# Building blocks of quantitative genetics
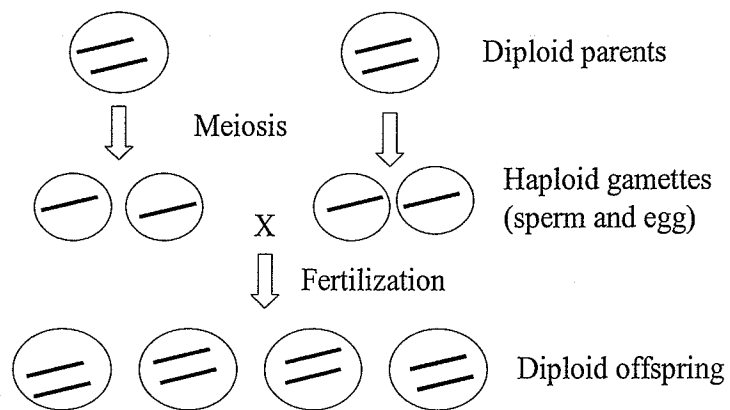
Karen Marshall

UNE
THE UNIVERSITY
OF NEW ENGLAND
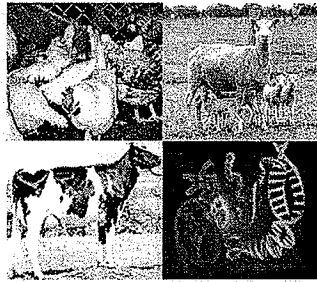
IAEA, Korea, April, 2006

# Basis of inheritance



Diploid parents

Meiosis

Haploid gamettes
(sperm and egg)

X

Fertilization

Diploid offspring

Basic quantitative genetics

# Polygenic model

As the number of genes controlling a trait increases, the distribution of genetic effects becomes more normal
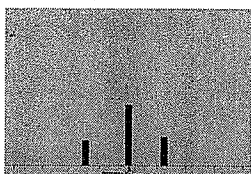
Quantitative traits are assumed to be controlled by genes at many loci: *the polygenic model*

Polygenic effects are the <u>action</u> and <u>interaction</u> of genes at a large number of loci, each with small effect
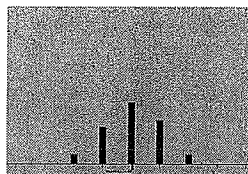
Basic quantitative genetics
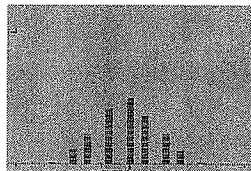
# Distributions of genetic effects

1 locus, 2 alleles / locus

2 loci, 2 alleles / locus

5 loci, 2 alleles / locus

150 loci, 2 alleles / locus

Basic quantitative genetics

# Phenotypic variation

$$P = G + E$$

$$V_P = V_G + V_E$$

Many loci, Genetic value  G:

Environmental deviation  E:

Phenotype,  P = G + E :

$$V_P = V_G + V_E$$

Basic quantitative genetics

| h²=0.1 | | | |
|---|---|---|---|
| $V_P$ | 0.030 | $\sigma_P$ | 0.173 |
| $V_A$ | 0.003 | $\sigma_A$ | 0.054 |
| $V_E$ | 0.027 | $\sigma_E$ | 0.164 |

Basic quantitative genetics

10

| h²=0.5 | | | |
|---|---|---|---|
| $V_P$ | 0.030 | $\sigma_P$ | 0.173 |
| $V_A$ | 0.015 | $\sigma_A$ | 0.122 |
| $V_E$ | 0.015 | $\sigma_E$ | 0.122 |
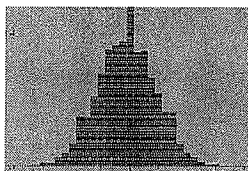


