­­Name \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date \_\_\_\_\_\_\_\_\_\_

AP Biology Mr. Collea





**Corn Genetics Lab**

**PreLab**: Go to Collea’s Corner to watch the Bozeman Science Chi-Square Video and answer each of the questions that follow.

***www.bozemanscience.com/chi-squared-test***

**1.** Label what each element represents in the

 Chi-square formula to the right.

**2.** Why do you use the Chi-Square Test?

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**3.** Define the Null Hypothesis.

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

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**4.** What is the whole point or cool thing about Chi-Square?

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**5.** What is the whole point of a Chi-Square test?

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**6.** What is the definition of and how do you calculate the “**Degrees of Freedom**”?

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

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**7.** What is the ***probability*** (**p**) we will most likely use in this class (*AP Biology at NSU*)? \_\_\_\_\_\_\_\_\_\_

**8.** What does a ***probability*** (**p**) of **.05** actually mean?

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

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**9.** What happens if you get a Chi-Square **HIGHER** than your critical value?

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

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**10.** What happens if you get a Chi-Square **LOWER** than your critical value?

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

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**11.** Complete the Chi-square question Paul Andersen uses as an example involving coin flipping.

 **(a)** State your **null hypothesis** (Ho) for this problem:

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

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|  |  |  |
| --- | --- | --- |
|  | **Heads** | **Tails** |
| ***Expected*** |   |   |
| ***Observed*** |   |   |

 **(b)** Fill in the data table to the right with the sample

 data Mr. Andersen give you and then solve.

 **Please SHOW ALL WORK in the space below.**

 (***E****quation –* ***S****ubstitute –* ***A****nswer = ESA*)



 **(c)** What is the ***probability*** (**p**) we will use in this problem and **MOST** problems at NSU? \_\_\_\_\_\_\_\_\_\_

 **(d)** What is your ***critical value*** for this problem? \_\_\_\_\_\_\_\_\_\_

 **(e)** What is your ***degrees of freedom*** for this problem? \_\_\_\_\_\_\_\_\_\_

 **(f)** What is the Chi-square value you calculated? \_\_\_\_\_\_\_\_\_\_

 **(g)** Is your Chi-square **HIGHER** or **LOWER** than the critical value from the table? \_\_\_\_\_\_\_\_\_\_\_\_\_\_

 **(h)** Do you ***ACCEPT*** or ***REJECT*** your null hypothesis? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

 What **EXACTLY** does this mean: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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**12.** Complete the 2nd Chi-square question Paul Andersen uses as an example involving dice.

 **(a)** State your **null hypothesis** (*Ho*) for this problem:

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

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 **(b)** Fill in the data table below with the sample data Mr. Andersen give you and then solve.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **1** | **2** | **3** | **4** | **5** | **6** |
| ***Expected*** |   |   |   |   |   |   |
| ***Observed*** |   |   |   |   |   |   |



 **Please SHOW ALL WORK in the space below.**

 (***E****quation –* ***S****ubstitute –* ***A****nswer = ESA*)

 **(c)** What is the ***probability*** (**p**) we will use in this problem and ALL problems at NSU? \_\_\_\_\_\_\_\_\_\_

 **(d)** What is your ***critical value*** for this problem? \_\_\_\_\_\_\_\_\_\_

 **(e)** What is your ***degrees of freedom*** for this problem? \_\_\_\_\_\_\_\_\_\_

 **(f)** What is the **Chi-square value** you calculated? \_\_\_\_\_\_\_\_\_\_

 **(g)** Is your Chi-square **HIGHER** or **LOWER** than the critical value from the table? \_\_\_\_\_\_\_\_\_\_\_\_\_\_

 **(h)** Do you ***ACCEPT*** or ***REJECT*** your null hypothesis? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

 What **EXACTLY** does this mean: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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

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**13.** Complete the 3rd Chi-square question Paul Andersen uses as an example involving pill bugs.

 **(a)** State your **null hypothesis (***Ho***)** for this problem:

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

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|  |  |  |
| --- | --- | --- |
|  | **Wet** | **Dry** |
| ***Expected*** |   |   |
| ***Observed*** |   |   |

 **(b)** Fill in the data table to the right with the sample

 data Mr. Andersen give you and then solve.

 **Please SHOW ALL WORK in the space below.**

 (***E****quation –* ***S****ubstitute –* ***A****nswer = ESA*)



 **(c)** What is the ***probability*** (**p**) we will use in this problem and ALL problems at NSU? \_\_\_\_\_\_\_\_\_\_

 **(d)** What is your ***critical value*** for this problem? \_\_\_\_\_\_\_\_\_\_

 **(e)** What is your ***degrees of freedom*** for this problem? \_\_\_\_\_\_\_\_\_\_

 **(f)** What is the ***Chi-square*** value you calculated? \_\_\_\_\_\_\_\_\_\_

 **(g)** Is your Chi-square **HIGHER** or **LOWER** than the critical value from the table? \_\_\_\_\_\_\_\_\_\_\_\_\_\_

 **(h)** Do you ***ACCEPT*** or ***REJECT*** your null hypothesis? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

 What **EXACTLY** does this mean: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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**Corn Genetics Lab**

