

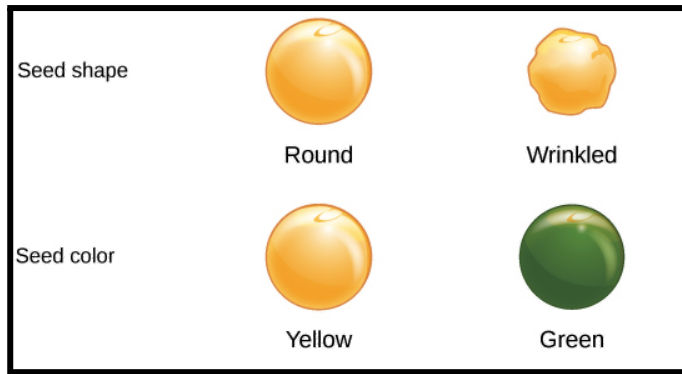
A Level Biology.

Linked & Unlinked Genes.

Name:

LINKED GENES VERSUS UNLINKED GENES	
LINKED GENES	UNLINKED GENES
Genes that are inherited together with the other gene(s) as they are located on the same chromosome	Genes located farther apart from each other
Occur in the same chromosome	Occur either in the same chromosome or in different chromosomes
Sit closely together	Sit farther apart
Do not undergo homologous recombination	Undergo homologous recombination
Inherited together	Have a less chance to be inherited together
Chance of inheriting together is more than 50%	Chance of inheriting together is less than 50%
Do not follow Mendel's second law	Follow Mendel's second law
Dihybrid ratio is 3:1	Dihybrid ratio is 9:3:3:1
Test cross ratio in a dihybrid cross is 1:1	Test cross ratio in a dihybrid cross is 1:1:1:1.
	Visit www.PEDIAA.com

Inheritance patterns with two genes - Dihybrid crosses.

