Single-step genetic evaluation of resistance to parasites in the Swiss Alpine goat population

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Resistance to parasites

- Gastrointestinal nematodes are source of one of the most important disease in small ruminants in pasture-based production system.

- After decades of the use of anthelminic products, parasites developed resistances.

- As alternative to anthelminic product, breeding for more resistant animals was proposed in sheep and goats

Previous study

PARASiTE
Available online at:
www.parasite-journal.org

RESEARCH ARTICLE   **OPEN ACCESS**

The genetic basis for the selection of dairy goats with enhanced resistance to gastrointestinal nematodes

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Phenotypes

- Measures of fecal egg count (FEC), packed cell volume (PCV) and FAMACHA© eye color score (FAA).

  - 948 Alpine goats in 17 Swiss herds

- Higher parasitic load leads to:

  - higher fecal egg count

  - lower percentage of packed cell volume, and

  - whiter FAMACHA© eye color score.

- All traits used together could build a resistance index

Dataset

- Pedigree contained 5652 animals
  - Of which 1277 were genotyped (60K Goat Chip V2)
- Heritability estimates, genetic (above diag) and phenotypic (below diag) correlations:

	FEC	FAA	PCV
FEC	**0.07**	-0.03	-0.39
FAA	0.18	**0.22**	-0.60
PCV	-0.27	-0.17	**0.22**

Qualitas.

Phenotyping

- Two measures
  - Early summer (after 3-4 months on pasture)
  - Early autumn (3-4 months after helminthic treatment)
- FEC transformed to obtain normal distribution:
  $FEC_t = (FEC + 1)^{0.36}$
- FEC reduction test (FECRT) done to account for level of resistance in each herd

Multi-traits animal model

FEC_t = season + anthelmintic + FECRT + age class + *herd* + *pe* + *a* + *e*

FAA = season + anthelmintic + FECRT + age class + *classifier* + *herd* + *pe* + *a* + *e*

PCV = season + anthelmintic + FECRT + age class + *herd* + *pe* + *a* + *e*

Reproduction of PBLUP by Heckendorn et al.

- Differences expected:
  - Multibreed vs only Alpine
  - Different pedigrees
    2012 vs 2021
  - Different evaluation software
   aireml90 vs MiX99 suite

BUT

- Same variance components
- Same phenotypic dataset
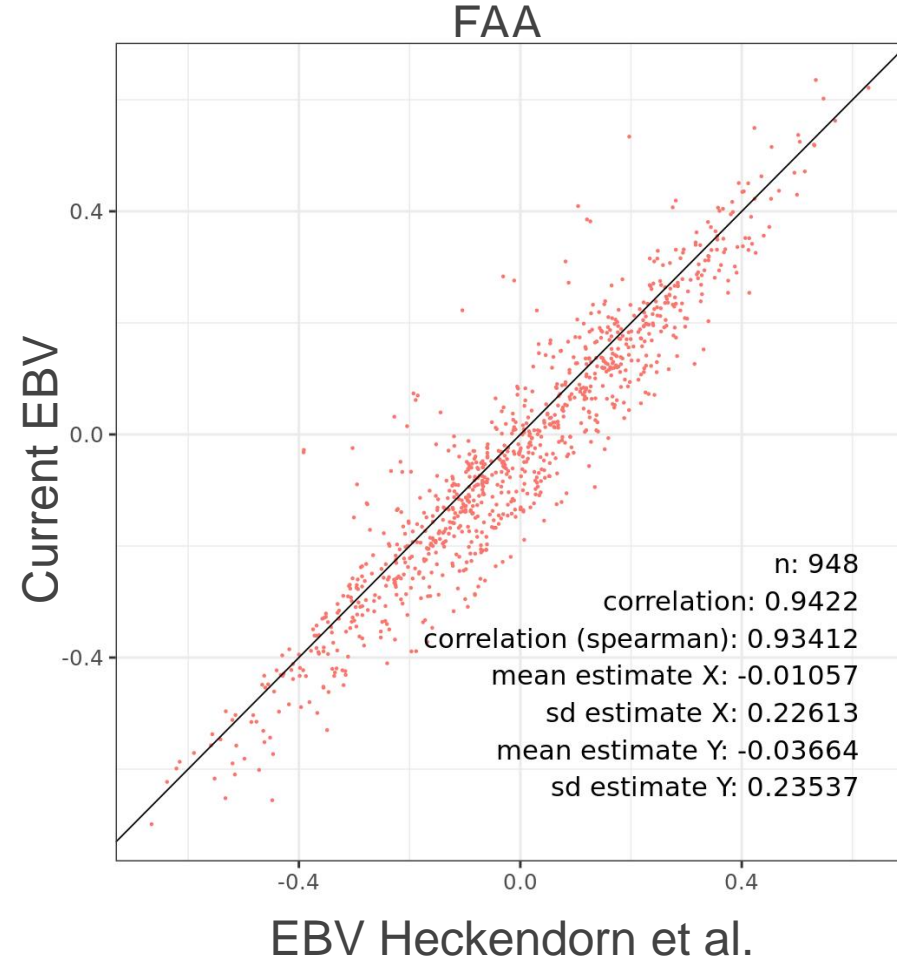
FAA

