

G19.6



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CONTROL OF THE COANCESTRY IN BREEDING PROGRAMS FOR AQUACULTURE SPECIES

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$$R = \rho_A i/L \sigma_A$$

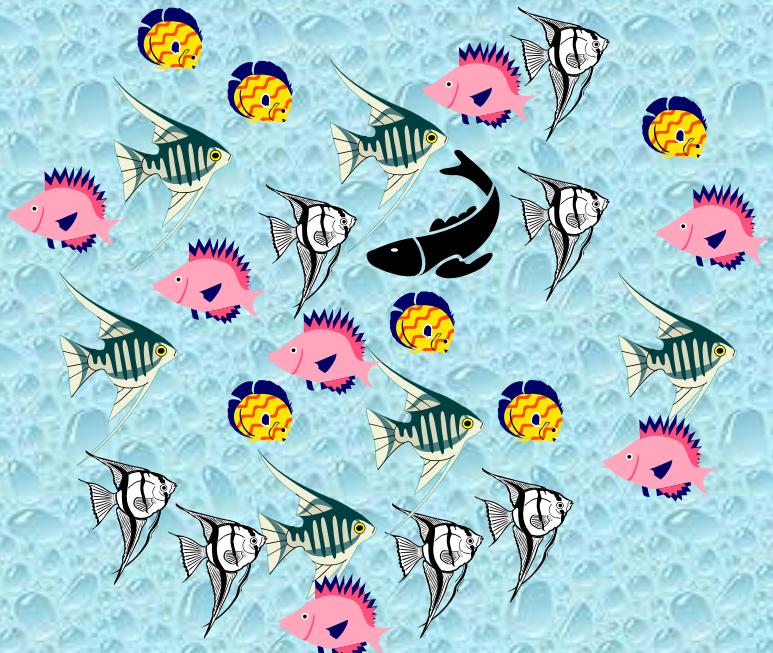
$$R = \rho_A i/L \sigma_A$$

$$R = \rho_A i/L \sigma_A$$

✓ higher selection
pressure

✓ use of relatives'
information

AQUACULTURE



High reproductive rate



DISADVANTAGE

⇒ rise of inbreeding

⇒ loss of diversity



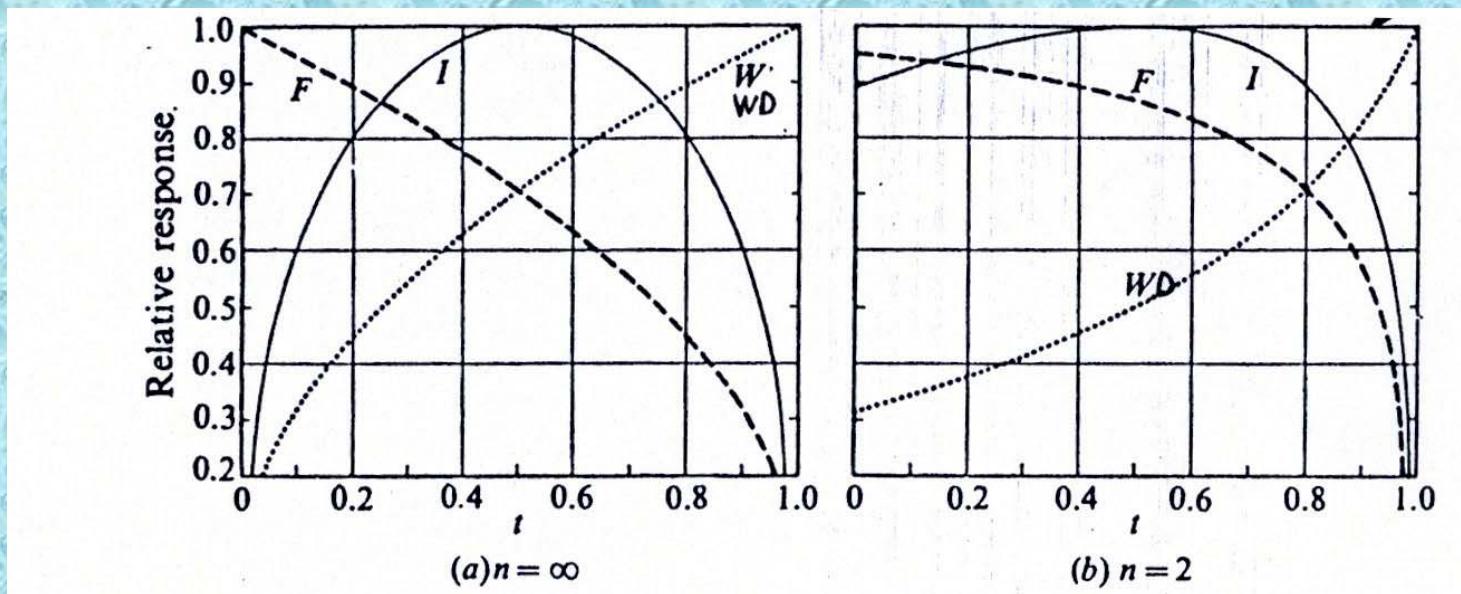
*long-term
response*

*new selection
objective*

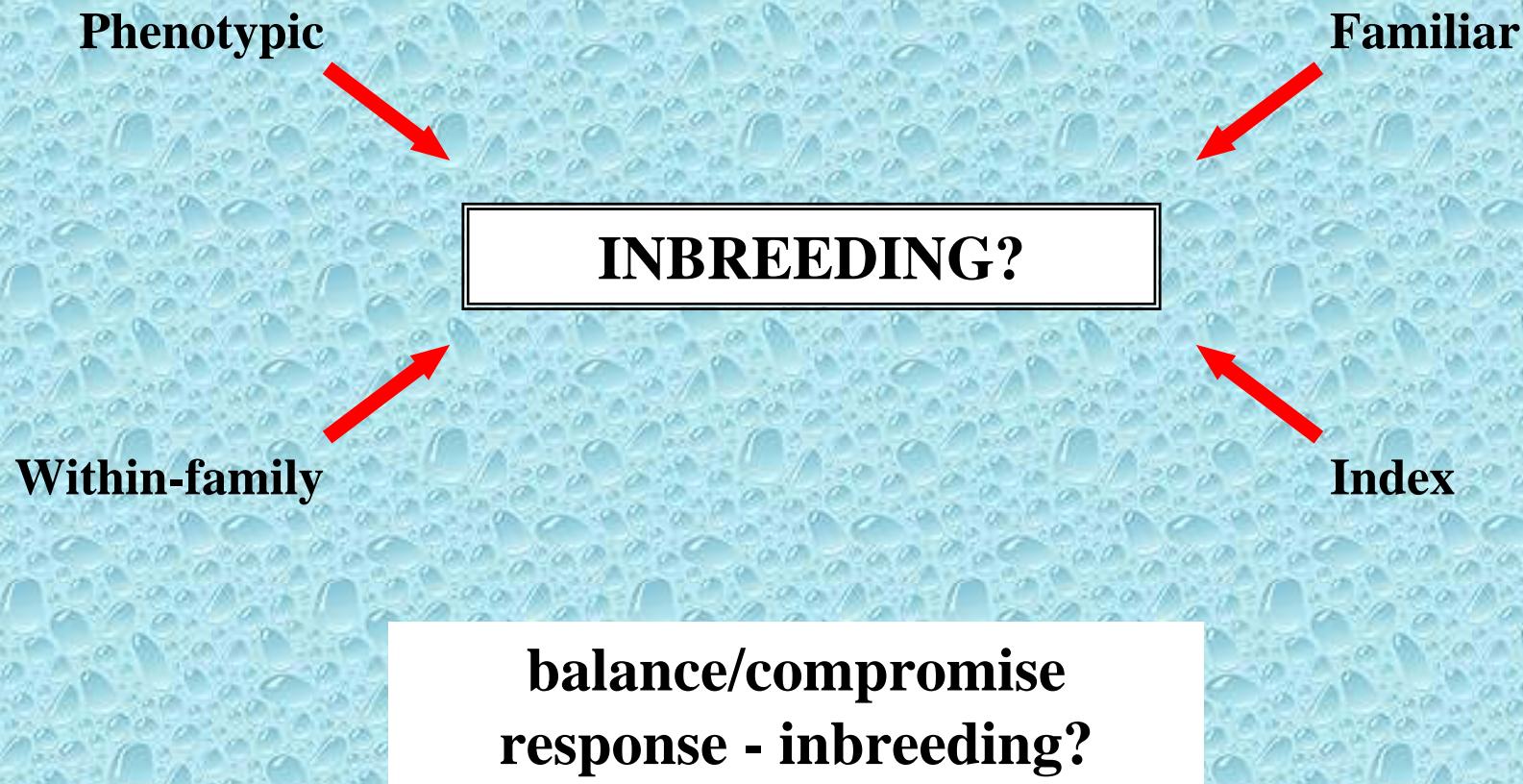
Influence of relative's information

$$R_f = ih\sigma_A \frac{1+r(n-1)}{\sqrt{n[1+t(n-1)]}}$$

