Quantitative Genetics

- Polygenic inheritance

Continuous variation

Additive alleles

Calculating the number of genes

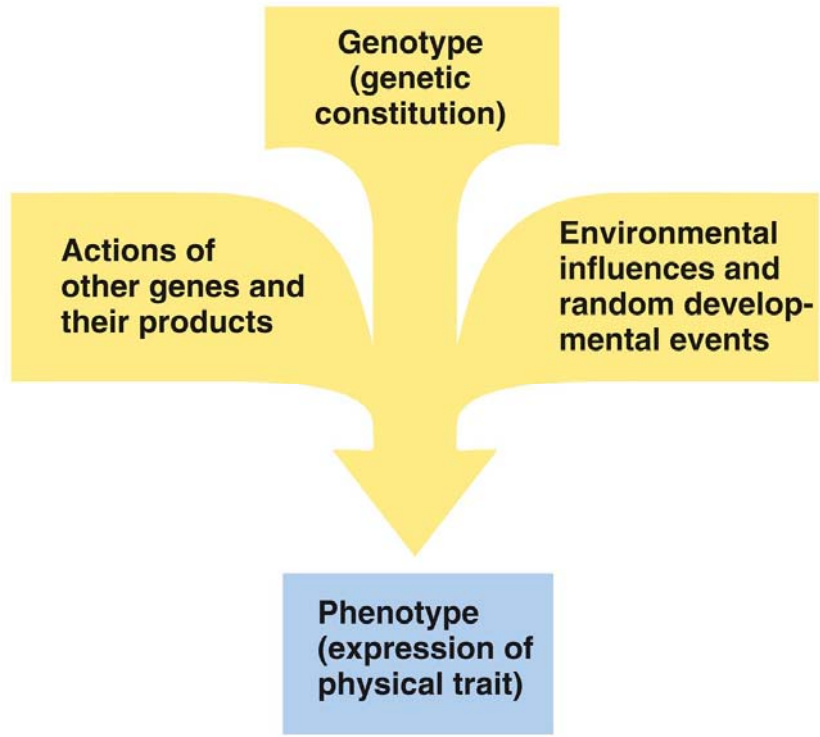
- Heritability

Statistical tools: Mean, variance

Broad sense heritability

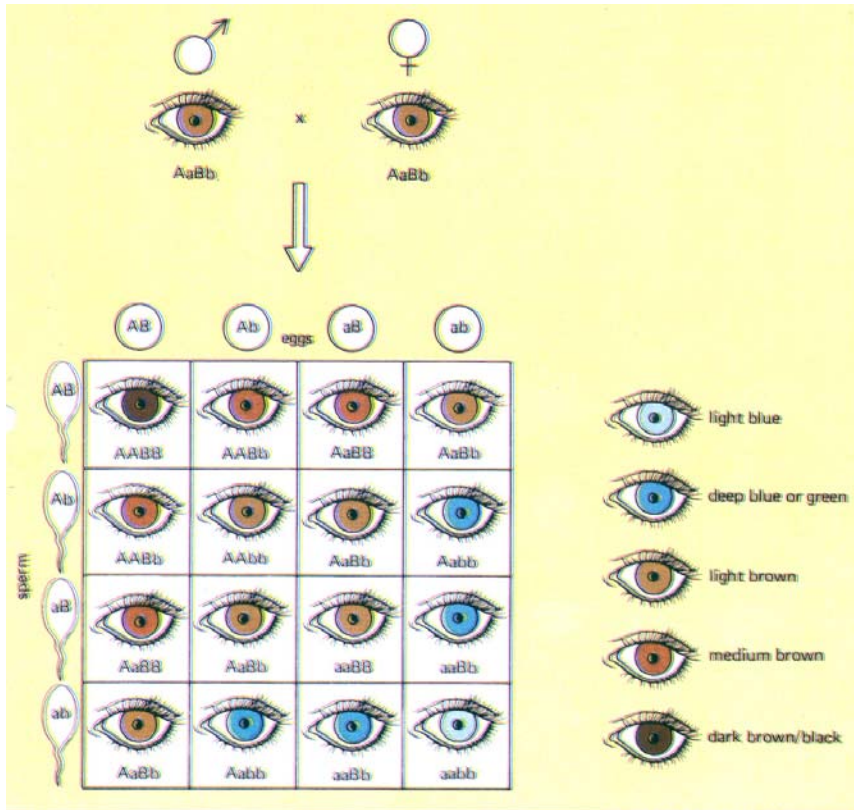
Narrow sense heritability

