How to Determine Dominance in a Fruit Fly Cross

Inheritance possibilities: autosomal recessive or dominant inheritance, non-linked genes with independent assortment, linked genes, sex-linked recessive or dominant

1. The goal of the lab is to determine the genotypes from the given phenotypes and determine the pattern of inheritance that the cross represents
2. First, determine if the cross is involving **one trait or two traits** which would indicate a MONOHYBRID or a DIHYBRID cross
   a. This means you will be using a single gene with 2 alleles or two genes with 4 alleles
3. Next, determine if the trait(s) appears to be **sex-linked or autosomal inheritance**
   a. Look at the F1 and F2 generation's numbers and if there is a significant difference in numbers between males and females, then it is SEX-LINKED
   b. If the numbers are pretty similar across the phenotypic groups then the trait(s) is AUTOSOMAL inheritance
4. If the inheritance is SEX-LINKED, determine if the gene is recessive or dominant by looking at all the phenotypes and data across the P, F1, and F2 generations.
   a. Keep the male and the female data separate and each sex with the different traits will be its own phenotypic group (Ex: male with wild type and male with mutant type are two different phenotypic groups)
   b. You will need to do some sample Punnett squares to figure out the dominance using the XX and XY with a superscript big and little letters to represent the gene
5. If the inheritance is AUTOSOMAL, determine if the gene is recessive or dominant by looking at all the phenotypes and data across the P, F1, and F2 generations.
   a. **Combine the numbers for the males and females and then evaluate the data. If the inheritance is not sex-linked then the different numbers obtained for males and females does not matter.** This will make each trait listed in the data chart the phenotypic groups NOT traits separated by sex. (Ex: wild type – males and females and mutant type – males and females make two phenotypic groups)
   b. You will need to do some sample Punnett squares (monohybrid or dihybrid depending on the number of genes involved) to figure out the dominance using big and little letters to represent the gene(s).
6. Finally, using the data from the **F2 generation** determine what your expected numbers would be based on the ratios predicted for the outcome of the F1 cross using the total numbers of fruit flies that were actually counted
   a. Ex: If a 3:1 ratio is predicted for an autosomal recessive cross and 100 fruit flies were counted, the expected numbers would be 75 showing the dominant trait and 25 showing the recessive trait
7. Writing a null hypothesis (This is one example of how to write the null hypothesis)
   a. Must include: type of inheritance, parents, and expected ratios/outcomes
   b. If _____ inheritance cross is done between _____ parents, then _____ ratio is expected in the F2 generation (or what fractions will occur for each phenotype)
   c. If you suspect linked genes, then the null hypothesis will be non-linked genes with independent assortment
   d. Ex: If a sex-linked recessive cross is done between a red-eyed male and white-eyed female, then there will be all red-eyed females and white-eyed males in the F2 generation.
8. Complete the Chi square analysis using the observed numbers in the F2 generation and the calculated expected numbers for each phenotypic group in the F2 generation. Fill in the data requested on the handout and justify whether you accept or reject your null hypothesis.