Linkage and crossing over

World's first chromosome map

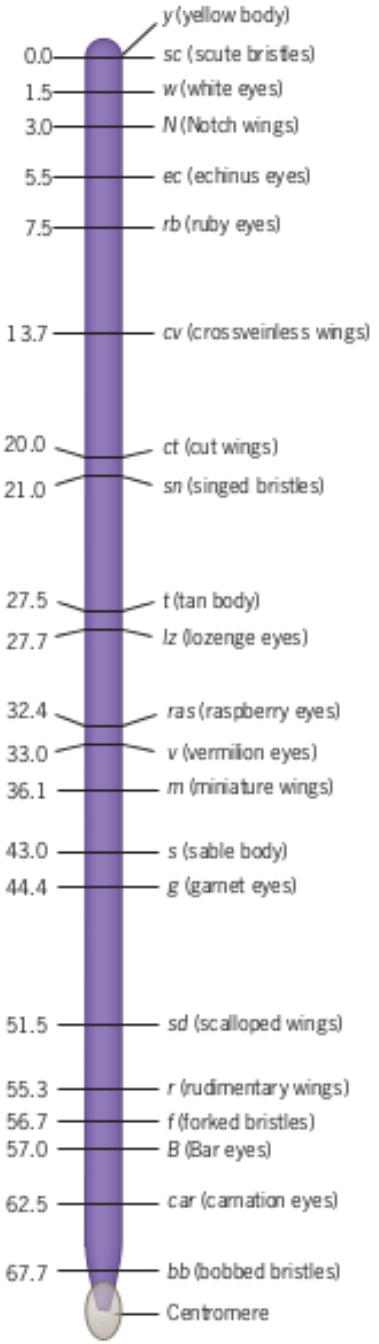
T. H. Morgan laid the foundation for these studies when he demonstrated that the gene for white eyes in Drosophila was located on the X chromosome.

Soon afterward Morgan's students showed that other genes were X-linked, and eventually they were able to locate each of these genes on a map of the chromosome. This map was a straight line, and each gene was situated at a
particular point, or locus, on it.

Sturtevant constructed the world's first chromosome map.

No microscope was powerful enough to see genes, nor was any measuring device accurate enough to obtain the distances between them.

Sturtevant did not use any sophisticated instruments in his work. Instead, he relied completely on the analysis of data from experimental crosses with Drosophila.



■ FIGURE 7.1 A map of genes on the X chromosome of *Drosophila melanogaster*.

Sturtevant based his mapping procedure on the principle that genes on the same chromosome should be inherited together.

Because such genes are physically attached to the same structure, they should travel as a unit through meiosis. This phenomenon is called **linkage**.

The early geneticists were unsure about the nature of linkage, but some of them, including Morgan and his students, thought that genes were attached to one another much like beads on a string. Thus, these researchers clearly had a linear model of chromosome organization in mind.

It was known that genes on the same chromosome could be separated as they went through meiosis and that new combinations of genes could be formed - the phenomenon is called **recombination.**

During meiosis, when homologous chromosomes paired, a physical exchange of material separated and recombined genes.

At the switch points, the two homologues were crossed over, as if each had been broken and then reattached to its partner.

A crossover point is called a **chiasma** (plural, **chiasmata**).

Early evidence for linkage and crossing over

The first evidence for linkage came from experiments performed by W. Bateson and R. C. Punnett.

