Lots of small changes make a BIG DIFFERENCE

Sheep Ireland Industry Meeting
18/04/2018
Why do we need EuroStars?

To make the most informed breeding decisions possible in order to have a more profitable & sustainable industry and farms
Since the last Meeting

Genomic Results
Displaying Animals for which Genotype Results are available

Flock Summary

<table>
<thead>
<tr>
<th>Summary of Your Flock Parentage Result</th>
<th>Size</th>
<th>Sex</th>
</tr>
</thead>
<tbody>
<tr>
<td>Where SheepCam is a match</td>
<td>8</td>
<td>4</td>
</tr>
<tr>
<td>Where SheepCam is not a match</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Where SheepCam Requires a Resample</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Where SheepCam has no DNA Available</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Where SheepCam is not Registered on the Database</td>
<td>11</td>
<td>13</td>
</tr>
<tr>
<td>Where SheepCam is not Registered on the Database</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

In progress
Across-breed Eval

Sheep Ireland: Profit through science
LambPlus membership

No of LambPlus breeders by year

Year

No of LambPlus Breeders

LambPlus began

2017 Premier Sale results

$y = 77.982x + 476.6$

$R^2 = 0.9073$
Genetic Gain

Replacement Index

Terminal Index
Research Projects

- **OviGen** - Genomics
- **OviData** – Using DNA to assign parentage
- **SusShep** – Ewe Longevity, Labour & Cervical AI
Calculating economic values using a whole farm bio-economic model

A. Bohan¹,², L. Shalloo¹, P. Creighton³, D.P. Berry¹, T. M. Boland², A.C. O’Brien¹, T. Pabiou⁴, E. Wall⁴, K. McDermott⁴ and N. McHugh¹

¹Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.
²School of Agriculture & Food Science, University College Dublin, Belfield, Dublin 4, Ireland.
³Animal & Grassland Research and Innovation Centre, Teagasc, Athenry, Co. Galway, Ireland.
⁴Sheep Ireland, Highfield House, Shinagh, Bandon P72 X050, Co. Cork, Ireland
Breeding objectives

- **Economic Value**
  - €

- **Genetic Component**
  - Breeding Values

= 

- **Terminal Index**

- **Replacement Index**
Bio-economic model

Flock net energy

Grass, Silage & Concentrate

Land
Animals
Production
Mortalities
Variable costs
Fixed costs
Labour

1. Financial
2. Economic
3. Physical

Net profit

The Irish Agriculture and Food Development Authority
Clinical mastitis increased from 5% to 20%

- Increased vet costs
- Increased labour costs
- Reduced lamb sales

Does not accounted for:
- Ewe mortality
- Ewe culling
- Lamb performance
EV Calculation: Days to slaughter

- Growth rate reduced by 5% (221 to 210g/day)
- Increased days to slaughter (+29 days)
## Maternal traits

<table>
<thead>
<tr>
<th>Trait Group</th>
<th>Trait</th>
<th>Unit</th>
<th>Economic value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maternal</td>
<td>Number of lambs born</td>
<td>Lamb</td>
<td>€39.76</td>
</tr>
<tr>
<td></td>
<td>Ewe mature weight</td>
<td>Kg</td>
<td>-€1.40</td>
</tr>
<tr>
<td>Trait Group</td>
<td>Trait</td>
<td>Unit</td>
<td>Economic value</td>
</tr>
<tr>
<td>-----------------</td>
<td>--------------------------------</td>
<td>------</td>
<td>----------------</td>
</tr>
<tr>
<td>Lambing</td>
<td>Lambing difficulty single</td>
<td>%</td>
<td>-€0.27</td>
</tr>
<tr>
<td></td>
<td>Lambing difficulty single (mat)</td>
<td>%</td>
<td>-€0.30</td>
</tr>
<tr>
<td></td>
<td>Lambing difficulty multiple</td>
<td>%</td>
<td>-€0.25</td>
</tr>
<tr>
<td></td>
<td>Lambing difficulty multiple (mat)</td>
<td>%</td>
<td>-€0.27</td>
</tr>
<tr>
<td></td>
<td>Lamb survival</td>
<td>Lamb</td>
<td>€54.84</td>
</tr>
</tbody>
</table>
## Production traits

