Creating a Wooly Booger

The study of quantitatively inherited traits

Overview

In this experiment, students will study the genetics of quantitatively inherited traits by examining the concepts behind a selective breeding program designed to encourage certain characteristics. Two populations of Wisconsin Fast Plants — very hairy and few to no hairs-- will help them determine the heritability of the trait and the results of a selective selection.

In the first part of the experiment, students will strive to create a population of intermediate hairiness and in the second part, they will strive to create a very hairy plant, the Wooly Booger.

This experiment may be terminated at any generation. However, one may find that the data and seed from the crosses may be carried from year to year as a continuous test for your school.

Biology and agriculture concepts

Plant growth and development
Genetics
Selective breeding
Statistics
Mathematics

The Teachable Moment

Biology and agriculture teachers can use this unit when teaching non-Mendelian genetics or when focusing on plant and animal selective breeding. These experiments also provide a solid foundation for the study of the plant life cycle.

Background

While introductory genetics often covers only simple Mendelian genetics, many of the genetic phenomena observed in our world do not follow this pattern. Quantitative genetics studies of the transmission of traits in which the phenotype of a characteristic is determined by the collective effect of several or many genes. Because of this effect, rather than observing 2 or 3 distinct phenotypic states for a given trait as is found in traditional Mendelian genetics, for instance, red versus white eyes in fruit flies, a range of expression of that trait is observed.

This range of expression allows a breeder to selectively choose those individuals with certain degrees of expression (the tallest 20%, for example) and interbreed them to create a population statistically different from the parent population. The genetics, mathematics and statistics involved in quantitative genetics and selective breeding will be explored in this unit.

Two genetic strands of Wisconsin Fast Plants (*Brassica rapa*), Hir(0-1) (few or no hairs) and Hir(3-6) (hairy), are used in this experiment to provide teachers and students with an observable and quantifiable trait that varies both in the location of the hairs (along the stem, on the upper and lower surfaces or margins of the leaves or even on the buds) and in the number of hairs found. The expression of the hairy phenotype is considered to be a polygenic trait, that is, it appears to be under the control of a number of genes. The number of different genes or alleles that control the quantity and location of hairs on the plant is unknown.

Observing and counting the numbers of hairs in parents and offspring will provide data that can be used in understanding statistical tools necessary for the study of quantitative genetics. Concepts of distribution (frequency, range, mean, mode, variance and standard deviation) should be introduced.

Not all variation observed is due to genetic influences; significant variation is affected by environmental conditions. When teaching this unit, it is good to keep in mind that observable variation is likely an interplay between genetic and environmental determinants.

Teacher Management

Preparation

Preparation time depends on how the activity will be used.

Activity time

Phase I-Introduction to Plant Breeding takes 55-60 days. In addition, four 50 minute class periods are necessary--two class periods for planting on days 1 and 40 and two class periods for data collection around days 16-18 and 55-60 are necessary.

Phase II-Creating a Wooley Booger
This unit take 55-60 days and approximately four 50 minute class periods as above.
Either activity can be shortened to approximately 35-40 days by providing the students with 16-18 day old flowering plants.

Materials

Hir(0-1) seed
Hir(3-6) seed
Quad pots or film canisters
Growing media
Osmocote fertilizer pellets
Materials for pollinating the plants (ie. bee sticks, cotton swabs, pipe cleaners, or tweezers)
Fluorescent light bank (minimum of six lights)
Reservoirs
Wicking material
Index cards
Bamboo sticks

Sources of materials

All Fast Plant materials and seed stock can be obtained from Carolina Biological Supply Company. After the initial purchase, seed can be grown and harvested for future classes and experiments.

Safety

General lab safety should be employed.

Tips

Hir(0-1) plants will have a green stem and Hir 3-6 will have a purple stem and can hence be distinguished early on in their life cycle.

Make sure all plants are properly labeled

Make sure all harvested seed is properly labeled

After harvesting, the next generation may be started as soon as the seed is dry.

