

When genes do not exhibit traditional Mendelian inheritance patterns by seemingly not following the Law of Independent Assortment, there is a possibility that these genes are linked. Linked genes are those that are contained on the same chromosome, thus during gamete formation, these genes have a higher probability of being inherited together. The more likely those genes are to be inherited together (the more closely linked), the closer those genes are to each other on the chromosome.

One way scientists determine how closely linked genes are on the same chromosome is by examining recombination frequencies. In essence they are measuring the rate of crossing over by comparing those individuals produced that match the parental phenotypes with those who exhibit recombinant (also called mutant or non-parental phenotypes).

In order to determine if genes are linked, you must first assume that they are not. This will involve determining the expected genotypic and phenotypic ratios for these organisms usually by making a Punnett square. This will often involve crossing individuals heterozygous for all traits in a testcross (crossing with an individual homozygous recessive for all traits).

Example: If two individuals with the genotypes AAbb and aaBB are crossed, the F₁ generation produced will consist of individuals with the genotype AaBb. To determine if genes A and B are linked, we must perform a testcross (crossing with aabb).

	AB	Ab	aB	ab
ab	AaBb	Aabb	aaBb	aabb

This cross shows that the expected outcome if the genes are not linked is 25% AaBb, 25% Aabb, 25% aaBb, and 25% aabb.

Through experimentation it was found that the observed outcome was 40% AaBb, 10% Aabb, 10% aaBb, and 40% aabb.

These results lead us to believe that the genes are linked because we see significantly more of the parental types (AaBb and aabb).

To determine the recombination rate (the rate of crossing over between these genes), we must take the number of recombinants and divide it by the total number of offspring.
 $20/100 = 20\%$ rate of crossing over.

This also tells us how far apart the genes are on the chromosome. 1% crossing over = 1 map unit between genes.

Directions: For each of the scenarios below, determine if the genes are linked, what the rate of crossing over is, and how many map units separate the genes. You must show your work.

1. Dogs have a gene that determines the size of their noses. Gene *N* codes for a protein that causes a large nose to develop and gene *n* codes for development of a small nose. It is suspected that this gene is linked to another gene for nose color. Gene *B* codes for a protein that causes black nose and gene *b* codes for proteins that cause pink nose. A purebred large nose, pink nosed dog is mated with a small nosed, purebred black nosed dog.

What are the genotypes and phenotypes of their offspring (F_1 generation)?

A member of the F_1 generation was test-crossed and it produced the following results.

Large, black nose - 18
Large, pink nose - 3
Small, black nose - 2
Small, pink nose - 17

Are the genes linked? Explain.

If so, what is the percent crossing over (recombination frequency)? What is the distance between the genes (in map units)?

2. In crayfish, gene *C* is epistatic to gene *R*. (Remember an epistatic gene turns other genes on or off.) When the *C* gene is present it allows color proteins to be produced by the *R* gene. Without the *C* gene, no color is deposited and the crayfish appear white. The allele *R* codes for proteins that produce red color while the allele *r* codes for proteins that produce blue color.

P: CCrr x ccRR

F_1 : _____

When the F_1 generation is test-crossed, the following results are observed.

Red - 225
Blue - 16
White - 240

Are these genes linked? Explain.

If so, what is the percent crossing over? What is the distance between the genes?

3. In mice a similar epistatic gene is present C (causing full color) is dominant to c (albino). Agouti mice are those that have two color tones is represented by A , and single color toned mice are represented by a . In a test-cross involving a hybrid individual, the following results were observed.

Agouti - 87

Albino - 166

Non-agouti - 85

Are these genes linked? Explain.

If so, what is the percent crossing over? What is the distance between the genes?

4. A wild-type fruit fly (heterozygous for both gray body color and normal wings), $b^+ b\ vg^+ vg$, is mated with a black fly with vestigial wings, $b b\ vg\ vg$. The offspring of this pairing have the following distribution of phenotypes: wild type = 856, black-vestigial = 887, black-normal = 182, gray-vestigial = 177.

Are these genes linked? Explain.

If so, what is the recombination frequency? What is the distance between the genes?

5. Fruit flies can also have red eyes (dominant) or purple eyes (recessive). A wild-type fruit fly for body color and eye color was mated with a black fruit fly with purple eyes. The offspring of this pairing have the following distribution of patterns: wild type = 815, black-purple = 811, gray-purple = 72, black-red = 67.

Are these genes linked? Explain.

If so, what is the recombination frequency? What is the distance between the genes?

6. Using the information from problems 4 and 5, construct a gene map for these characteristics. You must include map units between genes.

7. Create a gene map based on the following recombination frequencies: L-M = 8 map units, L-N = 28 map units, L-O = 25 map units, and M-O = 33 map units.

8. Four genes, J, K, L and M, reside on the same chromosome. Given that the crossover frequency between K and J is 3, between K and L is 8, between J and M is 12, and between L and M is 7. What is the order of the genes on the chromosome?