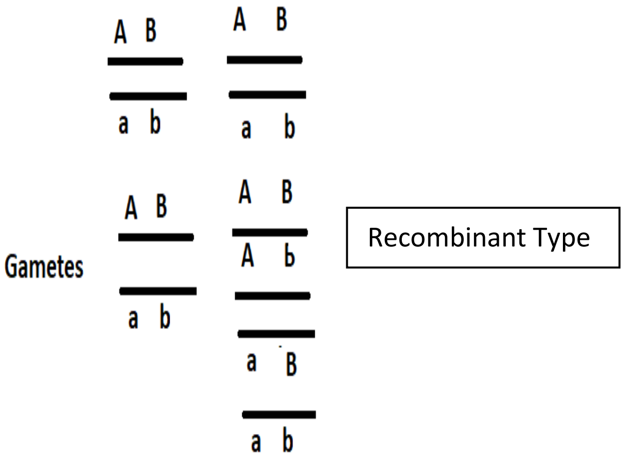
Gene Mapping

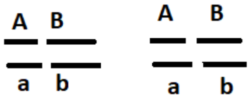
K.K.Gupta (www.dgen1996.wordpress.com)

Introduction

Genes are the hereditary unit located on the chromosomes .They are linearly arranged and together forms a linkage group. Location of genes on a chromosome decides the fate of inheritance. If the genetic distance are less , the two gene or group of genes are inherited together, and large distance in between the genes allow the inheritance in to different gametes as a consequence of gene exchange or crossing over (genetic Recombination) that occurs at pachytene stage of prophase I of Meiotic I during the gamete formation. Shown below is the formation of types of gametes in linkage and crossing over condition . Only parental type of gametes are produced in linkage while both parental and recombinant type are produced in crossing over condition. In Mendel's dihybrid cross the recombinant is due to independent assortment and not by crossing over. And does not produce the ratio of 9:3:3:1



Independent assortment



Gametes	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AaBb
Ab	AABb	AAbb	AaBb	Aabb
aB	AaBB	AaBb	aaBB	aaBb
ab	AaBb	Aabb	aaBb	aabb

F2 progenies
9:3:3:1

it will produce a ratio of 1:1:1:1 in F2 Ratio due to complete linkage

Gene mapping is a method to find out the

- Location of genes on the chromosomes
- Genetic distance between the two genes on chromosomes
- Order of genes on the chromosomes

The linkage map involves the mapping of linked gene . If the two geneare linked it shows linkage by inheriting two genes together and if at distance then forms recombinant by undergoing crossing over. The genetic distance is calculated by counting the number of recombinant phenotypes . It varies with respect to number of genes involved in the cross

i. Two point cross –for two genes
ii. Three point cross for three genes

Gene mapping by two point cross

A cross involving two loci is called two point cross. The mapping by this method can be understood in the following example using the cross over products in between the two autosomal linked gene vestigeal (Vg)i.e short wing and black body (b) i.e black body colour. The wild flies has normal long wing and brown body colour . A cross between the wild and mutant for these genes produces following no. of parental and recombinant after test cross. . Their recombination frequency will be calculated to find the distance .

