

Genomic selection in populations with low connectedness between herds

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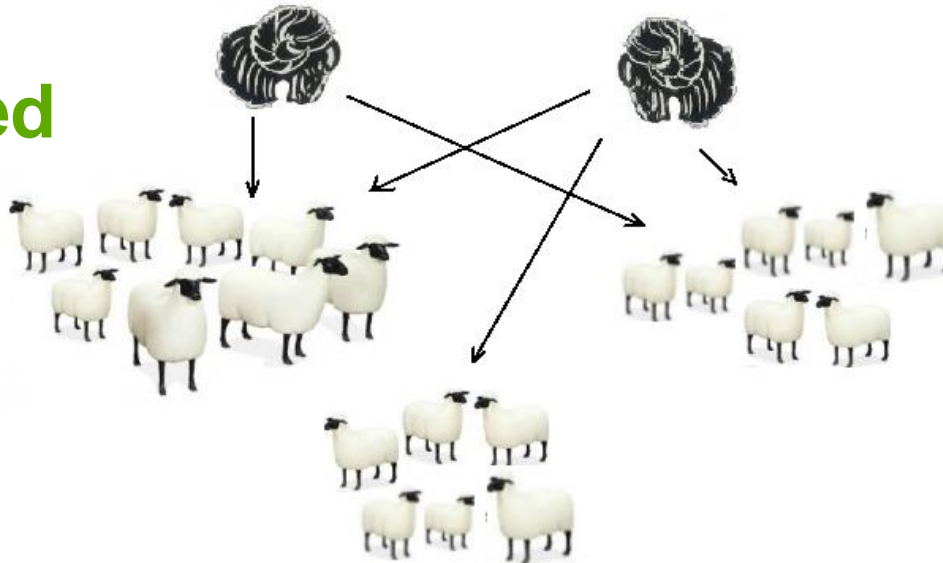
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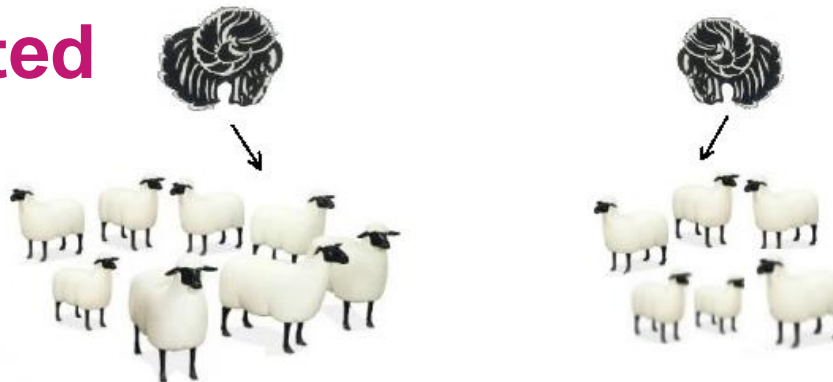
Genetic evaluation & Connectedness

$$\text{Phenotype} = f(\text{Genotype}, \text{Environment})$$

Connected



Disconnected



- Bias
- Comparison across sub-pops.?

The genomic promise

- Connectedness = estimability of contrasts between genetic effects
- Pedigree model
 - multiple sires in one environment or
 - one sire in multiple environments
- Genomic model
 - genome segments in multiple environments

AIM: Compare pedigree and genomic evaluation under varying levels of connectedness

