Council on Dairy Cattle Breeding

Enhancements to U.S. genetic and genomic evaluations in 2018 and 2019

Exciting times

- Introduction of all-breed system for genomics
- Genomic evaluations including crossbred animals
- Update of SNP set used for genomic evaluations to ~80k
- Update of SNP positioning to latest ARS-UCD assembly
- New traits + lethal recessives updates
- Future plans in 2019
Introduction of all-breed system in genomics

- All-breed AM from traditional evaluations introduced in 2007
  - Evaluations obtained on a common breed base using an all-breed pedigree
  - All animals (including crossbred) contribute to PTAs
- April 2018 – all-breed system extended to genomics
  - Major back-end recoding
  - Slight impact on evaluations for purebreds (larger for pedigrees with different breeds)
  - Required more frequent calculation of heterosis and expected future inbreeding
    - For new animals and animals whose pedigree changed.
Genomic evaluations including crossbred animals

• April 2019 first publication of genomic evaluation including crossbred animals
  • 31,894 animals without evaluation (+36,790 that were receiving one)
• BBR: % of DNA contributed to the animal by each of the 5 breeds in evaluation (Holstein, Jersey, Brown Swiss, Guernsey and Ayrshire).
• SNP effects (by breed) obtained from animals with BBR \geq 94 for that breed
  • Animals with BBR \geq 90 = evaluations from (single) breed SNP effects
  • Animals with BBR<90 = blended evaluations (based on BBR)
• No blending for type, calving and health traits.
Update of SNP set used for genomic evaluations to ~80k

- December 2018: 79,294 SNP panel used for evaluations
  - Evolution from the 60k panel (2014)
- Expected reliability increase of 1.4 % points across all traits for HO (Wiggans et al., 2016)
- Direct inclusion of causative mutations (DGAT1, lethal recessives)
- PTA correlations over 99% for yield traits (all breeds)
- Largest impact on:
  - foreign animals less connected to US population
  - Large proportion of missing pedigree
  - Genotyped at lower density

Wiggans et al. – Genomic predictions using more markers and gene tests
ADSA – 207/208 - WEDNESDAY 9.45am
Update of SNP positioning to latest ARS-UCD assembly

- Illumina and PacBio technology (longer reads)
  - Improvement to imputation (lower non-inheritance and fewer haplotypes per segment)
  - Better annotation
- Now 1000 bulls reference (run7)
- December 2018: SNP positions updated to ARS-UCD in CDCB.

Null et al. – Using the ARS-UCD1.2 reference genome in US evaluations - ITB meeting – Sunday 11.15am
New traits

- **April 2018** – Holstein - Resistance to: Hypocalcemia, Displaced abomasum, Ketosis, Mastitis, Metritis, Retained placenta.
  - DHIA records across country: +32% (+1.1 million in April 2019)
  - International validation (MAS) obtained in March 2019, using it in PTA calculation in August 2019
  - Pre-adjustment for variance across lactation included in April 2019

- **April 2019** - Early First Calving
  - DHIA calving records recorded for decades ($h^2$: 2.7%)
  - Defined in days with reverse scale (positive is desirable)
Lethal recessives updates

  - Lower frequency than in France (0.5%)
  - AGIL researchers traced it to “Skyliner” (1954)
- Discontinuation of:
  - BH1 (no longer significant effect)
  - JH2 (difficult to track with new ARS-UCD map)
- With 80k SNP panel update:
  - 9 gene tests added to improve haplotype calling
  - HH5 gene test *not* added (inconsistent and suspicious results)
Future developments

• Health trait evaluations for Jersey animals
• CDCB-FFAR co-sponsored project ($2 mln) for feed efficiency
• Enhancements to already published traits
• “Virtual parent” project – using MGS information in incomplete pedigrees
• Revisiting reliabilities in crossbred animals
• Including lethal recessive haplotype calling for crossbred animals
• Reduction of animals included in monthly imputation
• Update to SNP set used for evaluations

Jensen et al. – Extending genomic evaluations to direct health traits in Jerseys.
ADSA – 207/208 – TUESDAY 10.30am

VanRaden et al. – Genomic prediction and marker selection using high-density genotypes from 5 breeds
ADSA – 207/208 – WEDNESDAY 12.00pm
Acknowledgments

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• AGIL and CDCB staff
THANK YOU FOR YOUR ATTENTION