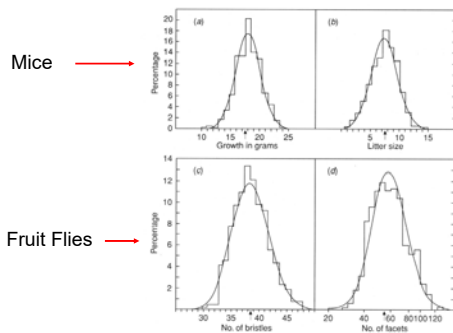
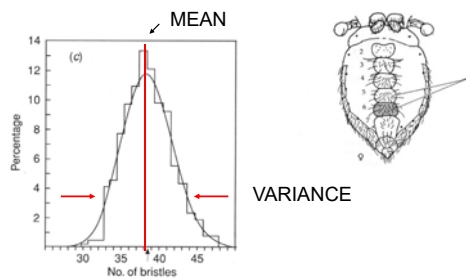


NORMAL DISTRIBUTIONS OF PHENOTYPES



In: Introduction to Quantitative Genetics Falconer & Mackay 1996

CHARACTERIZING A NORMAL DISTRIBUTION



Mean and **variance** are two quantities that describe a normal distribution.

USEFUL PARAMETERS FOR QUANTITATIVE GENETICS

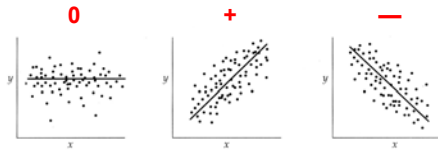
- **Mean:** The sum of all measurements divided by the number of measurements

$$\bar{x} = \frac{x_1 + x_2 + \dots + x_n}{N} = \frac{1}{N} \sum x_i$$

- **Variance:** The average squared deviation of the observations from the mean

$$\text{Variance} = \frac{(x_1 - \bar{x})^2 + (x_2 - \bar{x})^2 + \dots + (x_n - \bar{x})^2}{N} = \frac{1}{N} \sum (x_i - \bar{x})^2$$

CORRELATIONS AMONG CHARACTERS OR RELATIVES



Covariance:

$$Cov(x, y) = \frac{1}{N} \sum (x_i - \bar{x})(y_i - \bar{y})$$

COMPONENTS OF PHENOTYPIC VARIATION

$$V_P = V_G + V_E$$

- The total *phenotypic* variance for a character (V_P) is a function of:
- **Genetic variance (V_G)**– the variance among the mean phenotypes of different genotypes
- **Environmental variance (V_E)**– the variance among phenotypes expressed by replicate members of the same genotype



- Differences between monozygotic twins are due to environmental factors.

ENVIRONMENTAL VARIATION WITHIN PURE LINES

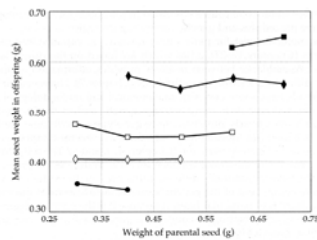


Figure 1.4 Mean offspring seed size as a function of parental seed size for some of Johansen's pure lines. The data for the different lines are denoted by different symbols. If there is a heritable component to seed weight within a pure line, a line with positive slope is expected — larger parents should yield larger offspring. However, within each line, mean offspring size is essentially independent of the parental phenotype. (Data from Johansen 1903.)

IN: Lynch & Walsh, 1998. *Genetics and Analysis of Quantitative Traits*. Sinauer Assoc.