**Background Information:**

A **gene** is a unit of heredity on a chromosome and can have alternate forms called **alleles**. In sexually reproducing organisms each parent contributes one allele to their offspring that may or may not be like the other parent's allele. Alleles for a particular gene occur in pairs. Alleles that mask expression of other alleles of a particular gene, but are themselves expressed are **dominant**, and are usually designated by a capital letter of that dominant allele (for example, "B"). Alleles whose expression is masked by dominant alleles are **recessive**, and are designated by a lower case letter (for example, "b"). The **genotype** (*genetic makeup*) of an organism includes all the alleles present in the cell, whether they are dominant or recessive. The biochemical manifestation of the trait is called the phenotype (*physical makeup*).

Why are fruit flies (*Drosophila melanogaster*) and corn (*Zea maze*) excellent choices for introducing Mendelian inheritance? **(1)** Fruit flies and corn have numerous contrasting phenotypes (*easily observable traits*). **(2)** Fruit flies and corn produce many offspring and seeds giving us an ample supply of data to work with. **(3)** Corn is a very important food crop and its genetics have been extensively investigated and modified (*genetically modified organism / GMO*) for better or worse.

**Figure 1: Examples of Phenotypes in Fruit Flies (***Drosophila melanogaster***)**





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

Morgan's conventions on notation

|  |  |
| --- | --- |
|   |   |
|   |   |

**1.** Genes symbol based on 1st mutant observed (non wild-type)

**2.** If mutant recessive, 1st letter lowercase (w = white eye)

**3.** If mutant dominant, 1st letter uppercase: Cy = curled wings

**4.** Wild-type designated by superscript + over symbol for trait:

 w+ = flies with normal red eyes

 vg+ = normal sized wings not vestigial in shape

 Cy+ = allele for normal or straight wings not curl

The corn phenotypes studied in this activity **Figure 2: Cross Section of a Corn Seed**

are kernel **color** and **endosperm** characteristics

(*starchy* and *sweet*). The two forms of kernel color

you will look at are *Colored Aleurone* (**R**) which

appears purple and *Coloredless Aleurone* (**r**) which

appears yellow. Normal corn endosperm is high in

starch or starchy (**Su**) and is dominant over the

recessive sweet (**su**) trait. As corn dries, its sugary

endosperm loses water, its kernels wrinkle and it tastes

sweet.

**Part I. Chi-Square Analysis of a Monohybrid Cross of Corn** (Color)

This monohybrid cross begins with the cross pollination of two corn plants that are **homozygous** (*pure*) for different forms of the kernel color trait. The offspring (F1) are then allowed to cross pollinate and the F2 offspring (*seeds*) are counted and analyzed.

 **P1**: RR x rr **F1**: Rr x Rr

|  |  |
| --- | --- |
|  **F1** |   |
|   |   |

|  |  |
| --- | --- |
|  **F2** |   |
|   |   |

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

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

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

Use a Chi-square test on the F2 generation data to analyze your prediction that the parental genotypes of the F1 were, in fact, heterozygous or hybrid.



|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **obs** | **exp** | **obs - exp** | **(obs - exp)2** | **(obs - exp)2 exp** |
| **Colored***(purple)* |   |   |   |   |   |
| **Colorless***(yellow)* |   |   |   |   |   |
| Degrees of Freedom = |   | X2 Total |   |

*Does the observed data fit the expected/predicted phenotypic ratio?*

**Part II. Chi-Square Analysis of a Dihybrid Testcross of Corn**

This dihybrid testcross begins with the cross pollination of two corn plants, one that is **heterozygous** or **hybrid** for both traits (kernel color/**Rr** and endosperm characteristics/**Susu**) and the other that is **homozygous** (*pure*) **recessive** for the same traits /**rr susu**. The offspring (F1) are then allowed to cross pollinate and the F2 offspring (*seeds*) are counted and analyzed. The results of such a cross can help you determine if the genes for any two traits are **linked** (*found on the same chromosome*) or not.

**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ X \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

|  |  |  |  |
| --- | --- | --- | --- |
|   |   |   |   |
|   |   |   |   |
|   |   |   |   |
|   |   |   |   |
|   |   |   |   |

*Dihybrid Organism Testcross Organism*

**Colored / Starchy Colorless / Sweet**

 *purple* / *inflated yellow* / *wrinkled*

 **Results:**

**\_\_\_\_\_\_: Colored / Starchy**

 *purple* / *inflated*

**\_\_\_\_\_\_: Colored / Sweet**

 *purple* / *wrinkled*

**\_\_\_\_\_\_: Colorless / Starchy**

 *yellow* / *inflated*

**\_\_\_\_\_\_: Colorless / Sweet**

 *yellow* / *wrinkled*

**\* Offspring/seeds that have a phenotype different from the parents are called RECOMBINANTS.\***

**If the genes are on different chromosomes (unlinked), *independent assortment* will produce a 1:1:1:1 ratio of gametes, which in turn will produce a 1:1:1:1 phenotypic ratio in the seeds or offspring.**

