# Genomic validation software: USA results

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## Abstract

The European Union requires a validation of genomic estimated breeding values (**GEBV**) for quality assurance to market the semen of young bulls. Countries such as the United States of America (**USA**) routinely validate GEBV internally. For practical reasons, there is interest in using standardized methods. The Interbull GEBV Test is conducted with the GEBVtest software and is an alternative to the conventional EBV validation including genomic information. New features recently added to GEBVtest software were a provision to allow countries with small populations a fairer opportunity to pass the test especially for more complex and less heritable traits. A GEBV validation was performed using the newest version of GEBVtest software with different features applied to USA dairy cattle populations. Five breeds and seven traits were tested: milk yield (**MIL**), fat yield (**FAT**), protein yield (**PRO**), somatic cell score (**SCS**), longevity (**DLO**) and calving interval (**INT**) were tested in all five breeds: Holstein (**HOL**), Jersey (**JER**), Brown Swiss (**BSW**), Ayrshire (**RDC**) and Guernsey (**GUE**), whereas direct mastitis (**MAS**) was tested for HOL. Genomic predictions, i.e., GEBV, from August 2022 were used as the full data set whereas GEBV from August 2018 were used as the reduced data set. Results varied due to population size, trait complexity, data ingestion and model differences. The HOL passed the test for all traits, except MAS due to large amounts of new data added and a model change between 2018 and 2022. The validation process for JER behaved as expected for more heritable traits (MIL, FAT, PRO and SCS), but performed poorly for more complex traits (DLO and INT). The analyses were more complicated and resulted in failures for breeds with smaller populations: BSW, RDC and GUE. The failures can be attributed to the complexity of traits, a small number of candidate bulls, and strict parameters within the GEBVtest software. Additionally, for these smaller population breeds and some traits, the parent average presented higher accuracies than GEBV. In summary, USA breeds with larger populations and traits with high heritability resulted in more stable results, whereas USA breeds with smaller populations and more complex traits are hard to validate with tests often failing. The use of TMACE-based genomic evaluations should be used when large data or model changes occur in target traits. Models that include extra regressions could also help to test for other biases and improve accuracies in small populations and/or for complex traits.

**Key words:** accuracy, bias, bull semen market, candidate bulls, deregressed breeding values

## Introduction

The GEBV Test (Interbull Centre, 2021a) is a valuable tool used to validate genomic breeding values (**GEBV**), comparable to trend validation tests when validating traditional estimated breeding values (**EBV**). Validating EBV and GEBV are prerequisite established by Interbull Centre (Uppsala, Sweden) for countries to participate in Multiple Across Country Evaluation (**MACE**) and Genomic Multiple Across Country Evaluation (**GMACE**), respectively.

The GEBV Test, based on methodology by Mäntysaari et al. (2011), performs quality assurance by reviewing the bias of the genomic evaluations and change in accuracy when using GEBV versus EBV. The bias is evaluated as the

stability of the genetic trend with GEBV and the stability of variation in GEBV and EBV.

Although the United States of America (**USA**) is not an active participant of GMACE, the Council on Dairy Cattle Breeding (**CDCB**) routinely validates USA GEBV to monitor the improvement over time that is due to the inclusion of genomics. The European Union regulation 2016/1012 states that GEBV validation for young bulls is required for their semen to be marketed in Europe (Regulation (EU) 2016/1012 of the European Parliament and of the Council, 2016). The USA has been validating GEBV independently for many years. However, as the largest semen exporter to Europe, the USA has interest in the validation process offered by Interbull. The GEBV Test, which uses GEBVtest software (Interbull Centre, 2021b), may be an easier and more practical way to validate GEBV. The Interbull GEBVtest software was first written in 2011 and now consists of a Python program gebvtest.py, and module ibutils.py. The software performs the GEBV validation tests for all currently evaluated Interbull traits, one breed and population at a time. Then, it creates a zip file with input and output files formatted to be sent to Interbull Centre for those who participate in GMACE.

In 2022, the GEBVtest software was modified for research and development purposes as proposed by a dedicated Interbull working group. New features include the flexibility to use different deregressed breeding values as validation target and other options such as performing GEBV base adjustments and modifying the initial birth year of bulls.