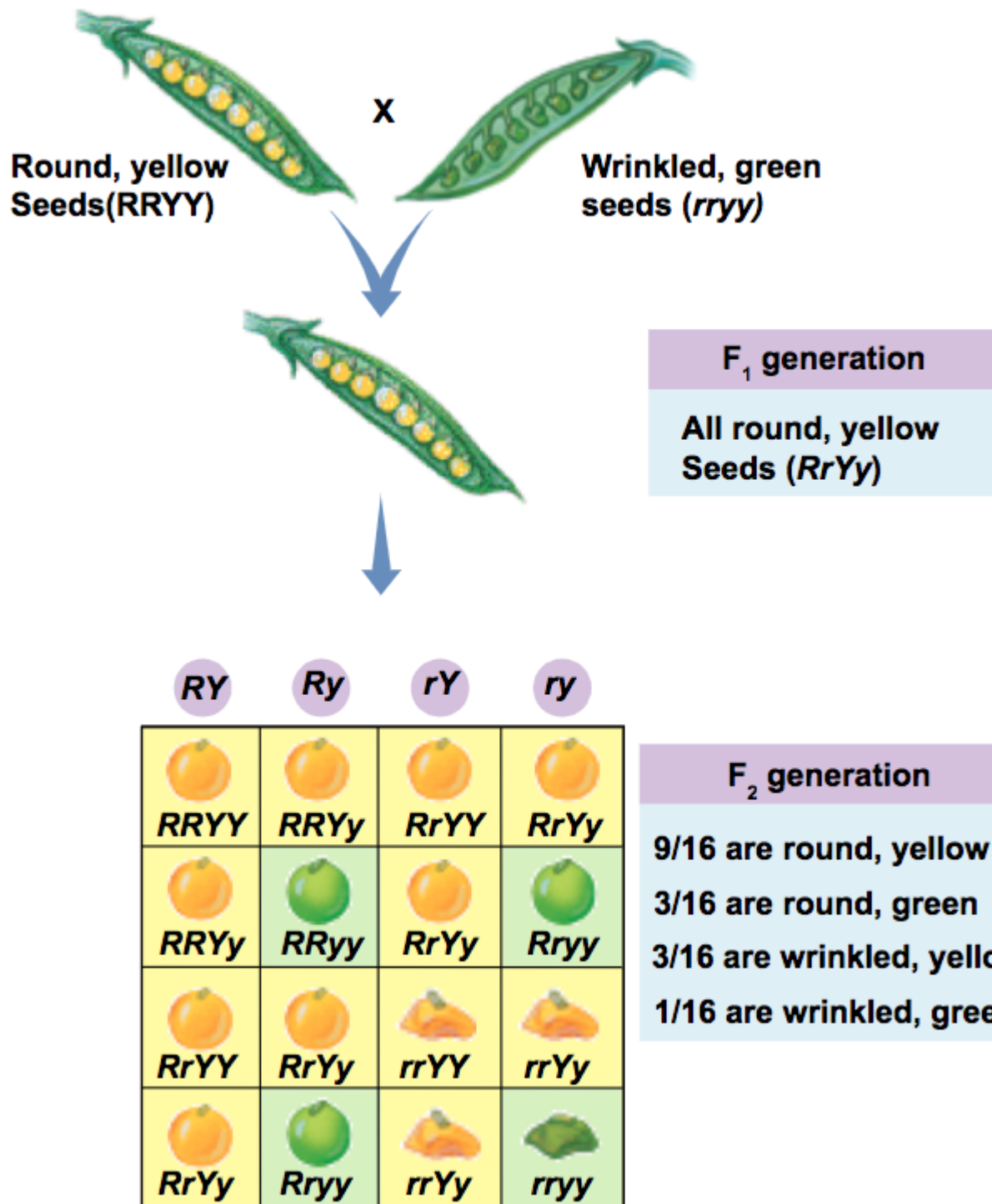


Trait	Allele
Yellow	Y
Green	y
Round	R
Wrinkled	r

F1 Generation - Carry out a cross between Homozygous round yellow and homozygous wrinkled green peas.

F2 Generation - Now carry out a cross of the offspring

Dihybrid Cross.



Note the expected ratio of 9:3:3:1

Linked and unlinked genes.

- Understand the inheritance of two non-interacting unlinked genes.
- Understand that autosomal linkage results from the presence of alleles on the same chromosome and that the results of crosses can be explained by the events of meiosis, including black/grey body and long/vestigial wing in *Drosophila*.
- Be able to use chi squared tests to test the significance of the difference between observed and expected results.

Linked and Unlinked Genes: Understanding Recombination and Gamete Formation

In genetics, the inheritance patterns of genes depend on their chromosomal locations. Genes can be either *linked* or *unlinked*. Linked genes are located close together on the same chromosome, while unlinked genes are either far apart on the same chromosome or on entirely different chromosomes. This difference influences whether or not recombination, specifically crossing over, can affect the alleles that gametes receive.

Unlinked Genes and Independent Assortment

Unlinked genes, which either reside on different chromosomes or are located far apart on the same chromosome, follow Mendel's law of independent assortment. During meiosis, the random orientation of homologous chromosome pairs in metaphase I means that these unlinked genes assort independently of each other. Because unlinked genes do not depend on recombination to produce variation in gametes, crossing over does not typically impact which alleles are inherited together. This independent assortment leads to a variety of possible allele combinations in gametes, allowing each gene to contribute independently to genetic variation.

Linked Genes and the Role of Crossing Over

Linked genes, in contrast, are located close together on the same chromosome. This proximity makes them more likely to be inherited together unless they are separated by a crossover event during meiosis. Crossing over involves the exchange of genetic material between homologous chromosomes and occurs during prophase I of meiosis. When crossing over happens between linked genes, it can produce *recombinant chromosomes*—chromosomes that contain new combinations of alleles not found in the original parental chromosomes.

The chance of a crossover occurring between two genes decreases with the proximity of the genes to each other. Therefore, genes that are very close together are less likely to be separated by recombination, while those further apart are more likely to produce recombinant alleles. This recombination process is essential for genetic diversity, allowing new allele combinations to appear in gametes that would otherwise be impossible if linked genes were always inherited together.

Impact on Gamete Formation

For unlinked genes, the formation of gametes does not rely on recombination to produce genetic variation since these genes are independently assorted. However, for linked genes, recombination through crossing over is a key contributor to genetic diversity. Without recombination, linked genes would always be passed on as a unit, leading to fewer possible allele combinations. The formation of recombinant chromosomes, therefore, allows for greater diversity in the gametes produced, which is critical in evolutionary adaptation and population variability.

In summary, while unlinked genes do not rely on recombination for varied allele combinations due to independent assortment, linked genes are heavily influenced by recombination. This distinction highlights the role of crossing over in promoting genetic diversity through the formation of recombinant chromosomes.

Observed and expected Ratios.

