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Accuracy of Genomic Selection in a Substructured Population of Large White Pigs

The Problem

In pig breeding, subpopulations within a breed are often
⇨ rather small
⇨ largely genetically disconnected
⇨ highly variable in level and accuracy of breeding values

Is it promising to implement a joint genomic breeding value estimation under these structural conditions?

Animals, Data Processing, Methods

Animals of two Large White populations were genotyped
Population 1: ■ 361 boars ○ 180 sows ⇨ 541 in total
Population 2: ■ 381 boars ○ 503 sows ⇨ 884 in total

Genotyping with Illumina PorcineSNP60V2 BeadChip

Quality control and filtering:
- only SNPs with known autosomal position
- call rate > 0.95 per locus and per animal
- minor allele frequency > 0.01
- missing genotypes imputed with Beagle [1]
⇨ 1'425 animals with 45'210 SNPs

Phenotypes are based on BLUP EBVs for 'piglets born alive'
- old boars ⇨ high accuracy, high and low EBVs
- young sows ⇨ low accuracy, high EBVs

Deregressed proofs (DRPs) obtained with the approach of Garrick *et al.* [2]

Genomic prediction via GBLUP[3] across or within populations

Predictive ability defined as correlation r_{DG} between DRPs and genomic breeding values was assessed by random fivefold cross-validations with 20 replicates
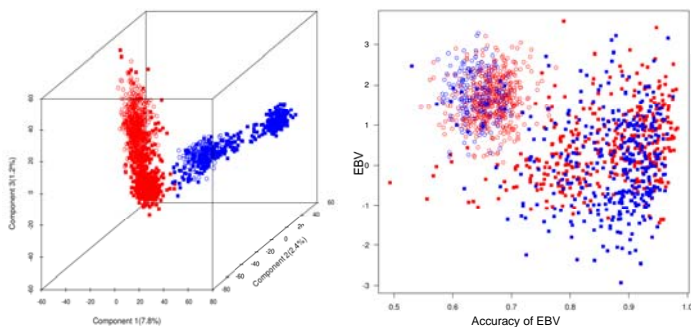
Populations are genetically disconnected: Plot of the first three principal components

Boars ■ ■ and sows ○○ differ systematically in accuracy and range of EBVs

References and Acknowledgements

[1] Browning, S. R. & Browning, B. L. (2007) *Am. J. Hum. Gen.*, **81**: 1084
[2] Garrick, D. J., Taylor, J. F. & Fernando, R. L. (2009) *Genet. Sel. Evol.*, **41**: 55
[3] VanRaden, P. M. (2008) *J. Dairy Sci.,* **91**:4414.

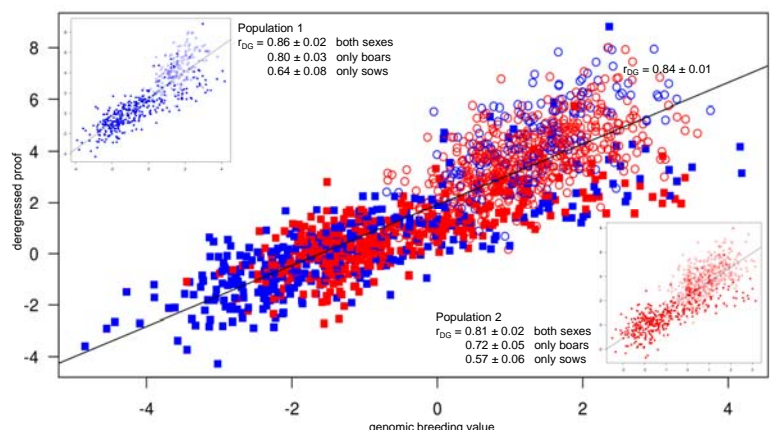## Conclusions

⇨ A joint genomic breeding value estimation across subpopulations can be implemented efficiently
⇨ The predictive ability across subpopulations is substantial (0.84)
⇨ Predictive abilities within subpopulations vary between 0.81 and 0.86
⇨ Joint genomic breeding value estimation in a substructured population improves predictive abilities within subpopulations only marginally
⇨ <u>But note:</u> Accuracies of genomic breeding values, defined as correlation between genomic and true breeding values, will differ from the reported predictive abilities and still need to be determined

Predictive Ability Across and Within Subpopulations

Joint analysis   Analyses within populations

Training set ⇨
Validation set ⇨
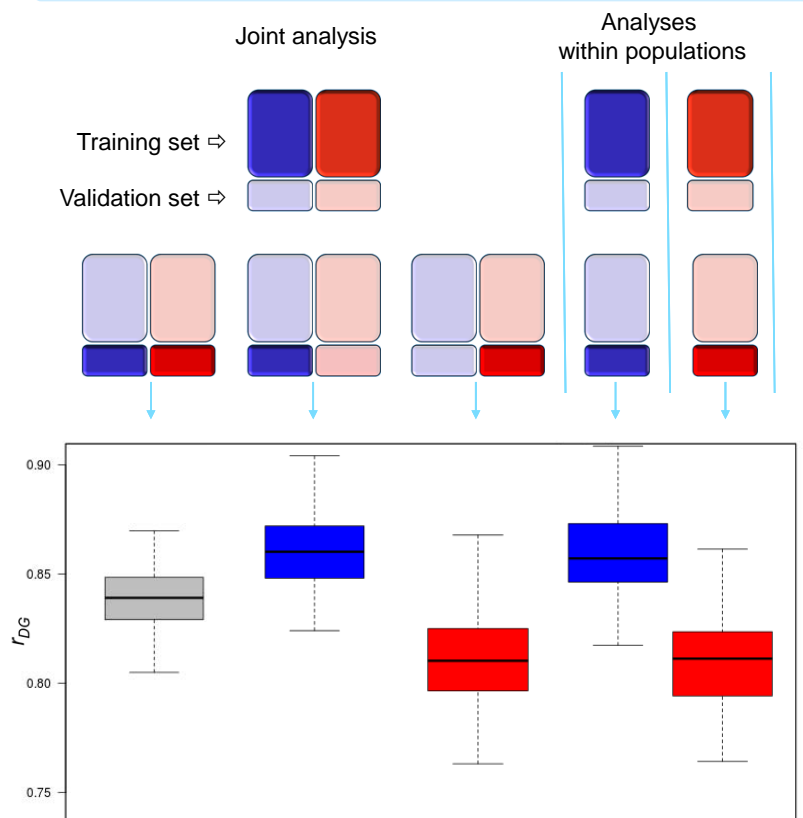
Predictive ability r_{DG} defined as correlation between deregressed proofs and genomic breeding values is almost identical when obtained with the joint analysis (left) or the within population analyses (right)

Population 1
r_{DG} = 0.86 ± 0.02 both sexes
0.80 ± 0.03 only boars
0.64 ± 0.08 only sows

r_{DG} = 0.84 ± 0.01

Population 2
r_{DG} = 0.81 ± 0.02 both sexes
0.72 ± 0.05 only boars
0.57 ± 0.06 only sows

Deregressed proofs and genomic breeding values are highly correlated both in the joint analysis (large window) and the within population analyses (small windows)