Key terms

Deviation: The individual observation minus the mean.

Frequency: The number of individuals in a population that show a trait. For example, in a population of 100 cats, 75 are black and 25 are white. The frequency of black would be .75 and the frequency of white would be .25. Expressed as a ratio of 3:1.

Heritability: The capacity for being transmitted from one generation to the next. A ratio of genetic variation to the total observed variation.

Mean: The sum of all numbers in the set divided by the total number of individuals in the set (the average).

Mode: The value represented by the greatest number of individuals

Polygenic trait: Inheritance of phenotypic characters that are determined by the collective effects of several or many genes.

Range: The difference between the largest and the smallest items in a sample

Standard deviation: The positive square root of the variance

Variance: The average of the total squared deviations.

References

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King, Robert C., A Dictionary of Genetics, 4th Ed., Oxford University Press, New York, 1990.

Edwards, M., T. Osborn and P.H. Williams, Quantitatively Inherited Characters. Crucifer Genetics Cooperative, Madison 1987.

Creating a Wooly Booger
A genetic study of quantitatively inherited traits

Introduction

Many of the genetic phenomena observed in our world do not follow a simple Mendelian genetics pattern. Quantitative genetics studies the transmission of traits in which a characteristic is determined by the collective effect of several or many genes. Because of this effect, rather than observing 2 or 3 distinct phenotypic states for a given trait as is found in traditional Mendelian genetics, for instance, red versus white eyes in fruit flies, a range of expression of that trait is observed.

This range of expression allows a breeder to selectively choose those individuals with certain degrees of expression (the tallest 20%, for example) and interbreed them to create a population statistically different from the parent population. The genetics, mathematics and statistics involved in quantitative genetics and selective breeding will be explored in this unit.

Two genetic strands of Wisconsin Fast Plants (*Brassica rapa*), Hir(0-1) (few or no hairs) and Hir(3-6) (hairy), are available to provide you with an observable and quantifiable trait that varies both in the location of hairs (along the stem, on the upper and lower surfaces or margins of the leaves or even on the buds) and in the number of hairs found. The expression of the hairy phenotype is considered to be a polygenic trait, that is, it appears to be under the control of a number of genes. Just how many different genes or alleles control the quantity and location of hairs on a plant is not known.

Observing and counting the numbers of hairs in parents and offspring will provide data that can be used in understanding statistical tools necessary for the study of quantitative genetics. Concepts of distribution (frequency, range, mean, mode, variance and standard deviation) will be examined.

Not all variation observed is due to genetic influences; significant variation is affected by environmental conditions. When working on this unit, keep in mind that variation is likely caused by a combination of genetic and environmental factors.

Procedure

Phase I: Introduction to Plant Breeding

Day 1

Following planting instructions in the Fast Plant introduction in this manual, each student should plant four Hir(0-1) and four Hir(3-6) seeds. All eight can be planted in one film can or in four quad cells (2/cell).

Day 7

Thin plants to two Hir(0-1) and two Hir(3-6) plants.
NOTE: Hir (0-1) plants will have a green stem and Hir(3-6) will have a purple stem.

Day 16-18--Early Flowering Stage

The students should count the hairs on the main stem of each of the plants. This data should be recorded on the data sheet for both sets of Fast Plants. Pool class data of number of hairs per plant.
Calculate the frequency range, mean, median, mode, variance and standard deviation for the data set.
Cross pollinate your Hir(0-1) x Hir(3-6) individuals.

Day 19-21--Three Days Later

Remove all buds from your plants. This insures that no seeds will be produced from other pollinations. **Buds should be removed every three days until the end of the experiment.**

Day 40

The seed should be harvested and prepared for planting.

Day 41

Following planting instructions in the Fast Plant introduction in this manual, plant eight seeds from the previous, first generation. All eight can be planted in one film can or in four quad cells (2/cell).