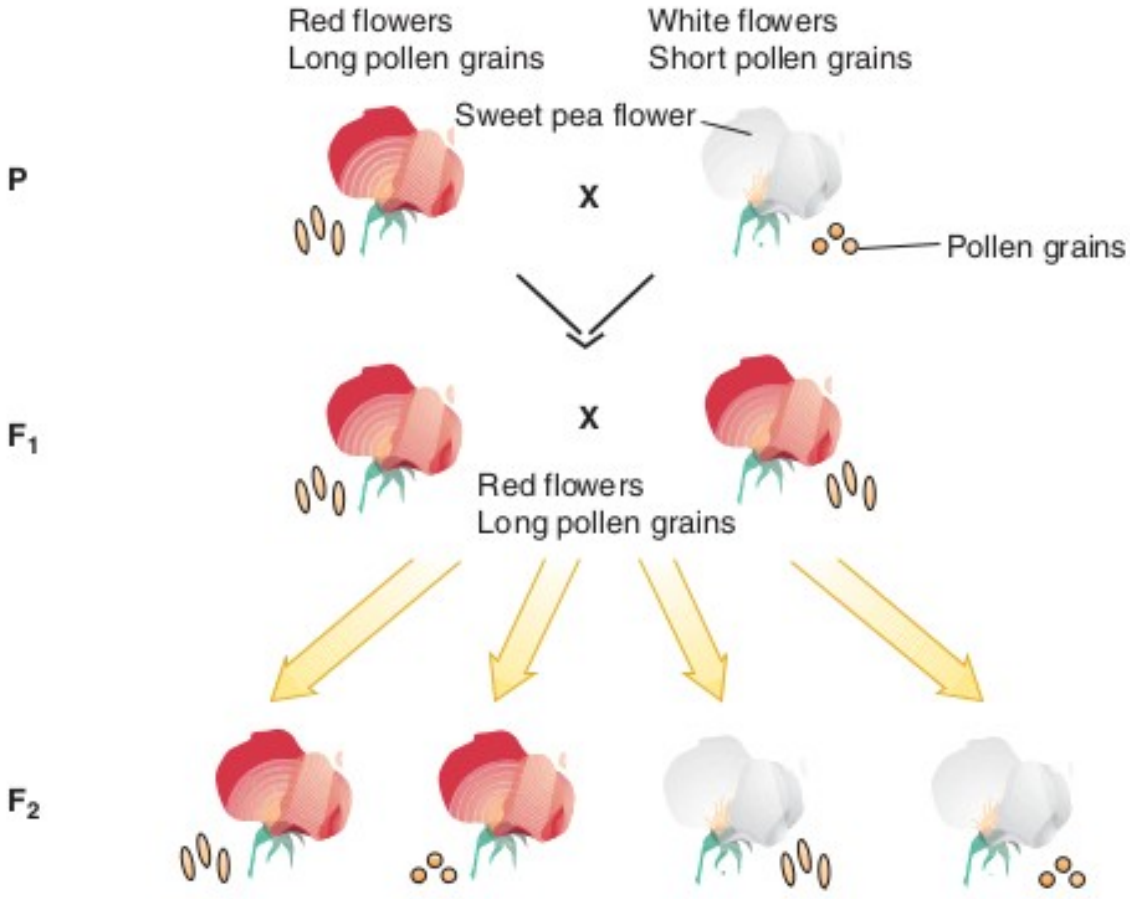
These researchers crossed varieties of sweet peas that differed in two traits, flower color and pollen length.

Plants with red flowers and long pollen grains were crossed to plants with white flowers and short pollen grains.

All the F1 plants had red flowers and long pollen grains, indicating that the alleles for these two phenotypes were dominant.

When the F1 plants were self-fertilized, instead of the 9:3:3:1 ratio expected for two independently assorting genes, they obtained a ratio of 24.3:1.1:1:7.1

They devised a complicated explanation for their results, but it turned out to be wrong. The correct explanation for the lack of independent assortment in the data is that the genes for flower color and pollen length are located on the same chromosome—that is, they are linked.



