Breeding for Breech Strike Resistance
Genomics Update

Sonja Dominik – CSIRO Agriculture and Food
17 July 2018
GOOD REASONS FOR A GENOMIC APPROACH

- Flystrike and indicator traits are heritable
- Correlations between flystrike and indicator 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

- **Find gene/s** and function

**Marker assisted selection**
Selection based on genetic marker profile

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

**Lots** of markers
*small* effect

**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