n: 948
correlation: 0.9422
correlation (spearman): 0.93412
mean estimate X: -0.01057
sd estimate X: 0.22613
mean estimate Y: -0.03664
sd estimate Y: 0.23537

Qualitas
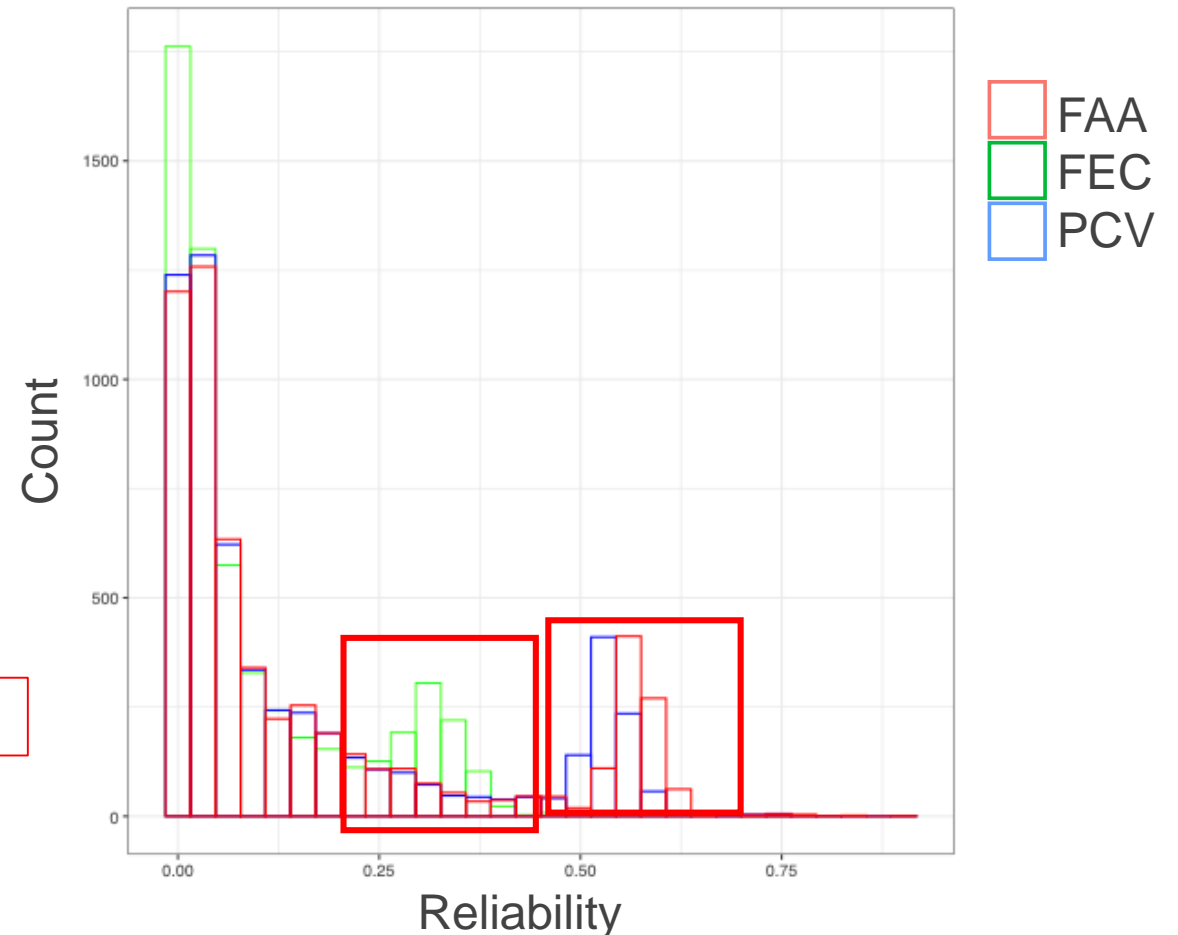
Reliabilities of non-genomic breeding values