<table>
<thead>
<tr>
<th>Trait Group</th>
<th>Trait</th>
<th>Unit</th>
<th>Economic value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Production</td>
<td>Days to slaughter</td>
<td>Day</td>
<td>-€0.25</td>
</tr>
<tr>
<td></td>
<td>Carcase conformation</td>
<td>Grade</td>
<td>€3.70</td>
</tr>
<tr>
<td></td>
<td>Carcase fat</td>
<td>Score</td>
<td>-€0.84</td>
</tr>
</tbody>
</table>
## Health traits

<table>
<thead>
<tr>
<th>Trait Group</th>
<th>Trait</th>
<th>Unit</th>
<th>Economic value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Health</td>
<td>Lameness ewe</td>
<td>%</td>
<td>-€0.24</td>
</tr>
<tr>
<td></td>
<td>Lameness lamb</td>
<td>%</td>
<td>-€0.08</td>
</tr>
<tr>
<td></td>
<td>Mastitis</td>
<td>%</td>
<td>-€0.25</td>
</tr>
<tr>
<td></td>
<td>Dag Score</td>
<td>Score</td>
<td>-€0.34</td>
</tr>
<tr>
<td></td>
<td>Faecal egg count</td>
<td>%</td>
<td>-€0.08</td>
</tr>
</tbody>
</table>
Indexes

Number of lambs born
Ewe mature weight
Lambing difficulty
Lamb survival
Days to slaughter
Carcass conformation
Carcass fat
Ewe lameness
Lamb lameness
Mastitis
Dag score
Faecal egg count

Replacement

12 traits

Terminal

8 traits

The Irish Agriculture and Food Development Authority
Relative emphasis

<table>
<thead>
<tr>
<th>Breeding Objective</th>
<th>Replacement</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maternal</td>
<td>40.24%</td>
</tr>
<tr>
<td>Lambing</td>
<td>21.70%</td>
</tr>
<tr>
<td>Production</td>
<td>37.71%</td>
</tr>
<tr>
<td>Health</td>
<td>0.35%</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Terminal</th>
</tr>
</thead>
<tbody>
<tr>
<td>33.09%</td>
</tr>
<tr>
<td>64.66%</td>
</tr>
<tr>
<td>2.24%</td>
</tr>
</tbody>
</table>

Relative Emphasis (%)
Conclusions

• Improved calculation using a whole farm model

• Updated and improved economic values

• Rapid response to industry change
Thank you

Questions ???
Genetic Evaluation Model Updates

Thierry Pabiou
+ SheepIreland, & Teagasc teams
Agenda

• What’s new for 2018
  • New genetic parameters for lambing
  • New economic values

• Impact on breeding values and accuracies
  • Using 1,412 rams with progenies in 2017
What’s new for 2018

• New Lambing Module
  • Applying Noirin’s research

• New Economic Values
  • Applying Alan’s research
Lambing module update

- Because last update was done in 2009
- More accurate data since from pedigree and commercial flocks
  - New genetic parameters

<table>
<thead>
<tr>
<th>Heritability for lambing traits</th>
<th>Ram traits (direct effect)</th>
<th>Ewe traits (maternal effect)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Birth weight</td>
<td>Lamb survival</td>
</tr>
<tr>
<td>‘Old’</td>
<td>15.0%</td>
<td>2.0%</td>
</tr>
<tr>
<td>New 2018</td>
<td>24.6%</td>
<td>2.7%</td>
</tr>
</tbody>
</table>

= More accurate breeding values
Economic value update

Calculating economic values using a whole farm bio-economic model

A. Bohan¹,², L. Shalloo¹, P. Creighton³, D.P. Berry¹, T. M. Boland², A.C. O’Brien¹, T. Pabiou⁴, E. Wall⁴, K. McDermott⁴ and N. McHugh¹

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The Irish Agriculture and Food Development Authority
Terminal index in April 2018

Terminal: no change

Terminal: +new data

Terminal: gain in accuracy

Terminal: +new data +new par.

