

Two (2) examples of proper Punnett Squares.

One (1.): ***Fruit Fly Eye Colour Punnett Square***

Punnett Square 1:  $E_1 E_4 \times E_1 E_4$

|       |           |           |
|-------|-----------|-----------|
|       | $E_1$     | $E_4$     |
| $E_1$ | $E_1 E_1$ | $E_1 E_4$ |
| $E_4$ | $E_1 E_4$ | $E_4 E_4$ |

Genotype ratios: **1**  $E_1 E_1$  : **2**  $E_1 E_4$  : **1**  $E_4 E_4$

Phenotype ratios: **3**  $E_1$  : **1**  $E_4$

In the python code, strings such as “E\_1” or “E\_4” represent “E sub 1” or “E sub 4” i.e. a subscript when copied from script output to rich text for presentation.

Two (2.): ***Pea Colour And Roundness Punnett Square***

Punnett Square 2:  $YyRr \times Yyrr$

|    |      |      |      |      |
|----|------|------|------|------|
|    | Yr   | Yr   | yr   | yr   |
| YR | YYRr | YYRr | YyRr | YyRr |
| Yr | YYrr | YYrr | Yyrr | Yyrr |
| yR | YyRr | YyRr | yyRr | yyRr |
| yr | Yyrr | Yyrr | yyrr | yyrr |

Genotype ratios: (not going to even bother)

Phenotype ratios: **6** YR : **6** Yr : **2** yR : **2** yr

The python code can do as many rows/columns as possible (practically infinite) and doesn't have to manually (cognitively, laboriously) count them – which is prone to human error! Not only does it save time and eye strain from staring at the tables in a rich text editor, but it is more practical realistically.

As realistically, humans have many thousands of genes, not just two. Some with complementary genetic interactions (such as human hair colour) which are *not* simple (Mendelian) phenotypic expressions as in: balding, mid-digit (human finger) hair, ABO blood type, or pea plant colour (yellow or green). I believe this is indeed what professional genomicists do in their sequencing and mapping work done on data from projects like the Human Genome Project—*automate!* Whether their software be made by a separate IT department or not—all the better if self-directed automation!

The biology teacher may not enjoy it, though.