

AWI Breech Strike R&D Technical Update
Maritime Museum, Sydney
20th August 2014

Breech Flystrike Genomics
Jen Smith for Sonja Dominik
CSIRO Agriculture Flagship

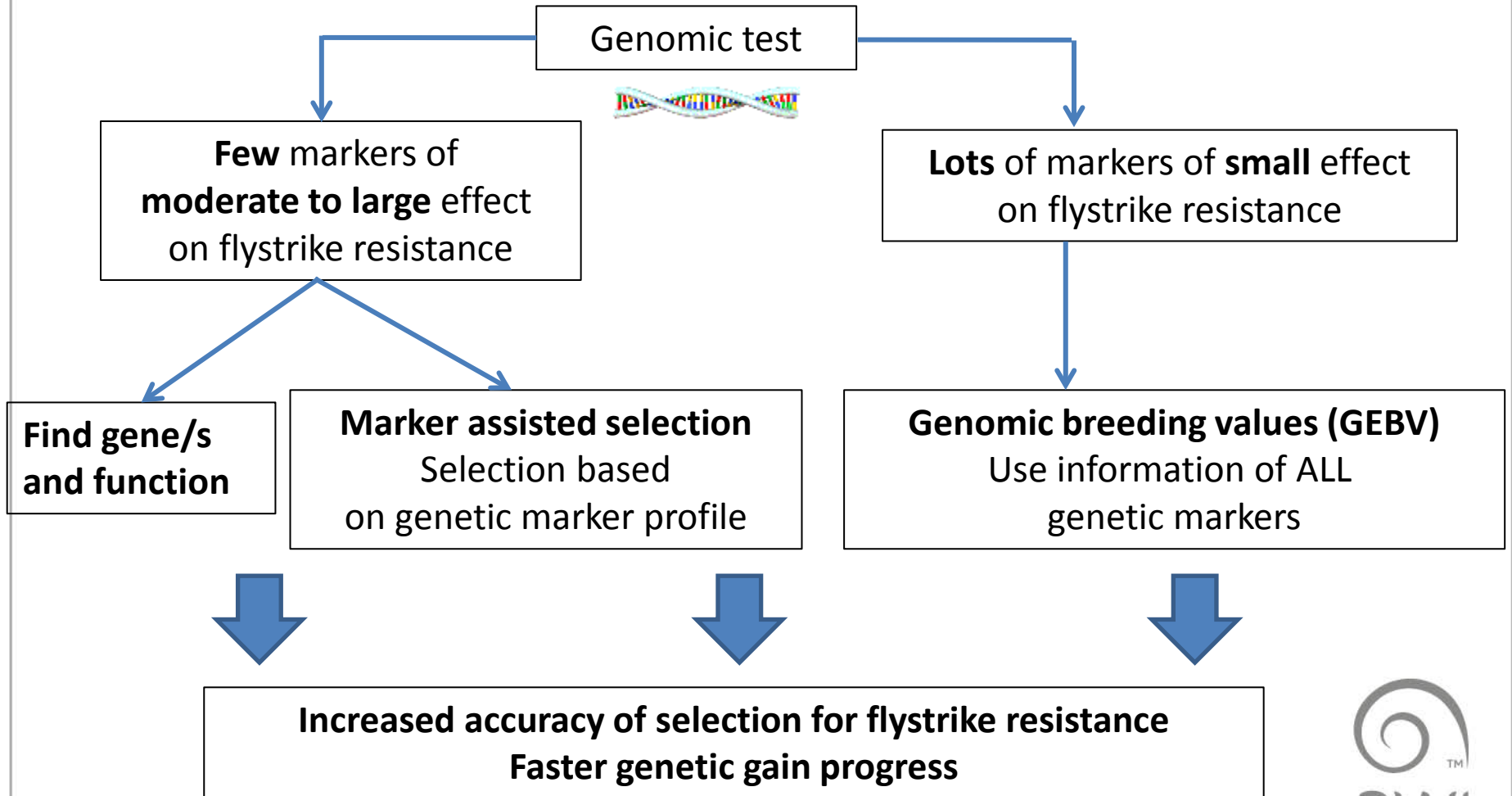


Good reasons for a genomic approach

- **The question:** Are genomic tools useful for genetic improvement of breech strike and indicator traits?
- 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
- Potentially an approach that can fast track genetic progress



Genomics and breeding programs



Genomics and breeding programs

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

For moderate to large effect on flystrike resistance

small effect on flystrike resistance

How can we use the information best in breeding?

