

# The concept of breeding value

Gene251/351

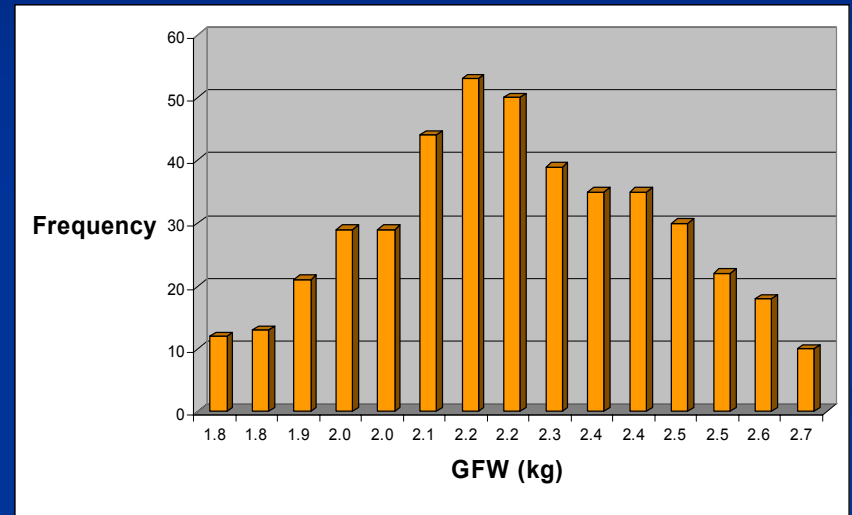
Lecture 5

# Key terms

- Estimated breeding value (EBV)
- Heritability
- Contemporary groups
  
- Reading: No prescribed reading from Simm's book.

# Revision:

- Quantitative traits show a normal distribution due to
  - An underlying genetic distribution, attributed to the polygenic model
  - An underlying environmental distribution



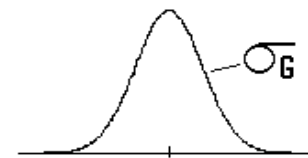
# Revision

## ■ Phenotypic variation

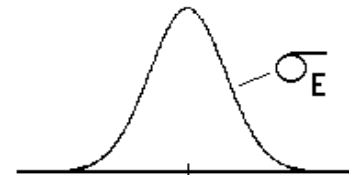
■  $V_P = V_G + V_E$

■ or  $V_P = V_A + V_{NA} + V_E$

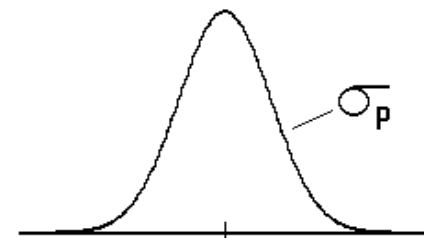
Many loci, Genetic value G:



Environmental deviation E:



Phenotype,  $P = G + E$  :



$$V_P = V_G + V_E$$

# Selection decisions

$$P = A + NA + E$$

- Q: Which component would you select on?
- A: A (additive genetic effects) as neither NA (non-additive genetic effects) or E (environment) can be passed on to progeny

# Breeding Value

- A (additive genetic effect) is also referred to as breeding value
- **Breeding value** = the value of genes to progeny
- **Genetic value** = the value of genes to self
  - it includes non-additive effects (such as dominance) which cannot be passed on to progeny

# More on the difference between genetic and breeding values

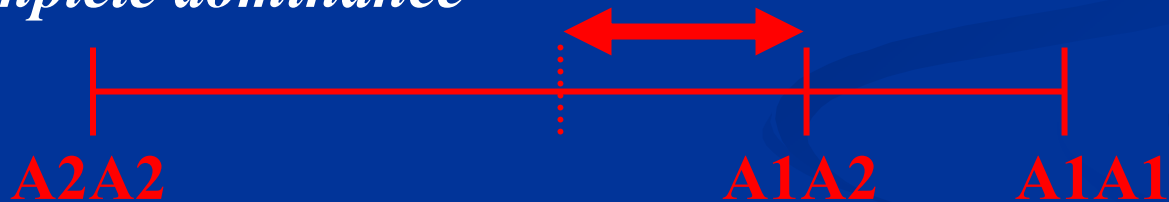
- The difference between genetic and breeding value is largely *dominance deviation*
  - An individual can express dominance deviation e.g. an  $A_1A_2$  heterozygote,
  - however an individual cannot pass on dominance deviation to its progeny as it only transmits one allele e.g. an  $A_1A_2$  heterozygote produces an  $A_1$  gamete and an  $A_2$  gamete.

