RECOMBINATION FREQUENCIES

A population of fruit flies trihybrid (*AaBbCc*) for potentially linked genes were crossed with a population of known homozygous recessives (*aabbcc)*. The Punnett Square and resulting number of progeny are shown at right.

If these genes are unlinked, we'd expect a 1:1:1:1:1:1:1:1 phenotype ratio. Given our observed progeny (which clearly is NOT following this ratio), its likely we are dealing with linked genes. If the genes are linked, we should be able to map them on a single chromosome.

	abc	Observed Progeny
aBC	aaBbCc	12
abc	aabbcc	373
AbC	AabbCc	50
Abc	Aabbcc	10
ABC	AaBbCc	400
abC	aabbCc	32
aBc	aaBbcc	29
ABc	AaBbcc	44

Step 1: Identify the parental and recombinant gamete genotypes
Parental = ABC, abc (have the greatest # of progeny)
Recombinants = all others

Step 2: Make a table that plots the gamete genotypes and # of offspring on the Y axis (vertical left side), and each combination of 2 genes on the X axis (horizontal top side):

2-gene combinations

Gamete Genotypes & Progeny numbers

		A&B	B&C	A&C
aBC	12	R		R
abc	373			
AbC	50	R	R	
Abc	10	R		R
ABC	400			
abC	32		R	R
aBc	29	R	R	
ABc	44		R	R
Totals: 950		101	155	98

Step 3: For every gamete genotype row, write on the table if it is Recombinant (R) for each 2-gene combination.
- For example, the "aBC" gamete is recombinant for both genes AB and AC
  (remember, the parental gametes are AB and ab)

Step 4: Add up the number of recombination progeny for each 2-gene column.
- For example, the total number of recombinants between A & B is
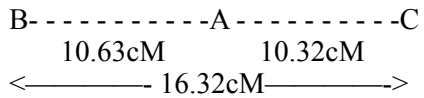 12 + 50 + 10 + 29 = 101

Step 5: Calculate the recombination frequencies between each pair of genes
AB: (101/950)100 = 10.63%
BC: (155/950)100 = 16.32%
AC: (98/950)100 = 10.32%

Step 6: Draw a recombination map, showing the proper gene order and distances.

B- - - - - - - - - - -A - - - - - - - - - -C
    10.63cM   10.32cM
<——————- 16.32cM——————->

Note that the recombinant-calculated length between B&C (16.32cM) does not = the sum of AB and AC (20.95cM).

Recombination calculations are hypothetical estimates of gene distances; they are not 100% accurate, and are impacted by things like double-crossovers.