

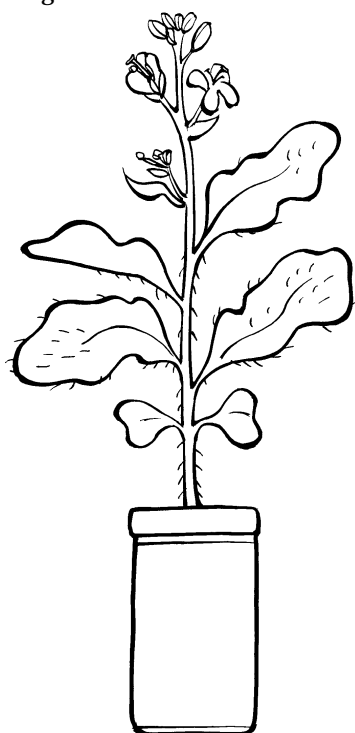


Hairy's Inheritance

Getting a Handle on Variation

Within the population of Fast Plants there is an observable trait (*phenotype*) that might escape some students' notice, but which lends itself easily to investigating variation and inheritance. Varying numbers of hairs can be seen along the stem, on the upper and lower surfaces of the leaves, on leaf edges and even on the buds of some Fast Plants (see Figure 1).

Figure 1:



The hairs found on the basic *Brassica rapa*, Fast Plants, constitute a trait that is variable, quantifiable and heritable. Scientists are not sure why plants have hairs although they have some ideas. Furthermore, very little is known about the genetics and inheritance of hairiness.

The number of different genes or alleles that control the number and location of hairs is also unknown. Observing and counting the

hairs on Fast Plants will challenge and sharpen students' observational skills and provide them with the opportunity to ask many questions.

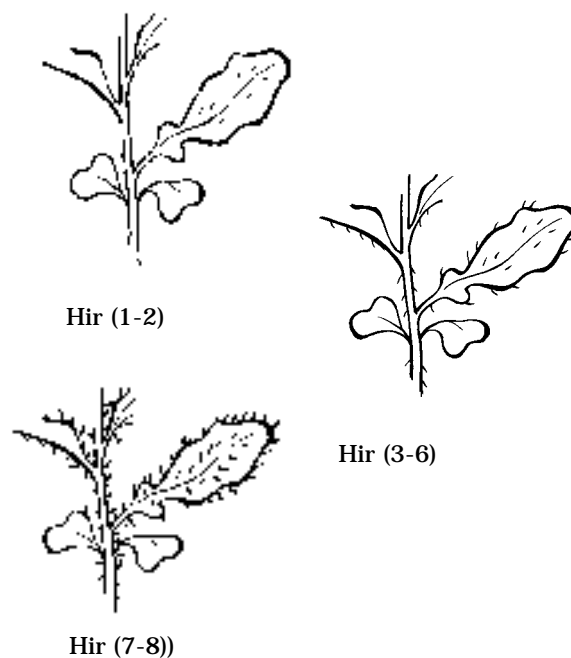
Students often measure the height of Fast Plants with a ruler and estimate the actual height in units such as millimeters. Determining the number of hairs is different than estimating height in that each hair is a meristic trait, a discrete unit that can be counted directly.

The expression of the hairy phenotype appears to be under the control of a number of genes and is considered to be a polygenic trait. (poly= Greek word for many).

For these reasons, two Fast Plants stocks, hairless, Hir (0-1), and hairy, Hir (3-6), have been developed for teachers, students, and scientists to investigate the quantitative nature of hairy's inheritance.

The hairy phenotype is described as Hir (3-6). This particular symbol, Hir, is for *hirsute* (after the Latin for hair). You will also note that since the specific genotype for hairiness is not yet known, the phenotype symbol is used, Hir. As with phenotypes which show a wide variation in their expression, a scale from (0-9) can be used to quantify the phenotype. On the scale from (0-9), 0 = no expression (no hair), 1-2 = low expression (few hairs) 3- 6 = intermediate expression (some hairs), 7-8 = high expression (many hairs) and 9 = very high expression (very hairy), (see Figure 2).