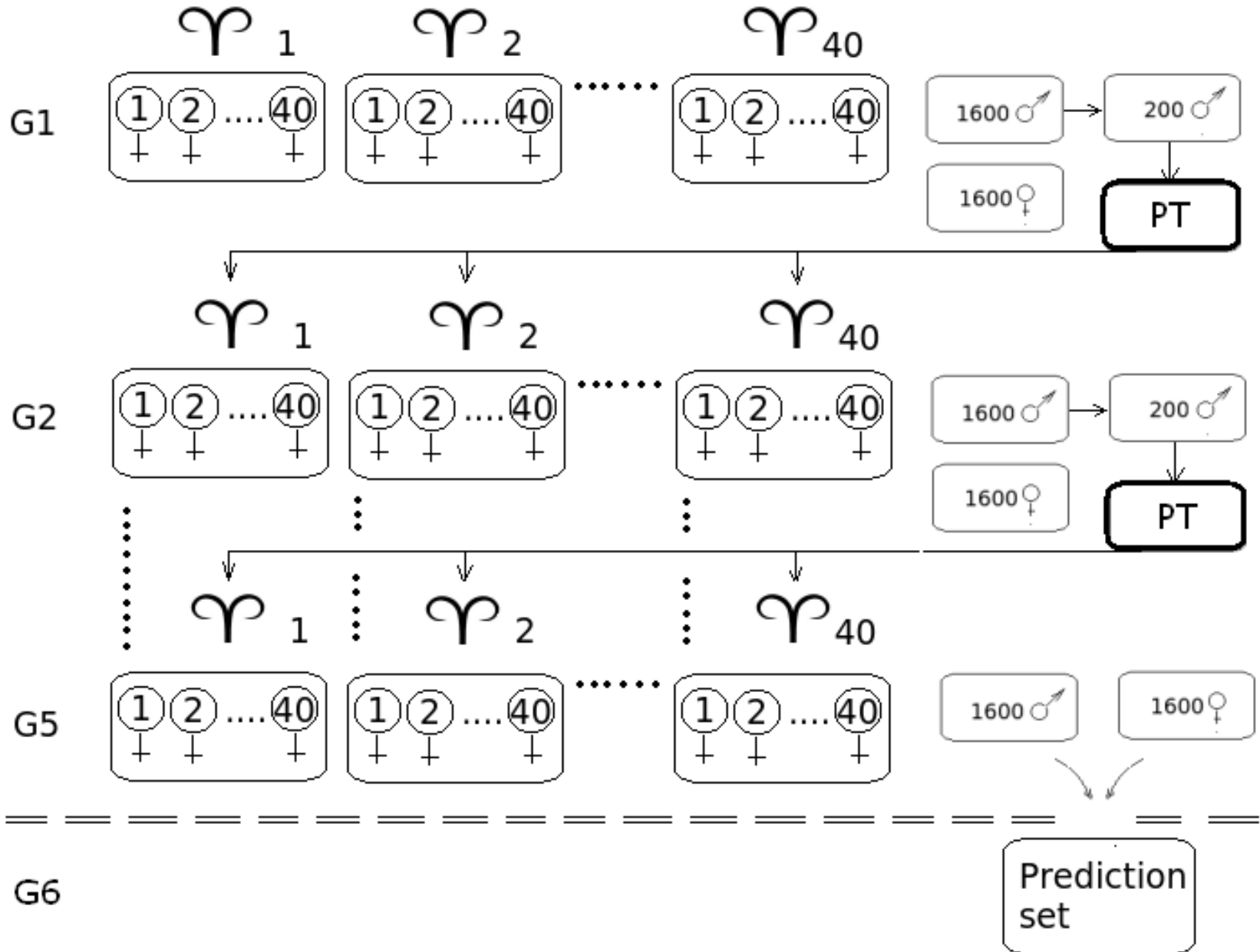


Simulation study (AlphaSim, R, & Wombat)

- Coalescent simulation of sheep genome
 - 300 causal loci per chrom.
 - 2000 markers per chrom. → 54K array
 - Sex-limited trait with 0.3 heritability
-
- Breeding program with progeny testing
 - Varying level of connectedness
 - Genotype tested males or their progeny
 - Pedigree evaluation
 - Genomic evaluation (GBLUP or HBLUP)



