Predicting the accuracy of multi-population genomic prediction

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LIVESTOCK RESEARCH
WAGENINGEN UR

Acknowledgements

BREED4FOOD

www.breed4food.com

CRV

www.crv4all.com

Designing breeding programs

Maximize response to selection

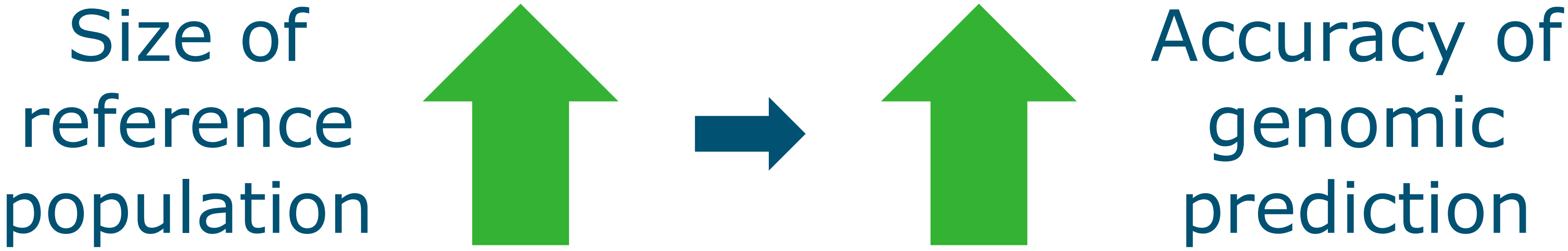
Designing breeding programs

Maximize response to selection

⬆

Accuracy for different designs

Accuracy of genomic selection



Size of reference population ↑ → ↑ Accuracy of genomic prediction

Accuracy of genomic selection

Size of reference population ↑ → ↑ Accuracy of genomic prediction

Combine populations:

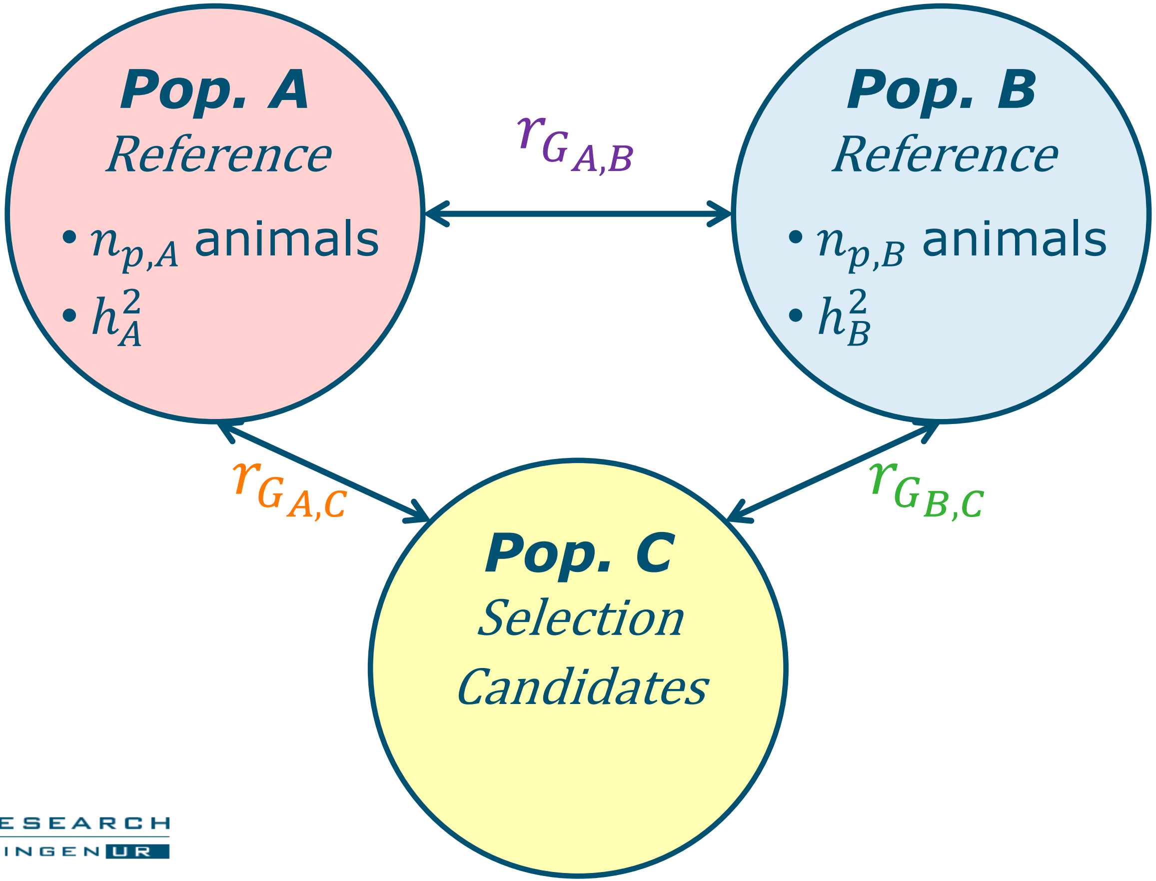
- Countries
- Lines
- Breeds
- Bulls/Cows

