

HOS 6236 Molecular Marker Assisted Plant Breeding Fall 2017

Last Class:

Introduction, Syllabus, and Expectations

Today's Class:

Important breeding concepts

Survey plant breeding methods

Types of Variation

Discontinuous Variation – categorical traits, small number of easily distinguished, discrete classes.

Monogenic Traits – Qualitative Inheritance






Character	Contrasting traits	
Seed shape	round/wrinkled	
Seed color	yellow/green	
Pod shape	full/constricted	
Pod color	green/yellow	
Stem height	tall/dwarf	

Fig. 3-1

Types of Variation

Most traits in breeding are more complex

Continuous Variation – classes can not be easily defined.

Examples:

Types of Variation

Most traits in breeding are more complex

Continuous Variation – classes can not be easily defined.

Examples:

Seed Yield

Fruit Yield

Plant Biomass

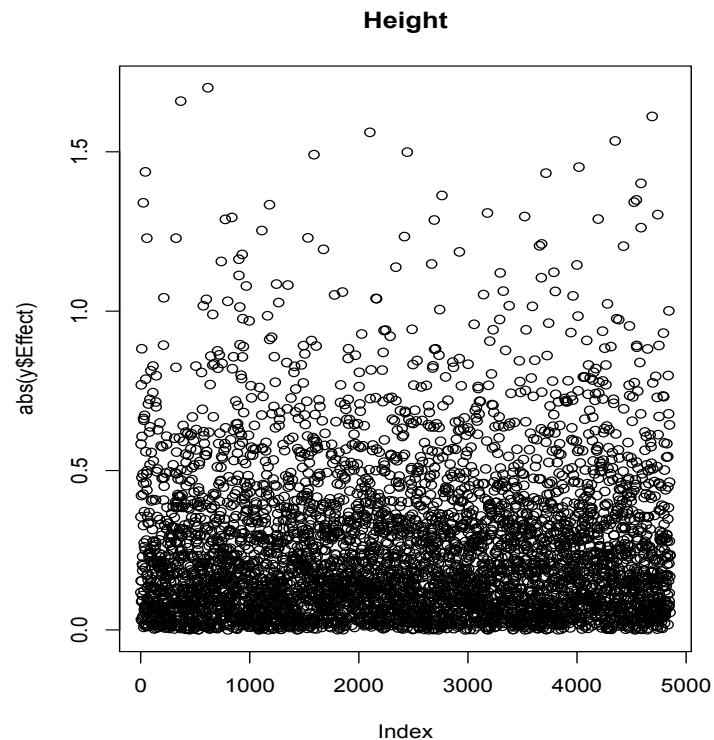
Tree height

Types of Variation

Polygenic (many genes): result of the input of multiple genes, each one with small effect in the phenotype.

The effect of a single gene on the phenotype is usually too small to be recognized.

Implications???

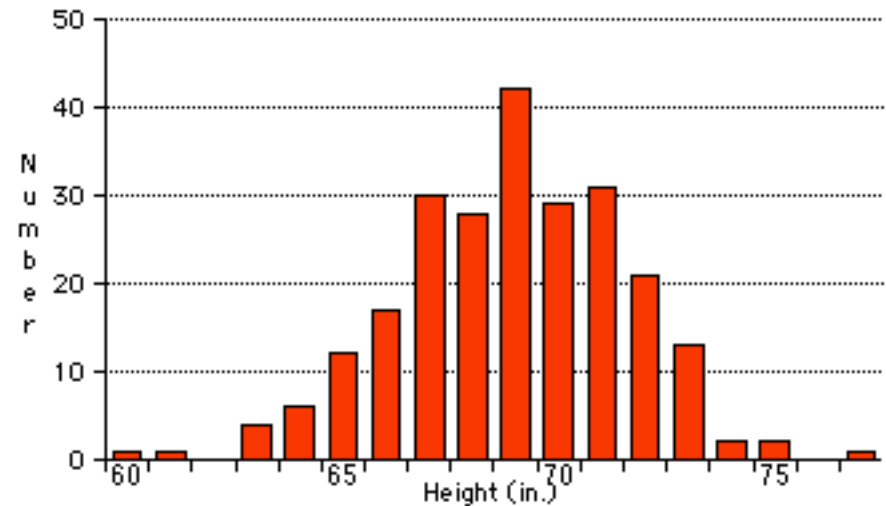


Types of Variation

Most traits in breeding are more complex

Continuous Variation – classes can not be easily defined.

