Using genomic technology to reduce mastitis in meat sheep

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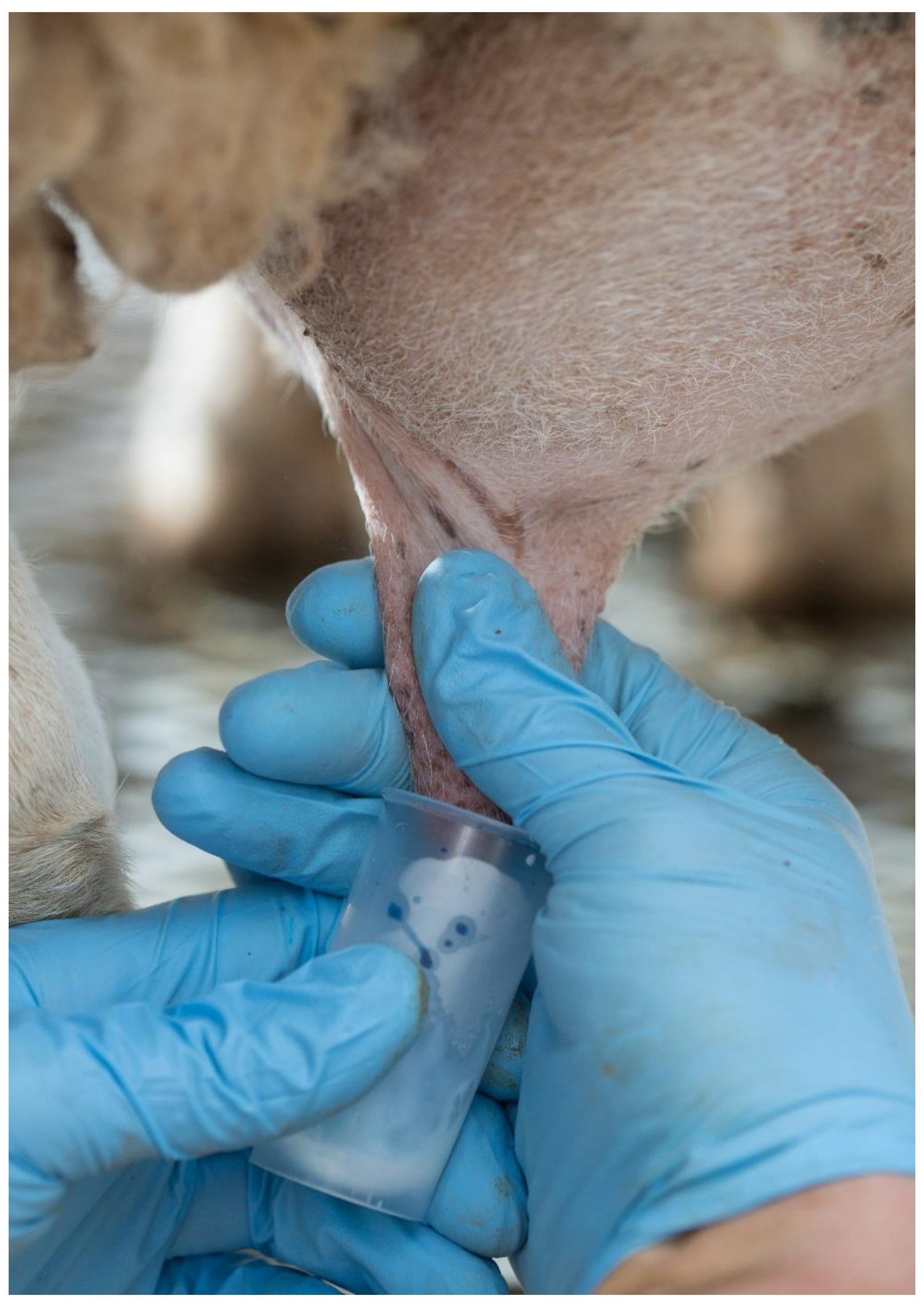
Introduction

- Performance-recorded Texel flocks, located throughout the UK, are involved in a new study to determine the 'best' way to breed more resistant sheep to mastitis.
- Mastitis in meat-producing sheep can cost the industry millions of pounds each year due to:
  - Poor performance. (e.g. poor lamb growth rates)
  - Increased medical costs.
  - Premature culling of affected animals.
- Preliminary results (433 Texel ewes from 5 flocks) found that 28% of ewes had abnormal udders.
- Reducing the risk of contracting mastitis by 10%
  - Could save the purebred Texel breed approximately £2.7 million pounds a year (Conington *et al., 2008*).
- Genomic technology provides an opportunity to identify genetically resistant animals.

