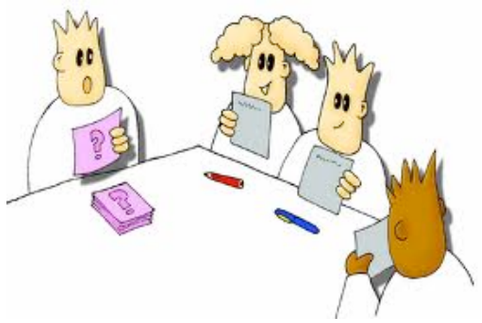
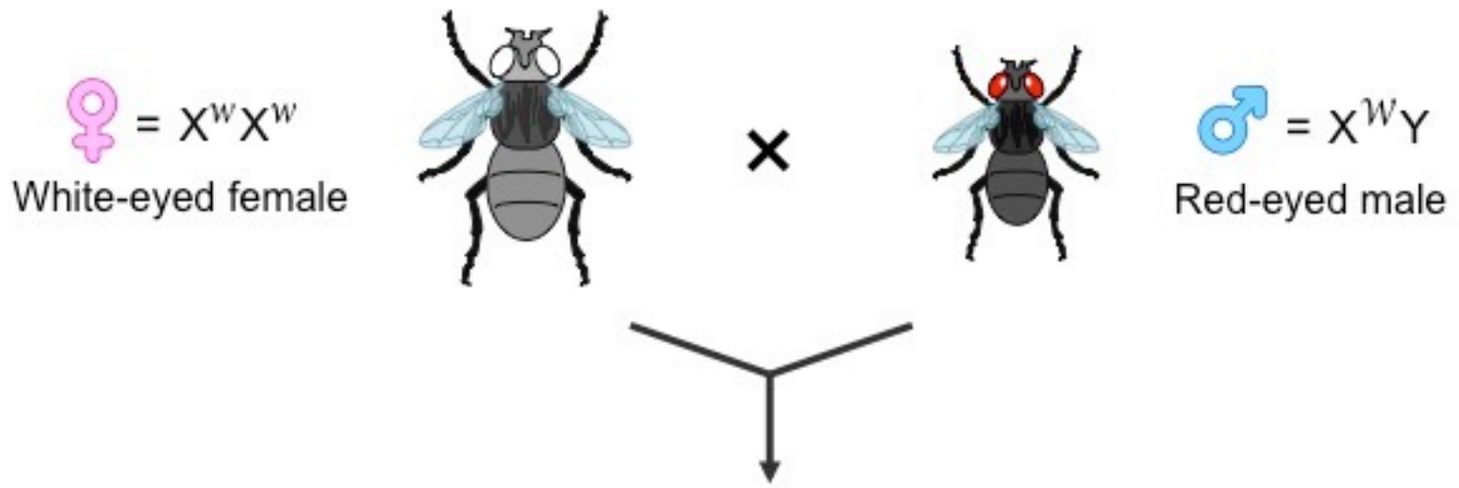
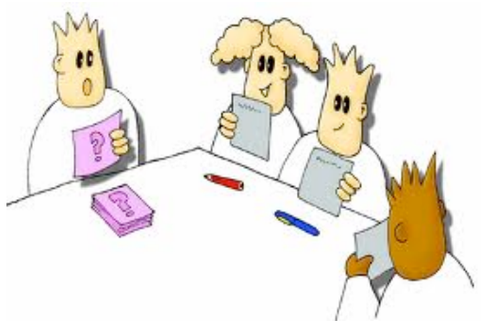


They don’t get any harder than this !