Day 48

Thin plants to four plants (in one film can or four quad cells)

Day 57-59--Early Flowering Stage

The students should count the hairs on the main stem of each plant.
Pool class data of number of hairs per plant.
Calculate the frequency, range, mean, median, mode, variance and
standard deviation for the data set.

If you are only doing Phase I, you can stop here. However, if you want
to continue the experiment or save the seed, identify each plant with a
number and record the number of hairs for each individual on the data
sheet and pollinate your plants.

Phase II: Creating a Wooley Booger

Day 1

Following planting instructions in the Fast Plant introduction in this
manual, 200 seeds should be planted. These can be Hir(3-6) or the
seeds from generation 2 of Phase I. They can be planted eight/film can
or two/quad cell.

Day 7

Thin plants to 100 plants (4/film can and 1/quad cell).

Day 16-18--Early Flowering Stage

Count the hairs on the main stem of each of the plants. Identify each
plant with a number and record the number of hairs for each indi-
vidual on the data sheet. Pool class data of number of hairs per plant.
Calculate the frequency range, mean, median, mode, variance and
standard deviation for the data set. Identify ten plants with the most
hairs. These will be the ten plants crossed and pollinated for the next
generation.

Thin out all other plants. NOTE: Only the ten hairiest plants will be
used for this experiment. However, if you want seed from these plants
for further experimentation, continue to grow, thin and harvest the
plants as before.
Randomly pollinate the ten plants amongst themselves.

Day 19-21--Three Days Later

Remove all buds from the ten plants. This insures that no seeds will be produced from other pollinations.
Buds should be removed every three days until the end of the experiment.

Day 40

Harvest seed from each plant individually and place in a small envelope. Label the envelope with the plant number and the number of hairs.

Day 41

Plant the seeds (up to 200) as outlined in the planting instructions in the Fast Plant introduction in this manual.

Day 48

Thin to 100 plants.

Day 57-59--Early Flowering Stage

Count the hairs on the main stem of each plant. Identify each plant with a number and record the number of hairs for each individual on the data sheet. Pool class data of number of hairs per plant. Calculate the frequency, range, mean, median, mode, variance and standard deviation for the data set. This data should be compared to the data that has been collected in the previous phases. This should reveal the results of your selection to increase the number of hairs on the plants.

Continue to thin, grow and harvest these plants as before if you wish to use this seed for future generations or experiments.

First Generation

Date Planted_____ Date Thinned_____ Date Pollinated_____

Individual Data on number of hairs

#1_____#2_____#3_____#4_____

Comments:

Class Data on number of hairs

_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____

Second Generation

Date Planted_____ Date Thinned_____ Date Pollinated_____

Individual data on number of hairs

#1_____#2_____#3_____#4_____

Comments:

Class Data on number of hairs

_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____
_____	_____	_____	_____

