

Summary of formula Quantitative Genetics**Basic genetics:**

General advice: use always a Punnett Square

Translate problem (usually given in phenotypes on parents) into genotypes on parents

Use a Punnett square to predict genotype frequencies in offspring

Translate those to 'phenotypes in offspring

1-locus model

Hardy Weinberg equilibrium:

Allele frequency of A1 = $f(A1) = p$

Allele frequency of A2 = $f(A2) = q$

Predicted genotype frequencies

A1A1: p^2

A1A2: $2pq$

A2A2: q^2

breeding value of A1A1: = $2 \times$ average effect of A1 = $2 \times [p \times A1A1 + q \times A1A2]$

breeding value of A2A2: = $2 \times$ average effect of A2 = $2 \times [p \times A2A1 + q \times A2A2]$

breeding value of A1A2 is mean of BV of A1A1 and BV A2A2.

Quantitative Genetics

From one locus to many loci

From discontinuous to continuous variation

Components of variation (phenotypic) \rightarrow Genetic ,Environmental

TERM	SYMBOL	MEANING
Phenotype	P	Observed merit
Genetic Value	G	Value of genes to SELF
Breeding Value	A	Value of genes to PROGENY
Environmental Value	E	'LUCK'

$$P = G + \text{Env.} = A + D + \text{Env.}$$

$$V_P = V_A + V_E$$

Total Variance = additive genetic variance + residual variance (note: V_E contains also dominance effects)

$$\text{Heritability} = h^2 = \frac{V_A}{V_P} = \text{proportion of phenotypic variance caused by variance in breeding values.}$$

= also proportion of parent's superiority expected to be transmitted to offspring

Estimating Breeding Value

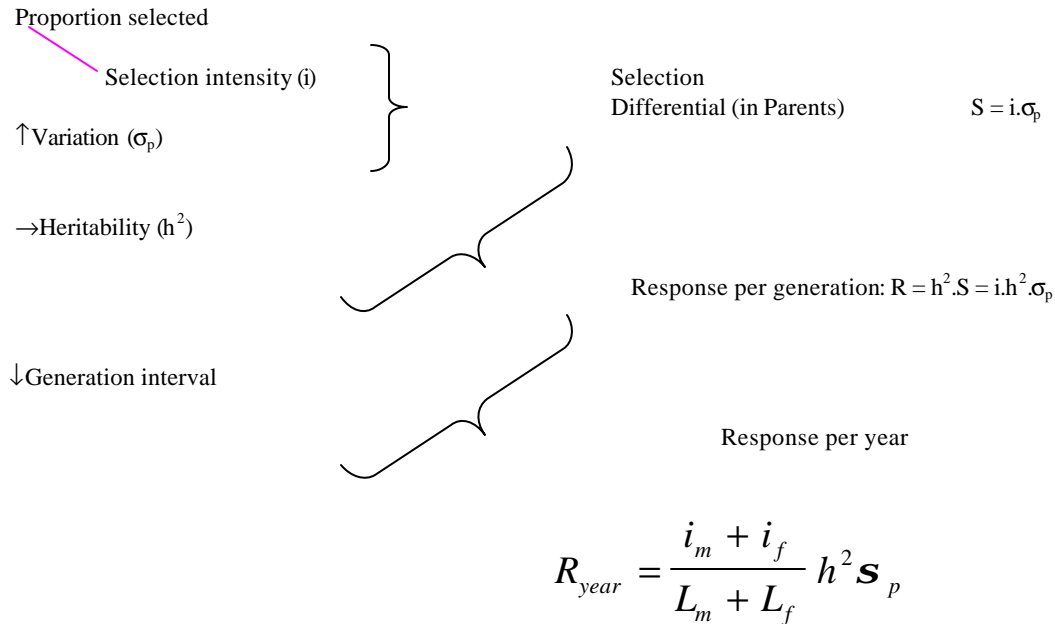
Estimated Breeding Value = EBV = heritability * phenotype (deviation)

$$EBV = h^2 \cdot P$$

$$EBV_{\text{offspring}} = \frac{1}{2} EBV_{\text{sire}} + \frac{1}{2} EBV_{\text{dam}}$$

Expected performance offspring = mean + EBV_{offspring}

Components of genetic gain: response to selection



Example:

Fleece weight in sheep.