$$R_w = ih\sigma_A (1 - \boxed{r}) \sqrt{\frac{n-1}{n(1-t)}}$$



Influence of relative's information



METHODS

✓ quantitative trait \Rightarrow infinitesimal model ($\mu = 50$ $\sigma^2_P = 100$)

✓ different combinations of h^2 and c^2

✓ two scenarios:

$$M = F = 25$$



$$N = 100 \text{ indiv. per family}$$

$$M = 10 \quad F = 50$$



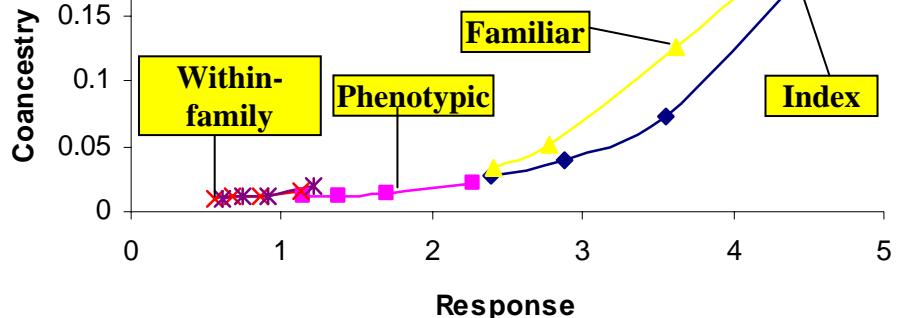
5 females per male

$$N = 100 \text{ indiv. per family}$$

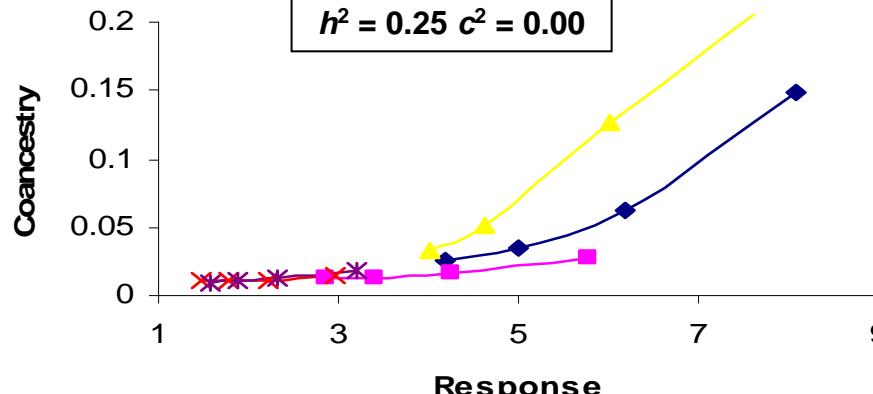
✓ selection \Rightarrow phenotype, within-family, familiar and index

$$I = b_1 P_{y - \bar{y}_{FS}} + b_2 P_{\bar{y}_{FS} - \bar{y}_{HS}} + b_3 P_{\bar{y}_{HS}} \Rightarrow \text{equivalent to BLUP}$$

