GWAS of meat quality traits using WGS data in a multi-breed sheep population

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WGS data can be helpful for

• Detecting QTLs and fine-mapping of QTL
  ▪ More variants
  ▪ Variants with low MAF
  ▪ Causative variant?
  ▪ Structural variants

• Increase accuracy genomic prediction
  ▪ Include significant SNPs from GWAS in prediction

work Moghaddar and Khansefid, presented yesterday, session Prediction 1.
What can we expect from WGS data?

- Detect more QTL, more peaks
- Fine map known QTL, sharper peaks
- Directly compare with functional studies such as RNA seq
What genotype data do we have?

- 726 sequenced sheep
  - 376 Australian sheep

- ~35,000 sheep with genotypes
  - 12/15K: 10,000
  - 50K: 23,000
  - HD: 2,600

→ All imputed up to sequence (Friday presentation Bolormaa session Imputation)

→ 27,896,226 variants (Minimac R² threshold=0.4)
Traits and model

- Pre-corrected for fixed effects
- Single SNP analysis
  - SNP Snappy WOMBAT
- Simultaneously fit
  - Grm (based on HD)
  - Qmatrix (breed proportions)

<table>
<thead>
<tr>
<th>Trait</th>
<th>N</th>
</tr>
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<tbody>
<tr>
<td>CCFAT</td>
<td>13,644</td>
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<tr>
<td>IMF</td>
<td>11,772</td>
</tr>
<tr>
<td>PEMD</td>
<td>21,412</td>
</tr>
<tr>
<td>PWT</td>
<td>26,769</td>
</tr>
<tr>
<td>SF5</td>
<td>13,363</td>
</tr>
</tbody>
</table>
Compare SNP density

A GWAS pemd 50K

N QTL regions = 4

FDR of 5%
Zoom of a region

GWAS imf 50K

GWAS imf HD

GWAS imf SEQ

Position (Mb) at OAR 23
## N QTL per trait

<table>
<thead>
<tr>
<th>Trait</th>
<th>50K</th>
<th>HD</th>
<th>WGS</th>
</tr>
</thead>
<tbody>
<tr>
<td>CCFAT</td>
<td>4</td>
<td>9</td>
<td>41</td>
</tr>
<tr>
<td>IMF</td>
<td>2</td>
<td>8</td>
<td>38</td>
</tr>
<tr>
<td>PEMD</td>
<td>4</td>
<td>15</td>
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<td>5</td>
<td>13</td>
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<tr>
<td>SF5</td>
<td>3</td>
<td>7</td>
<td>34</td>
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<tr>
<td>Total</td>
<td>20</td>
<td>52</td>
<td>250</td>
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</tbody>
</table>

**Significance SNPs**
(min and max $-\log_{10}(Pval)$)

- **50K**: 5-15
- **HD**: 5-22
- **WGS**: 5-29

→ More and higher peaks!
Affects body weight, height, bone and carcass traits in human, cattle, pigs, sheep etc.

Involved in lipid metabolism
GWAS trait PEMD for OAR 6 corrected for sign. SNP
WGS gives us

• More peaks

• More **significant** peaks
  • Use more data
  • And / or multi-breed pop. **LD exists over shorter distances**

• The basis for companion studies on **functional studies** to validate candidate genes and mutations
Acknowledgements

Work with sequence data

• Iona MacLeod, Sunduimijid Bolormaa, Hans Daetwyler, Majid Khansefid (Melbourne)

• Julius van der Werf, Cedric Gondro, Nasir Moghaddar and Sam Clark (UNE)

• Andrew Swan and Klint Gore (AGBU)

• Paul Stothard (University of Alberta)

Funding

• Co-operative Research Council (CRC) for Sheep Industry Innovation

• MLA (Meat Livestock Australia)