Impact of genotypic information on genetic evaluation accuracy for mastitis and footrot in the UK Texel Sheep



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What are footrot and mastitis?



- Important endemic diseases affecting animal welfare
- Hard to measure health traits

•Impacting productivity – can cause significant losses for the

industry







What are footrot and mastitis?



Losses:

- •Imp •
- Hard
- •Imp indu
- £3.60 per lamb loss in growth rate suckling from affected ewes with mastitis (unpublished results)
- **£8.40** per ewe if footrot prevalence was reduced by 10%

Conington, J., Cao, G., Stott, A., Bünger, L. (2008)

Breeding for resistance to mastitis in United Kingdom sheep – a review and economic appraisal. Veterinary Record 162: 369-376

March 22nd. DOI: 10.1136/vr.162.12.369





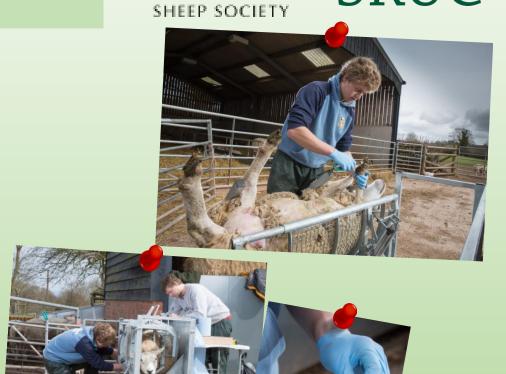




Collection of phenotypes

- 32 phenotype partner farms across the UK
- Footrot (FR)
 - Each hoof scored: range 0 to 4
 - Max total score 16
- Mastitis –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
 - Max total score 8
- Both FR and CMT log transformed to normalise distribution





Is there potential for selection?



Phenotypes collected between 2015 and 2019:

• Footrot: 9,123 records

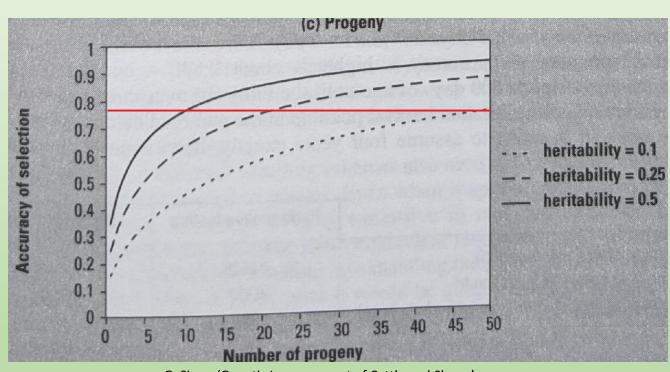
• CMT: 4,787 records

Estimated variance (SE)	direct	PE	residual	phenotypic	heritability
Footrot	0.04 (0.01)		0.28 (0.01)	0.32 (0.01)	0.12 (0.02)
California Mastitis Test	0.04 (0.01)	0.07 (0.02)	0.40 (0.02)	0.51 (0.01)	0.07 (0.03)



What accuracy can we expect?





G. Simm 'Genetic Improvement of Cattle and Sheep'

Conventional BLUP approach (pedigree + phenotypes):