- Reliability distribution similar for all three traits

- Averages are very low:
  - FAA: 0.164
  - FEC: 0.096
  - PCV: 0.156
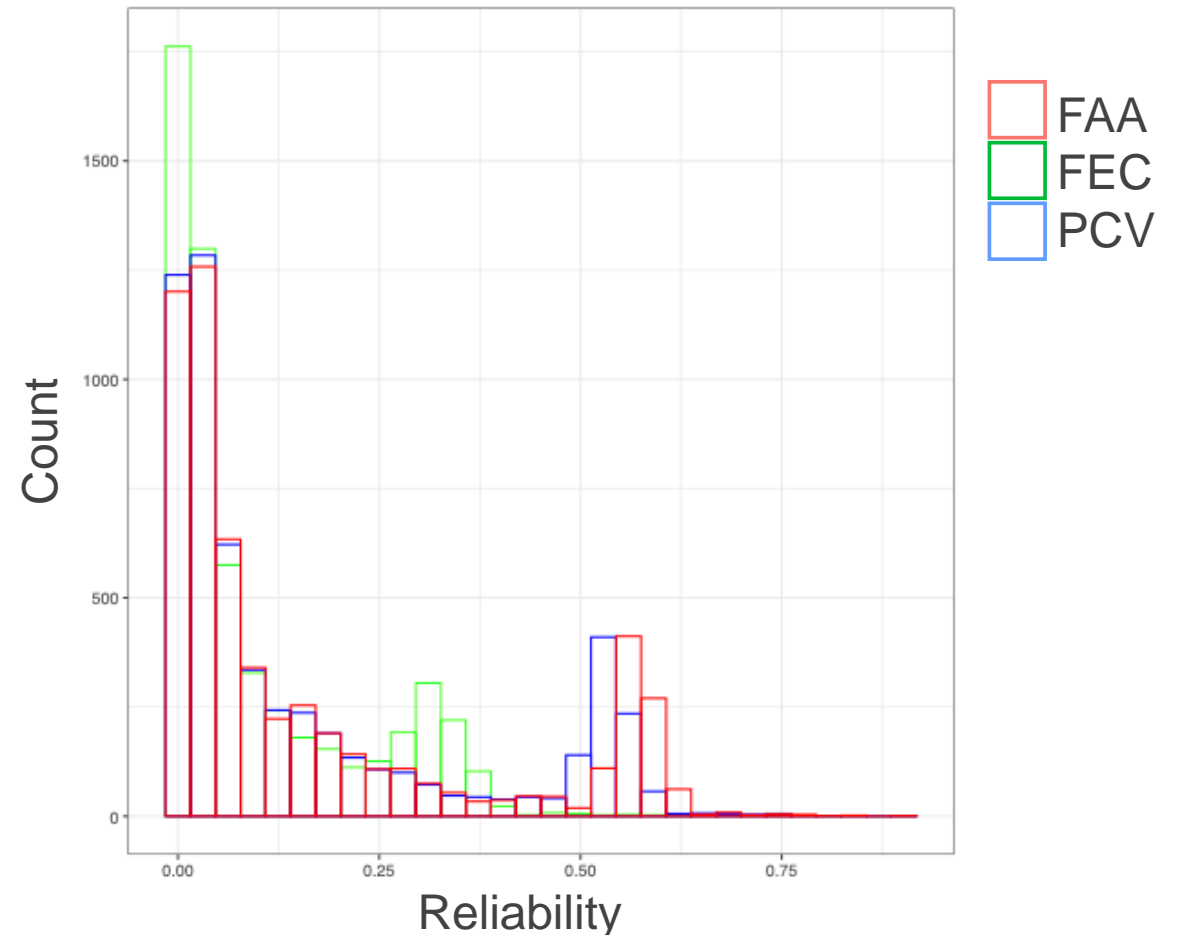
Reliabilities of non-genomic breeding values

