

Chi-square is a statistical tool that helps us to decide if the observed ratio is close enough to the expected ratio to be acceptable. Chi-square analysis can be used in any area, not just genetics. Whenever you have to determine if an expected ratio fits an observed ratio, you can use the Chi-square.

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

Chi Square Significance Table

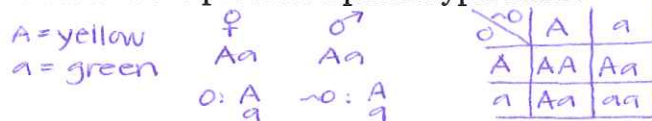
Degrees of Freedom (n)	5% Probability Value (P)
1	3.84
2	5.99
3	7.81
4	9.49

1. In peas, yellow seeds (A) are dominant over green (a) seeds. In a cross between two plants both heterozygous for seed color, the following was observed:

Yellow = 4400

Green = 1624

Does the data fit the predicted phenotypic ratio?



expected phenotypic ratio
3:1
yellow: green

Phenotype	Observed (O)	Expected (E)	O-E	(O-E) ²	$\frac{(O-E)^2}{E}$
Yellow	4400	6024(.75) 4518	-118	13924	3.08 = $\frac{13924}{4518}$
Green	1624	6024(.25) 1506	118	13924	9.24 = $\frac{13924}{1506}$
Totals	6024	6024			12.32

n = 2 - 1 = 1
P = 3.84

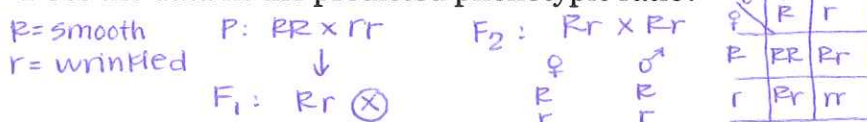
No, data does not fit predicted phenotype as
12.32 > 3.84

2. In peas, smooth seeds (R) are dominant over wrinkled (r) seeds. In the P generation, a plant homozygous for smooth seeds is crossed with a plant with wrinkled seeds. The resulting F₁ plants are crossed. The seeds of the observed F₂ generation were:

Smooth = 5474

Wrinkled = 1850

Does the data fit the predicted phenotypic ratio?



expected phenotypic ratio
3:1
smooth: wrinkled

Phenotype	Observed (O)	Expected (E)	O-E	(O-E) ²	$\frac{(O-E)^2}{E}$
smooth	5474	7324(.75) 5493	-19	361	0.07 = $\frac{361}{5493}$
wrinkled	1850	7324(.25) 1831	19	361	0.20 = $\frac{361}{1831}$
Totals	7324	7324			0.27

n = 2 - 1 = 1
P = 3.84

Yes the data fits the predicted phenotype
0.27 < 3.84

3. In a flowering plant, white flowers (B) are dominant over red (b), and short plants (E) are dominant over tall (e) plants. When two double heterozygote (BbEe) plants were crossed, the resulting phenotypes were observed:

White, short = 206
 Red, short = 83
 White, tall = 65
 Red, tall = 30

Does the data fit the predicted phenotypic ratio?

B = white E = short
 b = red e = tall

BbEe x BbEe

f white = 0.75 f short = 0.75
 f red = 0.25 f tall = 0.25

expected: white short : white tall : red short : red tall 9+3+3+1=16
 9 : 3 : 3 : 1 3/16 = 0.19
 (0.75)(0.75) (0.75)(0.25) (0.25)(0.75) (0.25)(0.25) 3/16 = 0.19
 0.56 : 0.19 : 0.19 : 0.06 1/16 = 0.06

Phenotype	Observed (O)	Expected (E)	O-E	(O-E) ²	$\frac{(O-E)^2}{E}$
white, short	206	384(0.56) = 215	-9	81	0.38 = $\frac{81}{215}$
red, short	83	384(0.19) = 73	10	100	1.37 = $\frac{100}{73}$
white, tall	65	384(0.19) = 73	-8	64	0.88 = $\frac{64}{73}$
red, tall	30	384(0.06) = 23	7	49	2.13 = $\frac{49}{23}$
Totals	384	384			4.76

n = 4 - 1 = 3
 P = 7.81

Yes, the data fit the predicted phenotype
 4.76 < 7.81

4. In corn, purple kernels (D) are dominant over yellow (d), and smooth kernels (G) are dominant over shrunken (g). An ear of corn has 381 kernels, illustrated at right:

A: purple, smooth = 216
 B: purple, shrunken = 79
 C: yellow, smooth = 65
 D: yellow, shrunken = 21

Does the data fit your predicted phenotypic ratio?
 (Your prediction would be the kernels are the result of a double heterozygous cross with a ratio of 9:3:3:1)



DdGg x DdGg
 purple = 0.75 = $\frac{3}{4}$
 yellow = 0.25 = $\frac{1}{4}$
 smooth = 0.75 = $\frac{3}{4}$
 shrunken = 0.25 = $\frac{1}{4}$
 purple, smooth = 3x3 = 9 0.75 x 0.75 = 0.56
 purple, shrunken = 3x1 = 3 0.75 x 0.25 = 0.19
 yellow, smooth = 1x3 = 3 0.25 x 0.75 = 0.19
 yellow, shrunken = 1x1 = 1 0.25 x 0.25 = 0.06

Phenotype	Observed (O)	Expected (E)	O-E	(O-E) ²	$\frac{(O-E)^2}{E}$
purple, smooth	216	381(0.56) = 213	3	9	0.04 = $\frac{9}{213}$
purple, shrunken	79	381(0.19) = 72	7	49	0.68 = $\frac{49}{72}$
yellow, smooth	65	381(0.19) = 72	-7	49	0.68 = $\frac{49}{72}$
yellow, shrunken	21	381(0.06) = 23	-2	4	0.17 = $\frac{4}{23}$
Totals	381	380			1.57

n = 4 - 1 = 3
 P = 7.81

Yes, the data fit the predicted phenotype
 1.57 < 7.81

6. Color blindness is a sex-linked trait in Bombats. A female who is a carrier of the color blind allele mates with a male who is color blind. The phenotypes of their offspring are:

Normal female = 132
 Color blind female = 124
 Normal male = 126
 Color blind male = 136

Expected Phenotypic Ratio

Normal ♀ = 1 = 0.25
 Colorblind ♀ = 1 = 0.25
 Normal ♂ = 1 = 0.25
 Colorblind ♂ = 1 = 0.25

Does the data fit your predicted phenotypic ratio?

X^B = normal
 X^b = colorblind
 Y = male

♀: $X^B X^b$
 ♂: $X^b Y$

♀ \ ♂	X^b	Y
X^B	$X^B X^b$	$X^B Y$
X^b	$X^b X^b$	$X^b Y$

Phenotype	Observed (O)	Expected (E)	O-E	(O-E) ²	$\frac{(O-E)^2}{E}$
Normal ♀	132	$518(0.25) = 129$	4	16	$\frac{16}{129} = 0.12$
Colorblind ♀	124	129	-5	25	$\frac{25}{129} = 0.19$
Normal ♂	126	129	-3	9	$\frac{9}{129} = 0.07$
Colorblind ♂	136	129	7	49	$\frac{49}{129} = 0.38$
Totals	518	~ 518			0.76

$n = 4 - 1 = 3$

$P = 7.81$

Yes, the data fit the predicted phenotype

$0.76 < 7.81$

7. In cats, fur color is determined by the codominant, sex-linked alleles: black (B) and orange (O). A calico female ($X^B X^O$) is bred (many times) with a black male ($X^B Y$). They produce the following offspring:

Black female = 78
 Calico female = 65
 Black male = 81
 Orange male = 45

Expected Phenotypic Ratio

Black ♀ = 1 = 0.25
 Calico ♀ = 1 = 0.25
 Black ♂ = 1 = 0.25
 Orange ♀ = 1 = 0.25

Does the data fit your predicted phenotypic ratio?

X^B = Black
 X^O = Orange
 Y = male

♀: $X^B X^O$
 ♂: $X^B Y$

♀ \ ♂	X^B	Y
X^B	$X^B X^B$	$X^B Y$
X^O	$X^B X^O$	$X^O Y$

Phenotype	Observed (O)	Expected (E)	O-E	(O-E) ²	$\frac{(O-E)^2}{E}$
Black ♀	78	$269(0.25) = 67$	11	121	$\frac{121}{67} = 1.81$
Calico ♀	65	67	-2	4	$\frac{4}{67} = 0.06$
Black ♂	81	67	14	196	$\frac{196}{67} = 2.93$
Orange ♂	45	67	-22	484	$\frac{484}{67} = 7.22$
Totals	269	~ 269			12.02

$n = 4 - 1 = 3$

$P = 7.81$

No, the data doesn't fit The predicted phenotype

$12.02 > 7.81$