

Extending genomic evaluation to crossbred cattle – U.S. implementation

G.R. Wiggans,¹ P.M. VanRaden,² E.L. Nicolazzi,¹
M.E. Tooker,² J.H. Megonigal, Jr.,¹ and L.M. Walton¹

¹ Council on Dairy Cattle Breeding, Bowie, Maryland, USA

² Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, Maryland, USA



**United States
Department of
Agriculture**

Background

- **Over 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., J. Dairy Sci. 100(Supp. 2) 409-410 2017)

Single-breed evaluations before April 2019

- **Genomic predictions for ~50 traits for 5 breeds: Ayrshire, Brown Swiss, Guernsey, Holstein, Jersey**
- **Crossbred animals excluded from evaluations based on presence of unlikely alleles in a set of breed-determining SNPs**
 - **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**
- **Evaluations for each breed on same base so that they can be combined**
- **Imputed genotypes for crossbreds**

Breed proportions (breed base representation; **BBR**)

- Reference population of ~36,000 purebred males across 5 breeds
- SNP effects estimated with same 80k 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

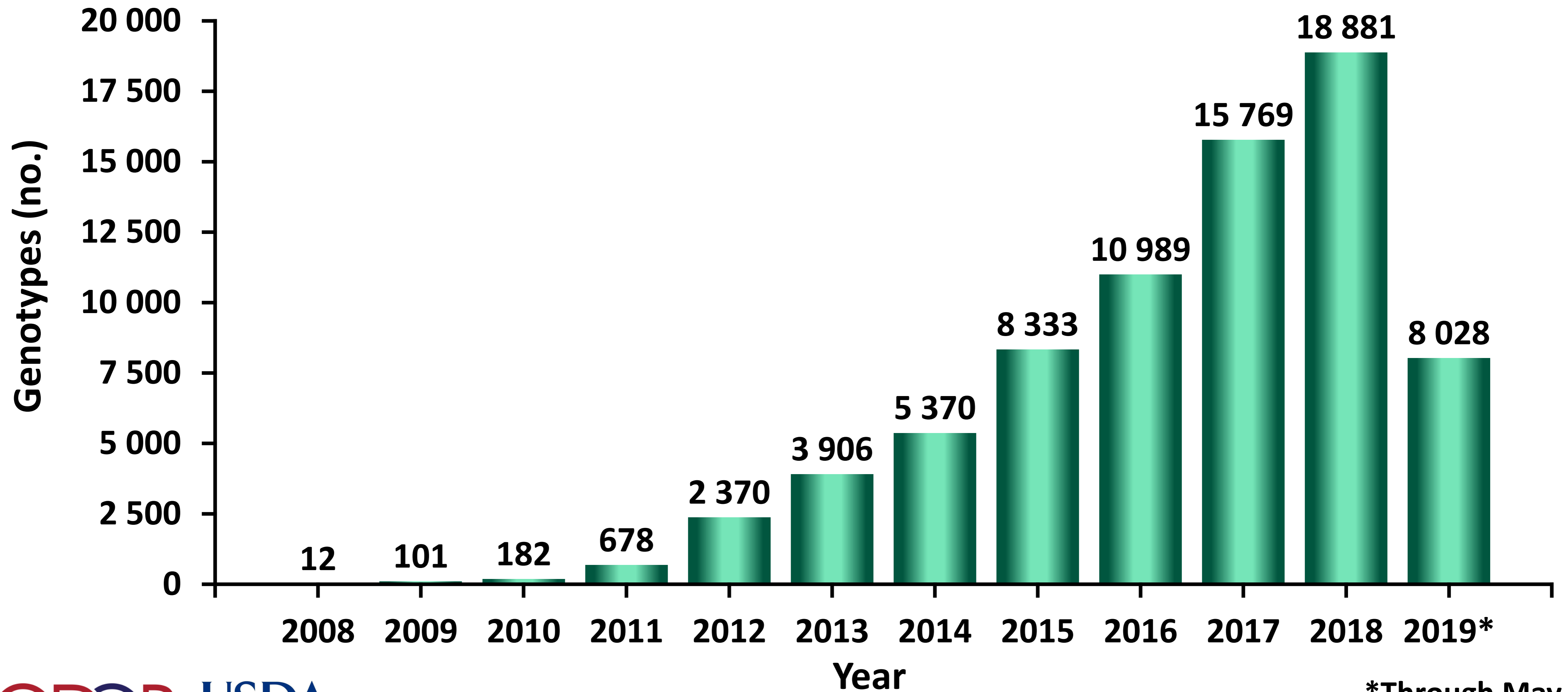
Imputation of crossbreds

- **Imputed separately from purebreds**
- **Parent genotypes from purebred directories added to improve imputation accuracy in crossbred directory**
- **Haplotype library from BBR reference population**
- **PTA released weekly, BBR delayed until monthly so released BBR is from imputation in appropriate reference population**

Evaluation of crossbreds

- **5 evaluations calculated for each trait of each animal (1 for each breed from 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, and health traits not blended because not comparable or not available for all breeds**

Frequency of crossbred genotypes



*Through May



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 ≥ 90 for different breed not evaluated due to possible misidentification**
- **Inbreeding of future progeny calculated with relationships from purebred directories**

Weekly evaluations

- **BBR first calculated in weekly evaluation (not released)**
- **Genotypes with >15% unlikely breed SNP alleles processed in crossbred directory**
- **Genotypes 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
- Breed of highest BBR becomes evaluation breed if highest BBR is >55
- Initial evaluation breed remains evaluation breed if its BBR is <10 lower than highest BBR to accommodate F_1
- Evaluations converted to individual breed bases for reporting

Recessive conditions

- **Initially not reported for crossbreds**
- **Most characteristics breed specific**
- **Bulls from all breeds w/ >100 daus added to inform the designation of carriers**
- **Reporting of more recessive tests of benefit, particularly for females**

Comparisons

- **Little effect on purebred evaluations because of requirement for BBR of ≥ 94 for reference population**
- **Largest effect for animals with $90 < \text{BBR} < 94$ when own 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 extended to crossbreds in April 2019**
- **Single-breed evaluations combined and weighted by breed proportions**
- **Number of crossbreds being genotyped increasing**
- **Routine updating of BBR when significant change**
- **Reduced influence of other breeds on purebred SNP effects**

Acknowledgments and disclaimers

- **Participating dairy producers for supplying pedigree and genomic data**
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Questions?