

Can genomics enable genetic evaluations for smallholder farmers?

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Kenyan Smallholders

Account for $\approx 70\%$ of milk production¹

- ~ 3 -5 acres of land.
- Mixed farming (crops, 1-5 cows)
- Low AI use.
- Weaker breeding & production infrastructure.
- Highly heterogeneous environment.



Poor penetrance of breeding practices.

Milk yields of ≈ 3 L of milk per day¹

Breeding hasn't been effective in this system

Kenyan Smallholders

- Low AI use.
- Small herd size.
- Weak Connectedness
- Highly Heterogeneous environments.
- Small herd size.

Advanced Economies

- High AI.
- Large herd size.
- Strong Connectedness
- Homogeneous environments.

Estimation of Breeding Values

ID	HerdID	BV	Residual	Pheno
1	1			-2.067
2	1			-0.201
3	2			1.435
4	1			2.382
5	2			-0.687

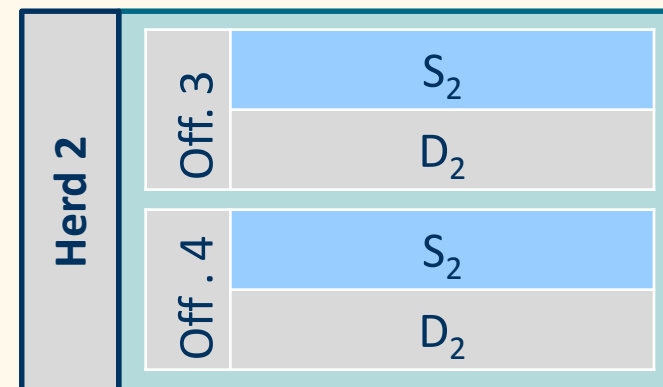
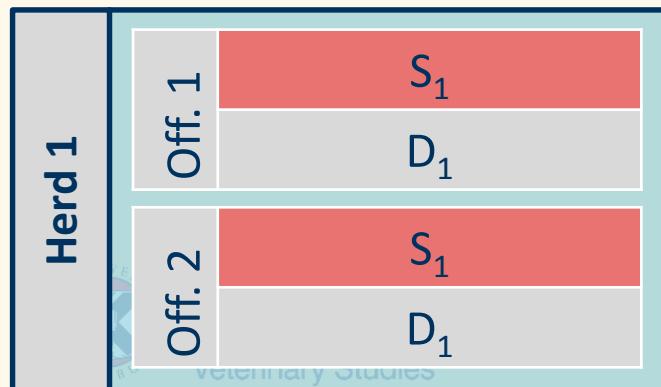
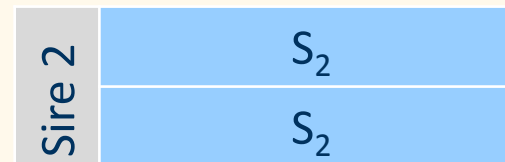
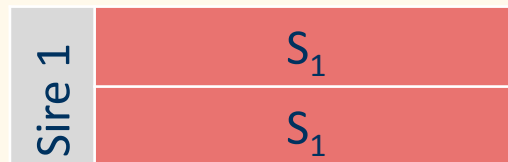
$$\textit{Phenotype} = \textit{HerdID} + \textit{BV} + \textit{Residual}$$

HerdID included to correct data for environment/herd.

Fixed OR Random

PBLUP versus GBLUP

- Currently:
 - Herd size too small
 - Connectedness too weak.
- Solve connectedness, the rest will follow.
- Genomics can strengthen connectedness by capturing shared haplotypes blocks across herds.



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Sire 1	1	0	1	1	0
	0	1	0	1	1

Sire 2	0	0	1	1	0
	0	1	0	0	1

Herd 1	Off. 1	0	1	0	1	1
		1	0	1	0	0
	Off. 2	1	0	1	1	0
		1	1	0	1	0

Herd 2	Off. 3	0	0	1	1	0
		0	0	0	1	0
	Off. 4	0	1	0	0	1
		0	0	0	1	0

Aims

In small holders systems:

- 1) Can GBLUP separate environment and genetics?
- 2) Should herd be fixed or random effects?
- 3) Impact of connectedness?