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



Collection of genotypes



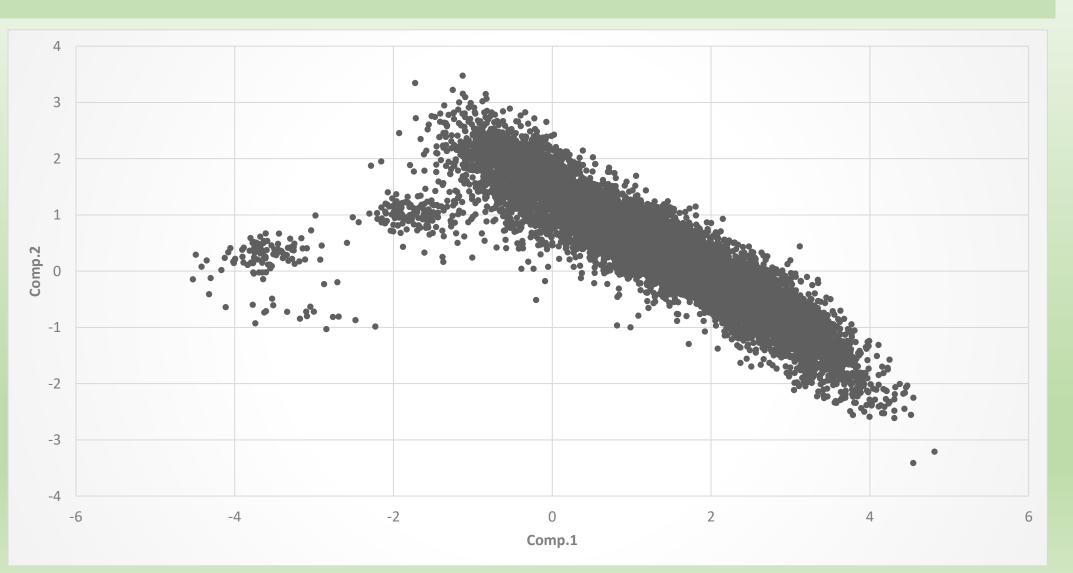
- Total of **10,193** Texel genotypes:
 - Illumina OvineHD BeadChip with 606,006 SNPs (HD)
 - Illumina OvineSNP50 with 54,241 SNPs (50K)
 - Illumina OvineLD BeadChip with 15,000 SNPs (LDv1)
 - Illumina OvineLD BeadChip with 16,560 SNPs (LDv2)
- Quality Control left 9,391 genotypes
- Reference population (genotyped + phenotyped)
 - Footrot: **3,779** ewes
 - CMT: **2,909** ewes





