Biol 2202: Genetics Laboratory
Laboratory 1: GloFish and Mendelian Genetics
Worksheet

You can use this worksheet for your laboratory notebook

Name_____

Date_____

Experiment Title_____
You must write you own title. Do not use the one from the handout or schedule.

Each table in the laboratory will have a tank containing the progeny of a cross between a single male and a single female-each tank is full of siblings. Each group of 3-4 students will move from table to table, gathering phenotype data and doing the analysis for each sibling group. This worksheet will take you through the process for each group.

Tank 1 (do the simplest one in this area-it has the fewest rows)
STEP 1: Observations
1. Move to a table with a tank of fish. Work with your group (the other students at the same table as you) to do the following steps.

2. Observe the fish and identify all of the phenotypes present. Refer to the laboratory handout for descriptions of the possible phenotypes and the genes associated with them.

3. Decide on the phenotypes that are important for understanding the genetics.

4. Count the number of fish that have each phenotype and record in columns 1 and 2 below.

Clutch 1 Table:

(1) Phenotype	(2) Observed Number,o	(3) Expected Number,e	(4) $d =(o-e)$	(5) d^2	(6) d^2/e
Total					

(7) X^2 = the sum of all of the numbers in column 6 =
(8) Degrees of freedom (df) = n-1 =

Conclusion:
(9) P-value and conclusion about your hypothesis:

STEP 2: Generate a Hypothesis

1. Compare the numbers of wild-type versus transgenic mutant fish in the clutch. It may be easier to consider each phenotype separately (striped vs. not striped, yellow vs. not yellow, etc.)

2. Form a hypothesis about what transgenes and mutant genes are present, and what type of inheritance they have (recessive, dominant, etc.-see lab handout for more information). Punnett squares will likely help you come up with a good hypothesis.

Hypothesis for clutch1:

STEP 3: Analysis
1. Use your hypothesis to calculate the expected values for each of the phenotypes. Fill in your calculated values in column 3 of the clutch 1 table.

Calculate here:

2. Chi-square test
How to do a chi-squared test:
A. Determine d and d^2 from the observed and expected numbers you have gathered/calculated. Enter these numbers in columns 4 and 5 of the clutch 1 table.
B. Calculate d^2/e for each phenotype.
C. Count the number of phenotypes you have listed in column 1. The number equals n. (if you observe two different phenotypes then n = 2)
D. The chi-squared value, X^2, is the total of all the values in column 6. Place this number in the total row of column 6 and in row 7.
E. Calculate the degrees of freedom (df). df= n-1. Place this number in row 8.
F. Use the chi square table, the chi-squared value, and the df to calculate your P value. You will probably end up with a range, such as $1.0 > P > 0.5$. Place this P value in row 9.
G. Make a conclusion-what does your P value tell you about your hypothesis? Place this statement in row 9.

Tank 2
STEP 1: Observations
1. Move to a table with a tank of fish. Work with your group (the other students at the same table as you) to do the following steps.

2. Observe the fish and identify all of the phenotypes present. Refer to the laboratory handout for descriptions of the possible phenotypes and the genes associated with them.

3. Decide on the phenotypes that are important for understanding the genetics.

4. Count the number of fish that have each phenotype and record in columns 1 and 2 below.

Chi Square Table for this clutch:

(1) Phenotype	(2) Observed Number,o	(3) Expected Number,e	(4) d =(o – e)	(5) d²	(6) d²/e
Total					

(7) X^2 = the sum of all of the numbers in column 6 =
(8) Degrees of freedom (df) = n-1 =

Conclusion:
(9) P-value and conclusion about your hypothesis:

STEP 2: Generate a Hypothesis

1. Compare the numbers of wild-type versus transgenic mutant fish in the clutch. It may be easier to consider each phenotype separately (striped vs. not striped, yellow vs. not yellow, etc.)

2. Form a hypothesis about what transgenes and mutant genes are present, and what type of inheritance they have (recessive, dominant, etc.-see lab handout for more information). Punnett squares will likely help you come up with a good hypothesis.

Hypothesis for this clutch:

STEP 3: Analysis
1. Use your hypothesis to calculate the expected values for each of the phenotypes. Fill in your calculated values in column 3 of the clutch 1 table.