In fruit flies, miniature wings are the results of a gene produced by a recessive **x-linked** trait (X^m). Normal length wings are (X^M). Wingless flies are **recessive** to winged flies which is controlled by an **autosomal gene.** A female that is a carrier for miniature wings and is heterozygous for having wings is crossed with a homozygous normal male with this female above. Construct a punnett for this cross

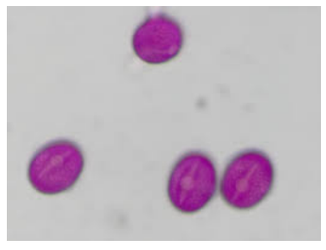
Linked Genes (Autosomal)





In sweet peas, purple flowers and long pollen grain plants were crossed with red flowers which round pollen grain plants. In sweet peas purple and long are dominant traits. Show the F1, and the F2 result when to purebred parents are crossed. State the expected phenotypical outcome.

vs



The actual results observed by William Bateson, Edith Saunders, and Reginald Punnett in 1903

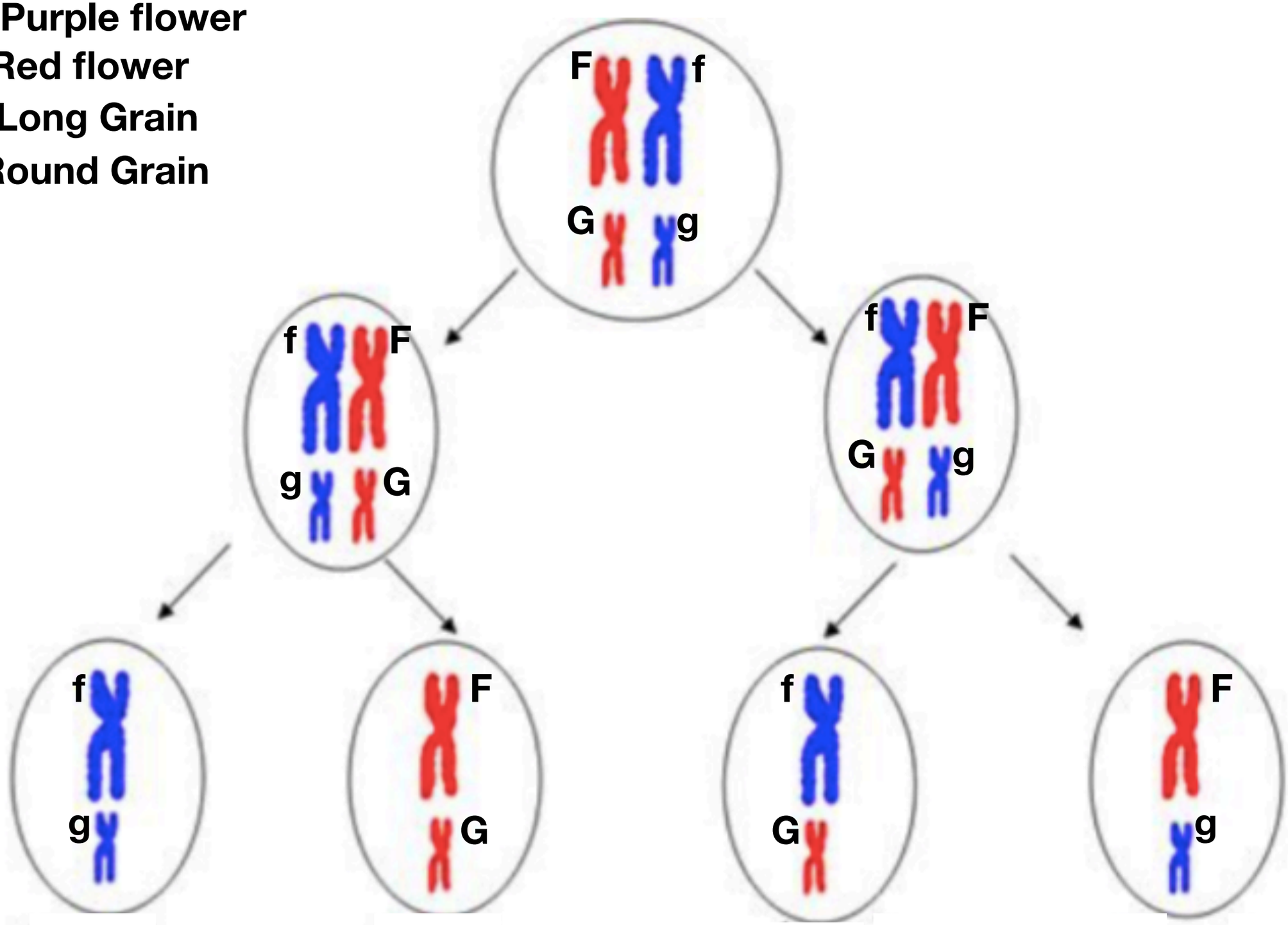
Phenotype	Expected outcome	Observed frequency	Observed outcome	Expected %	Observed %
purple long	9	4831	12.4	9/16 = 56.25%	69.5%
purple round	3	390	1	3/16 = 18.75%	5.6%
red long	3	393	1	3/16 = 18.75%	5.6%
red round	1	1338	3.4	1/16 = 6.25%	6.25%