Find gene/s and function

Marker assisted selection
Selection based

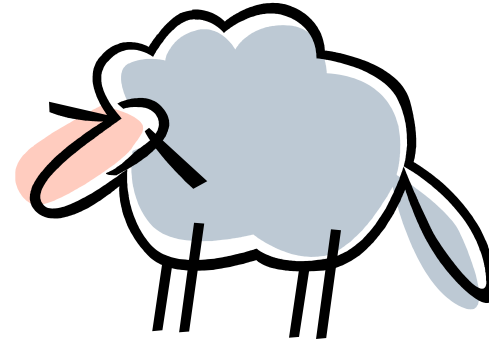
Genomic breeding values (GEBV)
Use information of ALL

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

Increased accuracy of selection for flystrike resistance
Faster genetic gain progress



Analysis protocol



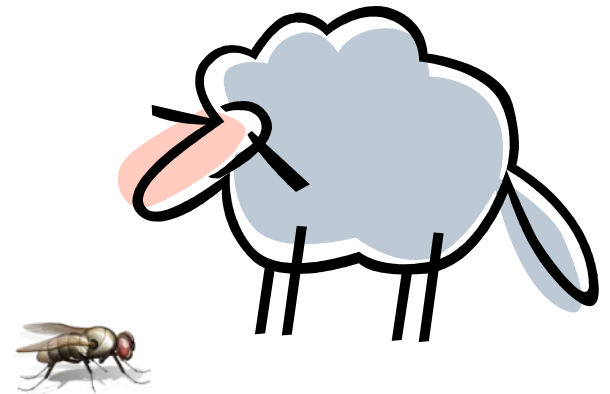
Illumina 600K HD
Genotype data
after quality control
948 samples
528,818 SNPs

Phenotype data

Genome-wide association study
Estimation and Validation of GEBV

Phenotypes

- Four traits
 - Breechstrike (STRIKE) (struck, not struck)
 - Breechcover (BCOV) (low, medium, high)
 - Wrinkle score (WRK) (low, medium, high)
 - Dag score (DAG) (low, medium, high)
- Other effects
 - Site (Armidale, Mt Barker)
 - Sex (male, female)
 - Drop ('05-'09 and '11)
 - Mules status (mulesed, unmulesed)



Genotyping strategy

Contemporary group

Phenotype group

Site (Armidale and Mt Barker)

Sex (male and female)

Birth year (2005 – 2011)

Mules status (mulesed and unmulesed)

Flystrike (struck and not struck)

Wrinkle Score (H,M,L)

Breech cover (H,M,L)

Dag Score (H,M,L)