Breeding program - nucleus

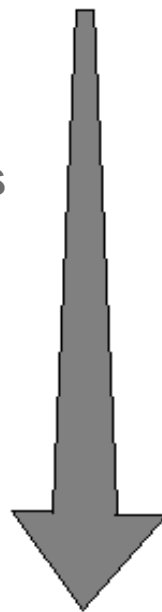


Breeding program – progeny test

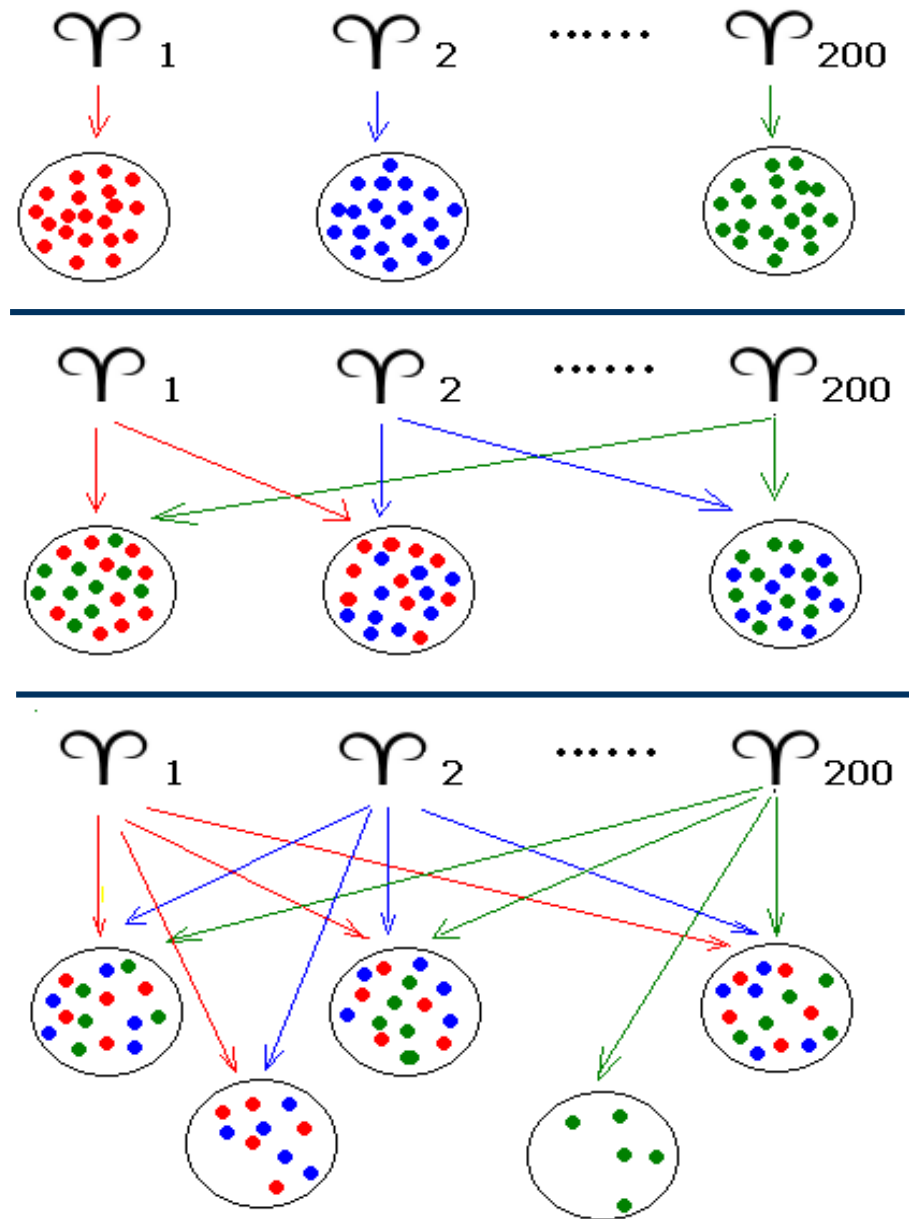
Separate from nucleus
to boost disconnectedness

dis-connected

Gradient of connectedness
20 progeny allocated to
1, 2, 4, 10, 20 management
units