COMPONENTS OF GENETIC VARIATION

$$V_G = V_A + V_D + V_I$$

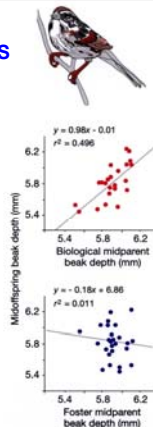
- The total *genetic* variance for a character (V_G) is a function of:
- **Additive genetic variance (V_A)** – variation due to the additive effects of alleles
- **Dominance genetic variation (V_D)** – variation due to dominance relationships among alleles
- **Epistatic genetic variation (V_I)** – variation due to interactions among loci

DOMINANCE VERSUS ADDITIVE GENETIC VARIANCE

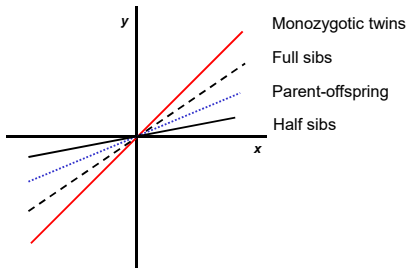
- Dominance variance is due to dominance deviations, which describe the extent to which heterozygotes are not exactly intermediate between the homozygotes.
- The additive genetic variance is responsible for the resemblance between parents and offspring.
- The additive genetic variance is the basis for the response to selection.

RESEMBLANCE BETWEEN RELATIVES

- When there is genetic variation for a character there will be a resemblance between relatives.
- Relatives will have more similar trait values to each other than to unrelated individuals.



RESEMBLANCE BETWEEN RELATIVES DEPENDS ON THE DEGREE OF RELATIONSHIP



Slope of a plot of two variables $(x,y) = \text{Cov}(x,y) / \text{Var}(x)$

DEGREE OF RELATEDNESS AND THE COMPONENTS OF PHENOTYPIC COVARIANCE

V_A = additive genetic variance
 V_D = dominance genetic variance
 V_{Es} = variance due to shared environment

Relationship	Phenotypic covariance
Monozygotic twins:	$V_A + V_D + V_{Es}$
Parent-offspring	$\frac{1}{2} V_A$
Full sibs	$(\frac{1}{2} V_A) + (\frac{1}{4} V_D) + V_{Es}$
Half sibs, or Grandparent – grandchild	$\frac{1}{4} V_A$

HERITABILITY

- The **heritability** (h^2) of a trait is a measure of the degree of resemblance between relatives.

$$h^2 =$$

additive genetic variance (V_A) / phenotypic variance (V_P)

Heritability ranges from 0 to 1

(Traits with no genetic variation have a heritability of 0)

HERITABILITY

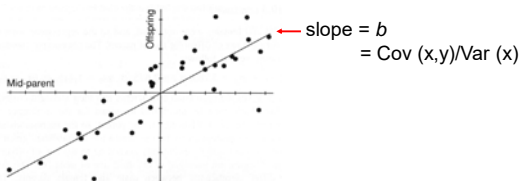
$$h^2 = V_A / V_P = V_A / (V_G + V_E)$$

- Since heritability is a function of the environment (V_E), it is a *context dependent* measure.

It is influenced by both,

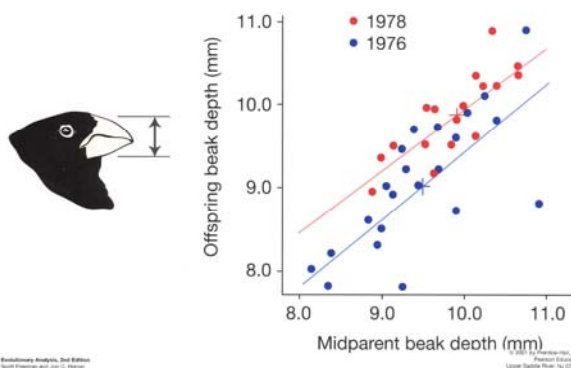
- The environment that organisms are raised in, and
- The environment that they are measured in.

ESTIMATING HERITABILITY FROM REGRESSION



Method of estimation	$COV_{(x,y)}$	h^2	Slope (b)
Offspring-Single parent	$\frac{1}{2} V_A$	$2b$	$b = \frac{1}{2} h^2$
Half-sib	$\frac{1}{4} V_A$	$4b$	$b = \frac{1}{4} h^2$
Offspring-Grandparent	$\frac{1}{4} V_A$	$4b$	$b = \frac{1}{4} h^2$
Offspring-Midparent	-	b	$b = h^2$