Figure 2:

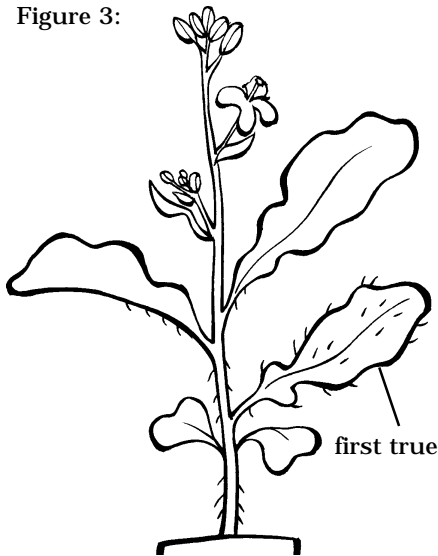


This WFPID is designed to give students and scientists ideas for investigating the variation and inheritance of hairs and is presented in "levels" each of which provides students with a given set of concepts and ideas. Moving up a level increases the skill and background requirements of students and teachers.

Level 1 **Observing, Counting and Analysis**

For this activity 10 day old Fast Plants are needed. The hairy stock of Fast Plants will work well for this activity unless more variation is desired, then the basic Fast Plant will work.

Figure 3:



Students first need to decide how and where to count the hairs on the plants. They can look over the plants and identify where hairs appear on the plant. Students should describe and map with sketches where the hairs are located (see Figure 3).

Next, they need to decide where on the plant they could accurately count the hairs. Younger students may have difficulty counting, for instance, the hairs all around one portion of the stem.

It may be easiest to count the hairs on the edge of the first true leaf. This should be done on or around day 10 in the life cycle when the first true leaf is well developed. Students will need good light coming over their shoulder and a hand lens.

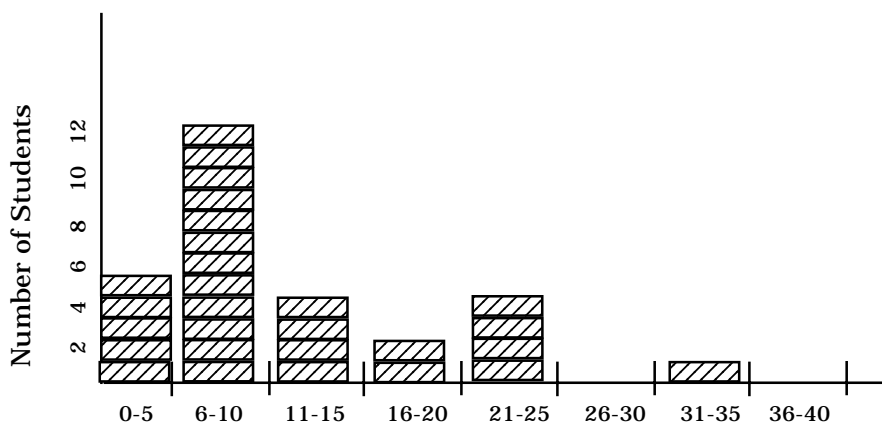
By observing the plant against a dark, contrasting background (construction paper, a classmates sweater, etc.) they can count all of the hairs on the edge of the leaf.

Each student can record the number of hairs at the particular agreed upon location on their plant and then all the data from the class can be incorporated into a *frequency histogram* as suggested in Figure 4. From observing the graph, students will be able to identify characteristics of the population with respect to the hairy phenotype.

Frequency histograms are an informative method of grouping class data. They may be created with the help of a computer program or simply worked out by hand. For younger students it may be helpful to do this as a group on a large graph (see Figure 4). The horizontal or X axis is the independent variable meaning that it defines the number of hairs counted. Each of the units on the X axis is called a "class" or a "bin" and is dependent on a predetermined class size. The class 0 - 5 denotes that if any student counts 0 to 5 hairs on the margin of the leaf then the student's data are recorded on the graph as a box. The vertical axis or Y axis is the dependent variable.