Terminal: gain in accuracy +new EV

April 2018: average = 51%

November 2017: average = 49%

Terminal: gain in accuracy
Replacement Index in April 2018

Replacement: no change

November 2017

Replacement: +new data

R² = 0.8371

April 2018

Replacement: gain in accuracy

R² = 0.736

November 2017: average = 44%

Terminal: +new data +new parameters +new EV

R² = 0.6737

April 2018: average = 48%

November 2017: average = 44%
Relation Terminal index with phenotypes

• Rams with progenies in 2017

<table>
<thead>
<tr>
<th></th>
<th>Texel</th>
<th>Suffolk</th>
<th>Charollais</th>
<th>Belclare</th>
<th>Vendeen</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of rams</td>
<td>404</td>
<td>230</td>
<td>298</td>
<td>97</td>
<td>62</td>
</tr>
<tr>
<td>%dead lambs</td>
<td>-2.1%</td>
<td>-4.1%</td>
<td>-2.2%</td>
<td>-3.8%</td>
<td>-4.4%</td>
</tr>
<tr>
<td>%lambing diff. single</td>
<td>-5.1%</td>
<td>-5.9%</td>
<td>0.2%</td>
<td>-0.2%</td>
<td>-0.3%</td>
</tr>
<tr>
<td>%lambing diff. multiple</td>
<td>-5.9%</td>
<td>-12.0%</td>
<td>-5.4%</td>
<td>-5.0%</td>
<td>-4.1%</td>
</tr>
</tbody>
</table>

• Better accuracy in 2018 compare to previous model: gain average -0.2%
Summary

• 2 major novelties
  • Revamping of lambing module
  • New economic values

• 2 major impacts
  • Better selection
  • Increase in accuracy
International Genetic Evaluations

Shauna Fitzmaurice
Success in Beef & Dairy
International data

Accuracy v. low
International data

Steps:
1. Identify UK animals in national database
2. Research phase
3. Implementation ??
Texel Data

8,392 common animals between Ireland and the UK

Males

- 2,594 with progeny in Ireland
- 1,188 with progeny in both countries

Females

- 5,798 with progeny in Ireland
- 2,323 with progeny in both countries

Animals must have breeding values in both countries

Shauna Fitzmaurice
Suffolk Data

3,313 common animals between Ireland and the UK

Males
1,040 have progeny in Ireland

Females
2,273 have progeny in Ireland
Charollais Data

1,727 common animals between Ireland and the UK

Males
604 have progeny in Ireland

Females
1,123 have progeny in Ireland

Shauna Fitzmaurice
Next Steps

➢ Compare Irish and UK breeding values for common animals

➢ Compare phenotypic data between the 2 countries
Measuring ewe efficiency

Nóirín McHugh
How to measure ewe efficiency

- What's the variation between ewes of the same weight??
- New concept → deviation in animal performance from a population
Data

Live weight records

Ewe weights

Lamb weights

Investigate the variation - combined litter weight relative to ewe weight at same time

Set relative to population
Ewe Efficiency

Combined litter weight relative to ewe weight at same time

$\sigma_p = 15.37 \text{ kg}$

$\sigma_g = 4.94 \text{ kg}$

Top 20%: 21.47 kg
Benchmarking – Flock A

Proportion of Litters vs. DEVwean (kg)

3rd parity ewe
Rearing 1 lamb
Ewe weight = 72.50 kg
Lamb weight = 21 kg

5th parity ewe
Rearing 2 lambs
Ewe weight = 59 kg
Lamb weight = 64 kg

5th parity ewe
Rearing 3 lambs
Ewe weight = 59 kg
Lamb weight = 106 kg

Rearing 3 lambs
Ewe weight = 72.50 kg
Lamb weight = 21 kg
Conclusion

- New ewe efficiency trait
- Information required to derive these phenotypes is routinely available

1. Exploitation through breeding programs
2. Routine benchmarking within and between flocks
Genomics

Áine O’ Brien
Sheep Ireland Industry meeting
Athenry, April 2017
DNA - From the tip of your nose to the tops of your toes!!