Correlation: Twin Studies and concordance

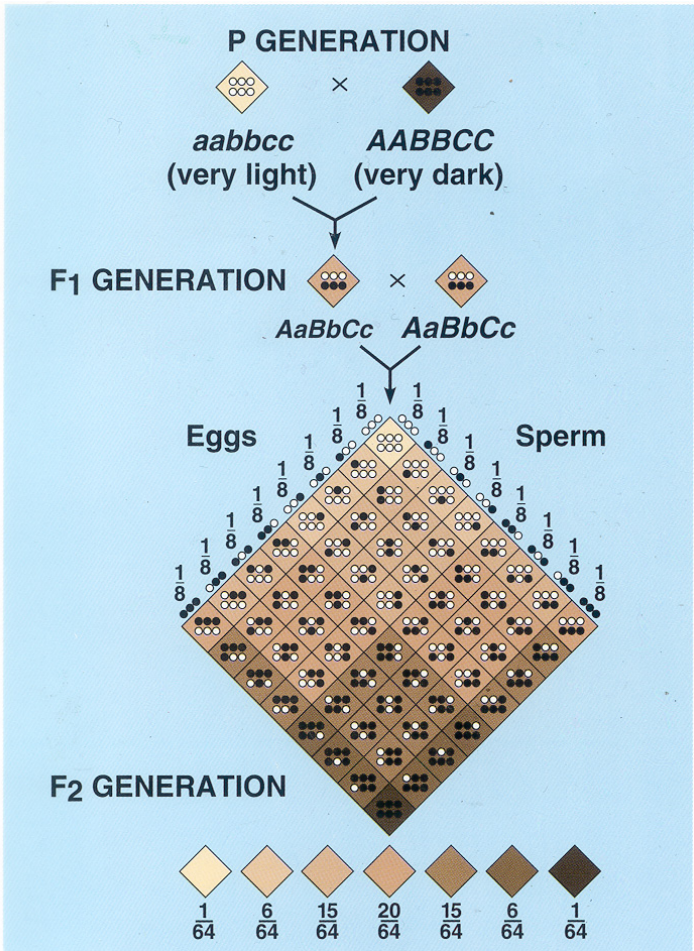


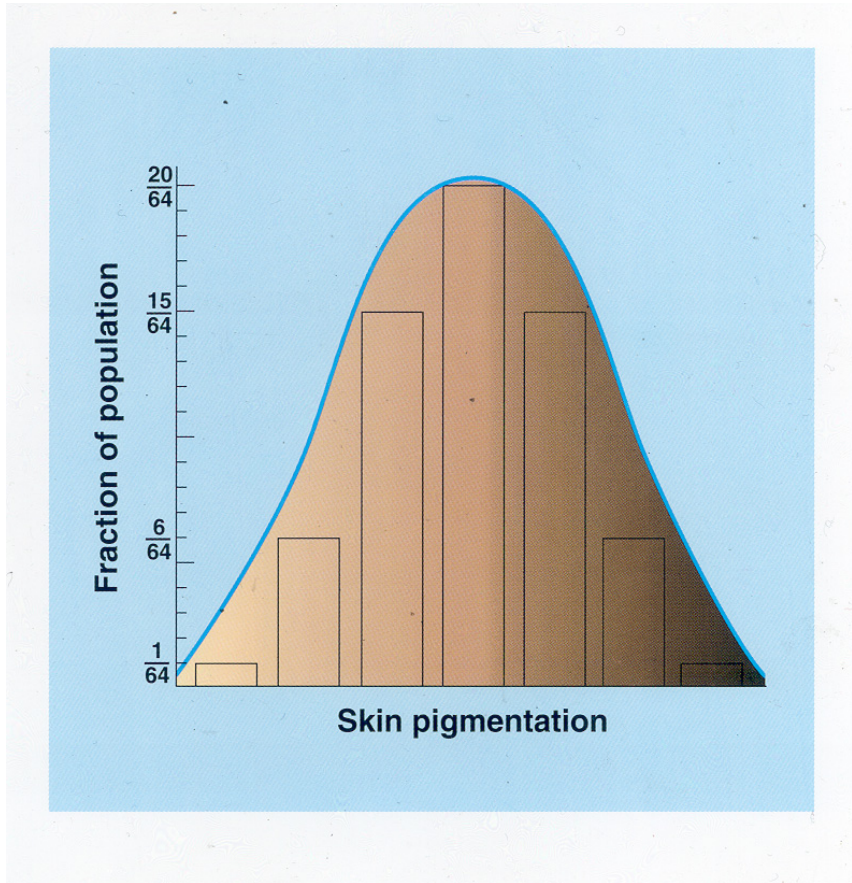
Polygenic inheritance

- 2 or more genes
- Show continuous variation vs discontinuous
- Additive component
- Distinct phenotypic classes
- Quantitative traits: size, weight, height,IQ



