

# Evaluation of crossbreds

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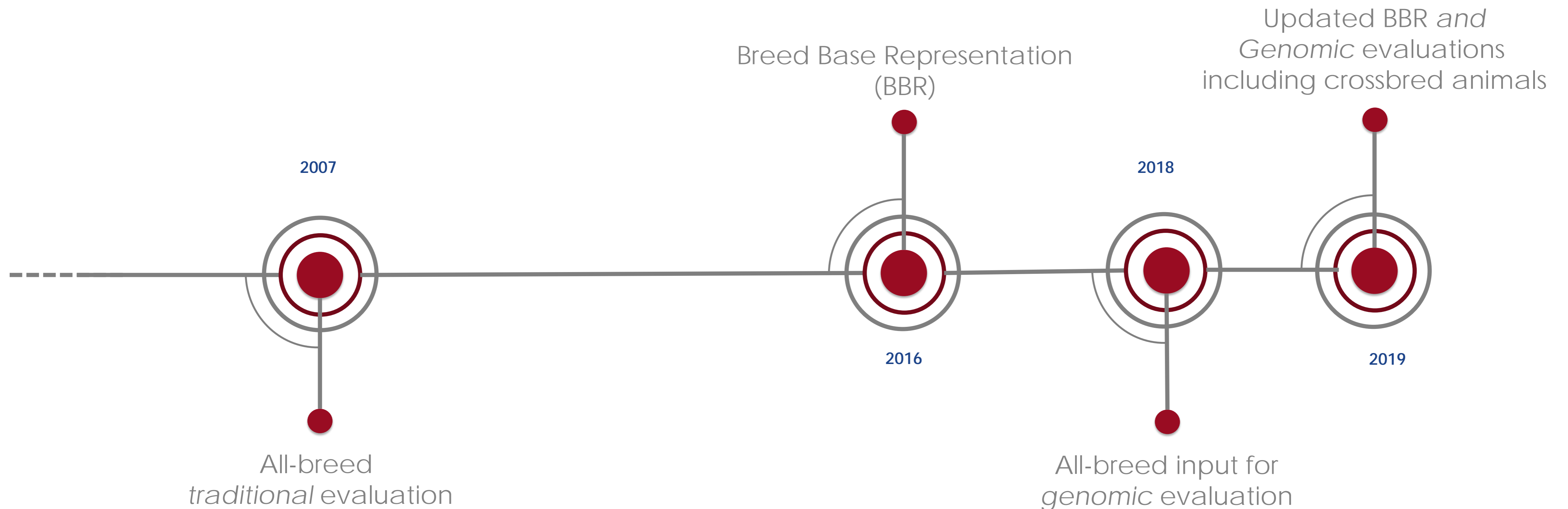
# Collaboration made it happen

- **For CDCB:** *George Wiggans* (application, coding and BBR research) and *Leigh Walton* (testing and implementation)
- **For AGIL-USDA:** *Mel Tooker and Paul VanRaden* (all research and methodology)

# 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**

# Steps to a genomic evaluation of crossbreeds



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

- Imputation requires multiple breed reference population. Possible “interference” of other breeds.
- 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?
- Animals currently getting an evaluation will receive a different evaluation if included in the multi-breed population.
- 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 sort animals between single-/multi-breed? What threshold?
- How to define the reference population for a single breed?
- What are the effects of these decisions on single-breed evaluation?
- What animals / breeds will be more impacted by this change?
- 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?)
- How to distribute results, how to label animals?
- etc...

# BBR (Breed Base Representation)

- % of DNA contributed to the animal by each of the 5 breeds in evaluation
  - An ***ESTIMATE***
  - Distributed once (except for **higher density re-genotyping**)
- Study on last 2 years of BBR evaluations:
  - Ancestry updates, availability of sire/dam genotypes, migration from 60K – 80k prediction set, genotype reassignments and **higher density re-genotyping**
  - *Breed means* correction discontinued.
    - Weekly breed means not representative so not reliable to reduce statistical noise

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

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

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

# Updated BBR (April 2019)

- BBR used to weight the breed contributions in the evaluations.
- Adjustment to BBR: remove small values not statistically different from 0
  - Set to 0 any breed proportion  $\leq 2$  and proportionally rescale 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, all animals received an new BBR from the updated procedure



# Previous (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 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)
- ***No haplotype calling 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
  - Nearly no difference in cow and bull trends in any single-breed.
- Animals in the multi-breed group **DO NOT** contribute to any PTA reference population.

# 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 changed (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 on single-breed animals (AY upwards)
- Impact on animals with BBR < 90 (some large).
  - More accurate now that their multi-breed composition is considered.
  - No haplotype calls for these animals (yet).

# Genomic evaluations including crossbred animals: What changed (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)



# 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

# Summary of evaluation of crossbreds

- Breed proportions called breed base representation (**BBR**) estimated as 5 genomic traits (**Ayrshire, Brown Swiss, Guernsey, Holstein, Jersey**) from purebred animals
- Animals with highest BBR < 90 evaluated by applying SNP effect solutions from each breed and then weighting by BBR
- Reference population limited to BBR  $\geq 94$
- Type, calving, and health traits not blended because not comparable or not available for all breeds

# Related changes

- PI=B no longer assigned. Retained for genotypes processed before April 3, 2019 to assist in applying fee codes.
- PI=B no longer prevents assignment of use weekly timestamp
- Animals w/ BBR  $\geq 90$  for different breed not evaluated
- All animals with the same breed of evaluation included in same csv
- Research continues on blend\_code=M evaluations to provide imputed recessive conditions, better reliabilities, and inbreeding/heterosis

# Adding discovered MGS to pedigree

- Query to search DHI data for cow in designated herd that is daughter of discovered MGS and calved on birth date
- Proposal to add sires where missing on fee code N pedigree with code to so indicate
- Creating constructed dam IDs to connect discovered MGS to genotyped animal



# Questions?