The new features were primarily implemented to use GEBV that account for selection as the dependent variable instead of daughter trait deviations or deregressed EBV and to assist all countries with validating their populations using the GEBV Test for a wide variety of traits. Therefore, the objective of this study was to perform a GEBV validation by using the new version of GEBVtest software with different features in USA dairy cattle populations.

## Materials and Methods

To conduct the GEBV Test, a full dataset and a reduced dataset consisting of 4 years prior are required. The genomic prediction datasets in USA dairy cattle populations were GEBV extracted from the August 2022 genomic evaluation (full) which included MACE input and from the August 2018 (reduced) genomic evaluation.

In this study, five breeds were evaluated: Holstein (**HOL**), Jersey (**JER**), Brown Swiss (**BSW**), Ayrshire (**RDC**) and Guernsey (**GUE**). Seven traits were tested: milk yield (**MIL**), fat yield (**FAT**), protein yield (**PRO**), somatic cell score (**SCS**), longevity (**DLO**), calving interval (**INT**), and direct mastitis (**MAS**). All breeds were evaluated for all traits with one exception: MAS was only tested in HOL. Although CDCB currently conducts a MAS evaluation for JER and BSW, these evaluations were not included in this study due to very recent data. MAS evaluations for JER and BSW were implemented after 2018 (CDCB Connection, 2022; CDCB Connection, 2023; Mota, et al., 2021).

As established by Interbull (2021a), the candidate bulls are males with an effective daughter contribution (**EDC**) > 20 in the full traditional data, EDC = 0 in the reduced traditional data and a reduced GEBV with reliability (**REL**) higher than zero. Thus, as can be seen in Table 1, the number of candidates bulls ranged from 7 to 3,562 depending upon the trait and breed.

In this study, several features from GEBVtest software were tested. The following parameters were applied: (1) predicted deregressed GEBV were used instead of the conventional deregressed EBV. This was done by using the option - - *target DGEBV*, derived by the software by using the method of VanRaden (2021); (2) GEBV were adjusted for a base equation by using the option - - baseadj. This option is useful to compare test results based on different options, especially for complex traits. The minimum birth year used

was 2014, which is the current year, 2022, minus 8, as recommended by Interbull.

## Results & Discussion

The GEBV validation results are presented in Table 1 for all breeds and traits tested.

**Table 1.** GEBV validation results for the five breeds evaluated in this study: Holstein, Jersey, Brown Swiss, Ayrshire and Guernsey

### Holstein

| Trait | Bulls | $B_1$ (±S.E.) | $R^2$ GEBV | $R^2$ EBV | Pass |
|-------|-------|---------------|------------|-----------|------|
| MIL | 3,562 | 1.10 (±0.01) | 0.74 | 0.35 | Yes |
| FAT | 3,562 | 1.08 (±0.01) | 0.77 | 0.41 | Yes |
| PRO | 3,562 | 1.04 (±0.01) | 0.74 | 0.43 | Yes |
| SCS | 3,502 | 1.12 (±0.01) | 0.69 | 0.27 | Yes |
| DLO | 3,330 | 1.01 (±0.01) | 0.61 | 0.30 | Yes |
| INT | 3,425 | 0.93 (±0.01) | 0.54 | 0.21 | Yes |
| MAS | 2,379 | 1.30 (±0.03) | 0.40 | 0.17 | No |

### Jersey

| Trait | Bulls | $B_1$ (±S.E.) | $R^2$ GEBV | $R^2$ EBV | Pass |
|-------|-------|---------------|------------|-----------|------|
| MIL | 648 | 1.06 (±0.03) | 0.73 | 0.49 | Yes |
| FAT | 648 | 1.05 (±0.03) | 0.63 | 0.33 | Yes |
| PRO | 648 | 1.05 (±0.03) | 0.69 | 0.45 | Yes |
| SCS | 604 | 1.01 (±0.05) | 0.45 | 0.21 | Yes |
| DLO | 571 | 0.88 (±0.05) | 0.36 | 0.27 | No |
| INT | 588 | 0.79 (±0.03) | 0.47 | 0.31 | No |