Aim of this study

Derive and **validate**:

Prediction equation for accuracy of GEBVs using multiple populations in the reference population

Schematic overview



Pop. A

Reference

- $n_{p,A}$ animals
- h_A^2

$r_{G_{A,B}}$

Pop. B

Reference

- $n_{p,B}$ animals
- h_B^2

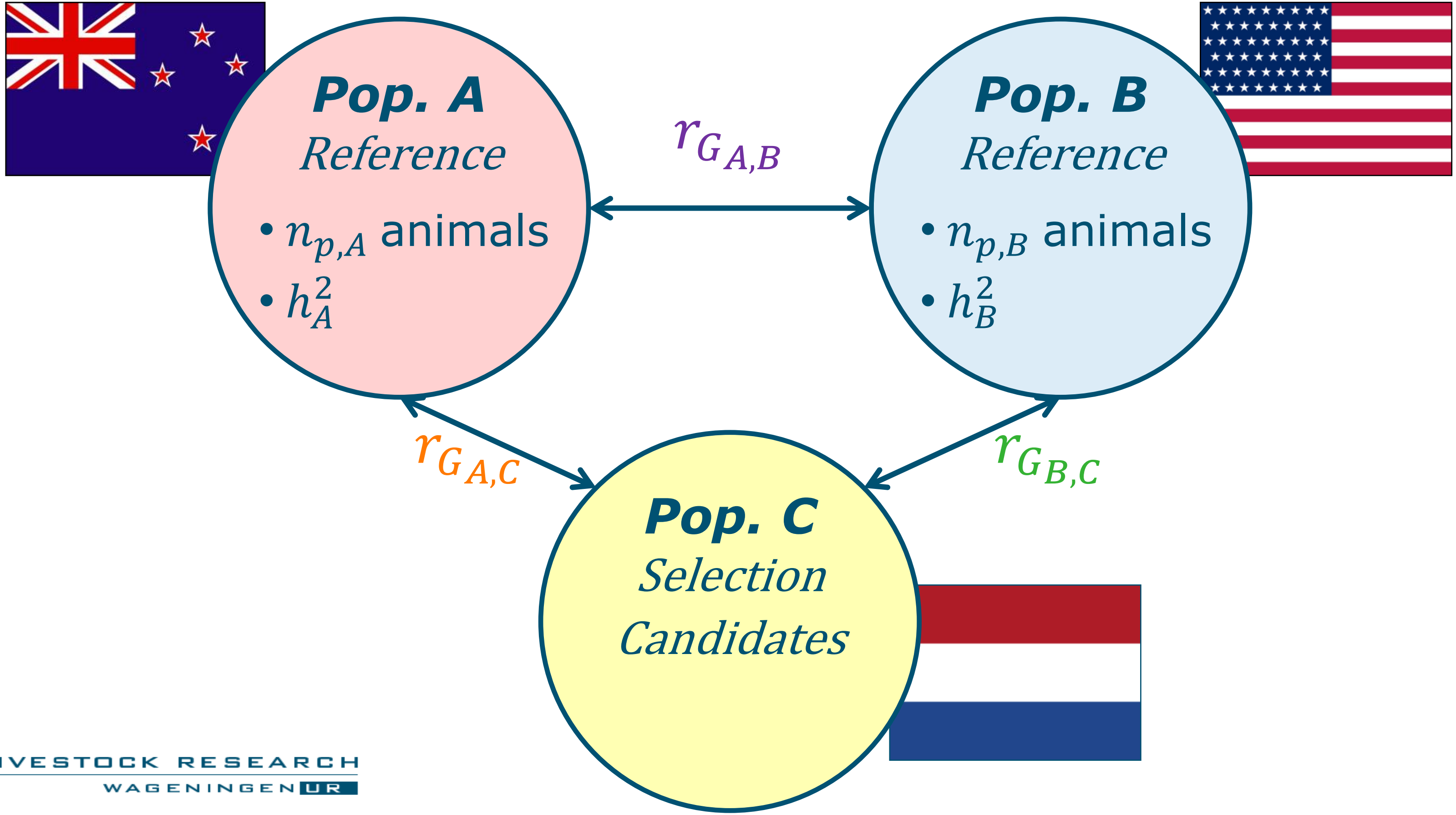
$r_{G_{A,C}}$

$r_{G_{B,C}}$

Pop. C

Selection Candidates

Schematic overview – an example



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$r_{G_{A,B}}$

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Reference

- $n_{p,B}$ animals
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$r_{G_{A,C}}$

