

Continuing the transformation



Genomic Selection in Sheep Breeding Programs

Julius van der Werf

Rob Banks, Sam Clark, Stephen Lee,

Hans Daetwyler, Ben Hayes and Andrew Swan

UNE
University of
New England

Outline

- What is different in sheep?
- Potential benefits to sheep breeding programs?
- Accuracy of prediction: expected and realized
- Reference population requirements
- Strategies for implementation
- Future developments

What is different in sheep?



- Existing data of high value as a RefPop
- Small N_e
- Only 1 breed (maybe 2)
- High genomic pred. acc.
- High Benefit/Cost ratio
- Large operators



- Existing data of limited value as a RefPop
- Higher N_e
- Many breeds
- Lower genomic pred. acc.
- Lower Benefit/Cost ratio
- Small operators/low cost

Challenges of implementing GS in sheep

- Economically viable? Cost vs benefit
 - How much genetic variation in profit?
 - How much increase in genetic gain?

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- Economically viable? Cost vs benefit
 - How much genetic variation in profit?
 - How much increase in genetic gain?
- Accuracy of genomic predictions?
 - Large genetic diversity, both within and across breeds
- Breeding program structure
 - Many small operators
 - Genetic improvement tends to be 'low cost'

Potential benefits of GS - some principles

% increase in EBV accuracy (male 1yo) and genetic gain

	$h^2 = 0.1 = r^2$		$h^2 = 0.3 = r^2$	
Trait Measurability	%Δ Acc	%Δ Gain	%Δ Acc	%Δ Gain
< 1 year, both sexes	15	7	7	7
> 1 year, both sexes	68	19	59	37
>1 year, females only	119	27	112	52
on Corr. Trait, $r_g = 0.9$	20	12	20	26
on Corr. Trait, $r_g = 0.5$	67	50	76	86

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These effects underestimated due to not accounting for Bulmer effect

Genomic breeding values

Hard to measure, late in life traits

HTML

- Lean meat yield, meat quality
- Number of lambs weaned
- Adult wool traits
- Parasite Resistance
- Milk production



Genomic prediction accuracies in sheep now

Trait group	Merino	Maternal	Terminal
Wool	0.30 to 0.50		
Body weight, muscle & fat scans	0.25 to 0.50	0.25 to 0.50	0.15 to 0.40
Worm egg count	0.30	< 0.10	0.30
Carcass	0.20	0.15	0.20
Reproduction	0.11 to 0.31	0.05 to 0.15	

Prediction across breeds has not been effective at 50K

Potential benefits of genomic selection for sheep

Wool Objective



1 st selection	GS	Relative response/year
2	No	100%
2	Yes	108%

Potential benefits of genomic selection for sheep

Wool Objective



1 st selection	GS	Relative response/year
1	No	100%
1	Yes	114%

Potential benefits of genomic selection for sheep

Wool Objective



1 st selection	GS	Relative response/year	
2	No	100%	
1	No	110%	100%
2	Yes	108%	
1	Yes	125%	114%

Potential benefits of genomic selection for sheep

Wool Objective



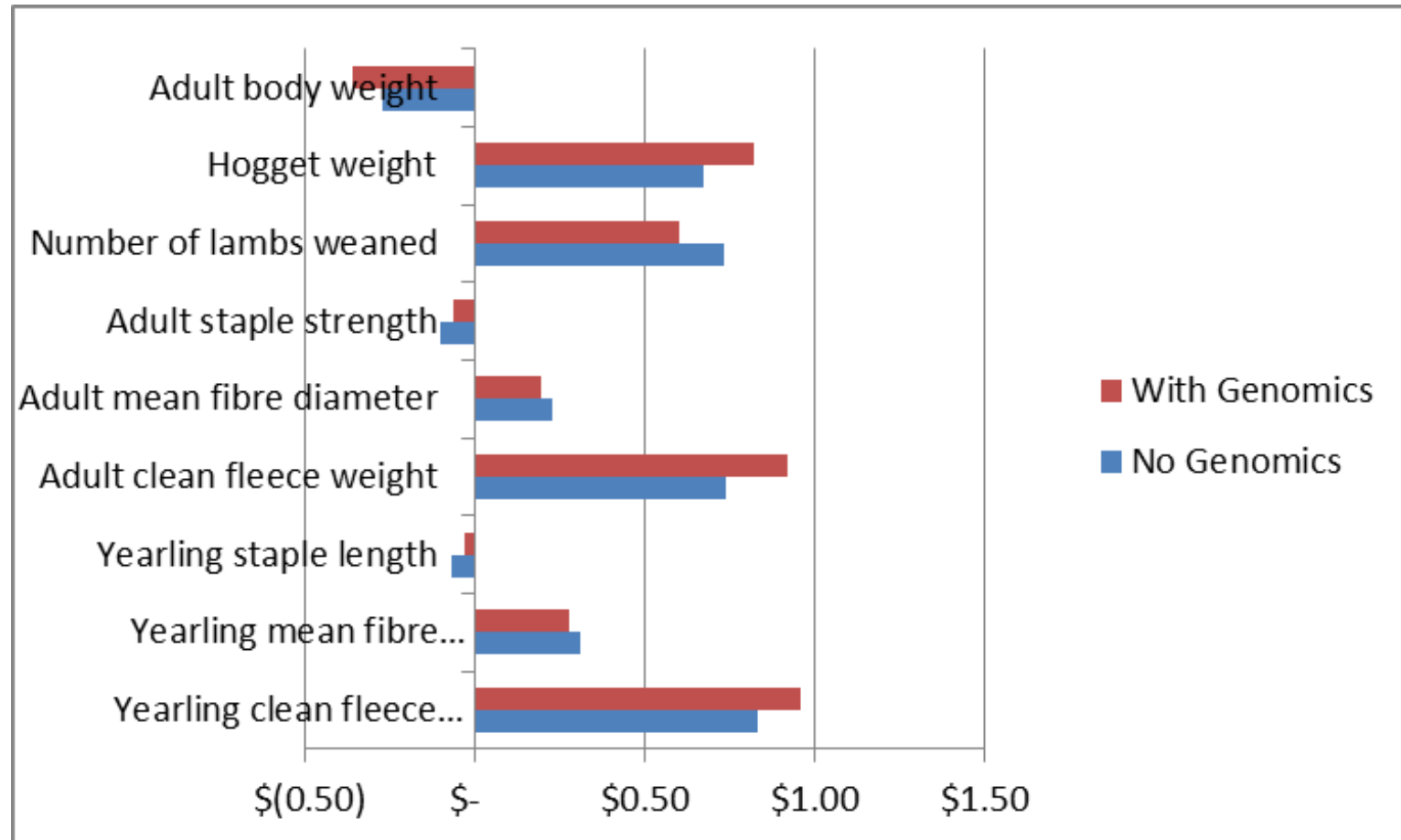
1 st selection	GS	Relative response/year	
2	No	100%	
1	No	110%	100%
2	Yes	108%	
1	Yes	125%	114%