### Brown Swiss

| Trait | Bulls | $B_1$ (±S.E.) | $R^2$ GEBV | $R^2$ EBV | Pass |
|-------|-------|---------------|------------|-----------|------|
| MIL | 94 | 1.29 (±0.11) | 0.59 | 0.20 | No |
| FAT | 94 | 0.89 (±0.11) | 0.41 | 0.18 | Yes |
| PRO | 94 | 1.03 (±0.11) | 0.47 | 0.16 | Yes |
| SCS | 93 | 0.60 (±0.09) | 0.31 | 0.09 | No |
| DLO | 65 | 0.53 (±0.12) | 0.24 | 0.12 | No |
| INT | 88 | 0.64 (±0.16) | 0.16 | 0.27 | No |

### Ayrshire

| Trait | Bulls | $B_1$ (±S.E.) | $R^2$ GEBV | $R^2$ EBV | Pass |
|-------|-------|---------------|------------|-----------|------|
| MIL | 22 | 0.61 (±0.21) | 0.35 | 0.17 | No |
| FAT | 22 | 0.91 (±0.20) | 0.54 | 0.33 | Yes |
| PRO | 22 | 0.85 (±0.21) | 0.50 | 0.29 | Yes |
| SCS | 21 | 0.79 (±0.30) | 0.21 | 0.26 | No |
| DLO | 7 | 1.36 (±1.26) | 0.01 | 0.38 | No |
| INT | 22 | 0.60 (±0.52) | 0.03 | 0.01 | No |

### Guernsey

| Trait | Bulls | $B_1$ (±S.E.) | $R^2$ GEBV | $R^2$ EBV | Pass |
|-------|-------|---------------|------------|-----------|------|
| MIL | 19 | 0.92 (±0.22) | 0.51 | 0.36 | Yes |
| FAT | 19 | 0.51 (±0.18) | 0.32 | 0.34 | No |
| PRO | 19 | 0.77 (±0.25) | 0.36 | 0.26 | Yes |
| SCS | 18 | 1.48 (±0.43) | 0.42 | 0.19 | No |
| DLO | 7 | 0.52 (±0.52) | 0.37 | 0.05 | Yes |
| INT | 19 | 0.62 (±0.62) | 0.18 | 0.30 | No |

MIL: milk yield; FAT: fat yield; PRO: protein yield; SCS: somatic cell score; DLO: longevity; INT: calving interval; MAS: direct mastitis; $B_1$: regression coefficient; S.E.: standard error; $R^2$: accuracy; GEBV: genomic estimated breeding value; EBV: (traditional) estimated breeding value; Pass: indication of passing (Yes) or failing (No) status of GEBV Test

Holstein, the breed with the largest population size in the USA, passed the test for all traits except direct mastitis. The failing status for mastitis can be attributed to the recent implementation of official health evaluations plus data and model changes. HOL health evaluations were first published in 2018. In 2019 and 2020, many more herds began sending health records to the CDCB which resulted in a large amount of new records from the entire country entering the evaluation. Furthermore, the models developed for health traits were upgraded in the official April 2020 evaluation (Gaddis et al., 2020). CDCB introduced the sire-by-herd effect which

addressed the overestimation of values for high-profile animals.

The validation for GEBV of Jersey, the breed with the second largest population size in the USA, performed as expected for more heritable traits (MIL, FAT, PRO and SCS) but performed below expectations for more complex traits (DLO and INT). The higher variation of the regression compared to the HOL breed may play a crucial role and explain how less heritable traits have greater difficulty passing the validation tests. It is important to note that the definition of DLO used for this study differs from the DLO trait Interbull receives from USA. The USA sends a DLO EBV obtained from a single-trait evaluation to Interbull. Alternatively, official evaluations published in the USA release DLO in an index as a multi-trait evaluation which uses correlations from all other traits published. Thus, comparison and validation for this trait might be more complex than others. The INT model also underwent fundamental changes in April 2019 (Dairy Producer, 2019). The INT GEBV compared in this study were *official* values obtained from the 2018 and 2022 evaluations.

