Australian Wool Innovation Limited

2018 BREECH FLYSTRIKE RD&E

TECHNICAL UPDATE

Breeding for Breech Strike Resistance – Genomics Update

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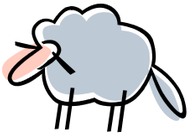
GOOD REASONS FOR A GENOMIC APPROACH



- Flystrike and indicator traits are heritable
- Correlations between flystrike and indictor traits favourable for selection purposes
- Flystrike itself remains difficult to measure, but excellent phenotype resource available in 2 research flocks
- Avenues that can fast track genetic progress can have a large impact on gain

Genomics and Breeding Programs

Genomic testing

Few markers
moderate to large effect

Lots of markers
small effect

Find gene/s and function

Marker assisted selection
Selection based on genetic marker profile

Genomic breeding values (GEBV)
Use information of ALL genetic markers

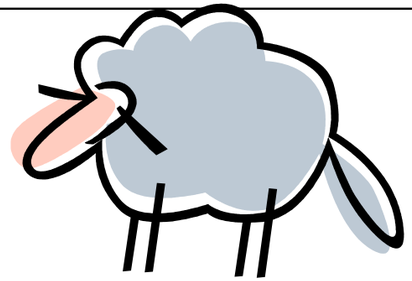
Increased accuracy of selection for flystrike resistance
Faster genetic gain progress

Can we identify regions on the genome associated with breech strike resistance?

Can we estimate genomic breeding values (GEBV) and how accurate are they?

How can we use the information best in breeding programs?

DATA & ANALYSIS

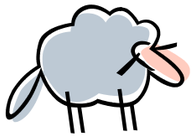


Illumina 700K HD
Genotype data
after quality control
948 samples
528,818 SNPs

Phenotype data
Breechstrike (STRIKE) (struck, no struck)
Breechcover (BCOV) (low, medium, high)
Wrinkle score (WRK) (low, medium, high)
Dag score (DAG) (low, medium, high)

Genome-wide association study
Estimation and Validation of GEBV

WHAT DID WE FIND IN PHASE 1? (First 5 drops)



- Found a large number of SNP with small effect
- Good indication for the use of Genomic Enhanced Breeding Values
- GEBV's accuracy currently around 11-15%
- Low density panels an option
- A closer look might reveal interesting genes

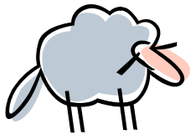
WE HAVE TAKEN A CLOSER LOOK

Differences in molecular signatures between Resistant vs Susceptible animals

The most promising region harbours a single gene with key role in the recognition of pathogens and initiation of immune response

RES and SUS are divergent for the SNP in that region, but needed more data

NEXT- PHASE 2 last 5 drops, final report due late 2018



50K genotypes of another 576 animals from NSW and WA Breech Strike Flocks

- Clearer phenotypic differentiation in the later 5 drops compared to first 5
- Another 576 animals in breech strike reference population, will increase accuracies
- Option to develop low density panels for cost-effect capture of variation
- Potential to follow up on interesting genes

This publication is based on information presented at the Australian Wool Innovation Limited (AWI) National Wool Research and Development Technical Update on Breech Flystrike Prevention held on 17th July 2018. Some information in this publication has been contributed by one or more third parties and licenced to AWI, and AWI has not verified whether this information is correct. This publication should only be used as a general aid and is not a substitute for specific advice. Any reliance on the information contained in this publication is done at your own risk and to the extent permitted by law, AWI and any third party contributors exclude all liability for loss or damage arising from the use of the information in this publication. Except to the extent permitted under Copyright Law no part of this publication may be reproduced by any process, electronic or otherwise without the specific written permission of AWI. Neither may information be stored electronically in any form whatsoever without such permission. AWI gratefully acknowledges the funds provided by the Australian government to support research, development and marketing of Australian wool. GD2792