$$h^2 = 0.10 \quad c^2 = 0.00$$

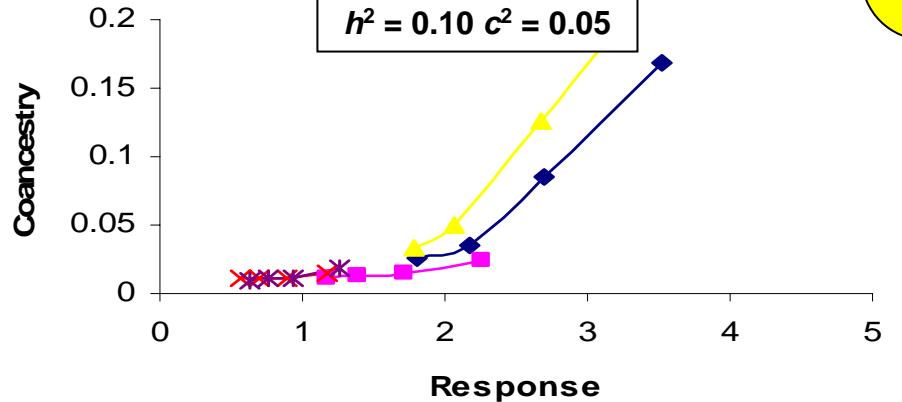


$$h^2 = 0.25 \quad c^2 = 0.00$$

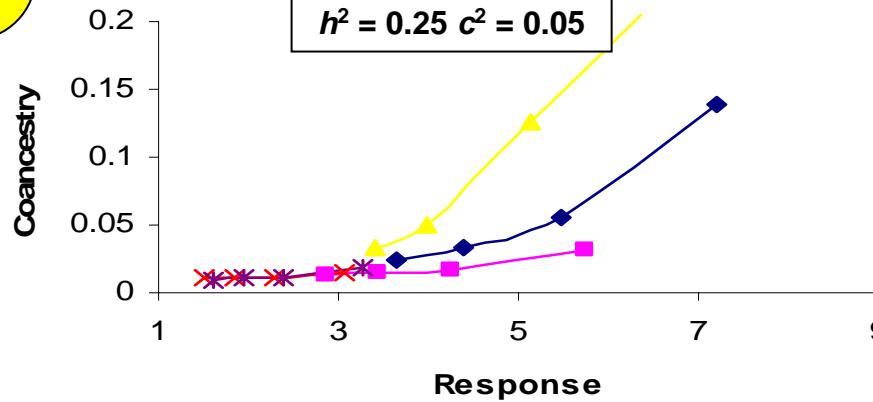


FS

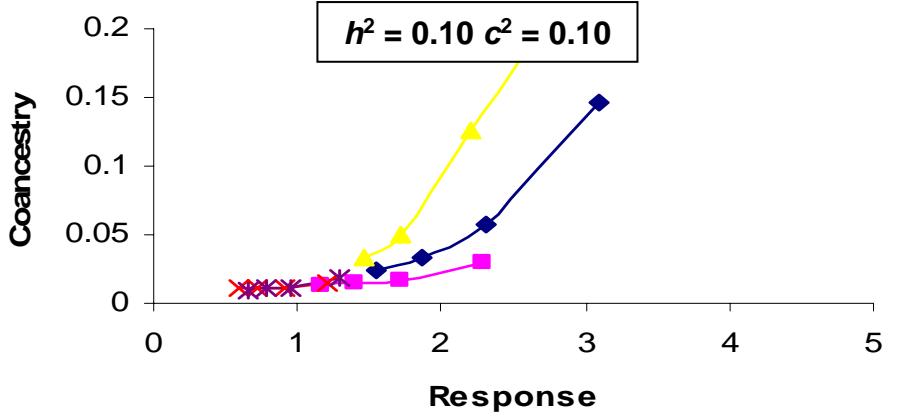
$$h^2 = 0.10 \quad c^2 = 0.05$$



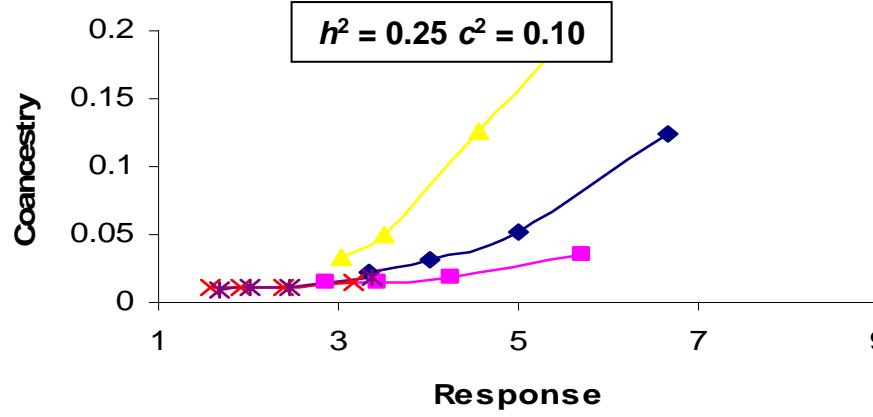
$$h^2 = 0.25 \quad c^2 = 0.05$$

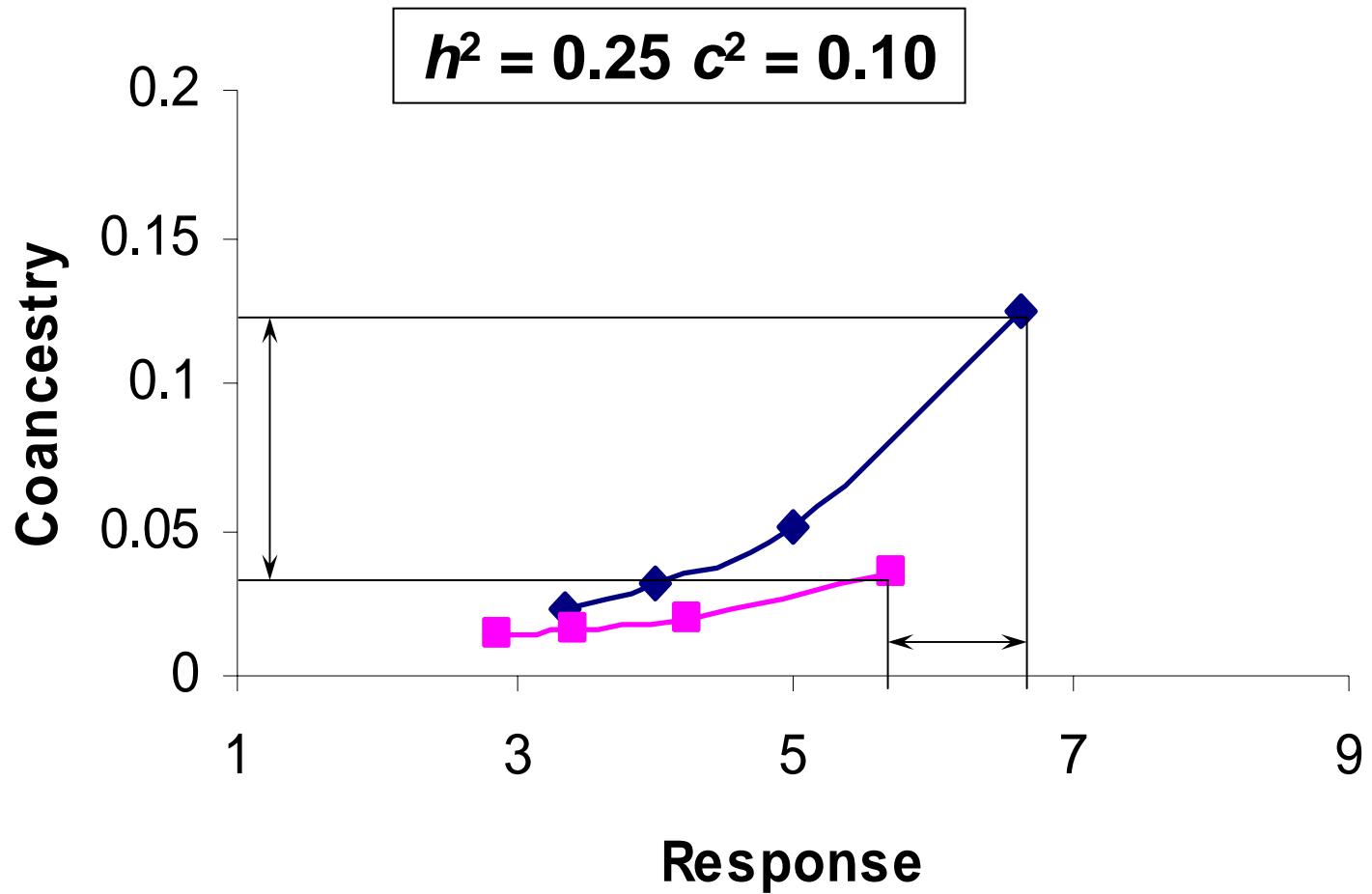


$$h^2 = 0.10 \quad c^2 = 0.10$$



$$h^2 = 0.25 \quad c^2 = 0.10$$





$t \approx 0.5 \ R_P = R_I$

$t = 0.35$

| | | Response | | Coancestry of selected | | |
|----|-------|----------|-------|------------------------|-------|------------|
| | h^2 | c^2 | Index | Phenotypic | Index | Phenotypic |
| FS | 0,10 | 0 | 4,46 | 2,27 | 0,18 | 0,02 |
| | | 0,05 | 3,51 | 2,27 | 0,17 | 0,03 |
| | | 0,10 | 3,09 | 2,28 | 0,15 | 0,03 |
| | 0,25 | 0 | 8,07 | 5,76 | 0,15 | 0,03 |
