

VIRTUAL FLYLAB

INTRODUCTION:

FlyLab will allow you to play the role of a research geneticist. You will use FlyLab to study important introductory principles of genetics by developing hypotheses and designing and conducting mating's between fruit flies with different mutations that you have selected. Once you have examined the results of a simulated cross, you can perform a statistical test of your data by chi-square analysis and apply these statistics to accept or reject your hypothesis for the predicted phenotypic ratio of offspring for each cross. With FlyLab, it is possible to study multiple generations of offspring, and perform testcrosses and backcrosses. FlyLab is a very versatile program; it can be used to learn elementary genetic principles such as dominance, recessiveness, and Mendelian ratios, or more complex concepts such as sex linkage, epistasis, recombination, and genetic mapping.

You will be responsible for mating the flies and collecting data concerning what happens as mutant traits are passed form one generation to the next. Assignments of crosses will be made for particular genetic crosses of flies having one or two mutations. The types of crosses available are:


1. *Monohybrid*. In these experiments, the method of inheritance is determined when a single contrasting pair of characteristics is involved.
2. *Dihybrid*. In these experiments, the method of inheritance is determined when two pairs of contrasting characteristics are considered simultaneously.
3. *Sex-linked*. In these experiments, the method of inheritance is determined when the mutant characteristic is associated with the X chromosome.

OBJECTIVES & GOALS:

- Simulate basic principles of genetic inheritance based on Mendelian genetics by designing and performing crosses between fruit flies.
- Help you understand the relationship between an organism's genotype and its phenotype.
- Demonstrate the importance of statistical analysis to accept or reject a hypothesis.
- Use genetic crosses and recombination data to identify the location of genes on a chromosome by genetic mapping.

PART I: ACCESSING THE VIRTUAL FLYLAB

1. Type in the following web address on the address line of the browser:
<http://biologylab.awlonline.com>

2. Click on the FlyLab **Free Trial** button when the  Welcome to Biology Labs Online window displays. Then click on **Register here**. Follow the directions. A username and password will be sent to your email.
3. Once you receive your username and password, the easiest thing to do is when you return to homepage and enter fly lab is to copy and paste them into the appropriate places.
4. Click on the Start Lab Button.

PART II: GETTING TO KNOW THE FLYLAB

7. Click on the Help Page link on the left of the screen. (although, if you follow my directions below, you won't need to use this!!!)
8. Read the information on this page to get an understanding of how the controls in the FlyLab work.

PART III: MATING FLIES – CROSS #1

9. In the FlyLab window, click on the drop down arrow and select **10,000** offspring.
10. Click on the **Design button** under the female fly.
11. The first cross will follow the **inheritance of eye color**. Click on the Eye Color button and make sure the **Wild Type (red) eyes** is selected.
12. Click on the Select button under the fly.
13. Click on the Design button under the male fly.
14. Click on the Eye Color button and select **Sepia (brown) eyes**.
15. Click on the Select button under the fly.
16. Now that you have designed the female and male fly, you are ready to mate the flies. Click on the Mate button located between the two flies.
17. Click on the **Analyze Results** button.
18. Click, on the **Add Data to Notebook** button. The data from the first cross should appear in the Notebook window. (I recommend you copy and paste this into a word document; labeling and keeping your data organized will be very helpful!!!)
19. Click on the **Return to Lab** button.
20. To perform the F₁ cross, click on the Select button under the female and male offspring. Notice that when you click on the Select button, the offspring fly is transferred to the top.

21. Click on the **Mate** button between the two flies.
22. The F₂ offspring should appear in the window. You can click on the green arrow to scroll through all the F₂ offspring.
23. Click on the **Analyze Results** button.
24. Click, on the **Add Data to Notebook** button. The data from the second cross should appear in the Notebook window. (Again, I recommend you copy and paste this into a word document; make sure you label. You will find keeping your data labeled and organized to be very helpful!)
25. Click on the **Export Notes** button in the Notebook window. Print one copy of your notes. Label your notes "**Results of Cross #1**". (If you have copied and pasted into a word document like I recommend, then you can print one copy once you finish all the Results below...otherwise, print and label as you go)
26. Once you have one copy of your notes, select all the information in the Notebook window and hit the delete button (everything will be deleted, so I hope you saved in word or printed!)