Accuracy -3%

Male generation interval -39%

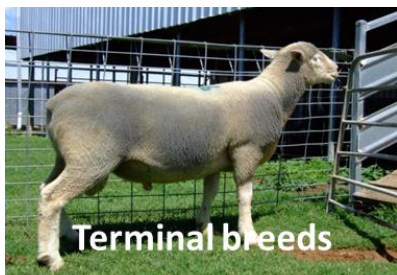
Potential benefits of genomic selection for sheep

Wool Objective



Potential benefits of genomic selection for sheep

Meat Objective



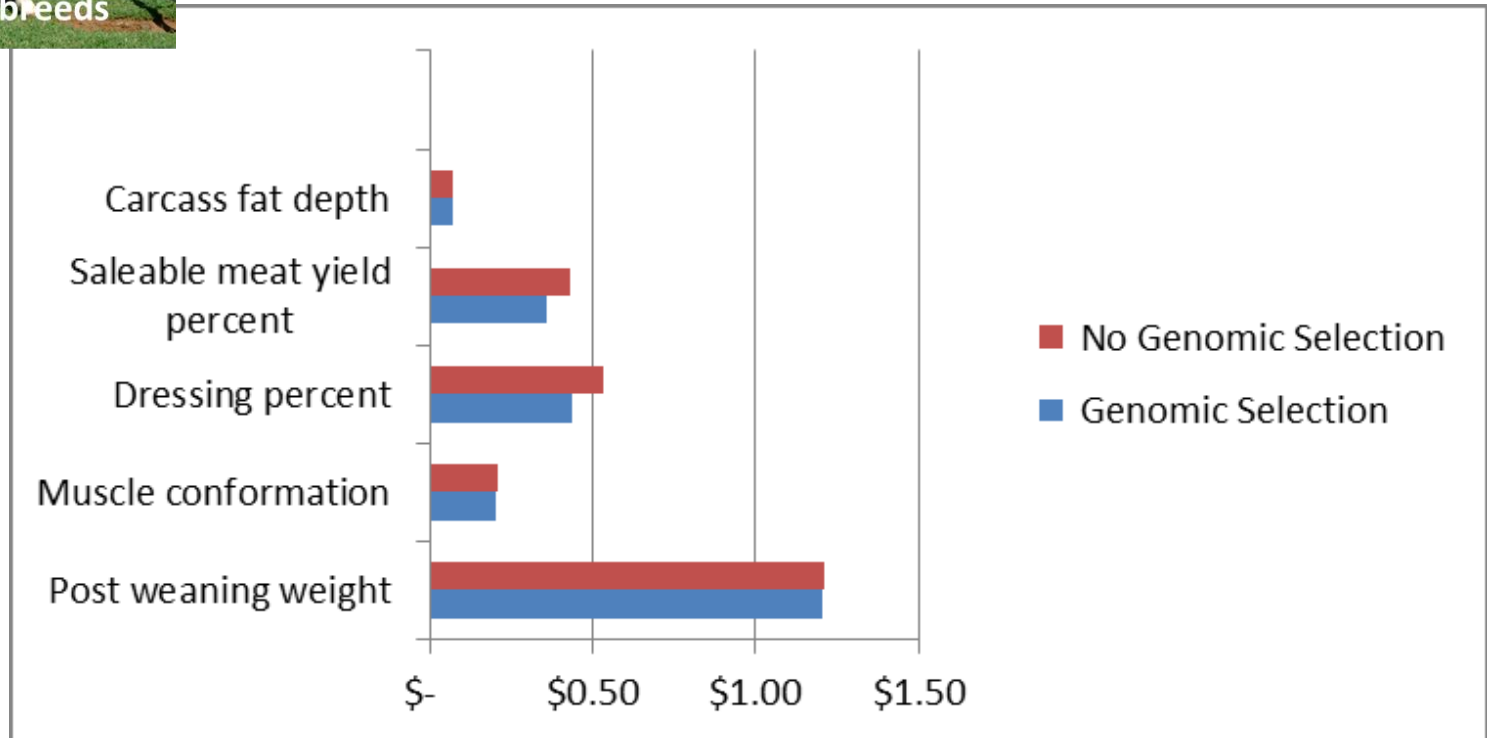
1 st selection	GS	Relative response/year
1	No	100%
1	Yes	108%