Population structure

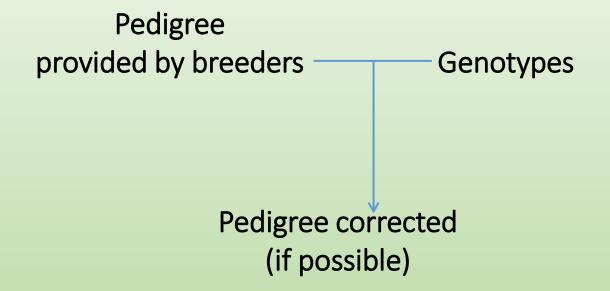




14.8% and 4.7% of variation explained by first and second component







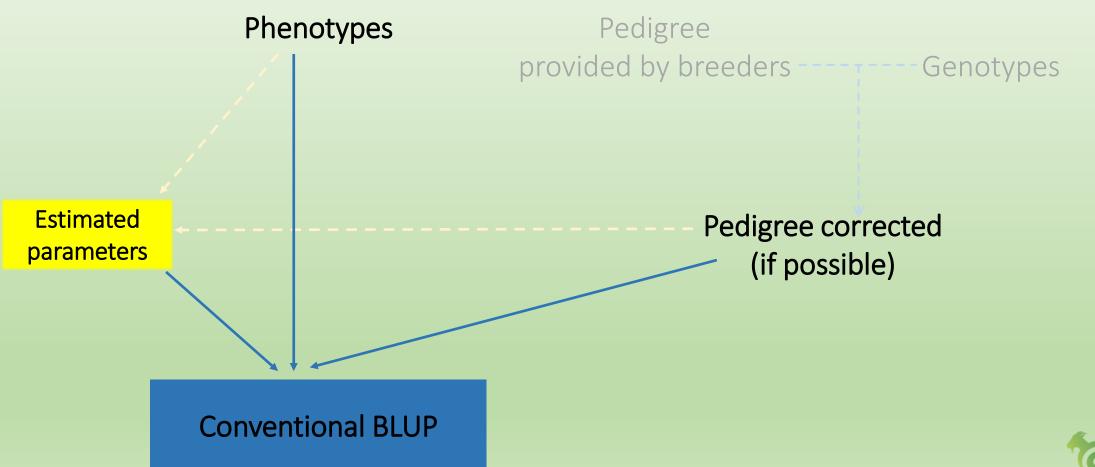








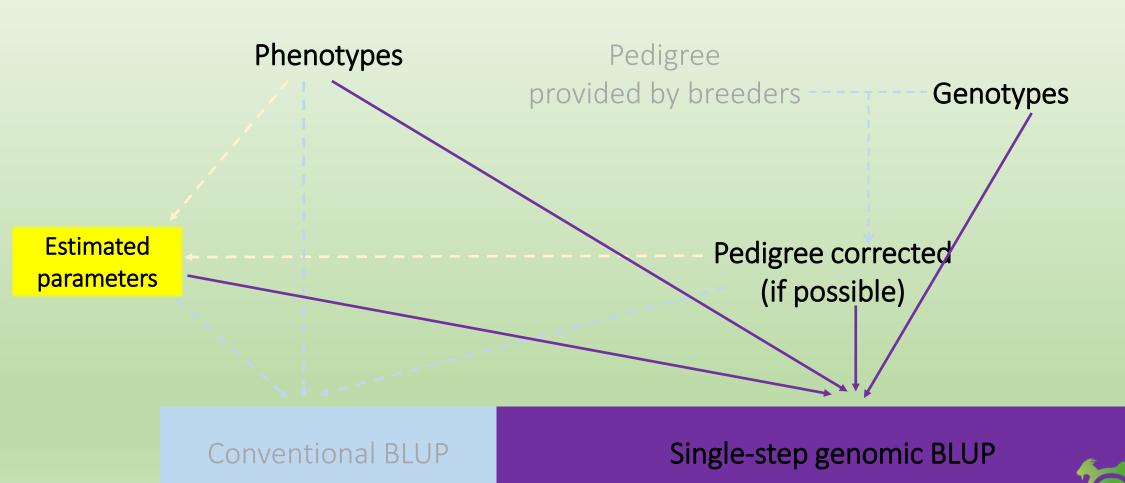


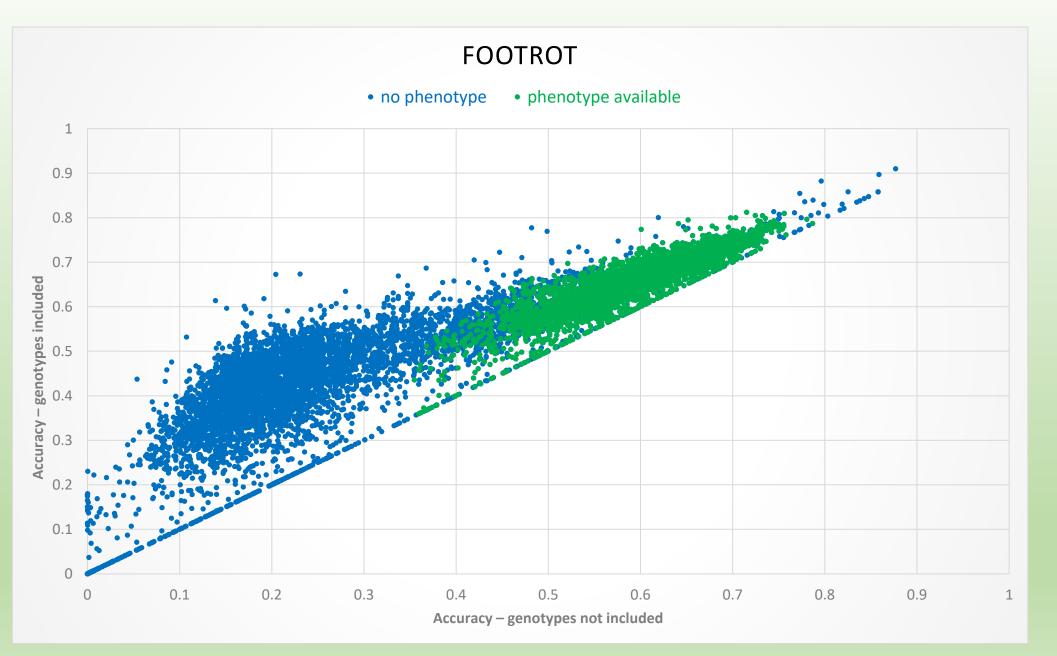






SMAII RuminanTs breeding for Efficiency and Resilience







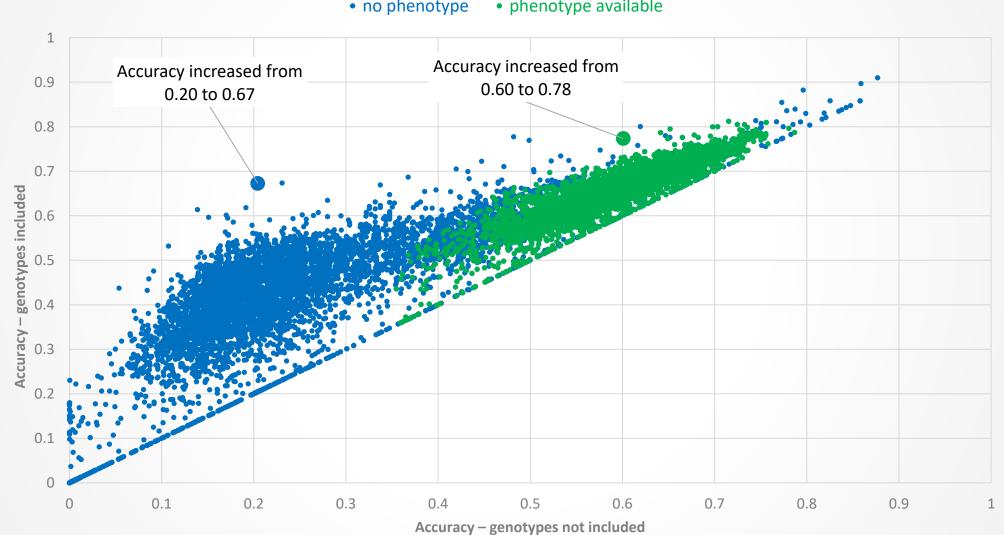
Heritability 12%

- +0.18 with phenotype
- +0.47 no phenotype



FOOTROT

- no phenotype
- phenotype available





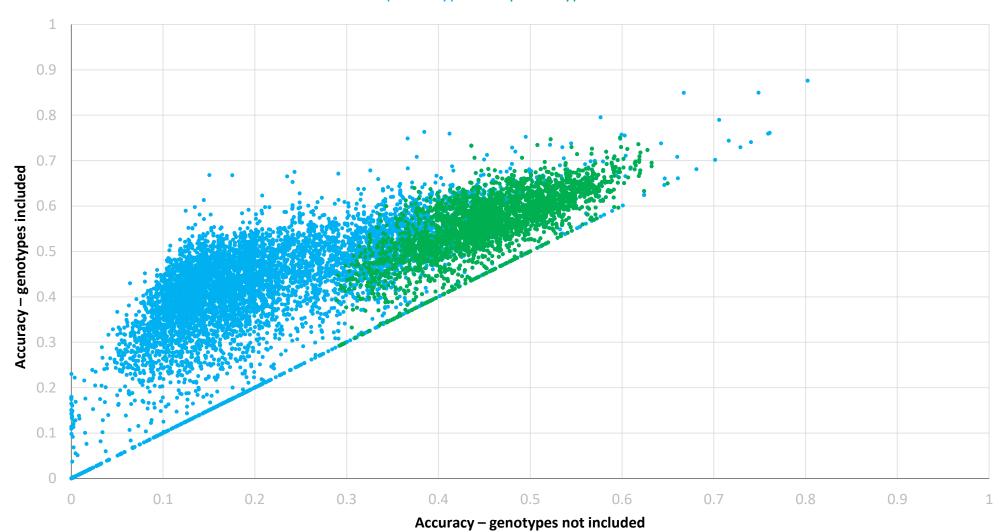