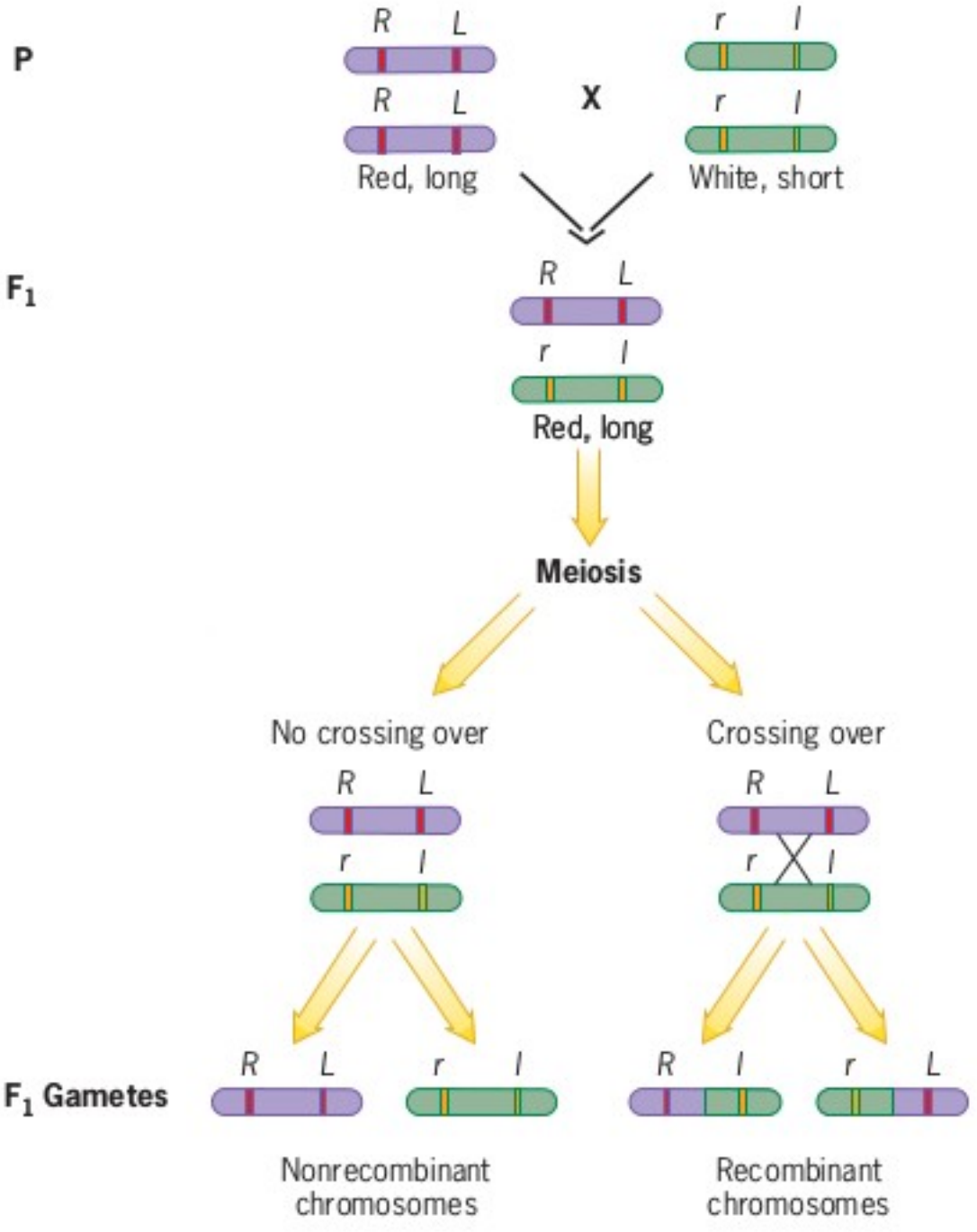
	Red flowers Long pollen grains (Parental)	Red flowers Short pollen grains (Nonparental)	White flowers Long pollen grains (Nonparental)	White flowers Short pollen grains (Parental)
Observed	583	26	24	170
Expected	451.6	150.6	150.6	50.2

$$\chi^2 = \sum \frac{(\text{Obs.} - \text{Exp.})^2}{\text{Exp.}} = 38.2 + 103.1 + 106.4 + 285.9$$

