

## Prediction of GEBV in Comparison with GMACE Value of Genotyped YYoung Foreign Bulls

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### Abstract

EBVs and GEBVs for milk yield of young genotyped Holstein bulls were predicted using a conventional Animal Model, RRBLUP, GBLUP, ssGBLUP and one-step blending procedures. For prediction, the nation-wide databases of domestic Czech production records from the first lactation combined with deregressed proofs from Interbull files through 2013, which had been transformed by MACE to domestic production conditions, and domestic test-day-records in the first three lactations were used. 2,627 genotyped bulls were used, from them 2,189 already proven in domestic condition. Analyses were run that used Interbull values only for these genotyped bulls, or used Interbull values for all available sires. Predictions were compared with GEBV of 96 young foreign bulls evaluated abroad and transformed by Interbull method GMACE 09/2013 into Czech scale. Correlation of predictions with GMACE value of foreign bulls ranged from 0.33 to 0.75. Combining domestic data with Interbull EBVs improved prediction of both EBV and GEBV. Prediction by Animal Model (traditional EBV) using only the domestic first lactation had correlation with GMACE value 0.33; whereas combining the nation-wide domestic database with all available deregressed proofs for genotyped and non-genotyped sires from Interbull resulted in of EBV correlation 0.60, compared to correlation 0.47 when using Interbull data only. Genomic enhanced breeding value has in all cases higher correlations than traditional EBV, the highest correlation were for predictions from the ssGBLUP procedure using combined data (0.75). ssGBLUP with domestic three lactations test-day-records has correlation with GMACE 0.69.

**Keywords:** genomic breeding value, single-step prediction, test-day-model, animal model

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Genomic enhanced breeding value (GEBV) is frequently predicted by multi-step procedure, using regression-based methodologies (Meuwissen *et al.*, 2001) and the GBLUP method using a genomic relationship (VanRaden, 2008). Input (pseudo-phenotype) data are daughter-yield-deviations (DYD) (Szyda *et al.*, 2011), or deregressed proofs (DRP) (Schaeffer, 1994). Genetic markers do not explain all genetic variability of traits (Liu *et al.*, 2011). Therefore direct genetic values (DGV) are combined with residual polygenic effect, or parent average (PA) to produce GEBV. Genotyped animals are usually strongly preselected, which influence

comparison with others animals (Patry *et al.*, 2013). GEBV of genotyped animals also influenced retroactively estimated breeding value (EBV) of un-genotyped animals (Christensen and Lund, 2010). Though test-day-model was developed for evaluation of milk production (Schaeffer *et al.*, 2000), genomic evaluation is according DYD/DRP, which are adequate to older lactation model.

Misztal *et al.* (2009), and Christensen and Lund (2010) developed a single-step procedure ssGBLUP, which overcomes several critical assumptions required by multi-step procedures, and allows common rank of all genotyped and

un-genotyped animals. Přebyl *et al.* (2012) used this methodology for the genetic evaluation of the Czech Holstein population. Gao *et al.* (2012) and Su *et al.* (2012) used in ssGBLUP as input data DRP of sires, instead of phenotypic production records, naming this approach one-step blending. Přebyl *et al.* (2013a, 2013b, 2014) combined in ssGBLUP nation-wide databases with all available Interbull DRPs.

Procedures are usually validated by comparing prediction of GEBV with results after progeny test and DYD according daughter yield are used as a response variable. Validated reliability is calculated (Su *et al.* 2012) which reflects correlation of prediction to DYD in domestic conditions, what is essential standpoint for selecting of animals.

Lot of bulls have progeny in several countries and therefore also several predictions of EBV. To convert EBV of foreign bulls the MACE method was developed (Schaeffer, 1994) and extended to GMACE for young genotyped bulls (Sullivan and Jakobsen, 2012). Into a country are imported foreign bulls frequently with abroad known EBV/GEBV. Additional domestic EBVs and GEBVs are calculated which reflect domestic production conditions.

The aim of this study was to compare genetic prediction of GEBV for young bulls using both domestic and global Interbull data into current year 2013. Predictions were compared with Interbull GEBV of young bulls, calculated according foreign data, transformed by GMACE (9/2013) into scale of Czech Republic.

## Material and Methods

### Files for predictions:

- I. First lactation milk yield of 1,257,462 Czech Holstein cows, calving years 1991-2013, with 2,314,856 animals in the pedigree file.
- II. Files for routine nation-wide evaluation of milk yield by MT-RRTDM for first three lactations. 19,435,367 Test-Day-Records of 1,086,267 Czech Holstein cows, calving years 1995-2013, with 2,142,354 animals in the pedigree file.