*** This data didn't appeared to follow Mendel's observations and seemed to defy the Law of Independent Assortment

Explanation- These Gene are LINKED (found on the same chromosome). First cased discovered.

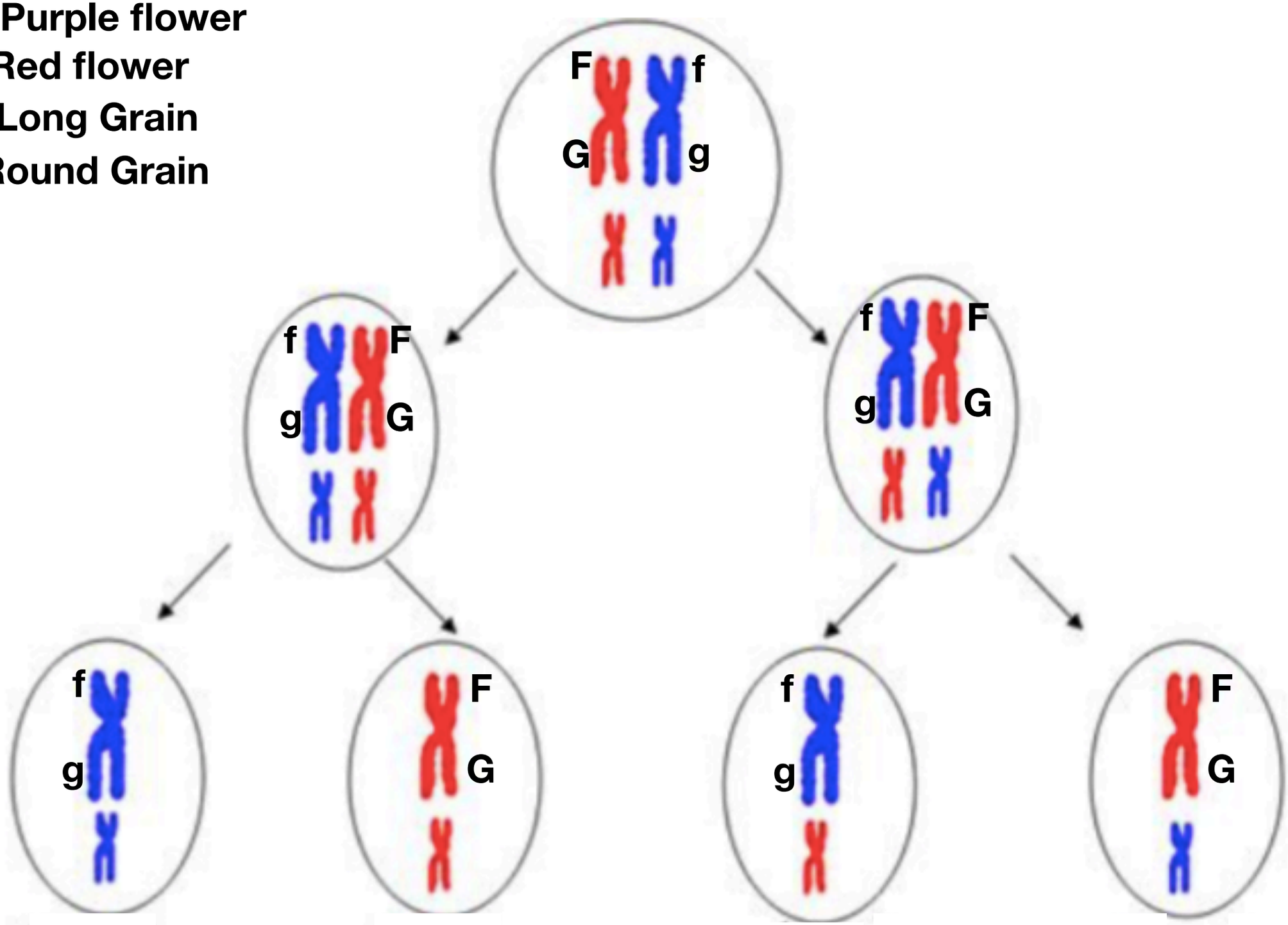
Recall Independent Assortment…

F = Purple flower
f = Red flower
G = Long Grain
g = Round Grain



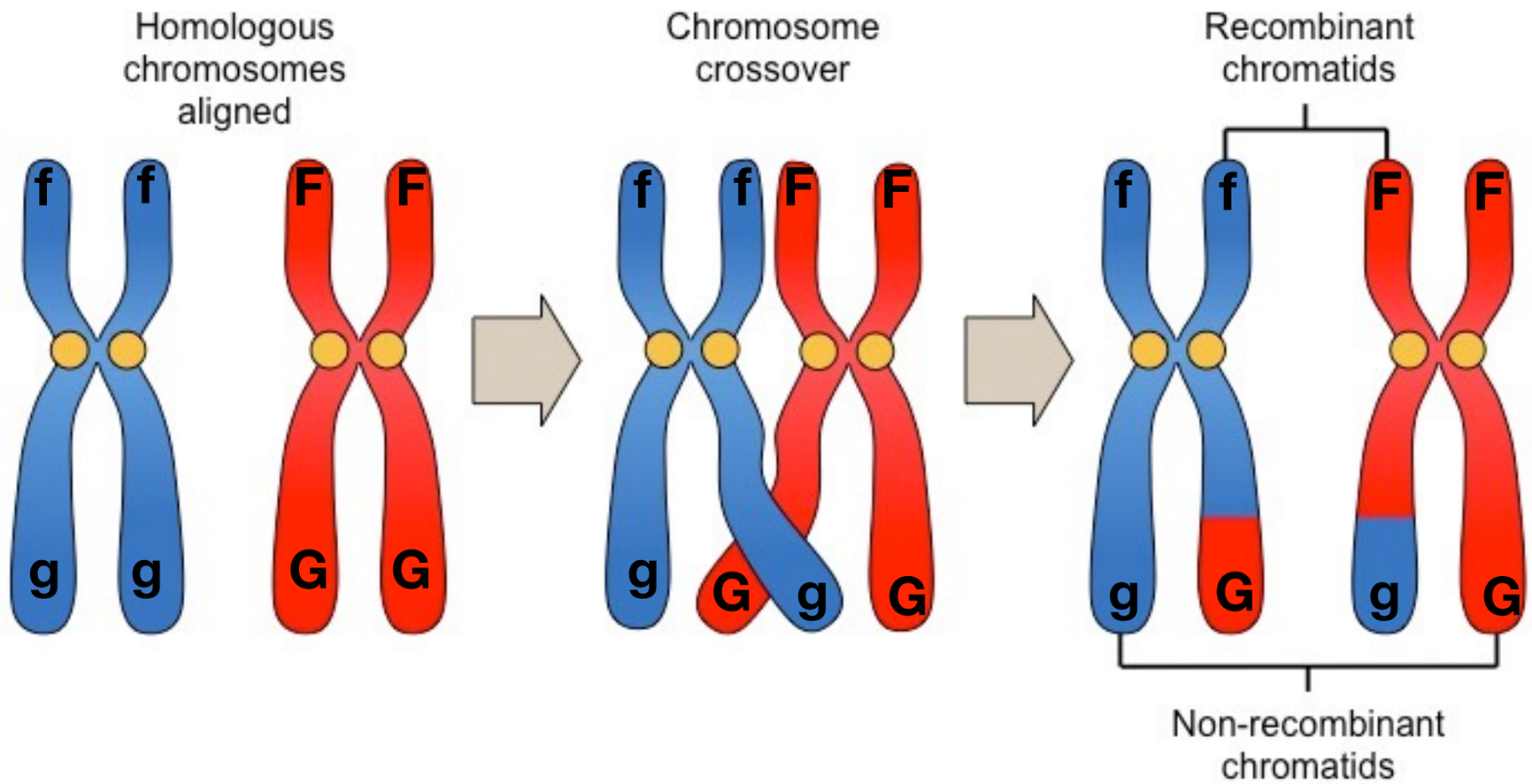
