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

- **2007**: All-breed traditional evaluation
- **2016**: Breed Base Representation (BBR)
- **2018**: All-breed genomic evaluation
- **2019**: Updated BBR and Genomic evaluations including crossbred animals
(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
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, all animals will receive a new BBR based on the updated procedure

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TOWARDS GENOMIC EVALUATIONS INCLUDING CROSSBRED ANIMALS
Current (single-breeds) 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≥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 F₁ (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)
- *No haplotype calling for blended animals at this stage (research ongoing)*
Genomic evaluations including crossbred animals

- Monthly evaluations: animals w/ trad eval + BBR ≥ 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 ≤ 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 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 changes (I)

- Single- and Multi-breed evaluations, affected by BBR
- Single-breed reference population for SNP effect estimation is based on “pure” (BBR > 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)
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
Thank you!

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