HERITABILITY OF BEAK DEPTH IN DARWIN'S FINCHES

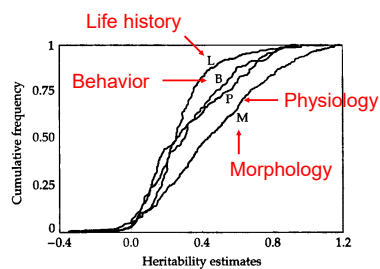


HERITABILITIES FOR SOME TRAITS IN ANIMAL SPECIES

	<u>h^2 (%)</u>
<i>Man</i>	
Stature	65
Serum immunoglobulin (IgG) level	45
<i>Cattle</i>	
Body weight (adult)	65
Butterfat, %	40
Milk yield	35
<i>Pigs</i>	
Back-fat thickness	70
Efficiency of food conversion	50
Weight gain per day	40
Litter size	5
<i>Poultry</i>	
Body weight (at 32 wks)	55
Egg weight (at 32 wks)	50
Egg production (to 72 wks)	10
<i>Mice</i>	
Tail length (at 6 wks)	40
Body weight (at 6 wks)	35
Litter size (1st litters)	20
<i>Drosophila melanogaster</i>	
Abdominal bristle number	50
Body size	40
Ovary size	30
Egg production	20

IN: Falconer & Mackay, *Introduction to Quantitative Genetics*, 1996, Longman.

HERITABILITIES FOR DIFFERENT TYPES OF TRAITS



FROM: Mousseau & Roff, 1987.

THE UNIVARIATE BREEDERS' EQUATION:

$$R = h^2 S$$

Response to Selection Selection differential

↑

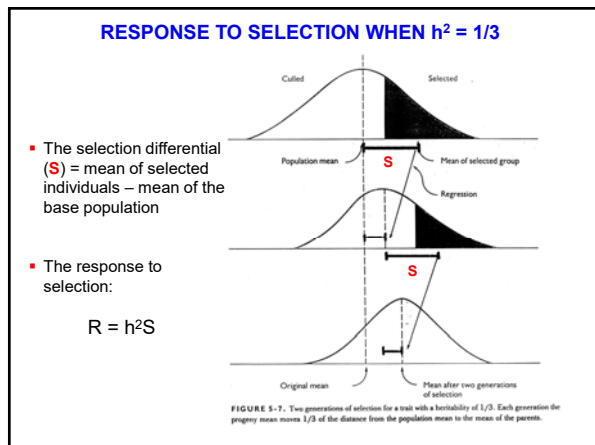
Heritability

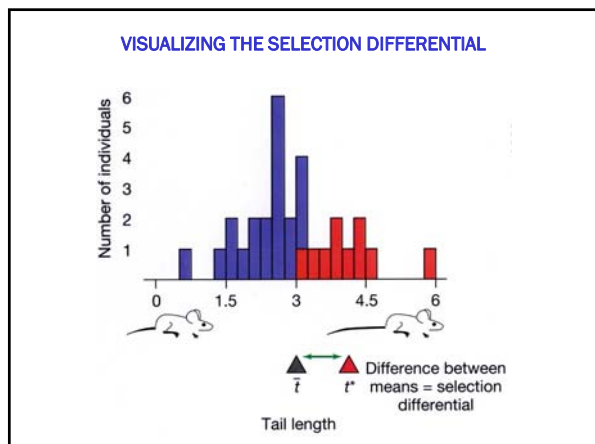
Where:

$$h^2 = \frac{V_A}{V_P}$$

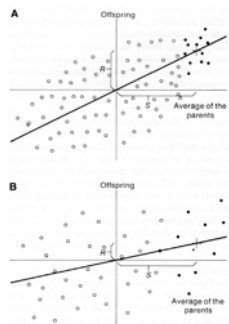
(Additive Genetic Variance)
(Phenotypic Variance)







RESPONSE TO SELECTION



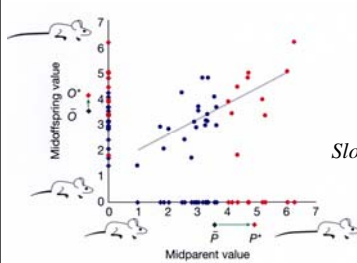
For a given intensity of selection, the response to selection is determined by the heritability.

