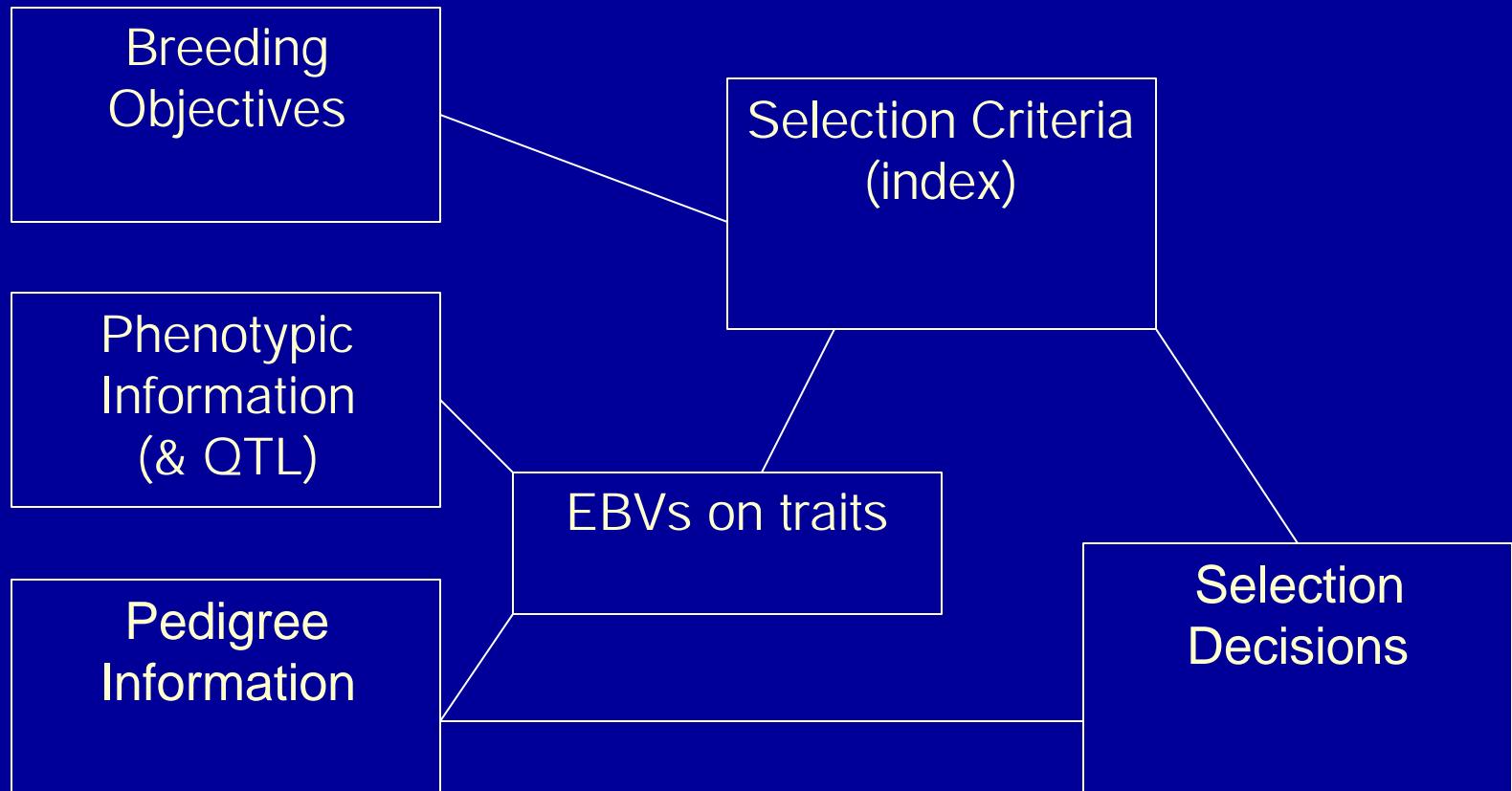


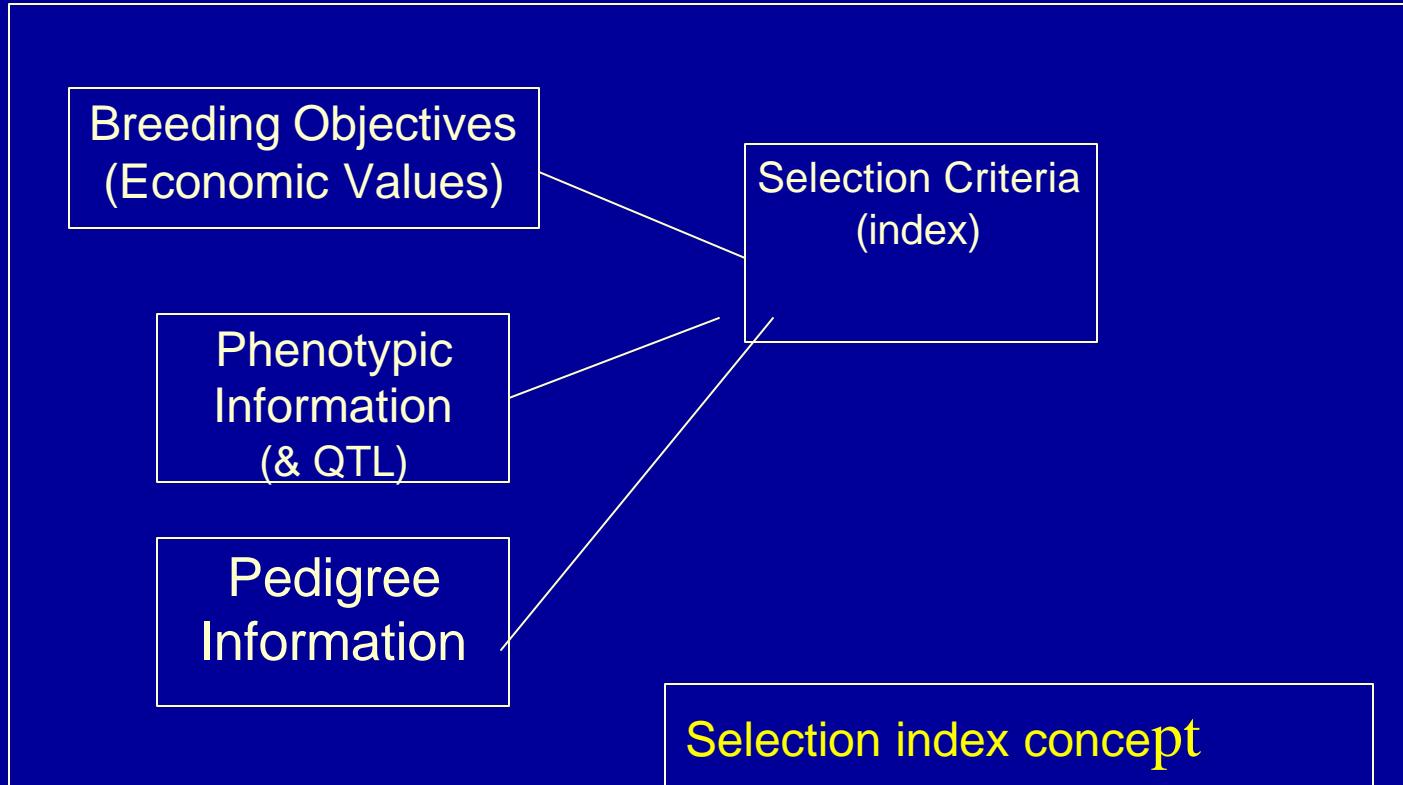
Multiple Trait Selection

- Defining Selection Criteria
- Prediction Selection Response
- Manipulating Selection Response