DNA is the same in every cell of your body and doesn't change throughout your life.
What is a SNP?

- 99.9% of our DNA is identical - most of the differences are in the form of SNPs

Single Nucleotide Polymorphism

Change
Genotyping panel (SNP chip)

DNA of one animal per section

- Each section has 51,135 SNPs
- Bind to DNA in specific locations

Process:
- DNA is stained with fluorescent dye
- Chips are washed, coated with preservative and dried
## Genotyping panels

<table>
<thead>
<tr>
<th>Year</th>
<th>Panel density (no. of SNPs)</th>
<th>Cost (€)</th>
<th>Cost per SNP (€)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2015</td>
<td>606,000</td>
<td>Research only</td>
<td>Research only</td>
</tr>
<tr>
<td>2015</td>
<td>50,000</td>
<td>62.50</td>
<td>0.00125</td>
</tr>
<tr>
<td>2016</td>
<td>15,000</td>
<td>28.50</td>
<td>0.00190</td>
</tr>
<tr>
<td>2017</td>
<td>11,000</td>
<td>25.00</td>
<td>0.00227</td>
</tr>
<tr>
<td>2018</td>
<td>50,000</td>
<td>22.00</td>
<td>0.000044</td>
</tr>
</tbody>
</table>
## Genotyping by breed and panel

<table>
<thead>
<tr>
<th>Breed</th>
<th>SNP panel</th>
<th></th>
<th></th>
<th></th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>50K</td>
<td>LD</td>
<td>HD</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Belclare</td>
<td>884</td>
<td>595</td>
<td>20</td>
<td></td>
<td>1499</td>
</tr>
<tr>
<td>Charollais</td>
<td>1049</td>
<td>2355</td>
<td>23</td>
<td></td>
<td>3427</td>
</tr>
<tr>
<td>Suffolk</td>
<td>1047</td>
<td>1293</td>
<td>14</td>
<td></td>
<td>2354</td>
</tr>
<tr>
<td>Texel</td>
<td>1353</td>
<td>3138</td>
<td>27</td>
<td></td>
<td>4518</td>
</tr>
<tr>
<td>Vendeen</td>
<td>699</td>
<td>129</td>
<td>9</td>
<td></td>
<td>837</td>
</tr>
<tr>
<td>Other - pedigree</td>
<td>379</td>
<td>249</td>
<td>189</td>
<td></td>
<td>817</td>
</tr>
<tr>
<td>Other - crossbred</td>
<td>1989</td>
<td>3490</td>
<td>14</td>
<td></td>
<td>5493</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>7400</strong></td>
<td><strong>11249</strong></td>
<td><strong>296</strong></td>
<td></td>
<td><strong>18945</strong></td>
</tr>
</tbody>
</table>
Genomic evaluations

Parentage

Traceability

Breed composition

Karyotyping

Inbreeding

Monitor lethal genes

Monitor major genes

Mating advice

Monitor

Breeding

Advisory
Parentage & Impact on Genetic Evaluations
Nóirín McHugh
Determining Parentage

Sire

Parents must also be genotyped

Dam

Animal genotyped
Parentage

17,991 animals genotyped

699 sires were incorrect (13.80%)
514 dams were incorrect (8.68%)

5,921 animals had a dam genotyped
5,066 animals had a sire genotyped

103 animals had both parents wrong (3.64%)
367 animals had either parent wrong (12.98%)

What's the impact of these errors??

