Genomic evaluation of crossbred dairy cattle in the United States

G.R. Wiggans,¹ P.M. VanRaden,² D.J. Null,² E.L. Nicolazzi,¹ G.B. Jansen,¹ and J.H. Megonigal, Jr.¹

¹ Council on Dairy Cattle Breeding, Bowie, Maryland, USA
² Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, Maryland, USA
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 [VanRaden et al., 2017, J. Dairy Sci. 100(Supp. 2):409–410]
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

- **Males**
- **Females**

![Graph showing the frequency of crossbred genotypes over years](image-url)
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 $\geq 94\%$ for reference population

• Largest effect for animals with $90\% < \text{BBR} < 94\%$ 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

• Participating dairy producers for supplying pedigree and genomic data

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