Relationship between information, pedigree, index and multiple trait selection

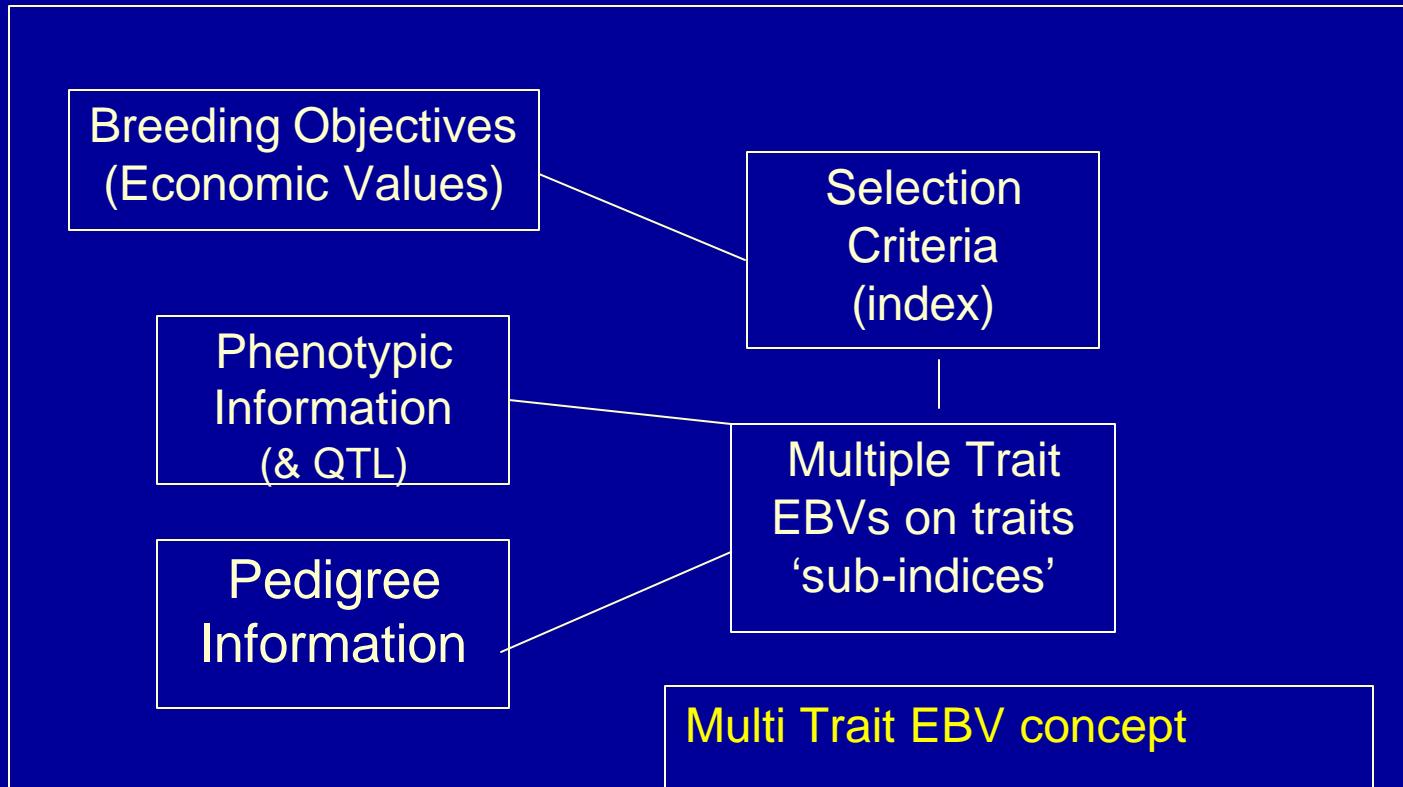


Relationship between information, pedigree, index and multiple trait selection



$$\text{Index} = 0.195.W_{\text{own}} + 0.056.W_{\text{sire}} + 0.164.W_{\text{HS}} - 0.916.FI_{\text{sire}}$$