2% failed genotyping

Total parentage errors (~20%)
Impact of parentage errors - theoretical

Costing industry €60,000/year

Proportional reduction in genetic gain

Number of progeny per parent

1% error
5% error
10% error
15% error
20% error
Impact of parentage errors - reality
Impact of parentage errors - reality

- Individual animal
  - -€0.13 (range -€1.37 to €0.69)

- Sire
  - <5 progeny -€0.08
  - Sire 6 to 30 progeny -€0.04
  - Sire >30 progeny -€0.02

- Dam
  - -€0.05

- Flock mates
  - -€0.17
Conclusion

• Genomics:
  • new accurate tool for parentage prediction
  • Impact of parentage errors
    • Individual animal, back pedigree and flock
• Future priorities:
  1. Routine parentage reports through LambPlus screens
  2. Parentage assignment from bank of available genotypes
Scrapie

Donagh Berry

Teagasc, Moorepark

donagh.berry@teagasc.ie

Sheep Ireland Industry Meeting, April 2018
Scrapie

- 5 different DNA variants
  - 1 + 1 + 3

<table>
<thead>
<tr>
<th>Name</th>
<th>Chr</th>
<th>Position</th>
</tr>
</thead>
<tbody>
<tr>
<td>oar3_OAR13_46225660</td>
<td>13</td>
<td>46225660</td>
</tr>
<tr>
<td>15k_OAR13_46225714</td>
<td>13</td>
<td>46225714</td>
</tr>
<tr>
<td>15k_OAR13_46225764</td>
<td>13</td>
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</tr>
<tr>
<td>15k_OAR13_46225765</td>
<td>13</td>
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</tr>
<tr>
<td>15k_OAR13_46225766</td>
<td>13</td>
<td>46225766</td>
</tr>
</tbody>
</table>
Codon 136

- **15K_OAR_46225660**
- **Determine amino acid at codon 136**: Alanine (A: GCC) or Valine (V: GTC)
- **Very nice**
Codon 154

15K_OAR13_46225714

Identify the amino acid at codon 154: (R: CGT) or Histadine (H: CAT)

Argenine
Codon 171 (3 bases)

- **15K_OAR13_46225764** – 1\textsuperscript{st} base

- Looks good
Codon 171

- 15K_OAR13_46225765 – 2\textsuperscript{nd} base
- Though one but now good
Codon 171

- **15K_OAR13_46225766 – 3rd base**
- **Problem one the last time (my fault)**

![Graph](image)
<table>
<thead>
<tr>
<th>Genotype result</th>
<th>Type</th>
<th>Degree of resistance/susceptibility</th>
</tr>
</thead>
<tbody>
<tr>
<td>ARR/ARR</td>
<td>1</td>
<td>Sheep that are genetically most resistant to scrapie.</td>
</tr>
<tr>
<td>ARR/AHQ</td>
<td>2</td>
<td>Sheep that are genetically resistant to scrapie, but will need careful selection when used for further breeding.</td>
</tr>
<tr>
<td>ARR/ARH</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARR/ARQ</td>
<td></td>
<td></td>
</tr>
<tr>
<td>AHQ/AHQ</td>
<td>3</td>
<td>Sheep that genetically have little resistance to scrapie and will need careful selection when used for further breeding.</td>
</tr>
<tr>
<td>AHQ/ARH</td>
<td></td>
<td></td>
</tr>
<tr>
<td>AHQ/ARQ</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARH/ARH</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARH/ARQ</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARQ/ARQ</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARR/VRQ</td>
<td>4</td>
<td>Sheep that are genetically susceptible to scrapie and should not be used for breeding unless in the context of a controlled breeding programme approved by NSPAC.</td>
</tr>
<tr>
<td>AHQ/VRQ</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARH/VRQ</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARQ/VRQ</td>
<td></td>
<td></td>
</tr>
<tr>
<td>VRQ/VRQ</td>
<td>5</td>
<td>Sheep that are highly susceptible to scrapie and should not be used for breeding.</td>
</tr>
</tbody>
</table>

First SNP differentiates type 4 & 5 from the rest V** v others

Only need to know ARR & VRQ

Courtesy of Hayley Baird & John McEwan
Testing

- 54 samples of Type 3, 4, & 5 from DAFM
- Type 1 & 2 from OVIGEN

- 100% correct in calling scrapie type
## Prevalence (n=2022)