Basic quantitative genetics
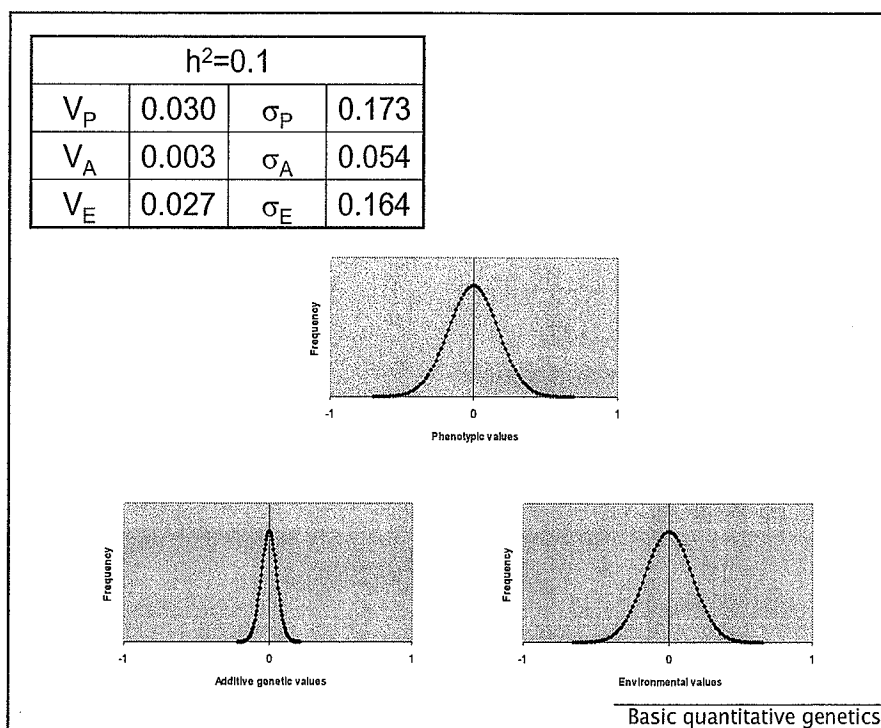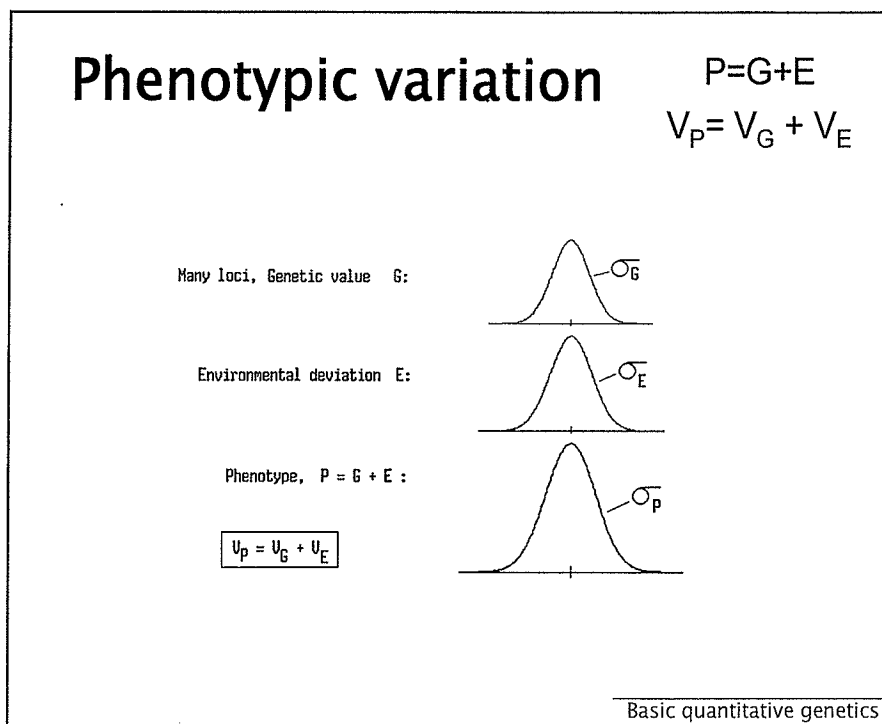
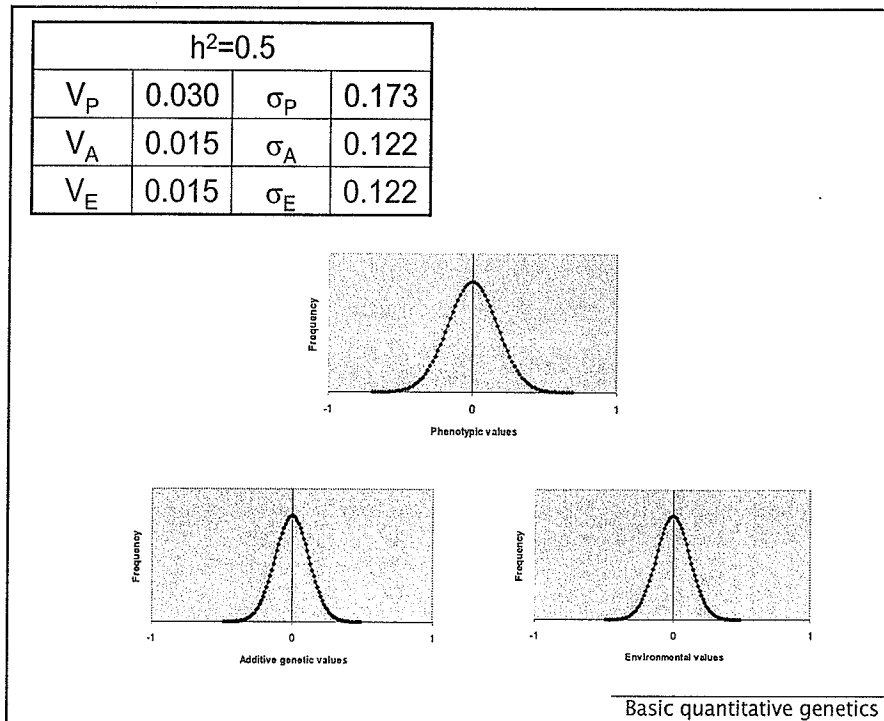# Breeding value versus genetic value