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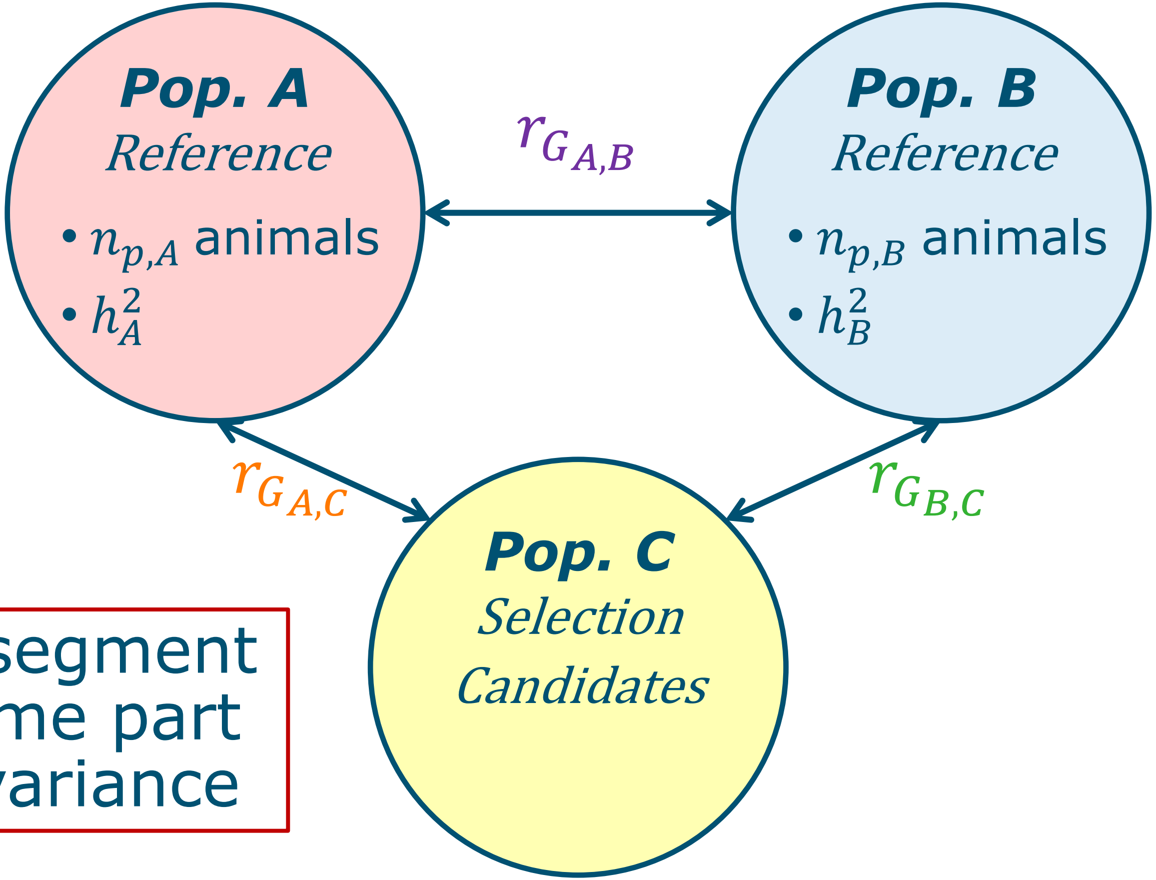
Pop. C

Selection Candidates

Schematic overview



Pop. A

Reference

- $n_{p,A}$ animals
- h_A^2

Pop. B

Reference

- $n_{p,B}$ animals
- h_B^2

Pop. C

Selection Candidates

$r_{G_{A,B}}$

$r_{G_{A,C}}$

$r_{G_{B,C}}$

Each locus/segment explains same part of genetic variance

Input parameters

Reference population

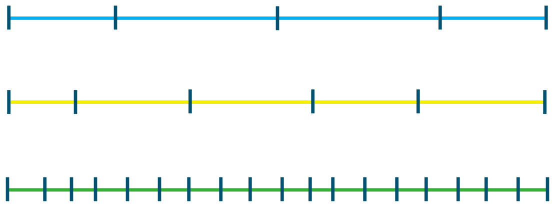
- Number of animals (n_P)
- Heritability (h^2)
- Genetic correlation (r_G)

Selection candidates – Reference population

- Genetic correlations (r_G)
- Number of independent chromosome segments shared (M_e)

M_e across populations

‘Effective number of estimated effects’



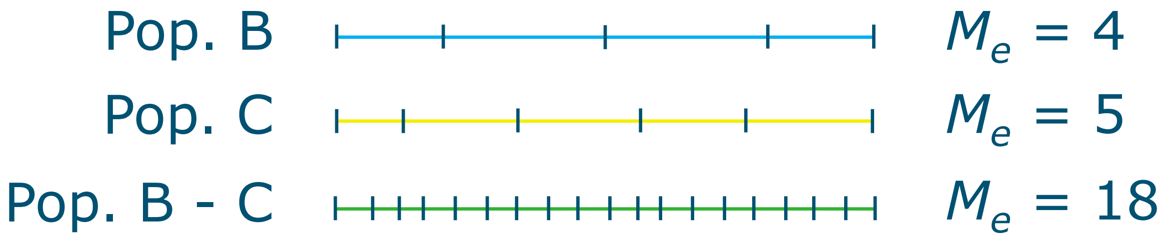
Pop. B $M_e = 4$

Pop. C $M_e = 5$

Pop. B - C $M_e = 18$

M_e across populations

'Effective number of estimated effects'



