Beef Genomic Evaluations.

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Replacement index Apr16 official v Jul16 NON genomic new milk

No of bulls 3795 correlation r = 0.931
Apr16 official = 56.96 \{stdev = 56.75\}
Jul16 NON genomic = 55.7 \{stdev = 50.8\}
Update since last meeting

- New blending method
- New data, pedigree and genotypes
- Combining of maternal wwt and cow milk score
Genomic evaluation steps

1. **Single trait evaluations**
   - \( n = 16 \) goal traits

2. **Adjustment of ebvs for influence of parents**
   - **SNP BLUP** (using selected animals)

3. **Genotypes**
   - Standardise to 50k SNPs

4. **7 multi trait evaluations**
   - 63 traits

5. **50k SNP effects**

6. **Direct Genomic Value**

7. **Blending** (influenced by reliability)

8. **Genomic ptas**
Blending method

- June method: Combined 2 sources of info: Traditional EBV and DGV
- Works okay where most of ancestry is also genotyped and where traits have a lot of data in traditional evaluations
- But: Many genotyped animals have no sire, dam or mgs genotyped
- Also traits like feed intake and cow live weight do not have a huge level of data
- Additional step needed
Genomic evaluation steps

Single trait evaluations
n = 16 goal traits

Adjustment of ebvs for influence of parents

SNP BLUP
(using selected animals)

Genotypes

Standardise to 50k SNPs

Genotypes

EBV and reliability using only genotyped animals in pedigree

50k SNP effects

Direct Genomic Value

Blending
(influenced by reliability)

Genomic ptas

7 multi trait evaluations
63 traits

All genotypes
Sire file circulated

- 3,795 beef AI sires
- 1,505 with a genotype and genomics
- 439 with a sire genotyped with genomics
- 2,290 sires with no genotype
- 86 sires requested but no sample back
- 51 with DNA received, awaiting genotypes
- 38 with poor DNA, DNA mis-match or other genotype problem
Replacement index Jul16 NON genomic v Jul16 with genomics new milk

No of bulls 3795  correlation r = 0.992
Jul16 NON genomic = 55.7  \{stdev = 50.8\}
Jul16 genomic = 56.62  \{stdev = 50.16\}
Replacement index Jul16 NON genomic v Jul16 with genomics: genotypes sires

No of bulls 1505 correlation r = 0.984
Jul16 NON genomic = 61.31 {stdev = 62.39}
Jul16 genomic = 63.12 {stdev = 60.79}
Combining maternal weaning weight and cow milk score

- Simple average of the two
- Weight according to single trait reliability
- If higher reliability for any one trait then more influence from that trait
- Not a huge difference as multi-trait evaluation will drive both in the same direction with correlation of 0.8
Milk combo5050 v Combo wtd : AI sires

No of animals 3696  correlation r = 0.996

Combo 5050 = 2.23 {stdev = 5.75}
Combo wtd = 2.15 {stdev = 5.68}
Milk combo5050 v Combo wtd : All geno animals

No of animals 336139  correlation r = 0.993

Combo 5050 = 3.6  {stdev = 5.17}
Combo wtd = 3.3  {stdev = 5}
Replacement index Apr16 official v Jul16 with genomics new milk

No of bulls 3795 correlation r = 0.927
Apr16 official = 56.96 {stdev = 56.75}
Jul16 genomic = 56.62 {stdev = 50.16}
Replacement index Apr16 official v Jul16 with genomics new milk

No of bulls 3795  correlation r = 0.927

Apr16 official = 56.96 {stdev = 56.75}
Jul16 genomic = 56.62 {stdev = 50.16}
Next Steps

- Updated calving run will be included
- Loading of files to the database
- Calculation of indexes for all animals
- New bull search facility to view impact of genomics on proofs
- Automation of evaluations (currently 197 different steps in process)
New bull search tab

### Replacement Index

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<tbody>
<tr>
<td></td>
<td>Replacement Index (Rel)</td>
<td>Replacement Index (Rel)</td>
<td>Replacement Index (Rel)</td>
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<tr>
<td></td>
<td>Within €150 (56%)</td>
<td>Across</td>
<td>Within €150 (56%)</td>
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<tr>
<td>Calving Difficulty</td>
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<td>4.8 6 42</td>
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Ability to see impact of genomics versus new data