$$P=G+E$$

$$P=A+NA+E$$

Genetic value (G)
  ❖ Value of genes to self

Breeding value (A)
  ❖ Value of genes to progeny

Difference (G-A)
  ❖ Non-additive effects e.g. dominance

Basic quantitative genetics

# Breeding value

Breeding values = the sum of the average effect of alleles ($\alpha$)

Example

- ❖ Singlue locus model;
  - Genotypic values are $G_{A2A2}$= -20, $G_{A1A2}$=0, $G_{A1A1}$=20
  - p=q=0.5

- ❖ An A1 gamete will meet an A1 or A2 gamete at equal frequency
- ❖ Progeny are thus 0.5 x A1A1 and 0.5 x A1A2
- ❖ The average value of the progeny is  0.5 x -20 + 0.5 x 0 = -10
- ❖ Thus $\alpha_{A1}$=-10 units
- ❖ Similarly $\alpha_{A2}$=10 units

Basic quantitative genetics

# No dominance, p=q=0.5

| Genotype | $A_2A_2$ | $A_1A_2$ | $A_1A_1$ |
|----------|----------|----------|----------|
| Value | 280 | 300 | 320 |
| Frequency | 0.25 | 0.50 | 0.25 |
| Pop'n mean | 300 | | |
| Genetic value | -20 | 0 | 20 |
| Breeding value | -20 | 0 | 20 |

$\alpha_{A1} = 10$

$\alpha_{A2} = -10$

- ❖ With no dominance the genetic and breeding values are equal.
- ❖ With equal allele frequency the average effects of A1 and A2 are of equal magnitude

Basic quantitative genetics

## Some dominance, p=q=0.5

| Genotype | $A_2A_2$ | $A_1A_2$ | $A_1A_1$ |
|---|---|---|---|
| Value | 280 | 310 | 320 |
| Frequency | 0.25 | 0.50 | 0.25 |
| Pop'n mean | 305 | | |
| Genetic value | -25 | 5 | 15 |
| Breeding value | -20 | 0 | 20 |

$\alpha_{A1} = 10$

$\alpha_{A2} = -10$

❖ With some dominance the genetic and breeding values differ.

❖ Dominance deviation is excluded from the breeding value.

Basic quantitative genetics

## p=0.1, q=0.9, No dominance

| Genotype | $A_2A_2$ | $A_1A_2$ | $A_1A_1$ |
|---|---|---|---|
| Value | 280 | 300 | 320 |
| Frequency | 0.81 | 0.18 | 0.01 |
| Pop'n mean | 284 | | |
| Genetic value | -4 | 16 | 36 |
| Breeding value | -4 | 16 | 36 |

$\alpha_{A1} = 18$

$\alpha_{A2} = -2$

❖ With unequal allele frequencies the average effects of A1 and A2 are of different magnitude.

❖ The average effect of an allele is greater if the allele is rare.