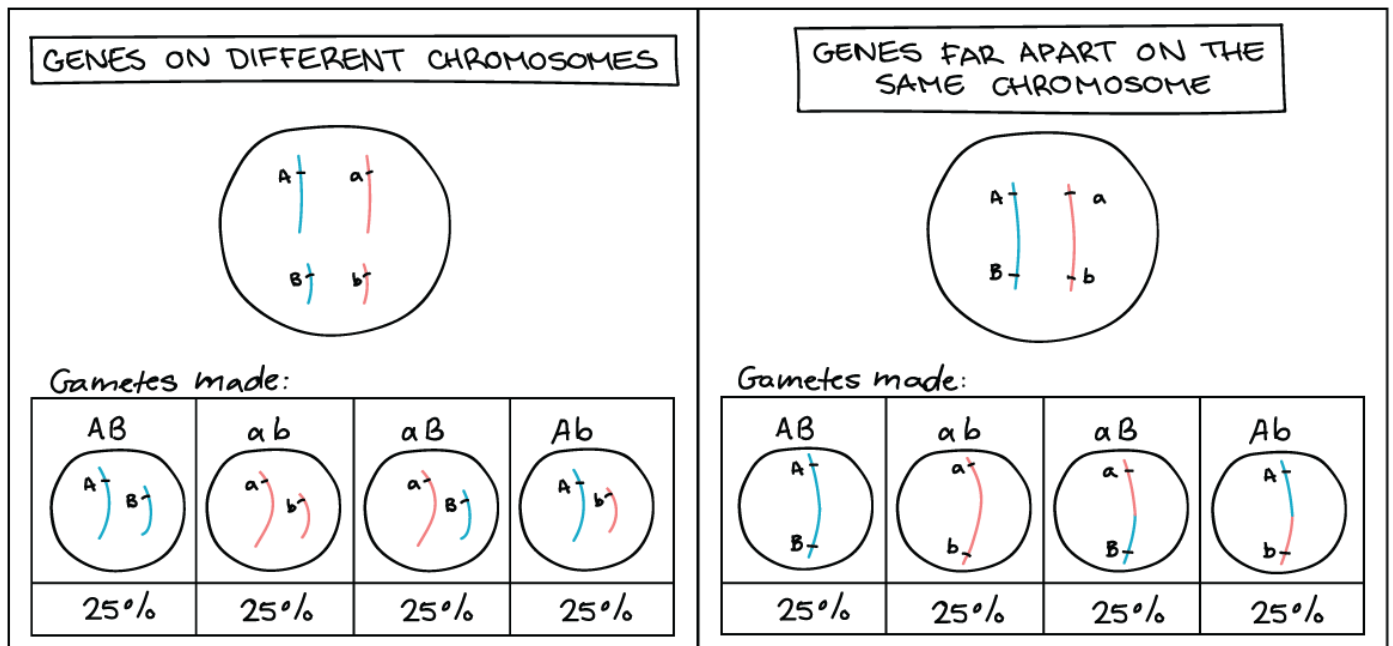
Mendelian ratios, such as the classic 9:3:3:1 ratio for a dihybrid cross, are not observed in linked genes because these genes are located close together on the same chromosome and do not assort independently during meiosis.

Here's why Mendelian ratios don't apply to linked genes:

1. **Independent Assortment Assumption:** Mendel's principles assume that each gene pair segregates independently during gamete formation. This independent assortment is possible when genes are unlinked (i.e., on different chromosomes or far apart on the same chromosome). Linked genes, however, are physically close to each other on the same chromosome, and they tend to be inherited together as a unit. This proximity makes independent assortment unlikely.
2. **Reduced Recombination:** Linked genes are less likely to be separated by crossing over because crossovers are more probable to occur between genes that are far apart. The closer two genes are, the less likely a crossover event will separate them. As a result, the genes are often inherited together in the same combinations found in the parent, known as **parental or non-recombinant phenotypes**.
3. **Deviation from Expected Ratios:** In a dihybrid cross involving linked genes, instead of the expected 9:3:3:1 phenotypic ratio, there are more offspring with the parental combinations of traits and fewer recombinant types. This deviation means that the ratios observed in offspring do not follow Mendel's predictions and vary based on the degree of linkage between the genes.

