

Multi-breed genomic prediction using biological information

Breed4Food seminar, 12th July, 2018

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ACKNOWLEDGEMENT

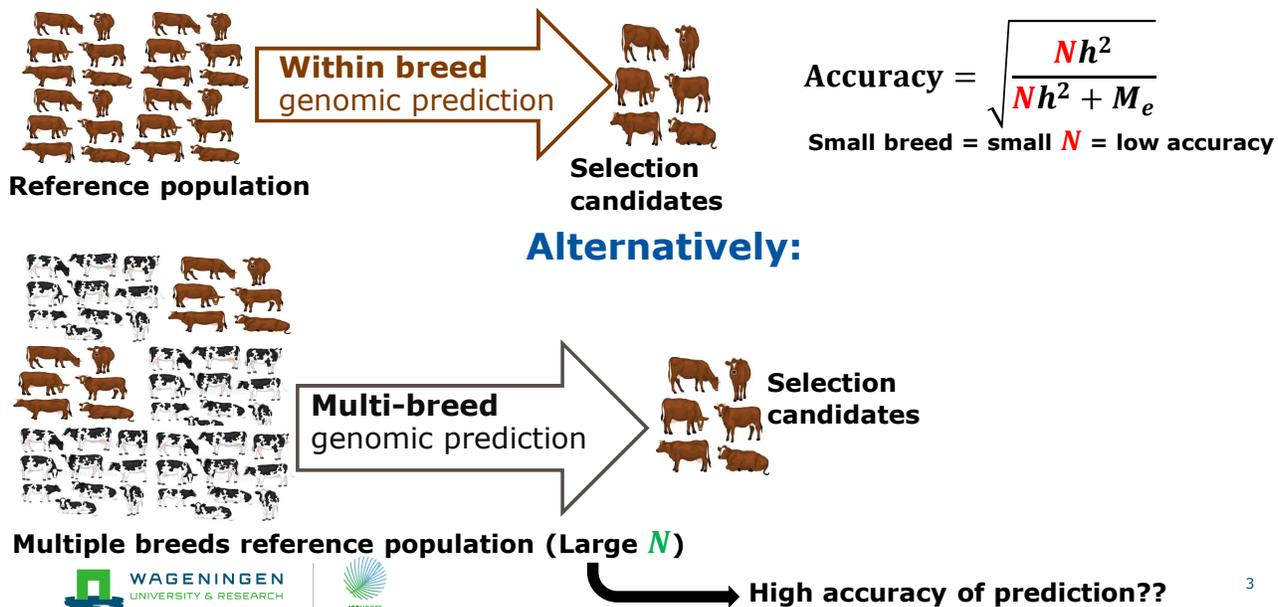


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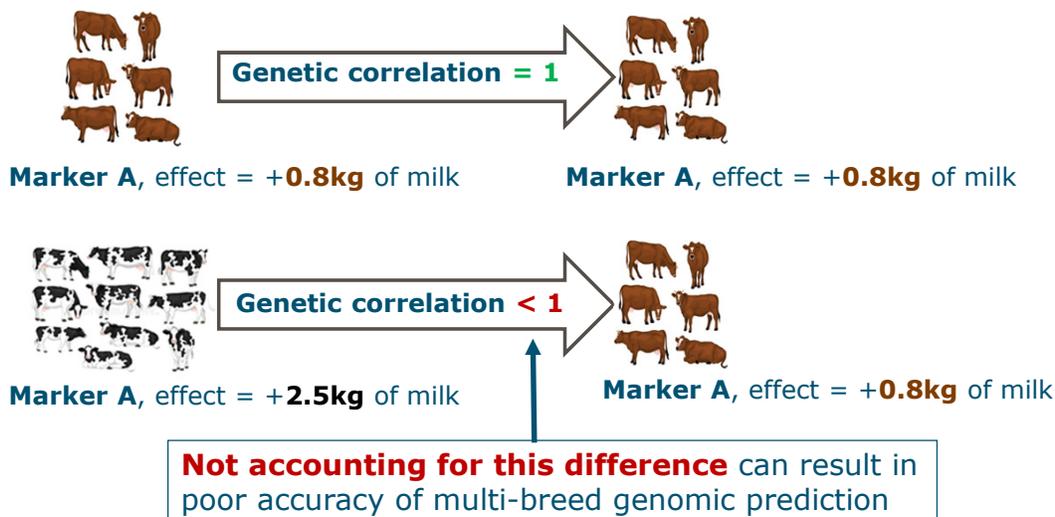
Applied and
Engineering Sciences

