

LINKAGE - TYPES OF LINKAGE AND ESTIMATION OF LINKAGE.

LINKAGE

Every individual organism bears several heritable characters which are represented by the innumerable genes present on the chromosomes. During meiosis, the chromosomes move into the gametes as units, all the genes present on any given chromosome will segregate as a group and move together from generation to generation. This tendency of the genes located on the same chromosome, to stay together in hereditary transmission, is known as linkage. The genes located on the same chromosome are called linked genes.

The principle of linkage was discovered by Bateson and Punnett in 1906 in the sweet pea, plant, *Lathyrus odoratus*. However, linkage, as a concept was put forth by Thomas Hunt Morgan in 1910 based on his experiment on *Drosophila melanogaster*.

Chromosome Theory of Linkage

Morgan, along with Castle formulated the chromosome theory of linkage. It has the following postulates;

1. Genes are found arranged in a linear manner in the chromosomes.
2. Genes which exhibit linkage are located on the same chromosome.
3. Genes generally tend to stay in parental combination, except in cases of crossing over.
4. The distance between linked genes in a chromosome determines the strength of linkage. Genes located close to each other show stronger linkage than that are located far from each other, since the former are less likely to enter into crossing over.

Linkage Groups

All the genes located on a particular chromosome, form a linkage group. Since, the genes present on a particular chromosome have their alleles located on its homologous chromosome, genes on a pair of homologous chromosomes. Hence, the number of linkage groups corresponds to the number of haploid chromosomes found in a species.

Drosophila melanogaster has four linkage groups which can be distinguished into three large and one small linkage groups corresponding to the four pairs of

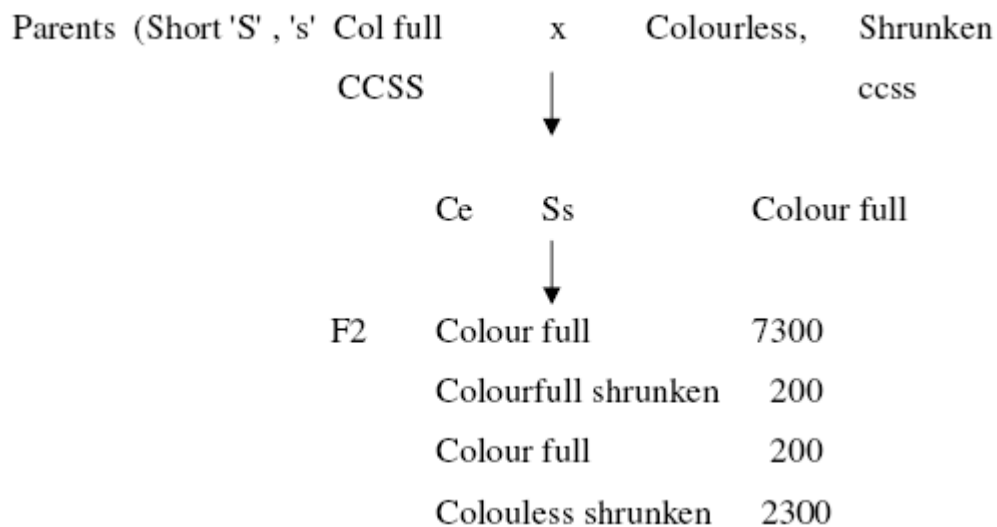
chromosomes. Twenty-three linkage groups are present in humans corresponding to 23 pairs of chromosomes.

Pea plant has seven linkage groups, corresponding to the seven pairs of chromosomes.

Linkage in maize

'C' for coloured aleurone is dominant over 'c' colourless

Sh for Full endosperm is dominant over 'sh' shrunken.



F2 did not show 9: 3: 3: 1 ratio. There were greater number of colour full, colour shrunken (parental types) than colourfull shrunken , colour full, If two character considered separately,they segregate 3 : 1

i.e . Colour - 7500

Full - 7500

Colouless - 2500

Shrunken - 2500

The large deviation of the observed F2 population form the excepted segregation is therefore not because the members of each pair of alleles do not segregate from each other but because of the separation in one pair of alleles is not independent of the separation in the other pair of alleles.

Test cross

	Colour full	x	Colourless shrunken
	CCSS		eess
F1		CeSs	x eess
F2	F2	Colour full	4800
		Col. Shrunken	200
		Col. Less full	200
		Col less shrunken	4800

The data show that, the two pairs of genes have not assorted independently.