Basic quantitative genetics

13

# Important points

Breeding values are expressed as a deviation of the population mean (with the population mean dependent on genotypic values and frequencies)

With no dominance G=A, with dominance G≠A

Animals with a rare allele will have a larger (either positive or negative) breeding value

Basic quantitative genetics

# Breeding values and can be used to predict progeny performance

❖ Using example 1 from before:
  • Genotypic values are $G_{A1A1}$= 20, $G_{A1A2}$=0, $G_{A2A2}$=-20
  • p=q=0.5

❖ Genetic value of offspring from an A1A1 sire is

$$G_o = \frac{A+0}{2} = \frac{20}{2} = +10$$

❖ Check:
  • sire passes on A1, dams have equal frequency of A1 & A2,
  • progeny are equally A1A1 and A1A2, and (20x0.5 +0x0.5)=10

Basic quantitative genetics

# Breeding values can be used to predict progeny performance

❖ Using example 3 from before:
- Genotypic values are $G_{A1A1}= 36$, $G_{A1A2}=16$, $G_{A2A2}=-4$
- p=0.1 and q=0.9
- average effect of A1=18, of A2= -2

❖ Genetic value of offspring from an A1A2 sire is

$$G_o = \frac{A+0}{2} = \frac{16}{2} = +8$$

❖ Check:
- sire passes on A1 and A2 in equal frequency, dams have frequency of A1 =0.1 & A2=0.9,
- progeny are  0.5 (0.1 A1A1 + 0.9 A1A2) + 0.5 (0.1 A2A1 + 0.9 A2A2) = 0.5 (0.1x36 + 0.9x16) + 0.5 (0.1x16 + 0.9x-4)=8

Basic quantitative genetics

# Breeding values are halved when used to predict progeny performance

❖ as breeding value represent the sum of the average effect of two alleles,

❖ only one of which is passed on.

Basic quantitative genetics

# Realised vs expected BVs

## Realised BVs
- ❖ are calculated from progeny performance
- ❖ BV=2 x (progeny mean – population mean)

## Expected BVs
- ❖ calculated from knowledge of genotypic values and allele frequencies

## These differ because
- ❖ Allele frequencies vary from expected, especially for small progeny group sizes
- ❖ Effect of environment - expectation of environmental effect is 0, but this is unlikely to be realised for small progeny group sizes.

Basic quantitative genetics

---

### Expected

| Genotype | $A_1A_2$ | $A_1A_2$ | $A_1A_2$ |
|---|---|---|---|
| Value | 280 | 300 | 320 |
| Frequency | 0.25 | 0.50 | 0.25 |
| Pop'n mean | | 300 | |
| Genetic value | -20 | 0 | 20 |
| Breeding value | -20 | 0 | 20 |

$$\alpha_{A1} = 10$$
$$\alpha_{A2} = -10$$

### Realised

**A1A1 sire**

| Progeny | Sire allele | Dam allele | G | E | P |
|---|---|---|---|---|---|
| 1 | A1 | A1 | 320 | 5.98 | 325.98 |
| 2 | A1 | A2 | 300 | -3.30 | 296.70 |
| 3 | A1 | A1 | 320 | .15.71 | 335.71 |
| 4 | A1 | A1 | 300 | 6.21 | 306.21 |
| 5 | A1 | A2 | 320 | -6.40 | 313.60 |
| 6 | A1 | A1 | 300 | -7.31 | 292.69 |
| 7 | A1 | A1 | 300 | -3.24 | 296.76 |
| 8 | A1 | A2 | 300 | -11.65 | 288.35 |
| 9 | A1 | A1 | 300 | 10.81 | 310.81 |
| 10 | A1 | A2 | 320 | 5.00 | 325.00 |
| | | Average | 308 | 1.18 | 309.18 |
| | | Expect | 310 | 0.00 | 310.00 |

Realised BV    21.78
Expected BV    20.00

**A1A2 sire**

| Progeny | Sire allele | Dam allele | G | E | P |
|---|---|---|---|---|---|
| 1 | A1 | A2 | 300 | -8.65 | 291.35 |
| 2 | A1 | A1 | 320 | -21.82 | 298.18 |
| 3 | A2 | A1 | 300 | -0.34 | 299.66 |
| 4 | A2 | A2 | 280 | 7.08 | 287.08 |
| 5 | A1 | A2 | 300 | -7.20 | 292.80 |
| 6 | A1 | A2 | 300 | 0.96 | 300.96 |
| 7 | A2 | A2 | 280 | -8.30 | 271.70 |
| 8 | A2 | A2 | 280 | -0.22 | 279.78 |
| 9 | A2 | A1 | 300 | 12.12 | 312.12 |
| 10 | A2 | A2 | 280 | 2.89 | 282.89 |
| | | Average | 294 | -2.35 | 291.65 |
| | | Expect | 300 | 0.00 | 300.00 |