The size of the variable was dependent on the number of students who's data fell into the predetermined class size on the X axis. If there is more than one student who counted between 0 and 5 hairs then their data point would also be added on the graph as a box. According to Figure 4 twelve students have between 6 to 10 hairs on the leaf edge of their plant. For the frequency histogram of basic *Brassica rapa*, Fast Plants, see Figure 5.

Figure 4:



Level 2
Analysis and Selection of Variation

Figure 5 depicts a frequency histogram of the number of hairs counted on the right margin of the first true leaf in a population of 104 Fast Plants. Notice that the outline of the frequency histogram roughly depicts a curve known as a *frequency curve*. Do the majority of plants in Figure 5 have few or many hairs? Could you assign a scale rating, Hir (0-9) to such a graph?

After looking at their graphed data and the population statistics, students could “brainstorm” ideas and develop questions relating to hairiness and inheritance.

Questions may include: Is hairiness inherited?

How is hairiness inherited? Could hairless or super hairy populations be produced? Could you produce a hairless population?

By choosing the top ten percent of the hairiest plants in the class population as an experimental group and intermating (pollinating) only those plants, students would be applying what Charles Darwin called *artificial* or *directed selection* on the population.

If hairiness were inherited through the combined effects of many different genes (*polygenically*), one would expect that by repeatedly selecting the hairiest parents for successive generations the number of genes contributing to hairiness in the population would be increased. Would this directed selection increase the population mean (average) for hairiness? Will the offspring of the first intermating have more hairs on average than the parents? Through how many generations would the students have to repeat the directed selection experiment before producing a super hairy plant?

Further investigations

Students, who ponder these questions and who are trying to understand the inheritance of the hairy trait, will continue to ask more questions. If all the hairy plants from the first (parental) generation are intermated, will all the offspring have hairs? Will the hairs show up in the same places on the offspring?

Will the progeny of a hairless and a hairy plant have hairs? Will all the offspring of the F_1 generation have hairs? If many genes are functioning to produce hairiness, can you keep increasing hairiness?

Is there a limit on the number of hairs that a plant can have? Conversely, if only the hairless progeny mated, how many generations would it take to develop a population of hairless plants?

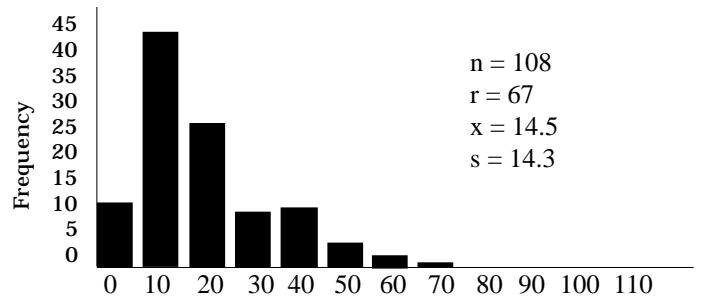
The environment and phenotype: Environment is ever present in the expression of the phenotype. The degree to which components of the environment, such as light, temperature and nutrition, contribute to the expression of phenotypes is an important part of genetics.

Little is known about the influence of environmental factors on the inheritance of hairiness. Investigation by students could provide insight into the influence of environment on the expression of the hairy phenotype.

Environmental applications:

Students may ask why plants have hairs at all. Do hairs confer an adaptive advantage to Fast Plants? If so, under what conditions? A few scientists have asked the similar questions.

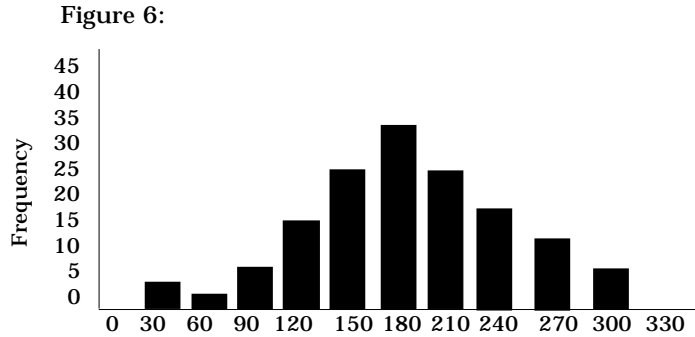
Figure 5: Hairs on First True Leaf of Margin on Basic *Brassica rapa* CrGC 1-33



Extension 1:

Consider the shape of the frequency histogram.

