WISCONSIN

FAST PLANTS

Unraveling the Mysteries of Hairy's Inheritance

Variation is one of the fundamental characteristics of life. All organisms exhibit some variation among individuals. Understanding the ways that variation is manifested in organisms, how it comes to be expressed through the development of the individual, and how it is transmitted from one individual to the next generation of individuals are central themes in biology.

Upon close observation of a population of rapid-cycling *Brassica rapa,* Fast Plants, students will become aware that any particular characteristic observed, (phenotype) on one plant varies more or less on other plants. The Crucifer Genetics Cooperative, CrGC, the genetic stock center of the Wisconsin Fast Plants Program, has developed many stocks of rapid-cycling *Brassica rapa* suitable for genetic investigation of the nature and inheritance of phenotypic variation. Some stocks contain traits in which only a few easily discernible or discrete phenotypic differences are exhibited and are suitable for Mendelian genetics. Other stocks exhibit phenotypes whose expression may vary continuously and which may be quantified as countable units, estimates of size , or as intensity of color saturation. The inheritance of such quantitative phenotypes maybe conditioned by a few (oligogenic) or many genes, (polygenic) and normally requires numerical descriptors in which statistical notations of population size (n), range (r), the mean (x), and the standard deviation (s) are applied. Understanding the inheritance of quantitatively inherited phenotypes is important to understanding the role of genotype in phenotypic expression, variation, and evolution.

Figure 1: Depicts a hairy Fast Plant. The hairs on Fast Plants allow students to investigate both Mendelain and quantitative inheritance.

Hairs found on Fast Plants, are an example of a continuously variable phenotype ideally suited for exploring the modes of inheritance underlying the trait. Hairs are a directly countable (meristic) trait and can be observed on the stem, petioles, leaf blades, margins, and occasionally on the sepals. How hairs are inherited in *Brassica rapa* is still not completely understood. However, the number of hairs on a plant or plant part appears to be conditioned polygenically, and is considered to be qualitatively inherited, (Agren, J. et al., 1992), while the absence of any hair on *Brassica rapa* is conditioned by a single Mendelian recessive allele (Song KM, et al., 1995).

The number of hairs on a specified plant part such as, on the margin of the first true leaf, can be used to represent the hairiness of an individual. Hairiness in a population of plants can be depicted as a statistical summary of individual plant counts. Graphing a frequency histogram of hairs can help students understand how Mendelian and quantitative inheritance contribute to the expression and variation of a trait (Figure 2).
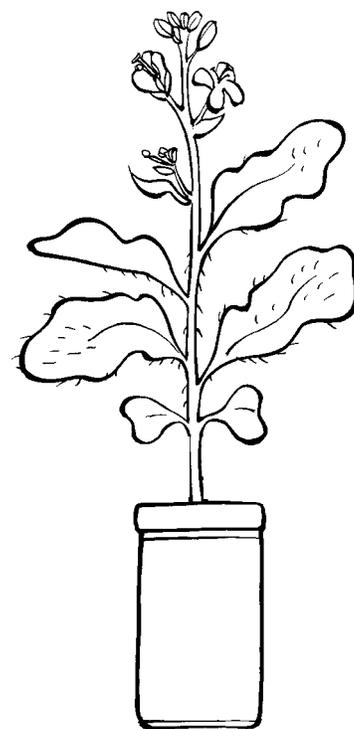
Hairs on First True Leaf Margin of Rapid-cycling *Brassica rapa, CrGC 1-33*
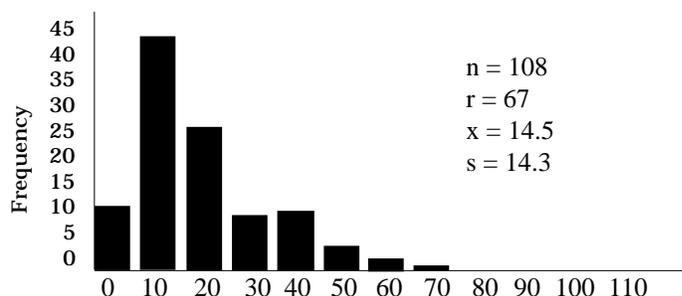

n = 108
r = 67
x = 14.5
s = 14.3

Figure 2: Frequency histogram shows the number of hairs in a population of Rapid-cycling *Brassica rapa,* CrGC 1-33

