PowerPoint® Lecture Presentation for

Concepts of Genetics

Ninth Edition

Klug, Cummings, Spencer, Palladino

Chapter 5 Chromosome Mapping in Eukaryotes

Lectures by David Kass with contributions from John C. Osterman.

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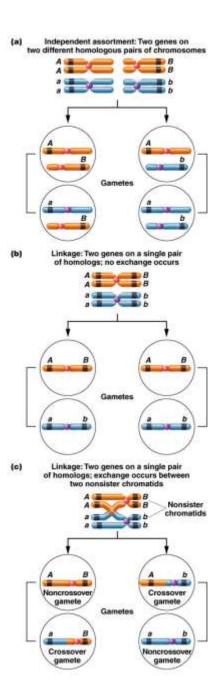
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5.1 Genes Linked on the Same Chromosome Segregate Together

 Genes assort independently if they are on different chromosomes but show linkage if they are on the same chromosome.

 If complete linkage exists between two genes because of their close proximity and organisms heterozygous at both loci are mated, a unique F₂ phenotypic ratio designated the linkage ratio results.

- In complete linkage, only parental (noncrossover) gametes are produced.
- If crossing over between two linked genes occurs between two nonsister chromatids, both parental and recombinant (crossover) gametes are produced (Figure 5.1).



Linkage Ratio

- Drosophila:
- heavy wing and brown eyes
- Normal alleles: hv+, bw+
- Cross thin, brown x heavy, red →
- all F1 are heterozygous
- normal
- F2 phenotypic ratio 1/4bw: 1/2wild: ¼ heavy

 The degree of crossing over between any two loci on a single chromosome is proportional to the distance between them, known as the interlocus distance.

- Genes on the same chromosome are part of a linkage group.
- The number of linkage groups should correspond to the haploid number of chromosomes.

5.2 Crossing Over Serves as the Basis of Determining the Distance between Genes in Chromosome Mapping

 The percentage of offspring resulting from recombinant gametes depends on the distance between the two genes on the chromosome.

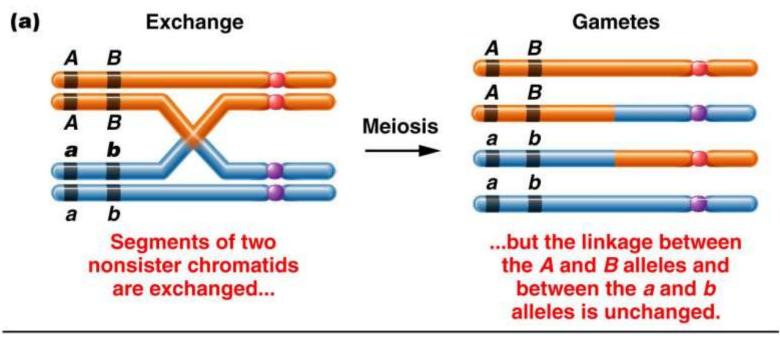
 Synapsed chromosomes in meiosis wrap around each other to create chiasmata that are points of genetic exchange.

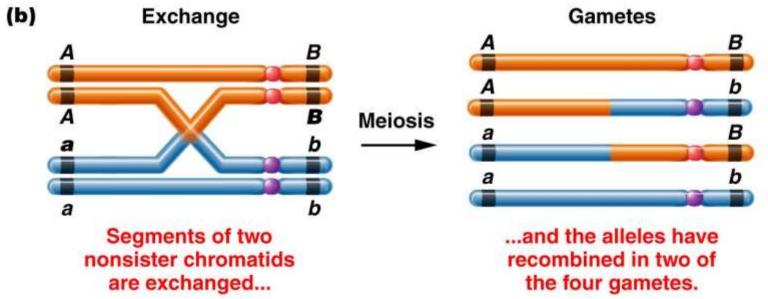
 Two genes located relatively close to each other along a chromosome are less likely to have a chiasma form between them, and it is less likely that crossing over will occur.

