LINKAGE AND CROSSING-OVER

During meiosis, a pair of synapsed chromosomes is made up of four chromatids, called a **tetrad**. The phenomenon of a **cross - over** occurs when homologous chromatids in the tetrad (one from each of the two parents) exchange segments of varying length during prophase. The point of crossover is known as a **chiasma** (pl. **chiasmata**). A tetrad typically has at least one chiasma along its length. Generally, the longer the chromosome, the greater the number of chiasmata. There are two theories on the physical nature of the process. The **classical theory** proposes that cross-over and formation of the chiasma occur first, followed by breakage and reunion with the reciprocal homologues. According to this theory, chiasma formation need not be accompanied by chromosome breakage. Alternatively, according to the **chiasmatype theory**, breakage occurs first, and the broken strands then reunite.

Linkage between loci is indicated when the recombinant phenotypes occur less frequently than the parental types. The frequency of crossing over (% recombination) between two loci is directly related to the physical distance between those two loci. Percent recombination in a test cross equals **map distance (1 map unit = 1 % recombination).**

EXAMPLE :

P1 **Ab//Ab** x **aB//aB** **(AAbb x aaBB)**

↓

F1 **Ab//aB** x ab//ab (test cross)

Gametes P+R Ab, aB , AB, ab x ab

F2: **Ab//ab** , **aB//ab** 90% - parental combinations

AB//ab, **ab//ab** 10% - recombinant

10% recombinant indicates that loci **a** and **b** are 10 map units apart.

Gene Map **a b = number of recombinant progeny / total number x 100**

= 10/100 x 100 = 10 m. u.

Three point test cross

Parental types have the maximum phenotypic frequencies, double crossovers have the lowest phenotypic frequencies, and the single crossovers have phenotypic

frequencies between these two classes. Suppose, ABC/abc are three linked genes located on two different chromosomes in F_1 of a cross between AABBCC and aabbcc parents.