Relationship between information, pedigree, index and multiple trait selection

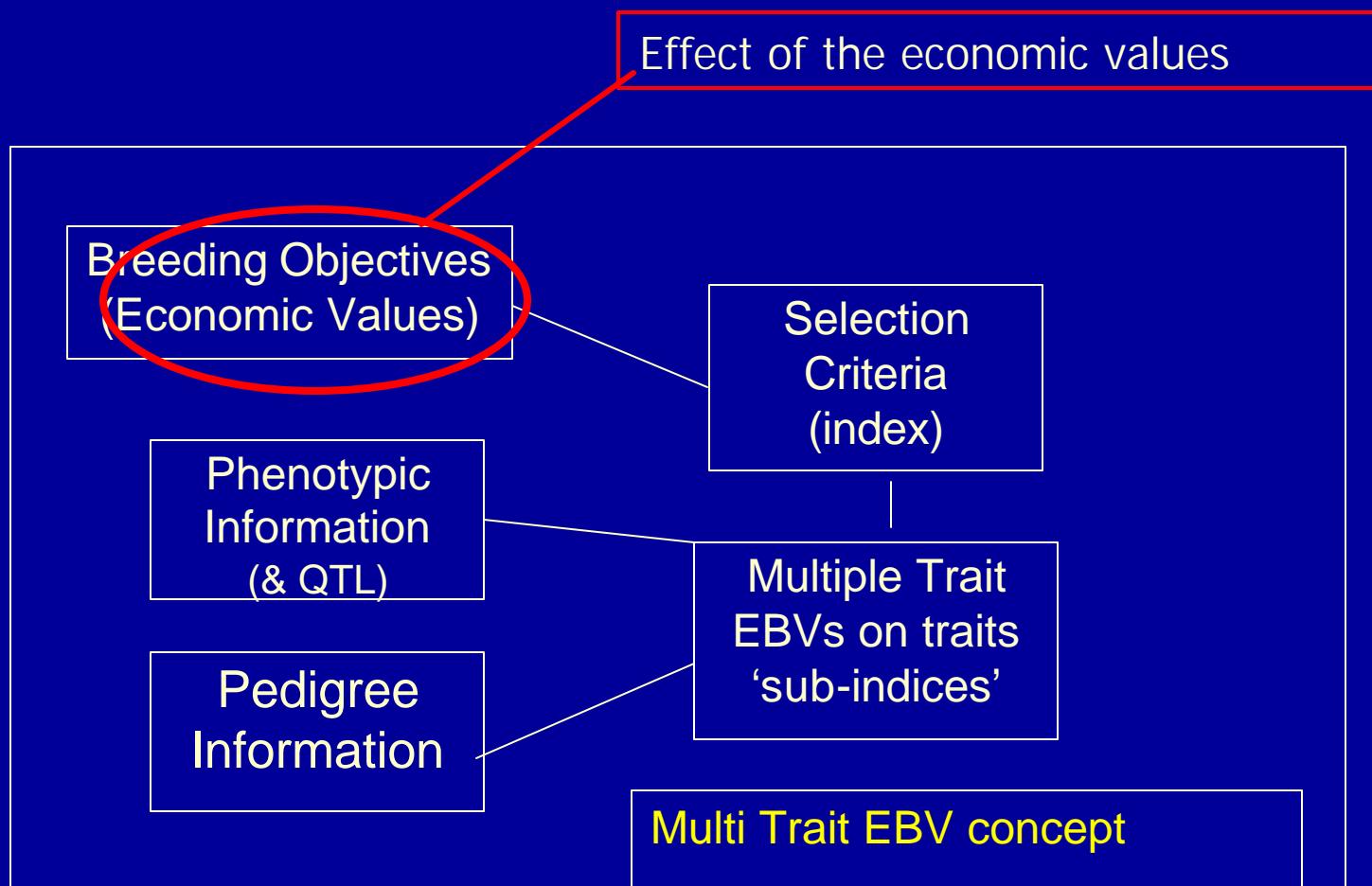


$$\text{Index} = 1.W_{\text{EBV}} - 10.FI_{\text{EBV}}$$

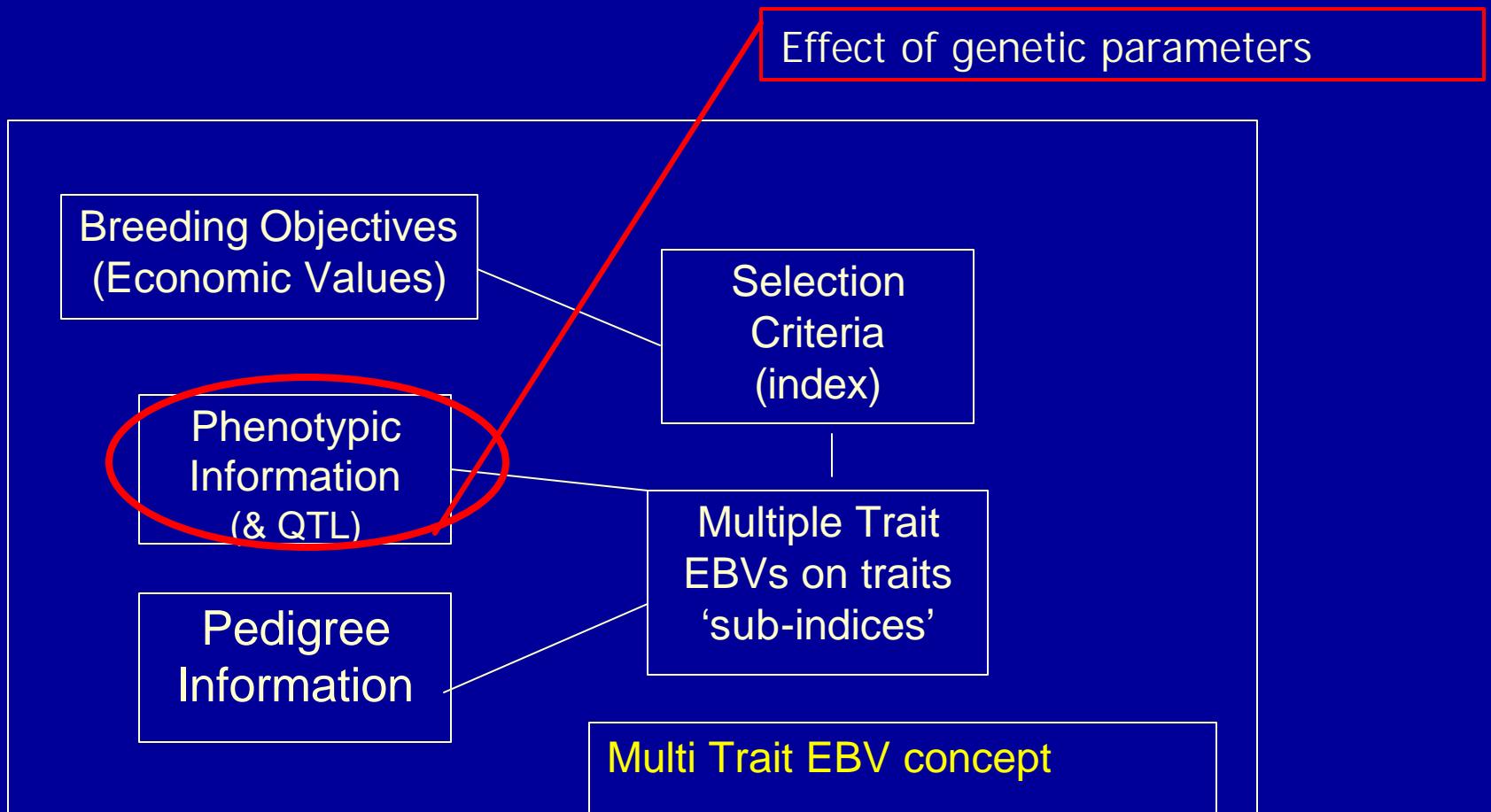
Outline MT Selection

- Properties of EBVs
- Single Trait Selection Index
- Multiple Trait Selection Index
 - Predicting Response
 - Manipulating Response
- MT Index and MTBLUP selection
- Increased Accuracy from MT Selection
- Effect of Incorrect Parameters
- Other Issues