Accuracy +5%

Male generation interval -1%

Potential benefits of genomic selection for sheep

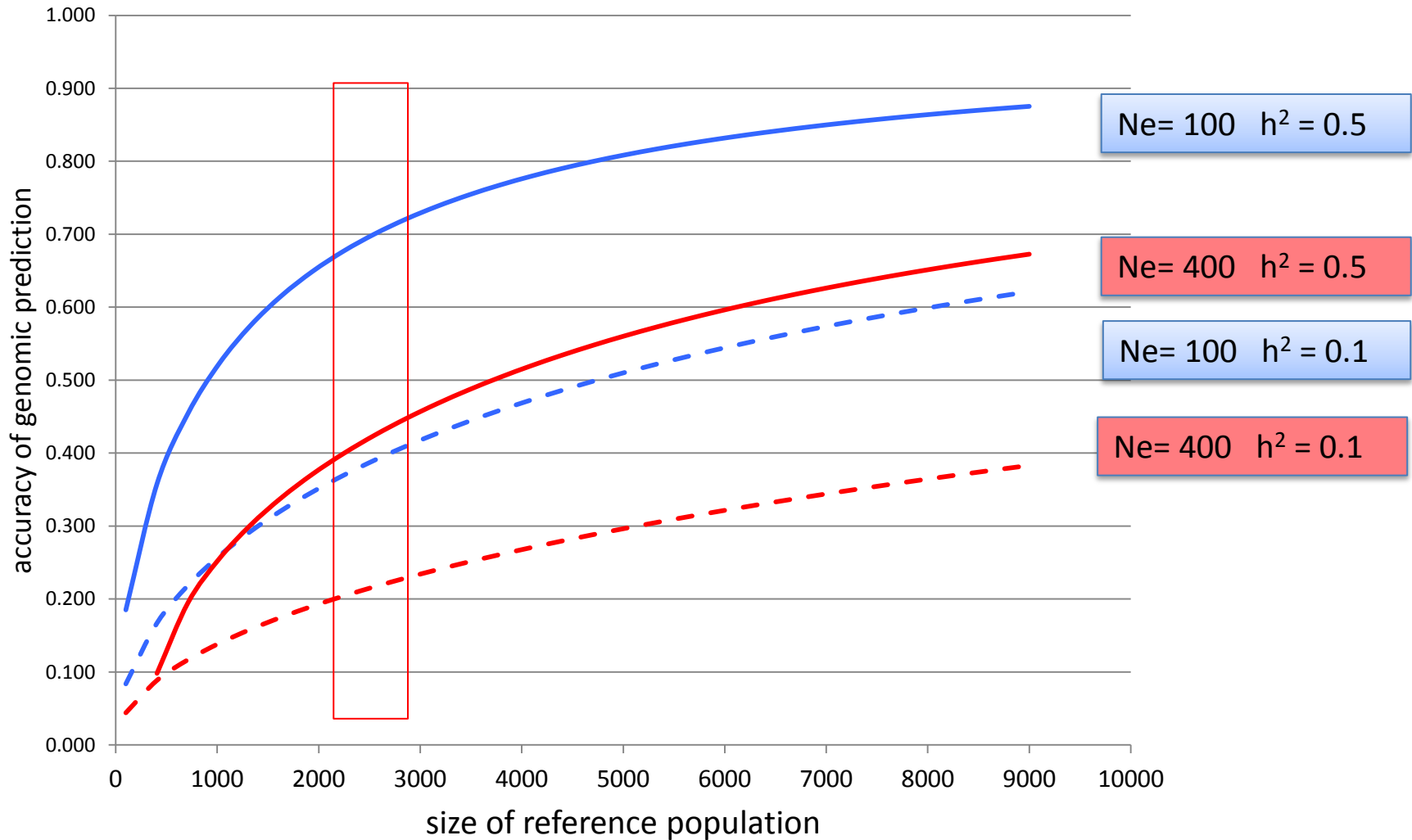
Meat Objective



Summary Potential Benefits

- 5 -15% more benefits for meat/wool objectives
- Not all benefits captured by current indexes
- Also a shift in benefit between traits

Genomic prediction accuracy *Using Goddard et al, 2011*



What effective population size?

Kijas et al 2012

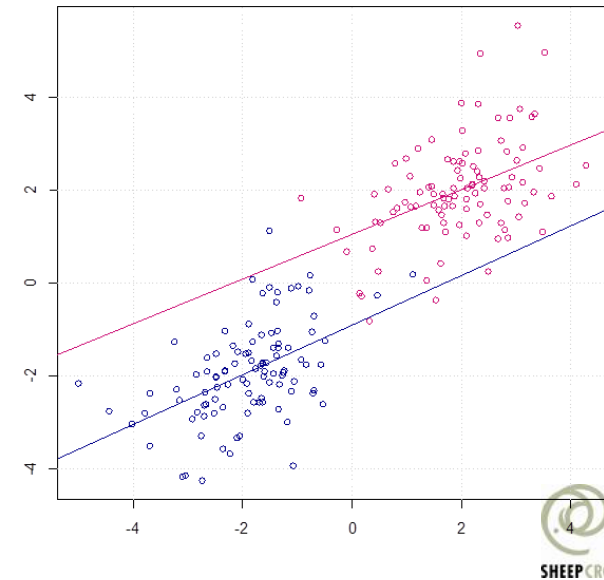
- Sampling?



Populations not homogeneous.