# What is dominance deviation?

*No dominance*



*Incomplete dominance*



*Complete dominance*





# Breeding value

- Breeding values = the sum of the average effect of alleles ( $\alpha$ )
- For example under a single locus model
  - If  $\alpha_{A_1} = 10$  &  $\alpha_{A_2} = -10$
  - Breeding value $_{A_1A_1} = 10 + 10 = 20$
  - Breeding value $_{A_1A_2} = 10 + -10 = 0$
  - Breeding value $_{A_2A_2} = -10 + -10 = -20$

# Average effect of alleles ( $\alpha$ )

- $\alpha$  can be defined as ‘the mean deviation from the population mean of individuals which received that allele from one parent, the other allele coming at random from the population’ (*Falconer, 1989*)
- The example on the next slide should help clarify this

# Average effect of alleles

## ■ Example

- Consider a single locus model where genotypic values (as deviations from the pop'n mean) are A1A1 -25, A1A2 5, A2A2 15.
- Within the population the two alleles are at equal frequency.
- *What is the average effect of A1?*
- An A1 gamete will meet either an A1 or A2 gamete at equal frequency
- Progeny are thus equally divided between A1A1 and A1A2
- The average value of the progeny is  $(-25 + 5) / 2 = -10$
- Which is equal to  $\alpha_{A1}$
- $\alpha_{A1} = -10$  units (and  $\alpha_{A2} = 10$  units: you should be able to work this out)

# Prediction of breeding values

In real life we observe  $P$  but want to estimate  $A$



We know phenotype of parent is +3  
(expressed as a deviation from the  
population mean)

But what is its breeding value  
(i.e. values of its genes to its progeny) ?

The contribution of each effect is proportional to the variance explained by the effect