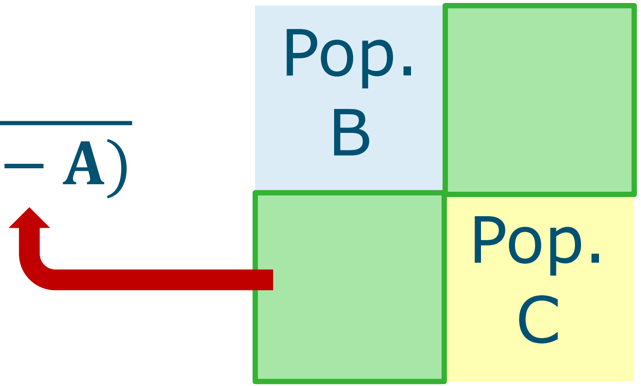
Pop. B $M_e = 4$

Pop. C $M_e = 5$

Pop. B - C $M_e = 18$

Relationship matrix

$$M_{e_{B,C}} = \frac{1}{Var(\mathbf{G} - \mathbf{A})}$$



Input parameters

Reference population

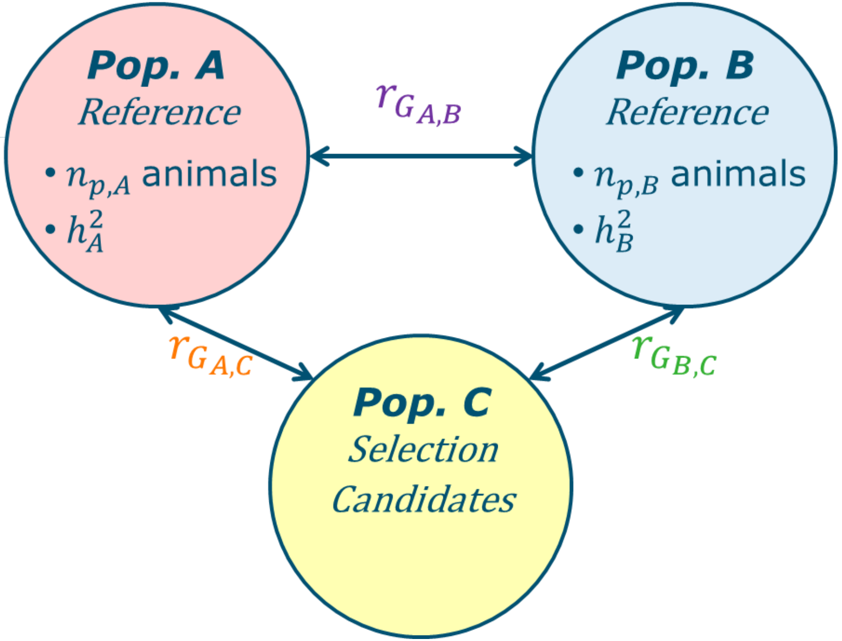
- Number of animals (n_P)
- Heritability (h^2)
- Genetic correlation (r_G)

Selection candidates – Reference population

- Genetic correlations (r_G)
- Number of independent chromosome segments shared (M_e)

$$r_{GEBV_{A+B,C}} = \sqrt{\begin{bmatrix} r_{G_{A,C}}\sqrt{\frac{h_A^2}{M_{e_{A,C}}}} & r_{G_{B,C}}\sqrt{\frac{h_B^2}{M_{e_{B,C}}}} \end{bmatrix} \begin{bmatrix} \frac{h_A^2}{M_{e_{A,C}}} + \frac{1}{n_{p,A}} & r_{G_{A,B}}\frac{\sqrt{h_A^2 h_B^2}}{\sqrt{M_{e_{A,C}} M_{e_{B,C}}}} \\ r_{G_{A,B}}\frac{\sqrt{h_A^2 h_B^2}}{\sqrt{M_{e_{A,C}} M_{e_{B,C}}}} & \frac{h_B^2}{M_{e_{B,C}}} + \frac{1}{n_{p,B}} \end{bmatrix}^{-1} \begin{bmatrix} r_{G_{A,C}}\sqrt{\frac{h_A^2}{M_{e_{A,C}}}} \\ r_{G_{B,C}}\sqrt{\frac{h_B^2}{M_{e_{B,C}}}} \end{bmatrix}}$$

Derived equation



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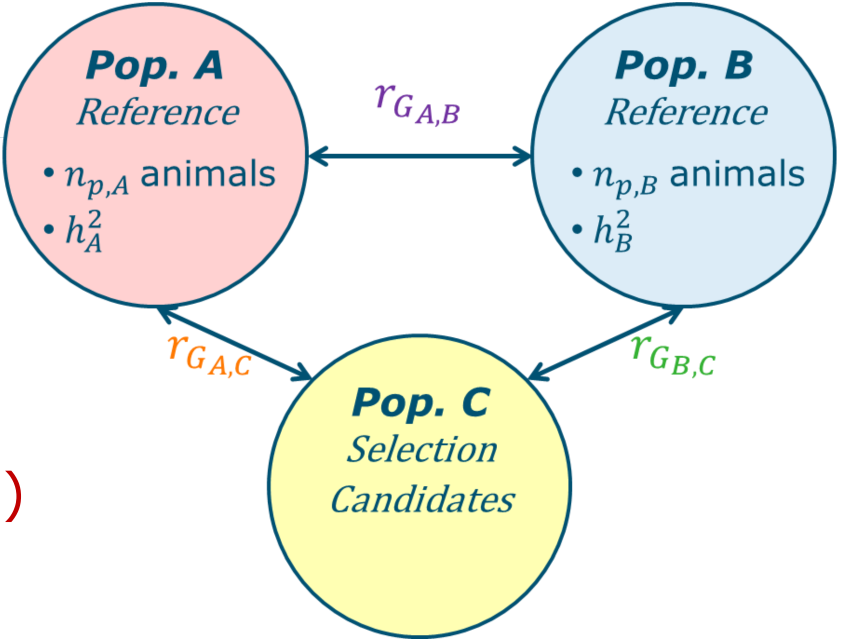
Derived equation



