

# GENOMIC EVALUATIONS INCLUDING CROSSBRED ANIMALS

Latest update: August 2020

## 0. REVISIONS

---

**December 2019:** The policy for F1 animals was simplified to allow animals to maintain the breed of evaluation when the breed in the animal ID has a BBR of at least 40%.

**August 2020:** Animals with an existing official (monthly) BBR that enter the evaluations as purebred will need to receive an updated BBR<85 to be considered crossbreds. This was introduced to avoid 4 Ayrshire cases that kept switching from pure to crossbred.

## 1. POLICY STATEMENT

---

The Council on Dairy Cattle Breeding (CDCB) calculates genomic predictions on over forty different traits separately for five different dairy breeds: Ayrshire, Brown Swiss, Guernsey, Holstein and Jersey. Genomic predictions for animals that have ancestors of more than one of these five breeds are calculated as a blended average of the respective single-breed marker effects, weighted by the estimated portion of the animal's DNA that came from each of the five breeds.

## 2. DEFINITIONS

---

**Breed Base Representation (BBR)**: Estimates of the percentage of DNA contributed to the animal by each of 5 evaluated breeds: Holstein, Jersey, Brown Swiss, Ayrshire, and Guernsey. These 5 proportions sum to 100 (with a minimum of 0 and a maximum of 100). Animals with BBR values of 94 to 99% are considered to have DNA from a single breed and therefore BBR is set to 100%.

**PTA reference population (PTA-RP)**: indicates the group of animals with genotype and phenotypes (e.g. traditional evaluations) used as **reference population** to estimate the SNP effects used to calculate genomic PTA (i.e.). Currently, there are 5 PTA-RP, one per each "genomic breed": HO (Holstein), JE (Jersey), BS (Brown Swiss), AY (Ayrshire), GU (Guernsey).

**Single breed group (SINGLE-group)**: Genotypes processed in these groups receive genomic evaluations based on estimates of SNP effects from a single breed. There are currently 5 different SINGLE-groups, one per each PTA-RP

**Multi breed group (MULTI-group):** *Genotypes processed in this directory receive a genomic evaluation based on a weighted average of the single breed SNP effects.*

### 3. OBTAINING GENOMIC EVALUATIONS INCLUDING CROSSBRED ANIMALS

---

#### 3.1. Processing of genotyped animals for weekly evaluations

- Animals with usable genotypes<sup>1</sup> and a valid fee code assigned<sup>2</sup> have an approximate SNP-based breed representation<sup>3</sup> method applied to verify the declared breed of the animal. If the approximate SNP-based breed method agrees with the declared breed, the animal is temporarily included in the single-breed group for the subsequent calculations. Alternatively, if the method reveals an excessive number of unlikely alleles, the animal is included in a multi-breed group for the subsequent calculations.
- Genomic imputation and breed weights calculations are performed separately for each of the SINGLE-groups and the MULTI-group. Animals with BBR < 90% in the SINGLE-group become part of the MULTI-group, and vice-versa.
- Similarly, animals in the MULTI-group are expressed on the breed base of the declared breed of the animal ID (if supported by the BBR value).
- If the SNP-based breed representation method indicates that the animal's most probable breed is not the declared breed, the animal will not receive a genomic evaluation until the breed is corrected.
- F1 generation animals will be allowed to maintain the breed of evaluation the same of the breed of the ID if their BBR is higher than 40%. In that case, an F1 animal with HO ID, will maintain the HO breed of evaluation if its HO BBR is higher than 40%. For XX and XD animals, the breed with the highest BBR will be used. This rule applies to monthly evaluation results as well.

#### 3.2. Processing of genotyped animals for monthly evaluations

- Breed weights obtained during weekly evaluations (instead of approximate SNP-based breed representation) are used to sort animals into SINGLE- and MULTI-groups. Similarly to the weekly procedure, animals with BBR < 90% are placed in the MULTI-group, whereas animals with BBR ≥ 90% are placed in the appropriate SINGLE-group (based on breed of evaluation).
- Genomic imputation and BBR calculation are performed separately on each of the 5 SINGLE-groups and on the MULTI-group. See 4 for further details.
- For each of the 5 SINGLE-groups, animals with a phenotypic-based evaluation and a BBR ≥ 94% for that breed are included in the PTA-RP. Animals with BBR above 90% receive an evaluation based on 100% BBR.
- No animal in the MULTI-breed group contributes to the PTA-RP. These animals receive an evaluation based on a weighted average of the SINGLE-breed groups SNP solutions