Calculate here:

2. Chi-square test
How to do a Chi-squared test:
A. Determine d and d^2 from the observed and expected numbers you have gathered/calculated. Enter these numbers in columns 4 and 5 of the clutch 1 table.
B. Calculate d^2/e for each phenotype.
C. Count the number of phenotypes you have listed in column 1. The number equals n. (if you observe two different phenotypes then n = 2)
D. The chi-squared value, X^2, is the total of all the values in column 6. Place this number in the total row of column 6 and in row 7.
E. Calculate the degrees of freedom (df). df= n-1. Place this number in row 8.
F. Use the chi square table, the chi-squared value, and the df to calculate your P value. You will probably end up with a range, such as $1.0 > P > 0.5$. Place this P value in row 9.
G. Make a conclusion-what does your P value tell you about your hypothesis? Place this statement in row 9.

Tank 3

STEP 1: Observations

1. Move to a table with a tank of fish. Work with your group (the other students at the same table as you) to do the following steps.

2. Observe the fish and identify all of the phenotypes present. Refer to the laboratory handout for descriptions of the possible phenotypes and the genes associated with them.

3. Decide on the phenotypes that are important for understanding the genetics.

4. Count the number of fish that have each phenotype and record in columns 1 and 2 below.

Chi Square Table for this clutch:

(1) Phenotype	(2) Observed Number, o	(3) Expected Number, e	(4) d =(o – e)	(5) d^2	(6) d^2/e
Total					

(7) X^2 = the sum of all of the numbers in column 6 =
(8) Degrees of freedom (df) = n-1 =

Conclusion:
(9) P-value and conclusion about your hypothesis:

STEP 2: Generate a Hypothesis

1. Compare the numbers of wild-type versus transgenic mutant fish in the clutch. It may be easier to consider each phenotype separately (striped vs. not striped, yellow vs. not yellow, etc.)

2. Form a hypothesis about what transgenes and mutant genes are present, and what type of inheritance they have (recessive, dominant, etc.-see lab handout for more information). Punnett squares will likely help you come up with a good hypothesis.

Hypothesis for this clutch:

STEP 3: Analysis
1. Use your hypothesis to calculate the expected values for each of the phenotypes. Fill in your calculated values in column 3 of the clutch 1 table.

Calculate here:

2. Chi-square test
How to do a Chi-squared test:
A. Determine d and d^2 from the observed and expected numbers you have gathered/calculated. Enter these numbers in columns 4 and 5 of the clutch 1 table.
B. Calculate d^2/e for each phenotype.
C. Count the number of phenotypes you have listed in column 1. The number equals n. (if you observe two different phenotypes then n = 2)
D. The chi-squared value, X^2, is the total of all the values in column 6. Place this number in the total row of column 6 and in row 7.
E. Calculate the degrees of freedom (df). df= n-1. Place this number in row 8.
F. Use the chi square table, the chi-squared value, and the df to calculate your P value. You will probably end up with a range, such as 1.0 > P > 0.5. Place this P value in row 9.
G. Make a conclusion-what does your P value tell you about your hypothesis? Place this statement in row 9.

Tank 4

STEP 1: Observations

1. Move to a table with a tank of fish. Work with your group (the other students at the same table as you) to do the following steps.

2. Observe the fish and identify all of the phenotypes present. Refer to the laboratory handout for descriptions of the possible phenotypes and the genes associated with them.

3. Decide on the phenotypes that are important for understanding the genetics.

4. Count the number of fish that have each phenotype and record in columns 1 and 2 below.

Chi Square Table for this clutch:

(1) Phenotype	(2) Observed Number,o	(3) Expected Number,e	(4) d =(o – e)	(5) d^2	(6) d^2/e
Total					

(7) X^2 = the sum of all of the numbers in column 6 =

(8) Degrees of freedom (df) = n-1 =

Conclusion:

(9) P-value and conclusion about your hypothesis:

STEP 2: Generate a Hypothesis

1. Compare the numbers of wild-type versus transgenic mutant fish in the clutch. It may be easier to consider each phenotype separately (striped vs. not striped, yellow vs. not yellow, etc.)

2. Form a hypothesis about what transgenes and mutant genes are present, and what type of inheritance they have (recessive, dominant, etc.-see lab handout for more information). Punnett squares will likely help you come up with a good hypothesis.