Pop. A
Reference
- $n_{p,A}$ animals
- h_A^2

$r_{G_{A,B}}$

Pop. B
Reference
- $n_{p,B}$ animals
- h_B^2

$r_{G_{A,C}}$

$r_{G_{B,C}}$

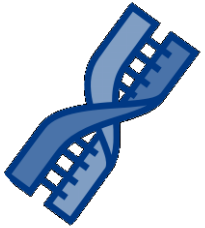
Pop. C
Selection Candidates

1 population in reference

→ Equal to Daetwyler *et al.* (2008)

$$r_{GEBV_{A+B,C}} = \sqrt{\begin{bmatrix} r_{G_{A,C}}\sqrt{\dfrac{h_A^2}{M_{e_{A,C}}}} & r_{G_{B,C}}\sqrt{\dfrac{h_B^2}{M_{e_{B,C}}}} \end{bmatrix} \begin{bmatrix} \dfrac{h_A^2}{M_{e_{A,C}}} + \dfrac{1}{n_{p,A}} & r_{G_{A,B}}\dfrac{\sqrt{h_A^2 h_B^2}}{\sqrt{M_{e_{A,C}} M_{e_{B,C}}}} \\ r_{G_{A,B}}\dfrac{\sqrt{h_A^2 h_B^2}}{\sqrt{M_{e_{A,C}} M_{e_{B,C}}}} & \dfrac{h_B^2}{M_{e_{B,C}}} + \dfrac{1}{n_{p,B}} \end{bmatrix}^{-1} \begin{bmatrix} r_{G_{A,C}}\sqrt{\dfrac{h_A^2}{M_{e_{A,C}}}} \\ r_{G_{B,C}}\sqrt{\dfrac{h_B^2}{M_{e_{B,C}}}} \end{bmatrix}}$$

Simulations for validation



Genotypes of

1033 HF animals

422 405 SNPs

50 000 candidate QTL

(Random or Low MAF)

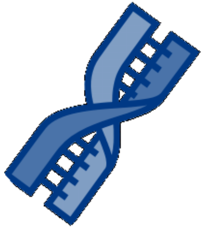
Phenotypes

Simulated

(4000 QTL)

TBV + E

Simulations for validation



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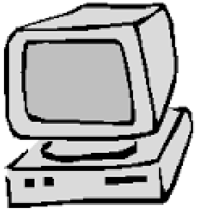