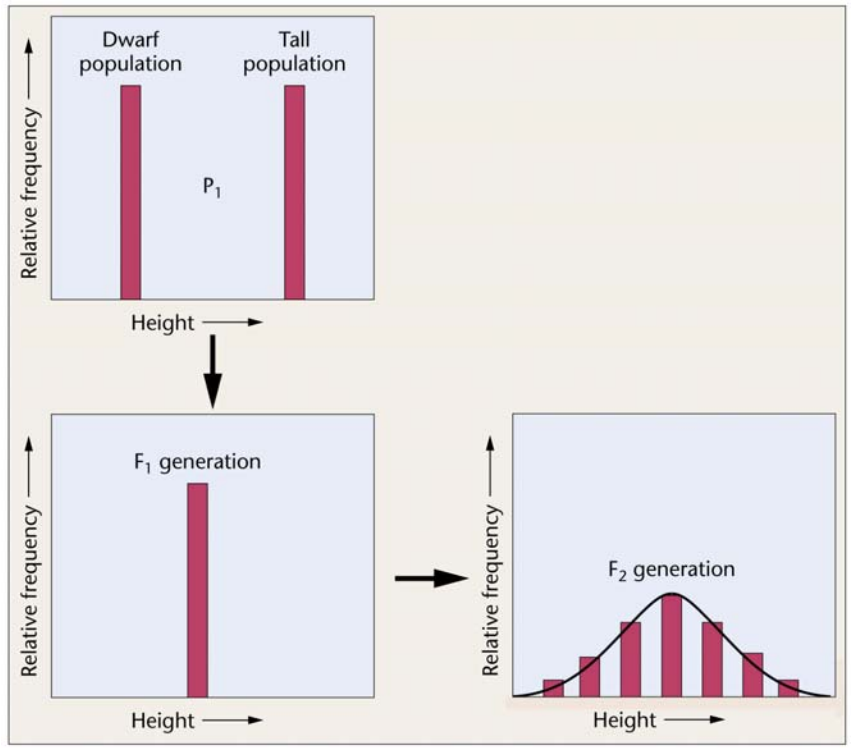
Polygenic inheritance





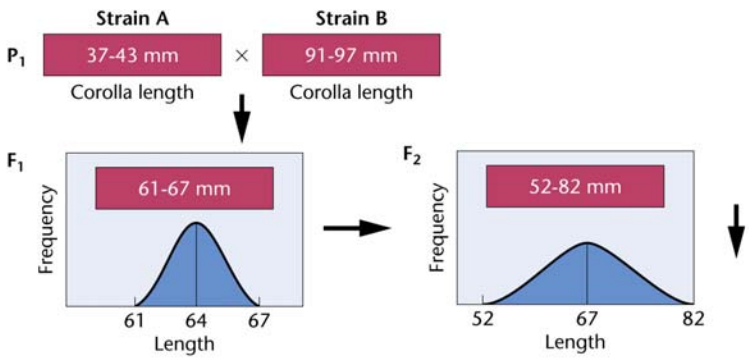
Continuous variation

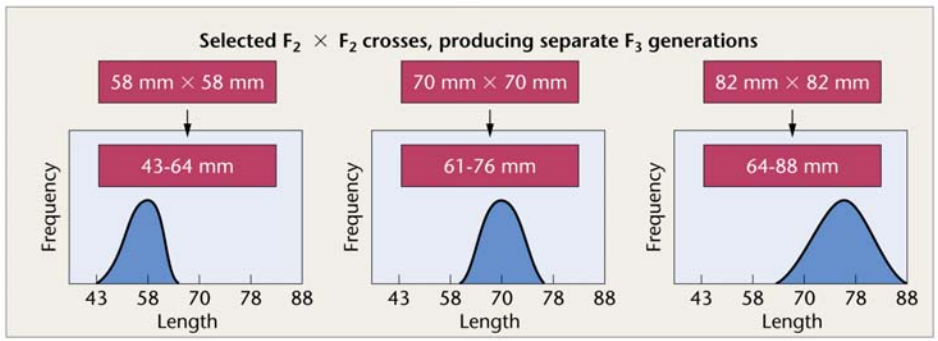
- Kolreuter's cross
- Dwarf x tall tobacco
- F1 intermediate
