be sure to show the map distances between the loci.

2. You are investigating 4 recessive alleles in corn. They are whimpy ears (*w*), striped leaves (*s*), shriveled kernels (*k*), and red tassels (*r*). Their dominant counterparts are generally just represented by the "+" symbol.

A plant that is homozygous recessive for all 4 genes (*ww ss kk rr*) is crossed with a plant that is homozygous dominant for all 4 genes. As expected, the F1 offspring of the cross display the dominant phenotypes of all 4 genes.

These F1 plants are then crossed with a plant that is homozygous recessive for all 4 genes. A total of 1,000 F2 offspring are produced. These F2 offspring display the following phenotypes:



w s k r	198
+ + + +	202
w s k +	201
+ + + r	199
w + k +	49
+ s + r	51
w + k r	48
+ s + +	52

*Analyze the data in 2 steps:*

a) First, calculate recombination frequencies between each of the 4 genes. (Because there are 4 genes, there are 6 gene pairs, and there will be a total of 6 recombination frequencies to calculate).

*(NOTE: The 6 gene pairs are: W-S W-K W-R S-K S-R and K-R)*

b) Next, Draw a genetic map for the location of these 4 genes. Be sure to show the map distances between the loci, and also be sure to indicate whether or not all 4 genes are located on the same chromosome.

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<sup>1</sup> That's right. The question doesn't tell us exactly what the parentage of this heterozygous plant is. However, you can figure it out from the test cross progeny, and that will help in making the genetic map.

*Finally, two more mapping problems to help develop your ability to recognize how unusual patterns of data affect a genetic map:*

**3.** The data below represent the offspring from a cross between one parent heterozygous for the three traits shown, and one parent homozygous recessive for all three traits.

wmf148  
+++141  
+mf6  
w++5  
++f306  
wm+305  
+m+43  
w+f46  
total1000

Construct a map that shows the correct order of the markers as well as the distances between them. (Don't worry about the phenotypes associated with the markers).

**4.**

Suppose the data from the same cross described in question **3** looked like this?

wmf238  
+++237  
+mf10  
w++12  
++f228  
wm+247  
+m+13  
w+f15  
total1000

Construct a map that is consistent with these data (it might be quite different from the one in question **3**!).



*Have fun working these sample mapping problems.*

*When you'd like to check your results, you'll find the answers posted on the Bio 20 Web site*