$$\hat{A} = \frac{V_A}{V_P} P$$

Breeding Value

$$\hat{D} = \frac{V_D}{V_P} P$$

Dominance

$$\hat{E} = \frac{V_E}{V_P} P$$

Environment

$$\hat{A} = \frac{V_A}{V_P} P = \hat{A} = h^2 P = EBV = h^2 P$$



Given  $P = +3.0$  units

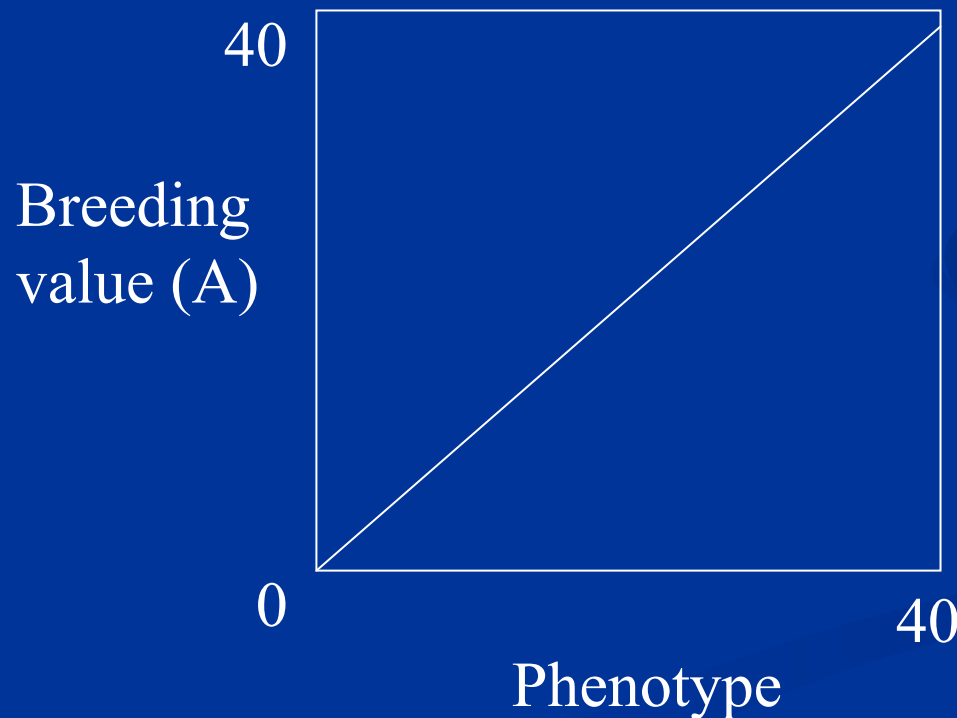
and  $h^2 = 0.333$

$EBV = +3 \times 0.333 = +1.0$  units

- *The breeding value of this parent is 1 unit superior to the flock average.*

# But how do you determine $h^2$ ?

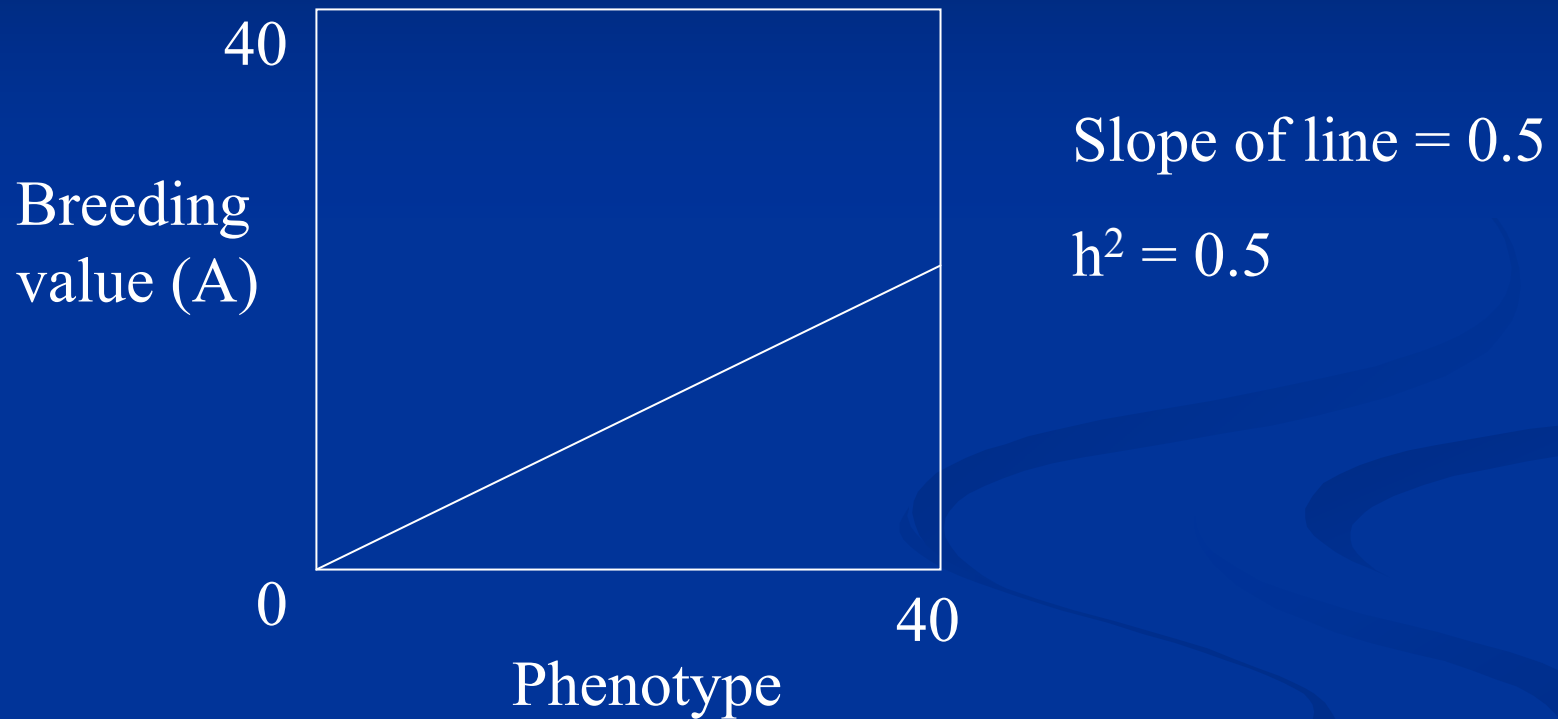
If all of the phenotype was heritable



Slope of line = 1

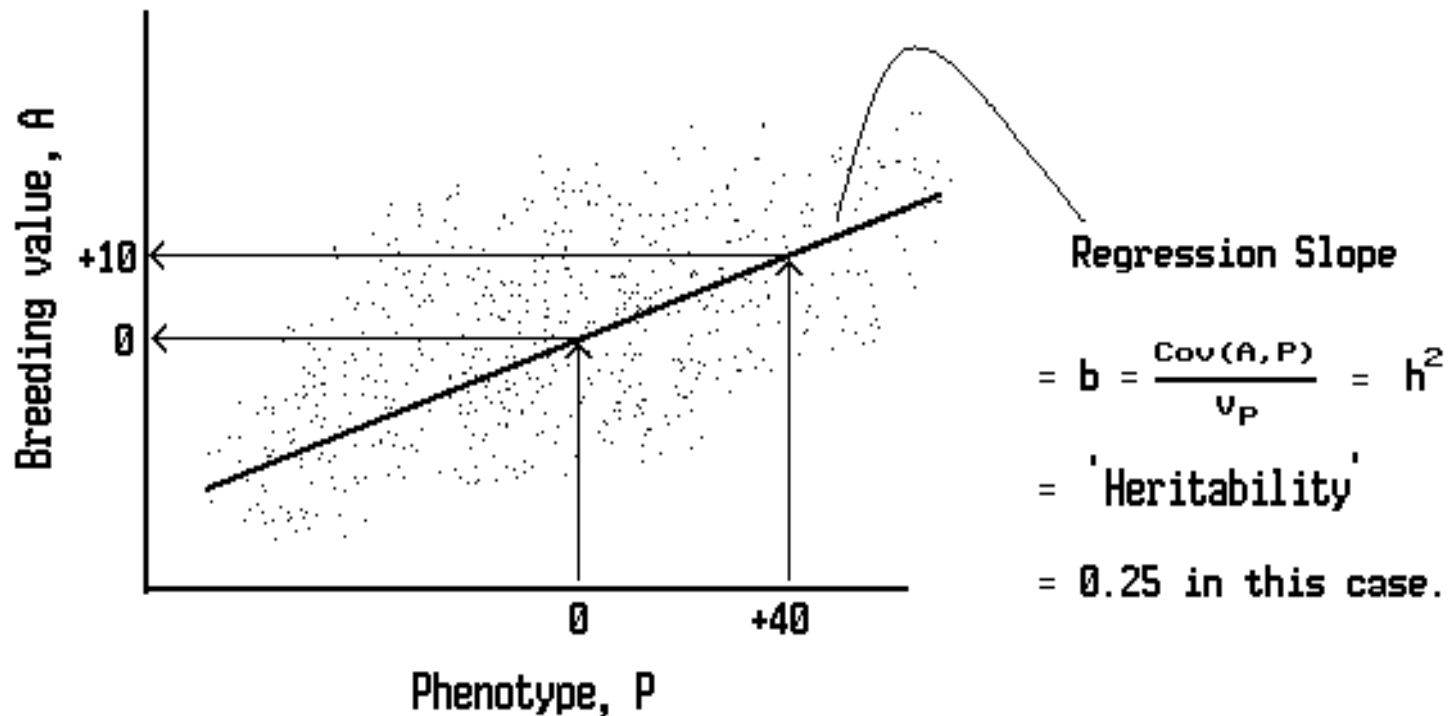
$$h^2 = 1$$

If say one-half of the phenotype was heritable





# Regression of A on P is equal to heritability



# Regression revision

- Regression coefficient (slope of regression line)  
= amount of units the y-axis variable changes  
per unit change of x-axis variable
- It can also be expressed as

$$b_{Y,X} = \frac{Cov_{Y,X}}{V_X}$$

Covariance

Variance

# Regression revision cont.

- Covariance

$$Cov(X, Y) = \frac{\Sigma(X - \bar{X})(Y - \bar{Y})}{n - 1}$$

- Regression - measures extent which changes in one trait are associated with changes in another, in units of measurement

