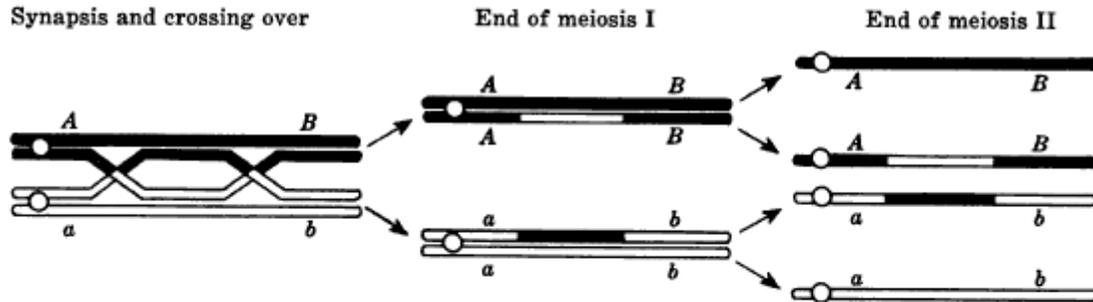


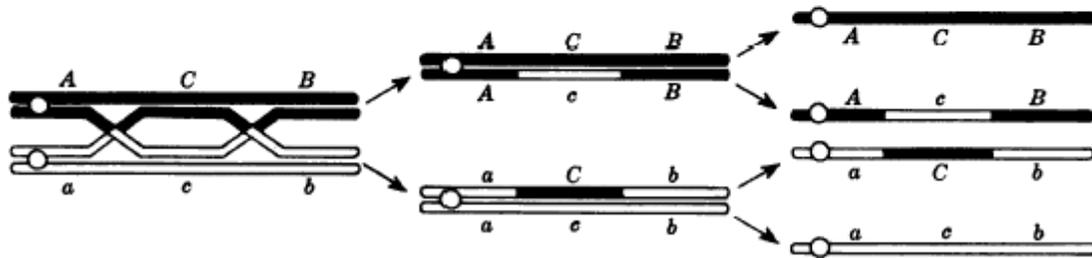
## Instructions for Solving Numericals

(a) Two-loci model

Synapsis and crossing over



(b) Three-loci model



**Fig. 6-2.** Multiple crossovers with two loci segregating (a) and three loci segregating (b).

- I All **linkage map distances** are calculated as the percentage recombination between two loci. This is reflected in the percentage of recombinant offspring.
  - A. If two genes are completely linked, all of the offspring will be **parental** (have the same linkage as the parents); there will be no **recombinant** offspring. Thus the linkage map distance between the two genes would be zero **LMU** (Linkage Map Units).
  - B. If the genes are on separate chromosomes (or are far enough apart that crossing over between them occurs in virtually all meioses), half of the offspring will be recombinant, the other half parental. Thus the distance between them would calculate as 50 LMU, and 50 LMU reflects **independence**.
  - C. Linkage Map Units are not additive, and there is no physical distance which is equal to one LMU.
    1. Locations of crossovers are not random; crossovers are repressed close to the centromere, and the presence of one crossover will repress a second one close by.
    2. Some crossover events are always missed because it is possible that multiple crossovers have occurred between the two points you are mapping; thus you will underestimate the total amount of recombination. The distance calculated between two genes will always be somewhat dependent upon how many interior points you are monitoring. (ie, you will calculate a greater distance between two genes

if you are doing a three point cross including a gene between the two in question than if you are doing a simply two point cross.

- II. Straightforward calculation of the percent recombination between two genes is called a **two point cross**.
  - A. To perform a mating cross, mate a parent who is heterozygous for both genes to one who is homozygous recessive for both genes. Thus the recombination in the offspring will reflect crossing over of only one parent, reducing the complexity of the problem.
  - B. X linked genes can be mapped by mating a female heterozygous for both genes in question to any male, then scoring only the male offspring, which will directly reflect what happens to the female's X chromosomes.
  - C. Establish linkage by determining that the results of the mating do not indicate independence.
  - D. Calculate the map distance between the two genes by calculating the percentage of the offspring which have recombined the two genes.

- III. Most useful linkage mapping is done with **three point crosses**, which involve mapping three genes relative to each other. The results of many three point crosses can be combined together to create an overall map of many genes.
  - A. Again, a useful mating for mapping would be between a parent heterozygous for all three genes and a homozygous recessive partner, or for X linked genes, between a triple heterozygous female and any male. Unless you have complete linkage, you will get eight phenotypic classes of offspring.
  - B. Confirm linkage by determining that the results of the cross do not meet expectations for independence.
  - C. Identify **parental** offspring and **double crossover** offspring. The most numerous offspring classes will be the parental classes. There should be two, and they should be **reciprocals**. The least numerous classes should be the double crossover classes (those that resulted from crossing over between **both** pairs of genes). Again, there should be two of these classes, and they should be reciprocals.
  - D. Determine **gene order** by determining which of the three genes is in the middle. This is done by comparing the parental and double crossover classes. Since the double crossovers crossed over between the first and second genes, then

- crossed **back** between the second and third genes, the only gene which is actually recombined is the middle one.
1. Select one parental class, then choose the double crossover class which is most like it. They should differ only in one gene. This is the middle gene.
  2. Examine the other parental and the other double crossover; they should give you the same result. See example.
- E. Rewrite all of your offspring phenotypic classes, putting the genes in the correct order. It doesn't matter which end gene you decide is the "first" gene, but you must get the correct one in the middle.
- F. You have four **single crossover** classes. Two of them resulted from crossing over between the first two genes; the other two from crossing over between the second and third genes. Figure out which of these are which, again by comparing them to the parental classes which are most like them. If a single crossover class differs from a parental class only in the first gene, then it represents a crossover between the first and second genes. If it differs only in the last gene, then it represents a crossover between the second and third genes. Again, you should have two pairs of reciprocal phenotypes. See example.
- G. Calculate the distance between the first two genes by calculating the percentage of your offspring that recombined those two genes. Remember that the double crossovers count as recombinants here.
- H. Calculate the distance between the second and third genes by calculating the percentage of your offspring that recombined those two genes. Again, the double crossovers count here.
- I. The distance between the end genes can be calculated simply by adding the two intervening distances.
- IV. Note that the distance you calculated between your end genes is different from the distance you would have calculated if you were simply doing a two point cross. You would have scored only the single crossovers as recombining the end genes; the double crossovers—each of which actually represents **two** crossovers between those end genes—would have been scored as parentals, since the end genes are still in the parental association.