Use a Chi-square test to analyze your prediction that these two traits are, in fact, unlinked.



|  |  |  |
| --- | --- | --- |
|  | **obs** | **exp** |
| **Colored / Starchy***purple* / *inflated* |   |   |
| **Colored / Sweet***purple* / *wrinkled* |   |   |
| **Colorless / Starchy***yellow* / *inflated* |  |  |
| **Colorless / Sweet***yellow* / *wrinkled* |  |  |
| Degrees of Freedom = |

*Does the observed data fit the expected/predicted phenotypic ratio and are these two genes unlinked?*

|  |
| --- |
|  |

**Part III. Crossover/Recombination Frequencies & Gene Mapping**

In Part II of this activity you determined that the two genes for kernel color and endosperm characteristics were in fact **UNLINKED** and *located on different chromosomes* because the 1:1:1:1 phenotypical ratio that resulted in the offspring. The first step in genetic mapping is to determine that the two genes in question are in fact **LINKED** and *located on the same chromosome*. Once this is determined, you can then **MAP** them.

Let’s use the data below (instead of the data from Part II) to determine if two genes are UNLINKED

**\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ X \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

*Dihybrid Organism Testcross Organism*

**Colored / Starchy Colorless / Sweet**

 *purple* / *inflated yellow* / *wrinkled*

|  |  |  |
| --- | --- | --- |
|  | **obs** | **exp** |
| **Colored / Starchy***purple* / *inflated* | 72 | 40 |
| **Colored / Sweet***purple* / *wrinkled* | 8 | 40 |
| **Colorless / Starchy***yellow* / *inflated* | *13* | 40 |
| **Colorless / Sweet***yellow* / *wrinkled* | *67* | 40 |
| Degrees of Freedom = |

 *Does the observed data fit the expected/predicted phenotypic ratio and are these two genes unlinked?*

Now that we have established that two genes in question are indeed linked (*because the* ***observed*** *results were* ***SIGNIFICANTLY*** *different from the* ***expected*** *results AND most of the organisms resemble the parental phenotypes*) the next question is:

**WHAT ARE THEIR RELATIVE POSITIONS (loci)** on the chromosome?

or

**HOW FAR APART ARE THEY** on the chromosome?

*(map unit = centimorgans****)***

Doing some simple arithmetic by calculating the crossover / recombination frequency

can answer this question and provide us with the first step in **GENE MAPPING**.

**Crossover/Recombination Frequency = Number of Recombinants**

 **Total Number of Offspring**

 **a)** Using the formula below, determine how far apart the genes for kernal color (*purple/yellow*) and endosperm characteristics (*inflated/wrinkle*) are in corn?

**Crossover/Recombination Frequencies & Gene Mapping Questions**

**1.** In guinea pigs, black fur is dominant over brown fur and solid color is dominant over spotted color.

 Determine the ratio of expected phenotypes in a **dihybrid testcross** between a **heterozygous** black, solid-colored guinea pigs and a **homozygous recessive** brown, spotted guinea pig.

P1: \_\_\_\_\_\_\_\_\_\_\_\_ X \_\_\_\_\_\_\_\_\_\_\_\_

|  |  |  |  |
| --- | --- | --- | --- |
|   |   |   |   |
|   |   |   |   |
|   |   |   |   |
|   |   |   |   |
|   |   |   |   |

*(dihybrid)**(homozygous recessive)*

 **Results:**

 \_\_\_\_\_\_: **black / solid**

 \_\_\_\_\_\_: **black / spotted**

 \_\_\_\_\_\_: **brown / solid**

 \_\_\_\_\_\_: **brown / spotted**

**2.** So based upon your results from above, how many of each type of guinea pig would you **expect** in a litter of **40** guinea pigs?

 black/solid = \_\_\_ *black/spotted* = \_\_\_ *brown/solid* = \_\_\_ brown/spotted = \_\_\_

 But let’s say when **you actually breed** the guinea pigs you **observe** and record the following results:

 black/solid = **17** *black/spotted* = **1** *brown/solid* = **3** brown/spotted = **19**

What do these observed results indicate: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

If linked genes are usually inherited together, then what explains the guinea pigs that have phenotypes different from their parents?

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

**Recombination Frequency = Number of Recombinants**

 **Total Number of Offspring**

 **a)** Using the formula above, how are far apart are the genes for coat color (*black/brown*) and coat pattern (*solid/spotted*) in guinea pigs?

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

**3.** By analyzing the results of many dihybrid test crosses (*to see if the genes are linked*) and calculating the recombination frequencies for these genes (*to see how far apart they are*), one can begin creating a map of where linked genes are located on chromosomes.

**a)** The following recombination frequencies were calculated after performing 4 dihybrid testcrosses. Determine the position of these genes (a, b, c and d) on the chromosome.

 a, c = 10% a, d = 30% b, c = 24% b, d = 16%