Heritability 12%

- +0.18 with phenotype
- +0.47 no phenotype



CALIFORNIA MASTITIS TEST

no phenotype
 phenotype available





Heritability 7%

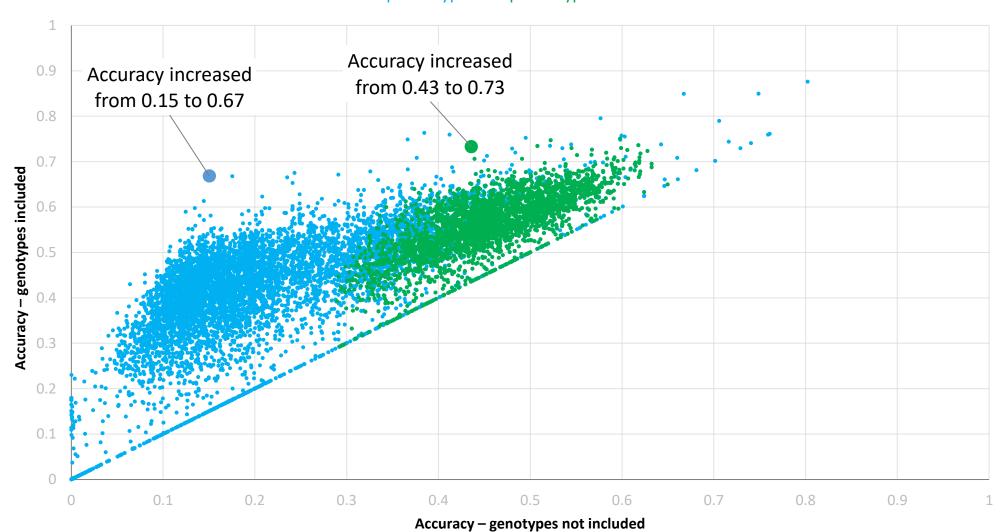
- +0.30 with phenotype
- +0.52 no phenotype



CALIFORNIA MASTITIS TEST

no phenotype

phenotype available





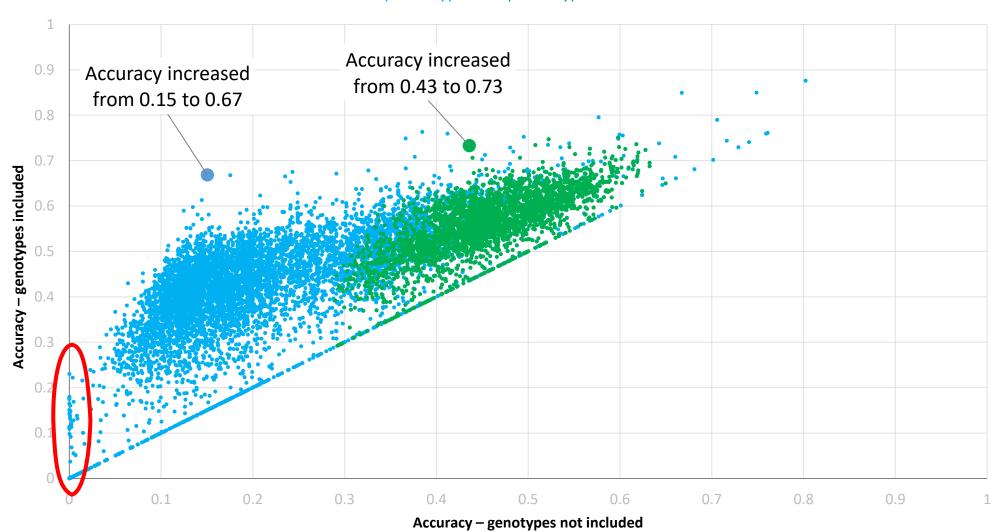
Heritability 7%

- +0.30 with phenotype
- +0.52 no phenotype



CALIFORNIA MASTITIS TEST

no phenotype
 phenotype available





Heritability 7%

- +0.30 with phenotype
- +0.52 no phenotype



Conclusions



• With a properly designed reference population, the use of genomic information is beneficial for non-phenotyped animals

 Improving both genotyping and phenotyping would enhance the accuracy of genetic evaluations for footrot and mastitis, which means Estimated Breeding Values (EBVs) for these traits could be published for more animals





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Innovate UK

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The Scottish Government Riaghaltas na h-Alba