

Ram Balak Mahto
 Guest faculty
 Zoology department
 v.s.j college Rajnagar Madhubani
 Class B.Sc 2nd yr. Paper 3, group-B
 7908055676

Non-Mendelian inheritance

If all traits were determined by a single gene locus, and if all alleles were inherited independently of each other, we would always observe Mendelian ratios in genetic crosses.

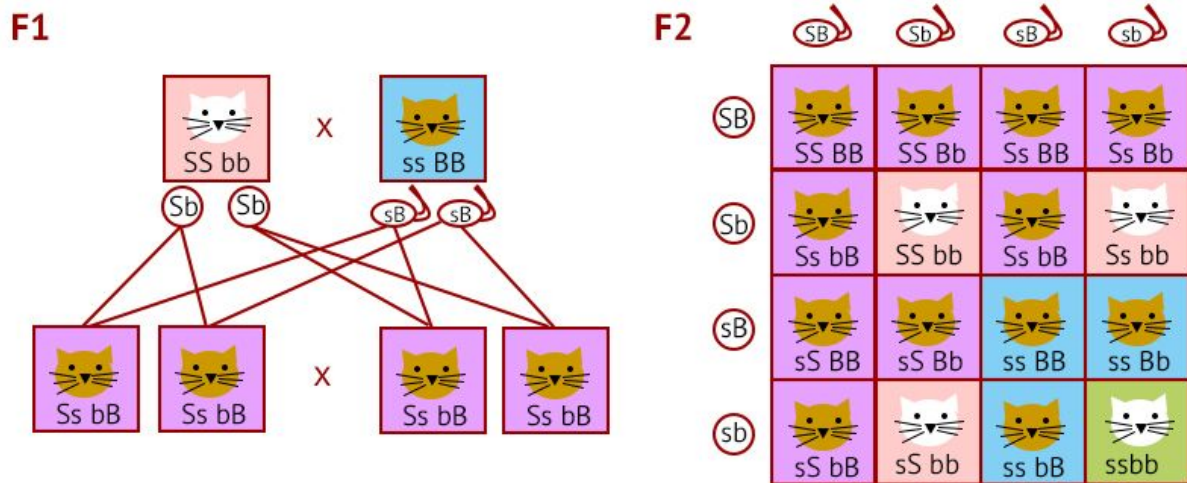


Figure : Mendelian genotypic ratio (9:3:3:1) resulting from a dihybrid cross

Polygenic traits

- Only a small number of observable traits are determined by a single gene locus. Most traits are polygenic, meaning that the trait involves a number of different genes at different loci.

	continuous variation	discrete variation
properties	- no distinct categories - no limit on the value - tends to be quantitative	- distinct categories - no in-between categories - tends to be qualitative (either/or)
examples	• height • weight • heart rate • finger length • leaf length	• cystic fibrosis • finger prints • sickle-shaped erythrocytes • blood groups
representation	line graph 	bar graph
controlled by	many genes, or genes and environmental factors → range of phenotypes between 2 extremes, e.g. height in humans	one, or few, genes → limited number of phenotypes with no intermediates e.g. A, B, AB and O blood groups in humans

Figure :

Discrete vs Continuous variation

- The phenotypes of polygenic traits tend to display continuous variation, as opposed to discrete variation. The more genes involved in the development of a specific phenotype, the greater the variation observed.
- Polygenic traits are often influenced by environmental factors, such as diet and exercise in humans, and various abiotic factors – pH, temperature, salinity, etc.

Linked and unlinked genes

- Gene loci from *different chromosomes* are called unlinked genes. Gene loci found on the *same chromosome* are linked genes.
- Alleles from different chromosomes assort randomly during meiosis, just as Mendel demonstrated.
- Alleles from linked genes are more likely to stay together during meiosis, do not assort randomly, and do not result in Mendelian ratios.