PART IV: MATING FLIES – CROSS #2

27. Click on the **Return to Lab** button.
28. Click on the **New Mate** button.
29. Make sure the **10,000 offspring** option is still selected.
30. Click on the **Design button** under the female fly and select the following traits:
Eye Color = Wild
Wing Size = Vestigial
31. Click on the **Design button** under the male fly and select the following traits:
Eye color = Sepia
Wing Size = Wild
32. Click on the **Mate** button between the two flies.
33. Click on the **Analyze Results** button.
34. Click on the **Add Data to Notebook** button. (copy and paste into word and label)
35. Click on the **Return to Lab** button.

36. To perform the F₁ cross, click on the Select button under the female and male offspring. Notice that when you click on the Select button, the offspring fly is transferred to the top.
37. Click on the **Mate** button between the two flies.
38. The F₂ offspring should appear in the window. You can click on the green arrow to scroll through all the F₂ offspring.
39. Click on the **Analyze Results** button.
40. Click, on the **Add Data to Notebook** button. The data from this cross should appear in the Notebook window.
41. Click on the **Export Notes** button in the Notebook window. Print one copy of your notes. Label your notes "**Results of Cross #2**". (or copy and paste into word document and label)
42. Once you have two copies of your notes, select all the information in the Notebook window and hit the **delete** button. (I hope you saved or printed, because it's gone!)

PART V: MATING FLIES – CROSS #3

43. Click on the **Return to Lab** button.
44. Click on the **New Mate** button.
45. Make sure the **10,000 offspring** option is still selected.
46. Click on the Design button under the female fly and select the following trait:
Eye Color = White
47. Click on the Design button under the **male fly** and select the following trait:
Eye color = Wild
48. Click on the **Mate** button between the two flies.
49. Click on the **Analyze Results** button.
50. Click on the **Add Data to Notebook** button.
51. Click on the **Return to Lab** button.
52. To perform the F₁ cross, click on the Select button under the female and male offspring. Notice that when you click on the Select button, the offspring fly is transferred to the top.

53. Click on the **Mate** button between the two flies.
54. The F₂ offspring should appear in the window. You can click on the green arrow to scroll through all the F₂ offspring.
55. Click on the **Analyze Results** button.
56. Click, on the **Add Data to Notebook** button. The data from this cross should appear in the Notebook window.
57. Click on the **Export Notes** button in the Notebook window. Print one copy of your notes. Label your notes "**Results of Cross #3**".
58. Once you have one copy of your notes, select all the information in the Notebook window and hit the **delete** button. (If you copy and pasted into word as I recommended, and labeled, you are now ready to print the whole document!)

PART VI: DATA ANALYSIS – CROSS #1

59. What mutation(s) were you following in this cross? (NOTE: Wild type is not a mutation. It is the normal condition in flies.)

60. Examine the data you collected from your crosses (F₁ Generation and F₂ Generation results). Make a hypothesis about the pattern of inheritance in this cross by answering the following questions:
 - a. Is the cross autosomal or sex-linked? _____
 - b. Is(are) the mutation(s) dominant or recessive? _____
 - c. Is the cross monohybrid or dihybrid? _____
61. Using the key below and the answers to the previous question, construct a Punnett square to predict results of the P (parental) cross and the F₁ cross. If you are sure that the cross is not sex-linked, you should combine the male and female numbers for the same phenotypes. **Remember: You have to have one allele from EACH parent of the trait you are crossing for each genotype! Go back to initial directions to verify your parental crosses.**

KEY:				
+	Wild type	SE	Sepia eyes	
W	White eyes	VG	Vestigial Wings	

P Cross: _____ x _____
 (female genotype) (male genotype)

Punnett Square:

F₁ Cross: _____ x _____
 (female genotype) (male genotype)

Punnett Square:

62. According to the Punnett square results, what are the expected phenotypic ratios of the F₁ and F₂ offspring? If you are sure your cross is not sex-linked, you should combine the male and female data for the same phenotypes.

CROSS	EXPECTED PHENOTYPIC RATIO
F ₁	
F ₂	

63. Look at the results of the F₁ cross (shows the F₂ generation). How many total flies were produced in this cross?
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64. Calculate the number of individuals you would expect to be produced from this cross. To do this you need to multiply the expected ratio (or percent) by the total number of flies produced in the cross. If you are sure that your cross is not sex-linked, you should combine the male and female data for the same phenotype.

PHENOTYPES	Expected Ratio or Percent	EXPECTED NUMBER

CHI-SQUARE ANALYSIS

Chi-square is a statistical test commonly used to compare observed data with data we would expect to obtain according to a specific hypothesis. For example, if, according to Mendel's laws, you expected 10 of 20 offspring from a cross to be male and the actual observed number was 8 males, then you might want to know about the "goodness of fit" between the observed and expected. Were the deviations (differences between observed and expected) the result of chance, or were they due to other factors? How much deviation can occur before the investigator must conclude that something other than chance is at work, causing the observed to differ from the expected? The chi-square test can help in making that decision. The chi-square test is always testing what scientists call the **null hypothesis**, which states that there is no significant difference between the expected and observed result.