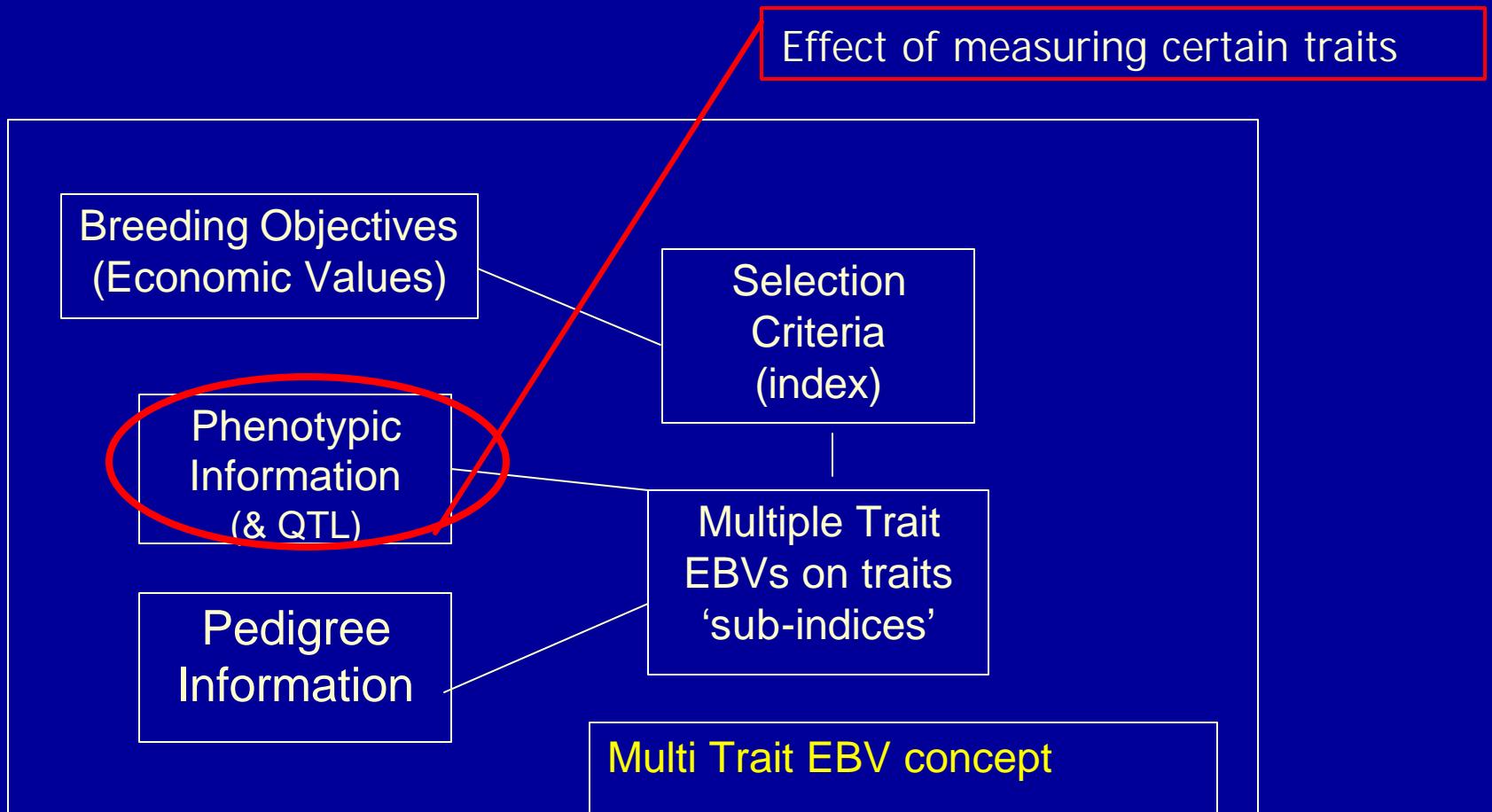
Selection Index framework allows to study.....



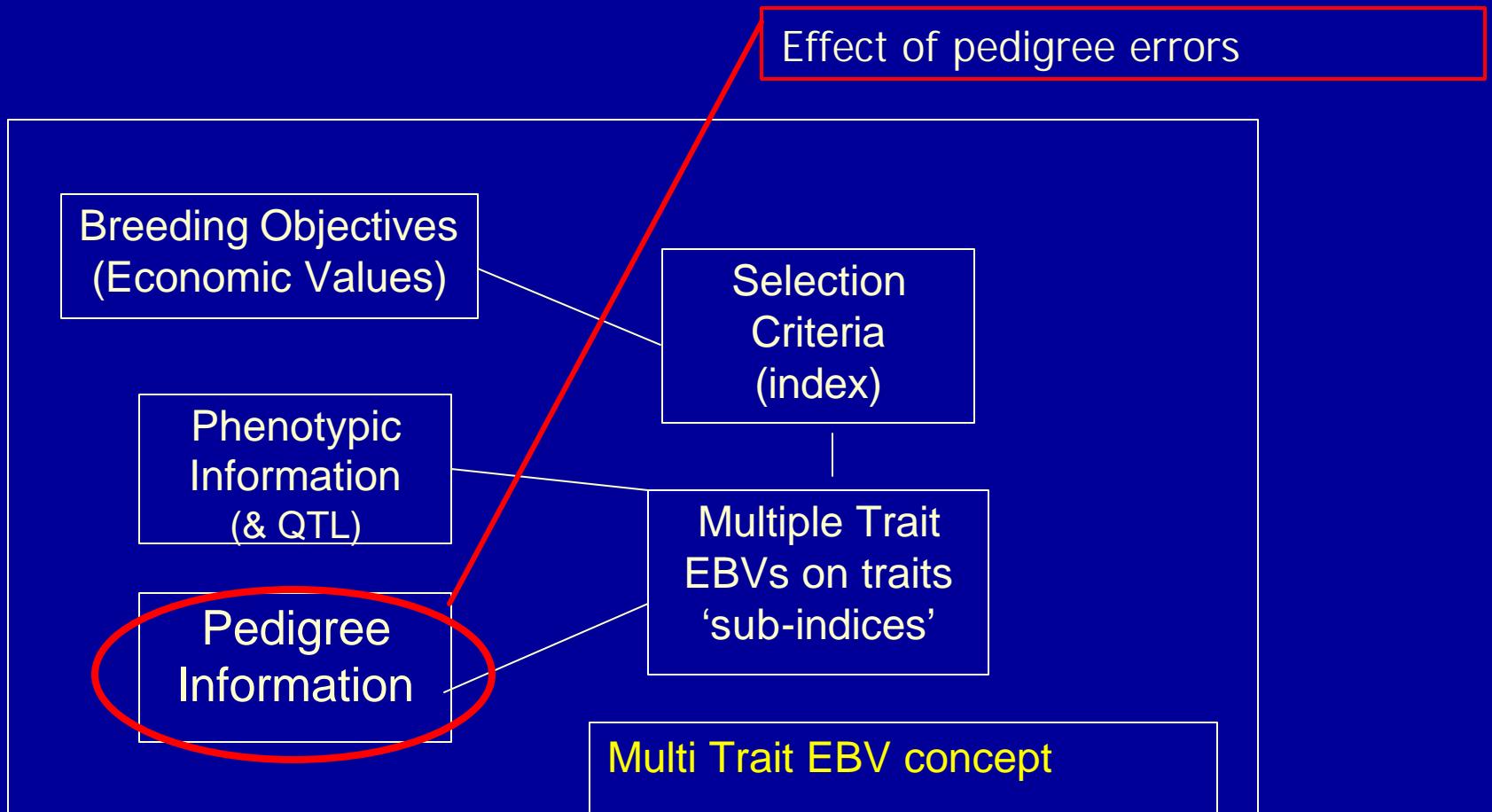
Selection Index framework allows to study.....



