Genomic selection in Irish beef cattle

Ross Evans ICBF
World Charolais Conference - Kilkenny – 08/08/2019
Overview of the different layers in the Irish beef Industry 2018

~ 249k cattle exported

~ 1.65 Million cattle slaughtered

32% of pedigree calves sired by foreign sires

45% of dairy herd calves sired by beef sires

42k F1 dairy-beef females replacements

Beef herd

Pedigree 55k cows 11.3k herds

Commercial 807k cows 62.7k herds 17% AI recorded

Dairy herd

1.36 m cows 18.1k herds

32% of pedigree calves sired by foreign sires
Breed Profile of Calves Born 2018

Births

- Pure/pedigree
- Same dam Suckler
- Dairy dam
- Different dam Suckler
The Beef Genomics Journey

- 2006+: Genotyping of AI straws (AI, Herdbooks, breeders)
- 2008–2012: Animal Welfare Recording and Breeding Scheme (Govt funded)
  - Sire recording, calving & weanling trait recording & weanling welfare
- 2013-2014: Beef Data Programme (BDP) (Govt funded)
  - Extension of BDP to cow traits
- 2014: Beef Genomics Scheme (BGS) Govt funded
  - 15% of herd genotype requirement
- 2015 - 2020: Beef Data and Genomics Program
  - Co-Funded by Irish Government and EU Rural Development program
  - Breeding Profitable, Sustainable, Carbon efficient cows
  - Farmers paid ~€80/cow/year to complete actions (Reference yr 2014)
- 2017 - 2020: Beef Data and Genomics Program II
Breeding More Efficient Cows

- REPLACEMENT INDEX

- Cows live longer +11%
- More weight at weaning +27kg
- More milk score (1-5) +0.72
- Younger at 1st calving -1.9m
- Reduced calving Int. -20d
- No extra gain in carcass weight

Estimated reduction -0.009kg CO₂/kg meat per breeding cow per year for a €1 increase in replacement index
Main Requirements

1. Commitment to stay for duration of scheme
2. Calf surveys: calving difficulty, calf size
3. Cow surveys: docility, milk
4. Genotyping 60% of animals / year
5. Replacement strategy: 50% females indexed 4 or 5 stars + (if any) 1bull 4 or 5 stars
6. Carbon navigator
7. Training
Participation

- Total signups BDGP 1: 29,889 herds
- Currently Active BDGP 1: 22,944 herds (77%)

- Total signups BDGP 2: 1,811 herds
- Currently Active BDGP 2: 1,489 herds (82%)

- Circa 400 herds merged into farm partnerships
Genotyping Chip

- Developed in Ireland
- 54,000 SNPs
- 160 Major genes/defects
- Imputation SNPs
- Microsatellite imputation SNPs
- 800 Parentage SNPs
- V1 to V3 - Illumina platform
- V4 - Thermofisher platform
- Lab services
  - Weatherbys Ireland
  - Eurofins Denmark

BDGP scheme: public EU tenders for
- SNP chip provision
- Lab services: DNA extraction, genotype reporting

IDB SNP CHIP
INTERNATIONAL DAIRY & BEEF
SNP CHIP
Choice of DNA sampling method
Biological sample failure rates

<table>
<thead>
<tr>
<th>Sample type</th>
<th>Count</th>
<th>% Fail (Call rate &lt;90%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ear punch</td>
<td>92,868</td>
<td>2.46%</td>
</tr>
<tr>
<td>Tail Hair</td>
<td>15,518</td>
<td>4.18%</td>
</tr>
<tr>
<td>Semen</td>
<td>309</td>
<td>16.80%</td>
</tr>
<tr>
<td>BVD diluent</td>
<td>341</td>
<td>20.50%</td>
</tr>
</tbody>
</table>

* The overall call rate of a sample is equal to the number of SNPs receiving an AA, AB, or BB genotype call divided by the total number of SNPs on the chip.
Selection of animals in BGS

- Farmers were required to genotype 15% of cows (100k)
- Algorithm developed to identify most informative animals to develop genomic selection
- Based on quantity of data and divergence