$$b_{Y,X} = \frac{Cov_{x,y}}{V_x}$$

- Correlation - measures association between traits, but on scale -1 to 1, rather than units of measurement

$$r_{X,Y} = \frac{Cov_{x,y}}{\sigma_X \sigma_Y}$$

# Regression revision cont.

$$\begin{array}{lll} Y = [2, 4, 6, 8, 10] & V_Y = 10 & \sigma_Y = 3.16 \\ X = [1, 2, 3, 4, 5] & V_X = 2.5 & \sigma_X = 1.58 \end{array}$$

$$\text{Cov}_{Y,X} = 5$$

$$b = \text{Cov}_{Y,X} / V_X = 5 / 2.5 = 2$$

*2 units change in Y for every 1 unit change in X*

$$r = \text{Cov}_{Y,X} / (\sigma_X * \sigma_Y) = 5 / (1.58 * 3.16) = 1$$

*1 stddev change in Y for every 1 stddev change in X*

# Back to regression of A on P

- We cannot derive regression coefficient of A on P from data as we do not know A (true breeding value)
- Thus calculate from theory as we can derive the covariance between A and P

$$b_{A,P} = \frac{Cov_{A,P}}{V_P}$$

# Derivation

$$b_{A,P} = \frac{\text{Cov}_{A,P}}{V_P} = \frac{\text{Cov}_{A,A} + \text{Cov}_{A,NA} + \text{Cov}_{A,E}}{V_P}$$

$$= \frac{V_A + 0 + 0}{V_P} = \frac{V_A}{V_P} = h^2$$

*You don't need to memorise this*

# Summary

- Breeding values are estimated from phenotype as

$$\hat{A} = h^2 P$$

- Both  $\hat{A}$  and  $P$  are expressed as deviations from their group means

- Regression of  $A$  on  $P$  is equal to  $h^2$

$$b_{A,P} = \frac{\text{Cov}_{P,A}}{V_P} = h^2$$

# Using estimated breeding values

Expected genotypic value of offspring is equal to the average of the estimated breeding value of its two parents

$$\hat{G}_o = \frac{\hat{A}_m + \hat{A}_f}{2}$$

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



# Using EBVs: Example

Ram = 90kg

Ewe = 80 kg

Average of flock = 70 kg

*Assume corrected for sex differences*

$$h^2 = 0.25$$

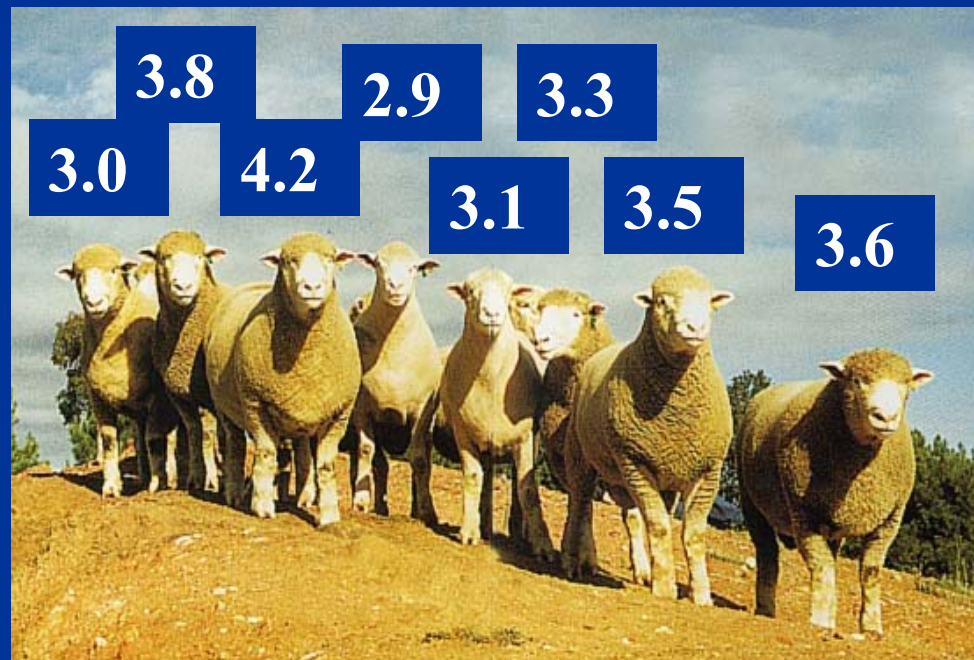
$$\text{EBV Ram} = P \times h^2 = 20 \times 0.25 = 5.0 \text{ kg}$$

$$\text{EBV Ewe} = P \times h^2 = 10 \times 0.25 = 2.5 \text{ kg}$$

Expected genetic value of progeny

$$= (5.0 + 2.5) / 2 = 3.75 \text{ kg (above average)}$$

Note that not all progeny will be +3.75 kg  
(this is average we expect for a large group of progeny)