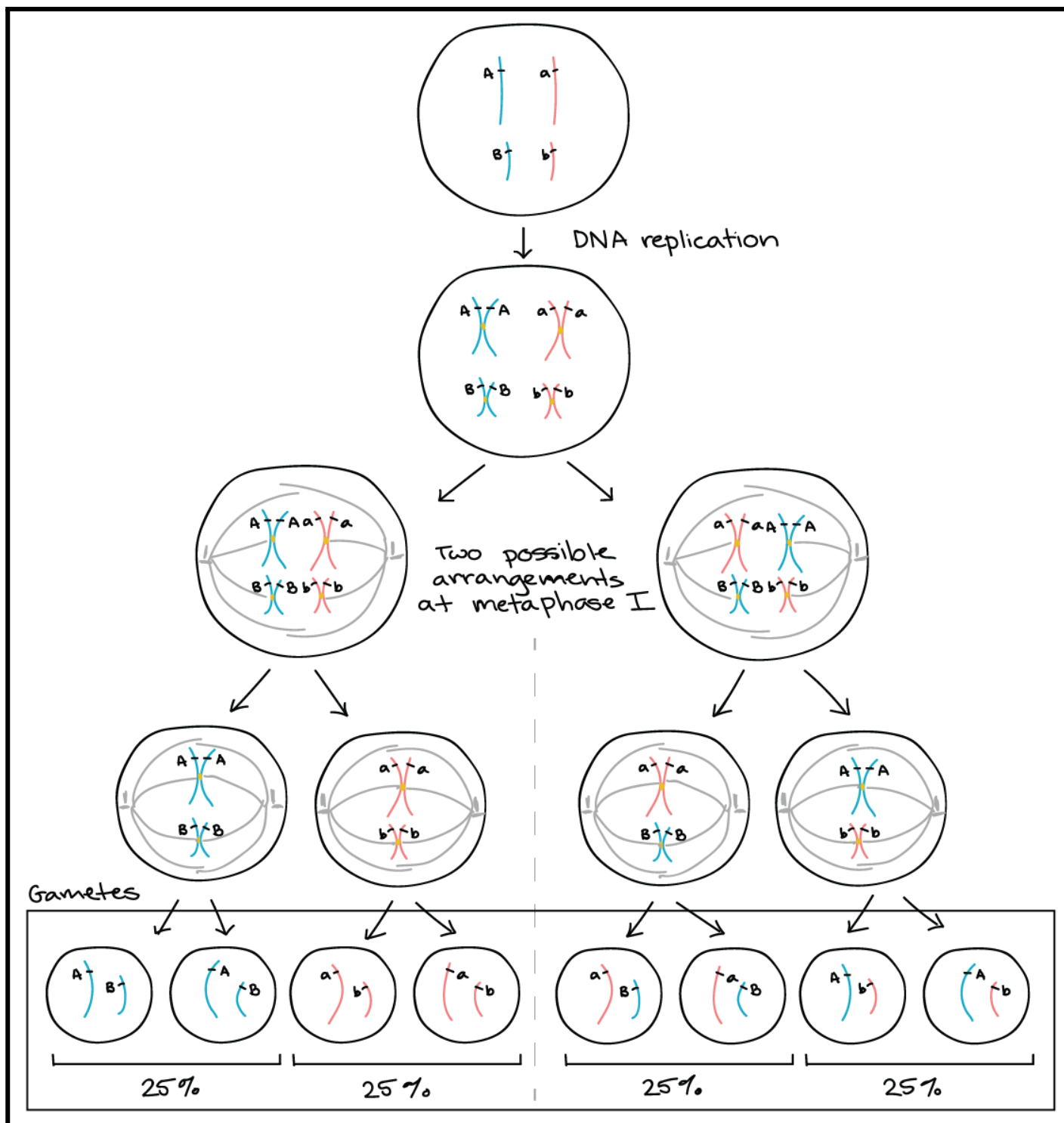
In summary, Mendelian ratios are not observed in linked genes because these genes do not assort independently. Instead, their proximity on the chromosome means they are often inherited together, leading to a greater proportion of offspring with parental phenotypes and fewer with recombinant phenotypes.

