

**Key info****Mouse Parent 1 phenotype** = Brown fur**Mouse Parent 2 phenotype** = Brown fur

We want to figure out the genotypes of these mice, but we only know their phenotypes. One way to address this issue is to conduct genetic crosses, then statistically assess the results.

We can use a punnett square to **hypothesize** what offspring phenotypes we **expect**, based on a hypothesis about the parental genotypes.

**Null Hypothesis #1:** If both mouse parents are monohybrids, the resulting offspring will exhibit a 3:1 phenotypic ratio.

**Expected Phenotype ratio:** 3:1

**Monohybrid Cross (H/h X H/h):****F1 offspring produced:** 100**Expected F1 Phenotypes:** 75 brown fur, 25 white fur**Observed F1 phenotypes:** 59 brown fur, 41 white fur

		MALE	
		H	h
FEMALE	H	H/h	H/h
	h	H/h	h/h

The observed number of brown and white fur offspring differ from our expected 3:1 ratio; are these differences just due to random chance, or is our null hypothesis wrong?

A Chi Square Goodness of fit test can help answer this question!

**Chi-Square Test:****Degrees of freedom (using classes):** 2 phenotypic classes - 1 = 1**Degrees of freedom (using variables):** 1 independent variable = 1**Fill out the Chi-Square Table:**

Phenotype	Observed number	Expected number	O - E	(O - E) <sup>2</sup>	$\frac{(O - E)^2}{E}$
Brown fur	59	75 (100 x ¾)	-16	256	3.41
white fur	41	25 (100 x ¼)	16	256	10.24
$\chi^2 =$					13.65

Percentage Points of the Chi-Square Distribution									
Degrees of Freedom	Probability of a larger value of $\chi^2$								
	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

For 1 d.f., our  $\chi^2$  of 13.65 gives a **P value far less than 0.05**. This means there is **less than a 5% chance** that the differences between our Observed and Expected values are due to random chance. **Some other factor is likely at play here!**

Our null hypothesis #1 is mostly likely wrong; **we should reject it** and consider alternative hypotheses.

**New Null Hypothesis:** If the mouse parents are a homozygous recessive and a heterozygote, the resulting F1 offspring will exhibit a 1:1 phenotype ratio.

**Expected Phenotype ratio:** 1:1

**Expected F1 Phenotypes:** 50 brown fur, 50 white fur

**Observed F1 phenotypes:** 59 brown fur, 41 white fur

		MALE	
		H	h
FEMALE	H	H/h	H/h
	h	h/h	h/h

### Chi-Square Test #2:

**Degrees of freedom (using classes):** 2 phenotypic classes - 1 = 1

**Degrees of freedom (using variables):** 1 independent variable = 1

### Fill out the Chi-Square Table:

Phenotype	Observed number	Expected number	O - E	(O - E) <sup>2</sup>	$\frac{(O - E)^2}{E}$
Brown fur	59	50 (100 x 3/4)	9	81	1.62
white fur	41	50 (100 x 1/4)	-9	81	1.62
				$X^2 =$	3.24

Percentage Points of the Chi-Square Distribution									
Degrees of Freedom	Probability of a larger value of $x^2$								
	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

For 1 d.f., our  $X^2$  of 3.24 gives a **P value between 0.10 and 0.05**. This means there is a **5-10% chance** that the differences between our Observed and Expected values are due to random chance. We generally do not consider P values greater than 0.05 to be significant; thus, **we do NOT reject our null hypothesis**.

**Based on current evidence**, it seems the mouse parent genotypes are (H/h) and (h/h). Remember, new evidence could change our assessment — **we have not proven this to be true.**