Example: A cross of two plants of sorghum (tall and short) create continue variation



Continuous variation is measured and described in quantitative terms: **Quantitative inheritance - Polygenic Traits**

Types of Variation

Question:

If we can not distinguish classes in a quantitative trait, then are these genes following Mendelian inheritance?

Fisher Infinitesimal Model (1918)

The character is determined by an infinite number of unlinked and non-epistatic loci, each with an infinitesimal effect on the trait.

Statistics and Complex Traits

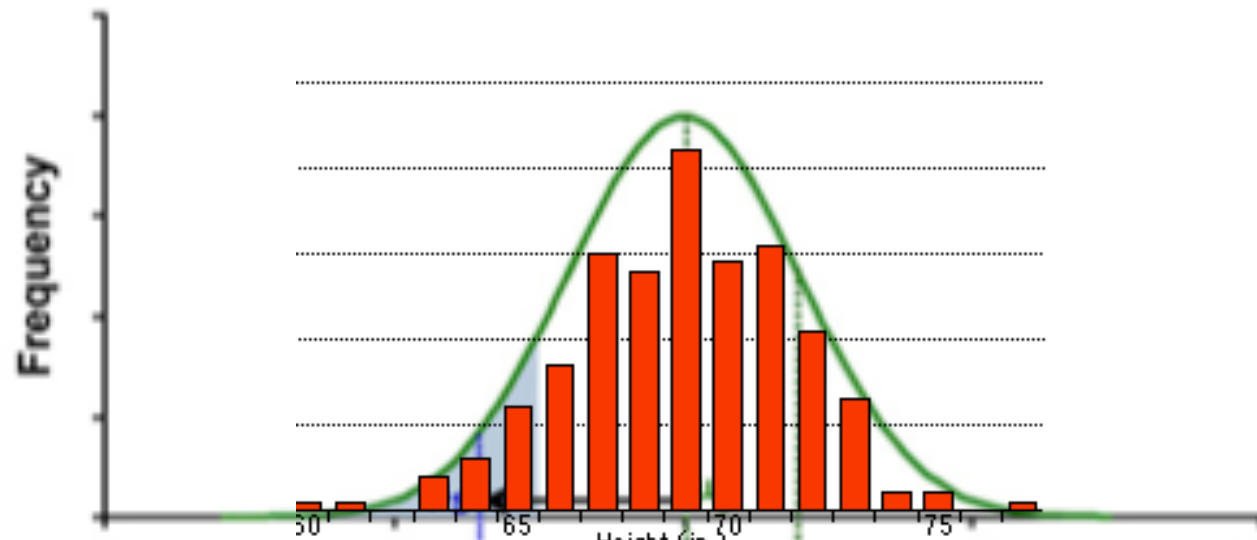
Several statistics parameters are used to describe a populations that has a continuous variation

Example:

Mean, Median, Mode

Variance, Standard Deviation, Coeff. Of Variation

Range, Minimum and Maximum



The most important for plant breeders are probably the Mean and Variance:

The Mean (\bar{x})

Provides information about where the central point lies in along the range of measurements of a quantitative trait

$$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$$

The Variance(s^2)

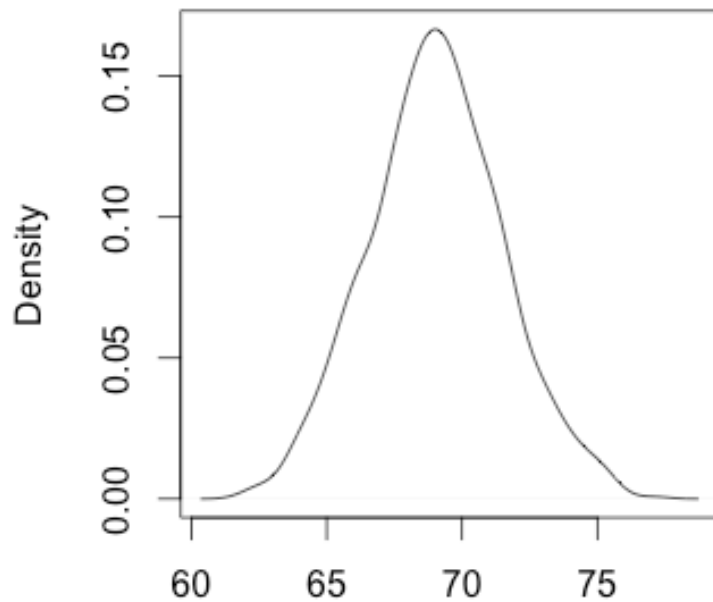
Measures the dispersion or spread of the set of measurements of a quantitative trait