<table>
<thead>
<tr>
<th>Type</th>
<th>BR</th>
<th>CL</th>
<th>SU</th>
<th>TX</th>
<th>VN</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>69</td>
<td>71</td>
<td>73</td>
<td>49</td>
<td>72</td>
</tr>
<tr>
<td>2</td>
<td>25</td>
<td>24</td>
<td>24</td>
<td>41</td>
<td>26</td>
</tr>
<tr>
<td>3</td>
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<td>0</td>
<td>5</td>
<td>2</td>
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<tr>
<td>4</td>
<td>2</td>
<td>1</td>
<td>3</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
<td>1</td>
<td>2</td>
<td>0</td>
<td>2</td>
<td>0</td>
</tr>
</tbody>
</table>

4.5% not called
Conclusion

• Genotypes now give 100% concordance with scrapie type (1, 2, 3, 4, 5)
  • Still a small proportion “didn’t work” – WIP
  • Calling of actual scrapie genotype – WIP
• Future validation with larger number
  • Work in retrospect
  • Locate different types from those already tested
• Continuous spot checks
Breed prediction

Áine O’ Brien
Sheep Ireland Industry meeting
Athenry, April 2017
Crossbreeding - dilemma 1

50% BR : 50% SU
(assuming both parents are pure)

50% CL : 25% BR : 25% SU

50% CL : 50% BR : 0% SU

50% CL : 0% BR : 50% SU

The Irish Agriculture and Food Development Authority
The Belclare

The question: How much Lleyn is in the modern day Belclare?
The Belclare

Galway

Finn

Lleyn

% in Belclare

• Minimum = 0%
• Maximum = 8.64%
• Average = 0.3%

Belclare

Texel

The Irish Agriculture and Food Development Authority
The Belclare

% in Belclare

- Minimum = 0%
- Maximum = 81.9%
- Average = 35.0%
The Belclare

- Galway
- Finn
- Lleyn
- Texel

% in Belclare
- Minimum = 0%
- Maximum = 91.7%
- Average = 16.0%

The Irish Agriculture and Food Development Authority
The Belclare

% in Belclare

- Minimum = 0%
- Maximum = 28.6%
- Average = 0.6%
On-going work

Quantifying breed proportion in crossbreds

- CPT flocks, Research Flock

Belclare and other composites

- EasyCare, Highlander, Primera
Major Genes and GWAS
Deirdre Purfield
deirdre.purfield@teagasc.ie
Sheep Ireland Industry Meeting 18/04/2018
**Major Genes**

**Major gene**: A gene that substantially influences a trait

<table>
<thead>
<tr>
<th>Gene</th>
<th>Symbol</th>
<th>Species</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Myostatin</td>
<td>GDF8</td>
<td>Sheep, Cattle</td>
<td>Double muscling</td>
</tr>
<tr>
<td>Bone morphogenetic protein 15</td>
<td>BMP15</td>
<td>Sheep</td>
<td>Ovulation rate</td>
</tr>
<tr>
<td>Growth differentiation factor 9</td>
<td>GDF9</td>
<td>Sheep</td>
<td>Ovulation rate</td>
</tr>
<tr>
<td>Diacylglycerol O-acyltransferase1</td>
<td>DGAT1</td>
<td>Sheep, Cattle</td>
<td>Milk yield</td>
</tr>
<tr>
<td>Melanocortin 1 receptor</td>
<td>MC1R</td>
<td>Cattle, Sheep</td>
<td>Coat colour</td>
</tr>
<tr>
<td>Calpains</td>
<td>CAPN</td>
<td>Cattle</td>
<td>Meat quality</td>
</tr>
</tbody>
</table>
Prevalence of major genes

All animals have “major” genes

Different DNA variants in major genes

Different Phenotypes

Prolificacy Genes

BMP15 Xb → associated with Belclare breed

1 copy of DNA variant (T) increased ovulation rate
2 copies sterile (TT)

