Council on Dairy Cattle Breeding
Genomic evaluations including crossbred animals

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Credits

- **For AGIL-USDA:** *Mel Tooker and Paul VanRaden* (all research and methodology)

- **For CDCB:** *George Wiggans* (application, coding and BBR research) and *Leigh Walton* (testing and implementation)

Background

- Over 35,000 animals excluded from genomic evaluation that were determined to be crossbreds based on breed SNPs.

    - > $1mln spent in genotyping with no genomic evaluation provided

- Mel Tooker and Paul VanRaden (2017) proposed that crossbreds could be evaluated by combining individual-breed (purebred) SNP effects weighted by **breed proportions**

Towards a genomic evaluation of crossbreds
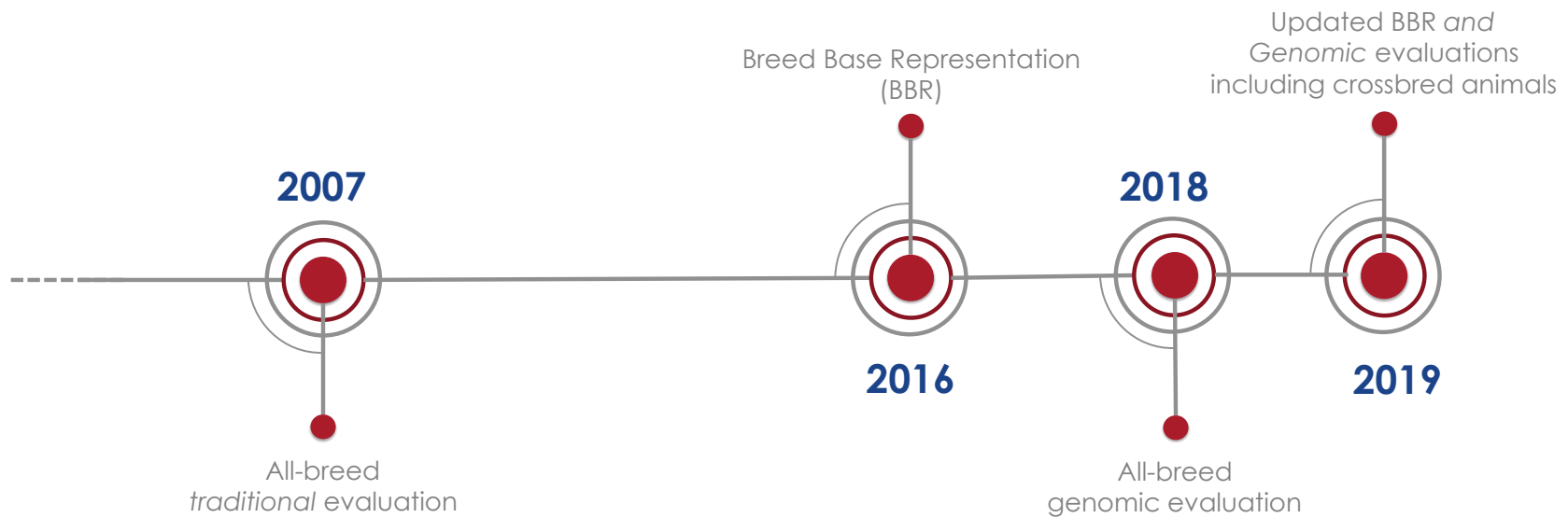
(some of the) Challenges of a genomic evaluation for crossbreds

- How to sort animals between single-/multi-breed? What threshold?
- Management of breed specific traits (type, calving and health traits)
- What breed base to use on all animals? What about F1's?
- What population parameters to use to obtain multi-breed PTAs?
- Is BBR the best method to "weight" breed composition? Is BBR "bulletproof"? How to manage evaluations on animals without starting BBR? (e.g. weeklies vs monthlies)
- How to define the reference population for a single breed?
- How to distribute results, how to label animals?

- What are the effects of these decisions on single-breed evaluation?
- Impact of any change in BBR on results.
- Impact PTAs of animals currently getting an evaluation when included in the multi-breed population.
- How to ensure stability of results in light of a BBR value that is an *estimate*? (e.g. expected to have a degree of variation?)
- Imputation requires multiple breed reference population. Possible "interference" of other breeds.
- etc...

BBR (Breed Base Representation)

- % of DNA contributed to the animal by each of the 5 breeds in evaluation
  - An **ESTIMATE**, corrected by breed mean to reduce statistical noise.
  - Distributed once per animal (except for higher density re-genotyping)
- BBR will have central role in genomic evaluations including crossbred animals. Used to:
  - Determine where the animal is obtaining an evaluation (single- / multi-breed group?)
  - Weight the breed proportions in the evaluations (if in multi-breed group)
- BBR revision of policy and methodology required.
- Study on last 2 years of BBR evaluations:
  - Ancestry updates, availability of sire/dam genotypes, genotype reassignments, migration from 60K – 80k prediction set and higher density re-genotyping

A (real) case scenario – March 2019

- HO cow:
  - First submitted in January
  - No pedigree.
  - Genotype fails breed checks, so imputation and BBR are obtained from multi-breed population.