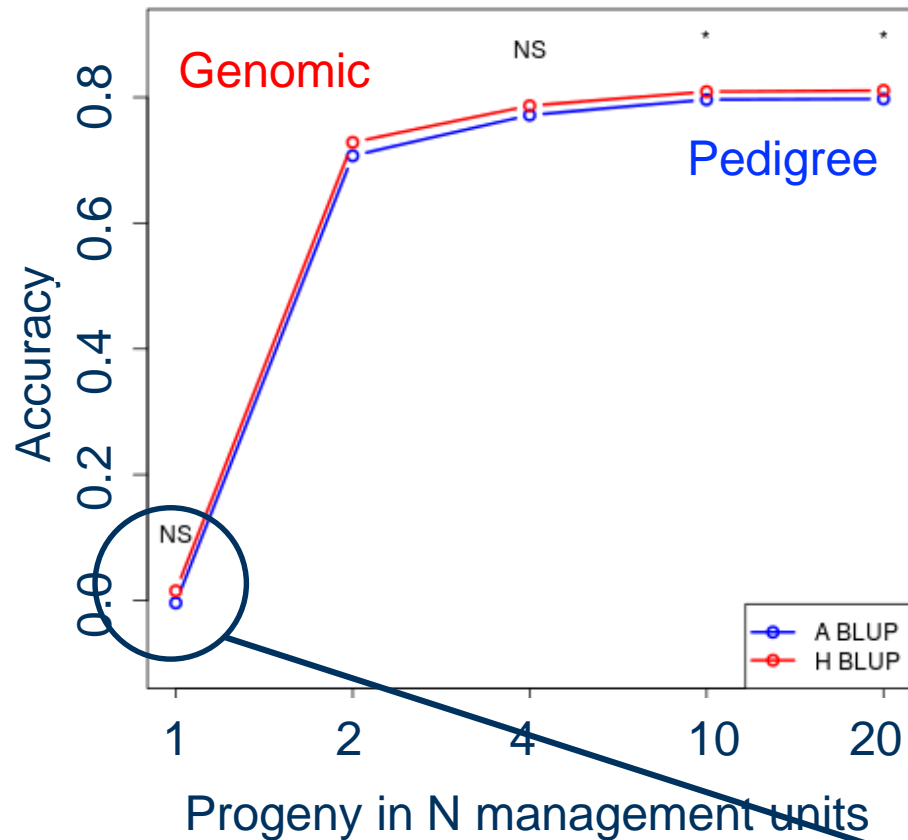


connected

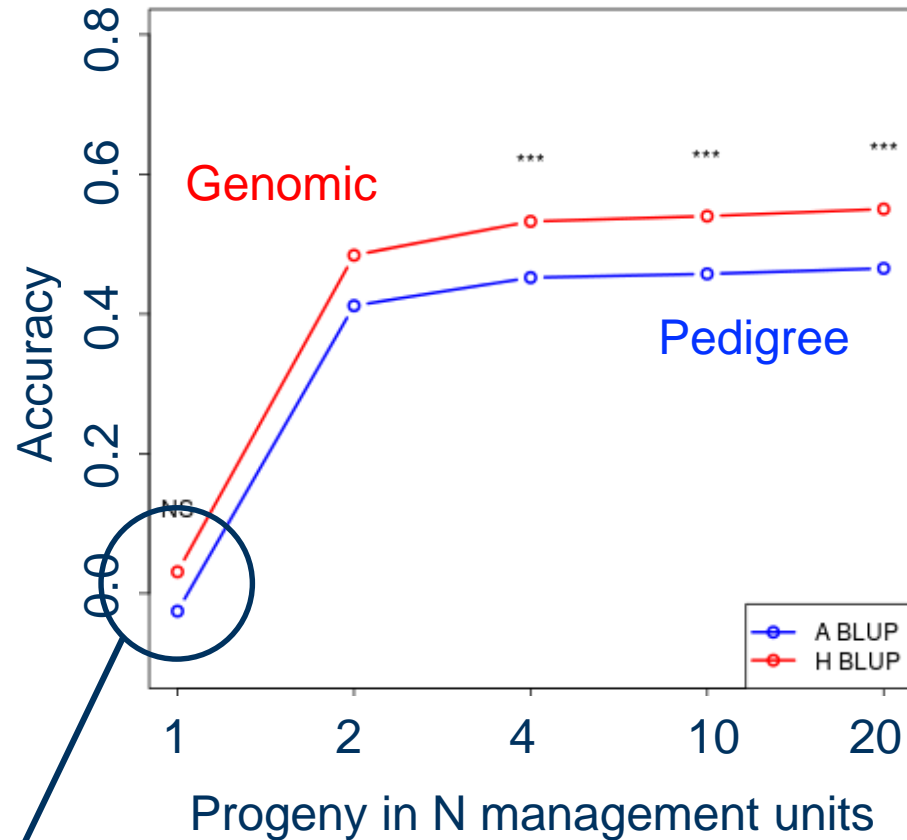


Results (ignore nucleus phenotypes → ~GBLUP)