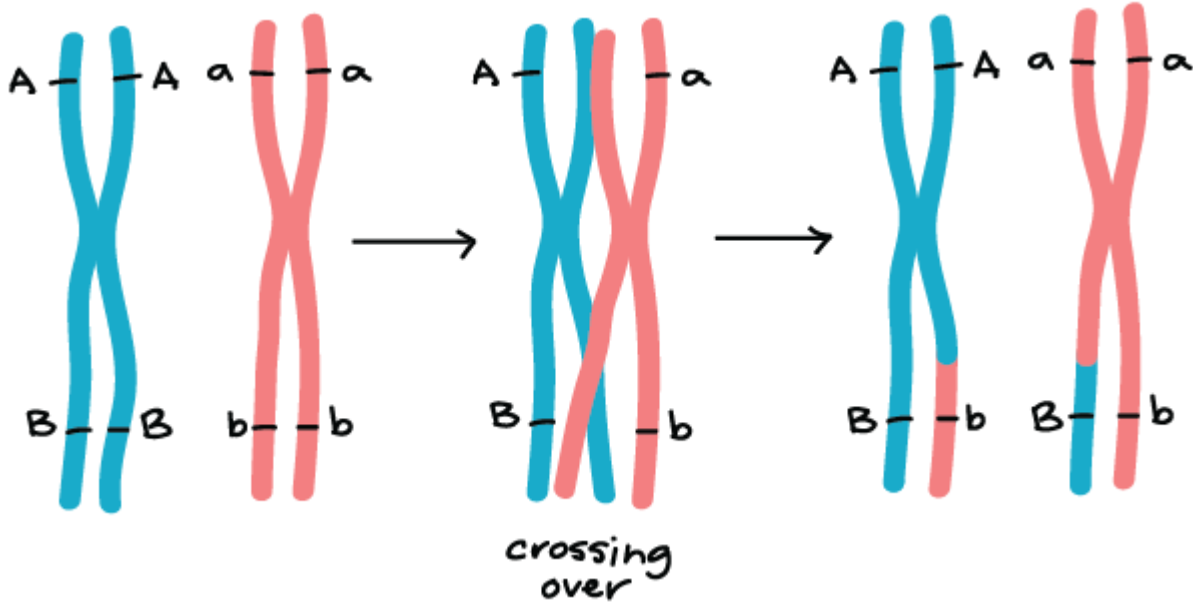
Unlinked genes.



1. Why are these genes unlinked?
2. Explain how the gametes shown have been formed?

[illegible]

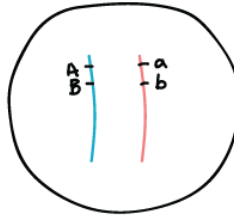




3. Explain why these genes are unlinked.

[illegible]

GENES CLOSE TOGETHER ON THE SAME CHROMOSOME



Gametes made:

AB 	Ab 	aB 	ab 
48%	2%	2%	48%

↳ Recombinant

- Parental

- 5. Why are gametes made in unequal proportions in this instance?**

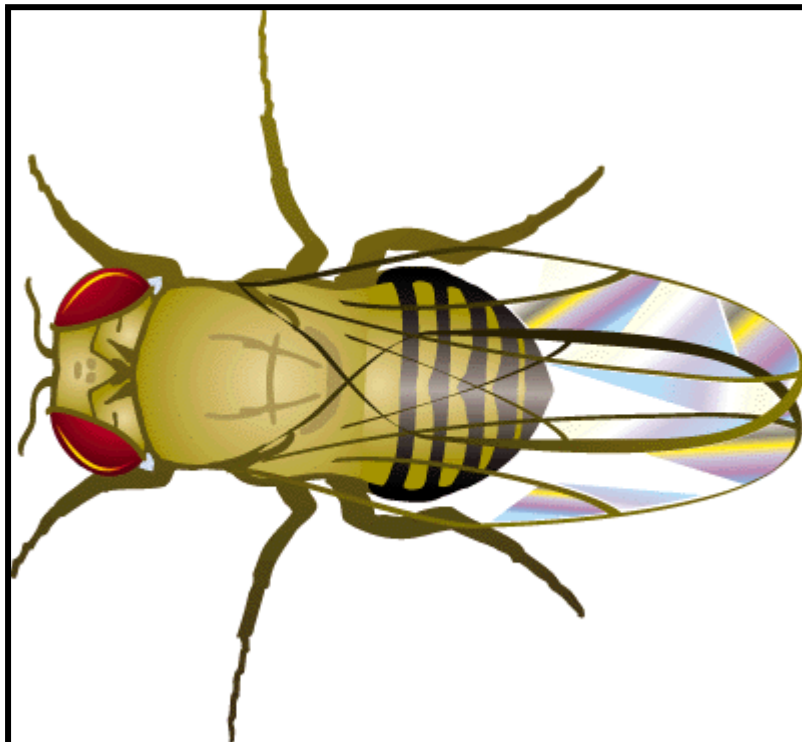
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Fruit fly Crosses.