Numerical representation of the population in tables or graphs, (Figure 2), enables students to understand the variation in the specified phenotype, e.g. hairs, in the population. By selecting and intermating individual plants to have none or a few hairs or plants having many hairs, the mean number of hairs can be decreased or increased demonstrating that hairiness is a heritable trait. Bruce Fall at the University of Minnesota has demonstrated the heritability of hairiness in an undergraduate biology lab by having his students select for the number of hairs on the petiole of the first true leaf. Starting with a population with a mean number of 8.8 hairs per individual, hairs had been completely eliminated from the smooth-selected lineages after 10 generations of recurrent selection for hairless. By selecting and intermating the 10% hairiest plants in each successive generation, the mean hair number has been increased to over 105 in 10 generations (Fall, B. et al., 1995)
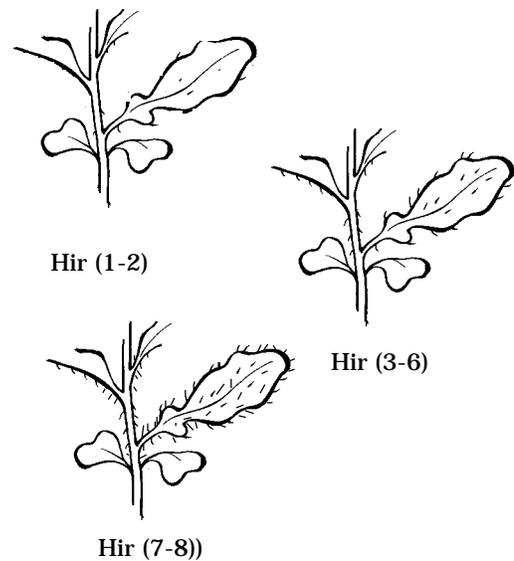
The CrGC has developed and maintains a number of Fast Plants stocks having varying numbers of hairs. Two stocks in particular, CrGC 1-54, hairless, Hir (0-1),

Hir (1-2)

Hir (3-6)

Hir (7-8))

Figure 3: A diagram illustrating the (0-9) point scale developed to quantify the number of hairs on a Fast Plant.

and CrGC 1-37, hairy, Hir (3-6), have been developed for students, and researchers to investigate the nature of the inheritance of hairs. Quantitative phenotypes such as hairiness which show a wide range in variation can be described using a scale from (0-9) to represent the relative expression of the phenotype. The hairy phenotype is described as Hir (3-6). This particular symbol, Hir, is for *hirsute* (after the Latin for hair). On the scale from (0-9), 0 = no expression (no hair), (1-2) = low expression (few hairs), (3-6) = intermediate expression (hairs), (7-8) = high expression (many hairs) and (9) = very high expression (very hairy), (see Figure 3). Hairless, Hir (0-1), and Hairy, Hir (3-6), are ideal stocks for researchers and students to conceptualize, hypothesize and experiment with the notions of how the hairy phenotype may be inherited.
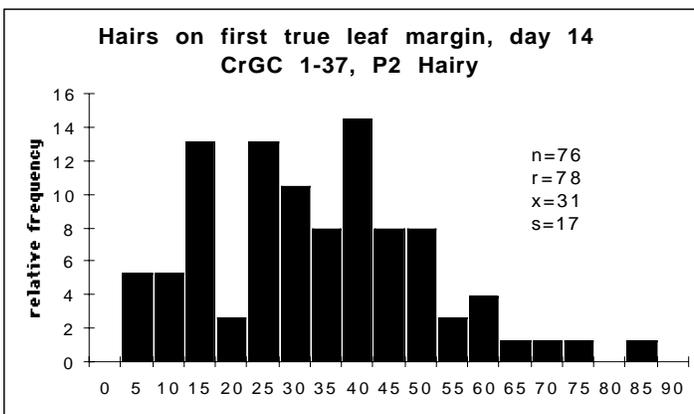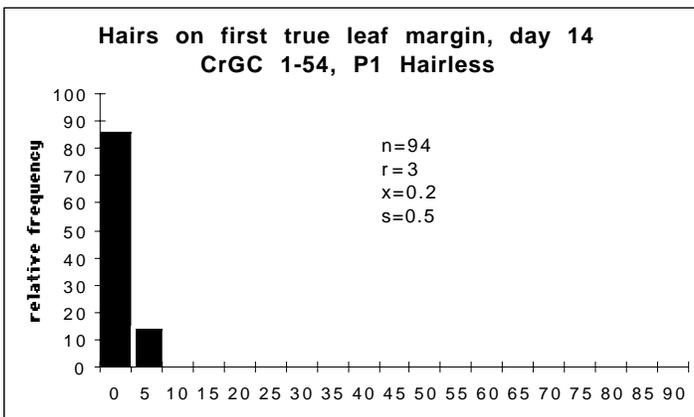
Crossing hairless and hairy parents to produce an F1 and then F2 progeny, should provide information indicating how hair number is inherited in *Brassica rapa*. The number of hairs on the margin of the first true leaf is used to characterize CrGC 1-54, Hir (0-1), and CrGC 1-37, Hir (3-6), for hairiness. Figure 4 shows the fre-quency histogram of both parents. Notice the difference in the standard deviation of the hairy stock compared to the hairless.

**Hairs on first true leaf margin, day 14
CrGC 1-54, P1 Hairless**

relative frequency

n=94
r = 3
x=0.2
s=0.5

**Hairs on first true leaf margin, day 14
CrGC 1-37, P2 Hairy**

relative frequency

n=76
r=78
x=31
s=17

Figure 4: Frequency histograms depicting the number of hairs on:
    Parent 1: CrGC 1-54: *anl/anl*, Hir (0-1), mst2/(1:1)
      (anthocyaninless, hairless, Hir (0-1), and
       50% of the plants male sterile)
    Parent 2: CrGC 1-37: *anl/anl*, Hir (3-6), mst2/(1:1)
      (anthocyaninless, hairy, Hir (3-6), and
       50% of the plants male sterile)

What questions about inheritance do these frequency histograms raise?