High heritability

Low heritability

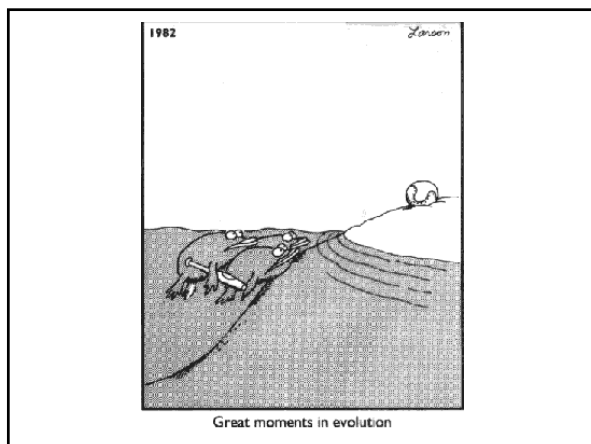
See Box 7.2 Z&E

ESTIMATING h^2 USING THE BREEDER'S EQUATION



$$R = h^2 S$$

$$\text{Slope} = h^2 = \frac{R}{S} = \frac{O^* - \bar{O}}{P^* - \bar{P}}$$



MODES OF SELECTION

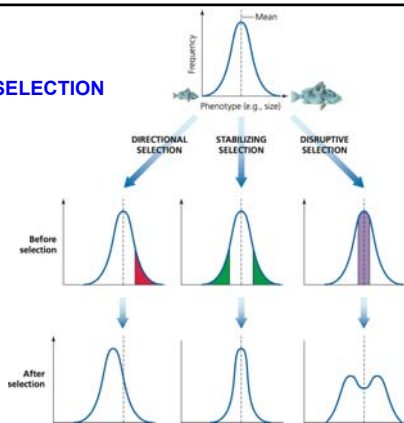
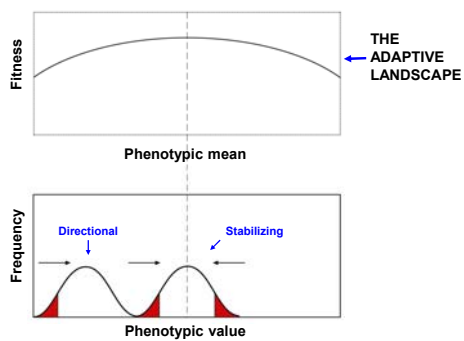


Fig. 7.6 Z&E

SELECTION ON QUANTITATIVE TRAITS

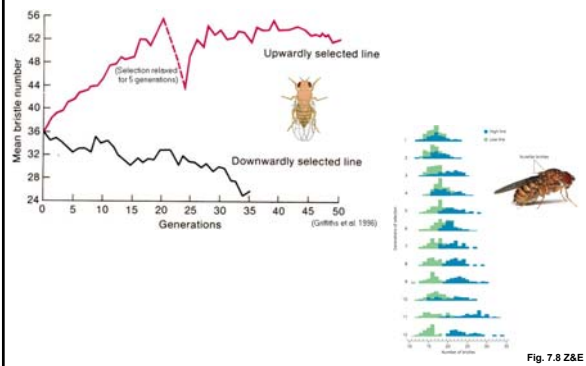
- Stabilizing and Directional selection



Response to Directional Selection:



Response to Directional Selection:



Response to Directional Selection:

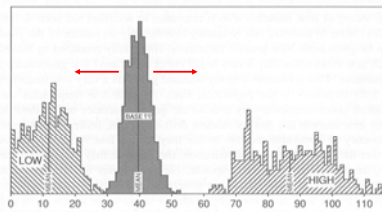


Fig. 12.4. Frequency distributions of abdominal bristle number in *Drosophila melanogaster* (females), in the base population and in the most extreme high and low lines after 35 and 34 generations of selection. (After Clayton and Robertson, 1957.)

In: Introduction to Quantitative Genetics Falconer & Mackay 1996