Population/flock size 1000 ewes Trait fleece weight: $h^2 = 0.3$; $\sigma_p = 0.4$
 reproductive rates weaning rate = 0.8 rams/ewe = 1/50
 some mortality (this makes it hard to figure out the distribution of animals over age classes!)

	rams	ewes
year of first drop	2	2
year of last drop	3	7
nr selected/yr	12	250

Age structure:

Age at drop of progeny:	2	3	4	5	6	7	TOTAL
No. of Rams:	12	8					20
No. of Ewes:	250	200	180	150	120	100	1000

Predicted response to selection per year.

Generation intervals: average age of parents 'dropping' progeny	
$L_m = \frac{12 \times 2 + 8 \times 3}{12 + 8} = 2.4$ years	
$L_f = \dots \dots \dots = 3.99$ years	
Selection Intensities	
1000 ewes give $0.8 \times 1000 = 800$ progeny, 400 male and 400 female.	
$p_m = 12/400 = 0.03 \rightarrow i_m = 2.268$	
$p_f = 250/400 = 0.625 \rightarrow i_f = 0.607$	
$R_{\text{year}} = \frac{2.268 + 0.607}{2.4 + 3.99} * 0.3 * 0.4 = 0.054$ Kg	is predicted increase in FW per year

Correlated Traits

$$\text{correlation} = r_p = \frac{\text{COV}(x, y)}{s_x s_y}$$

- phenotypic between observations
- genetic between breeding values
- environmental/ residual

phenotypic covariance = genetic covariance + environmental covariance

Correlated Response $CR_y = i r_{x_A} h_x h_y s_{py}$ Sometimes better to select

Direct Response $R_x = i_x h_x^2 s_{px}$ on a correlated trait

Using information from relatives

additive genetic relationships $a = \sum_{i=1}^p (1/2)^{n_i + n_j}$

- a_{ij} between full sibs = 0.5
- between half sibs = 0.25
- between parent-offspring = 0.5

Inbreeding

Inbreeding Coefficient $F_x = 1/2 a_{ij}$ where I and j are parents of x.

Using pedigree loops $F_x = \sum [(1/2)^n (1 + F_A)]$ where A is common ancestor, n is steps in loop, sum over loops

Effective Population size $N_e = \frac{4N_m N_f}{N_m + N_f}$

Rate of inbreeding (with no selection) $\Delta F = \frac{1}{2N_e}$

Response to selection should be balanced against inbreeding and risk!

Using information from relatives:

Note that a selection index is a general concept

$$EBV = \hat{A} = b_1P_1 + b_2P_2 + b_3P_3 + \dots + b_nP_n$$

Combines information from different sources of phenotypic information

$$\text{Response from index selection} = i r_{I,A} \sigma_A$$

$r_{I,A}$ is the selection accuracy (accuracy of index/ accuracy of EBV)
it is the correlation between Index and A!

Special case: Progeny testing $EBV_{\text{sire}} = b_1P_{\text{rogeny}}$ Deviation $b_1 = \frac{2n}{n+a}$ $a = \frac{4-h^2}{h^2}$

BLUP combines information like index, but UNBIASED i.e. corrects for fixed effects, selection, assortative mating, genetic trend)

Multiple Trait Selection Index

Breeding Objective: $a_1A_1 + a_2A_2 + a_3A_3 + \dots$
a = economic value, A = breeding value
Criteria Index : $b_xP_x + b_yP_y + b_zP_z + \dots$
b = weight, P = phenotypic information

Criteria traits and Objective traits not necessarily same
Criteria need to be measured, Objective contains all traits with a value

An index is an EBV (in dollars)

Estimation of parameters

Component:		Interpretation	
		HS groups	FS groups
Between groups variance	S_b^2	.25 Va	. 5 Va + Vd + V _{Ec}
Within groups variance	σ_w^2	.75 Va + Ve	. 5 Va + V _{Es}

CROSSBREEDING .

The following parameters are involved

Direct additive effects. Proportion of genes from each breed
Maternal additive effects These relate to dam genotype
Direct dominance effect (Heterosis) Depends on % heterozygosity
Maternal dominance effect D_m . Depends on % heterozygosity dam

Heterozygosity: Purebreds: 0 F1= 1 F2= 0.5 Back cross 0.5
Rotations have more heterozygosity than synthetics

Genetic Markers

When associated with/linked to QTL they help in predicting breeding value or determining QTL genotype.
Distinguish between linked/direct markers, each has different consequences in their use.