- F2 intermediate, normal distribution



Multiple gene hypothesis

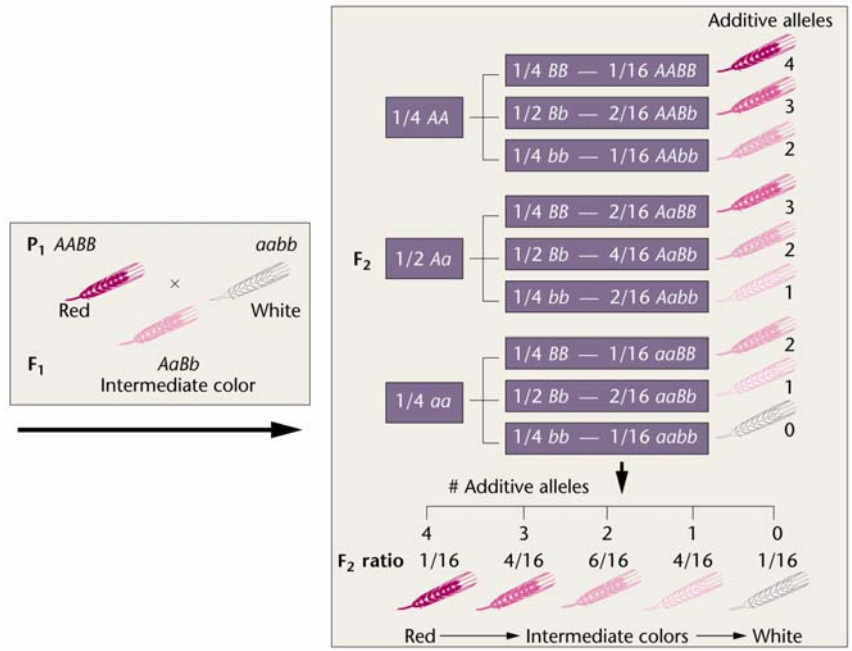
- East's cross of Nicotiana with different corolla length
- Indicates Mendelian segregation of different phenotypic classes
- Took subsets of F_2 and crossed.