Data Quantity = \( W_{T_{CIV}} \cdot \sum_{i=1}^{3} \text{Info}_{CIV_i} + W_{T_{MILK}} \cdot \sum_{i=1}^{3} \text{Info}_{MILK_i} + W_{T_{CALVING}} \cdot \sum_{i=1}^{3} \text{Info}_{CALVING_i} + W_{T_{CARCASS}} \cdot \sum_{i=1}^{3} \text{Info}_{CARCASS_i} \)

Divergence = \( W_{T_{CIV}} \cdot |\text{Diverge}_{CIV}| + W_{T_{MILK}} \cdot |\text{Diverge}_{MILK}| + W_{T_{CALVING}} \cdot |\text{Diverge}_{CALVING}| + W_{T_{CARCASS}} \cdot |\text{Diverge}_{CARCASS}| \)

\[ \text{INDEX} = 0.66 \cdot \text{Quantity} + 0.33 \cdot |\text{Divergence}| \]

\[ \text{Sire}_{\text{LIMIT}} = 10 + \left( \frac{(1 - \text{reliability})}{2} \right) \times 100 \]
BDGP Genotyping process

Genotypes

Priority based on urgency of sample e.g. AI, pedigree

Farmer option to change online

Selection algorithm: identify and prioritise animals for genotyping within herd

Lists sent to TAG providers

3-4 week turnaround

Empty sample: hair card

Barcode tracks sample

Priority based on urgency of sample e.g. AI, pedigree
ICBF genotype QC process

- Genotype call rate check (>90%)
- Sex check
- Breed composition check
- Duplicate check
- Parentage check (ISAG 200 parentage SNPs + 600 ICBF)
- Checks complete: Genotype is validated for further use
## Parentage verification/prediction

<table>
<thead>
<tr>
<th>Categories</th>
<th>Commercial</th>
<th>Pedigree</th>
<th>Ped Charolais</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number</td>
<td>1,499,259</td>
<td>277,328</td>
<td>48,186</td>
</tr>
<tr>
<td>Genotyped sire</td>
<td>68%</td>
<td>84%</td>
<td>87%</td>
</tr>
<tr>
<td>Sire to offspring conflict</td>
<td>14%</td>
<td>5%</td>
<td>5%</td>
</tr>
<tr>
<td>Sire changed</td>
<td>15%</td>
<td>6%</td>
<td>6%</td>
</tr>
<tr>
<td>Predicted sire where unknown</td>
<td>6%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Genotyped dam</td>
<td>51%</td>
<td>42%</td>
<td>42%</td>
</tr>
<tr>
<td>Dam to offspring conflict</td>
<td>6%</td>
<td>2%</td>
<td>2%</td>
</tr>
</tbody>
</table>

*Stats July 2019*
BDGP Herd progress

2018+ BDGP Herd Progress

% Available Requirements Completed

Carbon Navigator: 2018 Completed

BDGP Replacement Strategy Requirements

<table>
<thead>
<tr>
<th>1. Females</th>
<th>2. Stock Bulls</th>
<th>3. AI Requirement</th>
</tr>
</thead>
<tbody>
<tr>
<td>✓</td>
<td>✓</td>
<td>✓</td>
</tr>
</tbody>
</table>
Genotype levels

Count of genotypes

- Monthly
- Cumulative
- Dairy
- Beef

Year-month

BGS scheme
BDGP scheme

© Irish Cattle Breeding Federation Soc Ltd 2013
# Characteristics of Genotyped animals