The CrGC has also produced and characterized the stocks of the F1, CrGC 1-71, and the F2, CrGC 1-73, generations from the CrGC 1-37 and CrGC 1-54 parents. The production of the F1 seed was facilitated by incorporating in the parental stocks a single recessive allele, mst_2, which prevents any pollen formation thus, conferring male sterility on the plant. The mst_2 allele is maintained in the hairless, CrGC 1-54, and hairy, CrGC 1-37, parental stocks in order to ensure that one half of the plants will be male sterile and the other half male fertile. Removing the male fertile plants from one of the parents before pollen is shed enables strict pollen control in the pro- duction of the F1 generation.

Analysis of the F1 and F2 generation, (Figure 5), data provides interesting insight into the inheritance of the hairy phenotype. When F2 progeny are scored for the absence or presence of any hairs, the results support the model of a single recessive allele designated as *hir* for hairlessness. Chi-squared analysis of the F2 data in Figure 5 has a P value of approximately 0.05 for a 3:1 of hairy vs hairless. Observed values were 23 hairless of the total population of 95.

The F1 data are of interest in that they do not support the model of a single recessive allele for hairlessness with a completely expressed dominant, wild type allele conditioning presence of hair. The presence of 17 hairless in the F1 popula- tion of 93 suggests that interaction between the alleles for hairless and alleles for hairy may be occurring when the *hir* allele is in the heterozygous condition.

The data in Figure 5 and the above preliminary analysis are designed to raise a number of questions relating to the *Unraveling the Mysteries of Hairy's Inheritance*. It appears that the absence of hairs in Fast Plants is controlled by at least one allele having a major effect.

Hairs on first true leaf margin, day 14
CrGC 1-71A, F_1 Hairless x hairy

n= 93
r= 38
x= 8.4
s= 9.2

Hairs on first true leaf margin, day 14
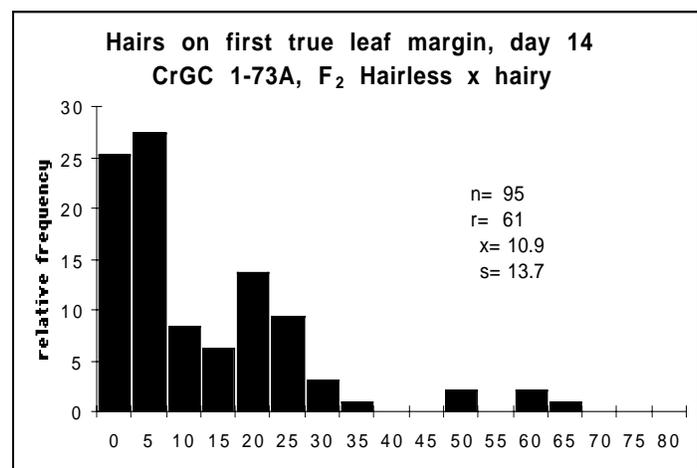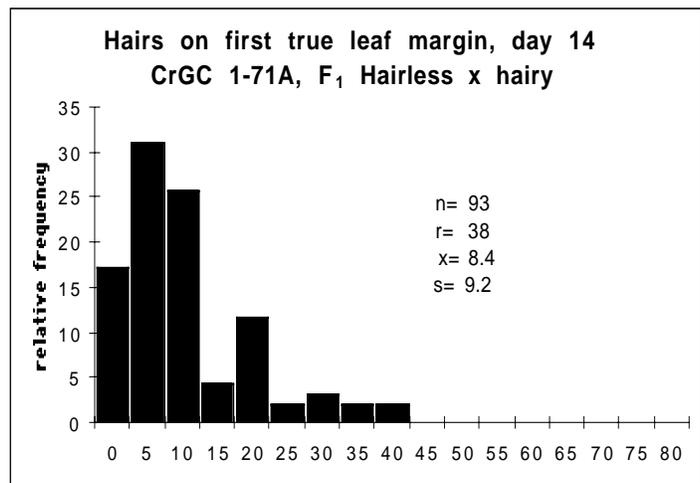**CrGC 1-73A, F_2 Hairless x hairy**

n= 95
r= 61
x= 10.9
s= 13.7

Figure 5: Frequency histograms depicting the number of hairs in the F1 and F2 populations from a cross between a hairless (CrGC 1-54) and a hairy (CrGC 1-37) Fast Plant.

The presence of one or more allele conditioning hairlessness cannot be ruled out since the crosses between the parental stocks were always made with massed pollen from a minimum of 32 plants. Thus, the contribution of multiple alleles at the hairless, *hir*, locus cannot be ruled out. If indi- vidual hairless and hairy plants were selected from a the parent populations and crossed would their progeny provide more explicit information on the inheritance of hairy? For example, would you expect the same results if you crossed a hairless plant with a plant with a few hairs as com- pared to a cross between a hairless plant and with a very hairy plant? These types of questions

and experiments will provide insight into the Mysteries of Hairy's Inheritance.

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