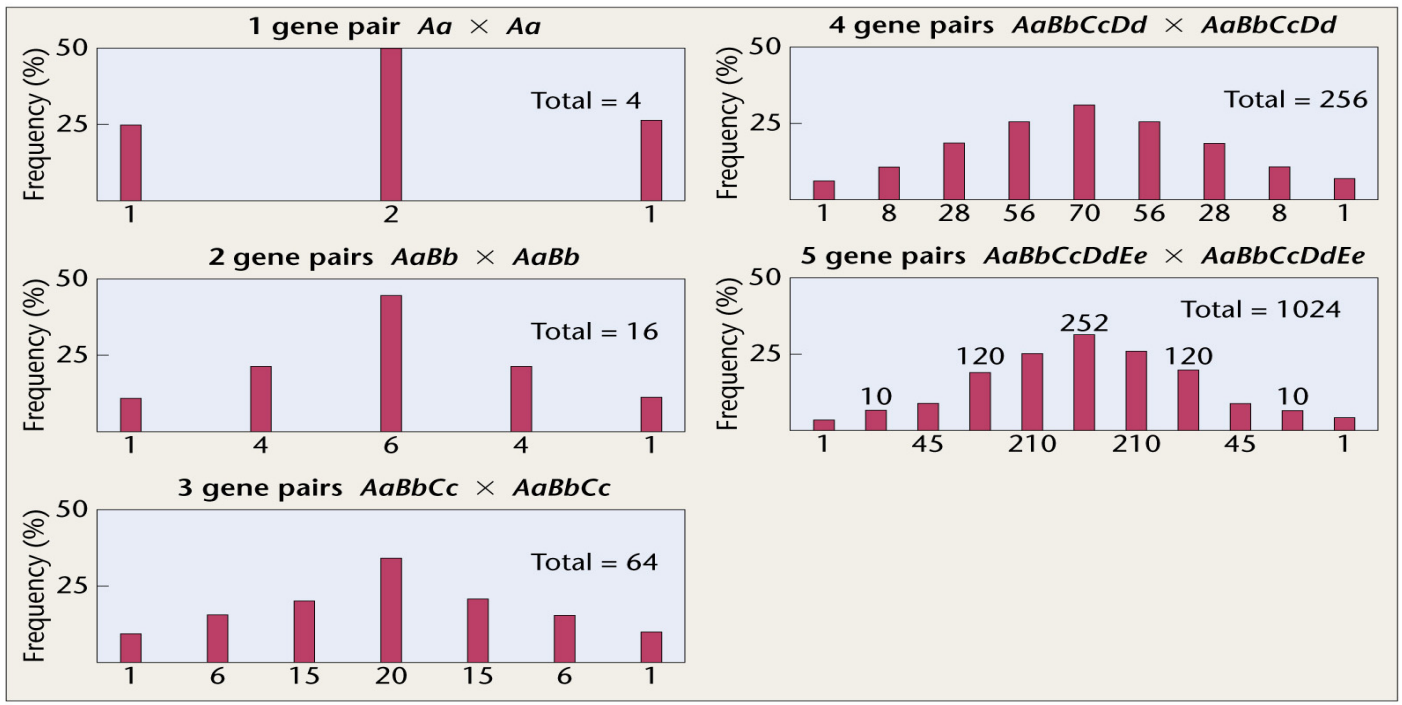
Multiple factor hypothesis

- Characters quantified
- Two or more genes
- Additive alleles
- Contribute a constant amount
- Non-additive add nothing
- All alleles add equally