Multi-breed genomic prediction



3

Challenges with multi-breed genomic prediction (1)



4

Challenges with multi-breed genomic prediction (2)



Genetic correlation = 0.8

Does not depend on LD patterns across breeds



Effect of causal variants

Effect of causal variants



Genetic correlation = 0.2

Depends on LD patterns across breeds



Effect of non-causal variants

Effect of non-causal variants

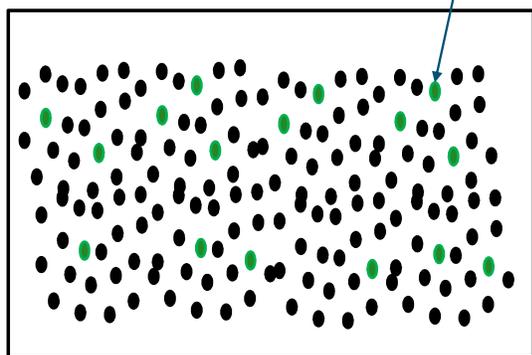
Difference in covariance structure of variants effects across breeds

❖ This difference must be accounted for



Challenges with multi-breed genomic prediction (3)

.....the use of whole genome sequence data

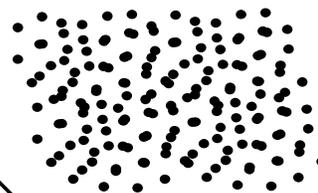


All markers in WGS

Effects are diluted by noise

Pre-select the most important markers and model them differently

Non-causal markers in WGS



Causal markers in WGS

There is need for an efficient marker pre-selection strategy



Objective



Develop and evaluate a multi-breed genomic prediction model that:

- ❖ Appropriately **utilise information on pre-selected functional markers**
- ❖ Capture **residual genetic variance** missed by pre-selected functional markers
- ❖ Weigh reference breeds information by their **genetic correlation** with validation breed

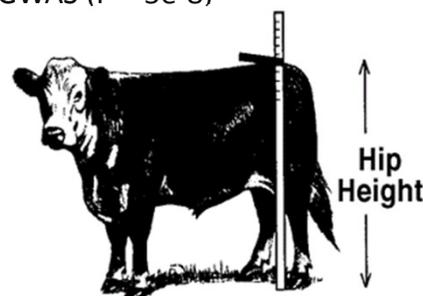
Material & Methods

Phenotype: Stature on **5503** Dutch Holsteins & **595** New Zealand Jerseys

Summary level results from a meta-GWAS on stature (58,265 Individuals)

Sets of DNA markers used in this study:

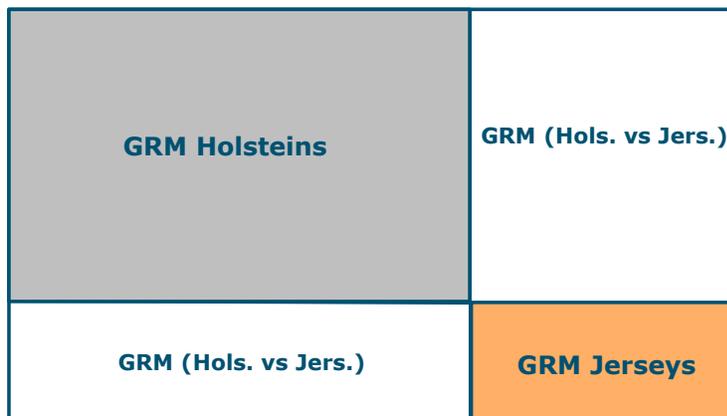
- **COJO8:** Independently significant markers from the meta-GWAS ($P = 5e-8$)
- **50K:** traditional 50k markers excluding COJO8 markers
- **50K+COJO8 :** COJO8 markers added to 50K



Statistical analyses (model 1)

- Individuals across breeds are related at all markers

A **single GRM** fitted in a bivariate model

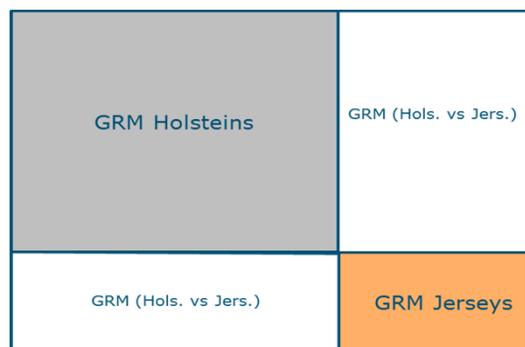


Statistical analyses (model 2)