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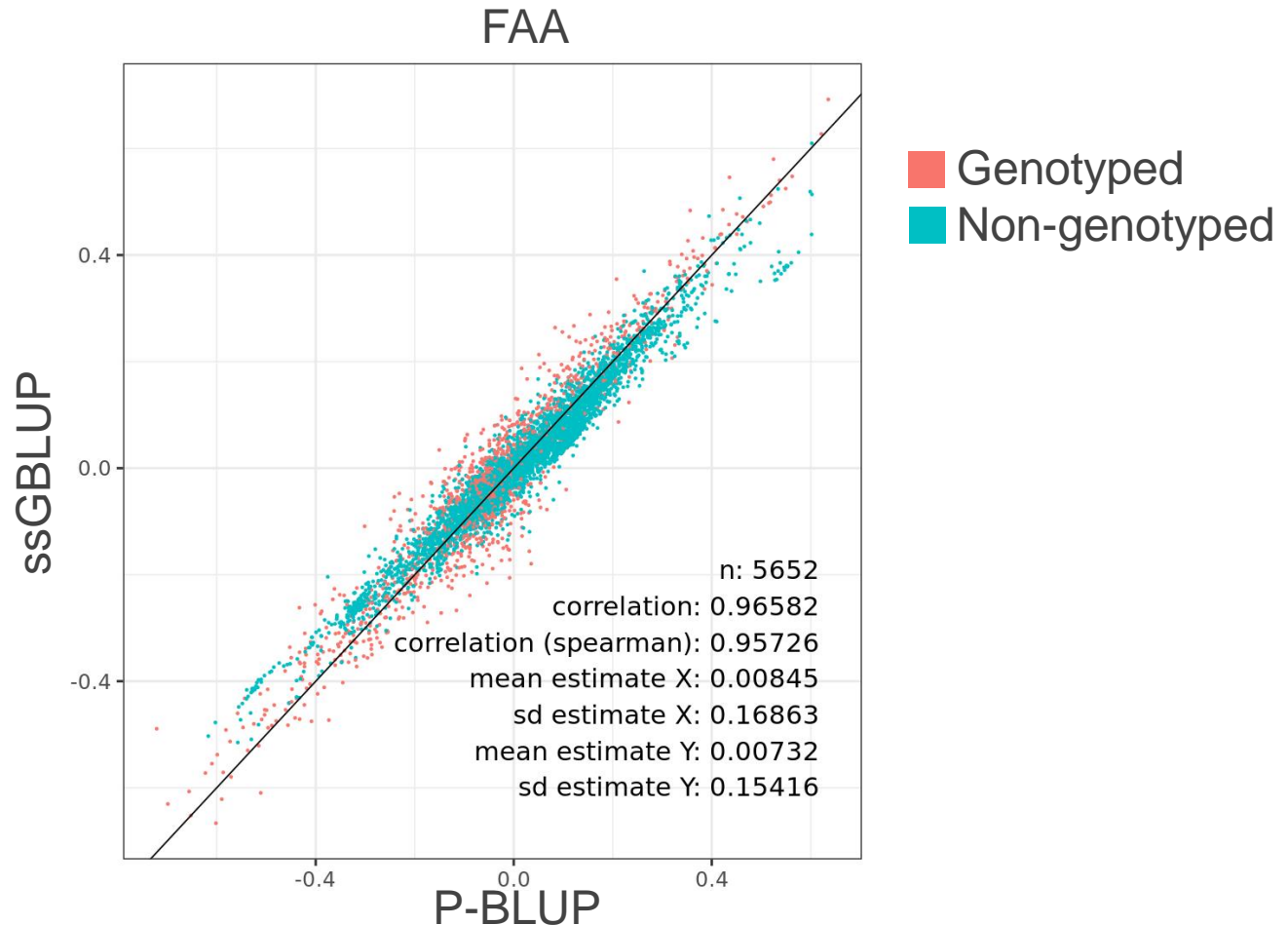 - FEC: 0.096
  - PCV: 0.156

