

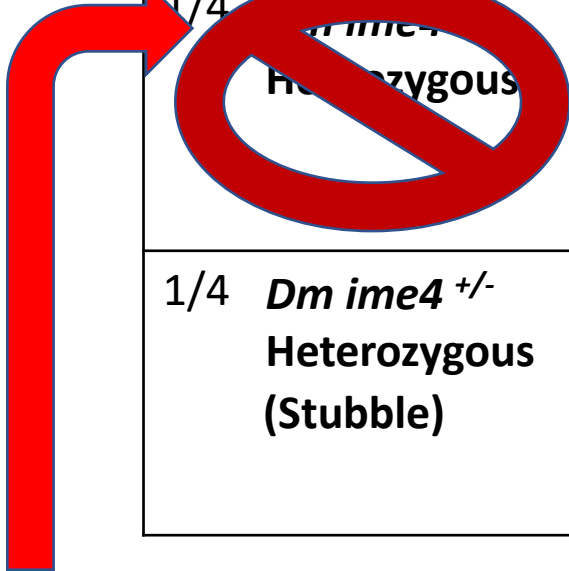
*Dm ime4* mutant/TM3<sup>Sb</sup> X *Dm ime4* mutant/TM3<sup>Sb</sup>

The corrected ratios are 2/3 heterozygous, 1/3 homozygous *Dm ime4* mutants

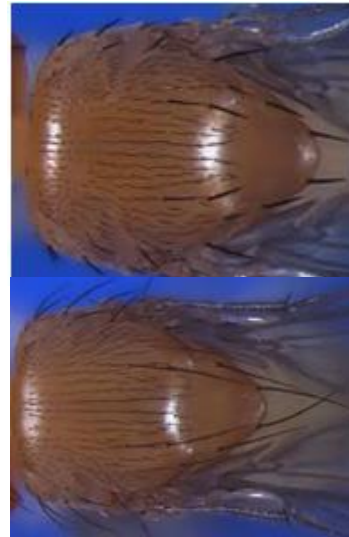
Adults: 1/3 expected to be *Dm ime4* <sup>-/-</sup> Homozygous.

E.g. out of 120 adults, 40 are expected to be homozygous *Dm ime4* mutant.

1/4 <i>Dm ime4</i> <sup>-/-</sup> Homozygous (Stubble)	1/4 <i>Dm ime4</i> +/- Heterozygous (Stubble)
1/4 <i>Dm ime4</i> +/- Heterozygous (Stubble)	1/4 <i>Dm ime4</i> <sup>-/-</sup> Homozygous (non-Stubble)



But TM3<sup>Sb</sup>/TM3<sup>Sb</sup> Homozygous balancer Dies before adulthood



Stubble

## Chi-square Goodness of Fit Test Formulas

Null Hypothesis  $\rightarrow H_0 : \text{Observed} = \text{Expected}$

Alternate Hypothesis  $\rightarrow H_a : \text{Observed} \neq \text{Expected}$

Test Statistic (that symbol is called "Chi-squared")  $\rightarrow \chi^2 = \sum \frac{(O - E)^2}{E}$

$df = (\# \text{ of categories}) - 1$

$P\text{-Value} = \chi^2 \text{cdf}(\chi^2, 9999, df)$

The null and alternate hypotheses are always the same with a Goodness of Fit Test.

O is the observed count for each category and E is the expected count for each category.

Instead of a normal or t distribution, we now have a chi-squared distribution