

# Council on Dairy Cattle Breeding

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

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# 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

*P. VanRaden, L. Bacheller,  
G. Fok, M. Tooker,  
L. Walton , J. Megonigal*

- 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

G. Wiggans, M. Tooker,  
L. Walton, E. Nicolazzi,  
P. VanRaden

- 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.

Wiggans et al. – Extending genomic evaluation to  
crossbred dairy cattle - US implementation  
**ITB meeting – SUNDAY 8.30am**

# 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

# Update of SNP positioning to latest ARS-UCD assembly

D. Null, D. Bickhart,  
G. Wiggans, L. Bacheller,  
P. VanRaden, J. Cole, J.  
O'Connell, B. Rosen *et al*

- Official release of ARS-UCD cattle DNA reference genome (*Rosen et al., 2018*)
- 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.



# New traits

K. Gaddis, J. Cole,  
L. Walton, D. Norman,  
J. Hutchison, D. Null,  
D. Bickhart, P. VanRaden

- **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

Gaddis et al. - Development, implementation, and future perspectives of health evaluations in the United States Joint  
**ADSA/ITB – Junior Ballroom C – MONDAY 4.30pm**

- **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

- December 2018 – Introduction of HH6 (*Fritz et al., 2018*)
  - Lower frequency than in France (0.5%)
  - AGL 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

- Participating dairy producers, owners of data used
- Dairy Herd Improvement organizations (DHIs) and the Dairy Records Processing Centers (DRCs) for processing and relaying the information on to the **Council on Dairy Cattle Breeding (CDCB)**
- Purebred breed associations for providing pedigree data
- AGIL and CDCB staff

**THANK YOU FOR YOUR ATTENTION**