

Exploring 1-Trait Crosses (Monohybrid) with Corn Ears

1) Examine the Corn Cross Card for the P → F₁ crosses (A & B) and complete the table below

Cross A		
Pure Breeding Parent (P)	A-1	A-2
Phenotype:		
Genotype:		

Cross B		
Pure Breeding Parent (P)	B-1	B-2
Phenotype:		
Genotype:		

2) Which 2 corn alleles are Dominant? Use this information to complete the P generation genotypes above

3) Examine the Corn Cross Card for the F₁ → F₂ cross and complete the table below

Cross A		
(Monohybrid)	F₁	F₁
Phenotype:		
Genotype:		

Cross B		
(Monohybrid)	F₁	F₁
Phenotype:		
Genotype:		

4) Draw the Punnett Squares for each of the F₁ → F₂ crosses below:

Cross A

Cross B

5) Summarize the F₂ **EXPECTED** Phenotype results below. Then examine the F₂ corn ears for cross A & B and record the actual phenotypes results. While working in pairs, one person should call out the phenotypes while the other organizes the data on a scratch paper. To organize the count, mark the beginning of each row with a transparency marker and continue marking rows as you count. Record final **ACTUAL** results in the data table below.

Cross A			
F ₂ Phenotypes	Expected Results (decimal)	Actual Results	Actual Results (decimal)

Cross B			
F ₂ Phenotypes	Expected Results (decimal)	Actual Results	Actual Results (decimal)

6) Now compile the F₂ Phenotype Class Results below:

Dominant Phenotypes		Class Total #	Dominant Combined Class Total #	Actual Totals (decimal)	Expected Totals (decimal)
Cross A				$\frac{\text{Dominant \#}}{\text{Total \#}} =$	
Cross B					
Recessive Phenotypes		Class Total #	Recessive Combined Class Total #	XXXXXXXXXXXX	XXXXXXXXXXXX
Cross A				$\frac{\text{Recessive \#}}{\text{Total \#}} =$	
Cross B					
Class TOTAL Phenotypes counted →				XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXX

7) Are the team or class results closer to the expected phenotypes results explain?

8) Use a X₂ analysis to determine if the variation between the actual and expected F₂ dominant & recessive phenotypes is above the 5% Probability Value (P) predicted by random chance alone?

GENETIC DATA SHEET

	1	2	3	4	Total
Phenotype Class					
Number of individuals (actual count)	a ₁	a ₂	a ₃	a ₄	
Expected number	e ₁	e ₂	e ₃	e ₄	

$$\chi^2 = \frac{(a_1 - e_1)^2}{e_1} + \frac{(a_2 - e_2)^2}{e_2} + \frac{(a_3 - e_3)^2}{e_3} + \frac{(a_4 - e_4)^2}{e_4}$$

χ² TABLE

d.f.	P = .95	.90	.80	.70	.50	.30	.10	.05	.01
1	.004	.016	.064	.148	.455	1.07	2.71	3.84	6.64
2	.103	.211	.446	.713	1.38	2.41	4.60	5.99	9.2
3	.352	.584	1.00	1.42	2.37	3.66	6.25	7.82	11.3

d.f. = degrees of freedom = number of classes - 1
P = probability

9) X² = _____

10) P = _____

11) CIRCLE below the correct interpretation of the P-value results:

- a) the variation in the F₂ results can be explained by natural random variation alone
- b) the variation in the F₂ results has been influenced by a **significant factor** other than natural random variation