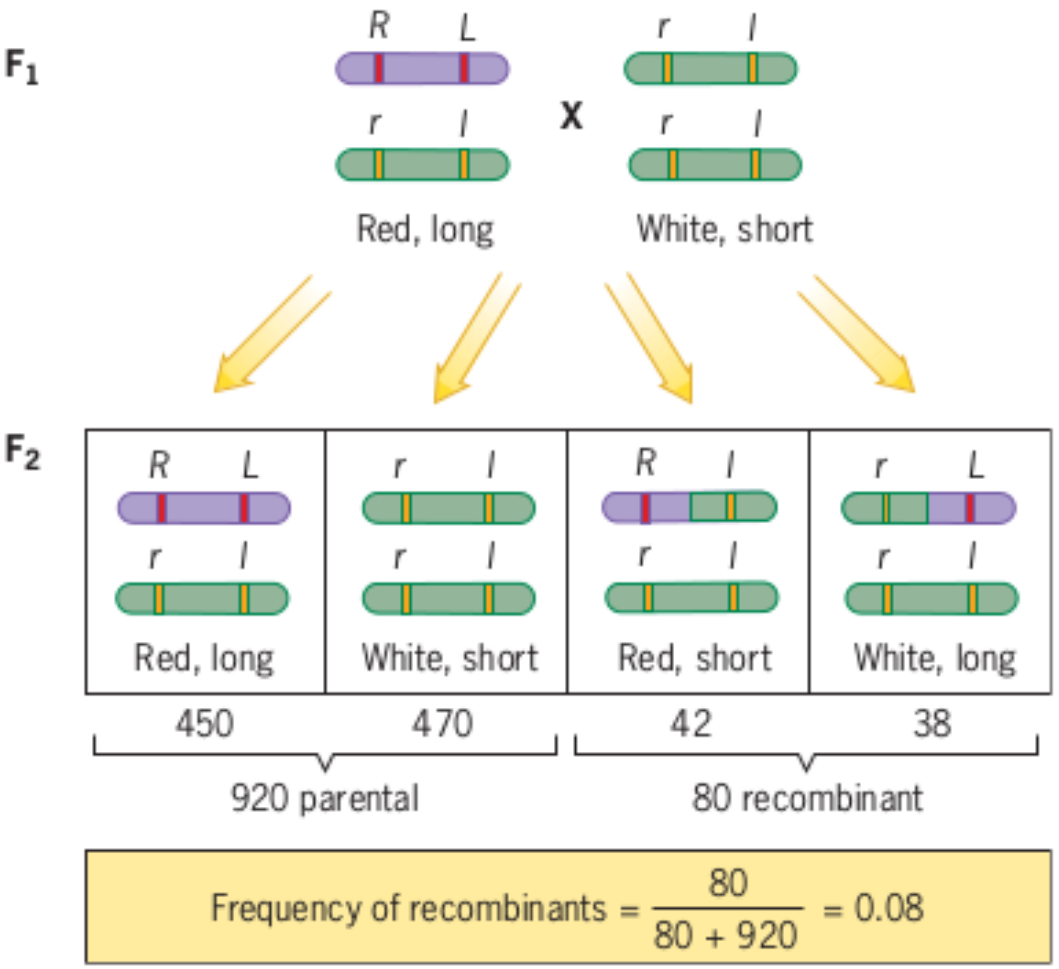
$$= 533.6$$

Hypothesis of linkage between the genes for flower color and pollen length in sweet peas.

In the F1 plants the two dominant alleles, R and L, of the genes are situated on the same chromosome; their recessive alleles, r and l, are situated on the homologous chromosome.



Bateson and Punnett might have come up with this explanation if they had performed a testcross instead of an intercross in the F1.



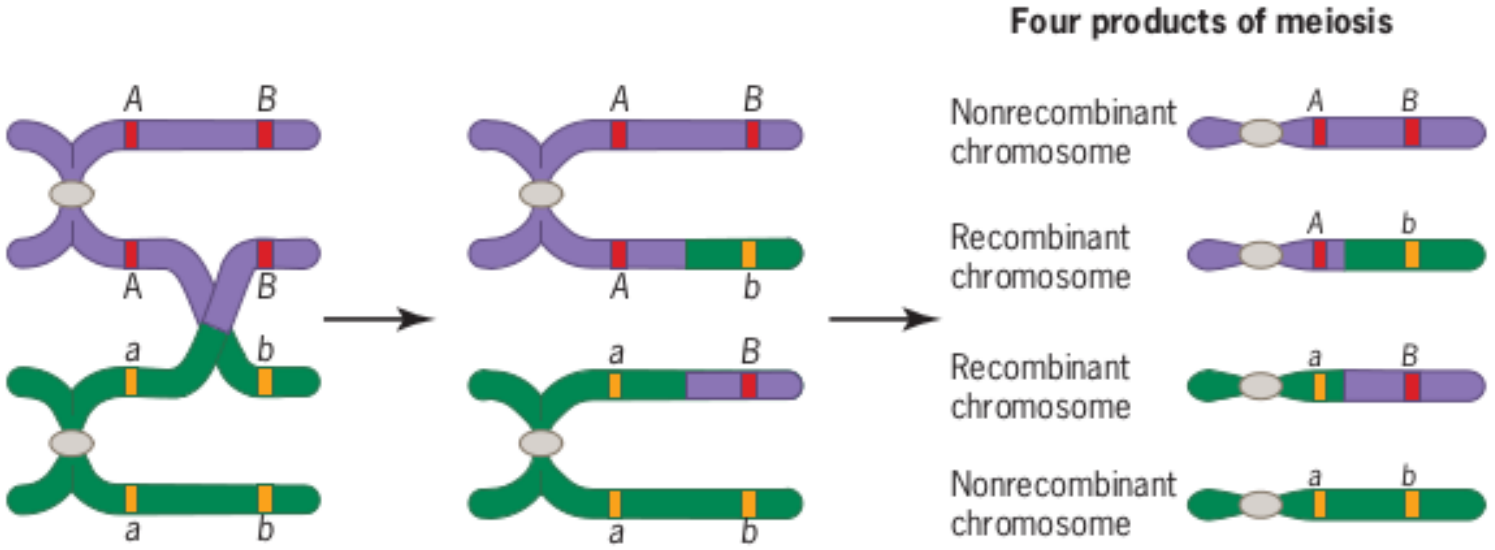
■ **FIGURE 7.4** A testcross for linkage between genes in sweet peas. Because the recombinant progeny in the F_2 are 8 percent of the total, the genes for flower color and pollen length are rather tightly linked.