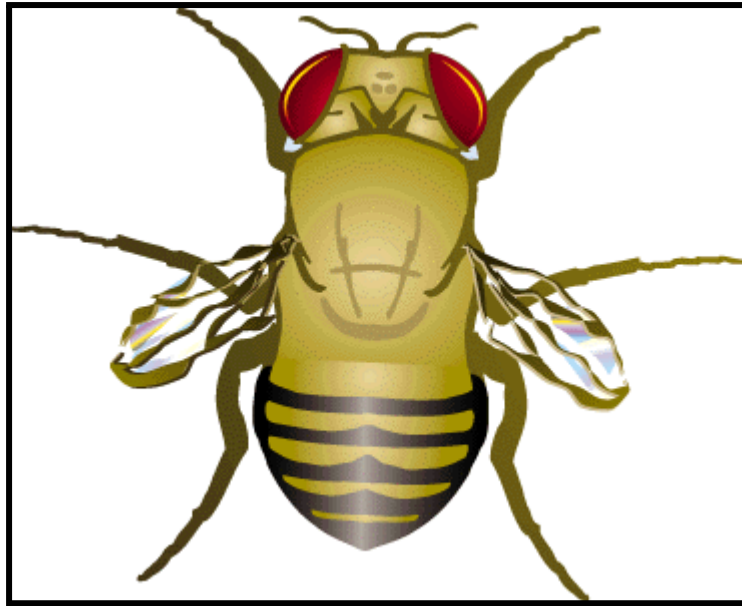
Linked & Unlinked genes

- Understand that autosomal linkage results from the presence of alleles on the same chromosome and that the results of crosses can be explained by the events of meiosis, including black/grey body and long/vestigial wing in *Drosophila*.

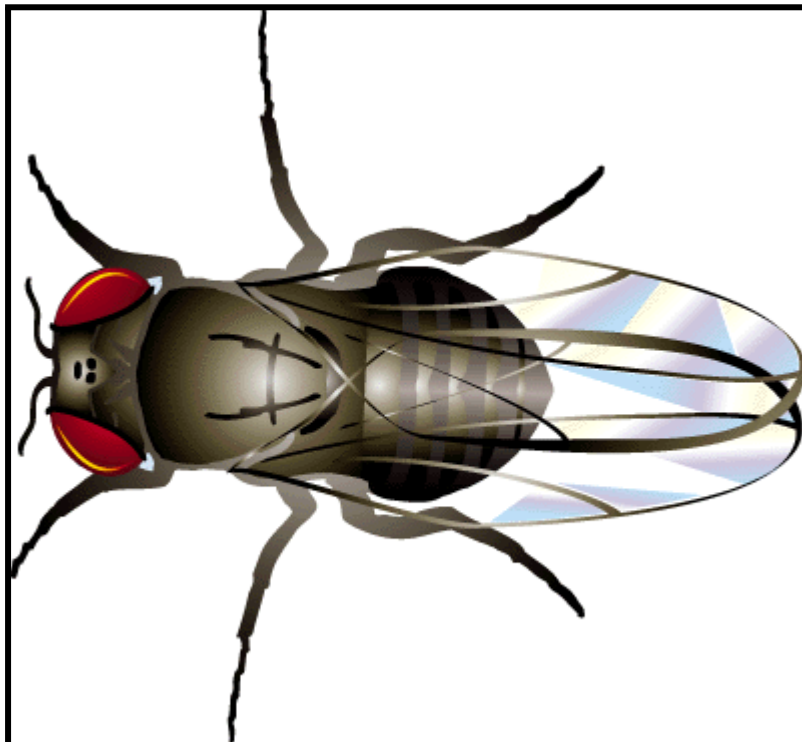
Gray body / Long wings.



