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

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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
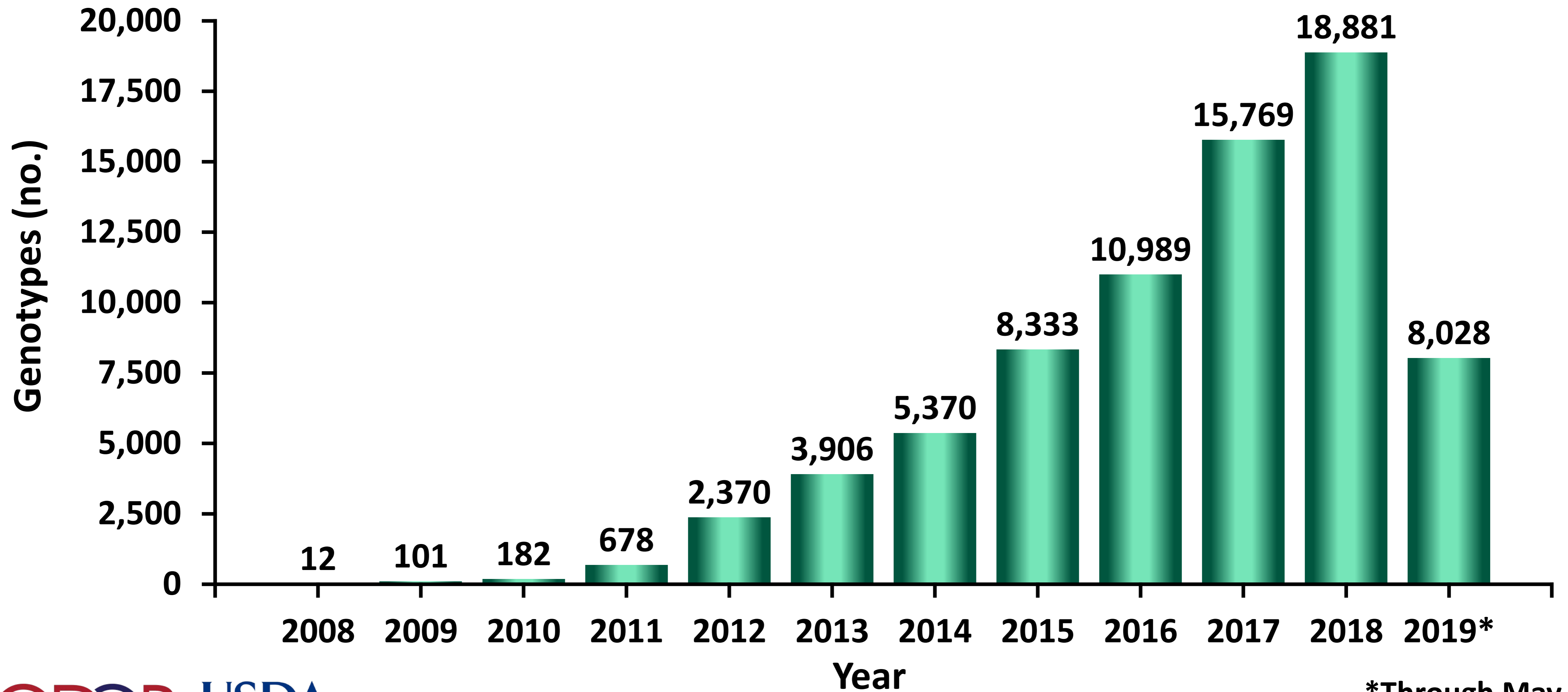
*Through May

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 < 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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- **Mention of trade names or commercial products in this presentation is solely for the purpose of providing specific information and does not imply recommendation or endorsement by USDA**

Questions?