Mapping of Chromosomes

our discussion of linkage and crossing over has madeclear so far, that

1. Because the number of genesusually exceeds the number of chromosomes in different species, therefore, many genes have to be located on same chromosomes.

2. The genes remain arranged linearly on the chromosomes and they have no option before them, except to behave according to the chromosomes during gameto-genesis and inheritance, therefore, all the genes on a chromosome inherit together and are said to be linked with each other to form linkage groups.

3. The number of linkage groups corresponds to the number of homologous pairs of chromosomes or bivalents of the species.

4. The linked genes do not always remain linked, but, occasionally are departed from other members of their linkage groups by crossing over.

5. The closely linked genes have less chances of departure or frequency of crossing over than the widely located genes.

6. And each gene has definite order and location in a linkage group or chromosomes, as the crossing over frequency has been found constant for two given linked genes of a species.

CONSTRUCTION OF A GENETIC MAPPING

The method of construction maps of different chromosomes is called **genetic mapping**. The genetic mapping includes following processes :

1- Determination of Linkage Groups

Before starting the genetic mapping of the chromosomes of a species, one has to know the exact number of chromosomes of that species and then, he has to determine the total number of genes of that species by undergoing hybridization experiments in between wild and mutant strains.

By the same hybridization techniques, it can also be easily determined that how many phenotypic traits remain always together or linked and consequently their determiners or genes during the course of inheritance. And thus, the different linkage groups of a species can be worked out.

2. Determination of Map Distance

The intergene distance on the chromosomes cannot be measured in the customary units employed in light microscopy, geneticists use an arbitary unit to measure the **map unit**, to describe distances between linked genes.

A map unit is equal to 1 per cent of crossovers (recombinants); that is, it represents the linear distance along the chromosome for which a recombination frequency of 1 per cent is observed. These distances can also be expressed in **morgan units**; one morgan unit represents 100 per cent crossing over. Thus, 1 per cent crossing over can also be expressed as**1 centimorgan**(**1cM**), 10 per cent crossing-over as **1 decimorgan** and so on. The Morgan unit is named in honour of **T.H. Morgan**; however, most geneticists prefer map units.

Quite interestingly, it is now possible to calculate the size of many genes, as well as distances separating them, and to photograph genes in the electron microscope (see **Burns** and **Bottino**, 1989).

Examples

1. If a F 1 hybrid having the genotype Ab/aB produces 8% of cross over gametes AB and ab, then the distance between A and B is estimated to be 16 map units or centimorgan.
2. If the map distance between the gene loci B and C is 12 centimorgan, then 12% of gametes of genotype BC/bc should be crossover types, i.e., 6% bC.

Because, each chiasma produces 50% crossover products, 50 percent crossing over is equivalent to 50 map units or centimorgans. If the mean number of chiasmata is known for a chromosome pair, the total length of the map for that linkage group may be predicted :

Total length = mean number of chiasmata × 50

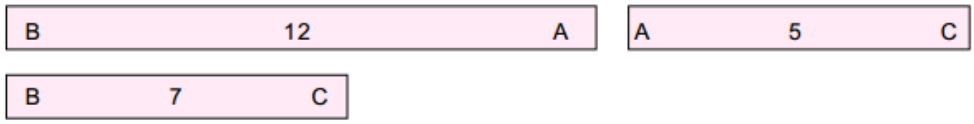
3. Determination of Gene Order

After determining the relative distances between the genes of a linkage group, it becomes easy to place genes in there proper linear order. For example, if the linear order of three genes ABC is to be determined, then these three genes may be in any one of three different orders depending upon that which gene is in the middle.

For the time being we may ignore left and right end alternatives. If double crossovers do not occur, map distances may be treated as completely additive units.

Now, if we suppose that the distance between the genes A–B = 12, B–C = 7 A–C = 5, we can determine the order of genes correctly in the following manner :

Case I. Let us assume that gene A is in the middle (e.g., B–A–C) :



In this case because, the distances between B–C are not equitable, genes A cannot be in the middle.

Linkage Maps of Different Organisms

By adopting the above mentioned techniques, geneticists have constructed the linkage or genetic maps of various organisms, such as, viruses, bacteria, fungi, tomato, barley, wheat, rice, sorghum, morning glory, garden pea, maize,Drosophila, chickens, mice, man etc. The first linkage map has been constructed for two chromosomes ofDrosophila by **Strutevant** in 1911. The linkage maps of other chromosomes ofDrosophila have been constructed by **C.B. Bridges**. The linkage or genetic mapping in maize has been done by **McClintock** under the leadership of**R.A. Emerson**.

Syntenic Genes

If two or more specific human gene products and a given human chromosome are both present in the same hybrid cells, then those genes are located in the same chromosome; that is, they are **syntenic**. The term **synteny** refers to genes that are located on the same chromosome, whether or not they show recombination; **linkage** refers only to genetic loci that have been shown by recombination studies to be in the same chromosome. Syntenic genes may be so far apart in their chromosome that they seem to segregate independently; that is, they may show as much as 50 per cent recombination as would be exhibited by non-syntenic genes.