The scenario was even more complicated for breeds with smaller population sizes in the USA such as BSW, RDC and GUE. These breeds failed the GEBV Test more often than they passed for specific traits (Table 1). The reoccurring failures seem mostly linked to the very small number of candidate bulls. As a result, the regression coefficients ($B_1$) variation was very pronounced (often much higher than the biological limit of 1.20 implemented by Interbull or unrealistically lower than 1). The standard errors (**S.E.**) of $B_1$ were much larger than those observed in HOL and JER, and in some cases, parent average (**PA**) presented higher accuracies ($R^2$) than GEBV.

Although the objective of this study was to perform a GEBV validation with a base adjustment, a control scenario was conducted without the base adjustment option (results not shown). The control scenario was evaluated for each trait and breed combination. Results were stable regardless of the base adjustment. The $R^2$ varied by a maximum of 2% between base adjustment and control scenarios. This was expected as the $R^2$ of GEBV and PA changed in the same direction. The S.E. of $B_1$ were stable except for the less heritable traits of the breeds with a small population size (Table 2). However, the changes for $B_1$ values were larger prior to the adjustment (Table 2) versus after the base adjustments (Table 1) especially for the breeds with smaller population sizes.

The use of base adjustments improved the

**Table 2.** Regression coefficients (**B₁**) and standard errors (**S.E.**) from the GEBV Test performed prior to base adjustments for the five breeds evaluated in this study: Holstein, Jersey, Brown Swiss, Ayrshire and Guernsey

| Breed | Holstein | Jersey | Brown Swiss | Ayrshire | Guernsey |
|---|---|---|---|---|---|
| *Trait* | | | $B_1$ (±S.E.) | | |
| MIL | 1.13 (±0.01) | 1.19 (±0.03) | 1.22 (±0.11) | 0.71 (±0.21) | 1.05 (±0.24) |
| FAT | 1.11 (±0.01) | 1.09 (±0.03) | 0.87 (±0.11) | 0.98 (±0.20) | 0.58 (±0.19) |
| PRO | 1.06 (±0.01) | 1.12 (±0.03) | 1.01 (±0.11) | 0.95 (±0.21) | 0.84 (±0.26) |
| SCS | 1.04 (±0.01) | 0.90 (±0.04) | 0.59 (±0.09) | 0.66 (±0.30) | 1.41 (±0.42) |
| DLO | 0.94 (±0.01) | 0.83 (±0.05) | 0.53 (±0.12) | 0.22 (±1.26) | 0.78 (±0.56) |
| INT | 0.95 (±0.01) | 0.88 (±0.04) | 0.94 (±0.14) | -0.51 (±0.64) | 1.42 (±0.58) |
| MAS | 1.25 (±0.03) | NA | NA | NA | NA |

MIL: milk yield; FAT: fat yield; PRO: protein yield; SCS: somatic cell score; DLO: longevity; INT: calving interval; MAS: direct mastitis; NA: not applicable for this study

validation results for the complex trait, DLO, but only for the breeds with large populations, HOL and JER. It is evident that base adjustments do not resolve all limitations of these methods in breeds with small population sizes. In fact, in this study, the inclusion of a base adjustment had no effect in BSW, RDC and GUE. It is important to note that GUE only had seven validation bulls available which resulted in the least informative estimates. The GEBV Test requires the $R^2$ for GEBV to be higher than for EBV so that breeders can justify the cost of genotyping. However, some individual traits have large $B_1$ S.E. when validating. For example, if the true $R^2$ is 10% better than PA but with a S.E. of 15%, some traits will have $R^2$ below PA. This could cause disappointment for those traits; however, we should not throw away the GEBV for those traits, because next time we validate those traits, some may pass and other traits will fail. USA breeds with large populations and small S.E. allow for the improvement and verification of models implemented. Often, these verified models need to be trusted regardless of the less than ideal results from breeds with small population sizes. In addition, averaging statistics across traits can be helpful.

## Conclusions

Breeds with larger populations and more heritable traits had more stable results. Breeds with smaller populations and more complex traits are more difficult to validate and showed unrealistically large variation. As a result, the breeds with smaller populations resulted in the GEBV Test failing often.

The use of Truncated MACE (**TMACE**) instead of 4-year-old official results is encouraged for GEBV validations, especially when substantial model or data changes occur in target traits (INT and MAS in our study). Methods with extra regressions could also help to test for other biases such as trend, parent average among others.

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