Crossing over is the physical basis of recombination

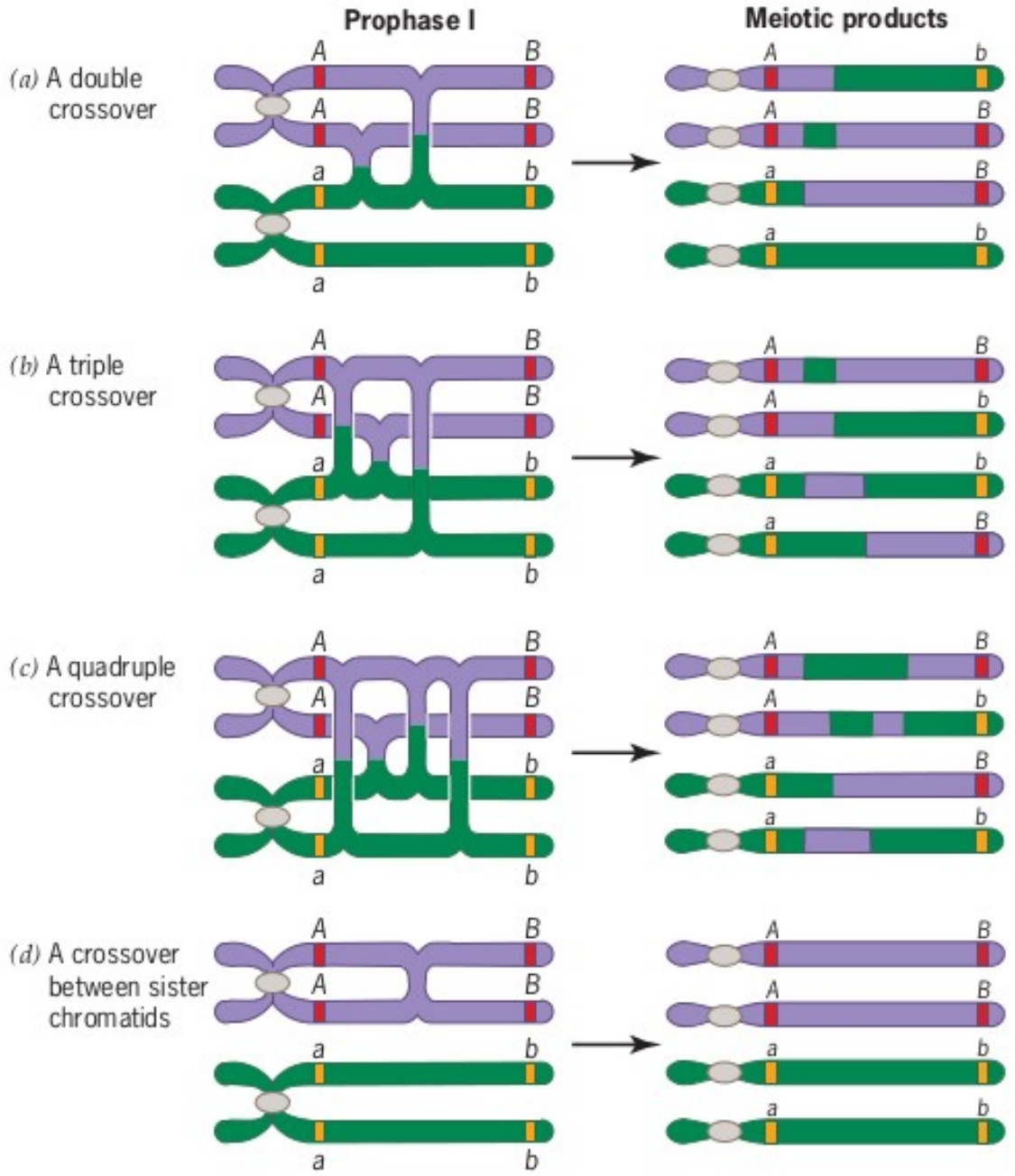
Recombinant gametes are produced as a result of crossing over between homologous chromosomes - involving a physical exchange between the chromosomes.