Selection Index framework allows to study.....



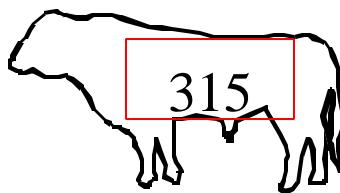
Selection Index framework allows to study.....



Estimated Breeding Values

- Properties accuracy, variance,....
- Selection Response select on EBV

| Observed | Phen. Dev. | Genetic Value | Env. Effects |
|----------|------------|---------------|--------------|
|----------|------------|---------------|--------------|



| |
|---|
| P |
|---|

| |
|---|
| G |
|---|

| |
|---|
| E |
|---|

| |
|-----|
| 315 |
|-----|

| |
|-----|
| +15 |
|-----|

| |
|-----|
| + 3 |
|-----|

| |
|-----|
| +12 |
|-----|

| |
|-----|
| 307 |
|-----|

| |
|-----|
| + 7 |
|-----|

| |
|-----|
| + 7 |
|-----|

| |
|---|
| 0 |
|---|

| |
|-----|
| 303 |
|-----|

| |
|-----|
| + 3 |
|-----|

| |
|-----|
| - 2 |
|-----|

| |
|-----|
| + 5 |
|-----|

| |
|-----|
| 294 |
|-----|

| |
|-----|
| - 6 |
|-----|

| |
|-----|
| + 8 |
|-----|

| |
|-----|
| -14 |
|-----|

| |
|-----|
| 287 |
|-----|

| |
|-----|
| -13 |
|-----|

| |
|-----|
| - 6 |
|-----|

| |
|-----|
| - 7 |
|-----|

$$h^2 = ?$$

| |
|----|
| SD |
|----|

| |
|----|
| 11 |
|----|

| |
|---|
| 6 |
|---|

| |
|----|
| 10 |
|----|

Observed Phen. Dev. Genetic Value Env. Effects

P

G

E

+27

+ 3

+24

+ 7

+ 7

0

+ 8

- 2

+10

- 20

+ 8

-28

-20

- 6

- 14

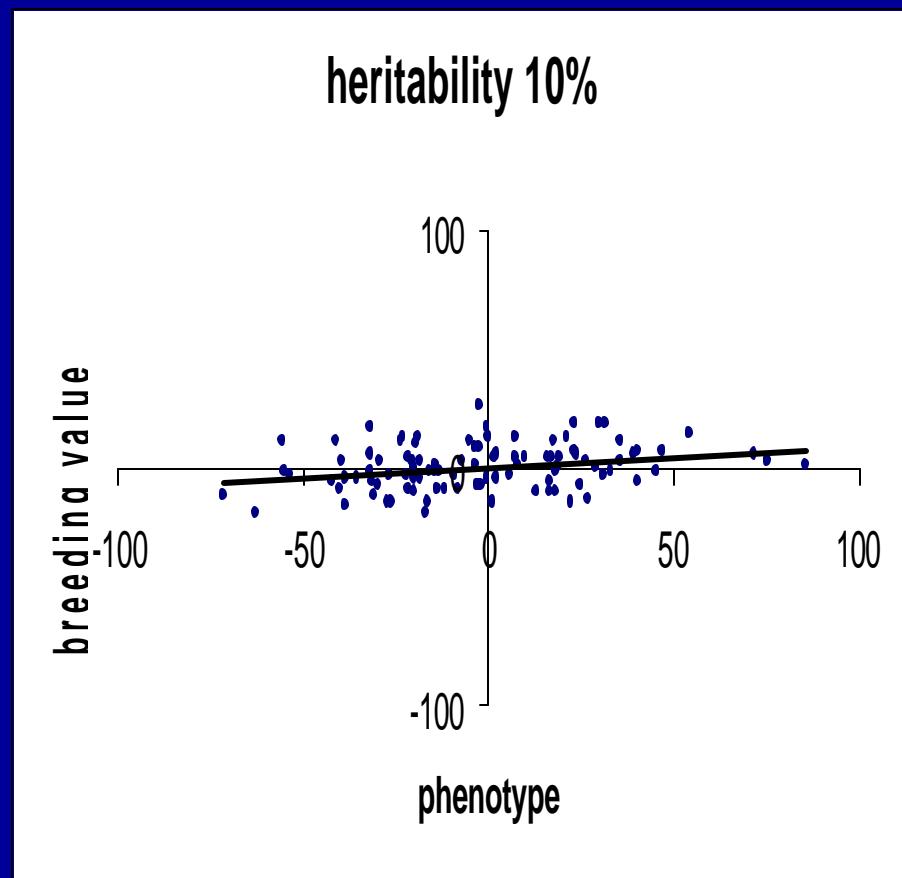
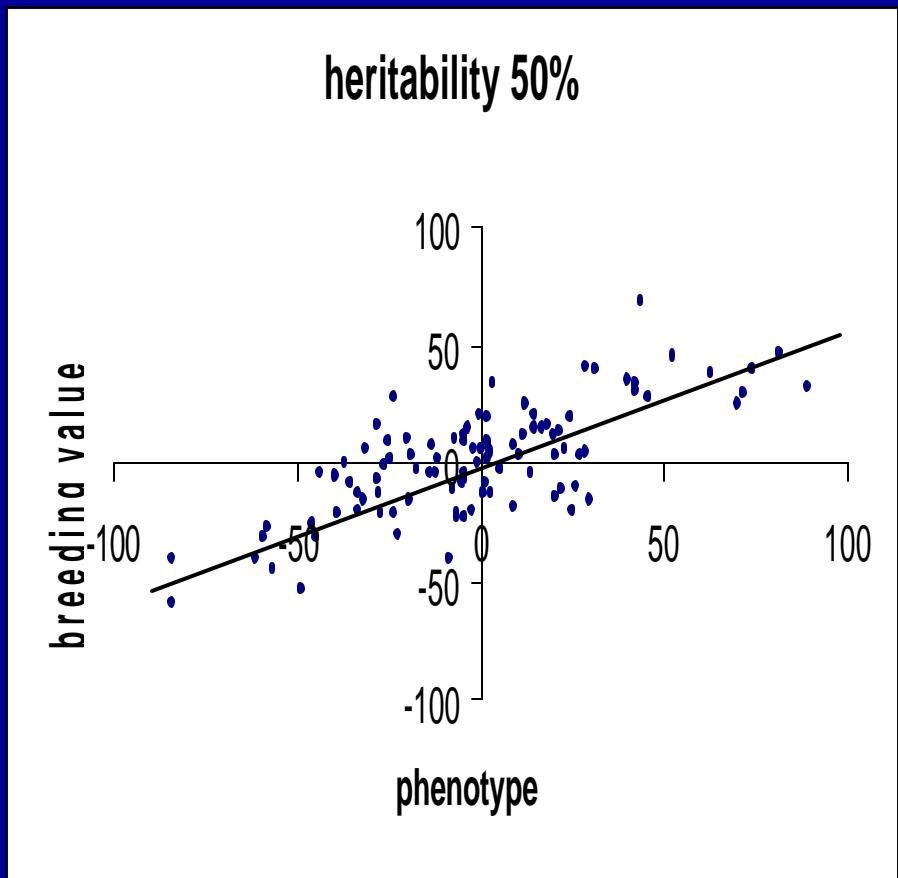
$h^2 = ?$

