Genomic evaluation of crossbred dairy cattle in the United States

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Background

• By 2019, >35,000 animals excluded from genomic evaluation
  • Determined to be crossbred based on breed SNPs
  • >$1 million spent in genotyping with no genomic evaluation provided

• Evaluate crossbreds by combining individual-breed (purebred) SNP effects weighted by breed proportions
Crossbreds excluded before April 2019

- Genomic predictions for ~50 traits for 5 breeds: Ayrshire, Brown Swiss, Guernsey, Holstein, Jersey

- Excluded from evaluations based on presence of unlikely alleles in a set of breed-determining SNPs because:
  - Imputation relies on breed-specific haplotype libraries and allele frequencies *(Holstein would overwhelm otherwise)*
  - Marker effects differ by breed
Requirements for evaluation of crossbreds

• Breed composition for weighting individual breed contributions
  • Pedigree often not reliable because of missing ancestors

• Evaluations for each breed on same base so that they can be combined

• Method to impute genotypes for crossbreds
Breed proportions (breed base representation; BBR)

- Reference population of ~36,000 purebred males across 5 breeds
- SNP effects estimated with same 79K SNPs as in genomic evaluation
- Phenotypic values for 5 breed traits: 100% for animal’s breed; 0% otherwise
- SNP-effect solutions updated each April
- BBR calculated and released for all animals every month
  - Adjusted to 0–100% range; values of ≤2 redistributed to other breeds
  - Animal BBR updated if any of its breed values differ by ≥4
Imputation of crossbreds

• Starts with Haplotype library from BBR reference population
  • For Holsteins, bulls and cows with progeny, trad evaluations required (only 1/3 of cows with single progeny included)
  • All genotypes from other breeds
• Parent genotypes from purebred directories added to improve imputation accuracy in crossbred directory
• PTAs released weekly; BBRs delayed until monthly so released BBR is from imputation using appropriate reference population
Evaluation of crossbreds

• 5 evaluations calculated for each trait of each animal
  (1 from each breed’s SNP-effect solutions)

• Animals with highest BBR of <90% evaluated by weighting
  individual breed solutions by BBR

• Reference population limited to BBR of ≥94%

• Type, calving, health traits, and feed saved not blended because
  not comparable or not available for all breeds
Frequency of crossbred genotypes

![Graph showing the frequency of crossbred genotypes from 2008 to 2020. The x-axis represents the year the genotype was submitted, and the y-axis represents the number of genotypes. The graph shows an increase in the number of genotypes submitted each year, with a significant spike in 2020. There are two categories: males (blue) and females (pink).]
Evaluation details

• Results from purebred and crossbred directories combined so that animals with same evaluation breed included in same distribution file

• Animals with BBR of $\geq 85\%$ for different breed not evaluated because of possible misidentification

• Inbreeding of future progeny calculated with relationships from purebred evaluations
Weekly evaluations

- Approximate BBR calculated as genotypes are loaded; uses only SNPs on chip
- Genotypes with BBR of ≥85% initially placed in purebred directory
- Genotypes based on imputation from purebred directories with BBR of <90% moved to crossbred directory
- Genotypes in crossbred directory with BBR of ≥90% receive single-breed evaluation
Breed of evaluation

• Initial breed of evaluation derived from preferred ID

• Remains breed of evaluation if BBR >40%; breed of highest BBR becomes breed of evaluation otherwise

• Change in breed of ID required if BBR of >85% for different breed

• Evaluations converted to individual breed bases for reporting
Recessive conditions

• Not reported for crossbreds

• Most characteristics breed-specific
Comparisons

- Little effect on purebred evaluations because of requirement for BBR of ≥94% for reference population

- Largest effect for animals with 90% < BBR <94% where own traditional evaluation not included

- Larger changes for animals previously with a single-breed evaluation and now with mixed breed ancestry reflected in evaluation
Summary

- Genomic evaluations of crossbreds began April 2019
- Single-breed evaluations combined, weighted by breed proportions
- Number of crossbreds being genotyped rapidly increasing
- Routine updating of BBR when significant change
- Extends pedigree validation, provides breed composition, lower reliability than purebreds
Acknowledgments and disclaimers

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