• Chromosomes are called linkage groups
  – They contain a group of genes that are linked together

• The number of linkage groups is the number of types of chromosomes of the species
  – For example, in humans
    • 22 autosomal linkage groups
    • An X chromosome linkage group
    • A Y chromosome linkage group

• Genes that are far apart on the same chromosome may independently assort from each other
  – This is due to crossing-over
Crossing Over May Produce Recombinant Phenotypes

- In diploid eukaryotic species, linkage can be altered during meiosis as a result of crossing over.

- Crossing over
  - Occurs during prophase I of meiosis at the bivalent stage.
  - Non-sister chromatids of homologous chromosomes exchange DNA segments.

Genetic maps allow us to estimate the relative distances between linked genes, based on the likelihood that a crossover will occur between them.

- Experimentally, the percentage of recombinant offspring is correlated with the distance between the two genes.
  - If the genes are far apart → many recombinant offspring.
  - If the genes are close → very few recombinant offspring.

- Map distance = \( \frac{\text{Number of recombinant offspring}}{\text{Total number of offspring}} \times 100 \)

- The units of distance are called map units (mu).
  - They are also referred to as centiMorgans (cM).

- One map unit is equivalent to 1% recombination frequency.
Trihybrid or 3-Point Crosses

• Data from trihybrid crosses yields information about map distance and gene order
  – Example, we will consider fruit flies that differ in body color, eye color and wing shape
    – $b$ = black body color
    – $b^+$ = gray body color
    – $pr$ = purple eye color
    – $pr^+$ = red eye color
    – $vg$ = vestigial wings
    – $vg^+$ = normal wings

• Analysis of the $F_2$ generation flies will allow us to map the three genes
  – The three genes exist as two alleles each
  – Therefore, there are $2^3 = 8$ possible combinations of offspring
  – If the genes assorted independently, all eight combinations would occur in equal proportions

• In the offspring of crosses involving linked genes,
  – Parental phenotypes occur most frequently
  – Double crossover phenotypes occur least frequently
  – Single crossover phenotypes occur with “intermediate” frequency
• The combination of traits in the double crossover tells us which gene is in the middle
  – A double crossover separates the gene in the middle from the other two genes at either end

<table>
<thead>
<tr>
<th>F₂ offspring</th>
<th>Observed number</th>
<th>Ratio</th>
<th>Expected number</th>
<th>Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Purple flowers, long pollen</td>
<td>296</td>
<td>15.6</td>
<td>240</td>
<td>9</td>
</tr>
<tr>
<td>Purple flowers, round pollen</td>
<td>19</td>
<td>1.0</td>
<td>80</td>
<td>3</td>
</tr>
<tr>
<td>Red flowers, long pollen</td>
<td>27</td>
<td>1.4</td>
<td>80</td>
<td>3</td>
</tr>
<tr>
<td>Red flowers, round pollen</td>
<td>85</td>
<td>4.5</td>
<td>27</td>
<td>1</td>
</tr>
</tbody>
</table>

• In the double crossover categories, the recessive purple eye color is separated from the other two recessive alleles
  – Thus, the gene for eye color lies between the genes for body color and wing shape
Which ones are the double crossover recombinants?

- **Calculate the map distance between pairs of genes**
  - To do this, one strategy is to regroup the data according to pairs of genes
    - From the parental generation, we know that the dominant alleles are linked, as are the recessive alleles
    - This allows us to group pairs of genes into parental and nonparental combinations
      - Parentals have a pair of dominant or a pair of recessive alleles
      - Nonparentals have one dominant and one recessive allele
    - The regrouped data will allow us to calculate the map distance between the two genes
3-Point Mapping

• vg-b recombinants are:
  – vg-b+
  – vg+-b

3-Point Mapping

• Now let's look at b-pr, recombinants?
  – b-pr+
  – b+-pr
3-Point Mapping

• Now let's look at vg-pr, recombinants?
  – vg-pr
  – vg+-pr
3-Point Mapping

• Now double check ourselves?
  12.3 + 6.4 = ?
  18.7

But 18.7 does not equal 17.7 why?

3-Point Mapping

• Didn’t include the double crossover events in your determination of vg and b:
  – A more accurate distance would be calculated using all numbers of recombinants
    • Need to count double crossover two times WHY?
      – Because in order to get all exchanges between vg and b then would occur twice
• When the distance between two genes is large
  – The likelihood of multiple crossovers increases
  – This causes the observed number of recombinant offspring to underestimate the distance between the two genes

Figure 5.11

Interference

• The product rule allows us to predict the likelihood of a double crossover from the individual probabilities of each single crossover

\[
P(\text{double crossover}) = P(\text{single crossover between } b \text{ and } pr) \times P(\text{single crossover between } pr \text{ and } vg)
\]

\[
= 0.064 \times 0.123 = 0.0079
\]

• Based on a total of 4,197 offspring
  – The expected number of double crossover offspring is

\[
= 4,197 \times 0.0079 = 33
\]
Interference

- Therefore, we would expect 33 offspring to be produced as a result of a double crossover.

- However, the observed number was only \((13+9)=22\)!
  - 9 with gray bodies, purple eyes, and normal wings
  - 13 with black body, red eyes, and vestigial wings

- This lower-than-expected value is due to a common genetic phenomenon, termed **positive interference**
  - The first crossover decreases the probability that a second crossover will occur nearby.

**Interference**

I = 1 – C
- where C is the coefficient of coincidence

\[
C = \frac{\text{Observed number of double crossovers}}{\text{Expected number of double crossovers}}
\]

\[
C = \frac{22}{33} = 0.67
\]

I = 1 – C = 1 – 0.67
= 0.33 or 33%
- This means that 33% or 1/3 of the expected number of crossovers did not occur.
• Since I is positive, this interference is positive interference.

• Rarely, the outcome of a testcross yields a negative value for interference:
  – Negative value would suggest that a first crossover enhances the rate of a second crossover.

• The molecular mechanisms that cause interference are not completely understood:
  – However, most organisms regulate the number of crossovers so that very few occur per chromosome.

---

**A 3-point cross**

\[ \frac{\text{P}}{\text{F}_1, \text{all identical}} \]

\[ \frac{\text{Test cross progeny}}{\text{Test cross}} \]

\[ \frac{125}{vg \ b \ pr} \]
\[ 135 \]
\[ 5 \]
\[ 7 \]
\[ 859 \]
\[ 775 \]
\[ 55 \]
\[ 65 \]
\[ 2017 \]