<table>
<thead>
<tr>
<th>Main Breed</th>
<th>Angus</th>
<th>Belgian Blue</th>
<th>Charolais</th>
<th>Hereford</th>
<th>Holstein</th>
<th>Limousin</th>
<th>Simmental</th>
<th>Other</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Total</strong></td>
<td>169,617</td>
<td>57,070</td>
<td><strong>367,998</strong></td>
<td>95,132</td>
<td>158,624</td>
<td>543,700</td>
<td>124,326</td>
<td>135,203</td>
</tr>
<tr>
<td><strong>AI sires</strong></td>
<td>306</td>
<td>313</td>
<td><strong>506</strong></td>
<td>223</td>
<td>2,904</td>
<td>509</td>
<td>378</td>
<td>1,465</td>
</tr>
<tr>
<td><strong>Natural service sires</strong></td>
<td>10,029</td>
<td>1,294</td>
<td><strong>20,797</strong></td>
<td>5,646</td>
<td>11,852</td>
<td>21,024</td>
<td>3,713</td>
<td>7,206</td>
</tr>
<tr>
<td><strong>Cows</strong></td>
<td>83,180</td>
<td>34,542</td>
<td><strong>146,905</strong></td>
<td>53,494</td>
<td>66,982</td>
<td>277,302</td>
<td>83,289</td>
<td>78,530</td>
</tr>
<tr>
<td><strong>Non parent Males</strong></td>
<td>13,577</td>
<td>2,083</td>
<td><strong>24,236</strong></td>
<td>8,026</td>
<td>60,370</td>
<td>29,535</td>
<td>6,320</td>
<td>14,938</td>
</tr>
<tr>
<td><strong>Non Parent Females</strong></td>
<td>62,556</td>
<td>18,862</td>
<td><strong>175,572</strong></td>
<td>27,765</td>
<td>16,703</td>
<td>215,352</td>
<td>30,694</td>
<td>33,200</td>
</tr>
<tr>
<td><strong>Pedigree registered</strong></td>
<td>34,010</td>
<td>2,608</td>
<td><strong>51,624</strong></td>
<td>20,389</td>
<td>24,702</td>
<td>63,328</td>
<td>16,769</td>
<td>23,451</td>
</tr>
<tr>
<td><strong>Single Breed Non ped</strong></td>
<td>4,914</td>
<td>1,474</td>
<td><strong>27,328</strong></td>
<td>3,707</td>
<td>5,415</td>
<td>37,238</td>
<td>11,897</td>
<td>8,245</td>
</tr>
<tr>
<td><strong>Multi-breed</strong></td>
<td>130,693</td>
<td>52,988</td>
<td><strong>289,046</strong></td>
<td>71,036</td>
<td>128,507</td>
<td>443,134</td>
<td>95,660</td>
<td>103,507</td>
</tr>
<tr>
<td><strong>Sired by AI</strong></td>
<td>53,470</td>
<td>36,967</td>
<td><strong>82,962</strong></td>
<td>23,115</td>
<td>114,324</td>
<td>151,985</td>
<td>35,788</td>
<td>45,778</td>
</tr>
<tr>
<td><strong>Known sire</strong></td>
<td>143,162</td>
<td>50,226</td>
<td><strong>324,791</strong></td>
<td>73,010</td>
<td>136,052</td>
<td>477,897</td>
<td>104,832</td>
<td>115,904</td>
</tr>
<tr>
<td><strong>Sire is also genotyped</strong></td>
<td>105,033</td>
<td>45,468</td>
<td><strong>270,393</strong></td>
<td>50,676</td>
<td>121,996</td>
<td>391,426</td>
<td>78,886</td>
<td>84,600</td>
</tr>
<tr>
<td><strong>Dam is also genotyped</strong></td>
<td>68,374</td>
<td>18,516</td>
<td><strong>200,372</strong></td>
<td>23,417</td>
<td>34,672</td>
<td>285,794</td>
<td>53,742</td>
<td>59,119</td>
</tr>
</tbody>
</table>
Development of genomic evaluations

• Scientific Advisory Committee established

  Esa Maantasari
  Ismo Stranden

  Roel Veerkamp
  Jeremie Vandeplas
  Jan te Napel

  Theo Meuwissen

  Peter Amer

  Dorian Garrick

  Donagh Berry

• Tasked with guidance in the rollout of genomic selection
  ➢ Computation Methods: GBLUP, SNPBLUP, Single step
  ➢ Validation
Genomic Evaluations

- SNP BLUP
  - DBV weighted by ERC
  - Random regression coeff matrix
  - Common marker $\sigma^2 \Sigma 2pq$

- ERC calculation
  - Identify Training population

- De-regression of EBVs
  - Weighted by ERC

- EBV

- Genotypes
  - Impute to 50k in FIMPUTE

- Univariate evaluations
  - n = 16 goal traits

- Reliability

- 7 multi-trait evaluations
  - 63 traits
  - Calving, Beef, Milk, Fertility, Docility

Published GEBV: Blending using selection index methodology
(Van Raden et al. 2009)
## Influence in SNP training: CH

