

## Mendel's Peas Exercise 4 – Part 1

### NON-MENDELIAN GENETIC INHERITANCE

#### Goal

In this exercise you will use StarGenetics, a software tool that simulates mating experiments, to explore the differences between traits that exhibit Mendelian versus non-Mendelian genetic inheritance.

#### Prerequisite knowledge

Before completing this exercise, students should be able to:

1. Infer and assign genotypes of individual organisms using proper nomenclature of alleles.
2. Determine if an organism is true breeding.
3. Explain how alleles are passed down from parents to progeny and how traits are inherited according to Mendel's laws of segregation and independent assortment.
4. Design experiments to distinguish between dominant versus recessive phenotypes.

#### Learning objectives

After completing this exercise, you will be able to:

1. Define incomplete dominance.
2. Identify whether a trait is inherited in a Mendelian versus a non-Mendelian manner through the use of Punnett Squares to identify expected genotypic and phenotypic ratios.

#### Getting started with StarGenetics

- To access StarGenetics, please navigate to: <http://star.mit.edu/genetics/>.
- Click on the **Start** button to launch the application.
- Click **Trust** when a prompt appears asking if you trust the certificate.
- Click on **File → New** in the drop-down menu in the upper left hand corner.
- Click on the **Mendel's Peas Exercise 4** file.

As a fearless explorer and geneticist, you decide to take a trip to the Near East to look for new species of popular crops, particularly plants related to the common/domesticated garden pea plant, in honor of your favorite gardening enthusiast/bee keeper/Austrian monk, Gregor Mendel, the “Father of Modern Genetics.” During an expedition to the Nile Delta in Egypt, one of few the places where wild pea plants grow, you discover what appears to be a new, uncharacterized species of peas, perhaps related to the pea plant species that Mendel studied (*Pisum sativum*). You decide to creatively name this new species *Pisum niledeltus*. You decide to further characterize *Pisum niledeltus* by performing a series of crosses with two different plants you have brought back from Egypt of this species: **Plant A** and **Plant B**.

**1** What are the flower color, plant height and pod shape phenotypes of these two new plants? Record the flower color, height, and pod shape phenotypes of **Plant A and Plant B** in the table below. These plants will be referred to as the ‘parent plants’ in the following questions.

Plant	Flower Color	Plant Height	Pod Shape
<b>A</b>			
<b>B</b>			

**2 a)** What are the phenotypes you observe in the F1 progeny when each parent plant is self-crossed? For each strain, produce 200 F1 progeny and record: i) the parental phenotype (the phenotype seen in the parent), ii) the phenotype(s) seen in the F1 plants, and iii) the number of F1 plants with each phenotype.

- Self-cross *Plant A* by dragging it to the **Mating site** twice, to act as both the ovum and pollen donor, and then click on the **Mate** button to generate F1 offspring.
- To add additional offspring to a cross, click on the **Add more matings** button and select the appropriate number of matings (or crosses) you would like to perform in the pop-up window.
- Each resulting offspring can be viewed within the **Individual** tab, and a summary of the results is available in the **Summary** tab.
- The flower color of individual offspring can be visually observed or obtained by selecting an offspring of interest and looking in the **Properties** window.
- Repeat the same steps with *Plant B*. Start a new mating experiment by clicking on the **New Experiment** button. Your current experiment will automatically be saved for you within the **Saved experiments** window.

		Parent	F1 progeny	
Plant	Trait	Parental Phenotype	Phenotype(s) observed in F1 progeny	# of F1 plants with each phenotype
<b>A</b>	Flower Color			
	Plant Height			
	Pod Shape			
<b>B</b>	Flower Color			
	Plant Height			
	Pod Shape			

**b)** Based on your experimental data with 200 F1 plants, is *Plant A* and/or *plant B* true breeding with regard to flower color, plant height, and/or pod shape? Fill in the table below to indicate whether each of the parent plants are true breeding with respect to each individual phenotype.

Plant	Trait	True Breeding? (Y/N)
<i>Plant A</i>	Flower Color	
	Plant Height	
	Pod Shape	
<i>Plant B</i>	Flower Color	
	Plant Height	
	Pod Shape	

**3** Now we will determine the mode of inheritance of the flower color, plant height, and pod shape traits in the two parent plants of the newly discovered pea plant species, *Pisum niledeltus*. We will examine how they compare with the known mode of inheritance of the pea species that Mendel studied, *Pisum sativum*. Recall that all the traits that Mendel characterized in peas, including flower color, plant height and pod shape, exhibited the following characteristics:

1. Each trait was controlled by one gene,
2. Each gene had 2 alleles, and
3. The phenotype conferred by one allele was dominant or recessive relative to the phenotype conferred by the other allele, with heterozygotes exhibiting the dominant phenotype.

From now on, we will refer to traits with these characteristics as those that exhibit '**Mendelian genetics**', or '**Mendelian inheritance**.'