21

6

20

The larger heritability, the more of phenotypic differences are due to (additive) genetic value



Estimation of Breeding Value

- Is based on regression

$$b = \text{covariance}(A, X) / \text{variance}(X)$$

$$\text{EBV} = b \cdot X$$

Accuracy of EBV

Symbol: r_{IA} =
correlation between
estimated ("I") and true breeding value ("A")

or: r_{IH} =
correlation between
estimated ("I") and true breeding objective ("H")

Accuracy of EBV

| Information used | $h^2 = 0.10$ | $h^2 = 0.30$ |
|---|--------------|--------------|
| Sire EBV ($r_{IA}=0.5$) | 0.25 | 0.25 |
| Sire EBV ($r_{IA}=0.9$) | 0.45 | 0.45 |
| Sire EBV ($r_{IA}=0.5$) + Dam EBV ($r_{IA}=0.5$) | 0.35 | 0.35 |
| Sire EBV ($r_{IA}=0.9$) + Dam EBV ($r_{IA}=0.5$) | 0.51 | 0.51 |
| Own Performance only | 0.32 | 0.55 |
| OP+ Sire EBV ($r_{IA}=0.9$)+ Dam EBV ($r_{IA}=0.5$) | 0.57 | 0.66 |

Accuracy of EBV

| Information used | $h^2 = 0.10$ | $h^2 = 0.30$ |
|--|--------------|--------------|
| Own Performance only | 0.32 | 0.55 |
| OP+ Sire EBV ($r_{IA}=0.9$) + Dam EBV ($r_{IA}=0.5$) | 0.57 | 0.66 |
| Mean of 5 full sibs | 0.32 | 0.48 |
| Mean of 10 half sibs | 0.23 | 0.33 |
| OP + 5 FS + 10 HS | 0.43 | 0.65 |
| Mean of 1000 half sibs | 0.49 | 0.50 |
| Mean of 1000 full sibs | 0.70 | 0.71 |
| Mean of 20 progeny | 0.58 | 0.79 |
| Mean of 100 progeny | 0.85 | 0.94 |
| Mean of 1000 progeny | 0.98 | 0.99 |

Examples of accuracies

| | $h^2=0.1$ | $h^2=0.3$ | |
|------------------------|-----------|-----------|------------------------------------|
| own information | 0.32 | 0.55 | <i>equal to sqrt h²</i> |
| mean of 10 half sib | 0.23 | 0.33 | |
| mean of 1000 half-sibs | 0.49 | 0.50 | <i>max is sqrt 0.25 = 0.5</i> |
| mean of 1000 full-sibs | 0.70 | 0.71 | <i>max is sqrt 0.5 = 0.71</i> |
| mean of 100 progeny | 0.85 | 0.94 | <i>max approaches 1.0</i> |

$$\text{Var}(A) = V_S + V_D + V_{MS} = .25V_A + .25VA + .5VA$$

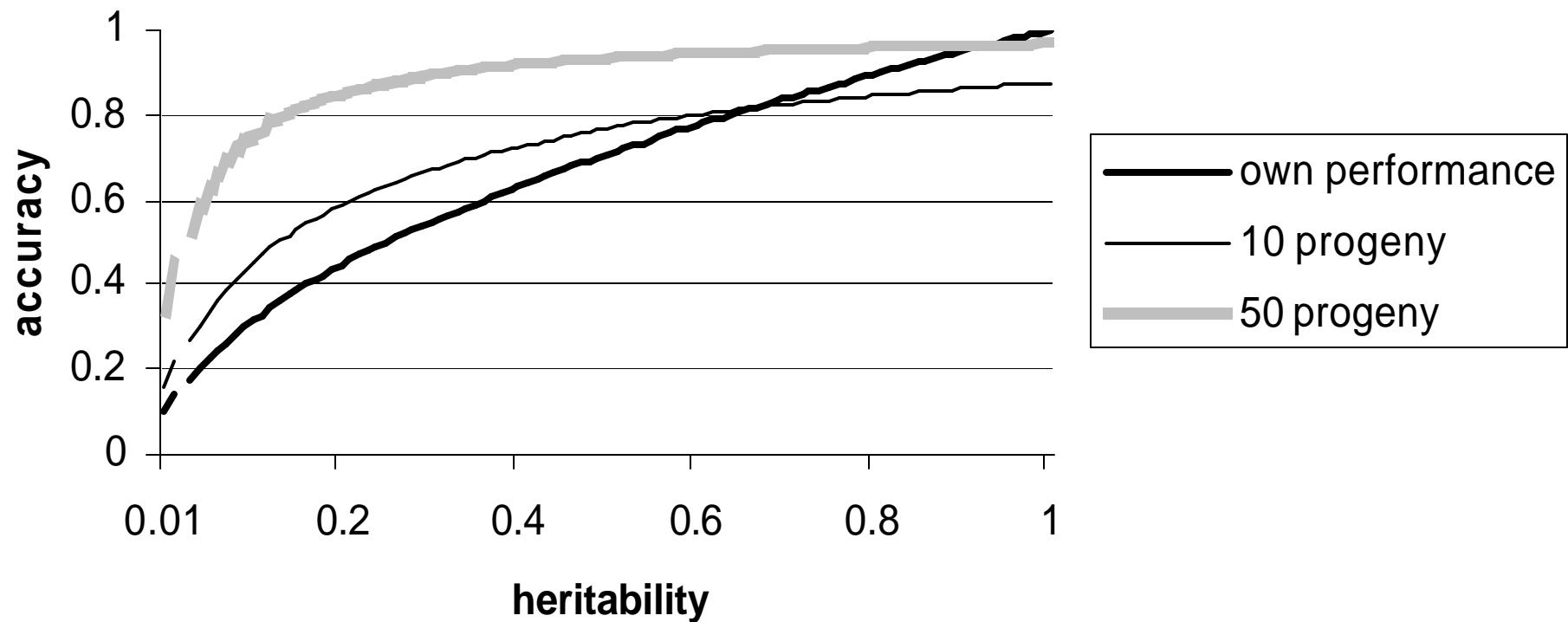
Accuracy of EBV

| <u>Information used</u> | <u>Index</u> | <u>Accuracy (approx)</u> |
|-------------------------|--|-------------------------------------|
| own performance | $EBV = h^2 \cdot P$ | h |
| progeny test | $EBV_{sire} = \frac{2n}{n+a} \cdot PM$ | $\sqrt{n/(n+a)}$ |
| | | $n = n_{prog}$ $a = (4-h^2)/h^2$ |
| Generic | $EBV = b_1 P_1 + b_2 P_2 + \dots$ | Use Selection Index Theory |

