

# Module 4C: Hypothesis Testing

Agenda:

- **Mendel!**

# Was Mendel's data 'too good'?

- RA Fisher (gently) accused Mendel of having data that fit too well (approx. 3/100,000 experiments should have data that fit as well as Mendel's)
- A raging debate ever since:
  - <http://www.istics.net/stat/>
    - Go to “Not random enough” in the sidebar
  - <http://arxiv.org/pdf/1104.2975.pdf>

The results of a **Monohybrid cross** between a (heterozygous) yellow pea plant (**Yy**) and a green pea (**yy**) plant are as follows: **14 yellow** and **6 green**. Are these results consistent with Mendel's first law (**segregation**) which should a 1:1 ratio in this case? (alpha = 0.05). Punnet square shown:

Yellow (Hetero)\Green (Homo)	y	y	
Y	Yy	Yy	← 14
y	yy	yy	← 6

- A. Yes – the results FTR the null hypothesis
- B. No – the results Reject the null hypothesis
- C. Yes – the results reject the null hypothesis
- D. No – the results FTR the null hypothesis

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### Step 1

**H<sub>0</sub>:**

*If the hypothesis (Yy is yellow and yy is green) is true then we would expect a 1:1 ratio in progeny (or, to put it into counts: 10 **Yellow** and 10 green)*

**H<sub>A</sub>:**

*The genotypes that result in **Yellow** and green are not simply Yy and yy (there may be something else going on)*

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### Step 2 Test Statistic:

assumptions: no category with expected freq < 1; no more than 20% categories have expected freq < 5

$$X^2 = (14-10)^2/10 + (6-10)^2/10 = 1.6 + 1.6 = 3.2$$

step 3 dof = # categories – 1 = 1

**critical value that corresponds to 0.05 = 3.84**

step 4 conclusion: since the critical value > value calculated from the **X<sup>2</sup>** test statistic; the ratio of progeny obtained is FTR Ho; **consistent** with a 1:1 ratio.