

**Problem Set 4**  
**Genetics 371**  
**Winter 2010**

1. A dihybrid YyZz is test crossed. The following phenotypic classes are observed:

442	Yz
458	yZ
46	YZ
54	yz

(a) What is the parental type of the heterozygous parent?

This is a test cross so the mating is YyZz x yyzz. The parental type of the heterozygous parent was Yz and yZ, which can be inferred from the two most abundant progeny classes.

(b) Determine the map distance between Y and Z.

$$(46+54) / (442+458+46+54) = 10 \text{ cM}$$

2. In corn...

Colored kernels (C) is dominant over colorless (c)  
Plump kernels (S) is dominant over shrunken (s)  
Starchy kernels (W) is dominant over waxy (w).

A trihybrid (Cc Ss Ww) plant is testcrossed and the following progeny are obtained:

2708 Colorless, plump, waxy  
2538 Colored, shrunken, starchy  
626 Colorless, plump, starchy  
601 Colored, shrunken, waxy  
116 Colorless, shrunken, starchy  
113 Colored, plump, waxy  
4 Colored, plump, starchy  
2 Colorless, shrunken, waxy

Determine linkage (including map distance) for the genes, and the phase in this cross.

The lack of the 1:1:1:1:1:1:1:1 ratio suggests linkage among the three genes. You can verify this through a chi-square test in less obvious cases.

The parental types of the fully heterozygous parent must be: C s W and c S w because they occur at the highest frequencies. At this point though, we do not know the order (i.e., phase) in which these genes occur along the chromosome.

To determine the order we can consider the map distance between each pair of genes. Specifically, since we know the parental types, we can calculate the map distance as the fraction of recombinant types for each pair of genes:

$$\text{C and S: } 100 * [(113+116+4+2)/6708] = 3.5 \text{ cM}$$

$$\text{S and W: } 100 * [(626+601+4+2)/6708] = 18.4 \text{ cM}$$

$$\text{C and W: } 100 * [(113+116+626+601)/6708] = 21.7 \text{ cM}$$

Determine gene order. Since 21.7 cM is the largest distance, we conclude that C and W are the outside genes, with S being in the middle:



Note that  $3.5 + 18.4 = 21.9$  cM is slightly larger than the 21.7 cM distance calculated above. The combined distance between C and S and S and W is a more accurate measure of distance between C and W because it compensates for undetectable double-crossovers in each interval.

Finally, it is also possible to determine gene order without calculating map distances. The two least frequent phenotype classes (Colored, plump, starchy and colorless, shrunken, waxy) had to have been produced by two crossovers: one between C and S and another between S and W. Because we know the parental types are C s W and c S w, a crossover in each interval (between C and S and S and W) results in CSw and csw, which are the phenotypes of the two least frequent progeny classes. Thus, S must be in the middle

3. RRSS is mated to rrss. The resulting RrSs progeny are mated to each other. R and S are 35 map units apart.

(a) Predict the frequencies of each gamete type produced from the RrSs individual.

RS: 32.5%

rs: 32.5%

Rs: 17.5%

rS: 17.5%

(b) Predict the frequencies of R\_ss and rrS\_ progeny classes from the RrSs x RrSs cross.

OK, I admit that I tried to answer this question without a Punnett Square – thanks to everyone who caught the error. To be clear, here is the Punnett Square:

	RS 0.325	rs 0.325	Rs 0.175	rS 0.175
RS 0.325	RRSS	RrSs	RRSs	RrSS
rs 0.325	RrSs	rrss	Rrss	rrSs
Rs 0.175	RRSs	Rrss	RRss	RrSs
rS 0.175	RrSS	rrSs	RrSs	rrSS

$$\begin{aligned} \text{Frequency of } R\_ss &= RRss + Rrss \\ &= .175^2 + .325 \cdot .175 + .175 \cdot .325 \\ &= 0.144 \end{aligned}$$

$$\begin{aligned} \text{Frequency of } rrS\_ &= rrSS + rrSs \\ &= .175^2 + .325 \cdot .175 + .175 \cdot .325 \\ &= 0.144 \end{aligned}$$

4. In a plant species, tall (**T**) is dominant over short (**t**) and red seed color (**R**) is dominant over white (**r**). The two loci are known to be linked; however, the frequency of recombinant gametes is different during production of eggs vs. production of pollen. A homozygous **TR/TR** plant is crossed to a homozygous **tr/tr** plant. The resulting heterozygote is allowed to self-fertilize. Assuming that 10% of eggs are recombinant between the **T** and **R** loci and that 8% of the pollen are recombinant, list the progeny phenotypes and proportions from this self-cross.

The gametes produced in pollen and eggs (which have the TtRr genotype) are:

Gamete	pollen	eggs
TR	0.46	0.45
tR	0.04	0.05
Tr	0.04	0.05
tr	0.46	0.05

The simplest way to answer the question is to construct a Punnett Square, which I'll leave for you to do. The four possible phenotypes are tall and red (T-R-), short and red (ttR-), tall and white (T-rr), and short and white (ttr). The frequencies of each phenotype can be obtained directly from your Punnett Square. For example the frequency of T-R- is:

$$\text{Freq}(T-R-) = 0.207+0.023+0.023+0.207+0.018+0.002+0.018+0.002+0.207 = 0.707.$$

The frequencies of the remaining three phenotypes is obtained in a similar fashion and is:

$$\text{Freq}(T-rr) = 0.043$$

$$\text{Freq}(ttR-) = 0.043$$

$$\text{Freq}(ttr) = 0.207$$

5. A family (mom, dad, and three kids) were genotyped at 6 different polymorphic loci on the X chromosome by allele specific (ASO) hybridization. At each locus, the four bases being tested are A, C, G, and T reading from top to bottom. Hybridization is indicated by shading and the base that actually was detected; no hybridization is indicated by blank boxes. The results for the mom and three kids are shown below.

Locus #					
1	2	3	4	5	6
A	A			A	
C			C		C
	G		G		
		T		T	T

Mom

Locus #					
1	2	3	4	5	6
A			A		A
		C	C		C
G	G				
		T		T	

Kid #1

Locus #					
1	2	3	4	5	6
	A		A		A
		C			
				G	
T					

Kid #2

Locus #					
1	2	3	4	5	6
	A		A	A	A
C		C			
G	G		G		
		T		T	T

Kid #3

(a) What is the sex of each child and how can you tell?

Kids 1 and 3 are female since they show heterozygous genotypes and kid 2 is male because this child only has homozygous genotypes.

(b) One of the kids was adopted. Which one and how can you tell?

Kid 2 is most likely to be adopted because the alleles that he has at locus 1, 3, 4, 5, and 6 do not match the alleles of the mom.