

# Including genotypic data in breeding values for mastitis in sheep increases accuracy of prediction

**K. Kaseja<sup>1</sup>, S. Mucha<sup>1</sup>, E. Smith<sup>2</sup>, J. Yates<sup>2</sup>, G. Banos<sup>1</sup>, J. Conington<sup>1</sup>**

<sup>1</sup> SRUC Easter Bush, Roslin Institute Building, Edinburgh EH25 9RG, UK

<sup>2</sup> The British Texel Sheep Society, Stoneleigh Park, Warwickshire, CV8 2LG

# What is mastitis?

- **Bacterial infection of the udder**
- **Hard to measure health trait**
  - Somatic Cell Count (SCC) has been used as the key indicator in mastitis – lab work
- **Great influence on the welfare of both ewe and lamb**
  - Severe cases can result in death of the ewe
  - Reduction in milk production, milk fat and milk protein lead to reduced lamb growth and higher risk of lamb mortality
- **Can cause significant losses for the industry**

# Collected phenotypes

- 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



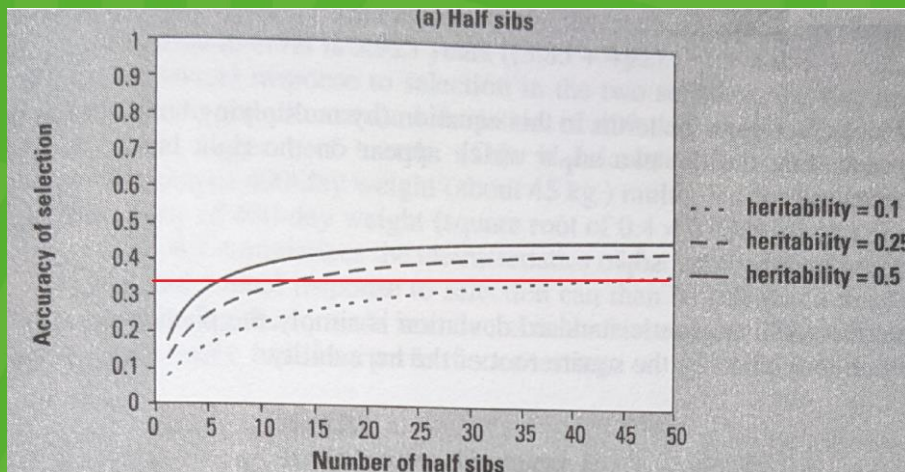
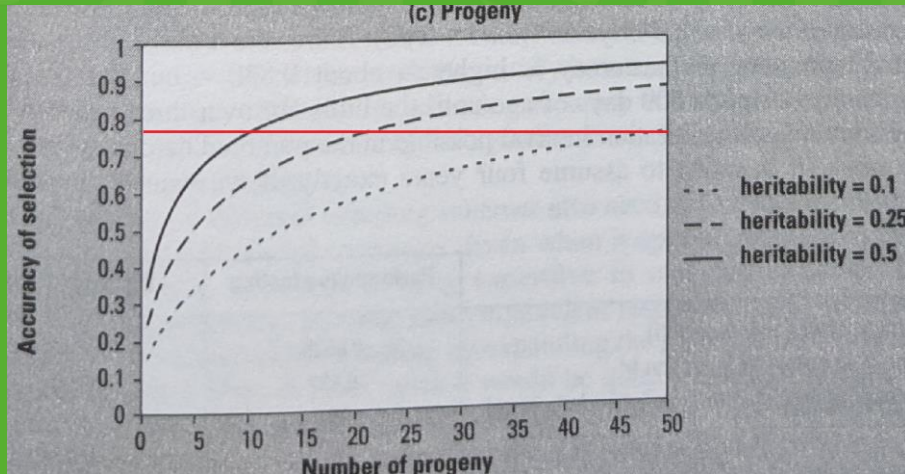
# Is there a potential for selection?

