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

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

**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.

But TM3<sup>SB</sup>/TM3<sup>SB</sup> homozygous balancer dies before adulthood.

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

**Chi-square Goodness of Fit Test Formulas**

**Null Hypothesis**

\[ H_0 : \text{Observed} = \text{Expected} \]

**Alternate Hypothesis**

\[ H_a : \text{Observed} = \text{Expected} \]

**Test Statistic**

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

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

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

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

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

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