Section 7.3 Gene Linkage and Mapping
Read pages 209-211 in your textbook.

Objectives

- Describe the discovery of gene linkage.
- Explain how linkage maps can be used to estimate distances between genes.

One of Mendel's conclusions from his work on inheritance in pea plants was the law of independent assortment, which stated that genes assort independently of each other during meiosis. However, later experiments suggested that some genes were linked together and did not assort independently. Eventually, research with fruit flies demonstrated that chromosomes, not genes, assort independently and that during meiosis chromosomes could exchange homologous genes.

The chance that two genes on a chromosome will be inherited together is related to the distance between the genes. If two genes are close together, it is very likely that they will be inherited together. If two genes are far apart, it is much more likely that they will be separated by the crossing over that occurs during meiosis. Crossing over takes place when segments of sister chromatids are exchanged.

The frequency of cross-overs is related to the distance between genes on a chromosome. By finding the percentage of times that cross-overs occur from observations of phenotypes in offspring, it is possible to make a map of the locations of the genes. A linkage map is a map of the relative locations of genes on a chromosome.

The distance between two genes on a linkage map is expressed in "map units." Two genes that cross over 1 percent of the time are one map unit apart. Two genes that cross over 20 percent of the time are 20 map units apart. Linkage maps can be made for several different genes at one time if all of their cross-over frequencies are known.

1. How was Mendel’s law of independent assortment inaccurate?
2. What is the relationship between the distance between two genes and the chance that they will be inherited together?
3. What is a linkage map?
4. How are the distances between genes determined for a linkage map?