Hypothesis for this clutch:

STEP 3: Analysis
1. Use your hypothesis to calculate the expected values for each of the phenotypes. Fill in your calculated values in column 3 of the clutch 1 table.

Calculate here:

2. Chi-square test
How to do a Chi-squared test:
A. Determine d and d^2 from the observed and expected numbers you have gathered/calculated. Enter these numbers in columns 4 and 5 of the clutch 1 table.
B. Calculate d^2/e for each phenotype.
C. Count the number of phenotypes you have listed in column 1. The number equals n. (if you observe two different phenotypes then n = 2)
D. The chi-squared value, X^2, is the total of all the values in column 6. Place this number in the total row of column 6 and in row 7.
E. Calculate the degrees of freedom (df). df= n-1. Place this number in row 8.
F. Use the chi square table, the chi-squared value, and the df to calculate your P value. You will probably end up with a range, such as 1.0 > P > 0.5. Place this P value in row 9.
G. Make a conclusion-what does your P value tell you about your hypothesis? Place this statement in row 9.

Tanks 5 and 6-do male and female phenotype analysis here

STEP 1: Observations
1. Move to the table with two tanks. Work with your group (the other students at the same table as you) to do the following steps.

2. Sort the fish in the first tank according to whether they are male or female. Refer to gender identification guides for help with this.

3. Count the number of female fish and male fish and record in columns 1 and 2 in the first table below.

4. Repeat for the second tank, and record the numbers in the second table below.

5. Add your two sets of numbers, and put it in the third table below

Chi Square Table for first male/female tank:

(1) Phenotype	(2) Observed Number,o	(3) Expected Number,e	(4) $d = (o - e)$	(5) d^2	(6) d^2/e
Total					

(7) X^2 = the sum of all of the numbers in column 6 =
(8) Degrees of freedom (df) = n-1 =

Conclusion:
(9) P-value and conclusion about your hypothesis:

Chi Square Table for second male/female tank:

(1) Phenotype	(2) Observed Number,o	(3) Expected Number,e	(4) $d = (o - e)$	(5) d^2	(6) d^2/e
Total					

(7) X^2 = the sum of all of the numbers in column 6 =
(8) Degrees of freedom (df) = n-1 =

Conclusion:
(9) P-value and conclusion about your hypothesis:

Chi Square Table for combined male/female data:

(1) Phenotype	(2) Observed Number,o	(3) Expected Number,e	(4) d =(o – e)	(5) d^2	(6) d^2/e
Total					

(7) X^2 = the sum of all of the numbers in column 6 =
(8) Degrees of freedom (df) = n-1 =

Conclusion:
(9) P-value and conclusion about your hypothesis:

STEP 2: Generate a Hypothesis

1. Compare the numbers of males and females in each tank and generate a hypothesis for how gender is determined in zebrafish.

Hypothesis:

STEP 3: Analysis
1. Use your hypothesis to calculate the expected values for each of the phenotypes. Fill in your calculated values in column 3 of each.

Calculate here:

2. Chi-square test
How to do a Chi-squared test:
A. Determine d and d^2 from the observed and expected numbers you have gathered/calculated. Enter these numbers in columns 4 and 5 of the clutch 1 table.
B. Calculate d^2/e for each phenotype.
C. Count the number of phenotypes you have listed in column 1. The number equals n. (if you observe two different phenotypes then n = 2)
D. The chi-squared value, X^2, is the total of all the values in column 6. Place this number in the total row of column 6 and in row 7.
E. Calculate the degrees of freedom (df). df= n-1. Place this number in row 8.
F. Use the chi square table, the chi-squared value, and the df to calculate your P value. You will probably end up with a range, such as 1.0 > P > 0.5. Place this P value in row 9.
G. Make a conclusion-what does your P value tell you about your hypothesis? Place this statement in row 9.

LAST STEP (do this only once):

1. Choose one of your hypotheses above to test.

Hypothesis to be tested:

2. Set up one single pair mating (see laboratory handout for instructions)
Note: some of our fish are quite small, so make sure to use the biggest fish for your mating

Phenotype of female fish:

Phenotype of male fish:

Anticipated phenotypes of progeny and their ratio: