Crossbred Evaluations and More

George R. Wiggans

Council on Dairy Cattle Breeding, Bowie, Maryland, USA

CDCB

COUNCIL ON DAIRY CATTLE BREEDING

Background of Crossbred Evaluations

- Over 34,000 animals excluded from genomic evaluation that were determined to be crossbreds based on breed SNPs
- Paul VanRaden proposed that crossbreds could be evaluated by combining individual-breed purebred SNP effects weighted by breed proportions
- Breed base representation (BBR) introduced in June 2016 to provide breed proportions
- In April 2018, calculations of genomic evaluations switched to an all-breed base to enable merging across breeds

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Challenges in Crossbred Evaluations

- Imputation to calculate BBR for crossbreds must be done using an across-breed haplotype library, but BBR not yet available to determine if animal is a crossbred
- Type traits evaluations not comparable across breeds; therefore, cannot be blended
- Health and calving traits not available for all breeds
- A breed base for expressing resulting evaluations must be selected
- Some animals now being evaluated as purebreds included in crossbred evaluation, causing changes in their evaluations

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Proposal for Crossbred Evaluations

- Animals with BBR of <94 (actually 93.5) receive genomic evaluation based on weighted average of SNP effects across breeds

- Evaluation expressed on base of breed of preferred ID if supported by BBR
  - For F1s in BBR range of 40 to 60%, breed base might not be breed of highest BBR
  - If no BBR above 40%, use breed of preferred ID if among the top 2
  - If XX (or XD), use breed of highest BBR
  - If BBR >60% for different breed, use BBR breed or report error

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Traits Included in Crossbred Evaluations

- Type traits cannot be combined across breed because trait evaluations not comparable across breeds
  - Type evaluation from evaluation breed reported
- Health trait evaluations only available for Holsteins and, therefore, only for crossbreds with HO evaluation breed
- Calving trait evaluations only provided for Holsteins and Brown Swiss (calving ease for both, stillbirth only for Holsteins)

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Modification of Evaluation Breed

- Format-1 record can change breed of preferred ID, which then causes evaluation breed to be updated
- No genomic evaluations for Milking Shorthorns, Montbéliardes, Linebacks, and Simmentals
- Wrong breed declared based on breed SNPs when different breed has <10% unlikely alleles and percentage of unlikely alleles lower than for evaluation breed

BBR Calculation

- BBR fundamental to evaluation of crossbreds, directly affects PTA
- Imputation required to calculate BBR
- Must decide which genotypes to impute using across-breed haplotype library
- Genotypes with >10% of unlikely breed SNP alleles to be imputed using across-breed haplotype library
- Weekly evaluations calculated using BBR from same run

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Grandsire Validation

- If parent not genotyped or not confirmed, grandsire checked
- Grandsire declared unlikely if animal and grandsire have more opposite homozygotes than threshold (declines as possible comparisons increase)b
- Possible grandsires suggested if low conflict percentage and birth date reasonable (94%)
- Animals with unlikely grandsires excluded from evaluation (4%)

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

MGS Changes

- If sire confirmed and MGS unlikely or unknown, haplotype method used
- As part of weekly evaluation, possible MGS discovered by matching with maternal haplotypes
- If discovered MGS matches pedigree MGS, unlikely MGS indicator removed
- Parentage verification records generated as part of weekly

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Ancestor Discovery

- Based on haplotypes, MGS discovered with 95% certainty and MGGS with >90% certainty
  - Both at least as accurate as average reported pedigree
- Discovered MGS added to no-pedigree dams and provided to DRPC and others
- When dam unknown, constructed dam ID allows use of discovered MGS (over 200,000 for Holstein)
- Procedure developed to detect actual dam based on herd code and calving date
- Constructed IDs could enable use of discovered MGGS (~200,000 for Holstein)

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

New SNP List

- Plan to increase number of SNPs used in genomic evaluations to around 77,000
- New bovine assembly used to determine SNP sequence on chromosomes
- SNPs selected to
  - Minimize gaps
  - Eliminate one of a pair of consecutive SNPs with high correlation
  - Have high impact on one trait or more
- More and better SNPs expected to increase evaluation accuracy by 3 percentage points

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Chip Validation

- Determine if new SNP included; if so, get location and probe
- Check that ICAR parentage and X/Y SNPs included
- Check each SNP for call rate and parent-progeny consistency
  - If not Illumina, check if any SNPs have A/B calls reversed
- Possibly revise SNP list if some SNPs not reliable

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

CDCB
COUNCIL ON DAIRY CATTLE BREEDING