Data Generation

BurnIn

- Effective Population Size (N_e) ≈ 100
- Sires per generation : 50
- Dams per generation : 500
- Population size : 1000

Coalescent
Population History

Historic Breeding
(4 Generations)

Recent Past Breeding
(3 Generations)

Dams
(4,000)

Recent Breeding

- Sires per generation: 50 -> 1000
- Dams per generation: 20000
- Select on TBV.

- Final generation subsets were created varying:
 - Population Size: 1000 -> 4000
 - Herd Size: 1 -> 32

Coalescent
Population History

Historic Breeding
(4 Generations)

Recent Past Breeding
(3 Generations)

Dams
(4,000)

Analysis

Bayesian Generalized Linear Regression (BGLR)²

- Populations of; 1000, 2000, 4000.
- Analysed each dataset with three P/GBLUP models;
 1. **excluding** herd effect,
 2. herd as a **fixed effect**,
 3. herd as a **random effect**.
- 12000 Iterations, 2000 BurnIn.

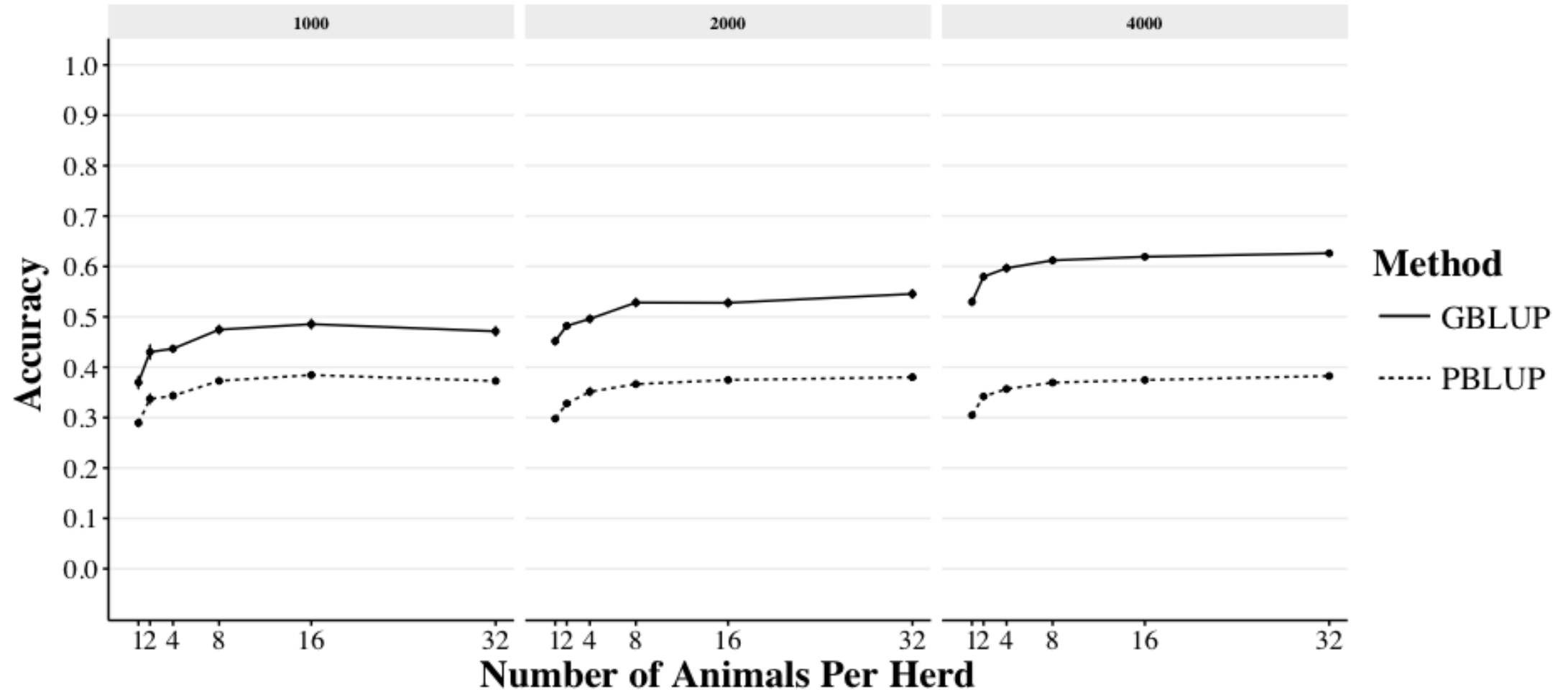


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Results

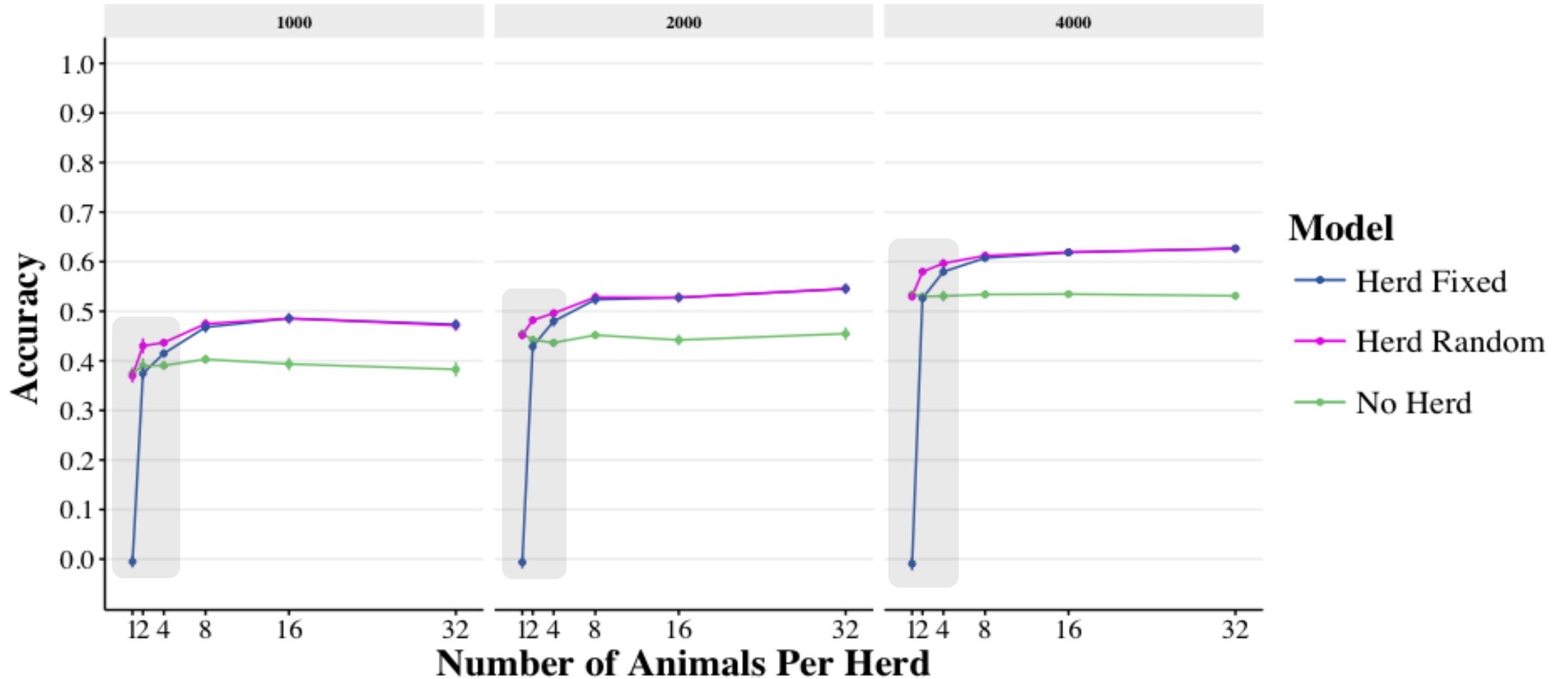
PBLUP versus GBLUP

Effect of Method on EBV Accuracy

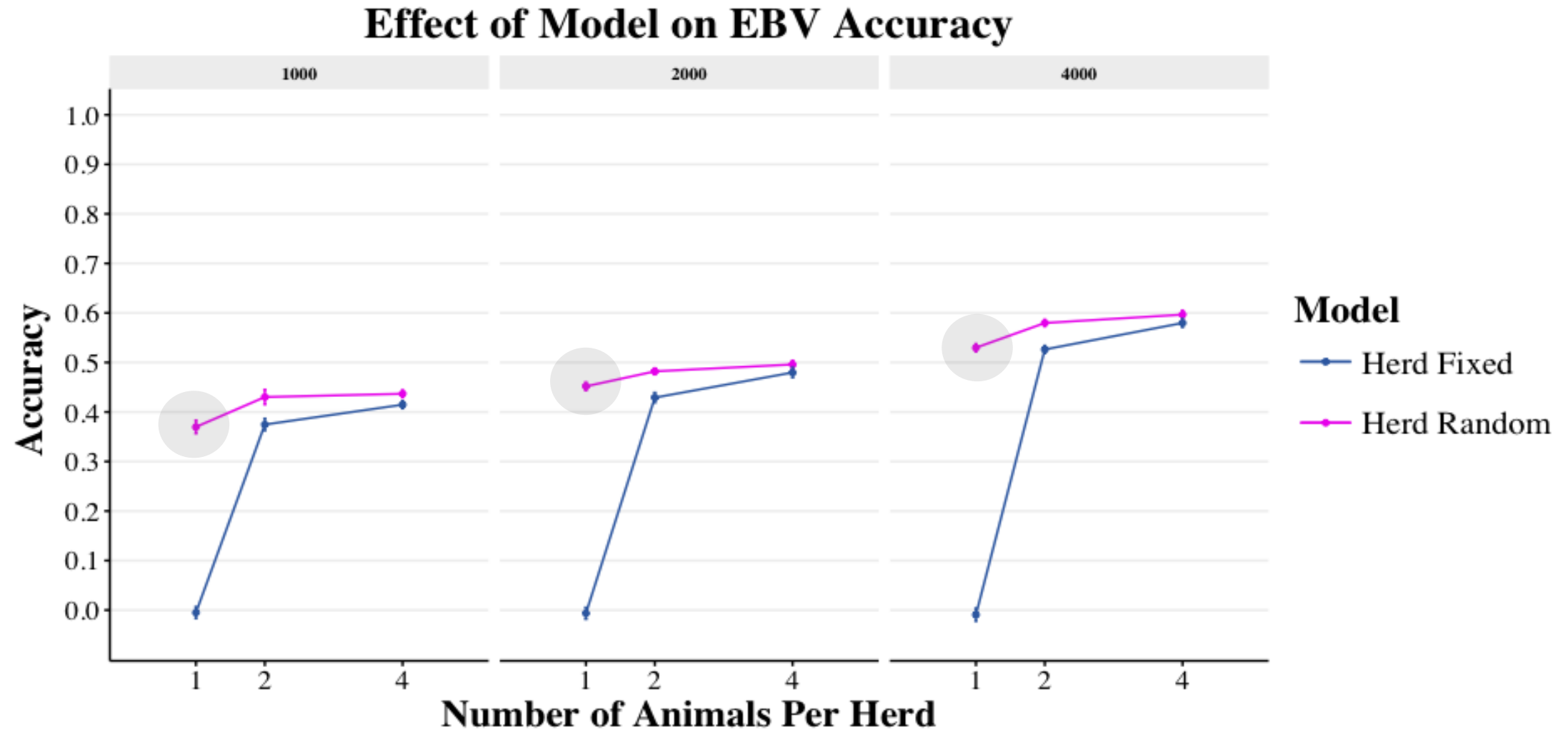


Fixed or Random

Effect of Model on EBV Accuracy



Fixed or Random - Small Herd Sizes



Connectedness

Population Size	Herd Size	Offspring per Sire	Accuracy	se
4000	2	4	0.580	0.007
		8	0.575	0.007
		16	0.588	0.006
		40	0.609	0.005
		80	0.635	0.008

Conclusions

- GBLUP is able to separate environment and genetics and outperform PBLUP estimates.
- At low herd sizes, herd should be modelled as random.
- Increasing the number of offspring per sire used, increases the probability of shared haplotypes across herds.
- **Genomic evaluations can exploit the existing architecture of smallholder farming systems.**

Future Work

- Accuracy of Genomic Prediction of:
 - Sons
 - International Sires
- Impact of non-random association of sire breeding value with herd value on accuracy and bias when modelling herd as a random effect.

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