$$s^2 = \frac{\sum_{i=1}^n (x_i - \bar{x})^2}{n - 1}$$

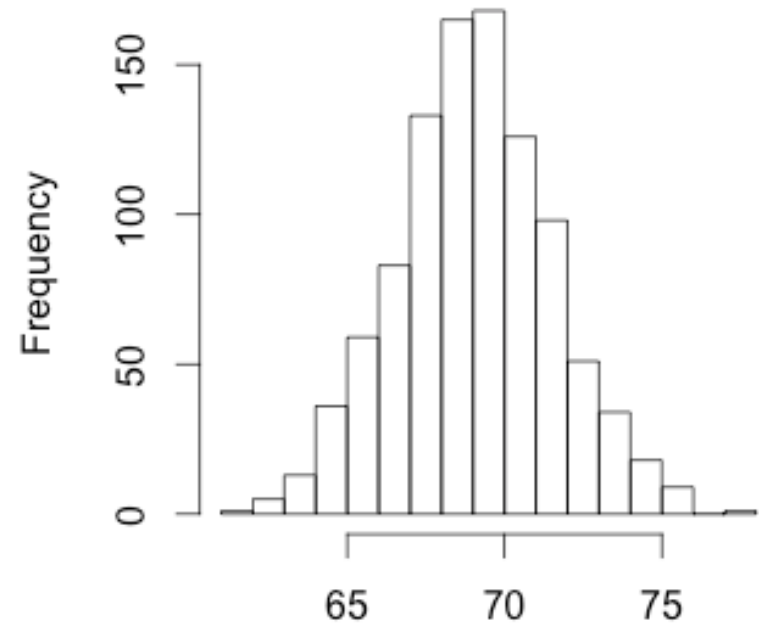
The standard deviation $s = \sqrt{s^2}$

The Statistics of Sorghum

density.default(x = example1)



Histogram of example1



Phenotypic data Sorghum height (in) n=1000

Min. : 60.34

1st Qu.: 64.94

Median : 69.54

Mean : 69.54

3rd Qu.: 74.14

Max. : 78.74

Environmental Effect

Quantitative or Complex traits: polygenic in nature usually also influenced by environment.

Plant Yield Example

The challenge of quantitative geneticist or breeder is to determine how much of the variation is due to genetic differences and how much is due to environment.

If **P**henotype = **G**enotype

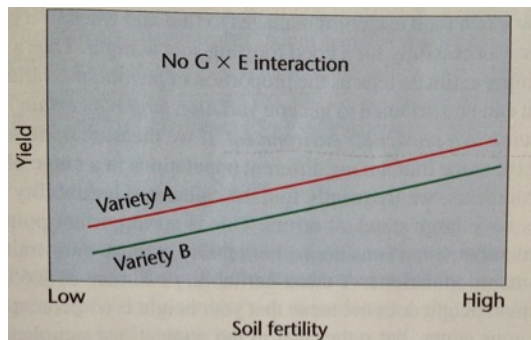
If **P**henotype = **G**enotype + **E**nvironment

but...

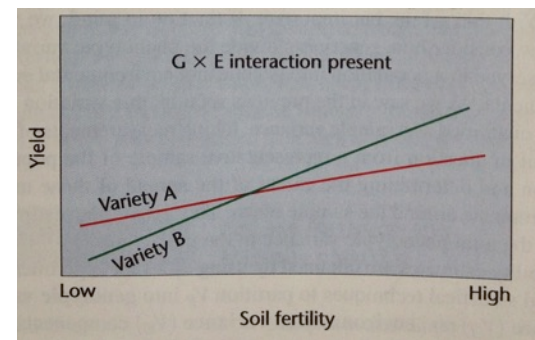
Genotype by Environment Interaction

There could be also an interaction between the genotype (G) and the environment (E):

Root Efficiency Example



No GxE interaction



GxE interaction

then

$$P = G + E + G \times E$$

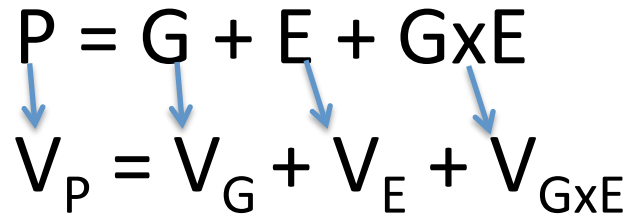
The Challenge

The challenge of quantitative geneticist or breeder is to determine how much of the variation is due to genetic differences and how much is due to environment.