<table>
<thead>
<tr>
<th>Trait</th>
<th>Category</th>
<th>count</th>
<th>avgERC</th>
<th>maxERC</th>
<th>Total ERC</th>
</tr>
</thead>
<tbody>
<tr>
<td>calving difficulty</td>
<td>AI sires</td>
<td>421</td>
<td>322</td>
<td>9,420</td>
<td>135,543</td>
</tr>
<tr>
<td>calving difficulty</td>
<td>Natural service sires</td>
<td>16,372</td>
<td>16</td>
<td>134</td>
<td>261,461</td>
</tr>
<tr>
<td>calving difficulty</td>
<td>Cows</td>
<td>17,979</td>
<td>3.5</td>
<td>11</td>
<td>64,234</td>
</tr>
<tr>
<td>carcass weight</td>
<td>AI sires</td>
<td>405</td>
<td>164</td>
<td>4,668</td>
<td>66,232</td>
</tr>
<tr>
<td>carcass weight</td>
<td>Natural service sires</td>
<td>14,942</td>
<td>8</td>
<td>74</td>
<td>118,229</td>
</tr>
<tr>
<td>carcass weight</td>
<td>Cows</td>
<td>32,338</td>
<td>1.1</td>
<td>6.6</td>
<td>33,925</td>
</tr>
<tr>
<td>maternal weaning wt</td>
<td>AI sires</td>
<td>250</td>
<td>34</td>
<td>877</td>
<td>8,497</td>
</tr>
<tr>
<td>maternal weaning wt</td>
<td>Natural service sires</td>
<td>378</td>
<td>2.0</td>
<td>11.5</td>
<td>754</td>
</tr>
<tr>
<td>maternal weaning wt</td>
<td>Cows</td>
<td>43,126</td>
<td>4.0</td>
<td>10</td>
<td>173,374</td>
</tr>
<tr>
<td>calving interval</td>
<td>AI sires</td>
<td>282</td>
<td>193</td>
<td>5,036</td>
<td>54,402</td>
</tr>
<tr>
<td>calving interval</td>
<td>Natural service sires</td>
<td>950</td>
<td>6.7</td>
<td>95</td>
<td>6,341</td>
</tr>
<tr>
<td>calving interval</td>
<td>Cows</td>
<td>69,383</td>
<td>5.9</td>
<td>18</td>
<td>411,081</td>
</tr>
</tbody>
</table>
Does genomics work?

- Forward prediction: 33% of phenotypes from animals with genotypes omitted
- Phenotype corrected for breed and evaluation fixed effects
- Then correlated with validation EBV, DGV and GEBV (without breed)
Benefit of correcting pedigree
160k ancestry changes

10% sire predicted, 9% sire changed
Impact of genomics by reliability

Difference GEBV-EBV Replacement Index

- Average difference
- Std of difference
- Bottom 1%
- Top 1%
Stability of first GEBV

Potential Change in Replacement Index between Evaluations based on Current Reliability

Stability depends on:
• Is pedigree known
• Reliability of sire/MGS
• Sire/dam/MGS genotyped
• Sire/dam/MGS in training population

Parental Average

Genomic evaluation

Proven sire 99%
In Reality

UK sire, Parents not genotyped
UK data integrated May 18

Average change is around 0 for each reliability band
Current research

• Single step evaluations
  ➢ Algorithms and knowledge have developed in last 2 years
  ➢ Currently testing on new calving evaluation with SAC partners

• Interbeef
  ➢ 8 countries participating: currently calving, weaning
  ➢ Integration of data into Irish evaluations

• New traits/indexes
  ➢ Dairy Beef index
    ➢ Specific calving traits: Dairy heifer, Dairy Cow, Beef heifer, Beef cow
    ➢ Specific beef traits: Dairy herd carcass, Beef herd carcass
  ➢ Meat Eating Quality
  ➢ Whole Herd Performance cow traits: udder, functionality, skeletal
  ➢ Cow intake: Greenbreed on farm project
  ➢ Carbon emissions: Greenfeed boxes in Tully performance centre

• Sire advice
  ➢ Genomic inbreeding, genetic defects, major genes (myostatin)
  ➢ Beef on the Dairy herd: expanding market
Thanks for listening!