

## Genetic Mapping Exercise - Extra Credit

Name \_\_\_\_\_

Section # \_\_\_\_\_

**Do not work together - each person to do their own work.**

When loci of different allelic groups are on the same chromosome, linkage occurs but is not absolute. Crossing-over always happens during meiosis. The probability of a cross-over event occurring between two loci is directly related to the distance (in base pairs) between them. Because of this simple relationship, we can use the frequency of cross-over events between two loci as a direct means to determine relative distances. By this idea, the frequency, in percent, is directly translated into map units where each percentage point is equal to one map unit.

The best procedure to determine crossover frequencies is to cross a heterozygous individual with a homozygous recessive one. The heterozygote should have the dominant alleles on the same chromosome (as opposed to having both dominant and recessive alleles on each chromosome). Note, this is a “test cross.” Every type of gamete produced by the heterozygote is represented by a type of phenotype in the next generation. Hence, that generation is a sample of the types and frequency of gametes produced.

Example: Flower color in a species of plant is determined by a pair of alleles, R = red flower color, and r = white color. Seed texture is determined by another pair, W = wrinkled texture and w = smooth texture. These loci are linked. To do a preliminary analysis of their distance, we need to develop pure breeding parental strains one of which has both dominant phenotypes and the other with the recessive phenotypes. Hence, the parental plants should have the following genotypes:

**P1**            WWRR            and            wwrr

We can cross these to generate the heterozygote:

W	R
—————	
w	r
—————	

We then cross this heterozygote back to a parental plant with the recessive phenotype.

WwRr x wwrr

Assuming no crossing-over, what phenotypes do we expect in the next generation and in what ratio?

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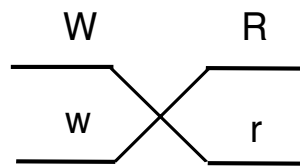
In practice, we generally will find all four phenotypic combinations. Let us assume the outcome below:

40 Red-Wrinkled: 39 White-Smooth: 11 Red-Smooth: 10 White-Wrinkled

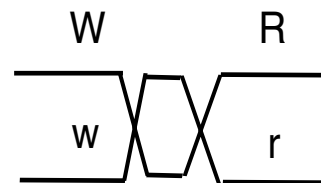
We can estimate the map units between these loci using the following calculation:

$$\frac{\# \text{ Crossover individuals}}{\# \text{ Of total offspring}} \times 100 = \underline{\hspace{4cm}}$$

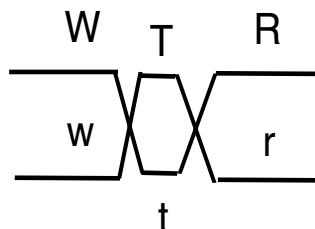
This value will give us an underestimate of the total distance because it does not take into consideration double-crossovers. A single cross-over can be shown as below



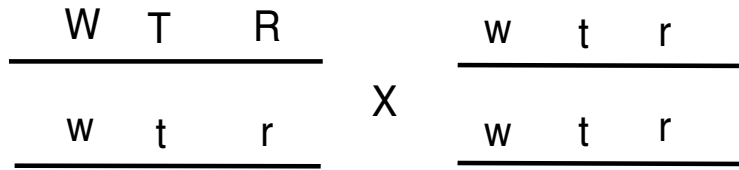
and results in the cross-over gametes Wr and wR. However, double-crossovers results in gametes (WR, wr) that also form when no crossover occurs (see below):



A double-crossover represent two cross-over events, but is not tallied as even one. To accurately determine the distance between loci, we need a way of determining double cross-overs between the two loci. This can be done using three loci on one chromosome in a trihybrid cross. If we consider a third locus (T,t) between the two loci previously considered, we can see that a double-crossovers result in unique gametes (WtR and wTr)



Let us define the genes at the “t” locus as T = tall and t= dwarf. We can now consider the cross illustrated below:

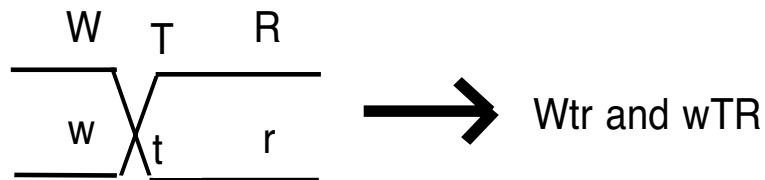
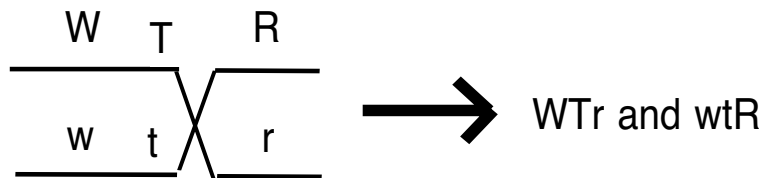


The types of gametes produced by the heterozygote are listed in the table below:

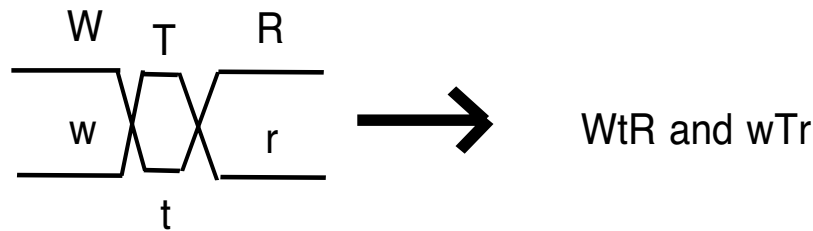
Gamete	Type	Resulting Phenotype
WTR	non cross-over	Wrinkled-Tall- Red
wtr	non cross-over	Smooth-Dwarf-White
Wtr	Single cross-over	Wrinkled-Dwarf-White
wTR	Single cross-over	Smooth-Tall-Red
WTr	Single cross-over	Wrinkled-Tall-White
wtR	Single cross-over	Smooth-Dwarf-Red
WtR	Double cross-over	Wrinkled-Dwarf-Red
wTr	Double cross-over	Smooth-Tall-White

How the various cross-over types develop are diagrammed below:

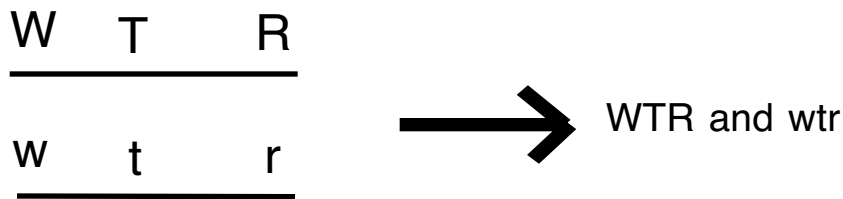
### Single-Crossovers



### Double-Crossover



### Non-Crossover



From this specific example we can generate some general rules for mapping linked loci.

1. All progeny like the original parents are derived from non-crossover gametes.
2. Progeny resulting from double-crossovers are recognizable as the least common phenotypes. Once we recognize these, we can determine which locus is in the middle. There will be two double-crossover phenotypes, each with two traits like one parent and a third like the other. It is this third trait that will identify the corresponding locus as residing between the other two (see the following example).
3. The true distance between the distal loci is the frequency of all the single crossover progeny summed with the frequency of the double-crossover progeny doubled.

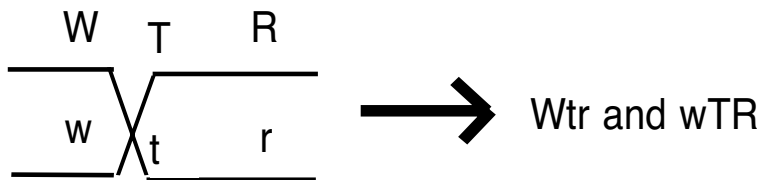
$$= \frac{\# \text{ Single Cross-over Offspring} + 2(\text{Double Cross-over Offspring})}{\# \text{ Of Total Offspring}} \times 100$$

4. The true distance between a locus on one end, and the center locus, is the sum of the frequency of the single crossover progeny between these loci, plus the frequency of the double crossover progeny (see the next page).

$$= \frac{\# \text{ Single Crossover Offspring} + \# \text{ Double Crossover Offspring}}{\# \text{ Of Total Offspring}} \times 100$$

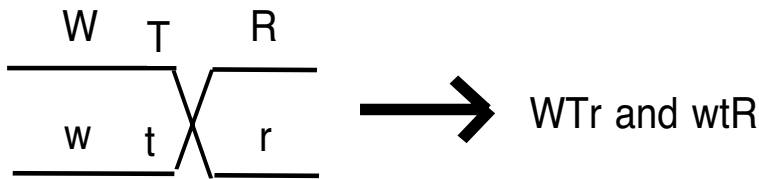
**In our example.....**

For loci “W” and “T” .....



The single crossover phenotypes are wrinkled-dwarf-white and smooth-tall-red.

For the loci “T” and “R” .....



The single crossover phenotypes are wrinkled-tall-white and smooth-dwarf-red.

**Procedure:** You will consider a cross with the three traits, “stem,” “stigma,” and “seed coat.” See the table below:

Trait	Phenotypes
Stem	Straight (dominant) vs. Twisted
Stigma	Kidney (dominant) vs Roughoid
Seed Coat	Engrailed (dominant) vs Furrowed

Our problem was set up by first crossing the following homozygous parents:

### **Straight-Kidney-Engrailed X Twisted-Roughoid-Furrowed**

The F<sub>1</sub> generation all have the phenotype:

### **Straight-Kidney-Engrailed**

An F<sub>1</sub> individual was then crossed with a homozygous recessive for all three traits

### **Straight-Kidney-Engrailed X Twisted-Roughoid-Furrowed**

Eight different phenotypic combinations resulted from this final cross. Your TA will provide you with a unique set of values for each phenotypic combination. As he reads it off to you fill in the table.

Phenotype	Count	Crossover type (parental, crossover, double crossover)
Straight-kidney-engrailed		
Straight-kidney-furrowed		
Straight-roughoid-engrailed		
Straight-roughoid-furrowed		
Twisted-kidney-engrailed		
Twisted-kidney-furrowed		
Twisted-roughoid-engrailed		
Twisted-roughoid-furrowed		

1. Which phenotypes are the result of double crossovers?

\_\_\_\_\_ and \_\_\_\_\_

2. Which locus is in the middle?

\_\_\_\_\_

3. Calculate the total map distance of the two loci farthest apart (show your work).

Map distance of the two loci farthest apart \_\_\_\_\_

4. Calculate the map distance between the middle locus and the two at each end (show your work).

Map distance 1 \_\_\_\_\_

Map distance 2 \_\_\_\_\_

Show all  
distances.

— Locus for \_\_\_\_\_

— Locus for \_\_\_\_\_

— Locus for \_\_\_\_\_