If **P**henotype = **G**enotype

If **P** = **G** + **E** + **G**x**E**

Heritability

$$P = G + E + G \times E$$
$$V_P = V_G + V_E + V_{G \times E}$$


Broad-sense heritability = the proportion of phenotypic variation that can be attributed to genetic variation within a **certain population** in a **particular environment**

$$H^2 = V_G / V_P$$

Range from 0 to 1

- Values close to 1 indicate that environment have little impact on phenotypic variance, which is then largely due to genetic differences
- Values close to 0 indicate that environment factors, not genotypic differences, are largely responsible for the phenotypic variation

Narrow-sense Heritability

$$P = G + E + G \times E$$

$$\text{But } G = A + D + I$$

A = additive effect of genes

D = dominance effect, results from the **interaction among alleles** within a locus

I = epistatic effect, results from the **interaction among genes**
thus

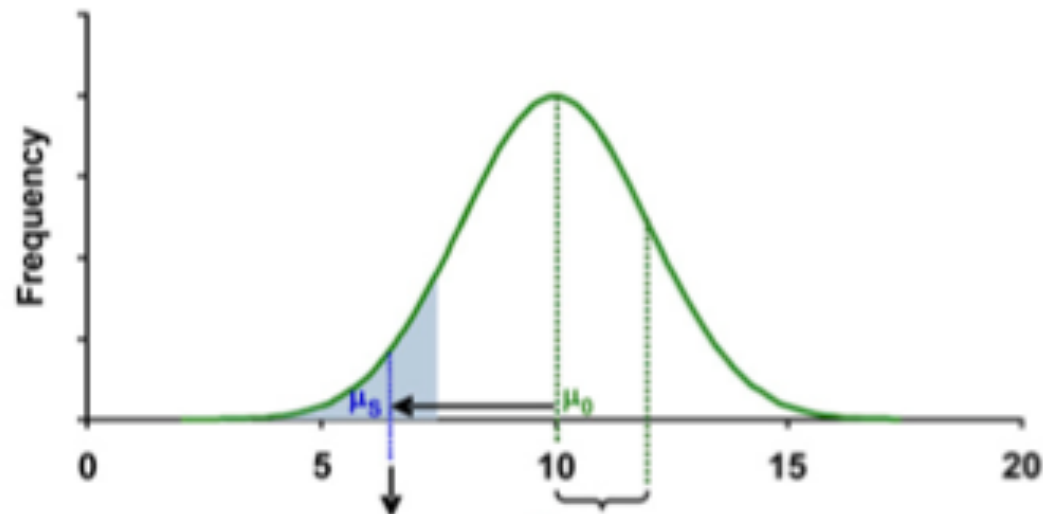
$$P = A + D + I + E + G \times E$$

$$V_P = V_A + V_D + V_I + V_E + V_{G \times E}$$

Narrow-sense heritability = is the portion of phenotypic variance due to additive genetic variation.

$$h^2 = V_A / V_P$$

The Goal!!



$$\text{Genetic Gain} = \Delta G = h^2 \sigma_P \frac{i}{L} \rightarrow \text{length of cycle interval (usually 1 generation)}$$

heritability

Selection Intensity
proportion of population selected
to produce the next generation

phenotypic variability in population

$$\sigma^2_{\text{Genotype}} - \sigma^2_{\text{Dominance}} - \sigma^2_{\text{Epistasis}} = \sigma^2_{\text{Additive}}$$

$$\sigma^2_{\text{Genotype}} + \sigma^2_{\text{Environment}} + \sigma^2_{\text{GxE}} + \sigma^2_{\text{error}} = \sigma^2_P$$

Breeder's Equation

$$\text{Genetic_Gain} = \Delta G = \frac{h^2 * \sigma_p^2 * i}{L}$$

h^2 = **Narrow-sense heritability** = is the portion of phenotypic variance due to additive genetic variation.

σ_p = **phenotypic standard deviation** = phenotypic variability in the population

i = **intensity of selection**

L = length of breeding cycle interval

Why this is important???