Geneticists know that normally distributed continuous phenotypic variation is usually produced by the combined effects of many genes. Such traits are said to be under *polygenic* control (poly = Greek for many.) Figure 6 is a frequency histogram showing a normal distribution curve. What questions about the inheritance of hairs does the frequency distribution in Figure 6 raise?

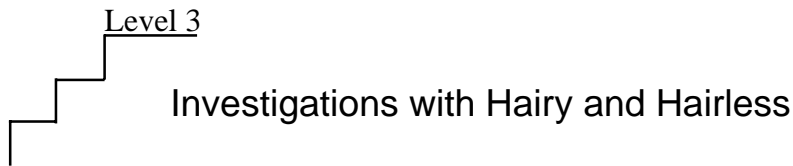


Extension 2:

Develop a scale for hairiness (Hir).

Since hairiness is a phenotype that shows wide variation in its expression, a scale from 0-9 can be used to define roughly the range in expression of hairiness, where 0 = no expression (no hair), 1-2 = very low expression (very few hairs), 3-6 = intermediate expression (intermediate numbers of hairs) to 9 = very high expression (very hairy).

By counting the number of hairs in a defined area on the plant, you can convert the 0-9 scale to a graph depicting the relationship of the scaling numbers 0-9 (the independent variable or x axis) and the actual count of number of hairs (the dependent variable or y axis.) What is the relationships of your scale to the number of hairs counted? Is it linear, logarithmic, etc.?



As mentioned earlier, the Fast Plants Program has developed two specialized stocks for investigating the inheritance patterns of hairs. Hairless, Hir (0-1) and Hairy (3-6) are ideal tools for researchers and students to conceptualize, hypothesize and experiment with the notions of how a trait or phenotype such as hairs may be inherited. Is hairiness controlled polygenically or by a few genes of unknown effect?

Figure 7 shows the frequency histogram of two stocks from the Crucifer Genetics Cooperative. Parent 1 (P1) is the hairless, Hir (0-1) CrGC 1-54 and Parent 2 (P2) is the hairy, Hir (3-6) CrGC 1-37 stock. Notice the difference in the standard deviation of the Hairy stock compared to the Hairless. What questions about inheritance do these frequency histograms raise?

Figure 7:

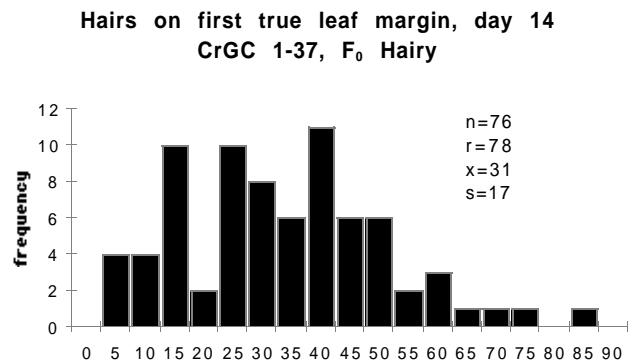
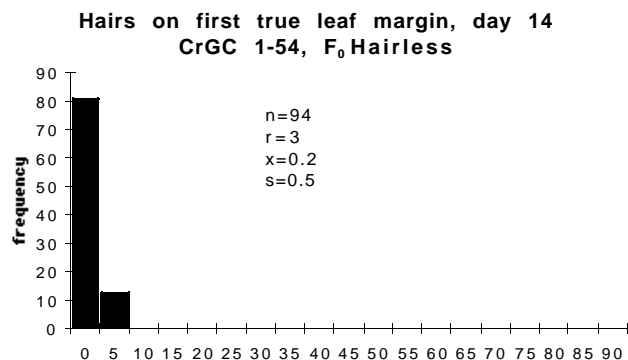
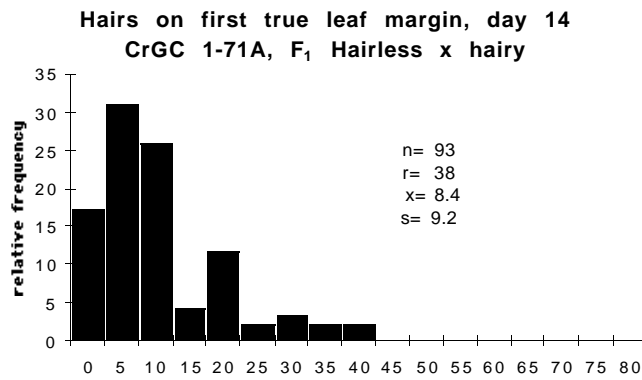
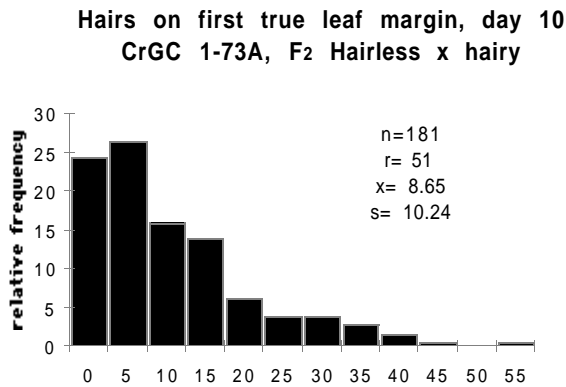