When Genes are LINKED…

F = Purple flower
f = Red flower
G = Long Grain
g = Round Grain



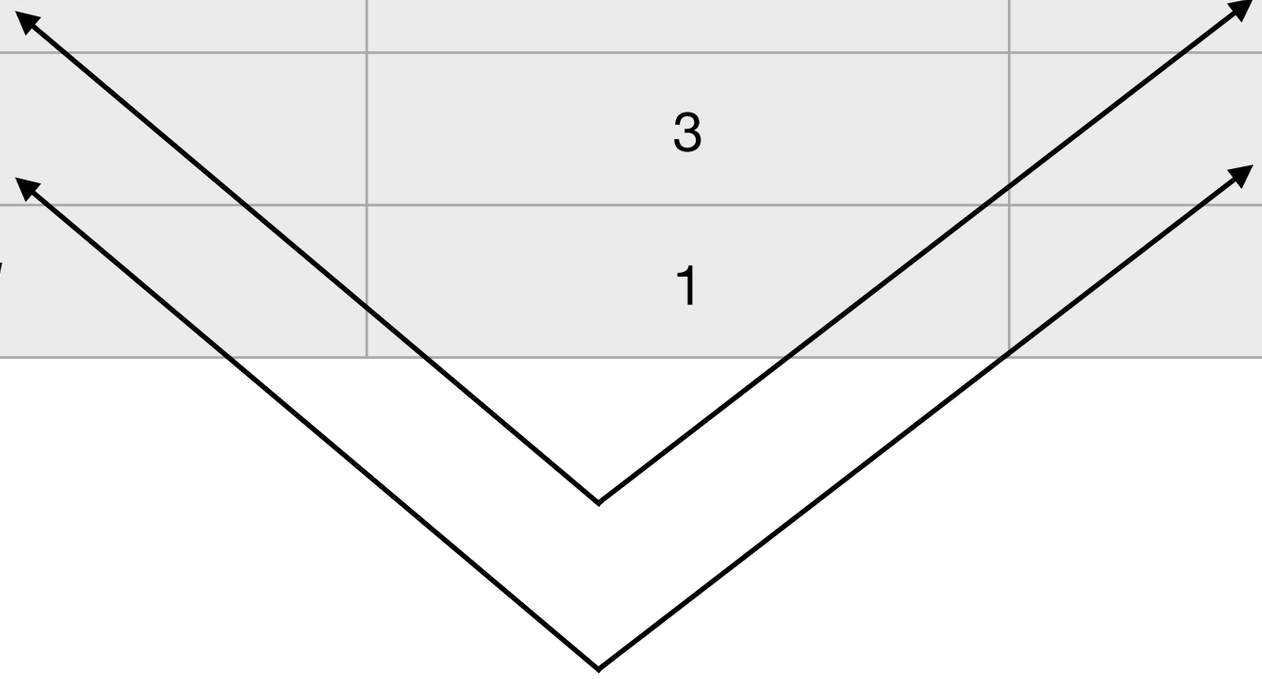
SO where did the Purple round and Long short come from ?

