Accuracy of genomic selection using multi breed reference populations

B. Gredler[1], J. Pryce[2], S. Bolormaa[2], C. Egger-Danner[3], C. Fuerst[3], R. Emmerling[4], J. Sölkner[1], B. Hayes[2]

[1]University of Natural Resources and Life Sciences Vienna
[2]Department of Primary Industries, Victoria
[3]ZuchtData EDV-Dienstleistungen GmbH
[4]Bavarian State Research Center for Agriculture

Introduction

- Accuracy of genomic breeding values (GEBVs) depends on the size of the reference population (e.g. VanRaden et al., 2008; Hayes et al., 2009)
- Assembling large reference populations is a major challenge for breeds with limited number of genotyped animals
- Use prediction equation from one breed to predict GEBVs in other breeds or use multi-breed reference population to predict GEBVs

Objectives

- To predict GEBVs for breeds not included in the reference population
- To predict GEBVs for single breed validation populations based on multi-breed reference populations

Populations

Australian Holstein bulls
Reference: 755 bulls
Validation: 386 bulls

Australian Jersey bulls
Validation: 364 bulls

Austrian/German Fleckvieh bulls
Reference: 1,247 bulls
Validation: 349 bulls

Genotypes

- All bulls were genotyped for 54,001 SNPs using the Illumina Bovine SNP50 Beadchip
- Quality checks within breeds
  - Call Rate, MAF, GC-Score, pedigree checking, …
- Genotypes of all breeds were merged according to SNPs present in all three breeds - 36,986 SNPs

Phenotypes

Daughter yield deviations for

- Milk yield
- Protein yield
- Fat yield
- Fertility
  - Australia: pregnancy within the first 42 days
  - Austria: 56 day non return rate in cows
- Daughter yield deviations were standardized to 0/1 within breed and corrected for breed

Methods

- **GBLUP** (Hayes and Goddard, 2008)
  - Genomic relationship matrix

$$y = 1_n \mu + Zg + e$$

- **BayesA** (Meuwissen et al., 2001)
  - Modified to include polygenic effect

$$y = 1n'\ldots + Xu + Zv + e$$

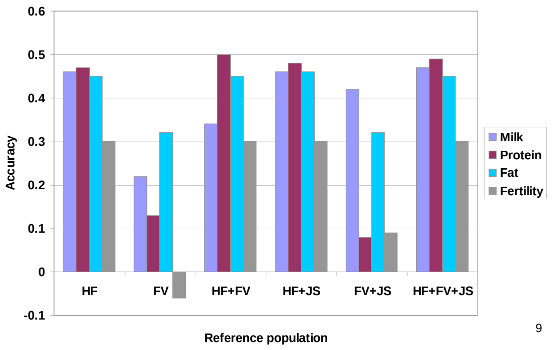
$$GEBV = \hat{v} + X\hat{u}$$

- Accuracy of GEBVs = r(GEBV/EBV)

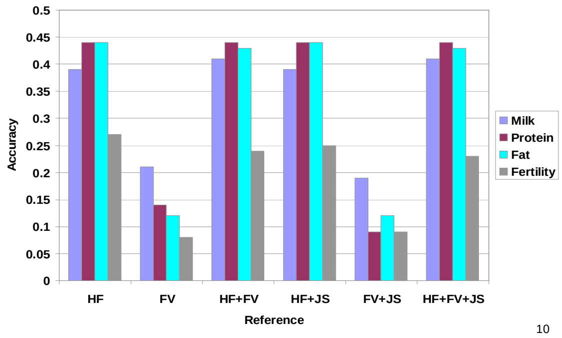
Scenarios

Reference population	N-Reference	Validation population
Single breed		
Holstein	755	Holstein
Fleckvieh	1,247	
Multi-breed		Jersey
Holstein + Fleckvieh	2,002	
Holstein + Jersey	1,119	
Fleckvieh + Jersey	1,611	Fleckvieh
Holstein + Fleckvieh + Jersey	2,366	

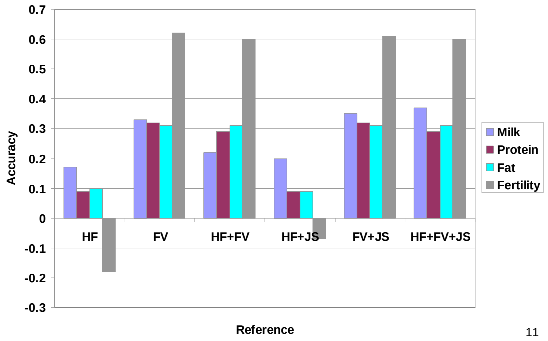
Accuracy of GEBVs for Holstein validation bulls (BayesA)