**a)** What are the possible genotypes, genotypic and phenotypic ratios would you expect in the F1 progeny resulting from a cross of *Plant A x Plant B* if all of the traits in question (flower color, plant height and pod shape) followed a **Mendelian inheritance pattern**?

Fill in the Punnett squares below with the possible genotypes of the parents and F1 progeny, and then determine the expected genotypic and phenotypic ratios for flower color, plant height, and pod shape for each cross according to what you would expect to observe if **Mendelian inheritance** applied in each case. Since you do not know which of the two possible phenotypes for a given trait is dominant or recessive relative to the other, **include ALL possible combinations**. For this question, assume that all 3 traits are **unlinked** to each other, and as a result, Mendel's Law of Independent Assortment applies.

#### **A Note on Nomenclature and Assigning Alleles:**

- Each allele in question is assigned a **single letter**. Use the **UPPERCASE** version of the letter to denote the allele that confers the **dominant** phenotype and the **lowercase** version of the letter to denote the allele that confers the **recessive** phenotype. For example, a plant that is homozygous dominant for a trait we will call *G* will have the genotype *GG*. A plant that is homozygous recessive for trait *G* will have the genotype *gg*.
- Usually the letter chosen describes the phenotype you observe. In this instance you may choose to use a "W" (for white) or a "P" (for purple) as the letter for the flower color trait, depending on your preference.
- Make sure to use the **SAME** letter for both the allele that confers the dominant and the allele that confers the recessive phenotype; just use different cases!

**Plant A x Plant B**

Flower Color: if **Red** is dominant)


Genotypic ratio:

\_\_\_\_\_

Phenotypic ratio:

Plant Height: if **Tall** is dominant


Genotypic ratio:

\_\_\_\_\_

Phenotypic ratio:

Pod Shape: if **Inflated** is dominant


Genotypic ratio:

\_\_\_\_\_

Phenotypic ratio:

Flower Color: if **White** is dominant


Genotypic ratio:

\_\_\_\_\_

Phenotypic ratio:

Plant Height: if **Short** is dominant


Genotypic ratio:

\_\_\_\_\_

Phenotypic ratio:

Pod Shape: if **Pinched** is dominant


Genotypic ratio:

\_\_\_\_\_

Phenotypic ratio:

**b)** What are the observed flower color, plant height, and pod shape phenotypes in 200 F1 progeny when **Plant A** is crossed with **Plant B**? For **each** trait, record i) the phenotype(s) observed in the F1 generation, ii) the number of plants with each phenotype, and iii) the phenotypic ratios.

- Cross **Plant A** with **Plant B** and produce 200 progeny.

**Answer**

**Flower color** Progeny:

Phenotypic ratio:

**Plant height** Progeny:

Phenotypic Ratio:

**Pod shape** Progeny:

Phenotypic Ratio:

**4 a)** Which, if any, of the 3 traits follow Mendelian genetics? Justify your answer by comparing the expected ratios in Question 3a with the observed phenotypic ratios in Question 3b. For each trait that follows Mendelian genetics, include which phenotype is dominant and which is recessive.

**Answer**

**b)** Which, if any, of the 3 traits follow a non-Mendelian inheritance pattern? Justify your answer by comparing the observed phenotypic ratios in Question 3a with the expected ratios in Question 3b.

**Answer**

**5** For the trait(s) you determined to be inherited in a non-Mendelian manner, provide a possible explanation or hypothesis that could explain how this trait is inherited. Include all possible genotypes and the phenotypes they correspond with.

**Answer**

**6** Now we are going to determine whether the phenotypic ratios you observe for the F2 generation for ALL phenotypes lend support to the hypothesis you proposed in Question 5 for any Non-Mendelian traits, and are also consistent with what you would expect for the traits do follow a Mendelian inheritance pattern. Based on your answers to Questions 4 and 5, what genotypic and phenotypic ratios would result from a cross between two F1 progeny? Fill in the Punnett Squares below.

Flower Color

Plant Height

Pod Shape




Genotypic ratio:

Genotypic ratio:

Genotypic ratio:

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

**7** Now, let's determine if your predictions correspond with the observed data from this cross. What are the flower color, plant height, and pod shape phenotypic ratios produced when two F1 individual plants from the **Plant A** x **Plant B** cross are crossed to produce 200 F2 progeny? For each trait, record the phenotype(s) observed in the F1 generation, the number of plants with each phenotype, and the phenotypic ratio.

- You can cross individual pea plants that you have generated in a previous saved experiment by dragging them from the appropriate **Saved experiments** window to the **Mating site**.
- Cross two F1 individual plants from the **Plant A** x **Plant B** cross you generated in Question 3b.

**Answer**

**Flower color**

**Phenotypes:**

**Phenotypic ratio:**

**Plant height**

**Phenotypes**

**Phenotypic ratio:**

**Pod shape**

**Phenotypes:**

**Phenotypic ratio:**

**8** Does your data in Question 7 support your hypothesis in Question 5? Explain. If not, suggest an alternate hypothesis for the inheritance pattern that is consistent with these new data.

**Answer**