Breeding for Tuberculosis and Liver Fluke Resistance

Siobhán Ring
Industry Concerns Prompt Research

“...My Beef HealthCheck report says 2 out of the cattle 7 I slaughtered had livers damaged by fluke ... are they a bad breed?”

“...why is it only a few cattle in herds get TB? ... are some cattle more attracted to wildlife carrying M.bovis?

Maybe genetics is responsible for some of the on-farm variability in resistance to TB & fluke??
Observing Genetic Variation

<5% of these sires progeny were diagnosed with TB despite being in multiple herds with TB infection

30-40% of these sires progeny were diagnosed with TB

Liver Fluke
Sourcing Data

TB
SICTT, lesion, & confirmed lab TB
(~1m records since 2000)

Liver Fluke
Damage & live fluke
(~300k records since 2012)

AgTech – it’s in our DNA
Quantifying Genetic Variation

Maybe genetics is responsible for some of the on-farm variability in resistance to TB & fluke!

<table>
<thead>
<tr>
<th></th>
<th>TB</th>
<th>Liver Fluke</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heritability</td>
<td>12%</td>
<td>1%</td>
</tr>
<tr>
<td>Genetic SD</td>
<td>0.09</td>
<td>0.04</td>
</tr>
<tr>
<td>Potential prevalence reduction per year</td>
<td>1.9%</td>
<td>0.09%</td>
</tr>
</tbody>
</table>

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**Graph:**
- **Y-axis:** Accuracy
- **X-axis:** Number of progeny records
- **Lines:**
  - Red line: heritability 0.01
  - Blue line: heritability 0.12

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AgTech – it’s in our DNA

#ISGC18
How well can breeding value predict performance when only pedigree known?

2.5% unit (TB) and 6% (Fluke) unit higher prevalence in worst EBV group compared to the best EBV group.
Presentation of Breeding Values

*(predicted % prevalence among animal’s progeny)*

- **TB**
  - Intercept = 18E-6
  - Slope = 1

- **Fluke**
  - Intercept = -38E-6
  - Slope = 1

Observed Progeny Prevalence (%) vs. Predicted Progeny Prevalence (%)

*AgTech – it’s in our DNA*
Breed Differences

(AI sires born ≥2000, reliability ≥40%)

Predicted Progeny Prevalence (%)

**TB**

- AA (205)
- BB (212)
- CH (282)
- HE (130)
- LM (304)
- SI (217)

**Fluke**

- AA (30)
- BB (6)
- CH (10)
- HE (16)
- LM (16)
- SI (7)

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Considerations for Using Breeding Values

- Screen-out worst males & females
  - Cut-off for ‘worst’ may vary
- Risk of infection
  - Proximity to restricted herds
  - Precedence of infection
- Emphasis on other traits
  - On average, high EBI and Replacement Index bulls have a lower TB prevalence
  - On average, high Terminal Index bulls have a higher TB prevalence

<table>
<thead>
<tr>
<th>Change per +€10 Index</th>
<th>TB (%)</th>
<th>Fluke (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>EBI</td>
<td>-0.026</td>
<td>-0.022</td>
</tr>
<tr>
<td>Replacement</td>
<td>-0.031</td>
<td>-0.012</td>
</tr>
<tr>
<td>Terminal</td>
<td>+0.029</td>
<td>+0.006</td>
</tr>
</tbody>
</table>
Under-review

GWAS for endo-parasite phenotypes using imputed whole-genome sequence data in dairy and beef cattle

Journal of ANIMAL SCIENCE
Genetic parameters for both a liver damage phenotype caused by Fasciola hepatica and antibody response to Fasciola hepatica phenotype in dairy and beef cattle

Journal of ANIMAL SCIENCE
Genetic correlations between endo-parasite phenotypes and economically important traits in dairy and beef cattle
Alan J. Twomey, Rebecca I. Carroll, Michael L. Doherty, Noel Byrne, David A. Graham, Riona G. Sayers, Astrid Blom, Donagh P. Berry

Journal of ANIMAL SCIENCE
Little genetic variability in resilience among cattle exists for a range of performance traits across herds in Ireland differing in Fasciola hepatica prevalence
Alan J. Twomey, David A. Graham, Michael L. Doherty, Astrid Blom, Donagh P. Berry

Under-review

RESEARCH ARTICLE
Genetic correlations between measures of Mycobacterium bovis infection and economically important traits in Irish Holstein-Friesian dairy cows

RESEARCH ARTICLE
Variance components for susceptibility to Mycobacterium bovis infection in dairy and beef cattle

RESEARCH ARTICLE
A genome-wide association study for genetic susceptibility to Mycobacterium bovis infection in dairy cattle identifies a susceptibility QTL on chromosome 23

Analysis of Imputed Whole Genome Sequence Data in Multiple Breeds Reveal Novel Single-Nucleotide Polymorphisms on BTA 15 and BTA 23 Associated with Bovine Tuberculosis Infection

#ISGC18
Take Home Message

- Considerable exploitable genetic variation
  - As much variation within breed as across breed
- Planned TB & Fluke EBV roll-out
  - Test proofs for AI sires Jan’19
  - Stand-alone traits
- Likely varying herd emphasis
  - Risk of infection
  - Emphasis on other traits (complimentary to EBI & Repl. Index)
ICBF.com

Our Farmer & Government Representation
- Department of Agriculture, Food and the Marine
- Irish Creamery Milk Suppliers Association
- IFA

Our AI & Milk Recording Organisations
- DoveaGENETICS
- Munster Cattle Breeding Group
- Progressive Genetics
- Tipperary Coop

Our Herdbooks
- Ayrshires
- Aberdeen-Angus
- IBBCS
- EASBB
- Irish
- Blonde d'Aquitaine
- Irish Charolais
- Irish Hereford
- MRI Cattle Society of Ireland
- Norwegian Red Cattle Society

Acknowledging Our Members