  BBR JAN: **50% Holstein, 25% Jersey, 12% Brown Swiss, 8% Ayrshire, 5% Guernsey**

- …two months later:
  - genotype re-submitted (same density)
  - sire and dam provided (confirmed)
  - breed test passed (gets imputation and BBR from HO population).

  BBR MAR: **100% Holstein, 0% Jersey, 0% Brown Swiss, 0% Ayrshire, 0% Guernsey**

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Updated BBR (April 2019)

- Updated BBR: value with a simpler correction to reduce statistical noise
- Reducing statistical noise:
  - Breed means correction discontinued. Weekly breed means not representative so not reliable to reduce statistical noise
  - Correction obtained by setting to 0 any breed proportion ≤ 2 and proportionally rescaling the remaining percentages.
- Example:

  BBR   : 80% Holstein, 16% Jersey, 2% Brown Swiss, 2% Ayrshire, 0% Guernsey
  BBRnew: 83% Holstein, 17% Jersey, 0% Brown Swiss, 0% Ayrshire, 0% Guernsey

- In April 2019, <u>all animals will receive a new BBR based on the updated procedure</u>

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TOWARDS GENOMIC EVALUATIONS INCLUDING CROSSBRED ANIMALS

Current (single-breed) evaluations

- Genomic predictions on ~50 traits for five breeds: Ayrshire (AY), Brown Swiss (BS), Guernsey (GU), Holstein (HO) and Jersey (JE)

- Crossbred animals excluded from evaluations (recognized by SNP–based check based on breed SNP)

- BBR values distributed once, except in case of genotyping at higher density – BBR values not used for evaluation purposes

Genomic evaluations including crossbred animals

- Updated BBR: active role in animal's genomic evaluation.

- Animals with BBR$\geq$90 = evaluations from (single) breed SNP effects.

- Animals with BBR<90 = blended evaluations (based on the BBR) – See exceptions to this rule in later slide.

  - Example BBR: 83% Holstein, 17% Jersey

  - Population parameters / relatedness have effect on final PTA

  - PTA base:

    - For purebred, breed of evaluation (breed in ID17)

    - For BBR<90, breed of highest BBR regardless their ID17. Exception for F1's

Breed of evaluation & fees

- For F_1 (2 breed cross) breed of ID17 used if second highest BBR breed and the highest BBR < 55 and second highest < 10 lower.

  - Gives owner some say in having comparable evaluations

- No genomic evaluation if BBR or SNP test indicate animal is nearly a purebred of different breed.

- For newly evaluated crossbred animals, fees will be charged only for those nominated on or after January 1, 2019

Genomic evaluations including crossbred animals

- *No blending* for multi-breed evaluations on

  - ***Type traits***: not comparable across breeds; DGV calculated based on 100% SNP solutions of the breed of evaluation.

  - ***Calving traits***: available for Holstein and Brown Swiss. DGV calculated based on 100% SNP solutions of the breed of evaluation (if HO or BS)

  - ***Health traits***: (currently) available for Holstein only. DGV calculated based on 100% SNP solutions of the breed of evaluation (if HO)

- ***<u>No haplotype calling</u> for blended animals at this stage (research ongoing)***

Genomic evaluations including crossbred animals

- Monthly evaluations: animals w/ trad eval+ BBR $\geq$ 94% included in breed PTA reference population
    - Evaluations of single-breed animals improved slightly by removing mixed breed animals from reference population.
    - Disadvantages:
        - fewer animals in reference population.
        - Animals with daughters and 90 $\leq$ BBR < 94 lose some of the impact of their own traditional evaluations on their evaluation
    - Test runs show nearly **no difference in cow and bull trends** in <u>any</u> single-breed.
    - Animals in the multi-breed group **DO NOT** contribute to any PTA reference population.

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Genomic evaluations including crossbred animals:
Publication rules

- All animals published in their respective breed of evaluation file (same PTA base).
  - No changes in files distributed
- Label (genomic files only – no changes in fmt 38/105)
  - BLEND_CODE="S" – single–breed based evaluations
  - BLEND_CODE="M" – multi–breed blended evaluations
- New BBR results distributed on **a monthly basis**
- Animals receive first BBR at their first monthly evaluation.
- Corrections to the initial BBR: only when genotype reassigned or recalculated value for any breed differs by more than 4
- Haplotype results for "M" animals are blank.

Genomic evaluations including crossbred animals:
What changes (I)

- Single- and Multi-breed evaluations, affected by BBR

- Single-breed reference population for SNP effect estimation is based on "pure" (BBR $\geq$ 94) animals.

  - Low impact expected on single-breed animals (AY upwards)

- Impact on animals with BBR < 90 (some may be large).

  - Expected to be more accurate now that their multi-breed composition is considered.

  - No haplotype calls for these animals (for now).

Genomic evaluations including crossbred animals:
What changes (II)

- Updated BBR is different from old BBR:
  - Different correction, results more consistent with pedigree.
  - Monthly vs Weekly distribution
  - *Can* change during an animal lifetime (some constraints to reduce variability)
- Label in genomic format (BLEND_CODE= "S" /"M")
- Merging of single- & multi-breed evaluation files (e.g. no changes in file distribution)

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Benefits

- Provide genomic evaluations on previously ineligible crossbreds.
- Improve accuracy of evaluations of animals currently evaluated with mixed breed ancestry
- Routine updating of BBR when significant change

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Thank you!

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