| | | 0,05 | 7,21 | 5,74 | 0,14 | 0,03 |
| | | 0,10 | 6,65 | 5,72 | 0,13 | 0,04 |
| HS | 0,10 | 0 | 4,16 | 2,35 | 0,14 | 0,03 |
| | | 0,05 | 3,42 | 2,33 | 0,13 | 0,03 |
| | | 0,10 | 3,13 | 2,31 | 0,13 | 0,04 |
| | 0,25 | 0 | 7,57 | 5,78 | 0,13 | 0,04 |
| | | 0,05 | 6,92 | 5,78 | 0,12 | 0,04 |
| | | 0,10 | 6,55 | 5,77 | 0,11 | 0,04 |

HOW TO COPE WITH INBREEDING?

- ✓ modification of the number of selected individuals and their contributions
- ✓ selection of non “elite” individuals

$$\max \quad \sum_{i=1}^{NF} EBV_i \cdot x_i - \lambda \left(\sum_{i=1}^{NF} \sum_{j=1}^{NF} x_i x_j f_{ij} \right)$$

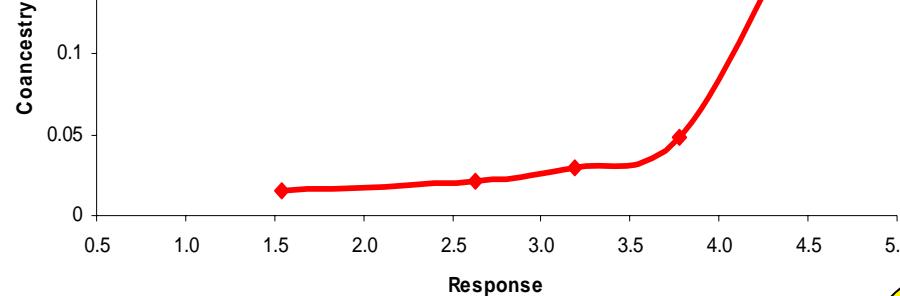
$$\boxed{EBV - \lambda f}$$

solved by “simulated annealing”

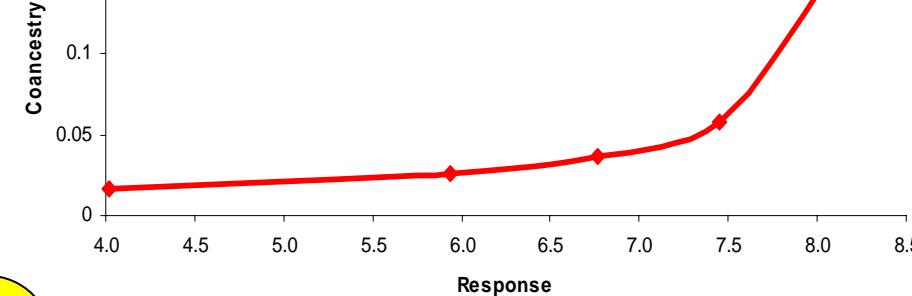
$\Rightarrow \lambda = 0$: truncation selection

