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 [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

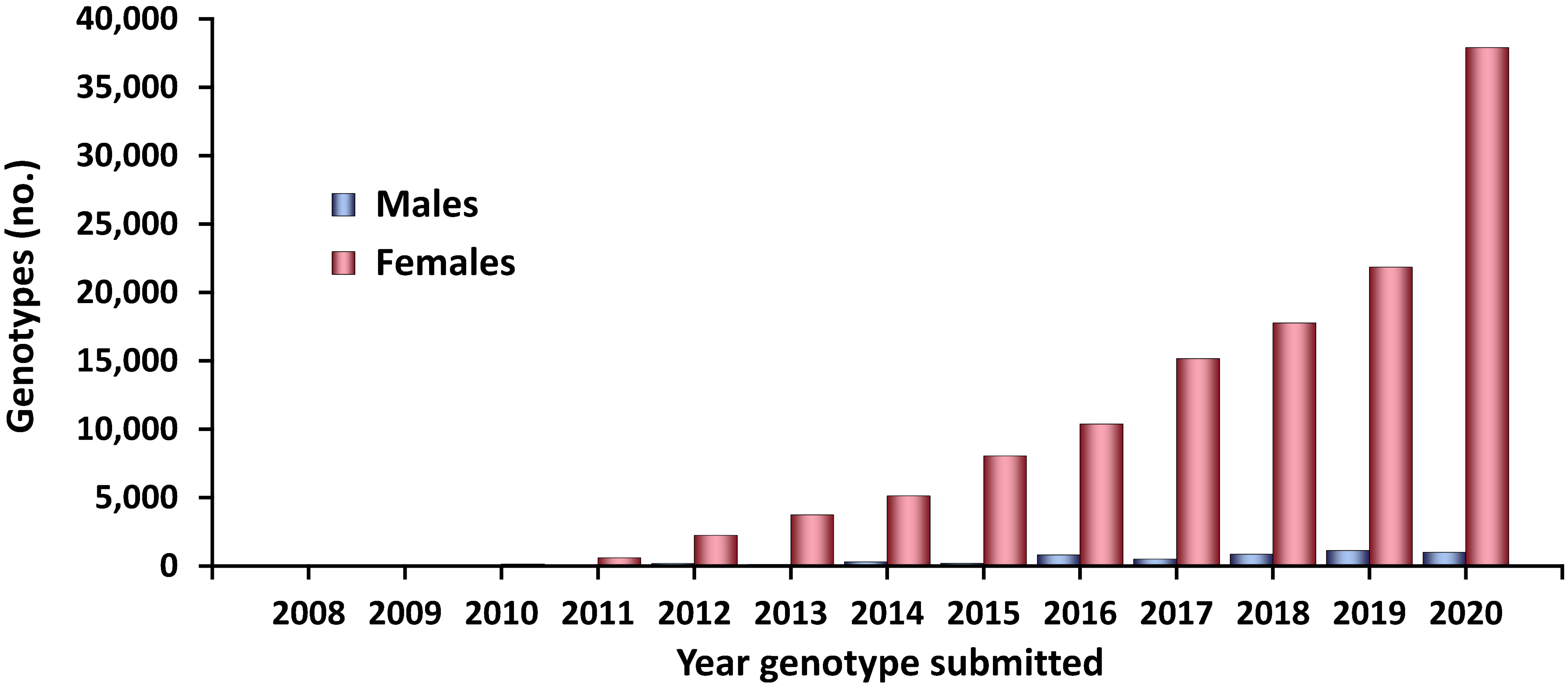
Imputation of crossbreds

- **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



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 ≥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

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Acknowledgments and disclaimers

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