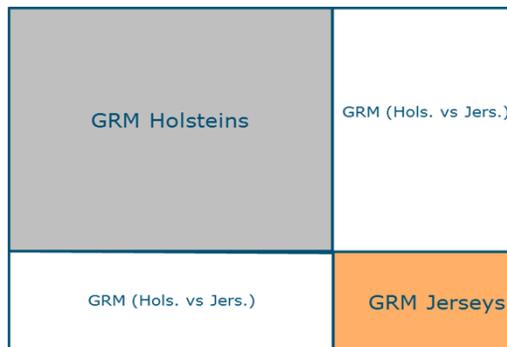
- Individuals across breeds are related at all markers
- **Differences in effect size variance** between **functional** and **non-functional** markers

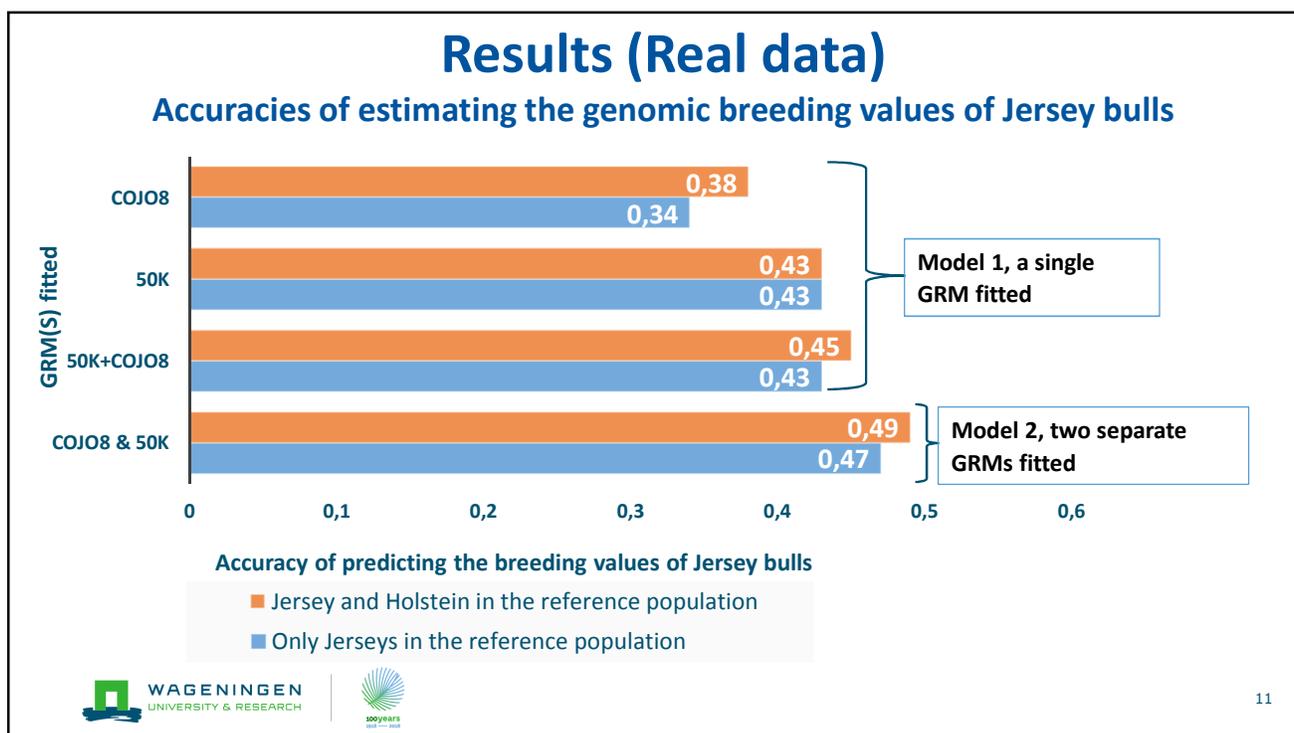
2 different GRMs fitted in a bivariate model

GRM1 (functional markers)



GRM2 (remaining markers)





Conclusion: Recipe for multi-breed Genomic prediction

- ❖ **Pre-select functional markers** from whole genome sequence
 - Weigh the pre-selected markers differently from others
- ❖ Use the remaining markers to **capture residual genetic variance**
- ❖ Weigh the information of breeds in the reference population by **their genetic correlation** with the validation breed



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