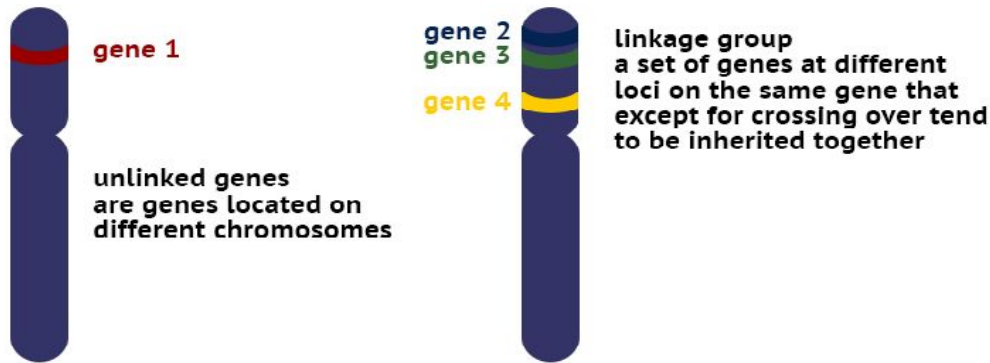


Figure : Linked and unlinked genes

- A linkage group is a group of genes that tends to be inherited together because of their proximity on a chromosome. When two loci are close together on a chromosome, there is less likely to be a crossing-over event between them during meiosis.

Chi-square tests

- We can determine if genes are linked using a chi-square (χ^2) test.

$$\chi^2 = \sum \frac{(o - e)^2}{e}$$

Figure : The chi-square value is equal to the sum of all the squared standard normal deviations, where O is the observed frequency, and E is the expected frequency

- When genes are unlinked, they assort independently and the F₂ ratio from a dihybrid cross will be 9:3:3:1. In a chi-square test, the null hypothesis (H_0) is that the alleles assort independently, so we expect these ratios.
- If the χ^2 value is greater than the critical value listed on the distribution table, for the correct degrees of freedom, then the difference we observe is statistically significant.
- In biology, we accept values at 95% confidence. This means that we always look at the value on the table where $p = 0.95$.

ν	Probability less than the critical value				
	0.90	0.95	0.975	0.99	0.999
1	2.706	3.841	5.024	6.635	10.828
2	4.605	5.991	7.378	9.210	13.816
3	6.251	7.815	9.348	11.345	16.266
4	7.779	9.488	11.143	13.277	18.467
5	9.236	11.070	12.833	15.086	20.515
6	10.645	12.592	14.449	16.812	22.458
7	12.017	14.067	16.013	18.475	24.322
8	13.362	15.507	17.535	20.090	26.125
9	14.684	16.919	19.023	21.666	27.877
10	15.987	18.307	20.483	23.209	29.588

Figure : Table of critical χ^2 values

- If the calculated χ^2 value is less than the one listed, then we accept the null hypothesis. We conclude that the variation we have observed will be due to chance 95% of the time – the genes are probably unlinked.

- If the calculated χ^2 value is greater than the one listed, then we reject the null hypothesis. It means that the variation we have observed is not due to chance 95% of the time – the genes are probably linked.

Worked example – Chi-square test for gene linkage

When true breeding pea plants with purple flowers and long pollen were crossed with pea plants having red flowers and round pollen, all of the F1 generation had purple flowers with long pollen.

- Ho: Purple flowers (P) are dominant to red flowers (p); long pollen (L) is dominant to round pollen (l). The genes are unlinked and will produce a Mendelian ratio of 9:3:3:1 in the F2.
- In the F2 generation the following pea plants were observed:

Purple flowers, long pollen: 296

Purple flowers, round pollen: 85

Red flowers, long pollen: 28

Red flowers, round pollen: 18

Total: 427

Let's compare the observed and expected frequencies for the F2:

Category	Expected ratio	Observed frequency (o)	Expected frequency (e)*	(o-e)	$(o-e)^2$ e
Purple, long	9	296	240	56	13.07
Purple, round	3	85	80	5	0.312
Red, long	3	28	80	-52	33.80
Red, round	1	18	27	-9	3.00
Total	16	427	427	-	$\chi^2 = 50.18$

*Calculation of e: [(Expected ratio/16) x total number of F2 plants]

- The value for χ^2 is 50.18. This is much greater than the critical value of 7.814 (see Figure 10.1.2e). The alleles have not assorted independently. The genes are linked.