Within and between breed/line accuracies

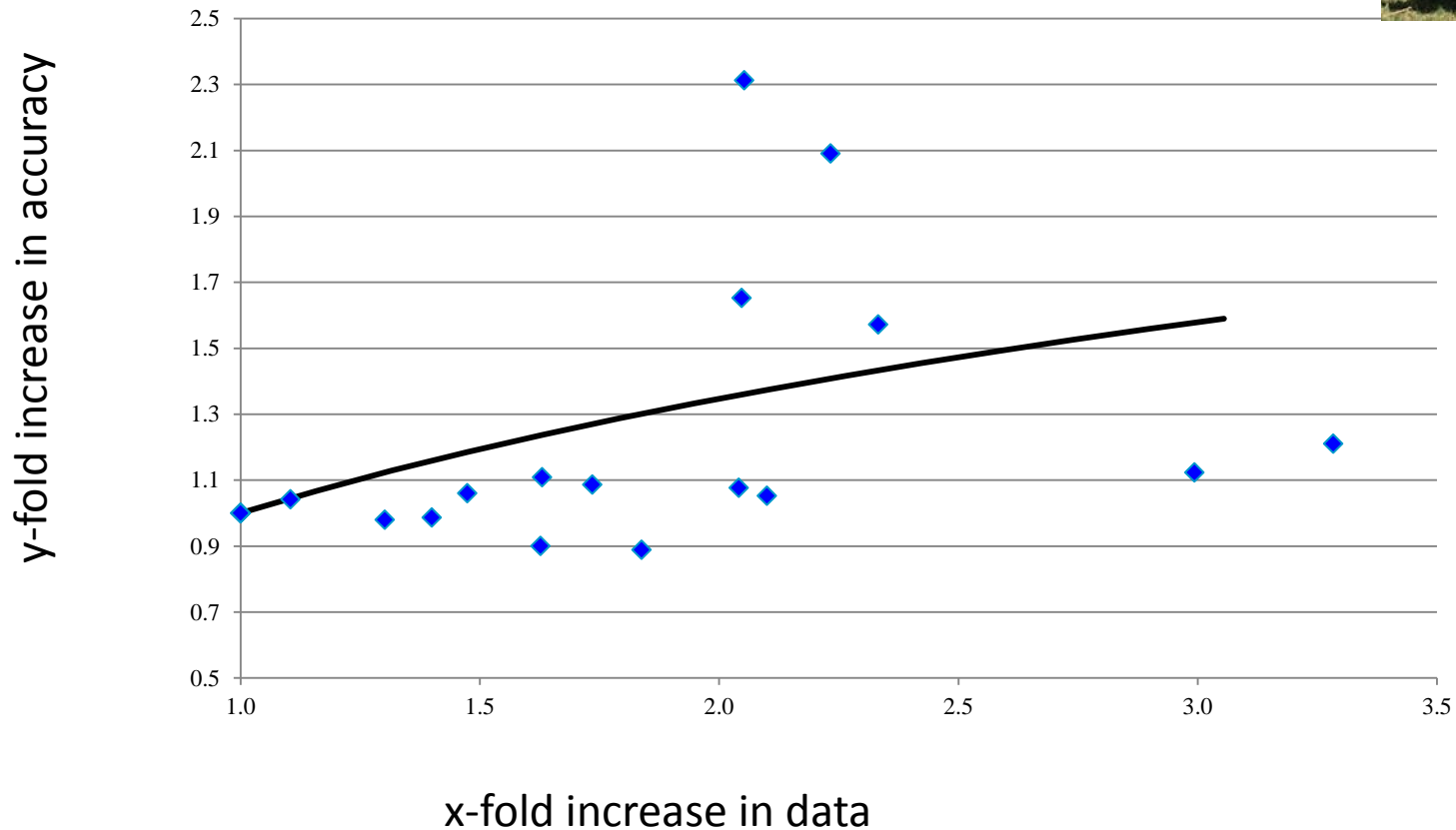
Some accuracy due to population structure



Validating 'Genomic Prediction Accuracy'

More data is always good

But does it increase accuracy as expected?



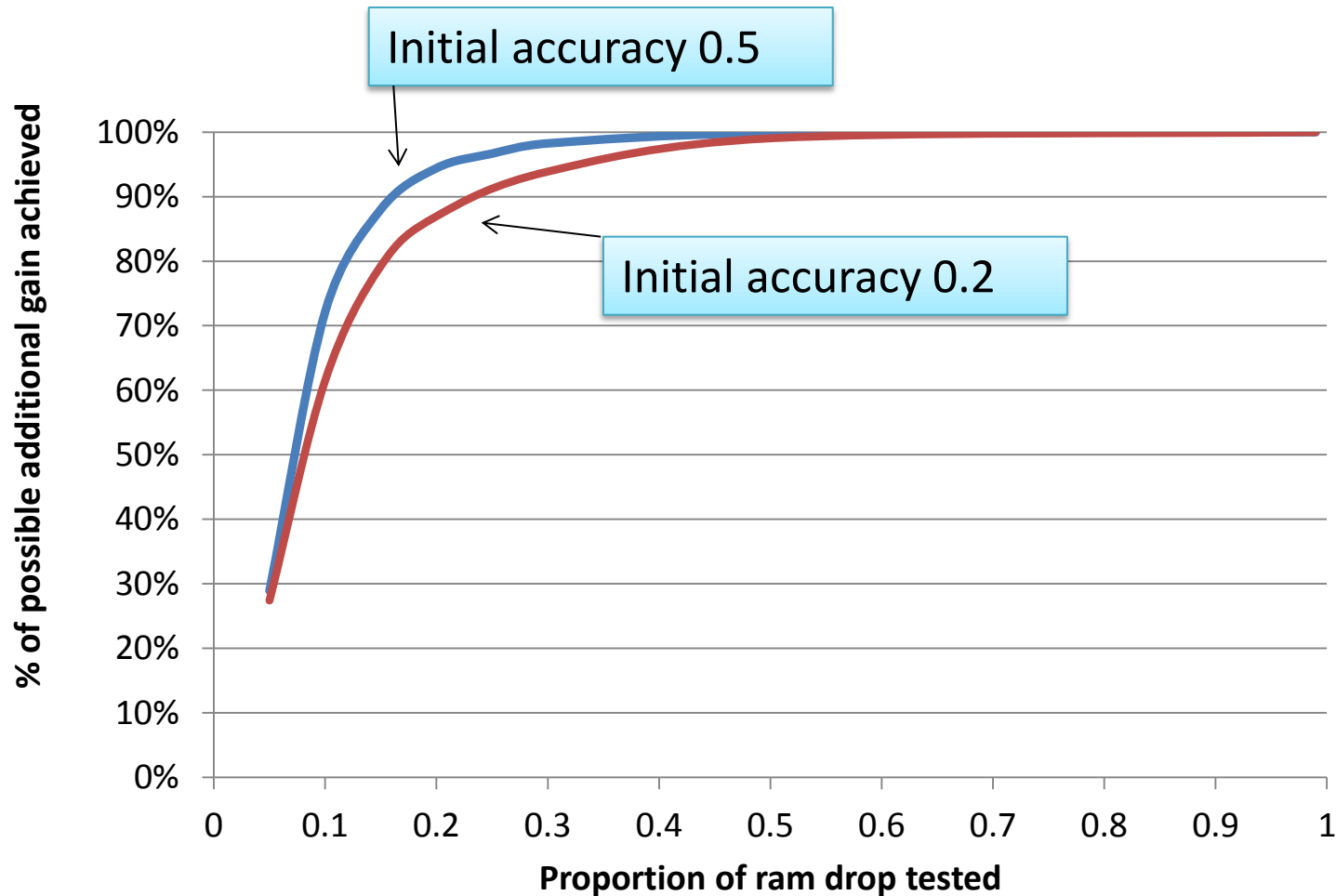
Strategies for implementation

- Reduce genotyping cost
 - Genotype males only ~ 3% loss
 - Genotype only the top ~20% ~10-15% loss
- Increase potential benefits
 - Earlier selection of candidates
- Benefit of reproductive technologies