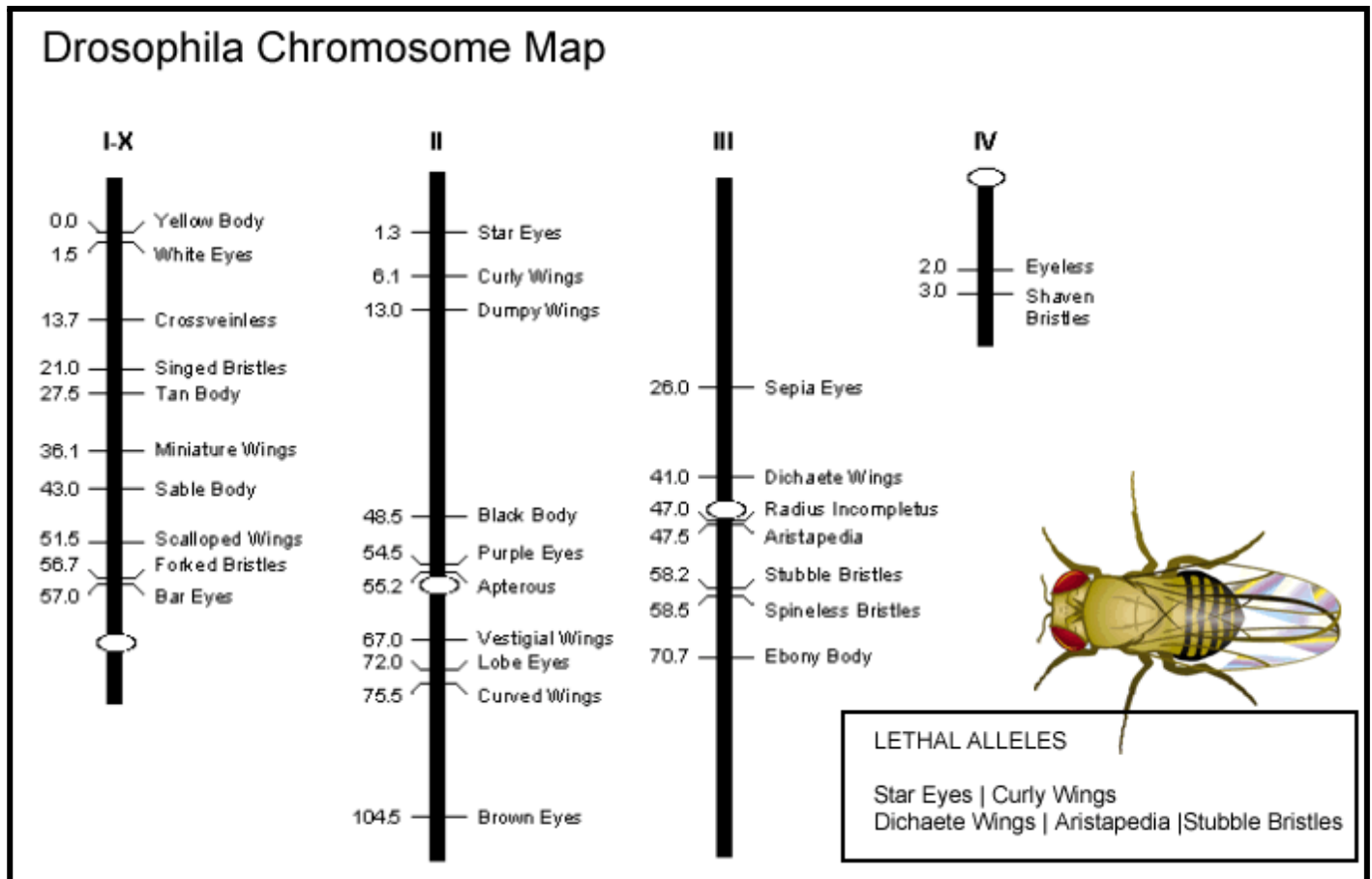
Grey Body / Vestigial wings.



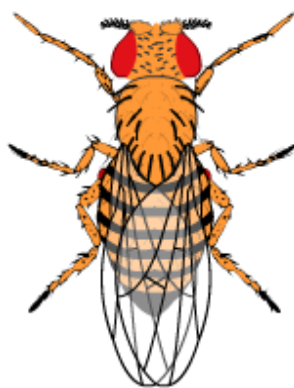
Black Body



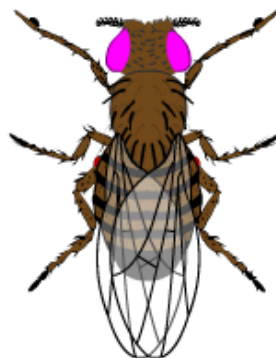
Investigating Linked and Unlinked genes.



Cross 1.



Wild type



Ebony Body Purple eyes

Linked or Unlinked? Using Chi Square.

A wild type with ebony body and purple eyes.

Trait	Allele
Wild (Body colour)	E
Ebony (Body colour)	e
Wild (Eye colour)	R
Purple (Eye colour)	r

1. Show the genotype for the parents.
2. Show the gametes produced
3. Complete a test cross to show the expected results for the F1 generation.
4. Complete a test cross for the expected results of the F2 Generation.

F1 Generation

Expected Ratio

Trait	Ratio

F2 Generation

Expected ratios.

Trait	Ratio

Null Hypothesis

Chi Square - Used to test null hypothesis.

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

O - Observed
E - Expected.