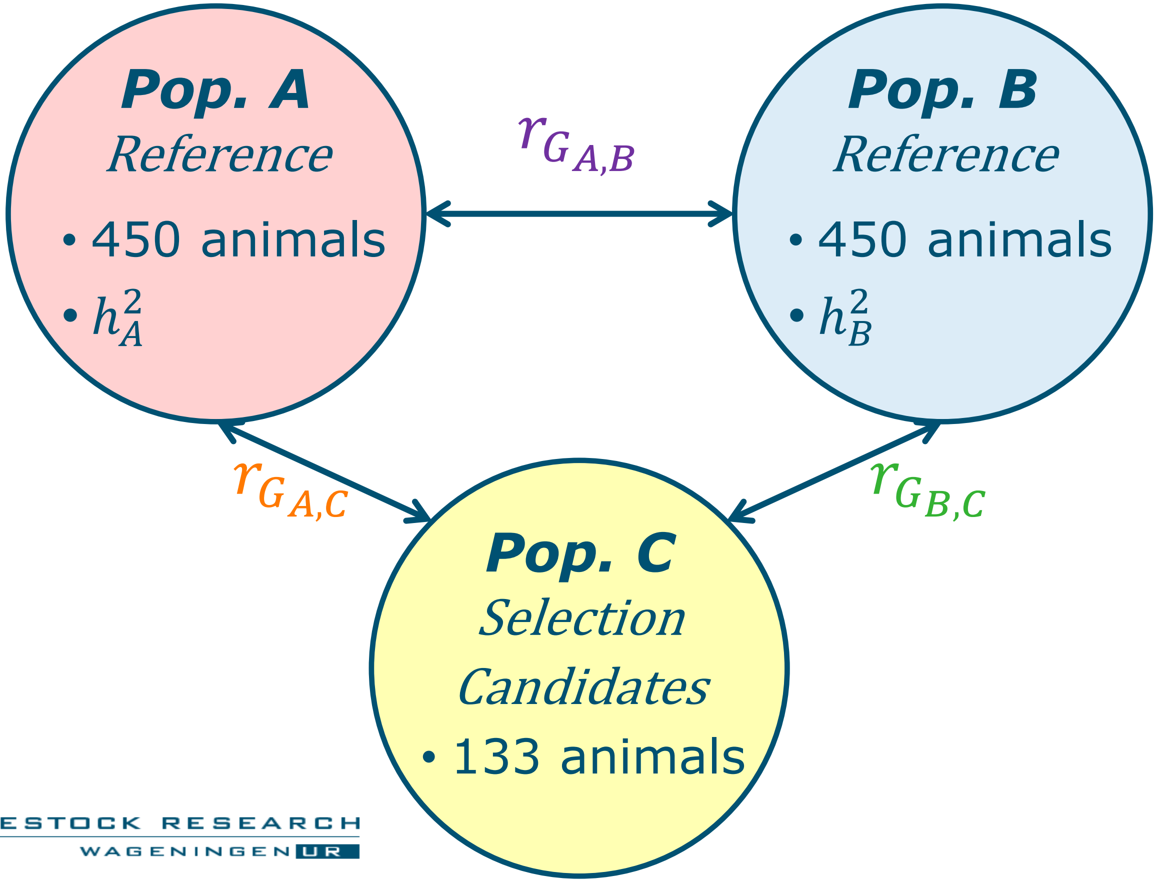
Breeding value (GEBV) estimation

Multi-trait GBLUP

Empirical Accuracy

Correlation GEBV with TBV

Populations for validation



Pop. A

Reference

- 450 animals
- h_A^2

$r_{G_{A,B}}$

Pop. B

Reference

- 450 animals
- h_B^2

$r_{G_{A,C}}$

$r_{G_{B,C}}$

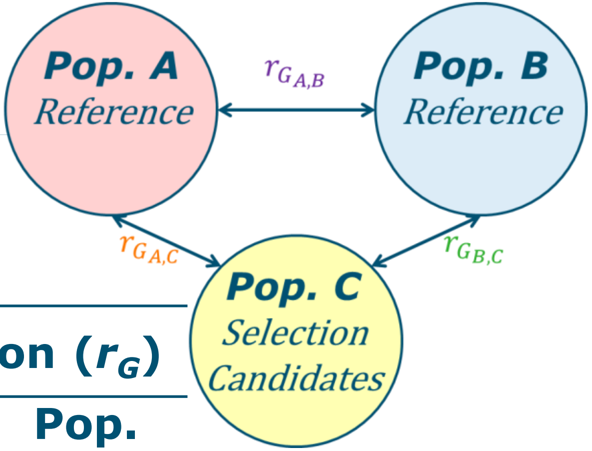
Pop. C

Selection Candidates

- 133 animals

Division:
Half-sib families kept in same population