Granleese WCGALP 25

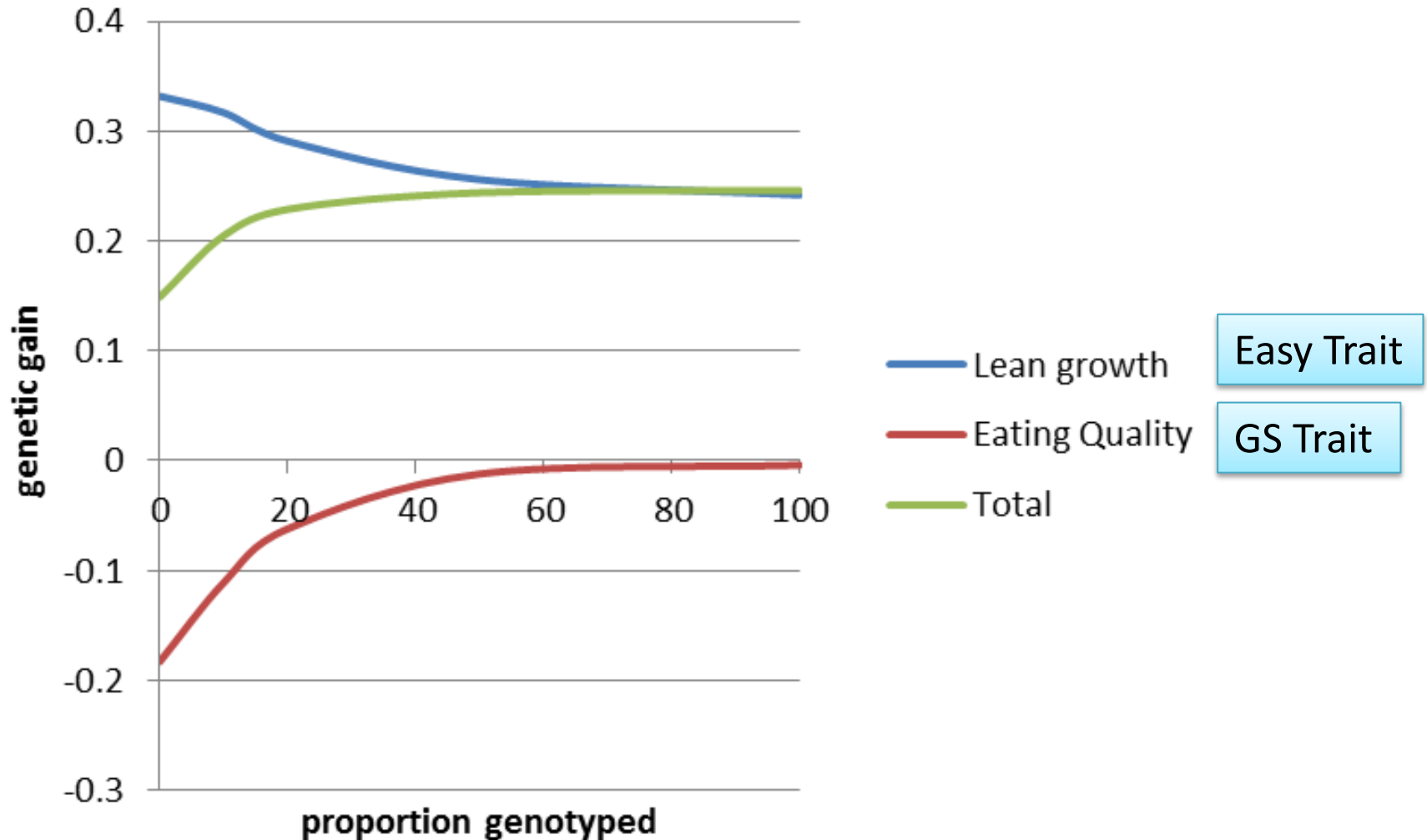
2-stage selection:

Testing 20% of drop gives most of benefit



2-stage selection

More traits and unfavourable correlations?



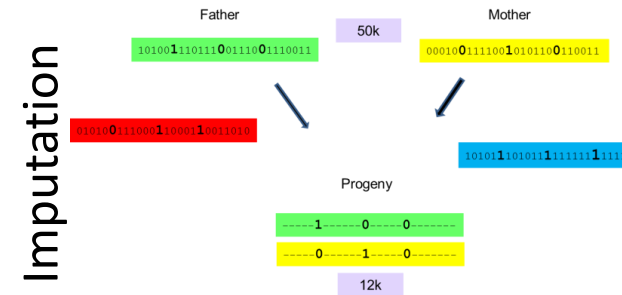
Future: Better and Cheaper testing

Whole genome sequencing (500 INF sires)

High density (600k, 2500 samples)

