

Council on Dairy Cattle Breeding
CDCB evolution 2018 to 2019

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Main projects in 2018 – 2019

- Introduction of all-breed genomic evaluation system
- 7 new traits (6 health evaluations + Early First Calving) + update of NM\$
- Update to existing traits
- Upgrade of SNP set from 60k to 80k and update to latest reference genome
- Changes to recessive haplotypes
- Update of BBR calculation
- **Genomic evaluations including crossbred animals**
- **Introduction of new genomic format**
- **Genomic laboratories auditing process.**
- Update(s) to genomic software and queries
- **New fee schedule**

All-breed system

- Introduced officially in April 2018
- **Major** re-writing of genomic evaluation software (drastic reduction of programs involved)
- Evaluation system now similar to the traditional evaluation since 2007
- Greatest benefit is the use of all pedigree from all breeds, and the calculation of genetic values on a common scale
 - First step towards crossbred evaluations

New traits

- April 2018: 6 new resistance (health) traits on Holstein
- August 2018:
 - HTH\$ included in NM\$ (~ 2%)
 - Much of the resistance in NM\$ was already accounted for by correlated traits.
 - International validation of Health traits (April 2019) – Inclusion of international MAS data in August 2019
- April 2019: Early First Calving

Update to existing traits

- **Productive Life (PL)**
 - Updated in April 2018. Stability of the multi-trait while including foreign evaluation was a problem. Changed the way foreign evaluations are considered.
 - Large initial change, large increase in stability
- **Fertility traits (DPR, CCR, HCR)**
 - Large negative variation in young bulls in April 2018. The way age-parity effects in the model was updated (each 5 years) caused periodic drops when new age groups were created. Corrected in August 2018 to a “rolling age-group” (updated every year)
 - Negative variation still present in April 2019, mostly on Holstein.
 - Investigation still in progress, AGIL identified possible reasons of the variation.
 - Still requires testing and validation of results

Update from 60k to 80k

- More accurate evaluations
- Improved imputation
- Using improved locations from new assembly
- Continuing review of SNP quality. Some SNP eliminated do to incorrect locations
- 28,516 SNP not on 60K
- 9,851 60K replaced by more informative SNP
- Future updates to add more informative SNP

Changes to recessive haplotypes

- Two new lethal recessive introduced:
 - AH2 (Ayrshire Second Fertility Haplotype) – December 2017
 - HH6 (Holstein Sixth Fertility Haplotype) – December 2018
- Discontinued two recessive haplotypes (December 2018)
 - BH1 – Brown Swiss First Fertility Haplotype (effect no longer significant)
 - JH2 (and JH2_PC) – Jersey Second Fertility Haplotype (no trace on new ARS map)

Update on BBR calculation

- Switched to 80K SNP set for estimation of SNP effects
- Use allele frequencies from purebred bull reference population where SNP missing
- Recalculated all BBR for April 2019
- Discontinued releasing BBR from weekly evaluations
- Recalculate BBR every month, update stored value if change > 4

Update to genomic software and queries

- Monthly genotype extract program changed to rely on BBR to determine directory for calculation
- Weekly extract uses threshold of 15% unlikely allele breed SNP to determine evaluation in XX (crossbred) directory
- Parentage only = B no longer used, not assigned to new genotypes
- Queries modified to accommodate new fee schedule
- Genotype query displays only current conflicts
- EDCLOB enhancements

THANK YOU FOR YOUR ATTENTION