Segregation of two pairs of genes on two pairs of chromosomes

Let us suppose that, gene 'C' is located on chromosome number 9 and 'S' on chromosome number 10 of maize. The segregation of chromosome bearing C and c is entirely independent of segregation of chromosome bearing S and s. So four types of gametes Cs, Cs, eS, eS are formed in F1 and F2 normal dihybrid ratio 9:3:3:1 and test cross 1:1:1:1

Segregation for two pairs of genes on one pair of chromosomes

Let us suppose that, two genes C and S are located on chromosome No. 9 during meiosis only 2 gametes will be formed Cs and cs gametes. So, Genes C and S situated on same chromosomes are said to be linked. Linkage is the association of character in inheritance due to fact that genes determining them are physically located on the same chromosomes.

Detection of Linkage

Compare the number of individuals observed in each class with those expected on the basis of independent assortment and then to test the deviation between these two values by chi-square test.

Linkage Group



Linkage studies revealed the following

1. Genes that assort at random are non linked genes. Genes that do not segregate at random are linked genes.
2. Linked genes are arranged in a lines fashion on the chromosome. Each linked gene has a definite and constant order in its arrangement.
3. The distance between the linked genes determines the degree of strength of linkage. Closely located genes show stronger linkage that the widely located genes.
4. Linked genes do not always stay together, but are often exchanged reciprocally by cross over.

Complete Linkage

The genes closely located in the chromosome show complete linkage as they have no chance of separating by crossing over and are always transmitted together to the same gamete and the same offspring. Thus, the parental combination of traits is inherited as such by the young one.

Incomplete Linkage

The genes distantly located in the chromosome show incomplete linkage because they have a chance of separation by crossing over and of going into different gametes and offspring.

Importance of linkage in breeding

When there is a close linkage between desirable and undesirable characters these genes are inherited in blocks and not individually and recombination is practically nil. In such cases linkage has to be broken by ' irradiation'.

Linked Genes on the Same Chromosome Exhibit Distorted Mendelian Ratios

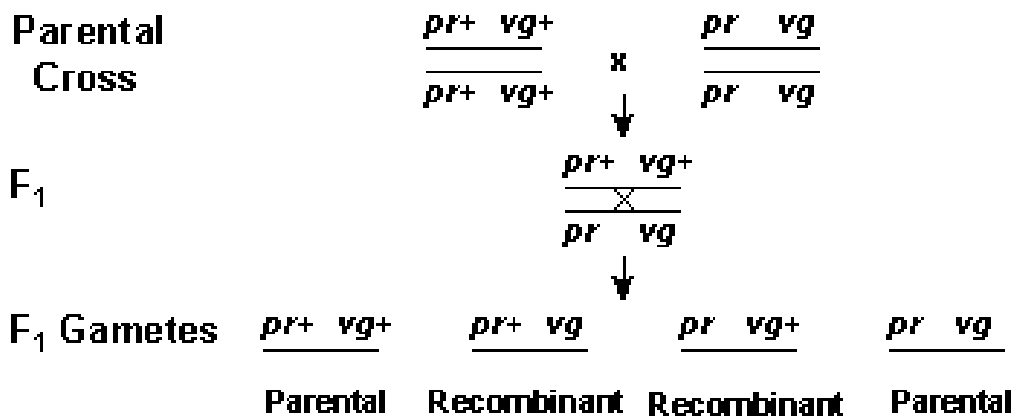
It was not long from the time that Mendel's work was rediscovered that new anomalous ratio began appearing. One such experiment was performed by Bateson and Punnet with sweet peas. They performed a typical dihybrid cross between one pure line with purple flowers and long pollen grains and a second pure line with red

flowers and round pollen grains. Because they knew that purple flowers and long pollen grains were both dominant, they expected a typical 9:3:3:1 ratio when the F₁ plants were crossed. The table below shows the ratios that they observed. Specifically, the two parental classes, purple, long and red, round, were over represented in the progeny.

	Observed	Expected
Purple, long (P_L_)	284	215
Purple, round (P_ll)	21	71
Red, long (ppL_)	21	71
Red, round (ppll)	55	24
Total	381	381

At the time of these experiments, Bateson and Punnett were not able to develop an acceptable hypothesis. The best explanation they posed was that in some manner the phenotypic classes (alleles) in the parents were **coupled**, and they did not sort independently into gametes as predicted by Mendel's second law.