O	E	O-E	(O-E) ₂	$\frac{(O-E)^2}{E}$
$\sum \frac{(O - E)^2}{E}$				

Making sense of χ^2

A chi-squared table shows the distribution of critical values according to each degree of freedom

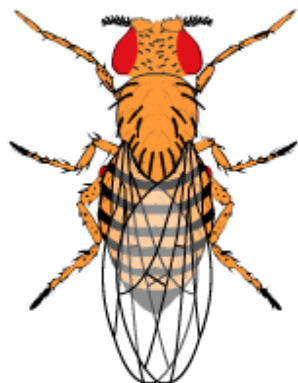
This allows for an assessment to be made as to whether the data is statistically significant ($p < 0.05$) or not

If the observed chi-square test statistic is greater than the critical value, the null hypothesis can be rejected.

Degree of Freedom	Probability of Exceeding the Critical Value								
	0.99	0.95	0.90	0.75	0.50	0.25	0.10	0.05	0.01
1	0.000	0.004	0.016	0.102	0.455	1.32	2.71	3.84	6.63
2	0.020	0.103	0.211	0.575	1.386	2.77	4.61	5.99	9.21
3	0.115	0.352	0.584	1.212	2.366	4.11	6.25	7.81	11.34
4	0.297	0.711	1.064	1.923	3.357	5.39	7.78	9.49	13.28
5	0.554	1.145	1.610	2.675	4.351	6.63	9.24	11.07	15.09
6	0.872	1.635	2.204	3.455	5.348	7.84	10.64	12.59	16.81
7	1.239	2.167	2.833	4.255	6.346	9.04	12.02	14.07	18.48
8	1.647	2.733	3.490	5.071	7.344	10.22	13.36	15.51	20.09
9	2.088	3.325	4.168	5.899	8.343	11.39	14.68	16.92	21.67
10	2.558	3.940	4.865	6.737	9.342	12.55	15.99	18.31	23.21
11	3.053	4.575	5.578	7.584	10.341	13.70	17.28	19.68	24.72
12	3.571	5.226	6.304	8.438	11.340	14.85	18.55	21.03	26.22
13	4.107	5.892	7.042	9.299	12.340	15.98	19.81	22.36	27.69
14	4.660	6.571	7.790	10.165	13.339	17.12	21.06	23.68	29.14
15	5.229	7.261	8.547	11.037	14.339	18.25	22.31	25.00	30.58
16	5.812	7.962	9.312	11.912	15.338	19.37	23.54	26.30	32.00
17	6.408	8.672	10.085	12.792	16.338	20.49	24.77	27.59	33.41
18	7.015	9.390	10.865	13.675	17.338	21.60	25.99	28.87	34.80
19	7.633	10.117	11.651	14.562	18.338	22.72	27.20	30.14	36.19
20	8.260	10.851	12.443	15.452	19.337	23.83	28.41	31.41	37.57
22	9.542	12.338	14.041	17.240	21.337	26.04	30.81	33.92	40.29
24	10.856	13.848	15.659	19.037	23.337	28.24	33.20	36.42	42.98
26	12.198	15.379	17.292	20.843	25.336	30.43	35.56	38.89	45.64
28	13.565	16.928	18.939	22.657	27.336	32.62	37.92	41.34	48.28
30	14.953	18.493	20.599	24.478	29.336	34.80	40.26	43.77	50.89
40	22.164	26.509	29.051	33.660	39.335	45.62	51.80	55.76	63.69
50	27.707	34.764	37.689	42.942	49.335	56.33	63.17	67.50	76.15
60	37.485	43.188	46.459	52.294	59.335	66.98	74.40	79.08	88.38
Not Significant								Significant	

Is there a significant difference between observed and expected?

Cross 2.



Wild type



Black body Vestigial wings

A wild type with black body and vestigial wings.

Trait	Allele
Wild Body color	B
Black Body color	b
Wild wing	A
Vestigial wing	a

- 5. Show the genotype for the parents.
- 6. Show the gametes produced
- 7. Complete a test cross to show the expected results for the F1 generation.
- 8. Complete a test cross for the expected results of the F2 Generation.

F1 Generation

Expected Ratio

Trait	Ratio

F2 Generation

Expected ratios.

Trait	Ratio

Null Hypothesis

Chi Square - Used to test null hypothesis.

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

O - Observed
E - Expected.

O	E	O-E	(O-E) ₂	$\frac{(O-E)^2}{E}$
835				
269				
55				
50				
$\sum \frac{(O - E)^2}{E}$				

Making sense of X²

A chi-squared table shows the distribution of critical values according to each degree of freedom

This allows for an assessment to be made as to whether the data is statistically significant ($p < 0.05$) or not

If the observed chi-square test statistic is greater than the critical value, the null hypothesis can be rejected.

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