GENETIC MAPPING / CHROMOSOME MAP

Genetic mapping, the linkage of the genes in a chromosome can be represented in the form of a genetic map or linkage map or chromosomal map. The first individual to construct a genetic map was Alfred Sturtevant. He used the frequency of crossing over between two genes to prepare the first genetic map of x-chromosome of Drosophila. There are two major aspects to genetic mapping — (1) The Determination of the linear order with which the genetic units are arranged with respect to one another (gene order) and (2) The Determination of the Relative distance between the genetic units (gene distance).

Because recombination tends to occur with increasing frequency as the distance between two specific gene loci increases, the percentage of recombination can be used to represent a measure of distance (map distance) between the two genes. The frequency of crossing over between two loci is directly related to the physical distance between the loci. One unit of map distance is equivalent to 1% crossing over or recombination. By analysing recombination frequencies among the progeny of parents that are heterozygous for a number of linked genes, a genetic map that places the genes in a linear array can be

constructed. ~~The distance b/w~~

$$\text{Map distance} = \frac{\text{No. of recombinant offspring} \times 100}{\text{Total no. of offspring}}$$

The unit of measurement for genetic linkage is known as a map unit or centi-Morgan (cM). One map unit is equal to 1 cM and 1 cM is equal to 1% recombination.

~~1 cM =~~

Two-Point Test Cross :

Example : Suppose two genes (A and B) are located on the same chromosome. An AABB individual is crossed two an aabb individual to produce AaBb offspring. The AaBb offsprings are then test crossed to aabb individuals. Let us assume this cross produces total 400 offsprings. Among these 325 offsprings are parental and 75 are recombinant.

Soln :

AABB × aabb

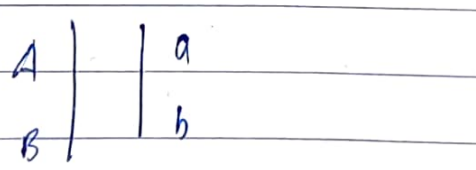
↓ A B

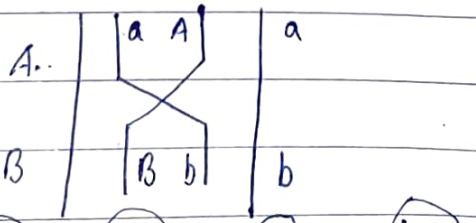
↓ a b

AaBb

AaBb × aabb

A B, A b, a B, a b (a b)





(A) (5)

Parental	AaBb	=	160
Recombinat	aaBb	=	39
Para "	Aabb	=	36
Parental	aabb	=	165

18.7
4 | 75
4
35
32
30

With the help of above data, we can calculate the recombination frequency and map distance in the following way —

$$\text{Map distance} = \frac{\text{No. of recombinant offspring}}{\text{Total no. offspring}} \times 100$$

$$= \frac{39 + 36}{160 + 39 + 36 + 165} \times 100$$

$$= \frac{75}{400} \times 100$$

$$= 18.8 \text{ cM}$$

The genes are approximately 18.8 cM apart

Genetic Map

$$a \xleftarrow{18.8} b$$

Q. In Drosophilla, cinnabar eye and vestigial wing are simple recessive traits. A female heterozygous for both genes was crossed with a male with cinnabar eyes and vestigial wings. The offspring resulting from these cross are listed in the table below.

Date :

Class	Phenotype	Number
I	Wild type eye, Wild type wing	455
II	Cinnabar eye, Wild Type wing	51
III	Wild type eye, Vestigial wing	49
iv	Cinnabar eye, Vestigial wing	455

On the basis of above data answer the following questions —

(i) Classes of recombinant phenotypes.

(ii) The distance between the cinnabar eye and vestigial wing genes.

Soln:- (ii)

$$\text{Map distance} = \frac{\text{No. of recombinant offspring}}{\text{Total no. of offspring}} \times 100$$

$$= \frac{51 + 49}{455 + 51 + 49 + 455} \times 100$$

$$= \frac{100}{1010} \times 1000$$

$$= \frac{1000}{101}$$

$$= 9.9 \text{ cM}$$

The genes are approximately 9.9 cm apart.

Genetic map = $a \xleftrightarrow{9.9\text{ cM}} b$

Three point test cross :

An individual heterozygous for three genes, A/a. B/b. C/c are test crossed to a/a. b/b. c/c and 1000 progeny are classified by the gametic contribution of the heterozygous parent as follows –

aBC	–	42	Single cross over type
Abc	–	43	
ABC	–	140	
abc	–	145	
aBc	–	6	Double cross over type
AbC	–	9	
ABc	–	305	Parental gametes
abC	–	310	

Draw a linkage map of the linked genes, showing the order and the distance in map units.

Soln: According to the data, given in the question, ABc and abC are parental types (most frequent) and aBc and AbC are double recombinant types (least frequent). The gene order can be determine either by the map distances or by comparing double recombinants with the parentals. The gene order BAc. Now, we can rewrite the progeny this time putting the genes in the proper order, and classify the progeny.

~~BaC~~ BaC - 42
bAC - 43
BAC - 140
bac - 145
Bac - 6
bAC - 9
BAc - 305
baC - 310

To construct the map of these genes, we can use the following formulae,

Distance betⁿ two genes = $\frac{\text{No. of single cross over} + \text{No. of double cross over} \times 4}{\text{Total no. of progeny}}$

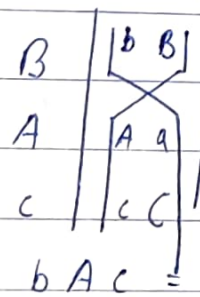
For A to B distance

$= \frac{42 + 43 + \ldots 6 + 9 \times 4}{42 + 43 + 140 + 145 + 6 + 9 + 305 + 310}$

$= \frac{100}{1000} \times 100$

$= 10$ cM ✱

Single cross over betⁿ A & B

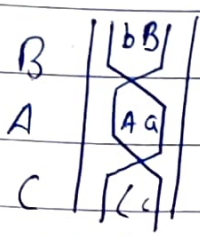


bAc = 43
Bac = 42

Single CO betⁿ A & C

BAC = 140
bac = 145

Double CO



bAC = 9
Bac = 6

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Date :

For A to C distance = $\frac{140 + 145 + 6 + 9}{1000} \times 100$

$= \frac{300}{1000} \times 100$

$= 30$ cM

Genetic map = $\underset{B}{\overset{\leftarrow 30\,cM \rightarrow}{\quad}} \underset{A}{\overset{\leftarrow 30\,cM \rightarrow}{\quad}} \underset{C}{\quad}$