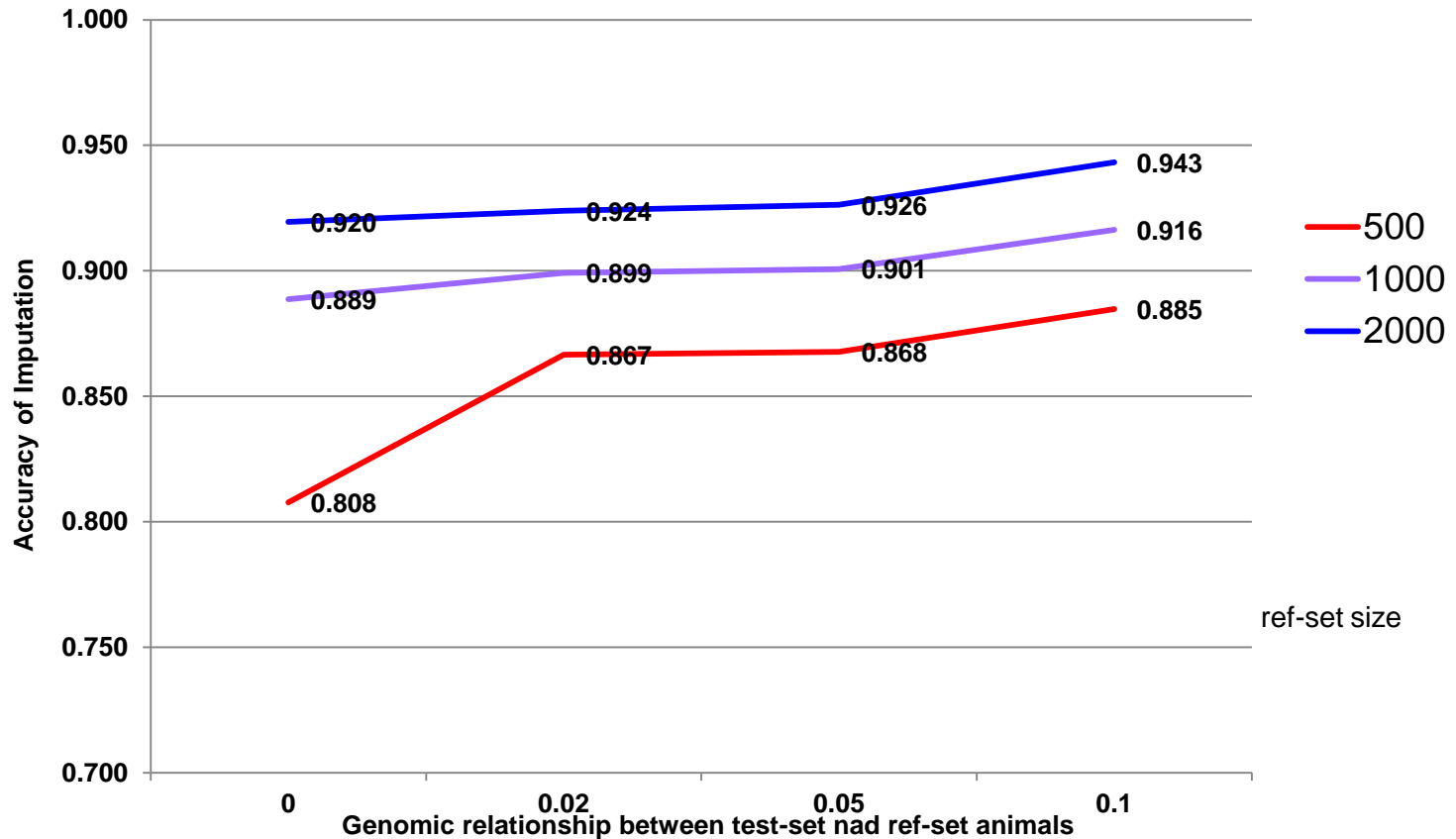
Medium (50k, ~18,000 INF progeny)

Low density (12k SNP chip, breeders)



- Use more info but cheaper for the breeder
- Testing across breeds
- More reliable
- Less costs for reference population

Accuracy of imputation (12>50k)