Phenotyped goats

Qualitas.

From P-BLUP to ssGBLUP

- 16% of the animals in evaluation were phenotyped and genotyped

- No clear EBV difference between genotyped and non-genotyped animals

- High correlation between PBLUP and ssGBLUP

==> Dataset still very small for traits with low heritability estimates

FAA

Genotyped
Non-genotyped

n: 5652
correlation: 0.96582
correlation (spearman): 0.95726
mean estimate X: 0.00845
sd estimate X: 0.16863
mean estimate Y: 0.00732
sd estimate Y: 0.15416

ssGBLUP (y-axis)
P-BLUP (x-axis)

Qualitas.

Reliabilities of single step genomic breeding values

- Use pipeline differentiating genotyped and non-genotyped animals:
  - Estimate reliabilities for all animals without genomic information (P-BLUP)
  - Estimate genomic reliabilities for genotyped animals (SNP-BLUP)
  - Integrate additional genomic information into P-BLUP model
  - Estimate genomic reliabilities for non-genotyped animals

Approximate individual animal reliabilities in single-step genomic model
H. Ben Zaabza[1], M. Taskinen[1], T. Pitkänen[1], G.P. Aamand[2], E.A. Mäntysaari[1] and I. Strandén[1]
[1]Natural Resources Institute Finland (Luke), 31600 Jokioinen, Finland, [2]NAV Nordic Cattle Genetic Evaluation, 8200 Aarhus, Denmark; hafedh.benzaabza@luke.fi

Qualitas.

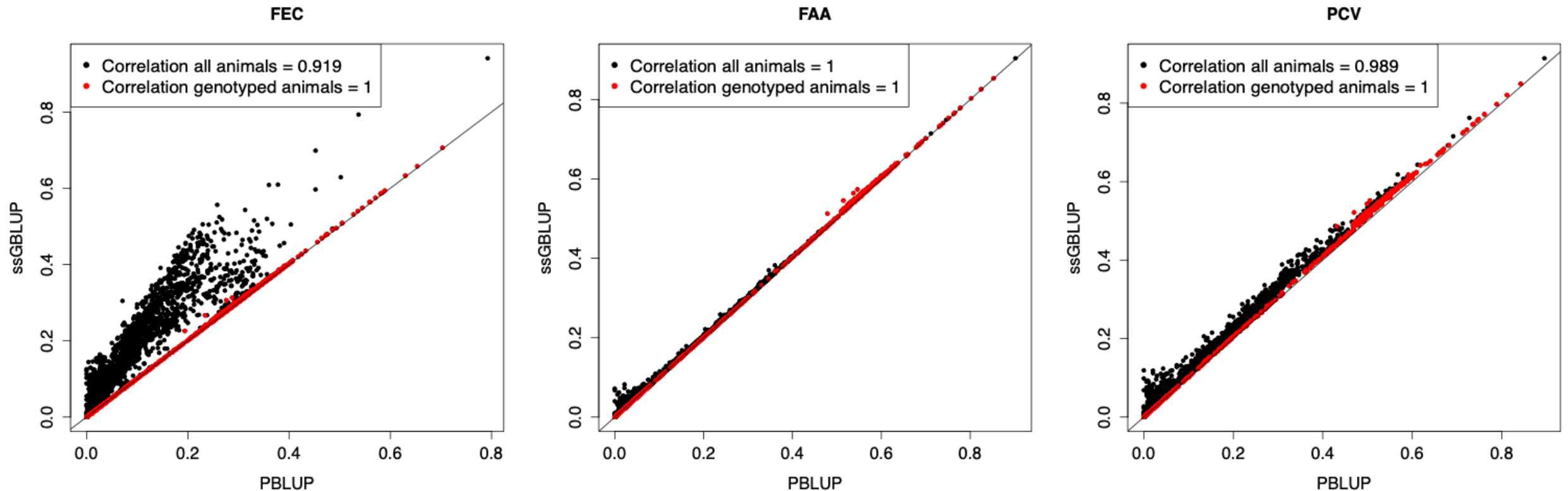# Reliabilities of single step genomic breeding values