Figure 8:



In order to provide more information on the inheritance patterns of these stocks the Fast Plants Program has produced and characterized the F₁ and F₂ of these two stocks. The production of the F₁ stocks was facilitated by using male sterile, *mst₂* genotype accompanying each of the two parent stocks, see WFPID *Nuclear Male Sterility in Facilitating Crosses*. The male sterile plants in each of the parental stocks appeared at a ratio of 1:1. Removing the male fertile plants from one of the parents before pollen is shed enables strict pollen control in the production of the F₁ generation.

Figure 9:



By using male sterile on both parents, reciprocal F₁ progeny can be produced and examined for potential maternal contributions to the expression of the hairy phenotype. Examples of hair counts for the first true leaf margins, in the F₁ and the F₂ progeny are depicted in Figure 8 and 9.

Populations such as CrGC 1-71, F₁ hairless X hairy, and CrGC 1-73, F₂ for hairless X hairy, could be used for many different investigations dealing with inheritance and expression of the hairy phenotype.

Level 4

Quantifying Gain from Selection, Heritability

To quantify any increase in number of hairs made by selecting and intermating the hairy portion of a population, students would first want to record the number of hairs on each plant in the experimental population (Generation 0) of size = n. Then calculate the average number of hairs on a representative plant = x. The standard deviation is a calculation that described the average amount that individuals vary from a population average and is a useful statistic in helping to understand how the hairy phenotype is inherited.

If students select the 10 percent hairiest plants from the population and calculate the average or mean number of hairs from this *subpopulation* then the difference between the population and the selected sub-population mean is the *selection differential*. Seed is produced on the selected plants. Then the progeny from the selected subpopulations are counted for hairs and averaged. The difference between average number of hairs from the original population, Generation 0 and the average of Generation 1 is known as the *response to selection*. The inherited change in the population due to the 10 percent selection for hairiness is known as the *realized heritability*, h^2 , and is the proportion of the response to selection to the selection differential.

$$h^2 = \frac{\text{response to selection}}{\text{selection differential}}$$

Estimates of realized heritability can range from low, < 0.1 to high, > 0.6 and are useful in predicting the rates at which a population can change through selection.

References

WFP Notes reprint, "Getting a handle on variation: quantifying differences in plant height."