Training set
Progeny tested males



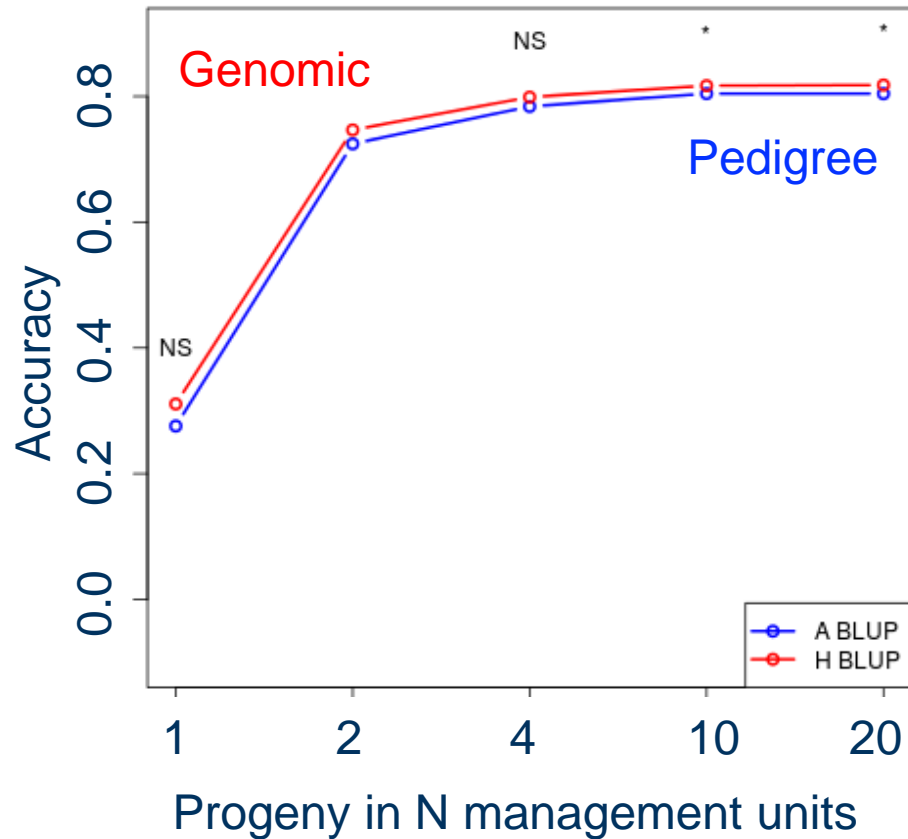
Prediction set
Non-phenotyped progeny



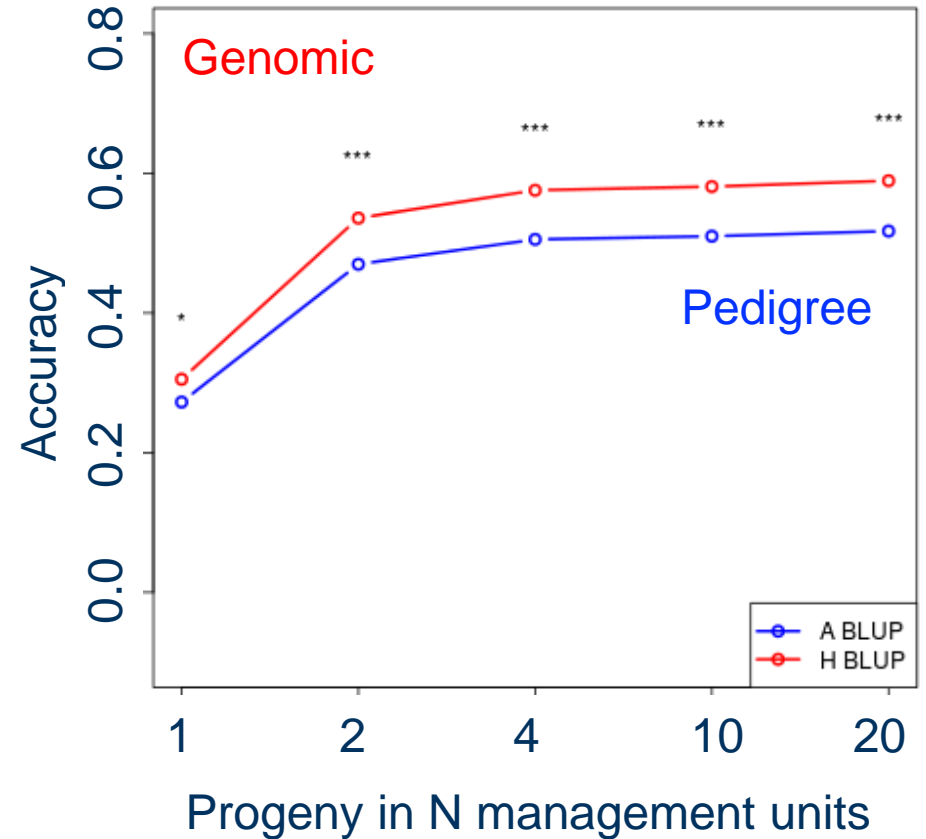
Inaccurate regardless of the method!

Results (utilize nucleus phenotypes → ~HBLUP)