<table>
<thead>
<tr>
<th>Genotyped</th>
<th>1 copy</th>
</tr>
</thead>
<tbody>
<tr>
<td>All population</td>
<td>0.07%</td>
</tr>
<tr>
<td>Belclare</td>
<td>9.78%</td>
</tr>
</tbody>
</table>

+0.53 lambs born
### GDF8-double muscling

<table>
<thead>
<tr>
<th>Breed</th>
<th>0 Copy (AA)</th>
<th>1 Copy (AG)</th>
<th>2 Copy (GG)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Texel</td>
<td>97.0</td>
<td>2.7</td>
<td>0.3</td>
</tr>
<tr>
<td>Beltex</td>
<td>97.8</td>
<td>2.2</td>
<td>0</td>
</tr>
<tr>
<td>Belclare</td>
<td>69.7</td>
<td>28.7</td>
<td>1.6</td>
</tr>
<tr>
<td>Charollais</td>
<td>2.6</td>
<td>26.6</td>
<td>70.8</td>
</tr>
<tr>
<td>Galway</td>
<td>0</td>
<td>21.1</td>
<td>78.9</td>
</tr>
<tr>
<td>Suffolk</td>
<td>0.2</td>
<td>0.3</td>
<td>99.5</td>
</tr>
<tr>
<td>Vendeen</td>
<td>0</td>
<td>0</td>
<td>100</td>
</tr>
</tbody>
</table>
How to identify DNA associations?

Genome Wide Association Study

SNP1G

SNP1A

~50,000 SNPs

Associate DNA variations with differences in performance
Most Performance traits are **polygenic**

Influenced by small effects of thousands of SNPs

Calving Interval

Genes associated with calving interval

SNP
Sheep example

- 9,909 Sheep with EBV for direct birth weight
- Five breeds
- No clear signal of association -> influenced by many SNPs

Charollais
N=2,895

Texel
N=3,148
Refine DNA associations

- Although can find DNA region, still difficult to identify which gene
- 1000 Rams project ~ 1000 Bulls genome project
  - Resource tool which each partner can use for imputation
  - Provides whole genome sequence (~50 million SNPs) on key rams

**Height of Withers**
Limousin cattle (n=39,821)

![Graphs showing genetic data analysis](image)

- 600,000 SNPs
- 15 Million SNPs

Pinpoint gene increase significance
On-going Work

- Complete association studies for multiple traits
  - Investigate if other major genes exist in sheep
  - Identify SNPs for possible inclusion in a custom panel
  - Validate association results
Genomics Next Steps

Eamon Wall
Current Situation

• **Ovigen budget**
  - Research completion – Dec 2018
  - Budget has now been spent – huge investment in pedigree sheep breeds
  - Long term legacy for Irish sheep breeding
Delivery of Genotype Results

• **Current status**
  - Results of 2017 genotyped animals are yet to be delivered
  - Why?
    - A change in SNP chip being used
    - Up to now a manual process of assessing the results
    - Work nearing completion on an automated system to process genotypes & results in SI
  - This will deliver results in a timeframe similar to beef (currently 3-4 weeks from sample submission)
  - Unable to commit to this turnaround in 2018
2018 Genotyping

• Genotyping in 2018
  • SI will subsidise genotyping in 2018
  • Females & Stock rams remain priority
  • Fee will be €10 per sheep (male or female)
  • SI will contribute €12 per animal (Total cost €22)
  • This will kick-in on April 30\textsuperscript{th}
  • Policy will need to be reviewed throughout the year
  • Alternative funding streams will be investigated!
Validation of genetic indexes

Fiona McGovern & Noirin McHugh

Sheep Ireland Industry Meeting
18th April 2018
Overview

• Why we need validation

• Results –
  – INZAC Flock
  – CPT

• Economic Efficiencies
Why we need validation...