- III. Interbull 112,880 EBVs of Holstein bulls through year 2013, average reliability 0.72 (>0.28), converted by MACE on a national scale, with 291,977 animals in the pedigree file. Values were modified in order that variability of EBVs of domestic proven bulls and of Interbull EBVs were similar, deregressed (Schaeffer, 1994) and pseudo-data yield deviation (YD) and effective record contributions (ERC) were calculated, considering sire as animal with its own production:

$$ERC = ((1 - h^2) / h^2) * (rel / (1 - rel))$$

where rel = reliability of EBV.

- IV. Bulls were genotyped by Illumina BovineSNP50 BeadChip V2. To eliminate possible input errors data were edited for: MAF < 0.05, number of loci per bull < 90%, number of bulls per locus < 90%, substantial error of prediction of old proven bulls in the training set - absolute difference of input DRP with predicted DGV > 539 kg, large discrepancy of relationship  $A_{22} : G$  - absolute difference in relationship to others > 3 animals > 0.30, and proportion of Holstein genes < 85%. After editing, 40,409 loci for 2,627 bulls, from which 2,189 were already proven in 2013 in the Czech Republic (training set), were used.

### File for verification:

- V. GMACE GEBV of 96 foreign young bulls from preliminary Interbull run 09/2013, without records in files I, II and III.

### Methods of evaluation

Data were evaluated by weighted analysis using several statistical procedures. Because ERC was used as the weight for individual records, for all domestic production records ERC was set equal to 1 (Přebyl *et al.*, 2013a).

- a) BLUP - Animal Model
  - Prediction of EBV of young animals according pedigree value.
- b) RRBLUP
  - Prediction on the basis of regression coefficients of all SNP loci.

- c) GBLUP
  - Prediction on the basis of genomic relationship of young and referenced old proven genotyped bulls.
- d) ssGBLUP
  - Single-step prediction of GEPH on the basis of entire domestic population, together for genotyped and un-genotyped animals.
- e) Blending ssGBLUP
  - ssGBLUP, working with DRP of all bulls from Interbull.
- f) Combination d + e
  - Joint evaluation in one step the entire domestic population + entire file from Interbull. To avoid the double counting, Interbull values of bulls with daughters in domestic population were eliminated.

RRBLUP was performed according to the following model:

$$y_j = \mu + \sum \delta_i \cdot g_{ij} + e_j \quad ,$$

where

- $y_j$  = DRP of milk production (adequate to lactation yield) for genotyped bull  $j$  ;
- $\mu$  = common constant (contemporary group) as a fixed effect ;
- $\delta_i$  = regression coefficient for locus  $i$ , with addition of diagonal matrix of constant value to the system of equations reflecting ratio of variances for one locus  $m \cdot (1-h^2) / h^2$  ;
- $m$  = number of loci;
- $g_{ij}$  = genotype value of bull  $j$  in locus  $i$  <0, 1, 2>;
- $e_j$  = random error.

Estimated and predicted right-hand side terms without random error are used to predict DGV of young animals.

GBLUP was done by the model:

$$y_j = \mu + a_{nj} + e_j \quad ,$$

where

- $a_{nj}$  = DGV of animal  $j$ , random effect with genomic relationship matrix  $\mathbf{G}$  for all genotyped animals.

BLUP, and ssGBLUP for the first lactation yield according to the animal model:

$$y_{ij} = \text{HYS}_i + \beta_1 \cdot ca_j + \beta_2 \cdot ca_j^2 + \beta_3 \cdot do_j + \beta_4 \cdot do_j^2 + a_{nj} + e_{ij},$$

where

- $y_{ij}$  = first lactation milk yield of cow, or DRP of milk production for bull;
- $\text{HYS}_i$  = contemporary group  $i$  within a herd in a 3-mo calving period (fixed effect);
- $\beta_1, \beta_2, \beta_3,$  and  $\beta_4$  = regression coefficients;
- $ca_j$  and  $ca_j^2$  = parameters for curvilinear regressions on calving age (fixed effect);
- $do_j$  and  $do_j^2$  = parameters for curvilinear regressions on days open (fixed effect);
- $a_{nj}$  = EBV, or GEBV of animal  $j$ , random effect with pedigree additive relationship matrix  $\mathbf{A}$  in BLUP, or matrix  $\mathbf{H}$  in ssGBLUP.