Scenarios for validation



Pop. A
Reference

Pop. B
Reference

Pop. C
Selection Candidates

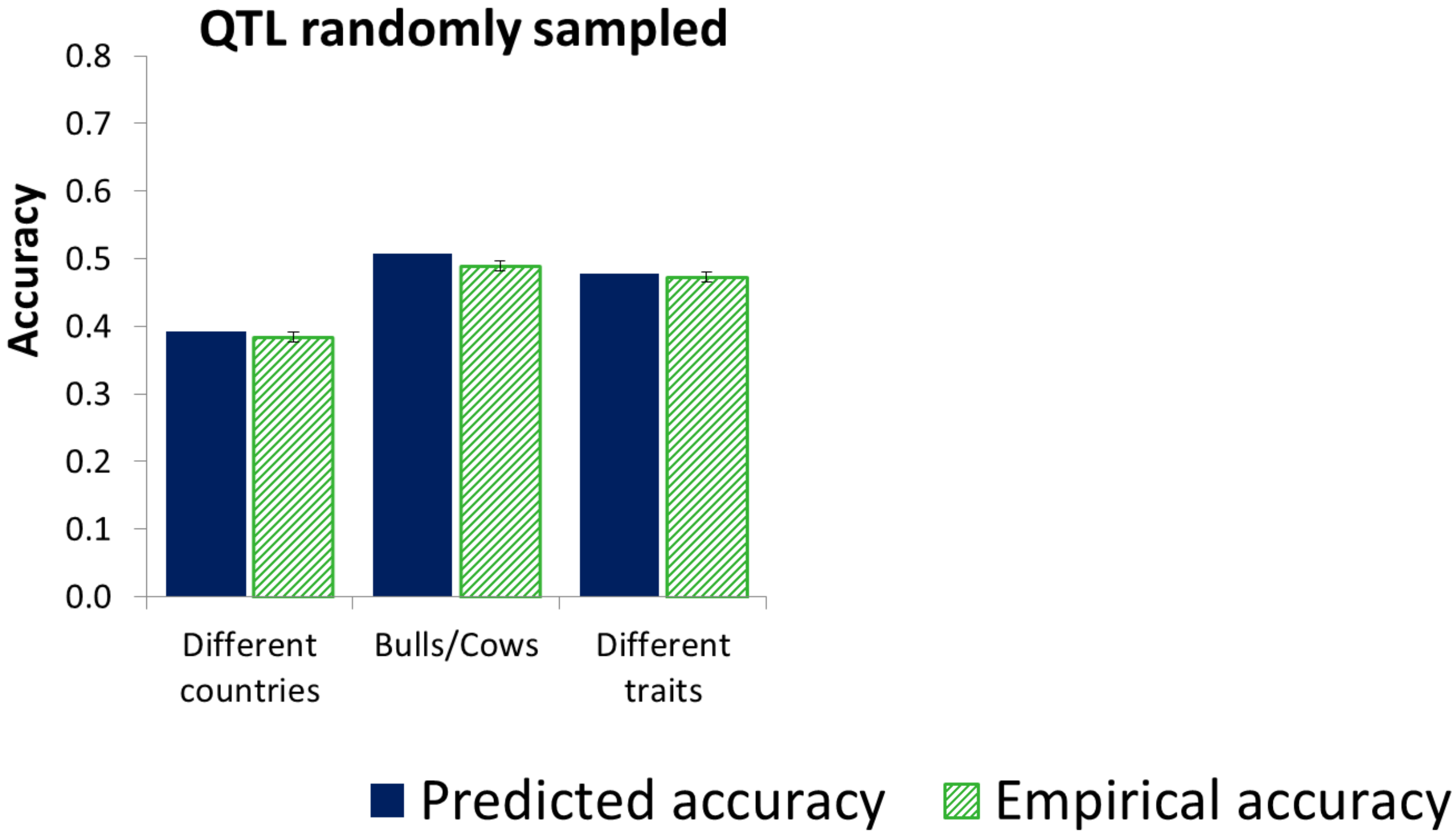
$r_{G_{A,B}}$

$r_{G_{A,C}}$

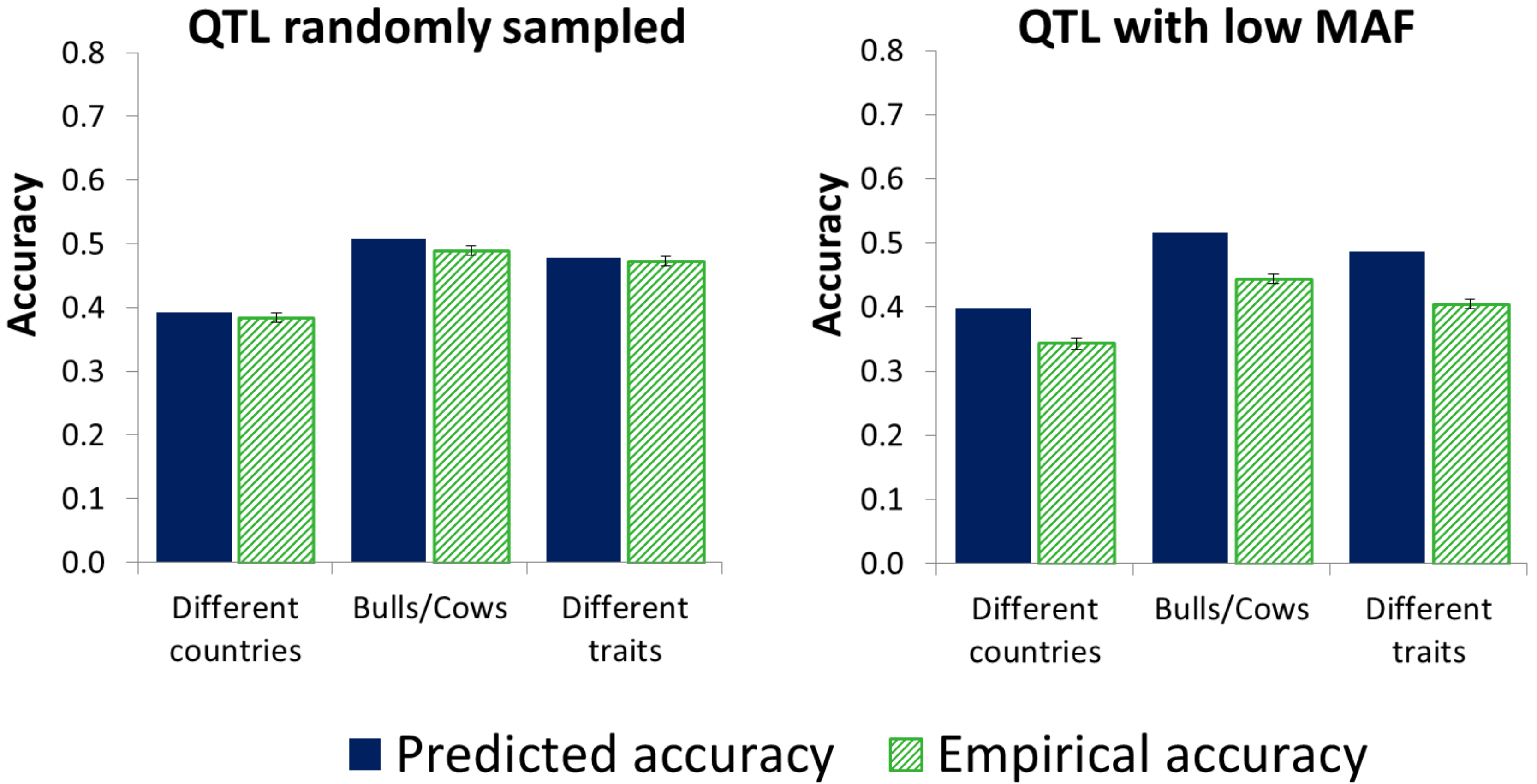
$r_{G_{B,C}}$

	Heritability (h^2)		Genetic correlation (r_G)		
Scenarios	**Pop. A**	**Pop. B**	**Pop. A - B**	**Pop. A – C**	**Pop. B - C**
Different countries	0.95	0.95	0.6	0.8	0.4
Bulls/cows	0.95	0.30	1.0	1.0	1.0
Different traits	0.95	0.30	0.6	1.0	0.6