$\Rightarrow \lambda \uparrow\uparrow$: only interested on inbreeding

$h^2 = 0.10 \ c^2 = 0.00$

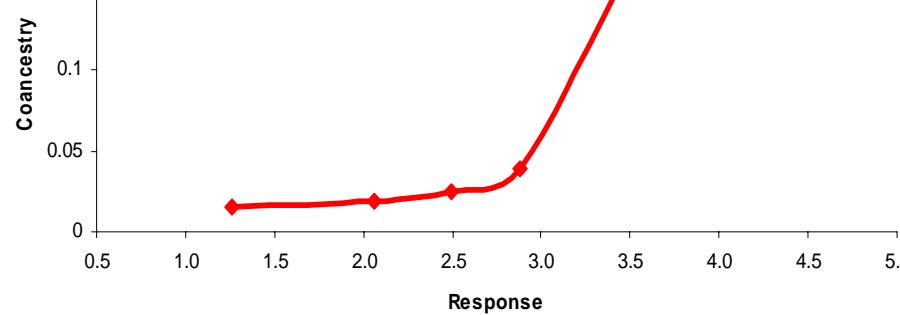


$h^2 = 0.25 \ c^2 = 0.00$

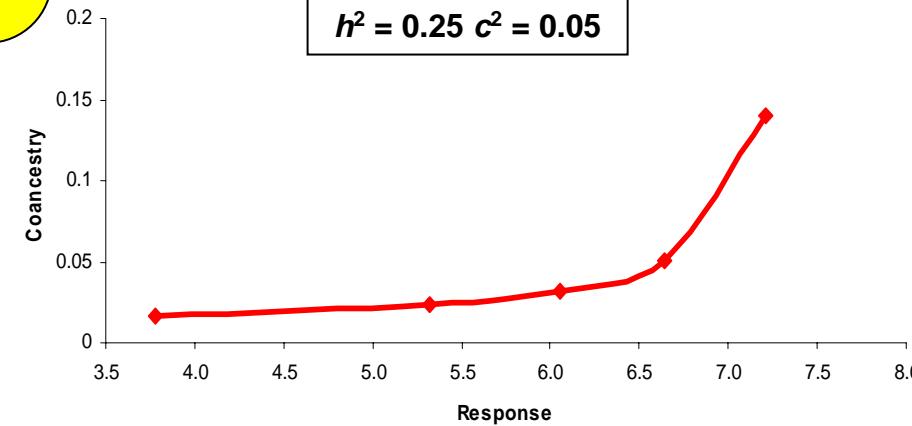


FS

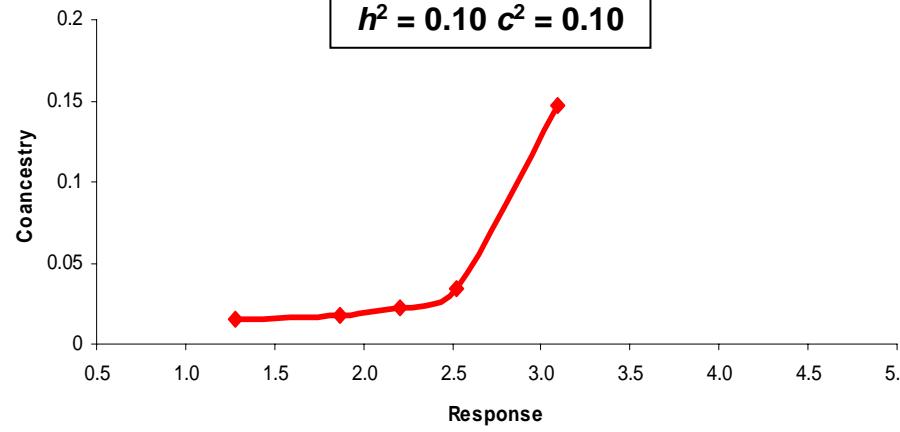
$h^2 = 0.10 \ c^2 = 0.05$



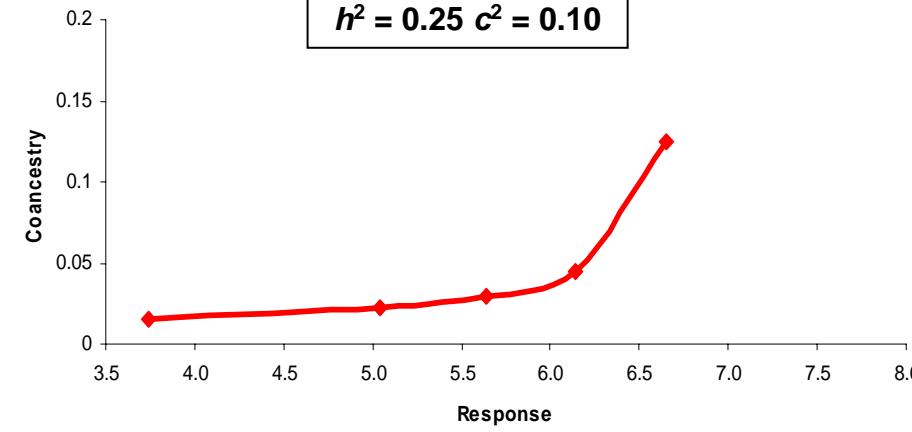
$h^2 = 0.25 \ c^2 = 0.05$



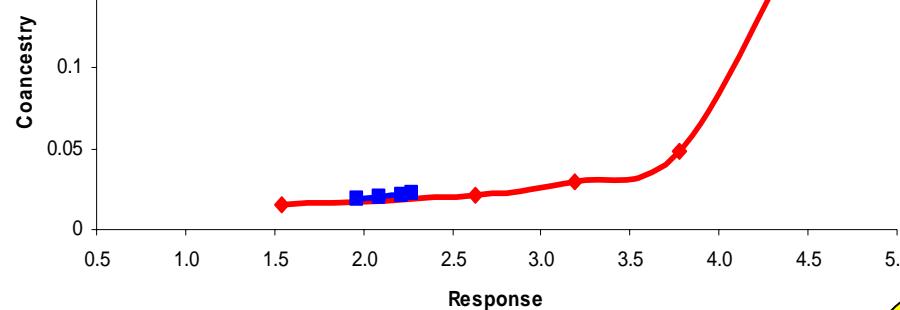
