## Genetics - Dihybrid Cross

Teacher's Guide

### 1.0 Summary

Dihybrid Cross is the ninth core Genetics activity. This activity is comprised of two sections. This activity is designed to be completed in one class period of 45-50 minutes.

### 2.0 Learning Goals

Driving Question: What is the likelihood that two traits will be inherited together?
The Dihybrid Cross activity focuses on the inheritance patterns for two traits at a time, and the differences that occur when the genes for those traits are parts of the same chromosome or parts of different chromosomes.

## Learning Goals

- Students will learn that offspring inherit entire chromosomes from their parents.
- Students will recognize that if two genes are parts of the same chromosome, they will inherit them together.
- Students will recognize that if two genes are parts of different chromosomes, they will inherit them independently.
- Students will distinguish the difference in inheritance patterns between two characteristics that are parts of one chromosome and two characteristics that are determined by genes that are parts of different chromosomes.
- Students will utilize the principles of probability to predict the outcome of genetic crosses for two traits.
- Students will utilize the principles of probability to explain genetic crosses involving more than one trait.
- Students will use Punnett Square and Pedigree Charts to examine patterns of heredity.


## Additional Teacher Background

In Dihybrid Cross, students will apply the information that they have acquired in the previous BioLogica core activities to complete activities of probability, segregation, and independent assortment. To appreciate fully the two laws of Mendelian genetics modeled in this activity, students should have basic comprehension of related terms and concepts.

Students should already have a firm grasp of Mendel's first law; the Law of Segregation of Alternate Factors, for single trait crosses, if the BioLogica activities were completed sequentially. This activity will reinforce those concepts and it will demonstrate Mendel's second law, the Law of Independent Assortment, for multiple trait crosses.

What we have learned since Mendel's studies is that his "Laws" have several exceptions. For example; there are eight known interactions between alleles that can form a phenotype. Incomplete and co-dominance, multiple alleles and polygenic traits as well as environmental influences are instances of these exceptions. In addition, we now know that genes are segments of chromosomes. Therefore, multiple traits assort independently if they are part of different chromosomes. However, different genes that are parts of the same chromosome are linked and will not, in the absence of crossing over, assort independently.

### 3.0 Standards Alignment

Alignment to National Math and Science Standards (NCTM or NSES)

| Objective | Standards |
| :--- | :--- |
| Students will be able to determine <br> whether the genes for $\mathbf{2}$ traits are parts <br> of the same or different chromosomes <br> through breeding experiments and <br> pedigree analysis. | Students will use representations to <br> model and interpret physical, social, <br> and mathematical phenomena. |
| Students will extend their <br> understanding of probability to the <br> inheritance of two traits. | Mathematical tools and models guide <br> and improve the posing cf questions, <br> gathering of data, constructing <br> explanations and communicating <br> results. |

### 4.0 Activity Sections

This activity is comprised of two sections: Genes that are parts different chromosomes and, Genes that are parts of the same chromosome. Students should use the notebook tool to keep track of useful information as they proceed through the screens. It may be helpful to print a copy of the Dragon Genome Chart for reference.

### 4.1 Table of Contents



### 4.2 Genes that are part of different chromosomes

Students review monohybrid predictions and probabilities and pedigrees for wings and horns. Then they are guided through the same procedures for dihybrid inheritance of the two traits together.

Step 1: Review genotypes in Punnett Squares and in Pedigrees.
Step 2: Complete the Punnett Square for Wings.
Step 3: Complete the Pedigree Chart for wings and horns.
Step 4: View the dragon offspring and count the number of dragons with the phenotypes for both traits.
Step 5: Practice Punnett squares for multiple traits, simplify the Punnett Squares for Dihybrid traits whenever possible.
Step 6: Complete the Quiz.
Step 7: Summarize the process.


Complete a Punnett Square for Wings.


Probability of wings is $50 \%$


Probability of horns is $50 \%$


Students scroll through the offspring created in the pedigree and count the number of dragons that have both horns and wings.


Mathematically speaking, the probability that two events, in this case the occurrence of two particular traits, will both occur is the product of the probabilities of the two separate events occurring, if the events are unrelated.

In other words, to predict the likelihood that a dragon will inherit both horns and wings, you multiply the probability that it will have horns times the probability that it will have wings ( $1 / 2 \times 1 / 2=1 / 4$ )
 $\geqslant$

Probability of simultaneous unrelated events


Explanation of Independent Assortment

| Results | horns <br> wings | horns <br> no wings | no horns <br> wings | no horns <br> no wings |
| :--- | :--- | :--- | :--- | :--- |
| Cross1 | $\mathbf{6}$ | $\mathbf{1 3}$ | $\mathbf{1 2}$ | $\mathbf{9}$ |
| Predicted | $\mathbf{1 0}$ | $\mathbf{1 0}$ | $\mathbf{1 0}$ | $\mathbf{1 0}$ |

The table above shows the results of Cross1 and the predicted results.
The results may or may not agree with the predictions. Geneticists would use statistics to test the agreement, but you don't need to.


