Gene Linkage and Mapping

**VOCABULARY**

- linkage map

**KEY CONCEPT** Genes can be mapped to specific locations on chromosomes.

**MAIN IDEAS**

- Gene linkage was explained through fruit flies.
- Linkage maps estimate distances between genes.

**Connect to Your World**

If you leave a banana out on a table until it is very ripe, you might see some of the most useful organisms for genetic research—fruit flies—buzzing around it. In your kitchen, fruit flies are pests. In the laboratory, early experiments with fruit flies showed not only that genes are on chromosomes, but also that genes are found at specific places on chromosomes.

**MAIN IDEA**

Gene linkage was explained through fruit flies.

Gene linkage, which you read about previously, was first described by William Bateson and R. C. Punnett, who invented the Punnett square. Punnett and Bateson, like Mendel, studied dihybrid crosses of pea plants. But their results differed from the 9:3:3:1 phenotype ratios that Mendel observed. The results suggested that some genes were linked together. But how could genes be linked and still follow Mendel's law of independent assortment?

American scientist Thomas Hunt Morgan, who worked with fruit flies (*Drosophila melanogaster*), found the answer. At first, Morgan was just looking for an organism to use in genetic research. He found fruit flies very useful because he could quickly and cheaply grow new generations of flies. He observed among fruit flies easily identifiable variations in eye color, body color, and wing shape. Knowing these variations, Morgan and his students set up experiments similar to Mendel's dihybrid crosses. They chose one type of fly with traits associated with the wild type, or most common phenotype. They crossed the wild type flies with mutant flies, or flies with a different, less common phenotype. You can see examples of fruit flies in **Figure 3.1**.

Morgan's results, like those of Punnett and Bateson, did not always follow the 9:3:3:1 ratio predicted by Mendel. But the results did differ in a noticeable pattern. Some traits appeared to be inherited together. Morgan called these traits linked traits, and they appeared to fall into four groups. As it turns out, fruit flies have four pairs of chromosomes. Each of the four groups of linked traits identified by Morgan matches one of the chromosome pairs. Morgan concluded that linked genes were on the same chromosome. The chromosomes, not the genes, assort independently during meiosis. Because the linked genes were not inherited together every time, Morgan also concluded that chromosomes must exchange homologous genes during meiosis.

**Synthesize** How did Morgan's research build upon Mendel's observations?
**Linkage maps estimate distances between genes.**

The probability that two genes on a chromosome will be inherited together is related to the distance between them. The closer together two genes are, the more likely it is that they will be inherited together. The farther apart two genes are, the more likely it is that they will be separated during meiosis.

One of Morgan’s students, Alfred Sturtevant, hypothesized that the frequency of cross-overs during meiosis was related to the distance between genes. This meant that the closer together two genes were, the more likely they were to stay together when cross-overs took place. Sturtevant identified three linked traits in fruit flies—body color, eye color, and wing size—and then crossed the fruit flies. He recorded the percentage of times that the phenotypes did not appear together in the offspring. This percentage represented the frequency of cross-overs between chromosomes.

From the cross-over frequencies, Sturtevant made **linkage maps**, which are maps of the relative locations, or loci, of genes on a chromosome. On a linkage map, one map unit is equal to one cross-over for each 100 offspring, or one percentage point. You can see an example of a linkage map in **Figure 3.2**.

Making a linkage map is fairly easy if all of the cross-over frequencies for the genes being studied are known. Suppose the following data were collected.

- Gene A and gene B cross over 6.0 percent of the time.
- Gene B and gene C cross over 12.5 percent of the time.
- Gene A and gene C cross over 18.5 percent of the time.

According to Sturtevant’s conclusions, genes A and B are 6 map units apart because they cross over 6 percent of the time. Similarly, genes B and C are 12.5 map units apart because they cross over 12.5 percent of the time. But where are the genes located in relation to each other on the chromosome?
Think about gene A as a point on a line. Gene B is either to the left or to the right of gene A. The same is true of the relationship between genes B and C. But if you only know the distances between genes A and B, and between genes B and C, you cannot determine the order of all three genes. You must also know the distance between genes A and C. As shown in Figure 3.3, the map distances between genes A and B and between genes B and C equal the map distance between genes A and C. Therefore, gene B must be located between genes A and C. If the map distance between genes A and C were 6.5 map units instead of 18.5 map units, then gene A would be between genes B and C.

Although linkage maps show the relative locations of linked genes, the maps do not show actual physical distances between genes. Linkage maps can give you a general idea about distances between genes, but many factors affect gene linkage. As a result, two pairs of genes may be the same number of map units apart, but they may not have the same physical distance between them.

**Summarize** How can a linkage map be made from observations of traits?

**7.3 Formative Assessment**

**REVIEWING MAIN IDEAS**

1. Summarize the importance of comparing wild type and mutant fruit flies in genetic research.
2. How is a **linkage map** related to cross-overs that take place during meiosis?

**CRITICAL THINKING**

3. **Compare and Contrast** How are linked genes similar to sex-linked genes? How are they different?
4. **Apply** Draw a linkage map based on the following cross-over percentages for three gene pairs: A – B = 8%, B – C = 10%, and A – C = 2%.

**SELF-CHECK Online**

**PREMIUM CONTENT**

**SCIENTIFIC PROCESS**

5. Punnett, Bateson, and Morgan found phenotype ratios that differed from Mendel’s results. Explain how these differences led to new hypotheses and new investigations in genetics.