$h^2 = 0.10 \ c^2 = 0.10$



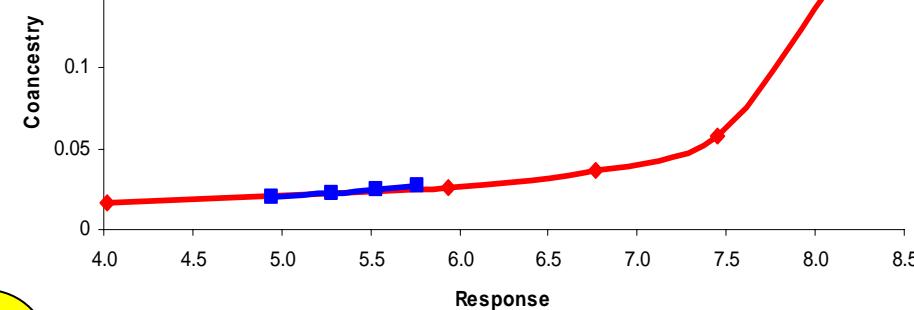
$h^2 = 0.25 \ c^2 = 0.10$



$h^2 = 0.10 \ c^2 = 0.00$

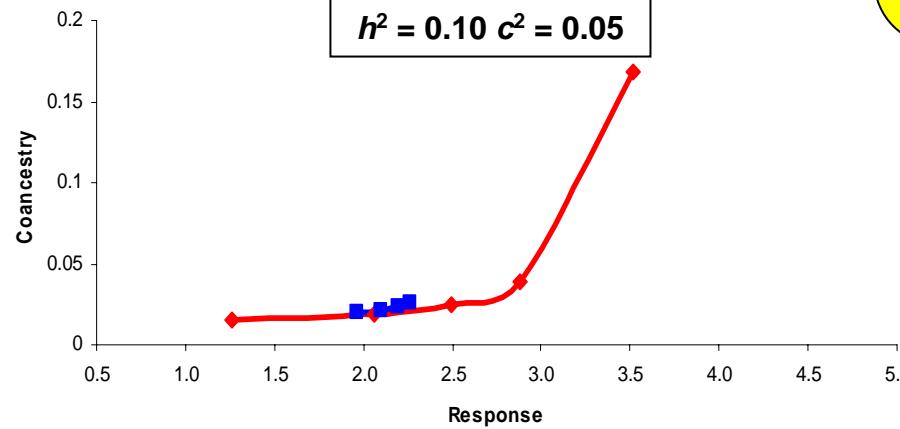


$h^2 = 0.25 \ c^2 = 0.00$

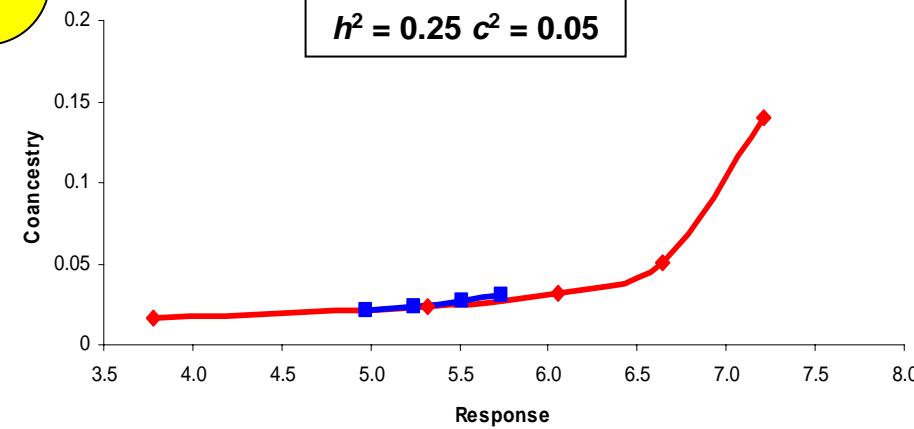


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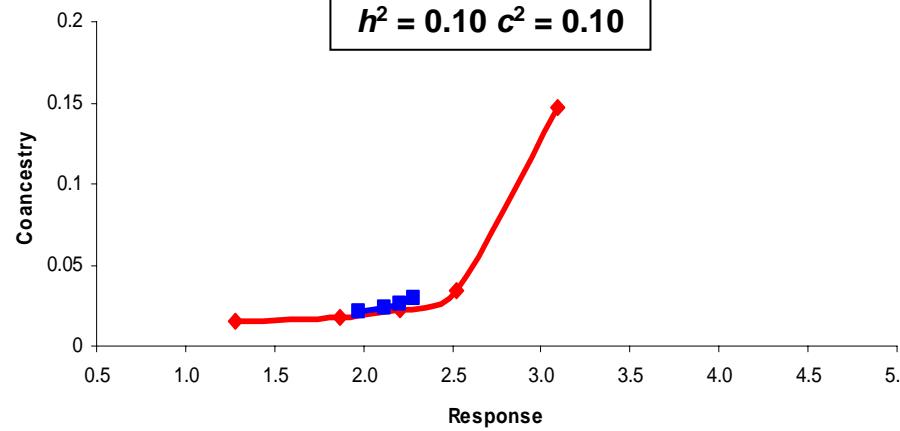
$h^2 = 0.10 \ c^2 = 0.05$