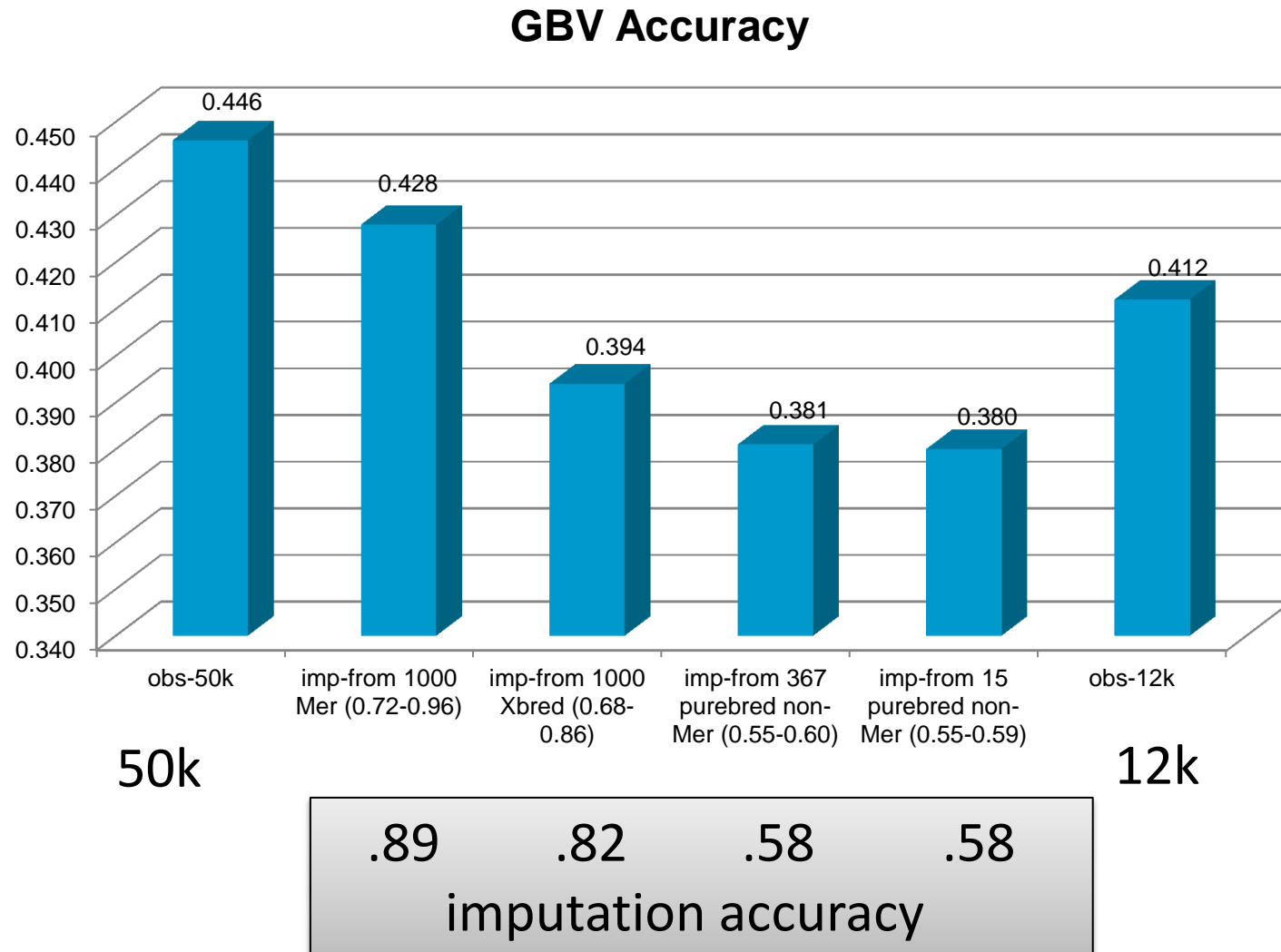


Test Set: 1328 crossbred

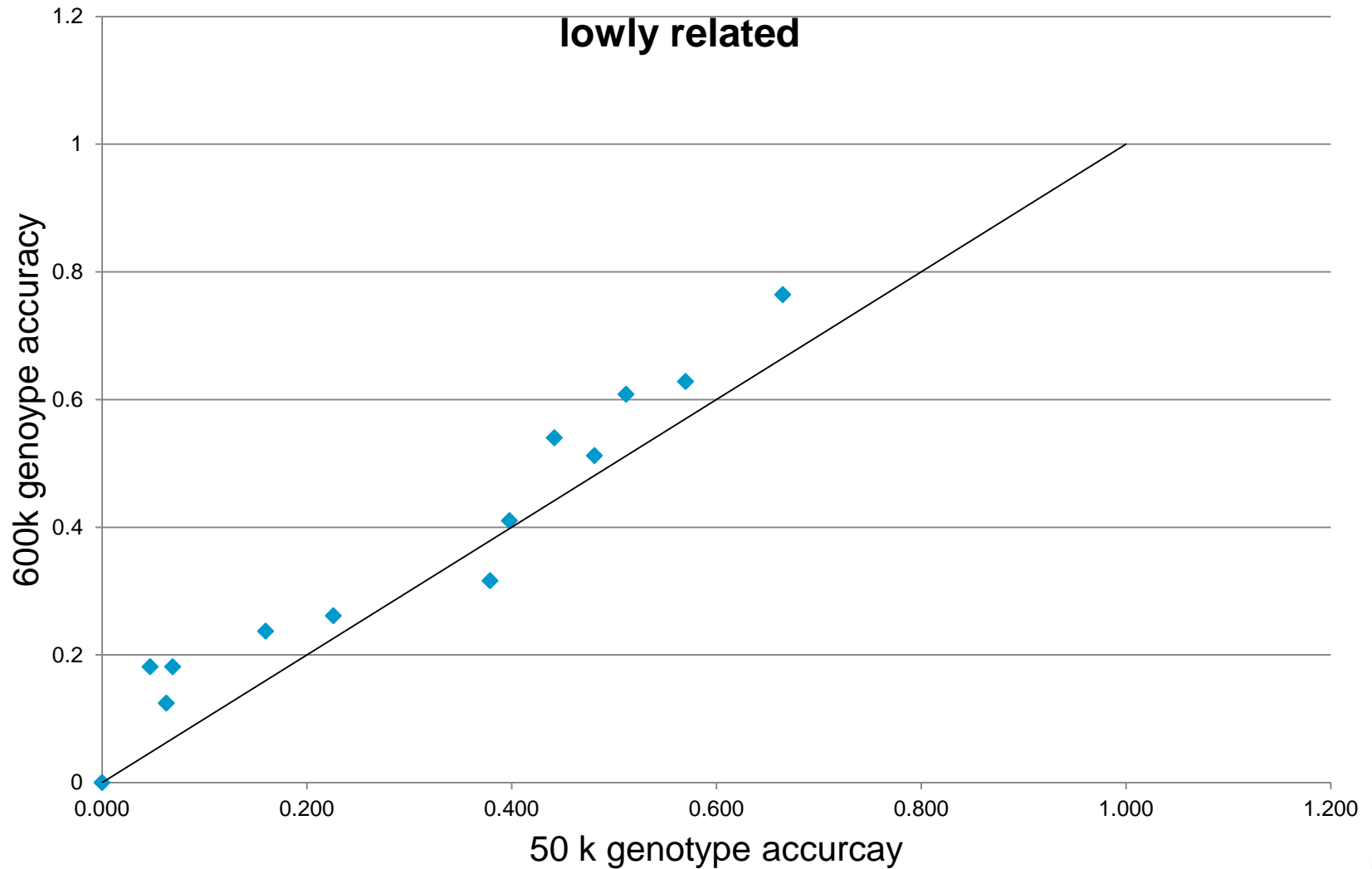
Ref Set: 500, 1000, 2000 crossbreds with 0%, 2%, 5% and 10% GRM

