

## Chi Squared Test for Genetics (Using TiNspire)

The chi squared ( $\chi^2$ ) test for comparing observed results in a genetics cross with the expected ratios (no linkage) is called a “**Goodness of Fit**” test. The test tells us if our sample significantly differs from the ratio we expect. If it doesn't, then we can assume no linkage, if it does differ significantly then we must suspect linkage between the genes.

### Degrees of Freedom

The  $\chi^2$  distribution is dependent on the number of degrees of freedom (df).

When you have an observed ratio of phenotypes that you are comparing to the ratios you get in a punnet square, the degrees of freedom are “**Number of phenotypes – 1**”

### $\chi^2$ values, p-values and critical values

We compare either the  $\chi^2$  value or the p-value (found with GDC) to another number to determine if the null hypothesis is accepted or rejected.

**Accepting the null hypothesis** means the observed ratio is **not significantly different** from the expected ratio (no linkage).

**Rejecting the null hypothesis** means the observed ratio is **significantly different** from the expected ratio (linkage).

We always test at the **5% significance level**. This means we are 95% confident that the differences between observed and expected values are only due to chance.

The **p-value** is calculated on your GDC. You can ALWAYS accept or reject using this (rather than the critical value).

If the **p-value is more than** the significance level ( 0.05 ) we **accept the null hypothesis**.

If the **p-value is less than** the significance level ( 0.05 ) we **reject the null hypothesis**.

In an exam, you may be given a **critical value** (at 95% significance level). This is used to compare with the  $\chi^2$  value.

If the  $\chi^2$  **value is less than** the **critical value**, we **accept the null hypothesis**.

If the  $\chi^2$  **value is more than** the **critical value**, we **reject the null hypothesis**.

Here is a set of results from one of Mendel's pea experiments:

Parental generation = heterozygous round + yellow

F <sub>1</sub> generation:	phenotype	observed	expected proportion	expected number
	round yellow	315	9/16	312.75
	round green	101	3/16	104.25
	wrinkled yellow	108	3/16	104.25
	wrinkled green	32	1/16	34.75
	total	556	1	556

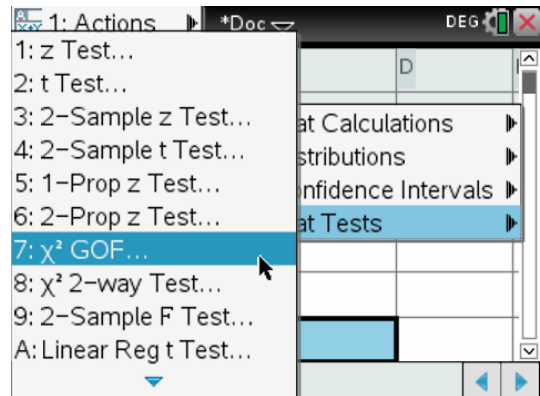
## Using the Calculator

Open spreadsheet document from home screen

- Enter observed results (NOT TOTAL) in column A
- Name Column A at top (eg OBS)
- Enter expected number in next column
- Name column B at top (eg EXPECT)

	A obs	B expect	C	D
1	315	312.75		
2	101	104.25		
3	108	104.25		
4	32	34.75		
5				

- MENU → 4. Statistics → 4. Stat Tests → 7.  $\chi^2$  GOF



- Click on each pop-up box to select the correct column
- Enter the correct number of degrees of freedom
- Click OK or press ENTER

$\chi^2$  GOF

Observed List: 'obs'

Expected List: 'expect'

Deg of Freedom, df: 3

1st Result Column: d[]

Draw:  Shade P Value

OK

The display will include the  $\chi^2$  value, p-value and df.

	D	E	F
=		= $\chi^2$ GOF('ot	
1	Title	$\chi^2$ GOF	
2	$\chi^2$	0.470023...	
3	PVal	0.9254259	
4	df	3.	