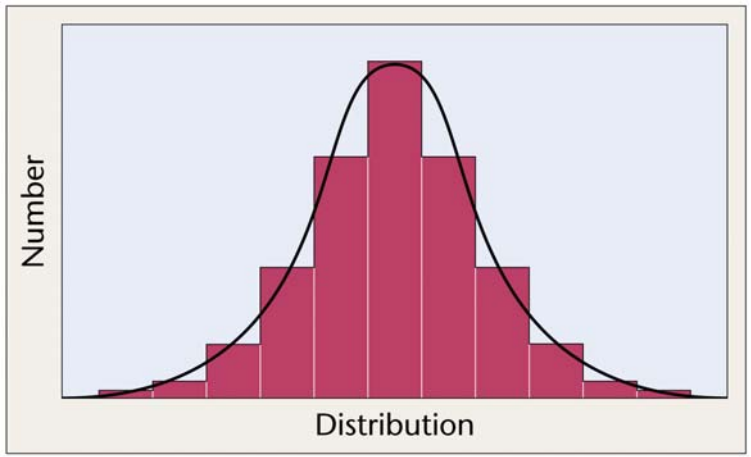


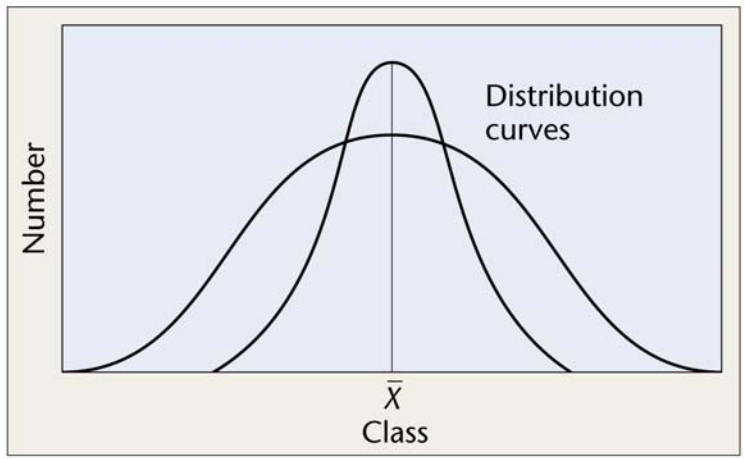
Calculation of number of genes

- $(1/4)^n$= ratio of f_2 individuals showing extreme phenotype
- n = (2n +1) phenotypic classes



Statistical Analysis





- Mean (X) = $\sum X_i/n$
- Variance (s^2) = $(\sum X_i - X)^2/n\text{-}1$
- Standard deviation (s) = $\sqrt{s^2}$

Heritabilty

- Genetic contribution to phenotypic variability
- Broad-sense Heritabilty (H^2)
- Narrow-sense Heritabilty (h^2)
- Quantitative trait loci (QTL)

Broad-sense Heritabilty

- H^2 = proportion of total variance caused by genetic variance
- H^2 = 1.0, all genetic
- H^2 = 0 all variation due to environment

- Vp= phenotypic var
- Vg= genetic var
- V_E= enviromental var
- $Vp = Vg + V_E$
- $H^2 = Vg/Vp$

Calculation of H^2(Broad-Sense)

- V_E= (3.1 + 3.9)/2
  (4.7 + 3.5)/2

V_E = 4.1

- Vp = 47.7

- Vg = Vp – V_E= 47.7-4.1

- H^2= Vg/Vp

	Mean	Var
P1 short	40.4	3.1
P2 tall	93.7	3.9
F1	63.9	4.7
F2	68.7	47.7

Estimation # of genes

- $n = D^2 / 8Vg$
- n = number of genes
- D = difference of means of two parents
- Vg = genetic variance
- Assumes: alleles equal and additive, assort independently, original parents are homozygous