Discussion of predictions vs. data
Students are then guided through the reasoning required to determine parental genotypes for Horns and Tails and then the phenotypes of their offspring, beginning with the genotypes and possible crosses through Punnett Squares and mathematical calculation of the probabilities.


Results for horns and fancy tails

The next section takes them through the same process but with an emphasis on the role of meiosis and independent assortment in producing possible combinations of alleles.

Remember, chromosomes are assorted
independently during meiosis
Since Duncan is heterozygous for both Horns and Wings, he could pass on an H allele. That H allele could end up in a gamete with either a W or w allele.

Or Duncan could pass on an h allele which could end up in a gamete with either a W or w allele.

This results in the 4 combinations shown in the diagram.


Possible combinations


Possibilities for Duncan's traits explained


> Students complete a 4X4 dihybriel Punnett Square, with the help of the "Show Me" button if desired.

Note: Students can copy and paste from one cell to another once they understand the pattern.


Simplified dihybrid Punnett Square gives same probability of offspring having both wings and horns as calculated previously with 2 Punnett Squares.


Students are asked a series of questions about calculating probabilities from Punnett squares. The correct answer to this question is $3 / 8$ of the offspring could have both horns and a fancy tail, which is explained in the next screen.


Explanation of answer

$1 \times 1 / 2=1 / 2$
Note: Karuna is homozygous dominant for Horns and Sam is homozygous recessive for Wings.

A 12-question quiz concludes the first section. Students are given their score, followed by an explanation of the answers.

|  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Sam |  |  |  |
| Karuna | $H$ | $h$ |  |  |  |
| $H$ | $H H$ | $H h$ |  |  |  |

> For Horns and Wings, again all of Karuna and Sam's offspring will have horns because Karuna can contribute only the dominant $H$ allele to her offspring. And as with Tails, Karuna is heterozygous for Wings (WW) and Sam is homozygous recessive ( $(\mathrm{Ww})$. So approximately $1 / 2$ of their offspring will have no wings (WW) and approximately $1 / 2$ of their offspring will have wings ( $W w)$.

From the individual Punnett squares for Horns and Wings, you can predict the probability that Karuna and Sam will have an offspring with both horns and wings by multiplying the probability that offspring will have horns (1/1) times the probability that offspring will have a plain tail ( $1 / 2$ ) which equals $1 / 2$ or $1 / 1 \times 1 / 2=1 / 2$

Now that you've explored how 2 characteristics are inherited when their genes are part of different chromosomes, it's time to investigate what happens when the genes for 2 characteristics are parts of the same chromosome.


Assessment questions explained.

### 4.3 Genes that are Part of the same Chromosome

The model of meiosis is used to help students explore inheritance patterns when genes for those characteristics are parts of the same chromosome. Note: While BioLogica has the capability to model crossing over, it is not used in the current set of activities. Students are guided through the reasoning from genotypes to pedigrees.

Step 1: Run meiosis and then run fertilization
Step 2: Use the cross tools to show a pedigree chart for Rosa and Boris
Step 3: Click the Show Organisms button view offspring.
Step 4: Complete the data table.
Step 5: Determine the probability of unrelated events, (traits on different chromosomes)
Step 6: Use your data to answer the questions.
Step 7: Review key concepts.


Students are challenged to produce a baby with wings and a plain tail. Both are recessive traits.

Note: Students must examine the gametes to select those with the recessive alleles for Wings and Tail.


Here are Rosita and Boris again, this time in a pedigree. As you've seen before, pedigrees are useful for looking at large numbers of offspring and multiple generations. But a pedigree shows just one characteristic at a time - you are looking at the Tail characteristic right now.

Cross Rosita and Boris then click the Show Organisms button so you can view the offspring Wings and Tails phenotypes at the same time.

Students then create lots of offspring in pedigree.


Students create data table by scrolling through the offspring and counting the different phenotypes and combinations.


Completed table looks like this but the numbers may be different, not because students miscount, which they might, but because organisms are generated randomly as they are in nature.