---

<sup>1</sup> [https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Usability\\_Codes](https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Usability_Codes)

<sup>2</sup> [https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Genomic\\_fee\\_codes](https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Genomic_fee_codes)

<sup>3</sup> The approximate method uses specific SNPs that have one allele with high frequency in one breed and low frequency in the others (named "breed SNPs"). Since not all SNP chips contain all breed SNPs, the determination is based on a percentage of the breed SNP available that have the unlikely allele for the declared breed of the animal.

(weighted by BBR), as described in 3.3

### 3.3. Publication of evaluations including crossbred evaluations

- Direct Genomic Values are obtained using:
  - Single-breed SNP solutions for all animals with  $BBR \geq 90\%$ .
  - Multi-breed SNP solutions (weighted average of the single-breed SNP solutions based on BBR) for all animals with  $BBR < 90\%$ , with a few exceptions:
    - *Type traits*: type evaluations are not comparable across breeds; therefore, type evaluations are provided using 100% of SNP solutions of the breed of evaluation.
    - *Calving traits*: currently available only for Holstein and Brown Swiss. Animals of those two breeds have a DGV calculated based on 100% BBR on the breed of evaluation.
    - *Health traits*: currently available for Holstein only. Only animals with Holstein as breed of evaluation receive a DGV based on 100% BBR on that breed of evaluation.
- No changes are envisaged to the way genomic PTAs are obtained, which is a combination of DGV and traditional evaluations<sup>4</sup>. The only difference is that animals in the multi-breed group for which phenotypic records are available receive a larger weight on their traditional evaluation, due to the fact that their phenotypes do not participate in the SNP effect calculation.
- Animals in both SINGLE- and MULTI-groups are published in their respective breed of evaluation file, since they all share the same breed base.
- CDCB labels single-breed based evaluations as “S” and multi-breed blended evaluations as “M” in the CSV genomic files only (formats 38 and 105 remain unchanged).

## 4. UPDATED BBR CALCULATION

---

- BBR values have been distributed only once for each animal, with the exception of updates for re-genotyped animals at a higher density. The reason for the re-calculation is that, since less imputation is involved, BBR is expected to be a more accurate estimate. A full review of the BBR methodology revealed that the following circumstances typically have a significant effect on BBR estimation accuracy:
  - Animal is genotyped at higher density
  - Animal changes ancestry (sire/dam)
  - A close relative (sire/dam) of the animal is genotyped
  - Animal genotype is reassigned

Furthermore, a breed mean correction to the results of the “raw” BBR calculations, put in place to reduce BBR “noise” values (statistical artifact of the BBR model yielding low percentages of other breeds that are not actually part of the animal genetic makeup), is now discontinued. Further investigation showed that weekly breed means are not as reliable to reduce the statistical noise as originally expected, especially for colored breeds.

---

<sup>4</sup> VanRaden, P. M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* 91:4414–4423

- Beginning in April 2019, CDCB publishes updated BBR. Updated BBR are obtained from the uncorrected BBR by setting to 0 any breed proportion  $\leq 2\%$  (considered statistical noise). The remaining percentages are proportionally rescaled. For example, an animal with a BBR:

80% Holstein, 16% Jersey, 2% Brown Swiss, 2% Ayrshire, 0% Guernsey

receives the following updated BBR:

83% Holstein, 17% Jersey, 0% Brown Swiss, 0% Ayrshire, 0% Guernsey

- In April 2019, CDCB calculates updated BBR values for all animals, based on the April 2019 purebred reference group and the 80k SNP set introduced in December 2018.
- BBR evaluations are distributed on a monthly basis (instead of weekly) in a separate file. This allows for corrections performed by genomic nominators between the weekly and the monthly releases to be reflected in the official BBR values.
- Animals receive their first official BBR when they receive their first month evaluation. Animals receive a re-calculated BBR if any of the breed percentages differs from its previous value by more than 4 percentage points, which is twice the standard error of the estimation (typically, such variation is due to the aforementioned circumstances).
- Animals with an existing official BBR entering a monthly evaluation as purebred will be considered crossbreds if they receive an updated BBR  $\leq 85$ .