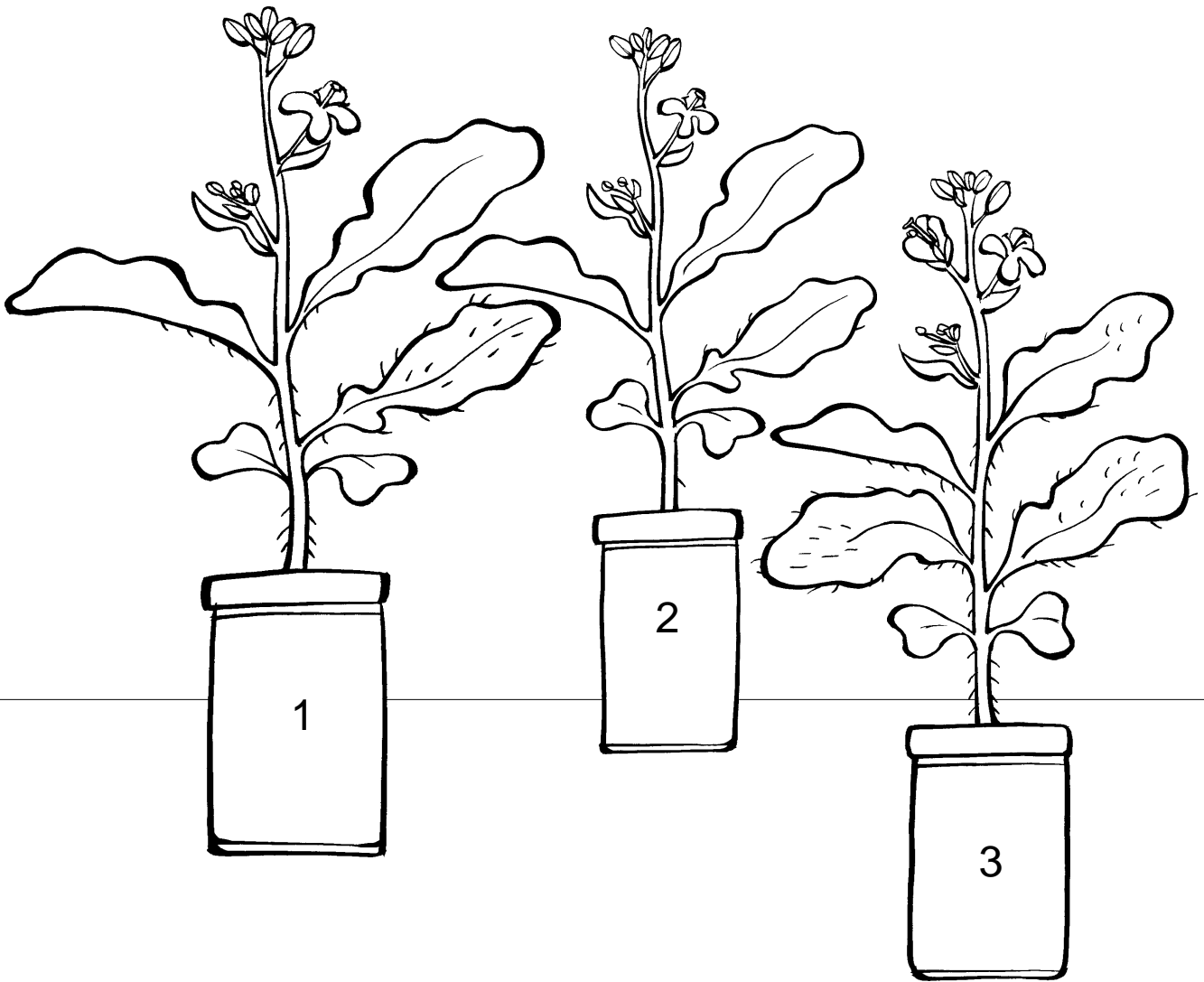
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How hairy is hairy?

- Directions:
1. Find the first true leaf on each plants and color it green.
 2. How many hairs can you find on the top of the first true leaf?
 3. How many hairs can you find around the edge (margin) of the first true leaf?
 4. Do you see hairs anywhere else on the plant?
 5. Circle the places where you find hairs.



Answers: Question 2: plant 1 = 7, plant 2 = 0, plant 3 = 9. Question 3: plant 1 = 11, plant 2 = 3, plant 3 = 11, do not count the hairs on the stem (petiole) of the leaf.