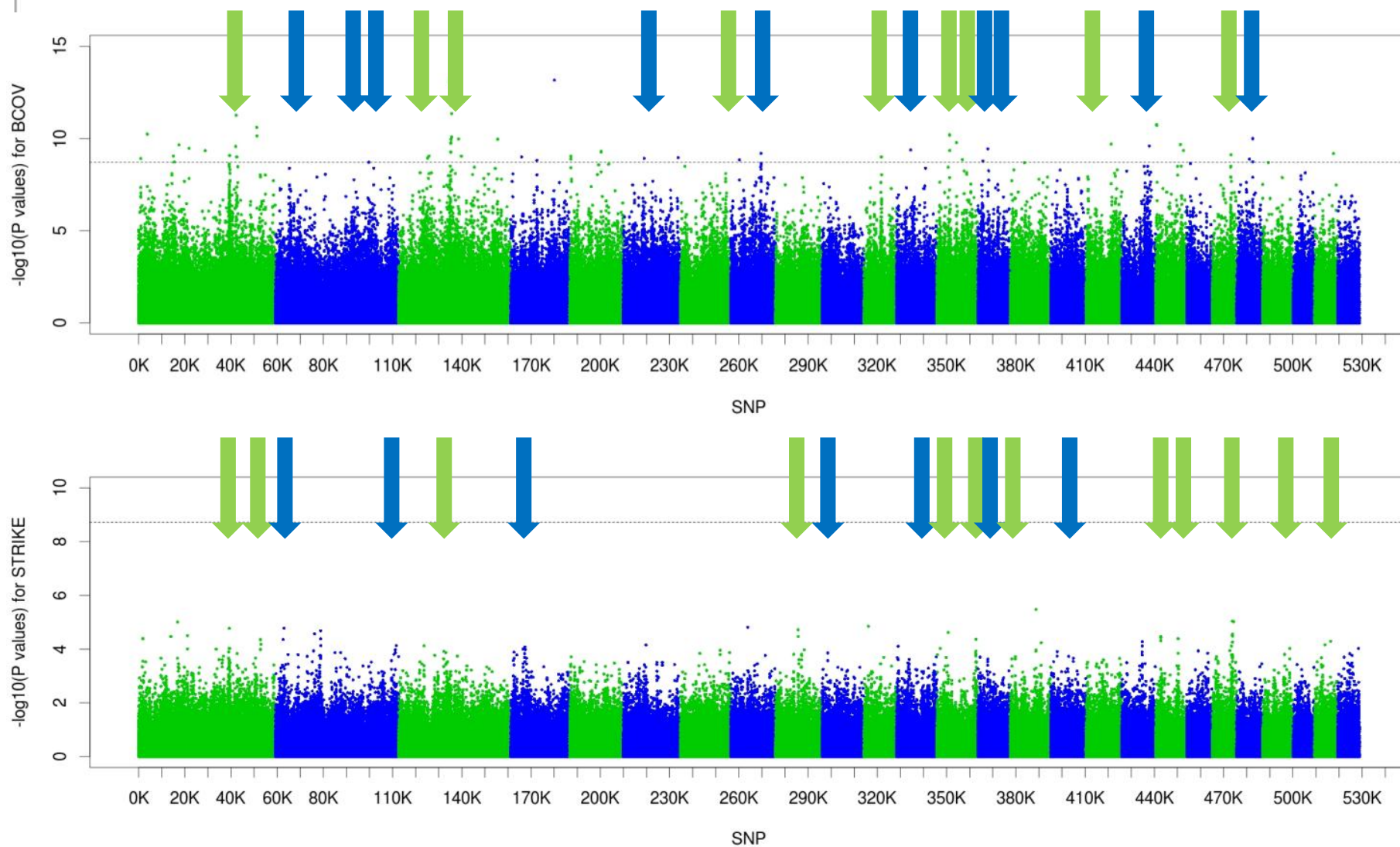
Groups for genotyping



awil

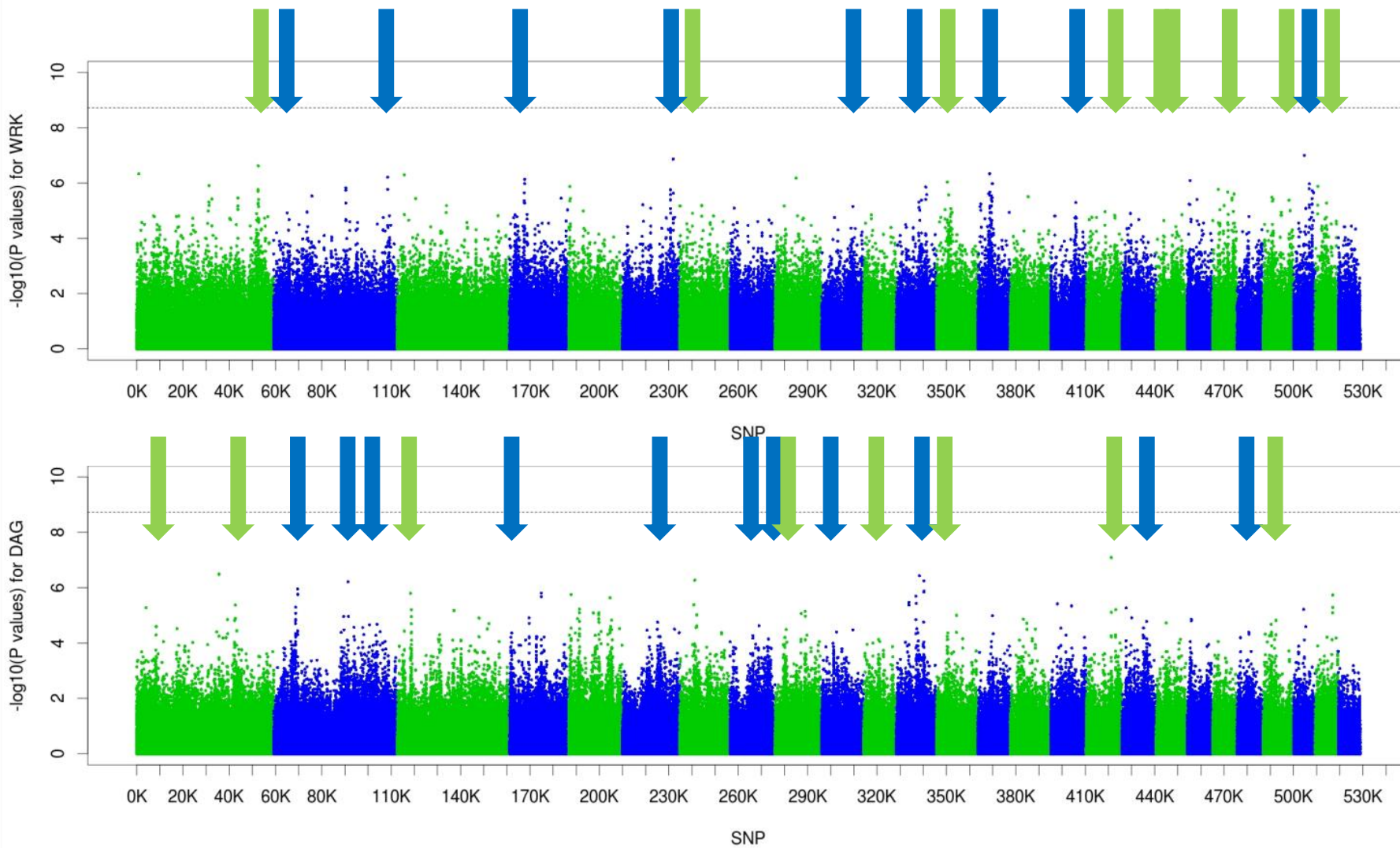
Australian
Wool Innovation
Limited

Results – BCOV and STRIKE



Manhattan Plots, cluster dots which peak are SNPs of interest¹

Results – BRWR and DAG



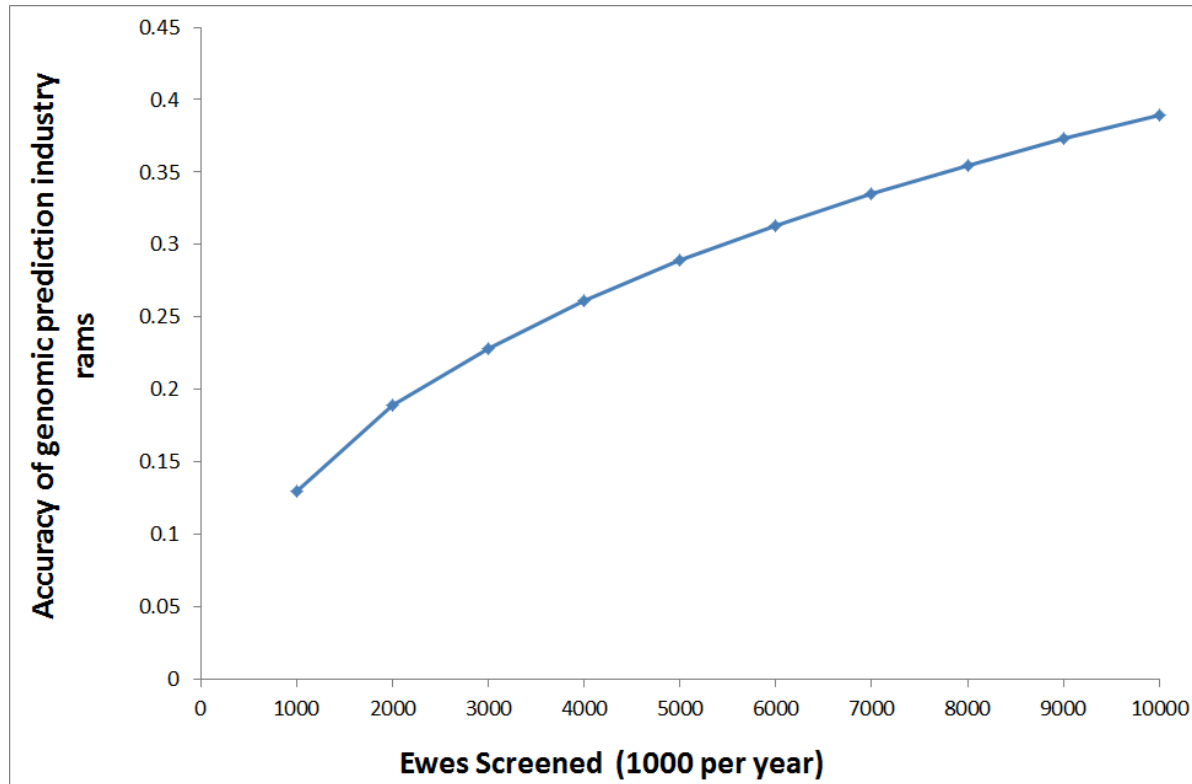
What does the Genome-Wide Association Study tell us?

- Found a large number of SNP with small effect
- Good indication for the use of GEBV
 - Potentially useful for these traits that don't express wide variation in all environments
- Low density panels an option
 - 3rd Generation LD Chip currently under discussion
- A closer look might reveal interesting genes
 - Detection of underlying genes?



Estimation and validation of GEBVs

Current accuracy of GEBVs for breech strike and indicator traits between 11-15%



Hayes, pers. comm



Where to from here?

- Additional analytical work on the genotypes obtained to date
- Possible linkage to the odour and bacteria work in WA
- Look for SNP associations with other traits, urine? Others?
- Co-evolution of parasite and host once fly and sheep genome are better detailed
- Continue to collect DNA to do additional genotyping when cost drops or use low density
- Genotype and indicator trait data will be added to Sheep CRC and industry data. Improvement in accuracies for the breed traits will be re assessed.
- No product for industry yet, but maybe in the future





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2008