The formula for calculating chi-square (χ^2) is:

$$\chi^2 = \sum \frac{(o-e)^2}{e}$$

That is, chi-square is the sum of the squared difference between observed (o) and expected (e) data, divided by the expected data in all possible categories. For example, suppose that a cross between two pea plants yields a population of 880 plants, 639 with green seeds and 241 with yellow seeds. You are asked to propose the genotypes of the parents. Your *hypothesis* is that the allele for green is dominant to the allele for yellow and that the parent plants were both heterozygous for this trait. If your hypothesis is true, then the predicted ratio of offspring from this cross would be 3:1 (based on Mendel's laws) as predicted from the results of a Punnett square.

To calculate χ^2 , first determine the number expected in each category. If the ratio is 3:1 and the total number of observed individuals is 880, then the *expected numerical values* should be 660 green and 220 yellow. **NOTE: Chi-square requires that you use numerical values, not percentages or ratios.**

Then calculate χ^2 using the formula.

$$\chi^2 = \frac{(639 - 660)^2}{660} + \frac{(241 - 220)^2}{220}$$
$$\chi^2 = 0.668 + 2.005$$
$$\chi^2 = 2.673$$

The next step is to interpret the χ^2 value. To do this you need to:

Determine the **degrees of freedom** (df). Degrees of freedom can be calculated as the number of categories in the problem minus 1. In our example, there are two categories (green and yellow); therefore, there is 1 degree of freedom.

Determine a relative standard to serve as the basis for accepting or rejecting the hypothesis. The relative standard commonly used in biological research is $p > 0.05$. The **p value** is the *probability* that the deviation of the observed from the expected is due to chance alone (no other forces acting). In this case, using $p > 0.05$, you would expect any deviation to be due to chance alone 5% of the time or less.

Refer to the chi-square distribution table below. Using the appropriate degrees of freedom, locate the value closest to your calculated chi square in the table. Determine the closest p (probability) value associated with your chi-square and

degrees of freedom. In this case ($\chi^2 = 2.673$), the p value is about 0.10, which means that there is a 10% probability that any deviation from expected results is due to chance only. Based on our standard $p > 0.05$, this is within the range of acceptable deviation. In terms of your hypothesis for this example, the observed chi-square is not significantly different from expected. The observed numbers are consistent with those expected under Mendel's laws.

CHI-SQUARE DISTRIBUTION

Degrees of Freedom	Probability (p)										
	0.95	0.90	0.80	0.70	0.50	0.30	0.20	0.10	0.05	0.01	0.001
1	0.004	0.02	0.06	0.15	0.46	1.07	1.64	2.71	3.84	6.64	10.83
2	0.10	0.21	0.45	0.71	1.39	2.41	3.22	4.60	5.99	9.21	13.82
3	0.35	0.58	1.01	1.42	2.37	3.66	4.64	6.25	7.82	11.34	16.27
4	0.71	1.06	1.65	2.20	3.36	4.88	5.99	7.78	9.49	13.38	18.47
5	1.14	1.61	2.34	3.00	4.35	6.06	7.29	9.24	11.07	15.09	20.52
6	1.63	2.20	3.07	3.83	5.35	7.23	8.56	10.64	12.59	16.81	22.46
7	2.17	2.83	3.82	4.67	6.35	8.38	9.80	12.02	14.07	18.48	24.32
8	2.73	3.49	4.59	5.53	7.34	9.52	11.03	13.36	15.51	20.09	26.12
9	3.32	4.17	5.38	6.39	8.34	10.66	12.24	14.68	16.92	21.67	27.88
10	3.94	4.86	6.18	7.27	9.34	11.78	13.44	15.99	18.31	23.21	29.59

65. Calculate the chi-square value for the F₂ generation in the space below. You must show all work.

$$\chi^2 = \underline{\hspace{2cm}}$$

66. Use the Chi-Square Distribution Table from the lab packet to determine the percent probability that the observed variation is due to random chance alone.

Degrees of freedom = _____

% Probability = _____

67. Was the deviation between the expected and observed data due to chance alone?

How do you know? _____

68. Based on the answer to the previous question, should you accept or reject your hypothesis regarding the pattern of inheritance for this cross?