Example: Accuracy of progeny test

| | Nr of progeny | | |
|-------|---------------|------|-------|
| h^2 | 5 | 50 | 100 |
| 0.1 | 0.34 | 0.75 | 0.85 |
| 0.5 | 0.91 | 0.99 | 0.995 |

Accuracy of own performance vs progeny test

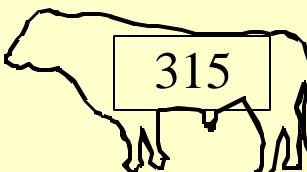


Accuracy of EBV

| <u>Information used</u> | <u>Index</u> | <u>Accuracy (approx)</u> |
|-------------------------|-----------------------------------|----------------------------|
| Generic | $EBV = b_1 P_1 + b_2 P_2 + \dots$ | Use Selection Index Theory |

Variance of EBV- *how much they differ*

- $\text{Var}(\text{EBV}) = r_{IA}^2 V_A$
- $\text{SD}(\text{EBV}) = r_{IA} \sigma_A$ = Standard deviation of EBVs

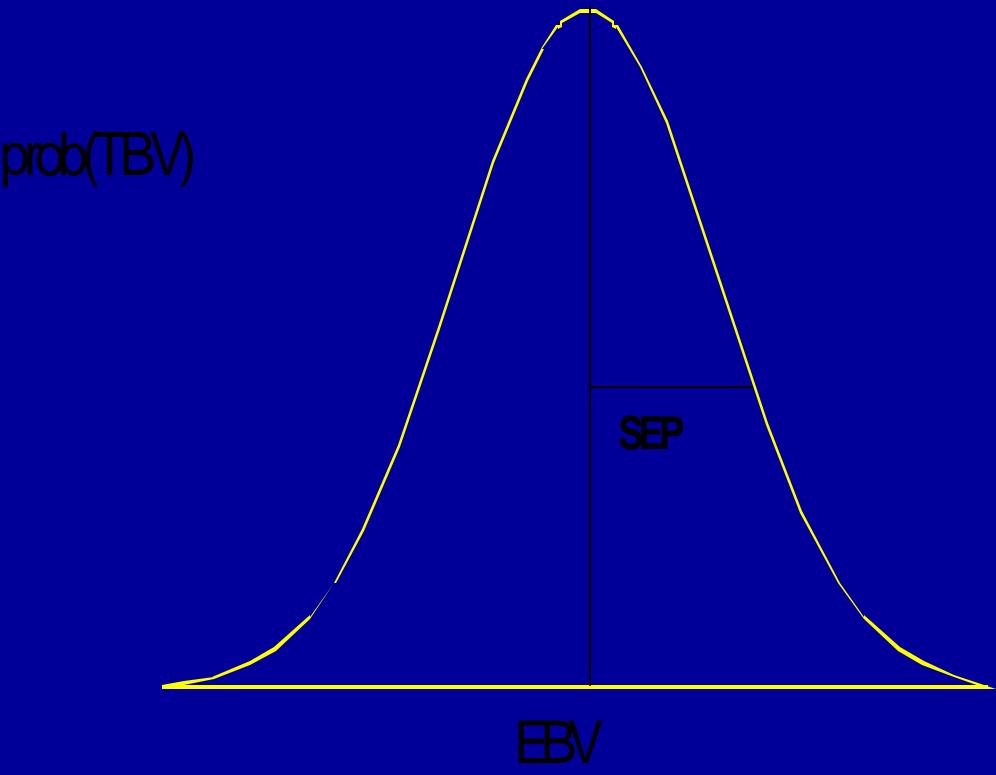
| Observed | Phen. Dev. | Genetic Value | Env. Effects | EBV ($h^2=0.3$) |
|---|------------|---------------|--------------|-------------------|
| | P | G | E | |
|  | +15 | + 3 | +12 | 4.5 |
| 307 | + 7 | + 7 | 0 | 2.1 |
| 303 | + 3 | - 2 | + 5 | 0.9 |
| 294 | - 6 | + 8 | -14 | -1.8 |
| 287 | -13 | - 6 | - 7 | -3.9 |
| SD | 11 | 6 | 10 | 3.3 |

| | Phen. Dev. | Genetic Value | Env. Effects | EBV (h ² =0.09) |
|----|------------|---------------|--------------|----------------------------|
| | P | G | E | |
| | +27 | +3 | +24 | 2.4 |
| | +7 | +7 | 0 | 0.6 |
| | +8 | -2 | +10 | 0.7 |
| | -20 | +8 | -28 | -1.8 |
| | -20 | -6 | -14 | -1.8 |
| SD | 21 | 6 | 20 | 1.8 |

Prediction Error Variance

- *how much they still may change*

- $\text{PEV} = \text{var}(\text{EBV}-\text{TBV}) = (1-r^2_{IA})V_A$



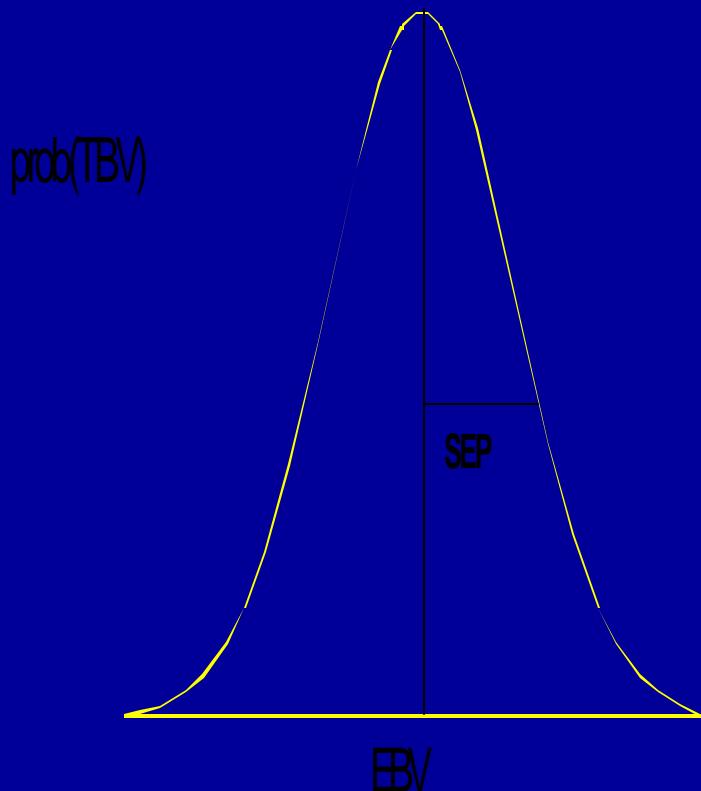
Let $s_a = 19$, $\text{EBV} = +12$,
Accuracy $^2 = r^2 = h^2 = 0.4$
Then $\text{SEP} = \sqrt{(1-0.4).19} = 14.7$