Generation One

Number of Hairs

Mean

Mode

Range

Variance

Standard Deviation

Generation Two

Number of Hairs

Mean

Mode

Range

Variance

Standard Deviation

Data Sheets for Phase II: Creating a Wooley Booger

First generation

Date Planted_____ Date Thinned_____ Date Pollinated_____

Individual data on number of hairs

#1_____ #2_____ #3_____ #4_____

Comments
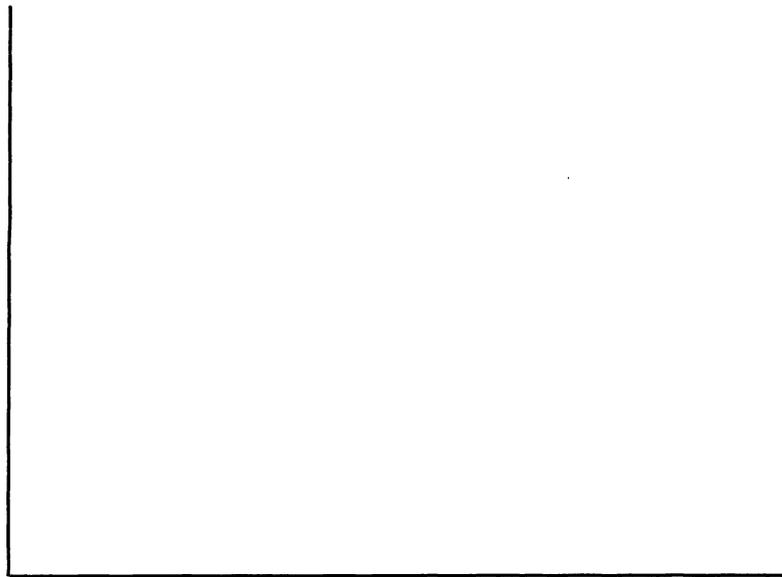

Class data on number of hairs (identify each individual with a number)

Second generation

Date Planted_____ Date Thinned_____ Date Pollinated_____

Individual data on number of hairs

#1_____#2_____#3_____#4_____

Comments

Class data on number of hairs (identify each individual with a number)

Generation One

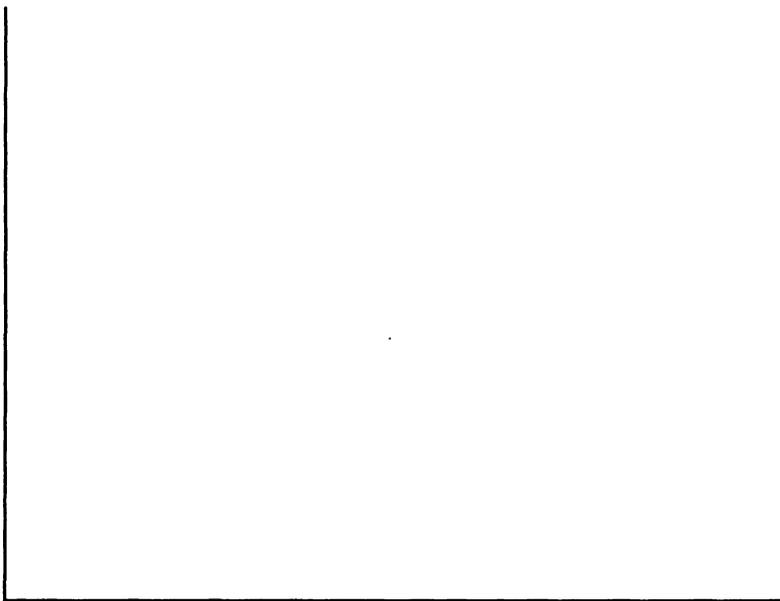Number of Hairs

Mean

Mode

Range

Variance

Standard Deviation

Generation Two

Number of Hairs

Mean

Mode

Range

Variance

Standard Deviation

Results and discussion

- Was the trait for the number of hairs heritable?

- How did the number of hairs in the population change from generation #1 to #2?

- Why do you need to calculate the average number of hairs for the population?

- How could you get the population to change faster?

- Do you think environment played a role in the number of hairs? How could you test this?

Extensions

- Continue to select the top 10 plants and cross for the hairy trait.

- Select for other traits such as
    pod length
    number of flowers
    length of pod
    # of seeds per pod
    total yield
    height

- Run a duplicate experiment in a different environment such as altered nutrient or light regieme.

Sample calculation of standard deviation

Hairy Plant

Plant #	# of hairs	Deviation	Sq. deviation
#1	15	15-11=4	16
#2	9	9-11=-2	4
#3	11	11-11=0	0
#4	12	12-11=1	1
#5	16	16-11=5	25
#6	7	7-11=-4	16
#7	9	9-11=-2	4
#8	11	11-11=0	0
#9	12	12-11=1	1
#10	11	11-11=0	0
	113		67

mean - $\dfrac{113}{10}$ = 11.3

variance - $\dfrac{67}{10}$ = 6.7

standard deviation   6.7 = 2.54