## Linked Genes- Example Problem and Explanation (in my own words...hope it helps!)

https://www.youtube.com/watch?v=QooJ6gPEiRk

Mendel P1 Dihybrid Cross (homozygous for both traits):

Ex- AABB x aabb

F1 = AaBb heterozygous (dom trait expressed)

Cross F1 with homo rec (test cross): AaBb x aabb

F2 Expected Genotypes: 1 AaBb; 1 Aabb; 1 aaBb; 1 aabb

## F2 Expected phenotypes = 1:1:1:1

In experiments, his actual data looked something like: 480: 520: 510: 490 (out of 2000). The actual data is very close to the expected data. It was later discovered that this was because the genes were on different c'somes, and they independently assorted (remember Metaphase I in meiosis?).

<u>Stanley Hunt Morgan</u>- Years later, he ran similar experiment to Mendel, but with fruit flies. His 'actual' data was NOT anywhere close to Mendel's actual data, or the expected data. He repeated the experiment many times and never saw the 1:1:1:1 ratio that Mendel did. His data looked something like this:

965: 944: 206: 105 (out of 2000).

Most offspring looked like the parents and few were recombinant. His student figured out that the genes were not on different chromosomes, but instead were on the SAME CHROMOSOME and that they must be very close together ("linked") with little crossing over.

This is the recombination frequency of the above data:

391/2300 x 100 = 17%

He converted the percentages to arbitrary units, called centimorgans (get it? Morgan was his name.)

The lower the percent, the closer together the genes are on a 'chromosome map'. Thus, the more likely they will stay linked together (not cross over) and be in a gamete together. This will reduce variation, but it explains Morgan's data.

Let's try to map some genes on a chromosome (pick up the worksheet).