Accuracy of GEBV from imputed genotypes

Moghaddar et al 2014

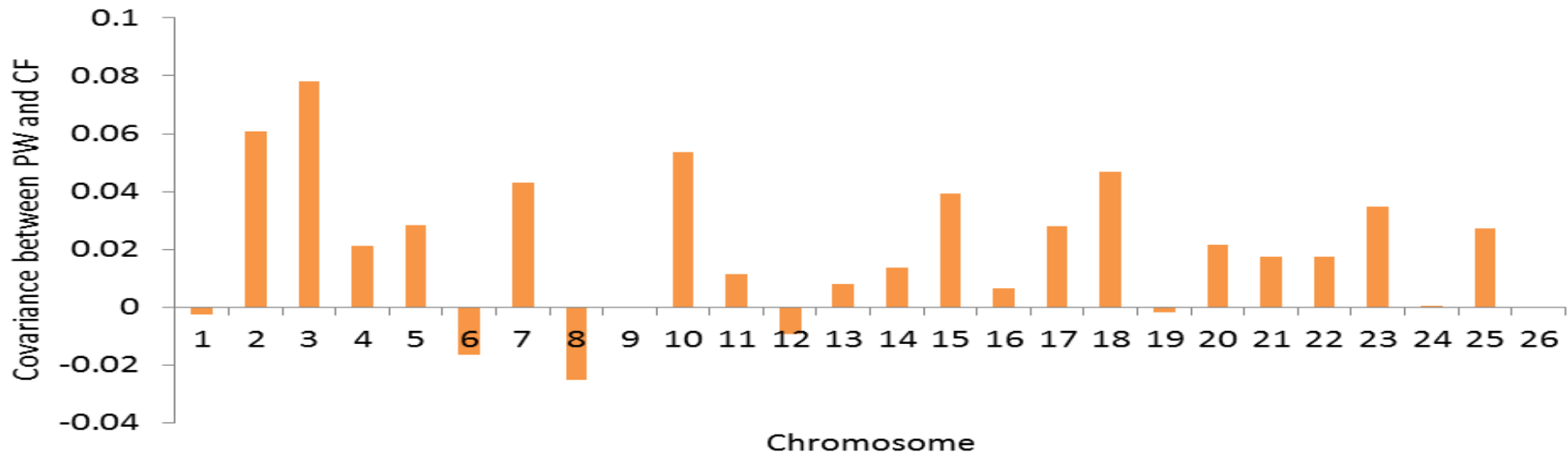
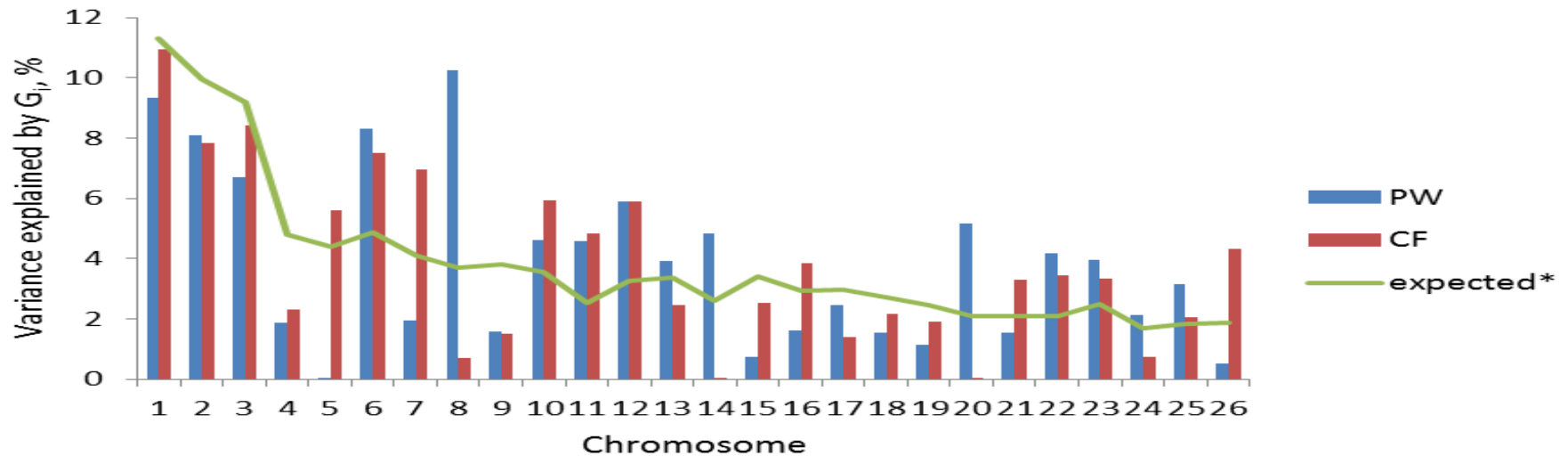


Higher accuracy with high density markers



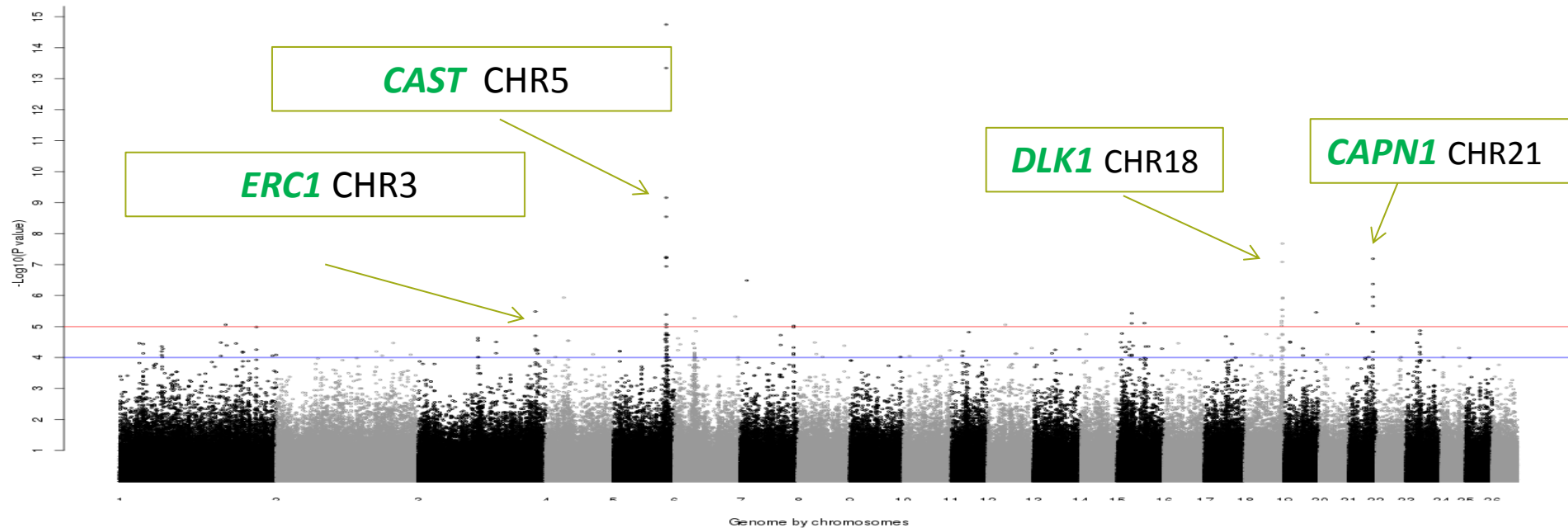
Breaking unfavourable correlations?

Esquivelzeta-Rabell et al



Genome Wide Association Studies

SHEARF5



Optimizing use of technologies

Proportion Captured	AI	MOET	JIVET	Dams Used	G/yr (\$)	L
0.06	0.95	0.00	0.05	261	\$2.26	1.87
0.32	0.77	0.04	0.19	221	\$2.82	1.46
0.64	0.36	0.10	0.54	136	\$3.96	1.21

Conclusions

- A number of challenges related to implementing genomic selection in sheep, but there are clear benefits
- We need to increase the accuracy and across breed prediction