F = Purple flower
f = Red flower
G = Long Grain
g = Round Grain



- During prophase I of meiosis, in some gamete formation, crossover events would've occurred.
- The frequency in which these genes combinations occur through crossover would have been smaller compared to the remaining linked genes.

Phenotype	Expected outcome	Observed frequency
purple long	9	4831
purple round	3	390
red long	3	393
red round	1	1338



Crossover events have occurred

Pure line white ones with a large single combs were mated with pure line chickens with dark feathers and small pea combs. All of the F1 were white with small pea combs. The F1 chickens were then mated in the following results were obtained: 111 white pea, 37 white single, 34 dark pea, and 8 dark single.

In this case which traits were dominant?

Which traits were recessive?

If you conducted a punnett square for this F2 cross what should your expected ratio be?

Do these results matched what is expected for independently assorted non linked genes?

Chi Squared Tests

The statistical test to determine differences between observed and expected results

Steps to do.

1. ***Draw up a contingency table of the absurd frequency***
2. ***Calculate the expected frequencies assuming independent assortment***

(punnett result x actual totals)

Phenotype	Observed frequency	Expected Ratio	Expected frequency
White Pea	111	9	9/16 x 190 = 106.9
White Single	37	3	3/16 x 190 = 35.6
Dark Pea	34	3	3/16 x 190 = 35.6
Dark Single	8	1	1/16 x 190 = 11.9
	Total=190	Mendelian in this case	

3. Calculate the degrees of freedom (Class totals -1)

… *in this case 4-1 Degrees freedom = 3*

Steps to do.

4. Using a **Critical Values Table** find the **critical region**

The critical region is any value larger than the critical value

ie >7.81

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

*** **NOTE -** In science, 0.05 level of significance is always used

Steps to do.

Phenotype	Observed frequency	Expected Ratio	Expected frequency
White Pea	111	9	9/16 x 190 = 106.9
White Single	37	3	3/16 x 190 = 35.6
Dark Pea	34	3	3/16 x 190 = 35.6
Dark Single	8	1	1/16 x 190 = 11.9
	Total=190	Mendelian in this case	

5. Calculate Chi-squared using this EQUATION $X^2 = \sum \frac{(obs- exp)^2}{exp}$

$$X^2 = \frac{(111-106.5)^2}{106.5} + \frac{(37-35.6)^2}{35.6} + \frac{(34-35.6)^2}{35.6} + \frac{(8-11.9)^2}{11.9}$$

$$= 1.56$$

Steps to do.

$$X^2 = \frac{(111-106.5)^2}{106.5} + \frac{(37-35.6)^2}{35.6} + \frac{(34-35.6)^2}{35.6} + \frac{(8-11.9)^2}{11.9}$$

$$= 1.56$$

the Critical Value			
0.25	0.10	0.05	0.01
1.32	2.71	3.84	6.63
2.77	4.61	5.99	9.21
4.11	6.25	7.81	11.34
5.39	7.78	9.49	13.28
6.63	9.24	11.07	15.09
7.84	10.64	12.59	16.81
9.04	12.02	14.07	18.48

In this case the chi-square value **is less than** the critical value!

Therefore, the observed data matches the expected results.

—> the traits comb and feather colour **are not linked** and therefore were independently assorted and exist on different chromosomes

IF the **chi-square value** had been **greater than** the critical value, then the traits don't match the expected values and therefore the **traits might be linked**

Assignment for the Weekend

Data-base questions: Gene linkage in Zia Mays found on page **452**

Databased questions: using the chi-squared test found on page ***454***

To be submitted Tuesday.