 The recombination frequencies between linked genes are additive, and the frequency of exchange is an estimate of the relative distance between two genes along the chromosome.

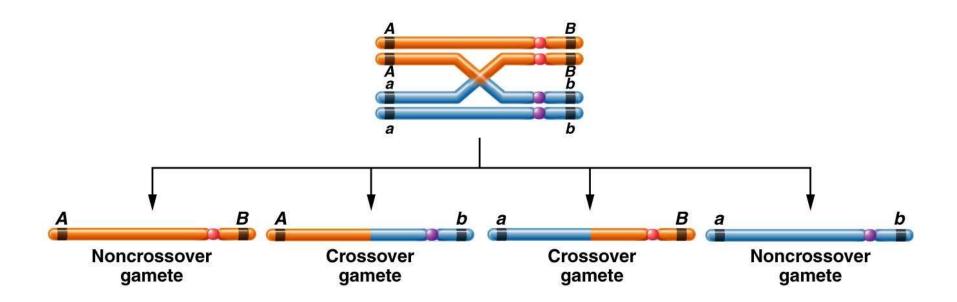
- One map unit (mu) is defined as 1 percent recombination between two genes on a chromosome.
- Map units are often called centimorgans (cM) and are relative distances, not exact ones.

 A single crossover (SCO) alters linkage between two genes only if the crossover occurs between those two genes (Figure 5.5).





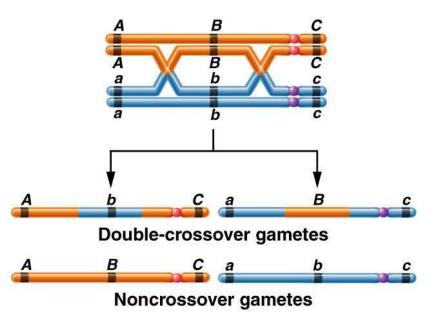
- The percentage of tetrads involved in an exchange between two genes is twice the percentage of recombinant gametes produced (Figure 5.6).
- When two linked genes are more than 50 map units apart, a crossover theoretically can be expected to occur between them in 100 percent of the tetrads.

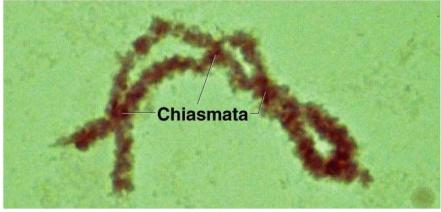


5.3 Determining the Gene Sequence during Mapping Requires the Analysis of Multiple Crossovers

 Single crossovers can be used to determine the distance between two linked genes, but double crossovers (DCOs) can be used to determine the order of three genes on the chromosome.

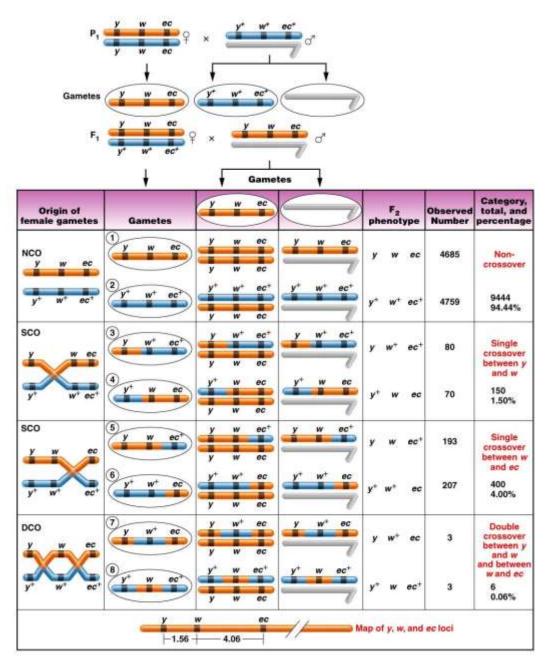
• To study double exchanges, three pairs of genes must be investigated, each heterozygous for two alleles (**Figure 5.7**).





 The expected frequency of doublecrossover gametes is much lower than that of either single-crossover gamete class.

