



## 023 – Monohybrid Genetics with Wisconsin Fast Plants

### Supports PA STEELS Standards

- 3.1.6-8.N Develop and use a model to describe why asexual reproduction results in offspring with identical genetic information and sexual reproduction results in offspring with genetic variation.
- 3.1.9-12.Q Make and defend a claim based on evidence that inheritable genetic variations may result from (1) new genetic combinations through meiosis, (2) viable errors occurring during replication, and/or (3) mutations caused by environmental factors.
- 3.1.9-12.R Apply concepts of statistics and probability to explain the variation and distribution of expressed traits in a population.

### Summary and Timing

Students investigate multiple generations of Wisconsin Fast Plant seedlings. P1, P2, F1, and F2 seedlings are analyzed for stem color at 4-6 days old to discover monohybrid inheritance patterns. The seedlings are easily grown on filter paper and can be thrown away or transferred to a pot with soil after the investigation. The lab kit includes a small greenhouse, seeds, and planting supplies. Suggested timing - 1-2 active class periods, 4-5 inactive days to germinate the seedlings.

### Materials \*Teacher Provided (view materials)

- Greenhouse or grow light
- Wisconsin Fast Plant seeds, 4 types - P1 non-purple stem (homozygous recessive), P2 purple stem (homozygous dominant), F1 purple stem (heterozygous), and F2 purple and non-purple stems (3:1)
- Petri dishes
- Filter paper
- Water bath container
- Forceps

### Suggested Background Resources

Visit the [Wisconsin Fast Plants website](#) to learn more about these plants.

### Guiding Questions

Create a genetic model to explain the inheritance pattern in the Wisconsin Fast Plant seedlings.

### Teacher Notes and Set-Up Instructions

Anthocyanin, a purple pigment found in plants, and the trait of interest in this monohybrid cross is best observed in the stem color on days 4-6. Germinate the seeds on day 0 and observe the seedlings on day 4-6. The characteristics of the seed types are described below. Share this information with the students as needed.



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- One gene controls stem color, simple dominance – the stems are either purple (dominant) or not-purple (recessive). Anthocyanin, a purple pigment found in plants, and the trait of interest in this monohybrid cross is best observed on days 4-6.
- P1 = parent 1 is homozygous recessive. Genotype: anl/anl. Phenotype: non-purple stem, hairless
- P2 = parent 2 is homozygous dominant. Genotype: ANL/ANL. Phenotype: purple stem, hairy
- F1 = heterozygous offspring from a P1 x P2 cross. Genotype: ANL/anl. Phenotype: purple stem
- F2 = 3<sup>rd</sup> generation offspring from a F1 x F1 cross. Genotype ratio: 1:2:1 for ANL/ANL: ANL/anl: anl/anl. Phenotype ratio 3:1 purple to non-purple stems.

### Procedure - days 0-3

1. Plan the “day 0” planting date so that you can observe the seedlings on day 4, 5, or 6. Recommended planting dates are Mondays, Thursdays, or Fridays.
2. On day 0, follow the petri dish protocol, but place only 10 seeds per dish. You will need 8 dishes for F1, 8 dishes for F2, and 8 split dishes for P1 and P2.

[petridishprotocol.pdf](#)

3. Place the dishes under 24-hour lights. The lights should be close to the dishes. Add water as needed.
4. Students can observe and measure the germination process, they will notice daily changes. View [p. 8 of the Wisconsin Fast Plant activity guide](#) for a measurement and graphing activity. Students can [read about how the Wisconsin Fast Plants were developed](#) through selective breeding.

### Procedure - day 4 or 5

1. Tell the students that we want to observe the traits of the plants and determine if any of the traits can be explained using a genetic model.
2. Provide each student group with a tray of F1 seedlings and instruct the students to create a sketch of one of the plants and label the physical characteristics they observe, such as color, shape, size, or texture.
3. Compile a class list of the observable plant traits. As a class, agree on 4 traits to observe. Stem color must be 1 of the 4 traits. Students typically include stem color in their list, but you may need to suggest ‘stem color’ in some classes. List the 4 traits in the first column of the data table.
4. As a group, students observe and record the 4 selected traits in the F1 seedlings.
5. Provide each student group with a split tray of P1 and P2 seedlings. Tell the students to observe and record the 4 selected traits in the P1 and P2 seedlings.
6. As a class, discuss the observed traits and describe any patterns observed. Project or draw a class data table to support a discussion about which of these traits can be described with a genetic model. Allow students to make mistakes and investigate traits other than stem color as time permits.
7. Determine the dominant and recessive stem colors. Purple is dominant and green is recessive, we know this because all of the offspring in a purple and green stem cross show the purple stem.



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8. Complete the Punnett's square to determine P1 and P2 genotype based on the observed phenotype for stem color (GG x gg, Gg x gg). P2 (purple stem) is homozygous dominant and P1 (green stem) is homozygous recessive; the cross between these parents produces 100% heterozygotes (F1) with purple stems.
9. Complete the Punnett's square to predict the result of an F1xF1 cross. Crossing two heterozygotes is expected to produce 75% of offspring with the dominant phenotype, and 25% will express the recessive phenotype (3:1). Expressed genotypically, we expect a 1:2:1 ratio of GG, Gg, and gg.
10. Provide each student group with a tray of F2 seedlings. How can we test the expectation of a 3:1 phenotypic ratio? Students can count the number of purple and green stems in each tray and calculate a class average - the observed average should be close to the expected 3:1.
11. The seedlings can be transplanted into soil and pots or thrown away.



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Student \_\_\_\_\_

Plant Sketch

### Wisconsin Fast Plant Traits

Trait	F1	P1	P2	F2

### Punnett Squares




P1 phenotype \_\_\_\_\_ genotype \_\_\_\_\_

P2 phenotype \_\_\_\_\_ genotype \_\_\_\_\_