Above are Punnett squares that show crosses with Rosita and Boris for Wings and for Tails. Each predicts that about $1 / 4$ of Rosita and Boris' offspring will have wings (ww) and about $1 / 4$ will have plain tails (tt) which may or may not be consistent with your counts in the tables below.

|  | no wings | wings |
| ---: | :---: | :---: |
| Rosita \& Boris: <br> Cross 1 | $\mathbf{3 0}$ | $\mathbf{1 0}$ |
| Ratios predicted by <br> Punnett square | $\mathbf{3 / 4}$ | $\mathbf{1 / 4}$ |
| Number of offspring <br> out of 40 predicted <br> by independent <br> assortment | $\mathbf{3 0}$ | $\mathbf{1 0}$ |


|  | fancy tail | plain tail |
| ---: | :---: | :---: |
| Rosita \& Boris: <br> Cross 1 | $\mathbf{3 0}$ | $\mathbf{1 0}$ |
| Ratios predicted by <br> Punnett square | $\mathbf{3 / 4}$ | $\mathbf{1 / 4}$ |
| Number of offspring <br> out of 40 predicted <br> by independent <br> assortment | $\mathbf{3 0}$ | $\mathbf{1 0}$ |

The difference between predicted and actual counts of phenotypes is discussed.


Students calculate what the probabilities would be if wings and tails were inherited independently.

|  | no wings \& fancy tail | no wings \& plain tail | wings \& fancy tail | wings \& plain tail |
| :---: | :---: | :---: | :---: | :---: |
| Rosita \& Boris: Cross 1 | 32 | $\mathbf{0}$ | $\mathbf{0}$ | $\mathbf{8}$ |
| Ratios predicted by <br> independent assortment | $\mathbf{9 / 1 6}$ | $\mathbf{3 / 1 6}$ | $\mathbf{3 / 1 6}$ | $\mathbf{1 / 1 6}$ |
| Number of offspring out <br> of 40 predicted by <br> independent assortment | about 22 | about 8 | about 8 | about 22 |

Clearly, your observations are not consistent with predictions based on independent assortment. Was Mendel wrong? Or is there a sound biological explanation about why the inheritance of the Wings and Tails genes does not act according to the Law of Independent Assortment?

Keeping in mind that

- during meiosis the chromosomes AND their included genes travel together, and
- fertilization combines chromosomes AND their included genes


Students are asked to explain why the counts predicted by independent assortment differ from those produced by pedigree.

## Mother



Your observations are not consistent with your predictions based on independent assortment because the Wings and Tail genes are part of the same chromosome. So they do not travel through meiosis independently of one another the way genes that are parts of different chromosomes do.

Click the play button, then carefully follow Rosita's Wings and Tail genes as they go through meiosis as parts of the same chromosome.


Students are asked to observe the action of the Wings and Tail genes as they go through meiosis, demonstrating that they do not sort independently.

$\frac{1}{2} \times \frac{1}{2}$

When you determined probabilities for the behavior of chromosomes as they assort independently, you multiplied the probability of offspring inheriting one specific trait (like horns) times the probability of the same offspring inheriting another specific trait (like no wings). You used this to determine the probability that the offspring will inherit both traits. In the language of mathematics, these are 'unrelated events'.

国
Comparison of unrelated events when genes are parts of different chromosomes is contrasted with what happens when genes are parts of the same chromosome and therefore do not assort independently.

But here we have two genes traveling through meiosis as part of the same chromosome. Therefore, how each gene gets from the beginning of meiosis to the end of meiosis is not a series of 'unrelated events'. So multiplying their independent probabilities to determine a combined probability is incorrect.

And it's important to understand that treating two genes as independent and creating data tables like the one you created is exactly what geneticists do as one way of finding out where different genes are located


|  | no wings \& fancy tail | no wings \& plain tail | wings \& fancy tail | wings \& plain tail |
| :---: | :---: | :---: | :---: | :---: |
| Rosita \& Boris: Cross 1 | $\mathbf{3 2}$ | $\mathbf{0}$ | $\mathbf{0}$ | $\mathbf{8}$ |
| Ratios predicted by <br> independent assortment | $\mathbf{9 / 1 6}$ | $\mathbf{3 / 1 6}$ | $\mathbf{3 / 1 6}$ | $\mathbf{1 / 1 6}$ |
| Number of offspring out <br> of 40 predicted by <br> independent assortment | about 22 | about 8 | about 8 | about 22 |

As you've seen many times already, data and predictions rarely agree exactly. This is true in genetics and in other sciences as well. Scientists build imperfect models of the natural world and use them to make predictions about how the world actually works. Then they observe and gather data from the actual world and look at how well their predictions and observations match the data. This gives scientists information about the quality of their models.

Discrepancies between data and predictions are discussed.