- Phenotypes collected on 30 Texel Sheep phenotype partner farms between 2015 and 2019:
  - CMT: 4,787

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



# Accuracy of Estimated Breeding Values (EBVs)



- Conventional approach (pedigree + phenotypes):
- requires many phenotypes
  - takes long time to achieve satisfactory (trustworthy) accuracy

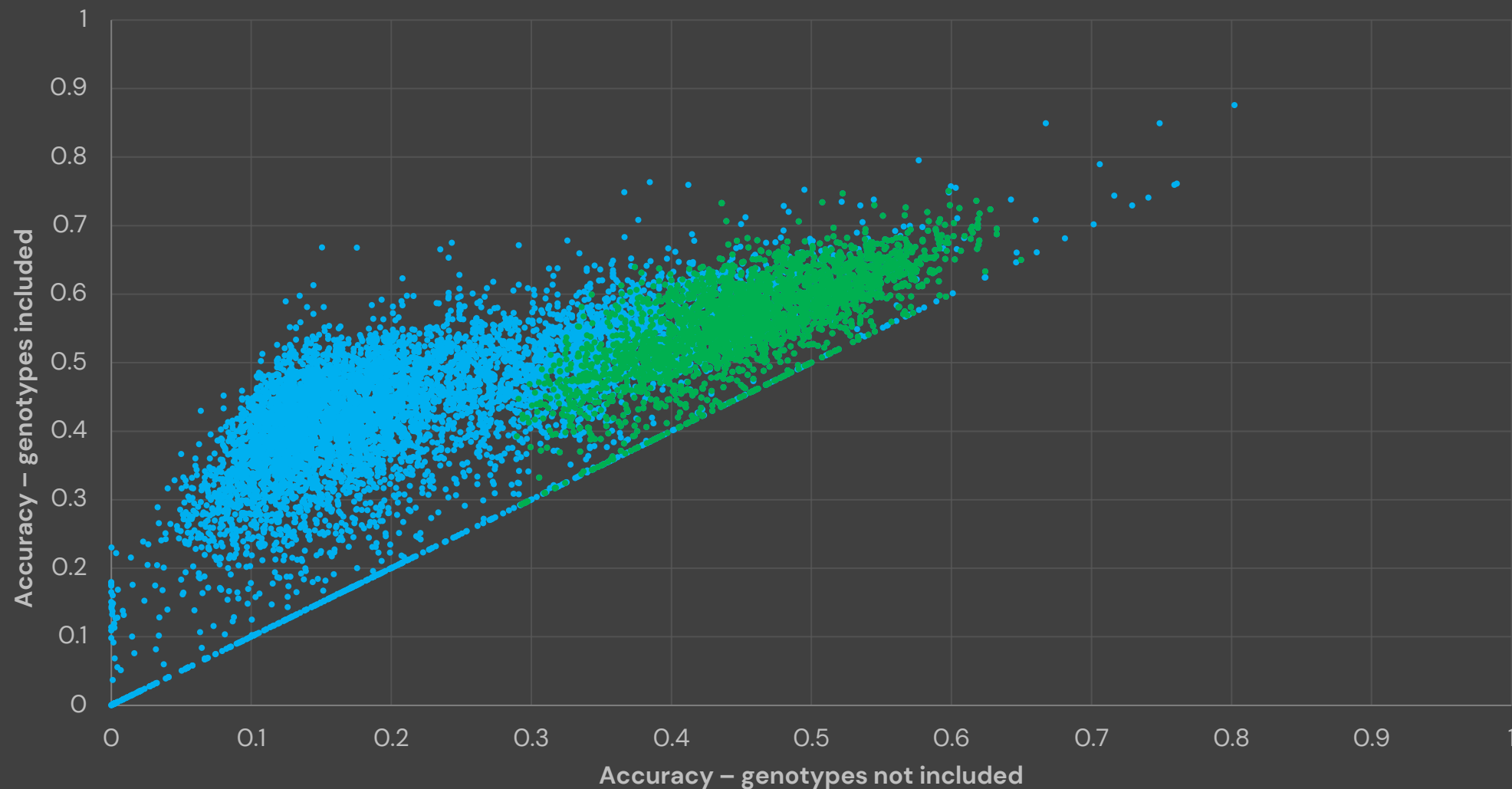
# Can we speed up?

