

Mendel Revisited: Distribution of Genotypes of Wildtype F2 hermaphrodites

D= wild-type allele d = mutant allele

Initials	Uu Dd	Uu DD	UU Dd	UU DD	<i>him trait?</i>
1GP	3	5	0	3	2 F2 moms
2 IO	5	0	6	1	3
3 WF	6	3	2	1	2
4 KS	7	2	2	1	
5KH	3	3	1	5*	0
6AG	5	4	1	2	-
7MO	4	3	3	2	-
8TCD	5	2	3	2	-
9NB	4	3	4	1	
10RK	6	3	0	3	
11 JRB	5	3	2	2	5
12KGB	6	2	2	2	1
13KAH	5	2	4	1	
14JY	8	4	0	0	-
15GLK	6	3	0	3	
16BK	6	2	3	1	8

* F3 progeny on the young side

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U = wild-type allele u = mutant allele D= wild-type allele d = mutant

GROUP		UuDd	UuDD	UUDd	UU DD	n	χ^2	p
	Expected ratio	4	2	2	1			
IO, KS, MO,TD	Raw data	21	7	14	6	48	2.390	0.187
	<i>Observed Ratio</i>	3.5	1.16	2.33	1			
AG, JY, KH, B	Raw data	24	13	7	4	48	1.813	0.758
	<i>Observed Ratio</i>	6	3.25	1.75	1			
GP,GK, BK,JRB	Raw data	19	13	6	9	47	6.68	0.0828
	<i>Observed Ratio</i>	2.11	1.44	0.66	1			
KH, RH, NB, KB	Raw data	19	11	7	11	48	7.586	0.1>p >0.05
	<i>Observed Ratio</i>	1.7	1	0.6	1			
Class totals	Raw data							
	<i>Observed Ratio</i>				1			

Observed ratio– to the nearest one decimal place

Interpreting the results of a chi square analysis

p value > 0.05

- *Your hypothesis may be correct and any differences between O and E due to chance.*
- *On the other hand, a p value > 0.05 Does NOT prove your hypothesis as competing hypotheses may also have a p value that is > 0.05.....*

p value < 0.05

- *Your hypothesis may be incorrect. The difference between E & O is not due to chance but due to an incorrect hypothesis. If we decide to reject the hypothesis based on the chi square analysis, what do we do or ask next?*
- *On the other hand, a p value < 0.05 does NOT disprove your hypothesis. Your hypothesis may be correct and something else is going that results in a difference between O and E that is not due to just to chance. We're not going to throw out our hypothesis just yet but:*

What should you do next?

Where would you go from here to resolve the problems? What could that something else be?