Narrow-sense Heritabilty

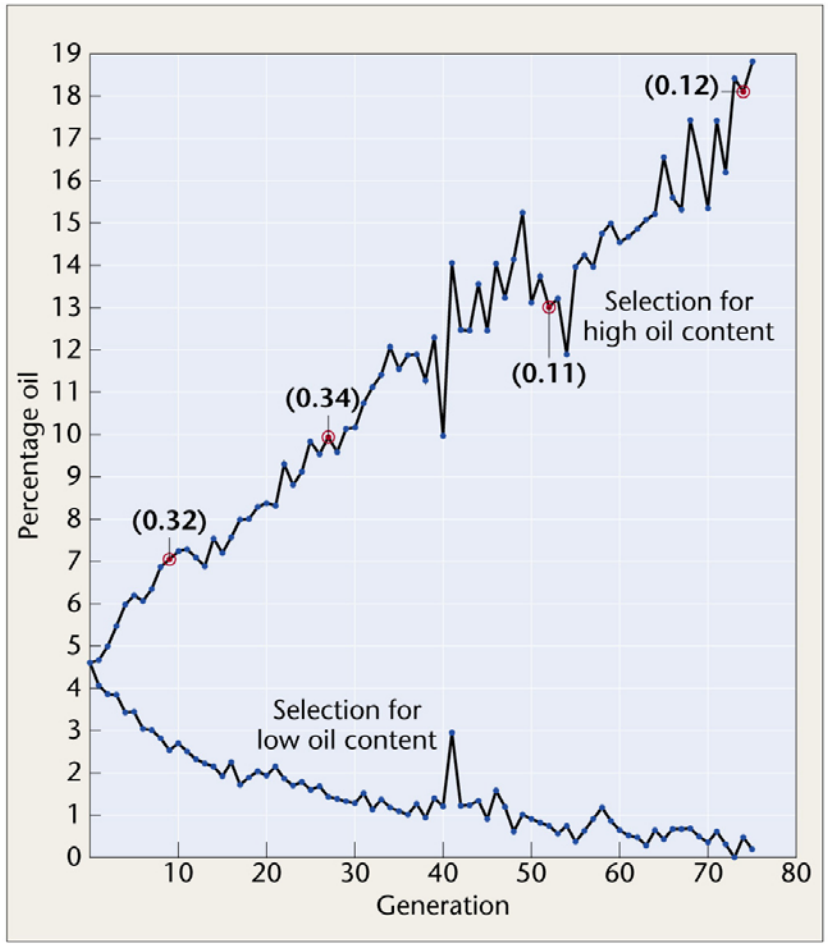
- **Potential response to selection**
- **Additive variance**
- **Dominance variance**

- **$V_G = V_A + V_D$**
- **$h^2 = V_A / V_E + V_A + V_D$**
- **High h^2 prediction of impact of selection in altering a population.**

Selection

- **h^2 = M2- M/ M1 – M**

  response/selection differential
- **M= mean of parental**
- **M1= mean of selected segment**
- **M2= mean of offspring**
- **Heritability low for traits essential for survival**



Narrow-sense Heritabilty

TABLE 5.5 Estimates of Heritability for Traits in Different Organisms

Trait	Heritability (h^2)
Mice	
Tail length	60%
Body weight	37
Litter size	15
Drosophila	
Abdominal bristle number	52
Wing length	45
Egg production	18
Chickens	
Body weight	50
Egg production	20
Egg hatchability	15
Cattle	
Birth weight	51
Milk yield	44
Conception rate	3

Twin Studies

TABLE 5.6 A Comparison of Concordance of Vario
Traits Between Monozygotic (MZ) and Dizygotic (DZ) Twins

Trait	Concordance MZ	DZ
Blood types	100%	66%
Eye color	99	28
Mental retardation	97	37
Measles	95	87
Idiopathic epilepsy	72	15
Schizophrenia	69	10
Diabetes	65	18
Identical allergy	59	5
Tuberculosis	57	23
Cleft lip	42	5
Club foot	32	3
Mammary cancer	6	3

TABLE 15.4 Heritability Estimates for Obesity in Twins (from several studies)

CONDITION	HERITABILITY
Obesity in children	0.77–0.88
Obesity in adults (weight at age 45)	0.64
Obesity in adults (body mass index at age 20)	0.80
Obesity in adults (weight at induction into armed forces)	0.77
Obesity in twins reared together or apart	
Men	0.70
Women	0.66

$$H = (V_{dz} - V_{mz})/ V_{dz}$$

Quantitative trait loci (QTL)

- DDT resistance polygenic
- Each chromosome makes a contribution to survival.