- 10,193 (**9,391** after Quality Control) Texel genotypes
  - Reference population (genotyped + phenotyped): **2,909** animals
- + Additional checks that can be done on genotypes: parentage, diseases, desirable genes



## CALIFORNIA MASTITIS TEST

• no phenotype    • phenotype available



SRUC



Heritability 7%

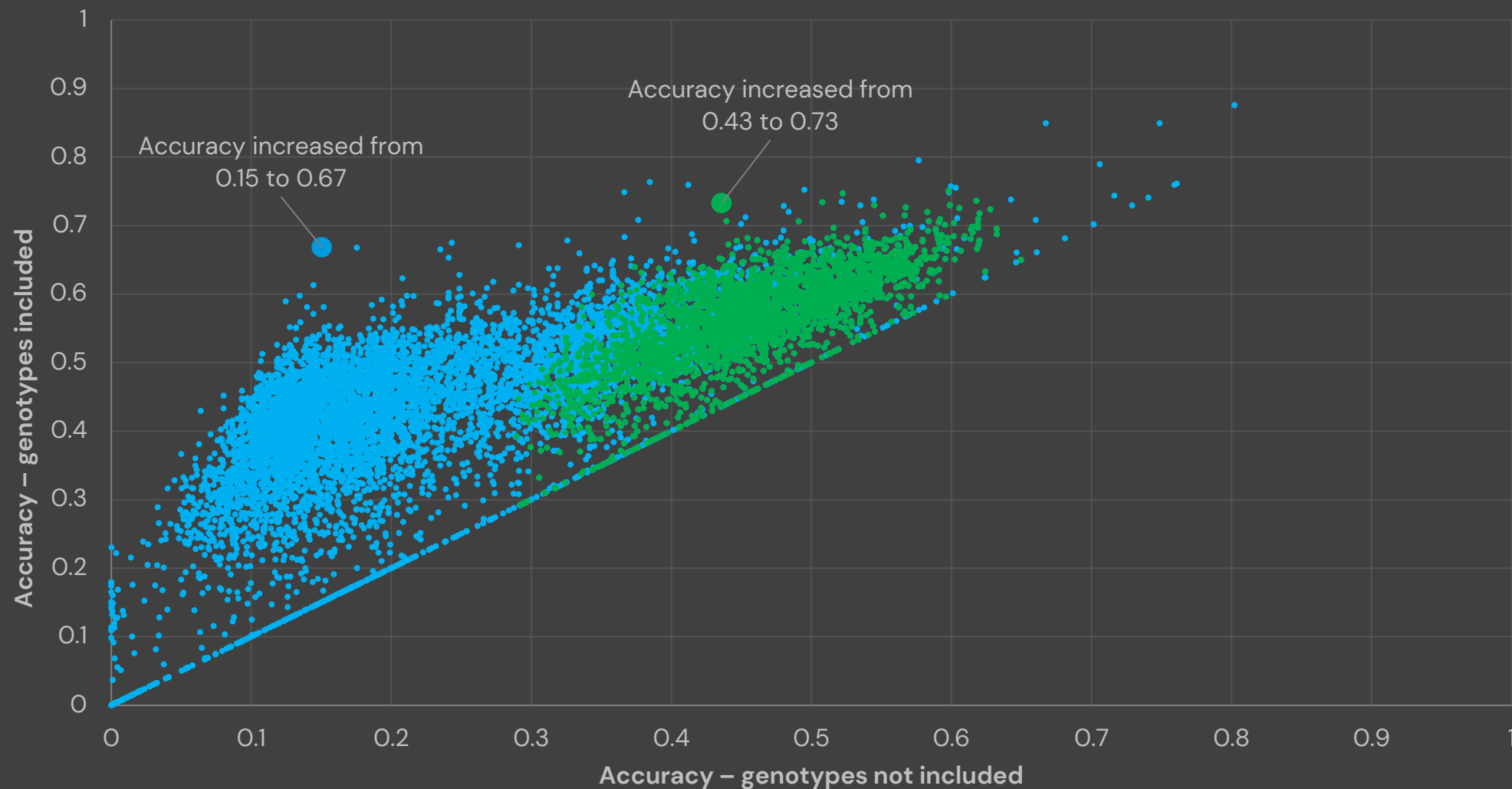
Max change:

- +0.30 with phenotype
- +0.52 no phenotype

K.Kaseja et al. (2021)

## CALIFORNIA MASTITIS TEST

• no phenotype    • phenotype available



SRUC



Heritability 7%

Max change:

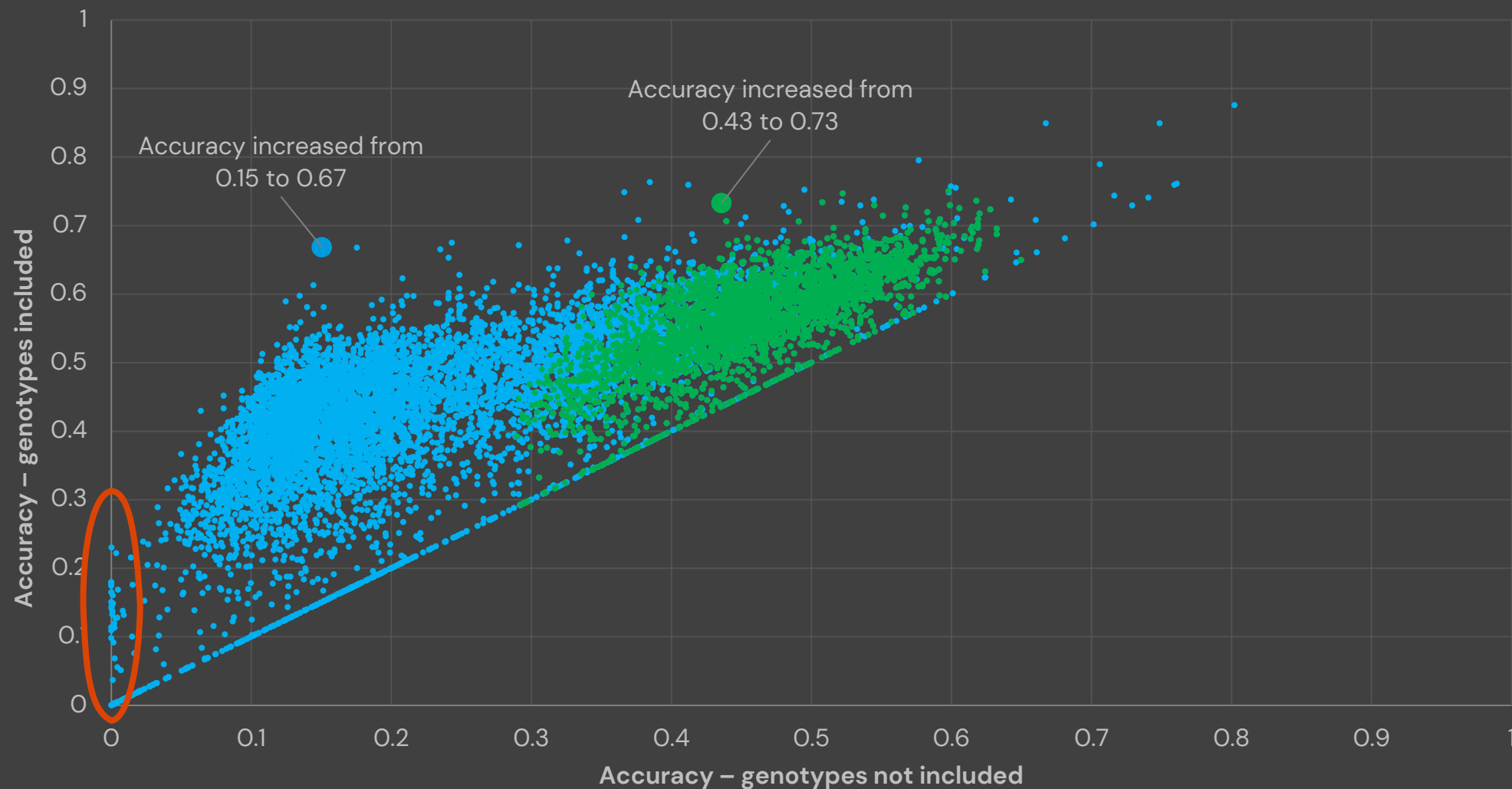
- +0.30 with phenotype
- +0.52 no phenotype

K.Kaseja et al. (2021)



## CALIFORNIA MASTITIS TEST

• no phenotype    • phenotype available



SRUC



Heritability 7%

Max change:

- +0.30 with phenotype
- +0.52 no phenotype

K.Kaseja et al. (2021)

# 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 prediction of breeding values



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



**The Scottish  
Government**  
Riaghaltas na h-Alba



[www.sruc.ac.uk](http://www.sruc.ac.uk)