Realised BV    -13.28
Expected BV    0.00

**A2A2 sire**

| Progeny | Sire allele | Dam allele | G | E | P |
|---|---|---|---|---|---|
| 1 | A2 | A1 | 300 | 5.57 | 305.57 |
| 2 | A2 | A2 | 280 | 1.46 | 281.46 |
| 3 | A2 | A1 | 300 | 2.61 | 302.61 |
| 4 | A2 | A2 | 280 | -1.49 | 278.51 |
| 5 | A2 | A1 | 300 | -3.48 | 296.52 |
| 6 | A2 | A2 | 280 | -7.54 | 272.46 |
| 7 | A2 | A1 | 300 | 8.13 | 308.13 |
| 8 | A2 | A1 | 300 | -2.66 | 297.34 |
| 9 | A2 | A1 | 300 | -1.33 | 298.67 |
| 10 | A2 | A1 | 300 | -0.88 | 299.12 |
| | | Average | 294 | 0.04 | 294.04 |
| | | Expect | 290 | 0.00 | 290.00 |

Realised BV    -8.50
Expected BV    -20.00

| | | Overall average | | | 298.29 |
| | | Expect | | | 300.00 |

Basic quantitative genetics

# Predicting effects

At simplest level, own phenotype can be used as the information source

$$\hat{A} = \frac{V_A}{V_P} P \qquad \hat{D} = \frac{V_D}{V_P} P \qquad \hat{E} = \frac{V_E}{V_P} P$$
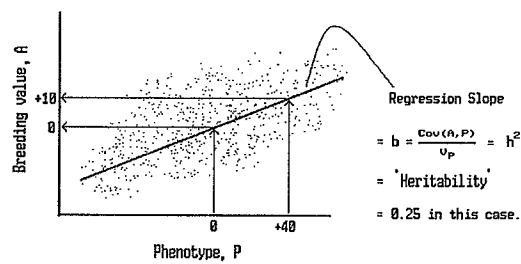
Breeding Value          Dominance          Environment

Basic quantitative genetics

# Heritability



Regression Slope

$= b = \frac{Cov(A,P)}{v_P} = h^2$

$=$ 'Heritability'

$= 0.25$ in this case.

Regression of A on P is equal to heritability

$$b_{A,P} = \frac{Cov_{A,P}}{V_P} = \frac{Cov_{A,A} + Cov_{A,NA} + Cov_{A,E}}{V_P} = \frac{V_A + 0 + 0}{V_P} = \frac{V_A}{V_P} = h^2$$

Basic quantitative genetics

# Predicting progeny performance

$$\hat{A} = \frac{V_A}{V_P} P = h^2 P \qquad \hat{G}_o = \frac{\hat{A}_m + \hat{A}_f}{2}$$

Note $G_o = (A_m + A_f)/2$ because
- ❖ G=A+NA+E
- ❖ NA and E are expected to be 0 on average
- ❖ $A = (A_m + A_f)/2$,

Basic quantitative genetics

# Example

Ram  = 90kg
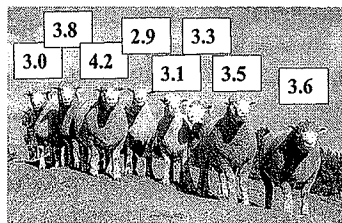
Ewe = 80 kg

Average of flock = 70 kg

$h^2$ = 0.25

$$\hat{A}_{Ram} = h^2 P = 0.25 x 20 = 5.0 kg$$

$$\hat{A}_{Ewe} = h^2 P = 0.25 x 10 = 2.5 kg$$

$$\hat{G}_0 = \frac{\hat{A}_{Ram} + \hat{A}_{Ewe}}{2} = \frac{5.0 + 2.5}{2} = 3.75 kg$$

Note that +3.75 kg is the average we expect for a large group of progeny, individuals will deviate



Basic quantitative genetics

18

# Why do progeny of the same parents differ?

Genetic variation within families
- ❖ each individual received a random one-half of genetic material from each parent
- ❖ Mendelian sampling effects
  - e.g. $V_{MS\text{-}full\ sib\ family}=0.5V_A$

Environmental variation
- ❖ systematic or random chance

Basic quantitative genetics

# Extending to a QTL model

Genetic variance under a QTL model
- ❖ Few genes of large effect
- ❖ Many genes of small effect

$$V_P = V_A + V_{QTL} + V_{NA} + V_E$$

Basic quantitative genetics