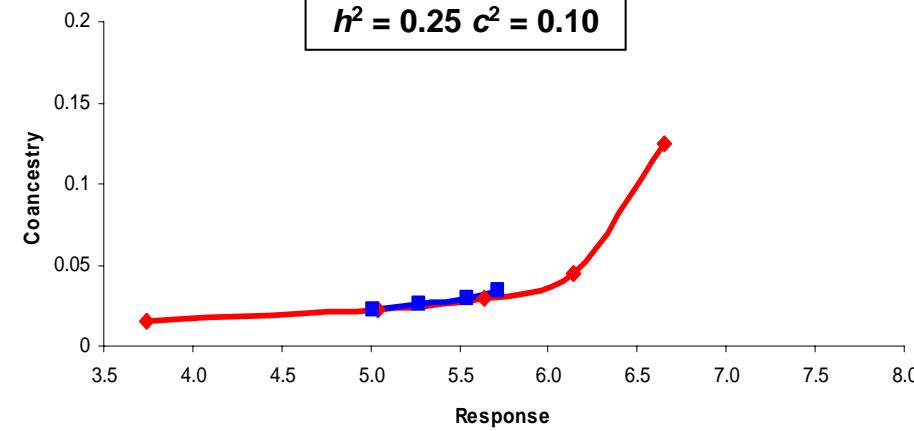
$h^2 = 0.25 \ c^2 = 0.05$



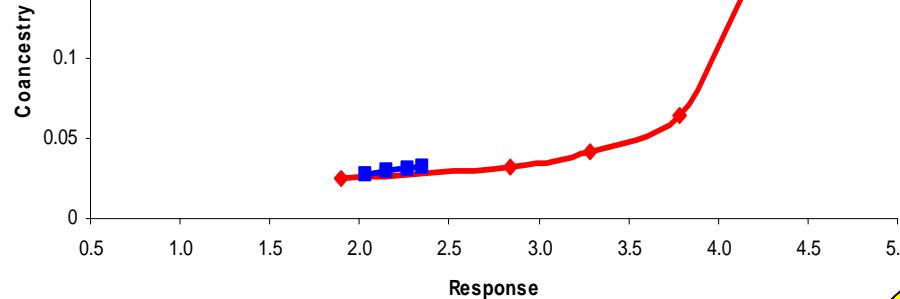
$h^2 = 0.10 \ c^2 = 0.10$



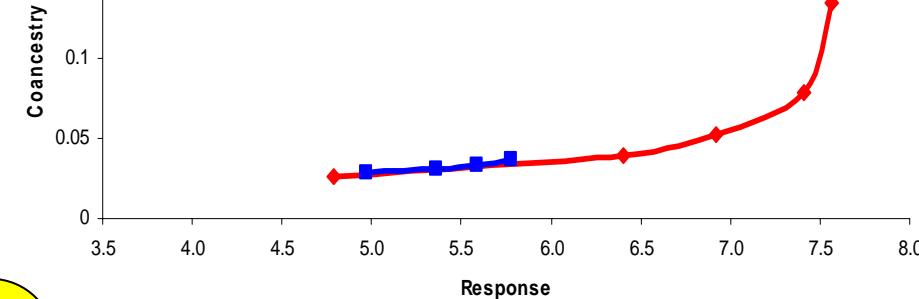
$h^2 = 0.25 \ c^2 = 0.10$



$$h^2 = 0.10 \ c^2 = 0.00$$

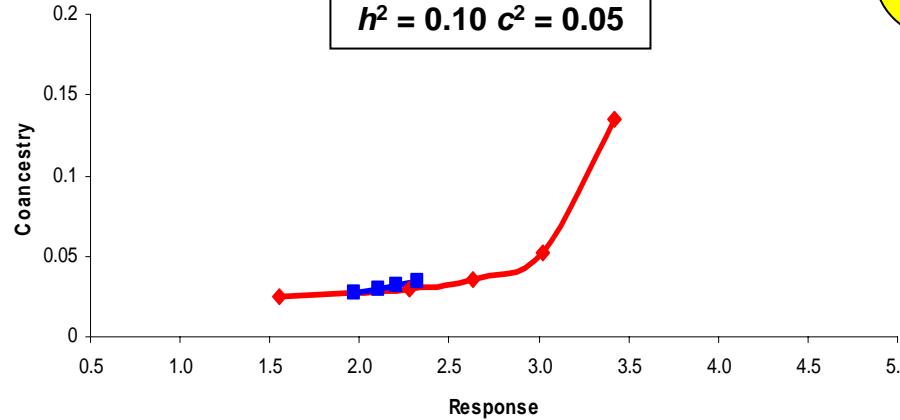


$$h^2 = 0.25 \ c^2 = 0.00$$

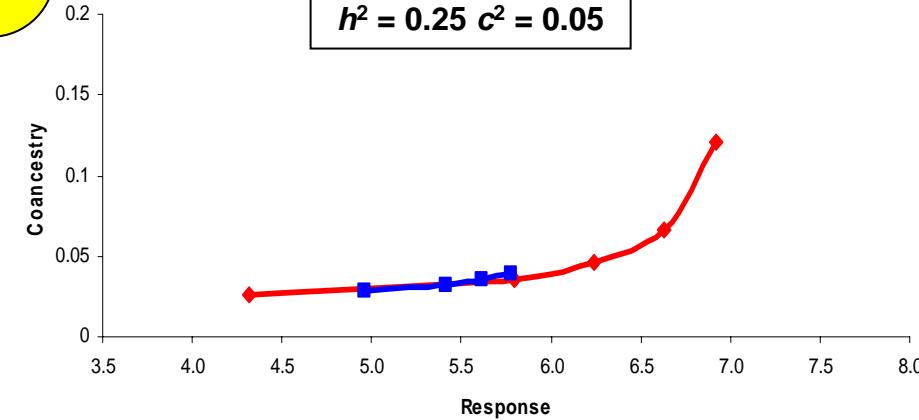


HS

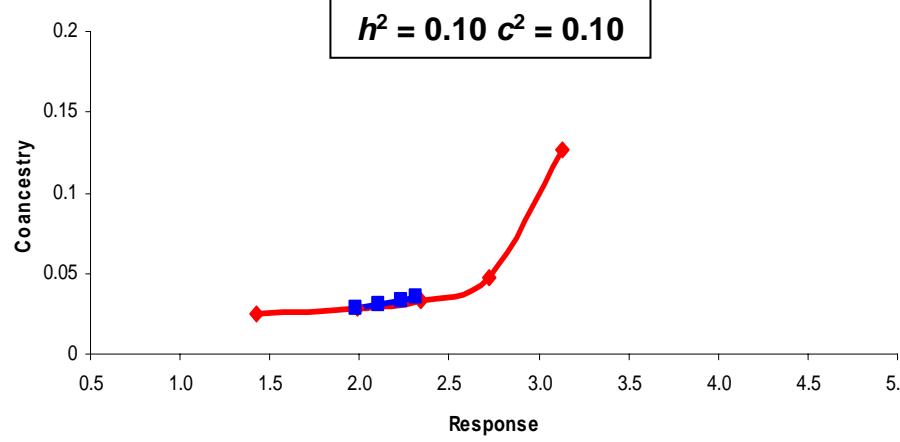
$$h^2 = 0.10 \ c^2 = 0.05$$



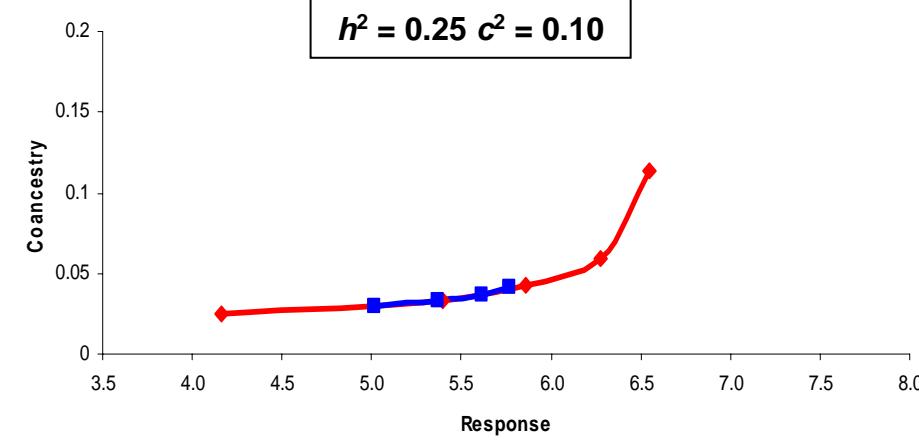
$$h^2 = 0.25 \ c^2 = 0.05$$



$$h^2 = 0.10 \ c^2 = 0.10$$



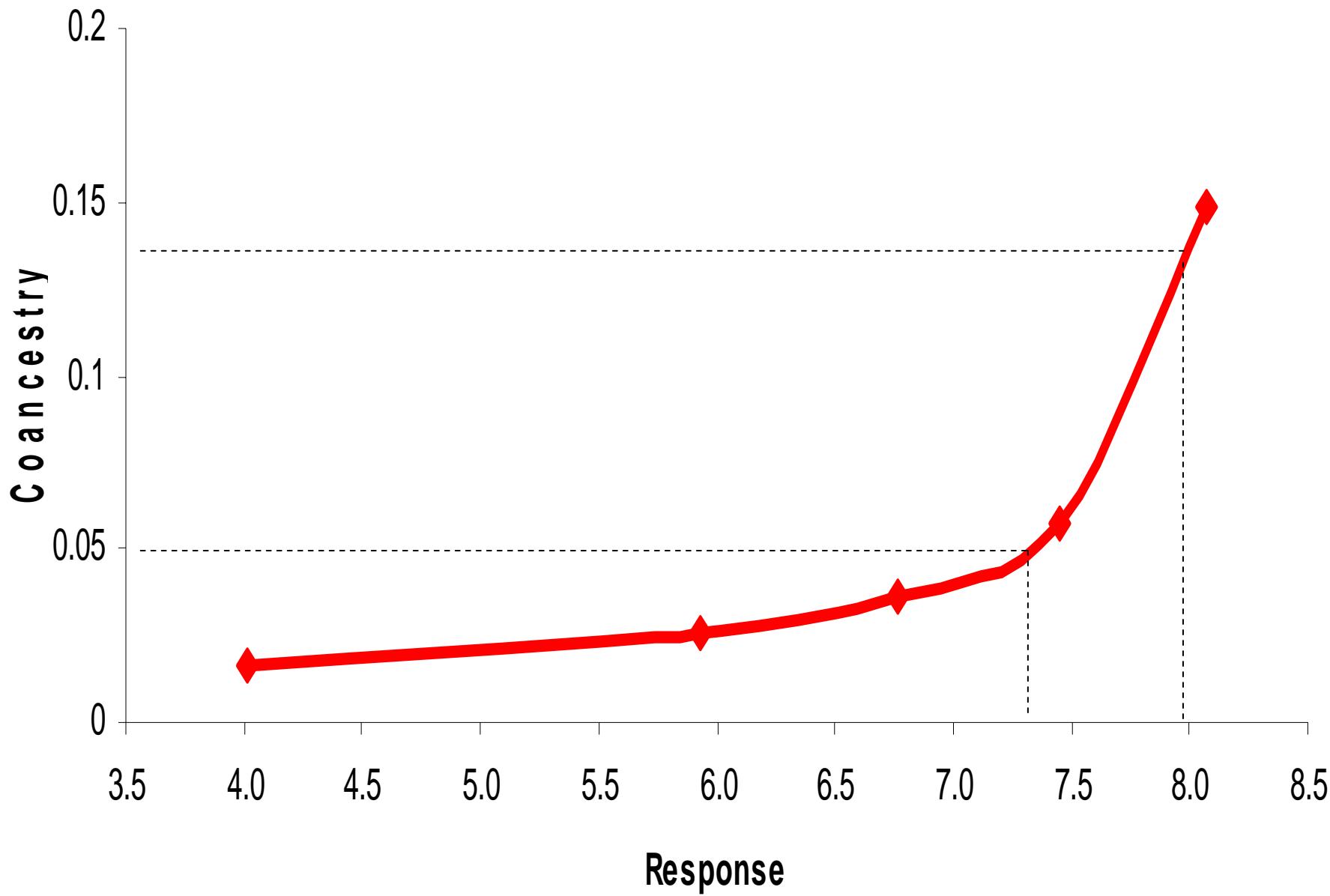
$$h^2 = 0.25 \ c^2 = 0.10$$



| | h^2 | c^2 | Index | Response | | Coancestry of selected | |
|----|-------|-------|-------|----------|------------|------------------------|------|
| | | | | I* | Phenotypic | Index | I* |
| FS | 0,10 | 0 | 4,46 | 3,77 | 2,27 | 0,18 | 0,05 |
| | | 0,05 | 3,51 | 2,87 | 2,27 | 0,17 | 0,04 |
| | | 0,10 | 3,09 | 2,52 | 2,28 | 0,15 | 0,03 |
| | 0,25 | 0 | 8,07 | 7,45 | 5,76 | 0,15 | 0,06 |