Proof those genes on the same chromosome can at times be inherited as blocks awaited the results of Thomas Hunt Morgan with *Drosophila*. Morgan crossed red eye, normal wing flies ($pr^+pr^+ vg^+vg^+$) with purple eye, vestigial wing ($prpr vgvg$) flies. The figure below shows the cross and the F₁ genotypes. (The bars are used to show that the genes reside on the same chromosome.) During meiosis, four different F₁ gametes are produced. The **parental gametes** are developed without any processing. The **recombinant gametes** though occur by a process called **crossing over**. (The X between the two F₁ chromosomes represents the crossing over event.)

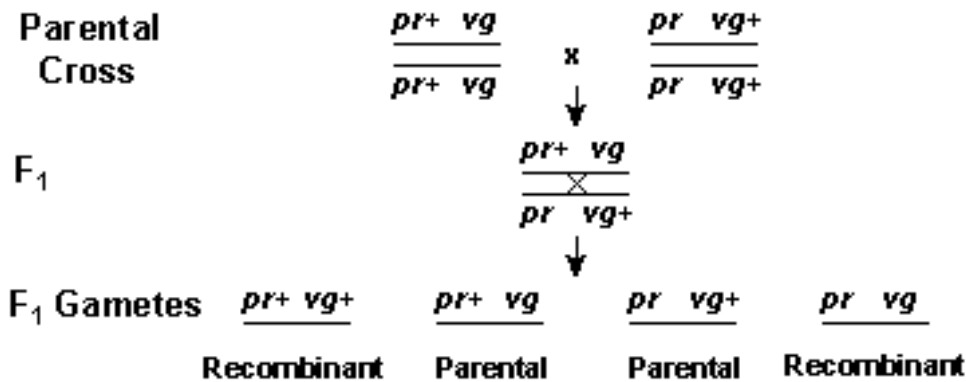


Morgan performed a testcross by crossing *prpr vgvg* flies to F₁. The testcross is powerful because it allows you to follow the meiotic events in one parent because all of the gametes from the test cross parent are homozygous recessive. For this example, the testcross genotype is *pr vg*. Therefore the testcross progeny will represent the distribution of the gametes in the F₁. Remember that a testcross to F₁ derived from a dihybrid cross gave a 1:1:1:1 ratio. But this is not what Morgan observed. The following table shows the result of this test cross.

F ₁ Gamete	Testcross Distribution	Gamete Type
<i>pr⁺ vg⁺</i>	1339	Parental
<i>pr⁺ vg</i>	151	Recombinant
<i>pr vg⁺</i>	154	Recombinant
<i>pr vg</i>	1195	Parental

These results confirm the Bateson and Punnett hypothesis that two genes do not always assort independently. A further confirmation experiment was performed by Morgan when he crossed red eye, vestigial wing flies and purple eye, normal wing flies. Whereas in the first cross, the two dominant alleles and two recessive alleles were on the same chromosome the F₁, in the is cross a dominant allele was on the same chromosome as a recessive allele. The term for the first chromosomal arrangement of the F₁ is called **coupling**, whereas the second arrangement is called **repulsion**. Another set of terms to describe these arrangements are **cis** and

trans, respectively. The following shows the chromosomal arrangement for the cross of two parents in repulsion.



As with the first cross, Morgan test crossed these F₁ flies. The following table shows the distribution of these F₁ gametes.

F ₁ Gamete	Testcross Distribution	Gamete Type
$pr^+ \quad vg^+$	157	Recombinant
$pr^+ \quad vg$	965	Parental
$pr \quad vg^+$	1067	Parental
$pr \quad vg$	146	Recombinant

It was expected that both the coupling and repulsion crosses would yield 1:1:1:1 ratios. How can we determine if the results deviate from this ratio. As with any ratio, we can use the chi-square test to determine if the observed results fit or deviate from the expected ratio. The two tables below show the results for the chi-square for the two crosses.

Coupling Cross Chi-Square Test

F ₁ Gamete	Observed	Expected	(O-E) ² /E
$pr^+ \quad vg^+$	1339	709.75	557.9
$pr^+ \quad vg$	151	709.75	439.9
$pr \quad vg^+$	154	709.75	435.2
$pr \quad vg$	1195	709.75	331.8

Total	2839	2839	$\chi^2 = 1764.8$
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Repulsion Cross Chi-Square Test

F₁ Gamete	Observed	Expected	(O-E)²/E
<i>pr⁺ vg⁺</i>	157	583.75	312.0
<i>pr⁺ vg</i>	965	583.75	249.0
<i>pr vg⁺</i>	1067	583.75	483.3
<i>pr vg</i>	146	583.75	328.3
Total	2335	2335	$\chi^2 = 1372.6$

It is quite clear that both of these large chi-square values indicate that neither of these ratios fit the 1:1:1:1