**Name: \_\_\_\_\_\_\_\_\_\_\_\_**

**Period: \_\_\_\_\_**

**Date: \_\_\_\_\_\_\_\_\_**

**MENDELIAN GENETICS: DIHYBRID CORN ACTIVITY WORKSHEET**

1. Expected number of corn kernels out of your total corn count from a dihybrid cross: (example: if you and your partner counted 300 total kernels… 9/16 of 300, 3/16 of 300, 1/16 of 300).

Purple, Starchy Kernels: \_\_\_\_\_\_

Purple, Sweet Kernels: \_\_\_\_\_\_\_

Yellow, Starchy Kernels: \_\_\_\_\_\_

Yellow, Sweet Kernels: ­\_\_\_\_\_\_\_

1. Observed number of corn kernels of each type out of you and your partner’s kernels.

Purple, Starchy Kernels: \_\_\_\_\_\_

Purple, Sweet Kernels: \_\_\_\_\_\_\_

Yellow, Starchy Kernels: \_\_\_\_\_\_

Yellow, Sweet Kernels: ­\_\_\_\_\_\_\_

1. What is your ratio? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ (divide by the lowest number of kernels)

Do your results exactly match your predicted ratio (9:3:3:1)? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

1. Are your (observed) results close enough to the expected values, a ratio (9:3:3:1), that you feel comfortable with the predicted mode of inheritance? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Would you accept the predicted mode of inheritance, or suggest testing a different model, if your results were:

1. 100:20:25:15? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
2. 30:30:30:30? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
3. 40:80? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
4. After observing an example of the chi-square test for a 9:3:3:1 ratio (by your instructor), carry out the chi-square test for your data from counting the corn kernels.

|  |  |  |  |
| --- | --- | --- | --- |
| Purple, Starchy kernels: | **(o – e)2** | = |  |
| e |
| Purple, Sweet kernels: | **(o – e)2** | = |  |
| e |
| Yellow, Starchy kernels: | **(o – e)2** | = |  |
| e |
| Yellow, Sweet kernels: | **(o – e)2** | = | **+** |
| e |
|  |  | = |  |

1. Determine your degrees of freedom (df): (number of events -1).
2. Use the chi-square chart on the lab using the 0.05 probability column and the df to find your value to compare your calculated chi-square value.
3. Set up your null hypothesis statement to verify if there is any significant difference between what you and your partner calculated you would have expected and what you both observed.

Example: Is 14.56 < or equal to 7.84 (df=3, p=0.05). If the answer is no then there is a SIGNIFICANT difference between observed and expected values, and your proposed parental genotypes are potentially incorrect.

If the answer is YES the value is less than or equal to the value on the chart, then you can state that you accept the null hypothesis there is no significant difference therefore you have surmised the correct genotypes and any different is due to acceptable random chance.

What is your null hypothesis statement? :

* 1. Do you now feel comfortable accepting your predicted mode of inheritance, or would you suggest testing a different model? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

1. What is the approximate percentage of probability that the class data differed from the expected data by chance alone? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
   1. Do you now feel comfortable accepting the predicted mode of inheritance, or would you suggest testing a different model? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

* 1. How did using more data (the entire class versus data from your group along) affect the outcome of the Chi-Square analysis? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_