The exchange event occurs during the prophase of the first meiotic division, when duplicated chromosomes have paired.

Although four homologous chromatids are present, forming what is called a **tetrad**, only two chromatids cross over at any one point.



■ **FIGURE 7.6** Crossing over as the basis of recombination between genes. An exchange between paired chromosomes during meiosis produces recombinant chromosomes at the end of meiosis.



■ **FIGURE 7.7** Consequences of multiple exchanges between chromosomes and exchange between sister chromatids during prophase I of meiosis.

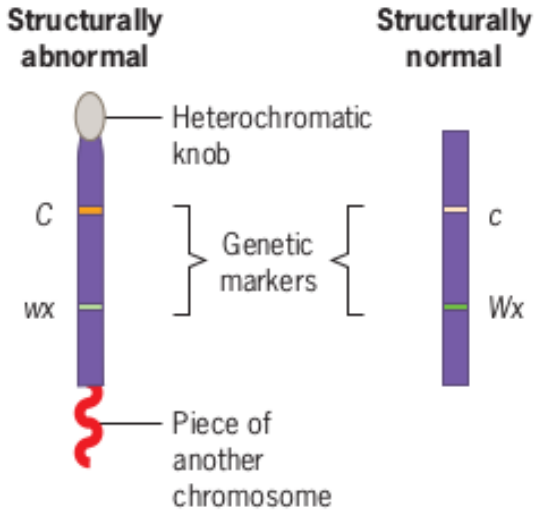
What is responsible for the breakage of chromatids during crossing over?

The breaks are caused by enzymes acting on the DNA within the chromatids.

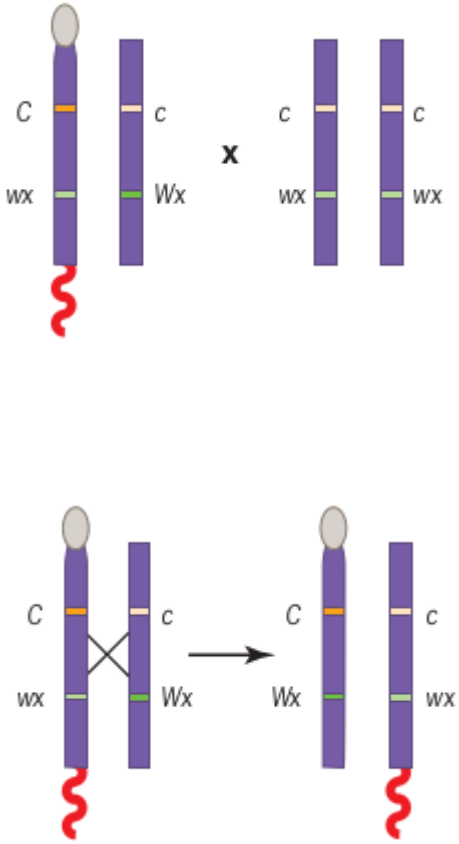
Enzymes are also responsible for repairing these breaks—that is, for reattaching chromatid fragments to each other.

Evidence that crossing over causes recombination

Harriet Creighton and Barbara McClintock (1931) obtained evidence that genetic recombination was associated with a material exchange between chromosomes.
They studied homologous chromosomes in maize that were morphologically distinguishable.



■ **FIGURE 7.8** Two forms of chromosome 9 in maize used in the experiments of Creighton and McClintock.



C – colored kernel, c – colorless
Wx – starchy kernel texture, wx- waxy

Chiasmata and the time of crossing over

The cytological evidence for crossing over can be seen during late prophase of the first meiotic division when the chiasmata become clearly visible.

At this time paired chromosomes repel each other slightly, maintaining close contact only at the centromere and at each chiasma.

This partial separation makes it possible to count the chiasmata accurately.

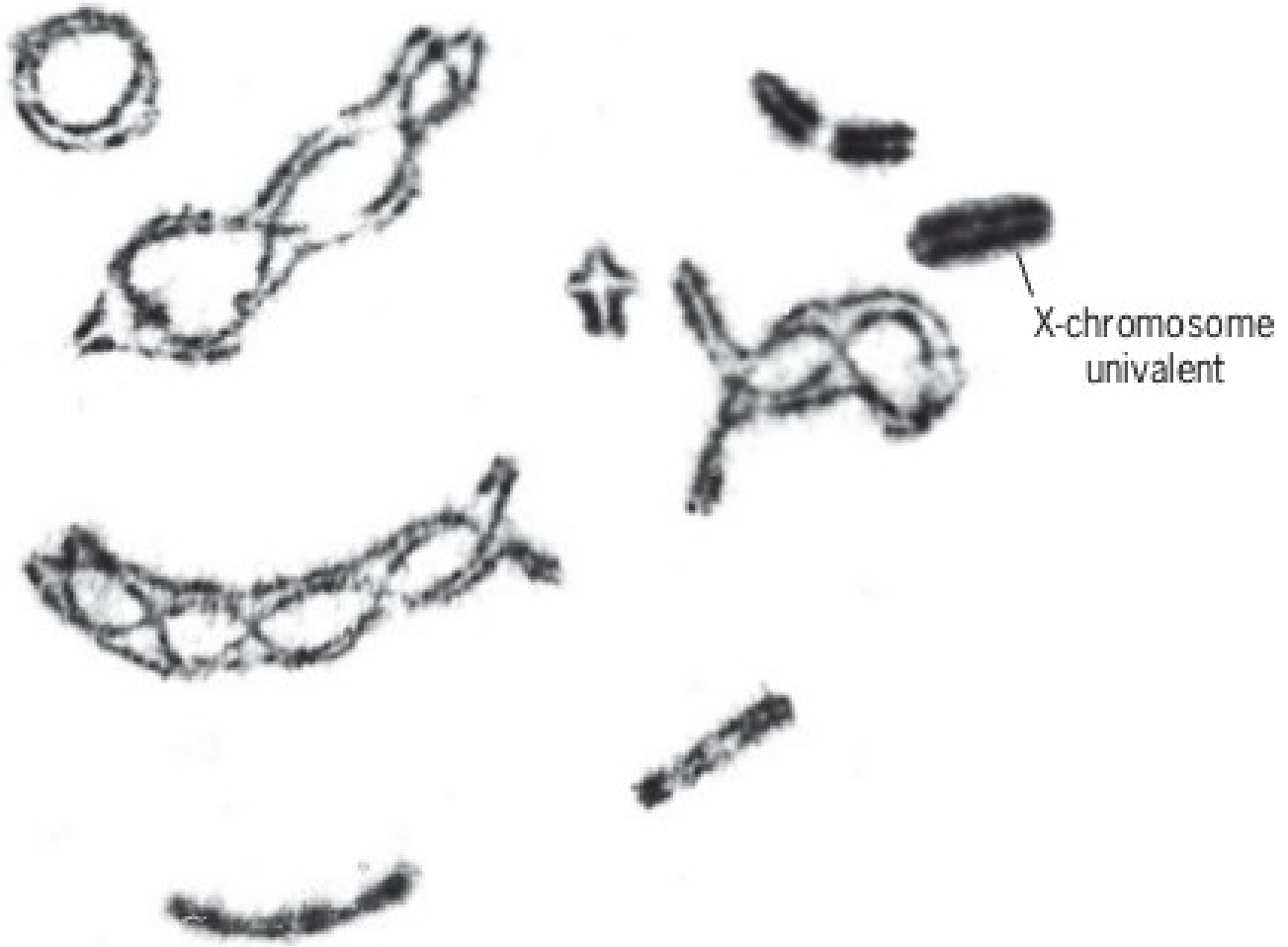
As we might expect, large chromosomes typically have more chiasmata than small chromosomes.

Thus, the number of chiasmata is roughly proportional to chromosome length.

Most geneticists believe that the chiasmata are merely vestiges of the actual exchange process.

Chromatids that have experienced an exchange probably remain entangled with each other during most of prophase.

Eventually, these entanglements are resolved, and the chromatids are separated by the meiotic spindle apparatus to opposite poles of the cell.



■ **FIGURE 7.9** Diplonema of male meiosis in the grasshopper *Chorthippus parallelus*. There are eight autosomal bivalents and an X-chromosome univalent. The four smaller bivalents each have one chiasma. The remaining bivalents have two to five chiasmata.

Why do these entanglements occur at all?

Many geneticists believe that the entanglements created by crossing over are a way of holding the members of a bivalent together during prophase I.

In some organisms, prophase I is protracted. In human females, for example, it may last as long as 40 years.

Without chiasmata, paired homologues might accidentally separate from each other during this long time, and homologues that have separated might not disjoin properly during the ensuing anaphase.

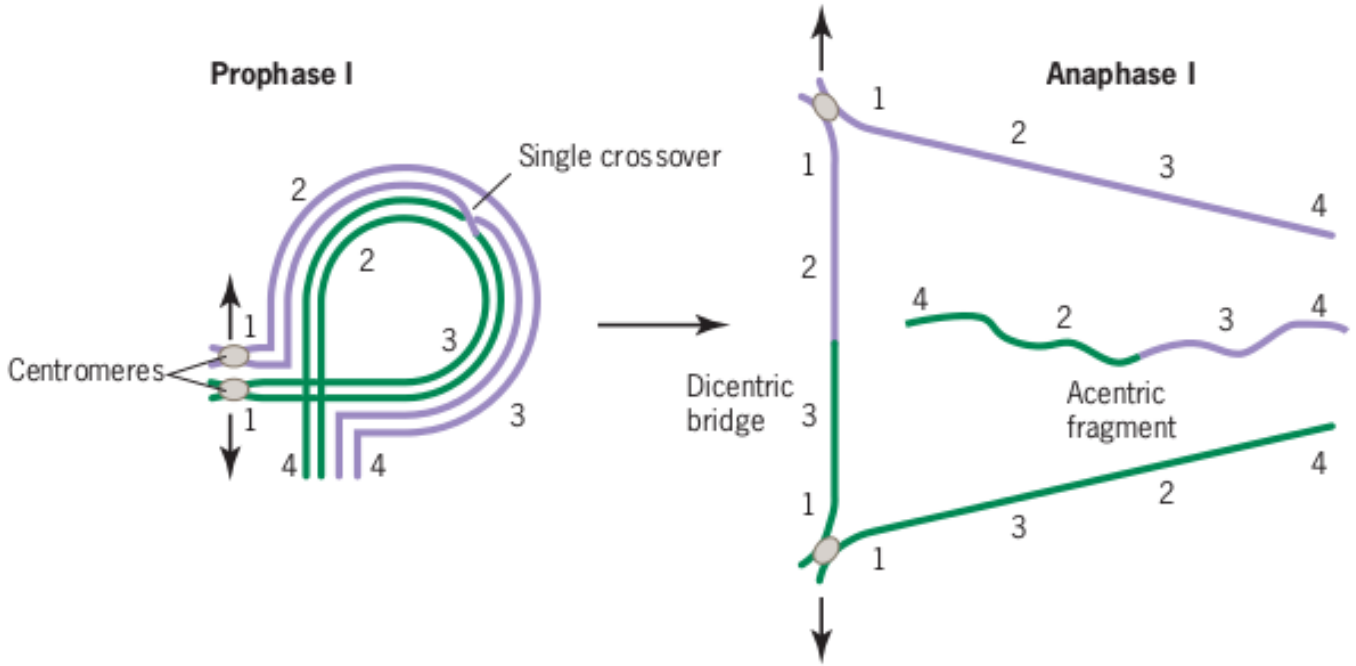
Faulty disjunction of the chromosomes during the first meiotic division would ultimately lead to aneuploid gametes.

Thus, chiasma formation appears to be a mechanism to hold paired homologues together so that when division does occur, the homologues are distributed appropriately to each of the daughter cells.

In this way, then, the possibility for nondisjunction is minimized, and aneuploidy in the gametes is largely prevented.

Suppression of recombination by inversions

In inversion heterozygotes the inhibition of crossing over that occurs near the breakpoints of the inversion is compounded by the selective loss of chromosomes that have undergone crossing over within the inverted region.



■ **FIGURE 7.23** Suppression of recombination in an inversion heterozygote. The dicentric (1 2 3 1) and acentric (4 3 2 4) chromosomes formed from the crossover chromatids are aneuploid and will cause inviability in the next generation. Consequently, the products of crossing over between the inverted and noninverted chromosomes are not recovered.

Evolutionary significance of recombination -

In evolutionary terms, recombination can allow favorable alleles of different genes to come together in the same organism.

It aso generates new combinations of alleles in the progeny thereby increasing genetic diversity.

Thank you

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