The impact of genotypic information on changes in breeding value accuracy for health traits in meat sheep

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Footrot and mastitis



- Hard to measure health traits
- Great influence on the welfare of the animals
- Can cause significant losses for the industry



Footrot and mastitis – phenotypes



- Footrot
 - Each hoof scored: range 0 to 4
 - All four scores summed together: range 0 to 16
- Mastitis as proxy trait: California Mastitis Test
 (CMT) correlated with SCC up to 0.98
 - Milk sample from each side of the udder scored: range 0 to 4
 - Two scores from two sides summed together: range 0 to 8





Is there a potential for selection?



 Phenotypes collected on 30 Texel Sheep phenotype partner farms between 2015 and 2019:

• Footrot: 9,123

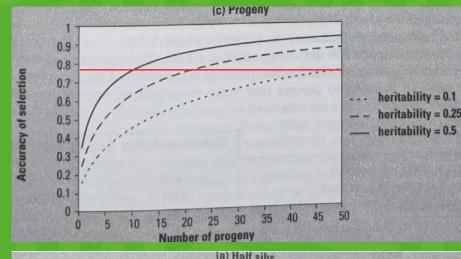
• CMT: 4,787

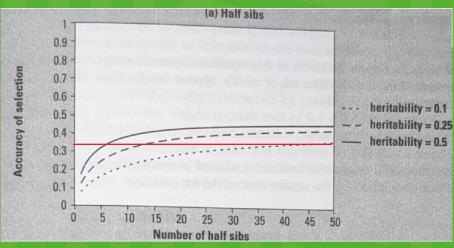
direct	PE	residual	phenotypic	heritability
0.04 (0.01)		0.28 (0.01)	0.32 (0.01)	0.12 (0.02)
0.04 (0.01)	0.07 (0.02)	0.40 (0.02)	0.51 (0.01)	0.07 (0.03)
	0.04 (0.01)	0.04 (0.01)	0.04 (0.01) 0.28 (0.01)	0.04 (0.01)



Accuracy of Estimated Breeding Values (EBVs)







Conventional approach (pedigree + phenotypes):

- requires many phenotypes
- takes long time to achieve satisfactory (trustworthy) accuracy



G. Simm 'Genetic Improvement of Cattle and Sheep'

Can we speed up?

- 10,193 (9,391 after Quality Control) Texel genotypes
- Reference population (genotyped + phenotyped)
 - footrot: 3,779
 - CMT: 2,909 animals

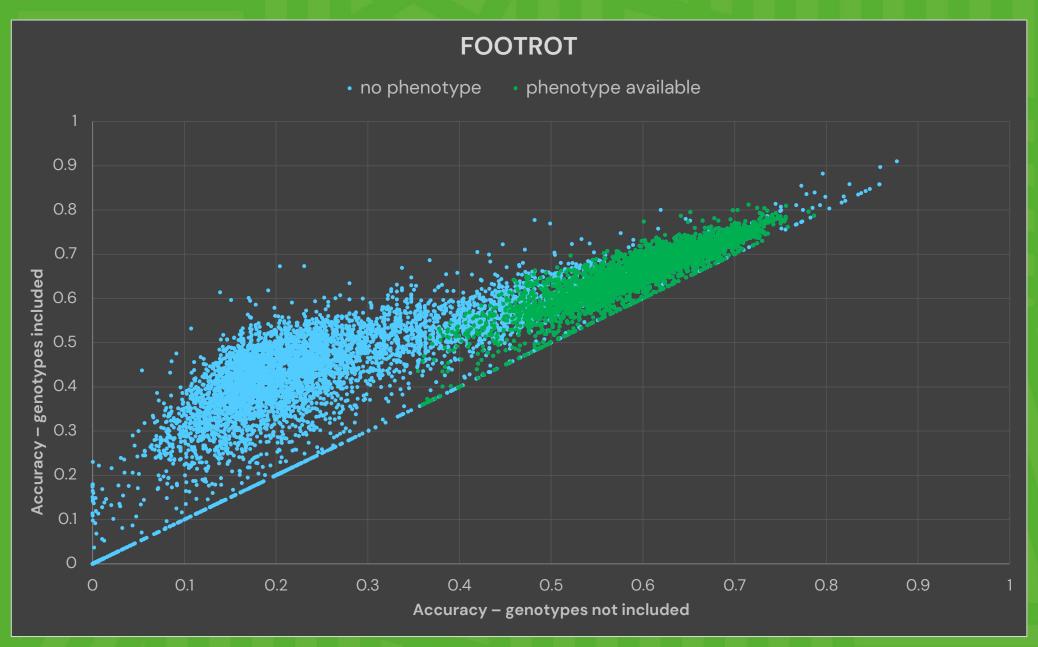
+Additional checks that can be done on genotypes: parentage, diseases, desirable genes