Methods

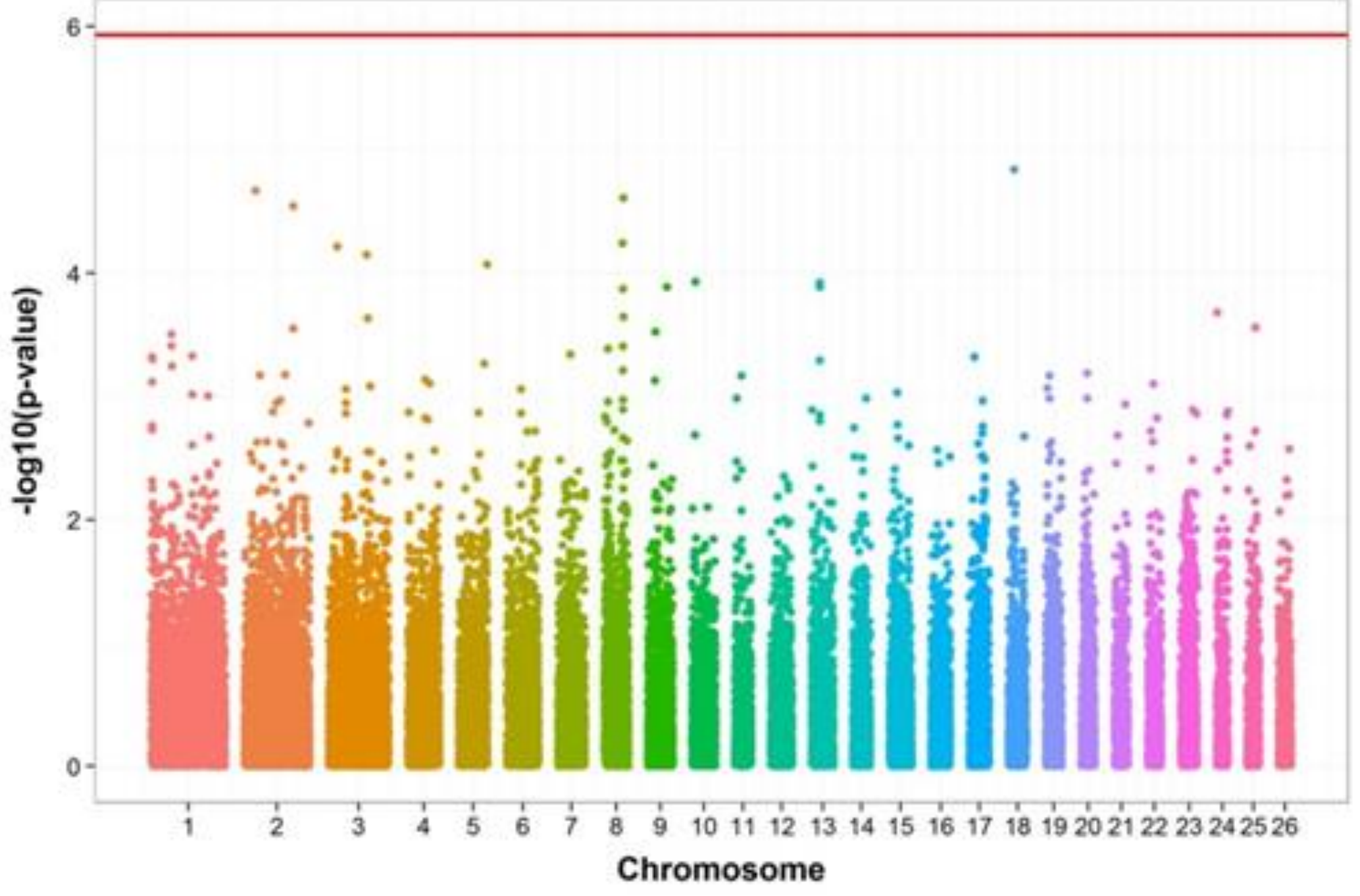
- Approximately 3,500 ewes (from 25 different flocks) will be scored and genotyped during two years of data collection.
- Visits made to each flock twice a year to record ewes post-lambing
  - Mid-lactation
  - Late-lactation/weaning
- Milk samples tested in different ways for signs of mastitis
  - Somatic Cell Counts
  - California Milk Test (CMT)
- Udder characteristics scored in a similar way to that of dairy animals.
  - Udder traits include:
    - Udder Attachment
    - Udder Drop
    - Udder Width
  - Teat traits include:
    - Teat Size
    - Teat Angle
    - Teat Placement
- Lumps and lesions also recorded



- DNA samples are collected using a nasal swab.
- These will be genotyped using high (700K) and medium (50K) density ovine single nucleotide polymorphism (SNP) bead chips.
- Genome wide association study (GWAS) will be carried out using the Multi-Locus Mixed Model (MLMM) algorithm.
- Genomic estimated breeding values (GEBVs) will be predicted using the single-step method
  - Integrates pedigree, genotype and phenotype data.
  - Imputation from 50K to 700K.

What do we hope to achieve?

- Identify if any existing SNPs on the sheep genome are linked to mastitis (similar to work carried out for footrot, Mucha *et al., 2015*).



- Predict both genetic (EBVs) and genomic (GEBVs) estimated breeding values for mastitis resistance.
- Identify the most appropriate phenotypes to record on-farm.
- Improve breed resistance to mastitis and reduce antibiotic use.
- Provide farmers with new tools to
  - Improve animal welfare
  - Improve production
  - Increase overall sustainability

Acknowledgements

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Conington, J., Cao, G., Stott, A. and L. Bunger. 2008. *Vet. Rec.* 162, 369-376
Mucha, S., Bunger, L and J. Conington. 2015. *Genet. Select. Evol.* 47:35 ,