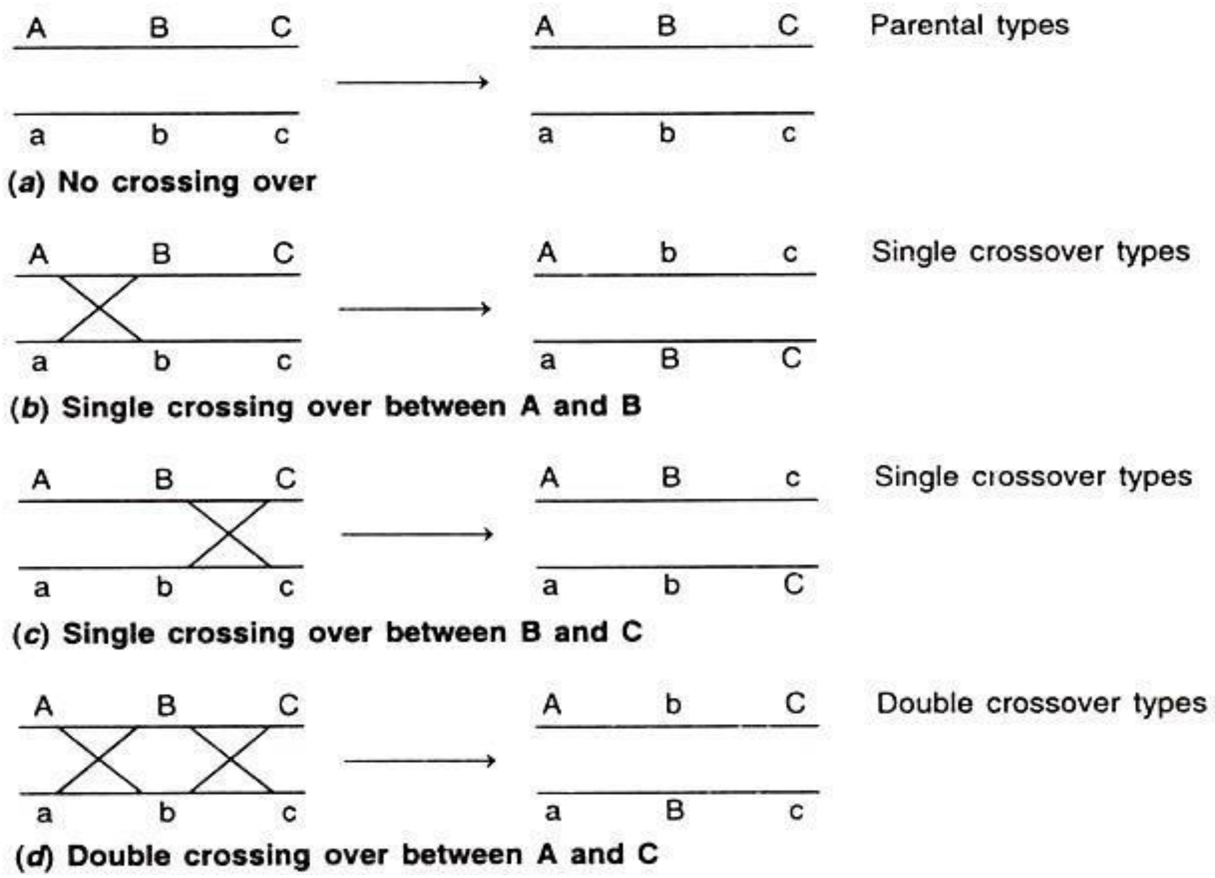


Fig. 9.3. Single and double crossing over between three linked genes.

If we consider three genes, (A), (B) and (C), the testcross tells us that the following offspring (reflecting the gametes produced) are

a B C	**580**		**aCB**
A b c	**592**		**Acb**
a b C	**45**		**aCb**
A B c	**40**	**The new**	**AcB**
a b c	**89**		**a c b**
A B C	**94**	→	**ACB**
a B c	**3**		**a c B**
A b C	**5**		**AC b**
total	**1448**		

Crossing over between A and B= 45+40+89+94=268

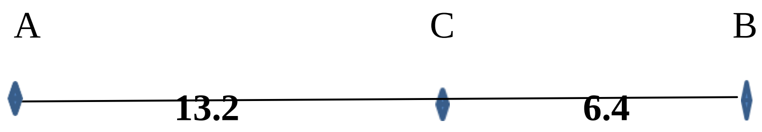
268/1448= 18.5%

Crossing over between B and C = 40+45+3+5 =93

93/1448 = 6.4%

Crossing over between A and C = 89+94+3+5=191

191/1448 = 13.2%



Note several important points here. First, we have deduced a different gene order from that of our listing of the progeny genotypes. Because the point of the exercise was to determine the linkage relation of these genes, the original listing was of necessity arbitrary; the order simply was not known before the data were analyzed.

The second point to note is that the two smaller map distances, 13.2 m.u. and 6.4 m.u., add up to 19.6 m.u., which is greater than 18.5 m.u., the distance calculated for *A* and *B* Why is this so? The answer to this question lies in the way in which we have analyzed the two rarest classes in our classification of recombination for the *A* and *B* loci. Now that we have the map, we can see that these two rare classes are in fact double recombinants, arising from two crossovers. However, we did not count the *a c B* and *A C b* genotypes when we calculated the RF value for *a* and *b*; after all, with regard to *a* and *b*, they are parental combinations (*a B* and *A b*). In the light of our map, however, we see that this led to an underestimate of the distance between the *v* and loci. Not only should we have counted the two rarest classes, we should have counted each of them twice because each represents a double recombinant class. Hence, we can correct the value by adding the numbers **45 + 40 + 89 + 94 + 3 + 3 + 5 + 5** = **284**. Of the total of 1448, this number is exactly **19.6** percent, which is identical with the sum of the two component values.

ANALYZING THE SYSTEM

To see how a system works, consider the system that is a single farm. The components of this system could be categorized in a number of ways. One choice would be to list them under the following headings:

• Animals (genotype)

• Physical environment

• Fixed resources and management

• Economics

The animal category contains the characteristic farm. On a dairy farm, for example, a typical genotype could be described genotype or genotypes—there may be more than one—of the animals on the as having small size, low feed intake, moderate yield, and high butterfat content. A contrasting genotype might have large size, high intake, high yield, and low butterfat.

Physical environment refers to those elements of the environment which out of humans control. Examples of physical environmental factors include weather, altitude, soils, and quality and quantity of native forages. For some production systems. physical environment is extremely important. Range cattle and sheep often exist under conditions. They must deal with the vagaries of the physical environment every day.

Fixed resources include things like the size of the farm, the ability of the farm to grow supplementary feeds.

Management involves all the policies implemented by the farmer. Some examples are level of supplementary feeding, health care, and the length of time animals remain on the farm.

Economics refers to the costs of farm inputs like feed, labor, and supplies, and the prices for farm outputs.