Recomination frequency = No. of recombinant /total no. of progenies produced

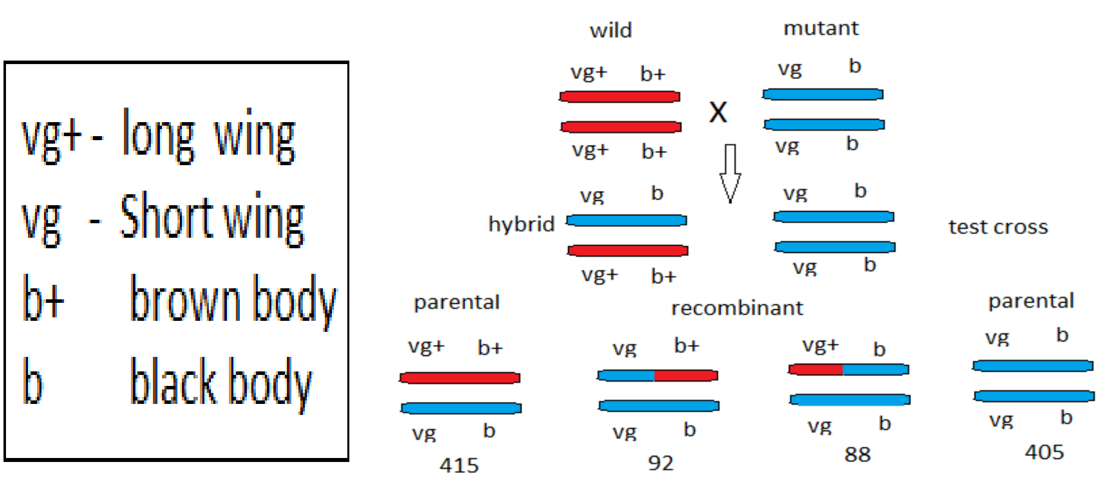
$$= \frac{92+88}{1000} = 0.18$$

Genetic distance = Vg 0.18 b

Average no .of cross over = Non recombinant (no cross over point) + recombinant (Cross over point)

= (0)X 0.82 + (1) X 0.18 =0.18

Average Cross Over indicates genetic distance



Recombinant frequency = 92+88/415+ 405+92+88

= 180/1000=0.18 morgan oe 0.18X100=18 centi morgan

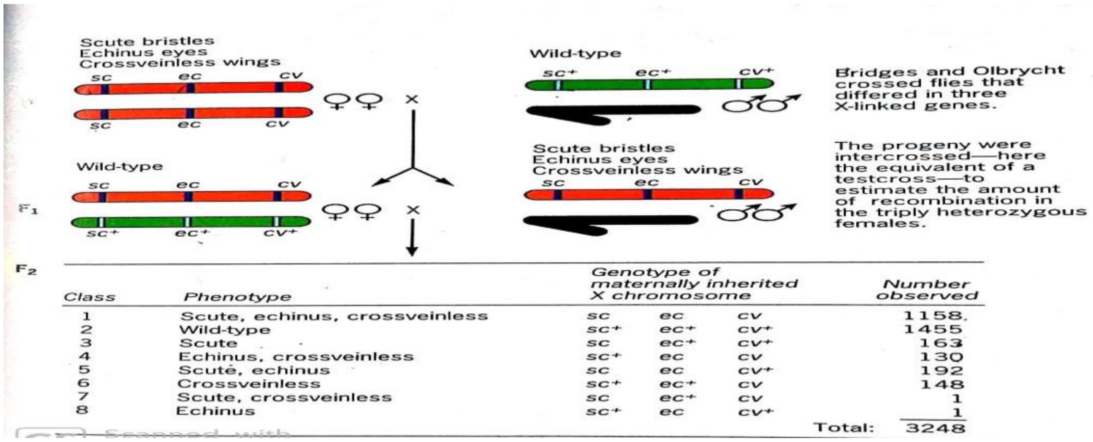
Thus Vg and b are separated by 18 units or 18 Centi Morgan or 0.18Morgan .

Recombination between three point cross

Bridge and Olbrycht studied the three point cross in similar way by crossing the wild type male with female homozygous for three recessive X linked genes

sc - scute bristles ; ec- echinus eye and cv- cross veinless wings

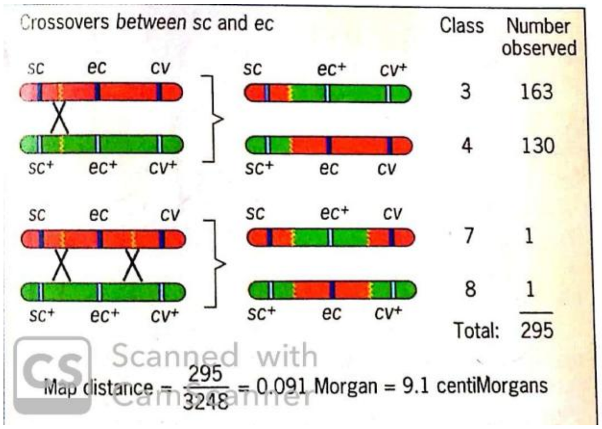
The F2 flies after test cross were counted phenotypically