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Reliabilities of single step genomic breeding values

Reliabilities of single step genomic breeding values

FEC

- Correlation all animals = 0.919
- Correlation genotyped animals = 1
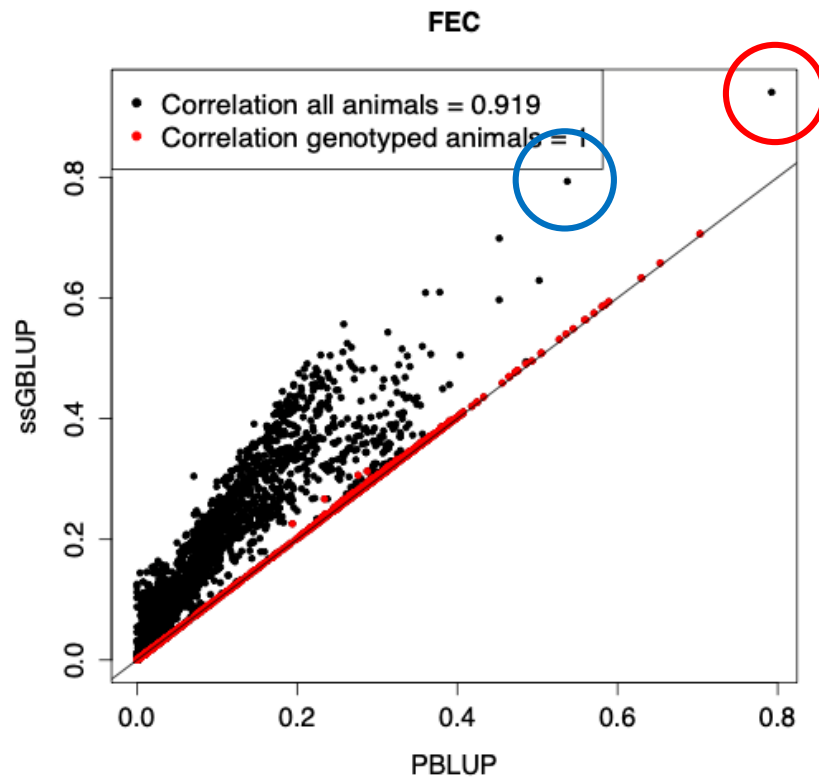
Buck of 87 animals in pedigree, of which 79 are genotyped.

Buck of 25 animals in pedigree, of which 17 are genotyped.

Conclusions

- Reproduction of the work by Heckendorn et al. was possible with MiX99 and additional pedigree information

  - EBV correlations of 0.94
  - Reliability estimates were still very low

- Change from PBLUP to ssGBLUP approach did not show any great impact on EBV for any genotyped or non-genotyped animals

- Reliability estimates are increased with additional genomic information, but data must be further expanded before any possible implementation.

Acknowledgements

Thank you for your attention

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