| | | 0,05 | 7,21 | 6,64 | 5,74 | 0,14 | 0,05 |
| | | 0,10 | 6,65 | 6,14 | 5,72 | 0,13 | 0,04 |
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| | | 0,10 | 3,13 | 2,72 | 2,31 | 0,13 | 0,05 |
| | 0,25 | 0 | 7,57 | 7,41 | 5,78 | 0,13 | 0,08 |
| | | 0,05 | 6,92 | 6,63 | 5,78 | 0,12 | 0,07 |
| | | 0,10 | 6,55 | 6,27 | 5,77 | 0,11 | 0,06 |

98 - 82 %

62 - 20 %



$$\max \quad \sum_{i=1}^{NF} EBV_i \cdot x_i$$

with the restriction

$$\left(\sum_{i=1}^{NF} \sum_{j=1}^{NF} x_i x_j f_{ij} \right) \leq f_{\max}$$

- ✓ more interest in response

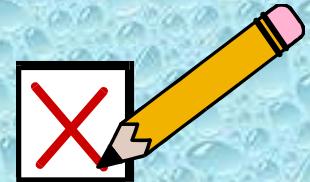
$$\min \quad \left(\sum_{i=1}^{NF} \sum_{j=1}^{NF} x_i x_j f_{ij} \right)$$

with the restriction

$$\sum_{i=1}^{NF} EBV_i \cdot x_i \geq R_{\min}$$

- ✓ more interest in inbreeding

- ✓ relatives' information does affect inbreeding
- ✓ a compromise solution can be found



- ✓ more generations extension
- ✓ implementing control of contributions

**THANK YOU
FOR YOUR
ATTENTION**