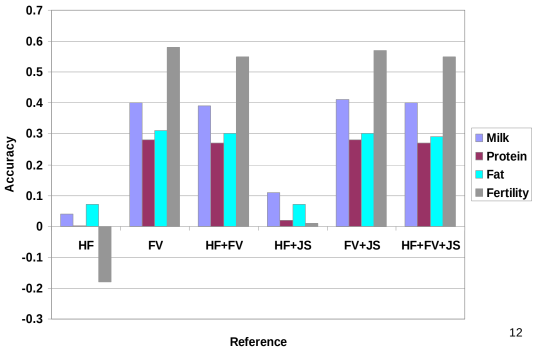
Accuracy of GEBVs for Holstein validation bulls (GBLUP)



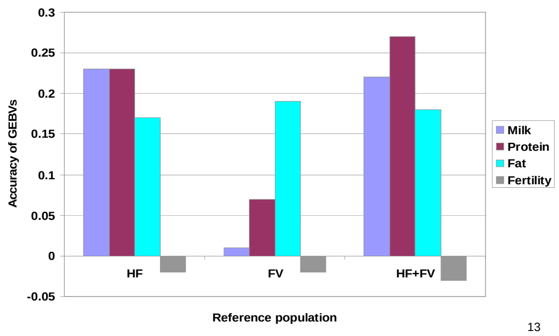
Accuracy of GEBVs for Fleckvieh validation bulls (BayesA)



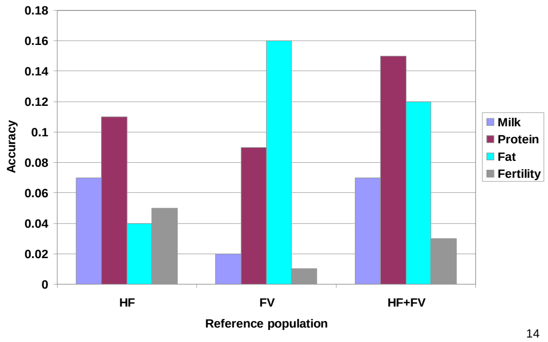
Accuracy of GEBVs for Fleckvieh validation bulls (GBLUP)



Accuracy of GEBVs for Jersey validation bulls (BayesA)

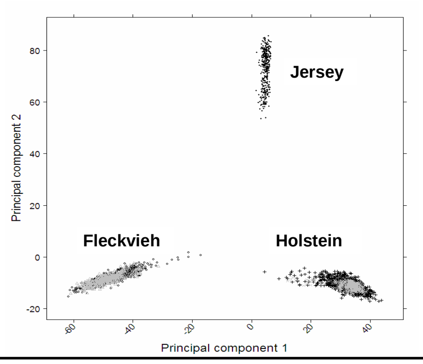


Accuracy of GEBVs for Jersey validation bulls (GBLUP)

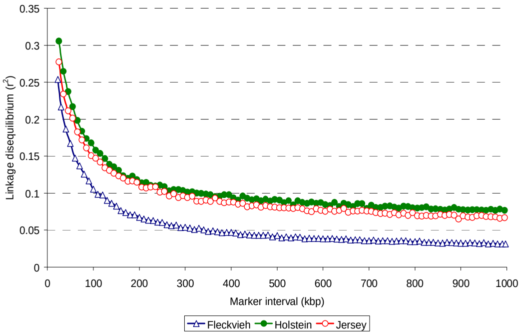


Genomic relationship between breeds

Principal component analysis



Extent of linkage disequilibrium in Holstein, Jersey and Fleckvieh



Summary

- In general, BayesA was superior to GBLUP in GEBV predictions across breeds
- Addition of other breeds to the reference population had only small effects
- Accuracy of GEBVs using multi-breed reference populations was not greater than that achieved with single breed reference populations
- Populations are too divergent to capture marker-QTL associations across breeds at current marker density

Acknowledgements

ADHIS (Melbourne, Australia) provided phenotype data of Holstein and Jersey bulls

Federation of Austrian Fleckvieh Cattle Breeders (AGÖF) provided genotypes of Fleckvieh bulls