Genetic architecture of resistance to virulent footrot in New Zealand Merino

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Multi-factorial disease

Bacteria
- Virulence: Benign, Virulent
- 19 serogroups & sub-types: A,B,C,D,E,F,G,H,I,M

Host
- Susceptibility: Res, Sus
- Management: limited & short term, Genetic variation

Environment
- Predisposition/transmission
Field study
Genetic variation
Virulent Footrot

72 flocks inspected
Predominantly Merino/Merino types

Footrot scores and flock prevalence

- Score 0: Clean and normal
- Score 1: Water maceration
- Score 2: Ovine interdigital dermatitis
- Score 3: Early footrot
- Score 4: Advanced footrot
- Score 5: Chronic footrot

Prevalence %
Sampling Case-Control

Each flock
2 inspections/ challenge

N = 40-80

N = 5836 sampled

N = 40-80
Genotype 5,008 sheep & impute to 51,713 SNP after QC

Final analyses- matched genotypes to phenotypes
Flock prevalence 30:70%, Merino types only
N=3,208  37 flocks

Model: logit FR (0,1)= Flock (observer), breed type, sex, age, GRM , residual

Heritability
Chromosome Heritability
QTL location-GWAS
Positional candidate
Heritability  0.41  (se0.04)

Chromosomal Heritability- OBS vs EXP
GWAS Outputs – Case / Control study

GRM = Fitted, Restricted to flock Ratio 30:70, fixed effects = flock, sex, breed, age class

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Haploview and impact of QTL markers

2 SNPs not close >>>> high likelihood of recombination between “key gene” & significant SNPS

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<tr>
<th>Trait</th>
<th>Markers fitted</th>
<th>Oar 23 Heritability</th>
<th>se</th>
<th>Residual genome heritability</th>
<th>se</th>
<th>Full Genome heritability</th>
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<td>FR (0,1)</td>
<td>0 fitted</td>
<td>0.14</td>
<td>(0.04)</td>
<td>0.27</td>
<td>(0.05)</td>
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<td>(0.04)</td>
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<tr>
<td>FR (0,1)</td>
<td>2 fitted</td>
<td>0.12</td>
<td>(0.04)</td>
<td>0.27</td>
<td>(0.05)</td>
<td>0.39</td>
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Significant QTL but
Relatively small effect
High Residual Va
GWAS-positional candidates

GRM = Fitted, Restricted to flock Ratio 30:70, fixed effects = flock, sex, breed, age class

Manhattan Plot Chromosome 23

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rs407911045 =OAR23:25972928
rs430746746 =OAR23:26109761

GSG 1-4 Desmoglein genes
DSG1-4 Candidate genes

Desmoglein genes

D nodosus fimbriae proteases
Conclusions

- Resistance Virulent FR - Heritable & polygenic
  - selective breeding Merino feasible
- Major QTL OAR23
  - but does not account for all variation
  - Needs validation & fine mapping
- Best option for gEBV – relationship+QTL+snp effects
  - See Walkom et al –these proceedings
- DSG gene family suitable candidates
Acknowledgements

- NZ Merino inc, NZ Primary industries & New Zealand Merino Co $$$
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- The NZ Merino inc field staff and veterinarians
- Dr Chris Mulvaney
- Assoc prof Imke Tammen