Explain. _____

PART VII: DATA ANALYSIS – CROSS #2

69. What mutation(s) were you following in this cross? (NOTE: Wild type is not a mutation. It is the normal condition in flies.)

70. Examine the data you collected from your crosses (F₁ Generation and F₂ Generation results). Make a hypothesis about the pattern of inheritance in this cross by answering the following questions:

a. Is the cross autosomal or sex-linked? _____

b. Is(are) the mutation(s) dominant or recessive? _____

c. Is the cross monohybrid or dihybrid? _____

71. Using the key below and the answers to the previous question, construct a Punnett square to predict results of the P (parental) cross and the F₁ cross. If you are sure that the cross is not sex-linked, you should combine the male and female numbers for the same phenotypes.

KEY:			
+	Wild type	SE	Sepia eyes
W	White eyes	VG	Vestigial Wings

P Cross: _____ x _____
 (female genotype) (male genotype)

Punnett Square:

F₁ Cross: _____ x _____
 (female genotype) (male genotype)

Punnett Square:

72. According to the Punnett square results, what are the expected phenotypic ratios of the F₁ and F₂ offspring? If you are sure your cross is not sex-linked, you should combine the male and female data for the same phenotypes.

CROSS	EXPECTED PHENOTYPIC RATIO
F ₁	
F ₂	

73. Look at the results of the F₁ cross (shows the F₂ generation). How many total flies were produced in this cross?

74. Calculate the number of individuals you would expect to be produced from this cross. To do this you need to multiply the expected ratio (or percent) by the total number of flies produced in the cross. If you are sure that your cross is not sex-linked, you should combine the male and female data for the same phenotype.

PHENOTYPES	Expected Ratio or Percent	EXPECTED NUMBER

75. Calculate the chi-square value for the F₂ generation in the space below. You must show all work.

$\chi^2 =$ _____

76. Use the Chi-Square Distribution Table from the lab packet to determine the percent probability that the observed variation is due to random chance alone.

Degrees of freedom = _____

% Probability = _____

77. Was the deviation between the expected and observed data due to chance alone?

How do you know? _____

78. Based on the answer to the previous question, should you accept or reject your hypothesis regarding the pattern of inheritance for this cross?

Explain. _____

PART VIII: DATA ANALYSIS – CROSS #3

79. What mutation(s) were you following in this cross? (NOTE: Wild type is not a mutation. It is the normal condition in flies.)

80. Examine the data you collected from your crosses (F₁ Generation and F₂ Generation results). Make a hypothesis about the pattern of inheritance in this cross by answering the following questions:

a. Is the cross autosomal or sex-linked? _____

b. Is(are) the mutation(s) dominant or recessive? _____

c. Is the cross monohybrid or dihybrid? _____

81. Using the key below and the answers to the previous question, construct a Punnett square to predict results of the P (parental) cross and the F₁ cross. If you are sure that the cross is not sex-linked, you should combine the male and female numbers for the same phenotypes.

KEY:			
+	Wild type	SE	Sepia eyes
W	White eyes	VG	Vestigial Wings

P Cross: _____ x _____
 (female genotype) (male genotype)

Punnett Square: Remember this is sex-linked so you have to put XX on one side and XY on the other (the trait is only carried on the X allele).

F₁ Cross: _____ x _____
 (female genotype) (male genotype)

Punnett Square: Remember this is sex-linked so you have to put XX on one side and XY on the other (the trait is only carried on the X allele).

82. According to the Punnett square results, what are the expected phenotypic ratios of the F₁ and F₂ offspring? If you are sure your cross is not sex-linked, you should combine the male and female data for the same phenotypes.

CROSS	EXPECTED PHENOTYPIC RATIO
F ₁	
F ₂	

83. Look at the results of the F₁ cross (shows the F₂ generation). How many total flies were produced in this cross?
-

84. Calculate the number of individuals you would expect to be produced from this cross. To do this you need to multiply the expected ratio (or percent) by the total number of flies produced in the cross. If you are sure that your cross is not sex-linked, you should combine the male and female data for the same phenotype.

PHENOTYPES	Expected Ratio or Percent	EXPECTED NUMBER

85. Calculate the chi-square value for the F₂ generation in the space below. You must show all work.

$\chi^2 =$ _____

86. Use the Chi-Square Distribution Table from the lab packet to determine the percent probability that the observed variation is due to random chance alone.

Degrees of freedom = _____

% Probability = _____

87. Was the deviation between the expected and observed data due to chance alone?

How do you know? _____

88. Based on the answer to the previous question, should you accept or reject your hypothesis regarding the pattern of inheritance for this cross?

Explain. _____
