

Drosophila Lab

Introduction

In this lab, we'll be doing virtual fly matings to study how traits are inherited. We will be using a python notebook to analyze data.

Directions:

Cross 1:	Choose a trait (this will be trait one). Cross a mutant male with a wild type female
Cross 2:	Choose trait number two. Cross a male with mutant trait one and normal trait two with a female of wild type trait one and mutant type trait two.
Cross 3:	Cross a wild type male with a female of a different mutation of trait one.

1. Go to <http://www.sciencecourseware.org/vcise/drosophila/>
2. Click the "Enter as a Guest" option
3. Do not back out of this page until you are completely done – or you will have to start over!
4. Order your fruit flies. Use the "Order Flies" icon. We are going to perform three different crosses. For each one, you will need to order the correct flies. Add the flies you want for cross 1 to your cart and then hit checkout.
5. After ordering your flies, you will have to work through the lab until you eventually have sorted your F1 progeny. Make sure you record all of the necessary data in your data table (page 2).
6. After you have recorded the data, you will need to establish a cross between members of your F1 generation. To do this, click on the piles of sorted flies to zoom in. Then click the "Use in New Mating" button. Do this for both a male and a female. Then return to your lab. Click on the mating jar.
7. Sort your progeny and record the necessary data in the F2 data table.
8. After you collect F2 data, clean out your incubator by clicking on the small trash can next to it. This resets your lab for the next cross.
9. Now that you have the F2 data, you can begin to formulate some conclusions about the mode of inheritance for the traits you are looking at.
10. Perform two other crosses. To order new flies, click on the computer and repeat.
11. When you have performed all of the crosses, move to the python analysis portion of the lab.

Example crosses:

- a. Cross 1: Cross a sepia eye male with a wild type female
- b. Cross 2: Cross a sepia eye, normal wing male with a wild type eye, vestigial wing female
- c. Cross 3: Cross a wild type male with a white eye female

DATA TABLES

Cross 1: P generation = mutant trait1 male * wild type female

Table 1: Phenotypes of F1 Generation

Phenotype	Number of Males	Number of Females

Table 2: Phenotypes of F2 Generation

Phenotype	Number of Males	Number of Females

Hypothesize the mode of inheritance of trait # 1: _____
Is this a monohybrid or dihybrid cross?

Cross 2: P generation = mutant trait1, normal trait2 male * wild type trait1, mutant trait2 female

Table 1: Phenotypes of F1 Generation

Phenotype	Number of Males	Number of Females

Table 2: Phenotypes of F2 Generation

Phenotype	Number of Males	Number of Females

Hypothesize the mode of inheritance of the sepia eye trait:

Hypothesize the mode of inheritance of the vestigial wing trait:

Do you think the two traits are linked?

Is this a monohybrid or dihybrid cross?

Cross 3: P generation = wild type male * mutant trait1 female

Table 1: Phenotypes of F1 Generation

Phenotype	Number of Males	Number of Females

Table 2: Phenotypes of F2 Generation

Phenotype	Number of Males	Number of Females

Hypothesize the mode of inheritance of the white eye trait:

Is this a monohybrid or dihybrid cross?

DATA ANALYSIS

1. In the space below, construct two Punnett squares for each cross to predict the expected results of both the parental and F1 crosses from your null hypothesis.

Cross 1: P generation = sepia male * wild type female

Parental Cross	F1 Cross

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Cross 2: P generation = sepia-eye, normal-wing male * wild type, vestigial wing female

Parental Cross	F1 Cross

Cross 3: P generation = wild type male * white eye female

Parental Cross	F1 Cross

2. Refer to the Punnett Squares above. In the boxes below, record the **expected** ratios for the genotypes and phenotypes of the F1 and F2 generations in the experiment.

Cross 1: P generation = sepia male * wild type female

	Expected Genotype Ratio	Expected Phenotype Ratio
F1		

F2		
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Cross 2: P generation = sepia-eye, normal-wing male * wild type, vestigial wing female

	Expected Genotype Ratio	Expected Phenotype Ratio
F1		
F2		

Cross 3: P generation = wild type male * white eye female

	Expected Genotype Ratio	Expected Phenotype Ratio
F1		
F2		

- Do the observed results deviate from your expected results? If so, explain how:

CHI SQUARE ANALYSIS IN PYTHON

- Download the example_data.csv and Fly_lab.ipymb files from canvas.
- Open Anaconda on your computer and navigate to the Jupyter notebook part and open up the Fly_lab.ipymb file.
- Follow the tutorial in the code.
- When you're done, move on to Step 5 so you can try the data analysis with your own data.
- Open up excel and type in the your F2 data for the first cross as shown below. Use the expected phenotype ratio based on your hypotheses from above.

	A	B	C	D
1	Observed	Expected		
2	70	75		
3	30	25		
4				
5				
6				

- Save the data as a csv file.
- Use Fly_lab.ipymb as a template to do data analysis on your Cross one F2 data. Copy the results into your chi square tables (below).
- When you're done, repeat the analysis for the other two crosses you did.

CHI SQUARE ANALYSIS

Cross 1: P generation = mutant trait1 male * wild type female

Phenotype	Observed	Expected	(o-e)	(o-e) ² /e

$\chi^2 =$

How many degrees of freedom are there? _____

What is the critical value? _____

Do you accept or reject your H₀? _____

Cross 2: P generation = mutant trait1, normal trait2 male * wild type trait1, mutant trait2 female

Phenotype	Observed	Expected	(o-e)	(o-e) ² /e

$\chi^2 =$

How many degrees of freedom are there? _____

What is the critical value? _____

Do you accept or reject your H₀? _____

Cross 3: P generation = wild type male * mutant trait1 female

Phenotype	Observed	Expected	(o-e)	(o-e) ² /e

$\chi^2 =$

How many degrees of freedom are there? _____

What is the critical value? _____

Do you accept or reject your H₀? _____