# GEBV Test for all Traits

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## Introduction

Interbull evaluations were started in 1995 with dairy production traits (milk, protein and fat), but since that have expanded into new trait groups: conformation (17 different traits), udder health (2), calving traits (3), female fertility (5), direct longevity (1), and workability traits (3). Currently international evaluations are provided for 6 different breeds from 30 countries, in a total of 79 populations. The natural goal is to extend the services into all the traits which member countries are considering in their selection.

During the last years, genomic evaluations (GEBV) have been introduced by many national evaluation centers for most of the traits evaluated by Interbull. The Interbull member countries have a desire to develop GEBVs for all the traits in their total merit indices. Genetic evaluation centers have published validation results for various traits with different genetic evaluation models and different levels of heritabilities. Consequently, the expectation is that Interbull would work towards implementing genomic MACE (GMACE), and not only for production traits, but perhaps for all the traits in the current MACE evaluations.

At first (2010) Interbull asked national evaluation centers to submit GEBVs from all the trait groups for running validation pilot studies. Based on the observed results, the Interbull Steering Committee decided to initially implement official validation of GEBVs only for protein yield, which was enough to conform to the European Commission decision 2006/427/EC that regulates minimum acceptance requirements for artificial insemination bulls within Europe. This was considered enough to get experiences on possible validation problems, and to start testing the GMACE alternatives. These first GEBV validation results opened discussion about acceptance regions of bias estimates and validation accuracies.

The objective of this discussion group was to give recommendations to Interbull about the policy for GEBV tests on different traits.

## Validation practice for all the traits

In June 2010 the Interbull Steering Committee made a decision that the first official validation for national GEBV are based on trait protein yield. Based on these GEBV validation results Interbull will maintain and publish a list of countries which have GEBV evaluation system tested and approved. The reason for concentrating only on protein was practical. Both the evaluation centers and the Interbull are still building up the systems for use of genomic evaluations, and moreover, the formats for data delivery or the definite requirements for the GEBV test were not yet final. The first validated protein GEBV has later been used to develop and test the GMACE methodology. Whenever the methodology is close to implementation, the GMACE model is to be implemented for all the traits that the countries can submit GEBV to international evaluations.

The discussion group did not see any reason why the validation policies for GEBV should be different than the validation policies for conventional EBV. Therefore the group suggests that the countries should submit GEBV for validation test for all the traits they consider to be included in GMACE. In the current code of practice the EBVs from the trait group conformation have been validated only for the traits stature and udder support. However, Interbull encourages the countries to

do validation test on all the traits, and that the same recommendation should be given to GEBV also.

For the first implementation of GMACE, the participating countries should submit evaluations validated by GEBV test. This is conformable with a practice that is applied currently to EBV validation. The suggestion by the discussion group is to apply the same requirements for revalidation of GEBVs as have been noted to be a good practice. With these requirements the countries should resubmit validation results every two years and every time when they make a major change in the genomic evaluation system or in the conventional evaluation. The increase in the size of reference population is not considered as a change in the evaluation system as long as change is due to new EBVs of own evaluation system. However, if the size change is because of a completely new source of information, such as merging reference populations of two countries, then the country should submit new validation data.

## Validation criteria for different traits

In the first completed GEBV validation tests the main emphasis was on the unbiasedness of the GEBVs. This was judged by testing whether estimated coefficient of regression ($b_1$) of young (test) sire de-regressed proofs (DRPs) on the GEBVs of the same bulls is one (see Interbull, 2010). However, it was recognized that for the countries that had not genotyped all the bulls in the birth years of the test candidates, the expected regression coefficient was not expected to be 1.0. For this reason the GEBV test included a rough estimation of selection differential for the trait in concern, and a derivation of expected regression coefficient $E[b_1]$ for the trait.

The discussion group noted that the $E[b_1]$ approximation is based only on the selection observed on the trait and by that means it tries to estimate the change in covariance between the DRP and the GEBV, and the reduction in variance in GEBV. The selection can be either direct or indirect due to undesired correlated responses. Moreover, the selection can be either negative or positive. In either case its' effect to regression is always downward. Therefore the $E[b_1] \leq 1.0$. In the group it was noted that this derivation might not always be clear. For example, the selection could be assortative. Then its' effect would not be visible because the mean of the EBVs of the test bulls would equal the mean of the corresponding year class. Also, if all the bulls in the age class have been genotyped, the approximated procedure assumes that $E[b_1] = 1.0$.

The other two GEBV test criteria were the test of equal mean of EBVs and GEBVs of test bulls, and the increase in accuracy due to use of genomic information. The first judgment is based on testing the intercept $b_0$ from the regression of test sire DRPs on their GEBVs. The latter is accessed by comparing the squared correlation ($R^2$) of DRP and GEBV of the test bulls to the $R^2$ between DRP and parent average EBV of the same bulls.

In the original GEBV test proposal, the judgment how large deviation $b_1$-$E[b_1]$ is acceptable was based on statistical inference through t-test. The first experiences have already shown that the t-test rejects the unbiasedness easier in a large population. When the standard error of $b_1$-estimate is very small biologically insignificant deviations from $E[b_1]$ are overemphasized. To avoid this the group suggested that the standard error of $b_1$ in the test should be at least 0.05, or larger if suggested by the regression model in the test. Thus, the acceptance region of the $b_1$ estimate would be at least ($E[b_1]$-0.1) to ($E[b_1]$+0.1), or larger.

In the original publication of GEBV test (Mäntysaari et al., 2010) it was stated that the $R^2$ between GEBV and DRP should be "notable higher" than $R^2$ between parent average EBV and DRP. Later on the "notable higher" has been replaced by "higher" (Interbull, 2010). It seems very difficult to set requirements how accurate the GEBV should be. One suggestion would be that the $R^2$ for GEBV should be always higher than 0.5, which has been used by EU to set a mark between pedigree index and progeny test. This limit could apply to production traits, but can be too high for many low heritable traits and might be difficult to reach by small

populations and minor breeds. Also, when the GEBV are to be used in GMACE, there does not need to be specific accuracy requirements as long as the country submits appropriate and correct genomic efficient daughter contributions (GEDC).

## Discussion and Recommendations

The main conclusion from the group was that the validation policy of GEBVs should be as similar with the current EBV validation as possible. It is likely that in the future the GEBVs have much larger importance than EBVs, and thus their reliability is important. For the both purposes of validation: for the GEBV evaluation system quality assurance and for the validation of the GMACE input, the unbiasedness and high reliability are required.

It was discussed if the test validation reliability, i.e. $R^2$ of GEBV validation regression equation (corrected with respect to accuracy of DRPs), should the same as the average of model reliabilities over all the bulls. The latter reliability is used to derive the bull GEDC for the GMACE weights. It will therefore control the influence of the population in the international evaluation and determine the standard deviations of GMACE proofs of the bulls. Because of selection the model based reliabilities for the parent average EBVs are notable higher than the $R^2$ from the validation regression model. The effect of selection might be different when the GEBVs are already derived from the selected genotypes of progeny tested bulls. Until the relationship with validation accuracy and model accuracy is clarified, it seems fair to only expect that the possible differences between published reliabilities, on average, should someway follow the differences in validation reliabilities.

There is no experience yet on the robustness and consistency of suggested GEBV validation test. Studies are needed to address the behavior of the test in different situations and different type of traits. Also new validation methods should be developed either to complement or replace the suggested test.

## References

Interbull, 2010. Interbull validation test for genomic evaluations – GEBV test. June 2010. http://www.interbull.org/images/stories/GEBV_validationtest_June2010.pdf. Accessed 10.5.2011.

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