- Accurate genetic evaluations are key to sustainable genetic gain
- Must be reflective of on-farm performance
- Access to accurate genetic evaluations → selection of superior animals for breeding
### Euro-Star Indexes 11/07/2016

<table>
<thead>
<tr>
<th></th>
<th>Replacement (€ 0.813)</th>
<th>Terminal (€ 1.026)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accuracy (%)</td>
<td>Acc 41%</td>
<td>Acc 44%</td>
</tr>
<tr>
<td>Rank (%)</td>
<td>Rank Top 8%</td>
<td>Rank Top 2%</td>
</tr>
</tbody>
</table>

A. 

<table>
<thead>
<tr>
<th></th>
<th>Replacement (€ -0.85)</th>
<th>Terminal (€ -0.197)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accuracy (%)</td>
<td>Acc 33%</td>
<td>Acc 37%</td>
</tr>
<tr>
<td>Rank (%)</td>
<td>Rank Btm 18%</td>
<td>Rank Btm 6%</td>
</tr>
</tbody>
</table>

B.
Index validation

Terminal Index      Replacement Index
Results:
Do genetic indexes work?
## CPT Data

<table>
<thead>
<tr>
<th>Index</th>
<th>Trait</th>
<th>1 Star</th>
<th>V's</th>
<th>5 Star</th>
<th>Diff</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Replacement</strong></td>
<td>Lamb Mortality (%)</td>
<td>10.65%</td>
<td>9.45%</td>
<td></td>
<td>-1.20%</td>
</tr>
<tr>
<td></td>
<td>Number of lambs born</td>
<td>1.92</td>
<td>1.97</td>
<td></td>
<td>0.05</td>
</tr>
<tr>
<td></td>
<td>Ewe mature weight (kg)</td>
<td>78.7</td>
<td>76.8</td>
<td></td>
<td>-1.9</td>
</tr>
<tr>
<td><strong>Terminal</strong></td>
<td>Lambing Difficulty (%)</td>
<td>23.06%</td>
<td>18.17%</td>
<td></td>
<td>-4.89%</td>
</tr>
<tr>
<td></td>
<td>40 day weight (kg)</td>
<td>18.1</td>
<td>20.2</td>
<td></td>
<td>2.10</td>
</tr>
<tr>
<td></td>
<td>Weaning weight (kg)</td>
<td>31.9</td>
<td>34.5</td>
<td></td>
<td>2.60</td>
</tr>
</tbody>
</table>
## INZAC Data

<table>
<thead>
<tr>
<th>Index</th>
<th>Trait</th>
<th>Index</th>
<th>Trait</th>
<th>Diff</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replacement</td>
<td>Lamb Mortality (%)</td>
<td>11.00%</td>
<td>5.10%</td>
<td>-6.00%</td>
</tr>
<tr>
<td></td>
<td>Number of lambs born</td>
<td>1.76</td>
<td>1.81</td>
<td>0.05</td>
</tr>
<tr>
<td></td>
<td>Lambing Difficulty (%)</td>
<td>22.00%</td>
<td>21.00%</td>
<td>-1.00%</td>
</tr>
<tr>
<td></td>
<td>Ewe weight (kg)</td>
<td>77.9</td>
<td>76.6</td>
<td>-1.3</td>
</tr>
<tr>
<td></td>
<td>40 day weight (kg)</td>
<td>16.9</td>
<td>18.4</td>
<td>1.5</td>
</tr>
<tr>
<td></td>
<td>Weaning weight (kg)</td>
<td>32.9</td>
<td>34</td>
<td>1.1</td>
</tr>
</tbody>
</table>
What does this mean for us??
Flock Scenario

A flock with 5 star animals has:
1. Less lambing difficulty - less labour
2. More lambs born & lower lamb mortality
3. Lighter ewes - increase stocking rate?
4. Heavier lambs at weaning - shorter DTS
Economic Efficiency - 100 ewe flock

€7
Net profit / ha

€217
Net profit / ha
Conclusion

• Genetic evaluations key to sustainable genetic gain

• Genetic merit for maternal and performance traits was associated with superior performance

• Importance of indexes for improving profitability across a range of traits