Training set
Progeny tested males



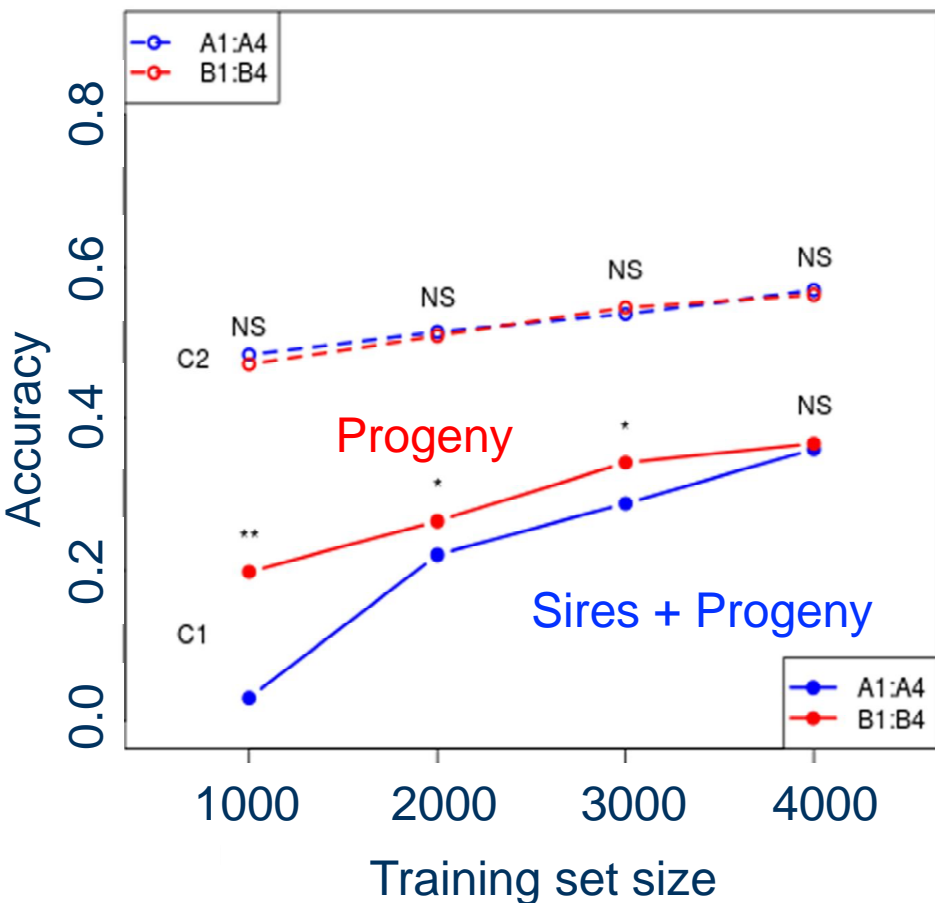
Prediction set
Non-phenotyped progeny



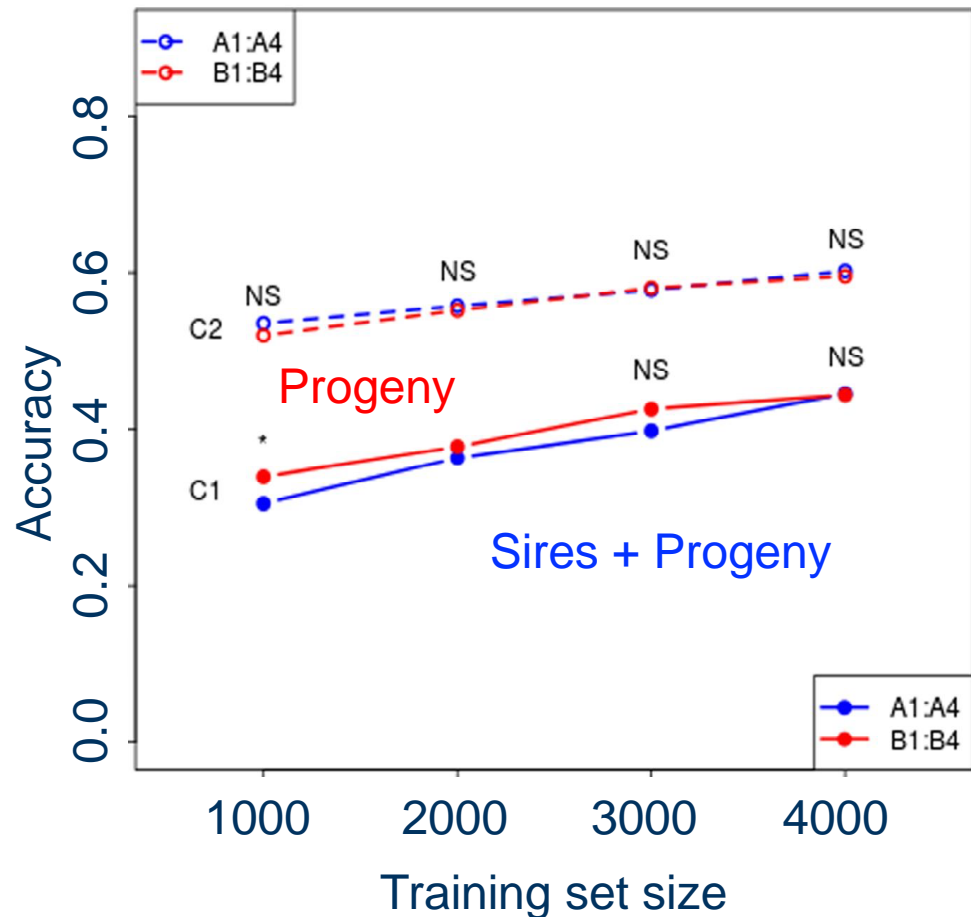
Increased accuracy due to improved connectedness/estimability

Results (alternative genotyping strategy)

Prediction set
(ignore nucleus phenotypes → ~ GBLUP)



Prediction set
(utilize nucleus phenotypes → ~ HBLUP)



In the case of complete disconnectedness,
genotype phenotyped individuals → genome segment testing!!!

Conclusions

- Connectedness an issue in some sectors
- It affects genomic and pedigree evaluation of males in the same way
- Single-step increases connectedness
- To kick-start genomic selection in disconnected programs focus on genotyping phenotyped individuals





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