Conf. Interval: $\text{EBV} \pm 2.\text{SEP}$
 $< -17.4 - 41.4 >$

Prediction Error Variance

- how much they still may change

- $\text{PEV} = \text{var}(\text{EBV}-\text{TBV}) = (1-r^2_{IA})V_A$



Let $s_a = 19$, $\text{EBV} = +12$,
Progeny Test: Accuracy $^2 = r^2 = 0.81$
Then $\text{SEP} = \sqrt{(1-0.81).19} = 8.3$

Conf. Interval: $\text{EBV} \pm 2 \cdot \text{SEP}$

$< -4.6 \quad - \quad 28.6 >$

Prediction Error Variance

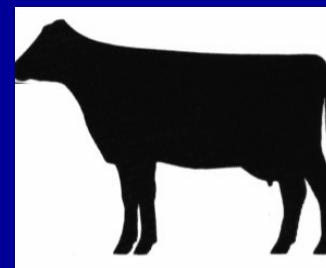
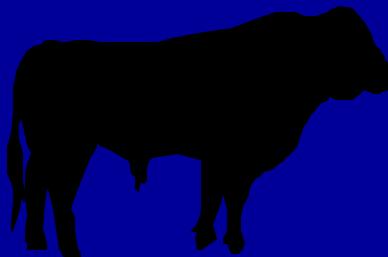
- *how much they still may change*

Consider Yearling weight EBV ($h^2 = 0.4$; $\sigma_a = 19$)

EBV = +12

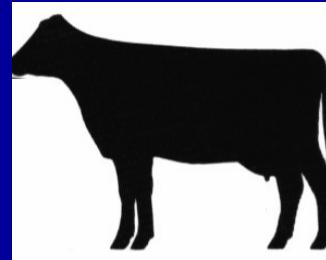
| Information for EBV | Accuracy (r_{IH}) | SEP | |
|---------------------|--------------------------|------|--------------|
| 95%CI_ EBV | | | |
| None | 0 | 19 | |
| Own performance | 0.63 | 14.7 | -17.4 - 41.2 |
| Progeny Test n=40 | 0.90 | 8.3 | -4.6 - 28.6 |
| Progeny Test n=200 | 0.98 | 3.8 | 4.4 - 19.6 |

Selection on EBV



50% of dad's
genes
1/2 EBV Sire

50% of mum's genes
1/2 EBV Dam



$$\text{Expected Value of progeny} = 1/2 \text{ } EBV_{sire} + 1/2 \text{ } EBV_{dam}$$

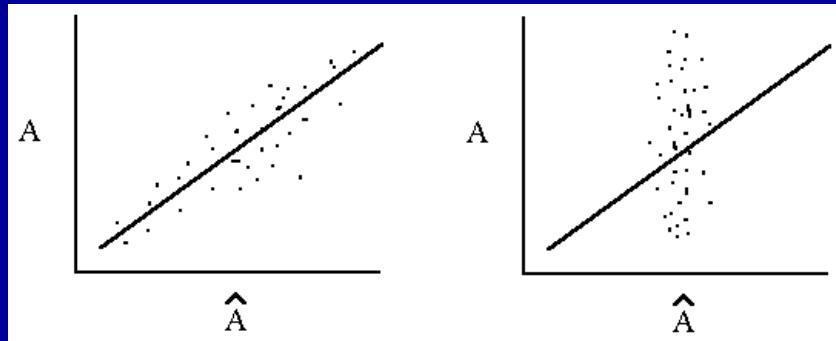
Some things to note

- EBV's on parents are additive
- Predicted performance of offspring does not depend on accuracy of the parents' EBVs
- Suppose $\text{EBV}_A = +56$ $r = 0.50$
 $\text{EBV}_B = +56$ $r = 0.95$
select A or B?

Answer: should not matter (if one is risk neutral)

Predicted Response

Regression of A on EBV = 1



Response = $i * \text{SD}(\text{EBV})$

Message:

One unit EBV relates to one unit BV, whether accurate or not

$$R = i * r * s_a$$

$$dG = \frac{R_{males} + R_{fem}}{L_{males} + L_{fem}}$$

Response to selection based on EBV

A Realistic Simulation

| Parent Average-EBV | Realized Performance | True BV | EBV_op |
|--------------------|----------------------|---------|--------|
| -11.5 | 291 | 1.4 | -3.5 |
| -9.0 | 279 | 21.3 | -8.4 |
| -8.8 | 245 | -22.9 | -22.2 |
| -4.8 | 315 | 17.0 | 6.0 |
| -3.1 | 295 | -6.6 | -2.0 |
| 4.0 | 278 | -23.5 | -8.6 |
| 4.2 | 291 | 0.4 | -3.7 |
| 4.4 | 323 | 12.2 | 9.0 |
| 5.9 | 278 | 1.9 | -8.7 |
| 9.7 | 333 | 34.4 | 13.0 |

EBV's may look inaccurate for individual, but they do provide selection response!

- Select top 50% on average BV
- PA_EBV +5
 - Own Perf_EBV +11
 - True_BV +17

Response to selection based on EBV

- Response = selection * selection * spread
intensity accuracy of TBV

$$= i r_{IA} \sigma_A$$

Example

$$\sigma_A = 19 \quad i = 0.80$$

| selection on accuracy (r_{IA}) | Expected Resp (R) | Realized Resp. |
|------------------------------------|-------------------|----------------|
| EBV_PA | 0.45 | +6.8 |
| EBV_op | 0.63 | +11 |
| BV | 1 | +17 |

See next slide

The more accuracy, the more response!

General to predict response per year

$$R_{yr} = \frac{i_{sires} r_{IA\ sires} + i_{dams} r_{IAdams}}{L_{sires} + L_{dams}} S_A$$

Should optimize i and L

Should maximize r_{IA} \rightarrow Information from correlated traits
 \rightarrow Information from relatives