

Crossbred Evaluations and More

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Background of Crossbred Evaluations

- **Over 34,000 animals excluded from genomic evaluation that were determined to be crossbreds based on breed SNPs**
- **Paul VanRaden proposed that crossbreds could be evaluated by combining individual-breed purebred SNP effects weighted by breed proportions**
- **Breed base representation (BBR) introduced in June 2016 to provide breed proportions**
- **In April 2018, calculations of genomic evaluations switched to an all-breed base to enable merging across breeds**

Challenges in Crossbred Evaluations

- **Imputation to calculate BBR for crossbreds must be done using an across-breed haplotype library, but BBR not yet available to determine if animal is a crossbred**
- **Type traits evaluations not comparable across breeds; therefore, cannot be blended**
- **Health and calving traits not available for all breeds**
- **A breed base for expressing resulting evaluations must be selected**
- **Some animals now being evaluated as purebreds included in crossbred evaluation, causing changes in their evaluations**

Proposal for Crossbred Evaluations

- **Animals with BBR of <94 (actually 93.5) receive genomic evaluation based on weighted average of SNP effects across breeds**
- **Evaluation expressed on base of breed of preferred ID if supported by BBR**
 - **For F1s in BBR range of 40 to 60%, breed base might not be breed of highest BBR**
 - **If no BBR above 40%, use breed of preferred ID if among the top 2**
 - **If XX (or XD), use breed of highest BBR**
 - **If BBR >60% for different breed, use BBR breed or report error**

Traits Included in Crossbred Evaluations

- **Type traits cannot be combined across breed because trait evaluations not comparable across breeds**
 - **Type evaluation from evaluation breed reported**
- **Health trait evaluations only available for Holsteins and, therefore, only for crossbreds with HO evaluation breed**
- **Calving trait evaluations only provided for Holsteins and Brown Swiss (calving ease for both, stillbirth only for Holsteins)**

Modification of Evaluation Breed

- **Format-1 record can change breed of preferred ID, which then causes evaluation breed to be updated**
- **No genomic evaluations for Milking Shorthorns, Montbéliardes, Linebacks, and Simmentals**
- **Wrong breed declared based on breed SNPs when different breed has <10% unlikely alleles and percentage of unlikely alleles lower than for evaluation breed**

BBR Calculation

- **BBR fundamental to evaluation of crossbreds, directly affects PTA**
- **Imputation required to calculate BBR**
- **Must decide which genotypes to impute using across-breed haplotype library**
- **Genotypes with >10% of unlikely breed SNP alleles to be imputed using across-breed haplotype library**
- **Weekly evaluations calculated using BBR from same run**

Grandsire Validation

- **If parent not genotyped or not confirmed, grandsire checked**
- **Grandsire declared unlikely if animal and grandsire have more opposite homozygotes than threshold (declines as possible comparisons increase)**
- **Possible grandsires suggested if low conflict percentage and birth date reasonable (94%)**
- **Animals with unlikely grandsires excluded from evaluation (4%)**

MGS Changes

- **If sire confirmed and MGS unlikely or unknown, haplotype method used**
- **As part of weekly evaluation, possible MGS discovered by matching with maternal haplotypes**
- **If discovered MGS matches pedigree MGS, unlikely MGS indicator removed**
- **Parentage verification records generated as part of weekly**

Ancestor Discovery

- **Based on haplotypes, MGS discovered with 95% certainty and MGGS with >90% certainty**
 - **Both at least as accurate as average reported pedigree**
- **Discovered MGS added to no-pedigree dams and provided to DRPC and others**
- **When dam unknown, constructed dam ID allows use of discovered MGS (over 200,000 for Holstein)**
- **Procedure developed to detect actual dam based on herd code and calving date**
- **Constructed IDs could enable use of discovered MGGS (~200,000 for Holstein)**

New SNP List

- **Plan to increase number of SNPs used in genomic evaluations to around 77,000**
- **New bovine assembly used to determine SNP sequence on chromosomes**
- **SNPs selected to**
 - **Minimize gaps**
 - **Eliminate one of a pair of consecutive SNPs with high correlation**
 - **Have high impact on one trait or more**
- **More and better SNPs expected to increase evaluation accuracy by 3 percentage points**

Chip Validation

- **Determine if new SNP included; if so, get location and probe**
- **Check that ICAR parentage and X/Y SNPs included**
- **Check each SNP for call rate and parent-progeny consistency**
 - **If not Illumina, check if any SNPs have A/B calls reversed**
- **Possibly revise SNP list if some SNPs not reliable**



Thank You!