Mendel's imperfect model of inheritance wasn't wrong. The chart below shows the general steps of how scientists use models and data on the left and the corresponding steps of your work with the inheritance of Wings and Tail on the right. The general 'steps' are actually part of a repeating cycle.

| In general ... | In this case ... |
| :--- | :--- |
| 1. Based on observations/data, build a <br> convincing model of the world. | 1. Mendel did this for you ©. You are <br> also doing something similar as you <br> learn about genetics and other new <br> things. |
| 2. Assume that model to be correct when <br> interpreting new data. | 2.Use Mendelian model of inheritance, <br> particularly independent assortment, to <br> predict possible Wings/Tail <br> phenotypes for Rosita and Boris' <br> offspring. Compare these predictions <br> with the actual Wings/Tail phenotypes <br> of Rosita and Boris' offspring. <br> 3. Decide if the model still basically makes <br> sense with some modifications or if the <br> new data indicate that the model is <br> fundamentally wrong and needs to be <br> replaced with a new model. |
| Modify Mendel's Law of Independent <br> Assortment so that it applies to genes <br> that are parts of different <br> chromosomes but not to genes that <br> are part of the same chromosome. |  |



Reasoning with models is discussed in general and in the context of what students have just done in Dihybrid.

Let's take a look at meiosis in Boris to understand independent assortment and gene location more fully and to think about what this means in terms of dihybrid offspring probabilities

Remember, chromosomes are assorted independently during meiosis
Since Boris is heterozygous for Horns (part of Chromosome1), he could pass on an H or h allele
Since he is also heterozygous for Wings (part of Chromosome2) his H allele could end up in a gamete with either a W or w allele and
his h allele could end up in a gamete with either a W or w allele.
The results of many of Boris' germ-line cells going through meiosis are the 4 combinations shown in the diagram


Independent assortment for Horns and Wings genes are contrasted with assortment of Wings and Legs genes that are parts of the same chromosome.

Remember that it's the chromosomes, not the genes, that assort independently.

Although Boris is heterozygous for Wings and Legs, he can only pass on Wings and Legs allele combinations as they occur in each of his Chromosome2s.

This results in just two combinations as shown in the diagram.


Here's a correctly filled in Punnett square
38. Using the Punnett square above, determine the probability of Rosita and Boris having offspring with different Wings and Legs phenotypic combinations

$$
\begin{aligned}
& \text { no wings \& no legs } \quad \bigcirc \quad 0 \quad 1 / 4 \bigcirc 1 / 2 \bigcirc 3 / 4 \bigcirc 1 / 1 \\
& \text { no wings \& } 2 \text { legs } \quad \bigcirc 0 \quad 1 / 4 \bigcirc 1 / 2 \quad \bigcirc \quad 3 / 4 \bigcirc 1 / 1
\end{aligned}
$$

$$
\begin{aligned}
& \text { wings \& nolegs } \quad 0 \quad \bigcirc 1 / 4 \bigcirc 1 / 2 \bigcirc 3 / 4 \bigcirc 1 / 1 \\
& \begin{array}{lllllll}
\text { wings } \& 2 \text { legs } & \bigcirc 0 & \text { (9) } 1 / 4 \bigcirc 1 / 2 \bigcirc 3 / 4 \bigcirc 1 / 1
\end{array} \\
& \begin{array}{llllll}
\text { wings } \& 4 \text { legs } & 0 & 1 / 4 & 1 / 2 & \bigcirc 3 / 4 & 1 / 4
\end{array}
\end{aligned}
$$

You're right! About $1 / 2$ of Rosita and Boris' offspring would have no wings and 4 legs (WWLL and WwLL). About $1 / 4$ would have no wings and 2 legs (WwLI). And about $1 / 4$ would have wings and 2 legs ( $w w L I$ ).国

Students are asked to reason through the probabilities of possible phenotypic combinations for the offspring of Rosita and Boris.

A series of quiz questions exercise and assess students' ability to reason about dihybrid.

To summarize.


Throughout your work with dihybrid inheritance and other concepts in BioLogica, you have been working with an incomplete, simplified model of meiosis as a way to help you build your own model and ultimately a more sophisticated understanding of genetics. When learning about complex things, like meiosis, it's useful and easier to build simple but incomplete models first and then add missing pieces and more complex details, such as corssing-over, as your learning continues.

### 5.0 Student Reports

Your students' work with Dihybrid is logged and viewable on the MAC Project Web Portal at http://mac.concord.org. For each student, you can view a report containing questions and answers.

Students have now completed the core instructional activities of BioLogica and are ready for Invisible Dragons, an assessment activity that requires that students figure out the genotypes of invisible parents from the phenotypes of their offspring.

Other optional activities include Scales, which guides students through reasoning about a previously unknown trait and Plates. Plates gives students a chance to explore an unknown trait with less guidance.