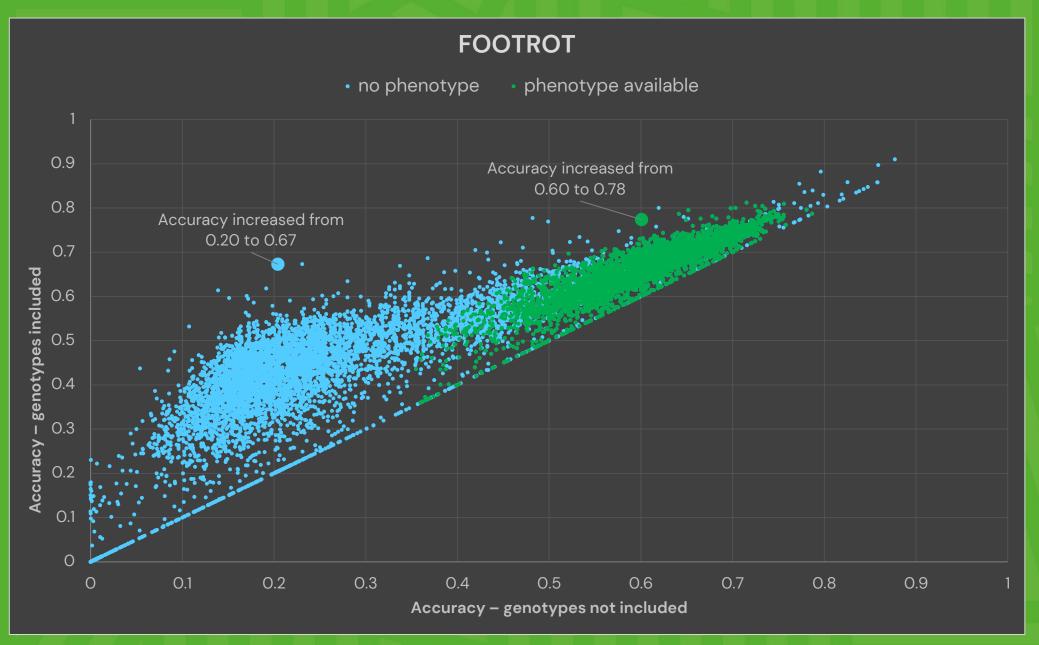




Heritability 12%

- +0.18 with phenotype
- +0.47 no phenotype



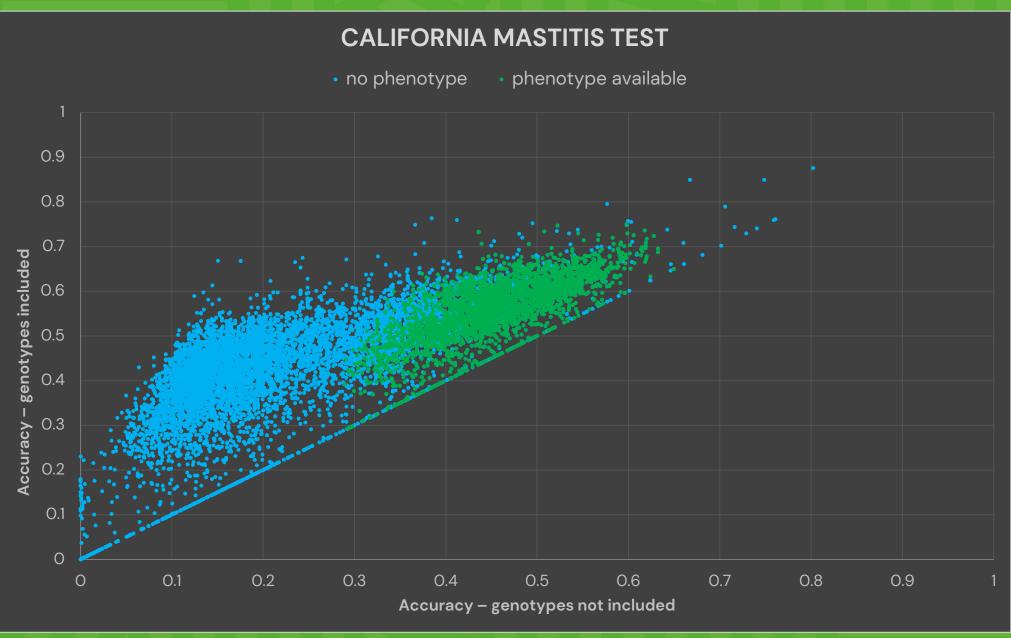




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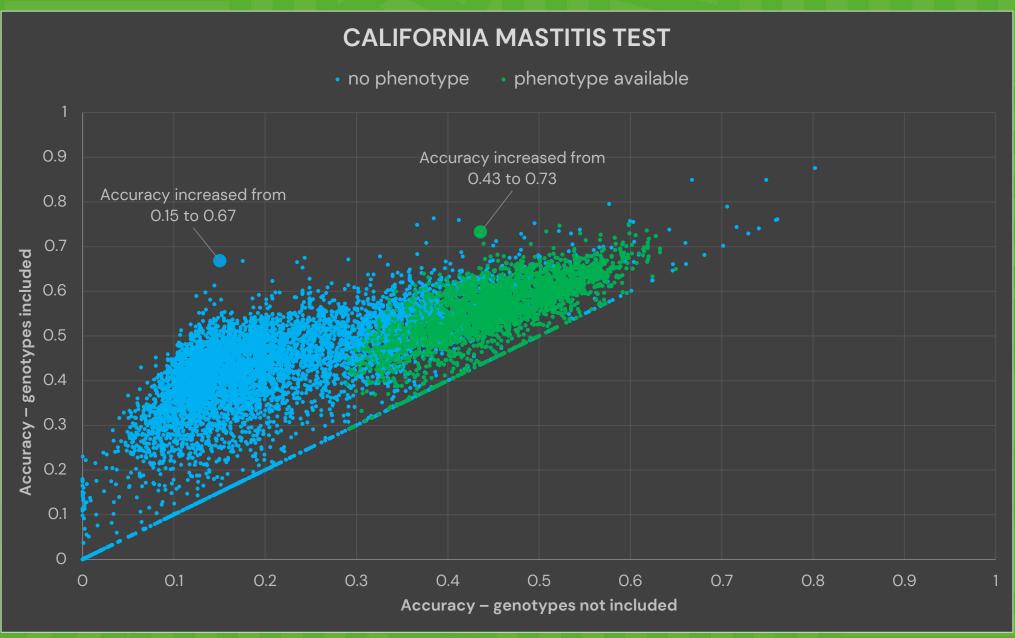




Heritability 7%

- +0.30 with phenotype
- +0.52 no phenotype



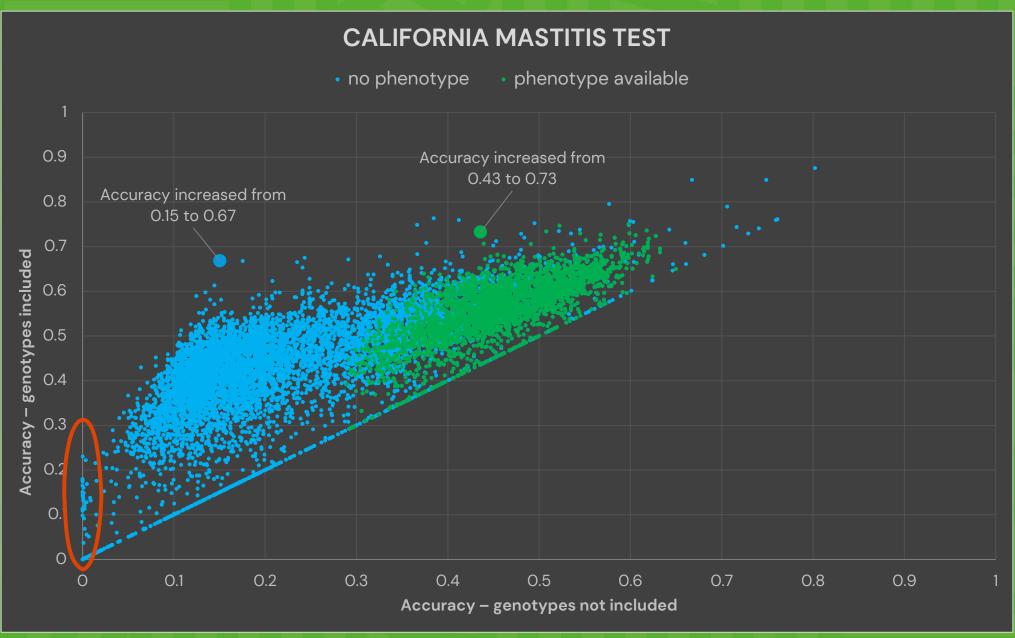




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conclusions



 Animals without phenotypic data gain the most in EBV accuracy when genotypic information is included

 Improving both genotyping and phenotyping would enhance the accuracy of genetic evaluations



This work was funded by H2O2O SMARTER project ID 772787, InnovateUK project ID 102646 (BBSRC project no. BB MO2833X/1) and InnovateUK project ID 131791.



Innovate UK