# Within family variation

(why do progeny of the same parents differ)

- Genetic variation within families
  - as each individual received a random one-half of genetic material from each parent
  - you are not identical to full sibs
- Environmental variation
  - systematic or random chance

# Using EBVs: Example

Ram = +5 mm EMD (eye-muscle depth)

Mated to a group of ewes

$$h^2 = 0.40$$

$$\text{EBV Ram} = P \times h^2 = 5 \times 0.4 = 2.0 \text{ kg}$$

Average EBV for group of ewes is zero

Expected genetic value of progeny

$$= (2.0 + 0) / 2 = 1.0 \text{ kg (above average)}$$

# The concept of fair comparisons

- Phenotypes and breeding values are expressed as deviations from group means
- However it is not fair to compare e.g.
  - weight of a 12 month bull versus a 15 month bull
  - weight of a single versus twin
  - weight of individuals raised in different paddocks
  - weight of individuals raised in different seasons / years
- The following 4 slides show how to overcome these types of problems

# Contemporary group

- Individuals can be compared only to other individuals belonging to the same contemporary group
- A contemporary group is generally defined as animals raised under similar conditions (born within the same year and season), the same sex, and with small age differences

# Comparing to contemporary group

	Single	Twins	
Males	60 Kg	55 Kg	<i>57.5 Kg</i>
Females	50 Kg	45 Kg	<i>47.5 Kg</i>
	<i>55 Kg</i>	<i>50 Kg</i>	<i>52.5 Kg</i>

Express P as deviation from contemporary group mean

e.g. 57 Kg male twin has a P of  $57 - 55 \text{ Kg} = 2 \text{ Kg}$

# Data correction

- Data can be adjusted for fixed effects
- Fixed effects that can influence phenotype include
  - sex
  - born as single versus twin
  - year / seasonal differences
  - age



# Adjusting for fixed effects

	Single	Twins	
Males	60 Kg	55 Kg	57.5 Kg
Females	50 Kg	45 Kg	47.5 Kg
	55 Kg	50 Kg	52.5 Kg

Adjust for effects separately- only applicable in absence of interactions between effects

- 57 Kg male twin is advantaged by 5 Kg for being male and disadvantaged by 2.5 Kg for being a twin
- Adjusted P =  $57 - 5 + 2.5 = 54.5$  Kg
- P (as deviation from overall mean) = 2 Kg

# How to tell if there is an interaction between effects

	Single	Twins	
Males	60 Kg	55 Kg	57.5 Kg
Females	50 Kg	45 Kg	47.5 Kg
	55 Kg	50 Kg	

	Single	Twins	
Males	60 Kg	55 Kg	57.5 Kg
Females	50 Kg	40 Kg	45.0 Kg
	55 Kg	47.5 Kg	

## ■ No interaction

- Effect of being male or female does not depend on birth type (i.e. males always 10kg heavier than females)
- Effect of being single or twin does not depend on sex (singles always 5kg heavier than twins)

## ■ Interaction

- Effect of being male or female depends on birth type (i.e. males 10kg heavier than females if single, 15 kg heavier if twin)
- Effect of being single or twin depends on sex (singles 5kg heavier than twins if male, 10 kg heavier if female)

# Summary

- The concept of fair comparisons is important when calculating EBVs
- This is achieved by
  - Comparison to contemporary group
  - Adjusting phenotypes for known fixed effects

# Equations from today

$$\hat{A} = h^2 P$$

$$EBV = h^2 P$$

$$b_{A,P} = \frac{Cov_{P,A}}{V_P} = h^2$$

$$\hat{G}_o = \frac{\hat{A}_m + \hat{A}_f}{2}$$