- In three-point mapping, the parent must be heterozygous for all three genes under consideration.
- A three-point mapping cross is shown in Figure 5.8.



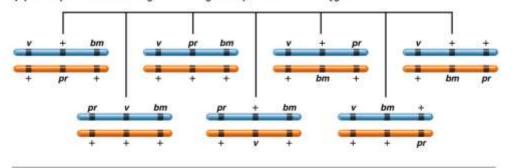
- The noncrossover F₂ phenotypes occur in the greatest proportion of offspring.
- The double-crossover phenotypes occur in the smallest proportion.

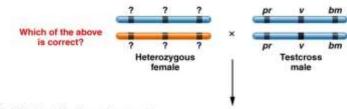
 Because the F₂ phenotypes complement each other (i.e., one is wild type and the other is mutant for all three genes), they are called **reciprocal classes** of phenotypes.

 The distance between two genes in a three-point cross is equal to the percentage of all detectable exchanges occurring between them and includes all single and double crossovers.

- There are two methods for determining gene order from a three-point cross.
- An example of a three-point cross and mapping of the three genes involved is shown in Figure 5.10 and Figure 5.11.

(a) Some possible allele arrangements and gene sequences in a heterozygous female





(b) Actual results of mapping cross*

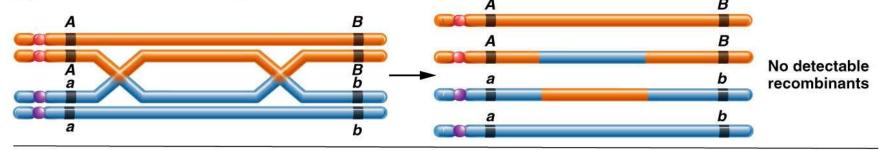
Phenotypes of offspring			Number	Total and percentage	Exchange classification	
+	v	bm	230	467	Noncrossover	
pr	+	+	237	42.1%	(NCO)	
+	+	bm	82	161	Single crossover (SCO)	
pr	v	+	79	14.5%		
+	v	+	200	395	Single crossover	
pr	+	bm	195	35.6%	(SCO)	
pr	v	bm	44	86	Double crossove	
+	+	+	42	7.8%	(DCO)	

^{*}The sequence pr - v - bm may or may not be correct.

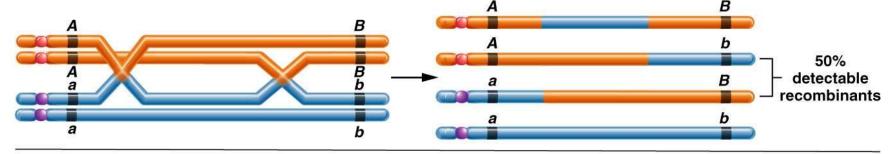
Possible allele arrangements and sequences				Explanation
(a) + pr	+	bm +	+ <i>v bm</i> and <i>pr</i> + +	Noncrossover phenotypes provide the basis for determining the correct arrangement of alleles on homologs
(b) +	v v	bm	+ + bm and pr v +	Expected double-crossover phenotypes if v is in the middle
(c) + pr	bm +	v v	+ + v and pr bm +	Expected double-crossover phenotypes if bm is in the middle
(d) v	, t	bm +	v pr bm and + + +	Expected double-crossover phenotypes if pr is in the middle (This is the actual situation.)
(e) _V	pr +	bm +	v pr + and + + bm	Given that (a) and (d) are correct, single- crossover phenotypes when exchange occurs between v and pr
(f) v	+ pr	bm	v + + and + pr bm	Given that (a) and (d) are correct, single- crossover phenotypes when exchange occurs between pr and bm
(g)	Final	v	pr	bm

- Two exchanges between linked genes that are far apart on a chromosome can involve two, three, or all four strands.
- They can result in production of different percentages of recombinant chromatids (Figure 5.12).

(a) Two-strand double exchange



(b) Three-strand double exchange



(c) Four-strand double exchange