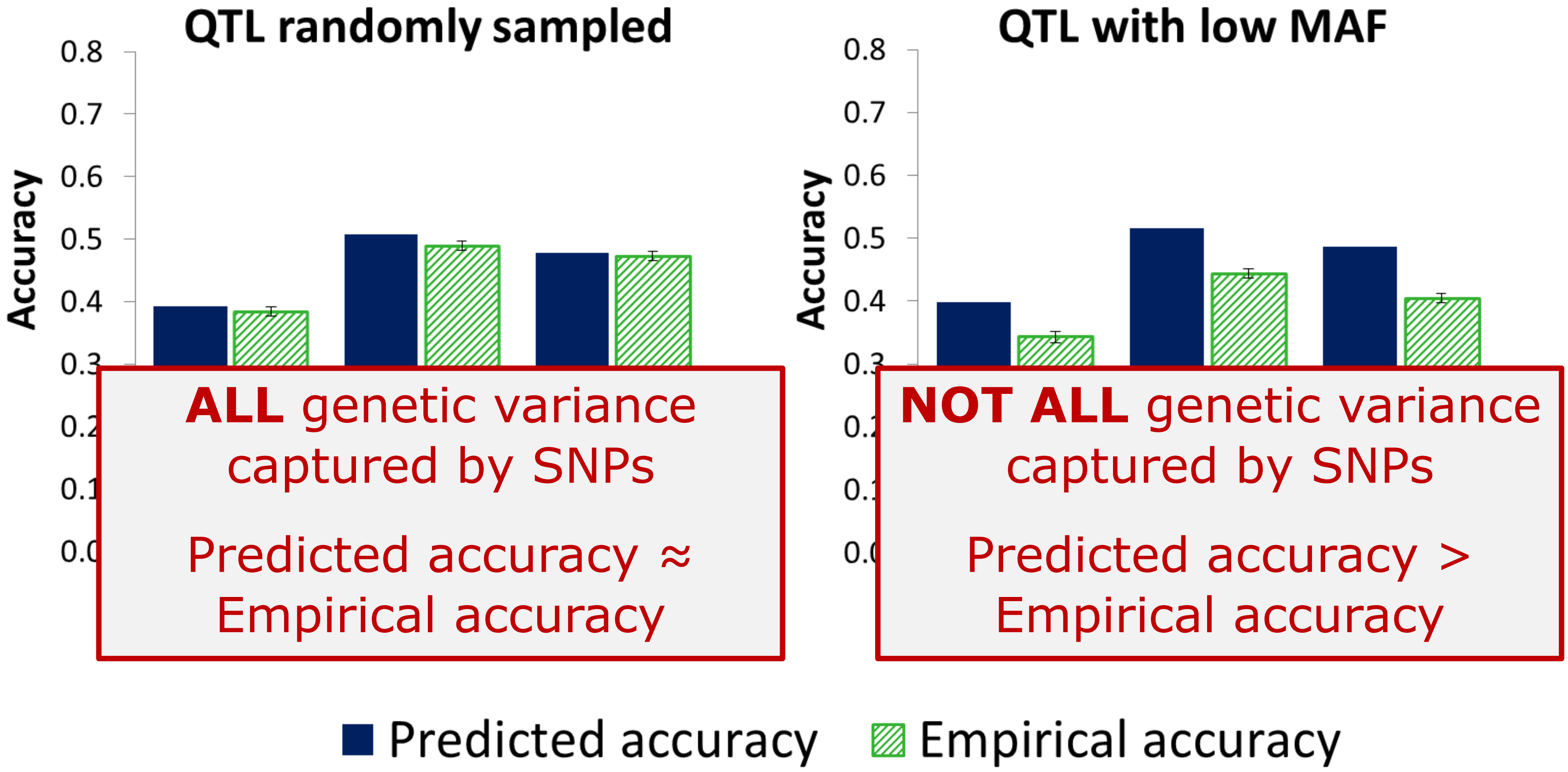
Results of validation



Results of validation



Results of validation



ALL genetic variance captured by SNPs

Predicted accuracy ≈ Empirical accuracy

NOT ALL genetic variance captured by SNPs

Predicted accuracy > Empirical accuracy

Conclusion

Equation accurately predicts GEBV accuracy

- Multiple populations:
    - Countries
    - Bulls/Cows
    - Traits
    - Breeds?
- All genetic variance captured

Conclusion

Equation accurately predicts GEBV accuracy

- Multiple populations:
    - Countries
    - Bulls/Cows
    - Traits
    - Breeds?

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- All genetic variance captured

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Thank you!