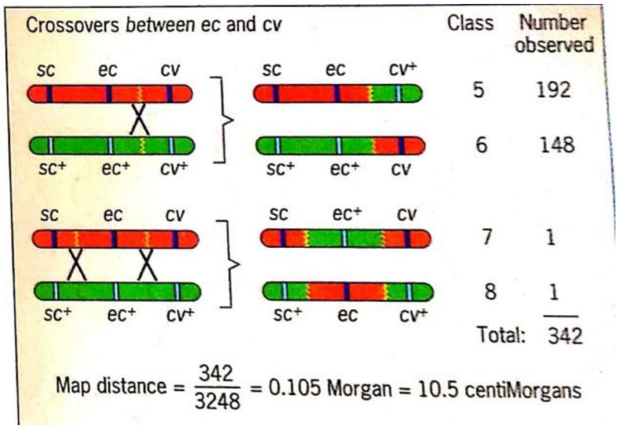


Bridges and Olbrycht crossed flies that differed in three X-linked genes.

The progeny were intercrossed—here the equivalent of a testcross—to estimate the amount of recombination in the triply heterozygous females.

Class	Phenotype	Genotype of maternally inherited X chromosome			Number observed
1	Scute, echinus, crossveinless	sc	ec	cv	1158
2	Wild-type	sc+	ec+	cv+	1455
3	Scute	sc	ec+	cv+	163
4	Echinus, crossveinless	sc+	ec	cv	130
5	Scute, echinus	sc	ec	cv+	192
6	Crossveinless	sc+	ec+	cv	148
7	Scute, crossveinless	sc	ec+	cv	1
8	Echinus	sc+	ec	cv+	1
				Total:	3248





There is doubt in the gene order in between the three gene . This can be sorted out by observing the double cross product In this case the rarely produced double cross number is one and by comparing it with parental cross (Max number) one can found that this product is only possible ec is in centre with sc & cv on the either side .

The genetic distance between sc & ec = <u>(SCO +DCO)</u> = <u>(163+130)+ (2)</u>
Total 3248
= 295/3248= 0.091 CM

Genetic Distance between ec & cv = <u>(SCO +DCO)</u> = <u>(192+148)+ (2)</u>
Total 3248
= 342/3248= 0.105 CM

So the c omplete Map after calculating recombinant frequency using the formula s mentioned , the Map is

Sc 9.1 ec 10.5` cv

Map distance are additive .so one can verify the result by directly counting and adding the cross over product as given below.

Non Cross Over + single cross over + double cross over

(1&2) (3, 4, 5, & 6) (7 & 8)

(0) X 0.805 (1) X 0.195 (2) X 0.0006 =0.196

The order of the genes are determined by observing the double cross phenotype.In the above double cross result the middle gene is ec ,therefore the two genes are on the either side . The order will be **sc ec cv** or **cv ec sc** .

A three point cross has advantage over two point cross . It demonstrates that whether the exchange between the two genes are independent of each other or either one is inhibiting the other to occur for exchange. The phenomenon by which one cross over inhibits the other is called **interference** .which can be measured by calculating the coefficient of coincidence given by :-

Coefficient of coincidence = <u>observed frequency of double cross over</u>
Expected frequency of double cross over

If the two cross over is independent then the expected frequency is multiple product of the frequency of two cross overs i.e 0.091 X 0.105 = 0.0095 and observed frequency of double cross is number of double cross over divided by total i.e 2/3248 =0.0006

Therefore coefficient of incidence = <u>0.0006</u> = 0.063
0.0095

The level of interference (I) is 1-0.063 =0.937

It means the coefficient of incidence is nearer to zero and interference is close to 1 , therefore interference is strong the chance of two cross over to occur independent is less.

Viewers : Please post ur comments