$\mathbf{H}$  is the pedigree additive relationship matrix  $\mathbf{A}$  augmented by genomic relationship matrix  $\mathbf{G}$ . Weights of 80%  $\mathbf{G}$  and 20% additive pedigree relationship matrix only for genotyped animals  $\mathbf{A}_{22}$  were used for incorporation into  $\mathbf{H}$  (Christensen and Lund, 2010; Pribyl *et al.*, 2012).

Matrix  $\mathbf{G}$  was constructed according to deviations from the averages of observed allele frequencies in the analysed population and was standardized by division by the average value of the diagonal of  $\mathbf{G}$  (Forni *et al.*, 2011), then shifted, so that the elements of the  $\mathbf{A}_{22}$  and elements of  $\mathbf{G}$  would have the same average (Vitezica *et al.*, 2011).

DRPs processed from MACE values are free from influence of systematic environmental effects and all of them are on the same scale. For inclusion into BLUP calculations, DRPs are therefore located into additional class of HYS, and for independent variables (ca, do) are used average values from domestic population.

ssGBLUP for MT-RRTDM

Evaluation is according to the MT three-lactations test day animal model with 4-parameter Legendre Polynomials (LP):

$$y_{ijn} = \text{HTD}_{in} + \beta_1 \cdot ca_j + \beta_2 \cdot ca_j^2 + \beta_3 \cdot do_{jn} + \beta_4 \cdot do_{jn}^2 + \beta_5 \cdot ci_{jn} + \beta_6 \cdot ci_{jn}^2 + f_{fg,n} + f_{pe,n} + f_{an,n} + e_{ijn} ,$$

where

$y_{ijn}$  = test-day record of milk yield of cow in lactation  $n < 1,2,3 >$ ;

$\text{HTD}_{in}$  = herd-test-day contemporary group  $i$  within a herd in lactation  $n$  (fixed effect);

$\beta_1, \beta_2, \beta_3, \beta_4, \beta_5$  and  $\beta_6$  = fixed regression coefficients;

$ca_j$  and  $ci_{jn}^2$  = parameters for curvilinear regressions on calving interval for second and third lactations (fixed effect);

$f_{fg,n}$  = average LP of lactation curve according to groups of cows within management classes of systematic environment (Zavadilová *et al.*, 2005b) (fixed effect);

$f_{pe,n}$  = permanent environmental within lactation LP of lactation curve of cows, random effect with covariance matrix (Zavadilová *et al.*, 2005a);

$f_{an,n}$  = genetic within lactation LP of lactation curve of animal, random effect with covariance matrix;

$e_{ijn}$  = random residual of test day records within lactation  $n$ , reflecting changes of variability along the course of lactation.

Procedures for the various models for genetic prediction are summarized in Table 1.

**Table 1.** Prediction procedures.

| Method of prediction | Predicted value | Sources of phenotype records        |                     |                       |                      |
|----------------------|-----------------|-------------------------------------|---------------------|-----------------------|----------------------|
|                      |                 | Domestic 1 <sup>st</sup> lactations | Domestic TD records | Interbull DRP         | D + I                |
| BLUP                 | EBV             | D-EBV                               |                     | I-EBV                 | DI-EBV               |
| PA <sup>1</sup>      | EBV             |                                     |                     | I-PA                  |                      |
| RRBLUP               | DGV             |                                     |                     | rI-DGV                |                      |
|                      | GEBV            |                                     |                     | rPA-GEBV <sup>3</sup> | rI-GEBV <sup>2</sup> |
| GBLUP                | DGV             |                                     |                     | gI-DGV                |                      |
|                      | GEBV            |                                     |                     | gPA-GEBV <sup>3</sup> | gI-GEBV <sup>2</sup> |
| ssGBLUP <sup>4</sup> | GEBV            |                                     | TD-GEBV             | I-GEBV <sup>5</sup>   | DI-GEBV              |

1) Parent average from Interbull: PA = 0,5\*EBV sire + 0,25\*EBV maternal grandsire ;

2) GEBV = 0.8 DGV + 0.2 D-EBV ;

3) GEBV = 0.8 DGV + 0.2 I-PA ;

4) Genomic relationship **G** is weighted 80 % and pedigree relationship **A**<sub>22</sub> 20 % into **H**;

5) One-step blending approach.

Domestic production of 1<sup>st</sup> lactation records were used in BLUP (D-EBV procedure), and domestic nation-wide test-day-records of official national evaluation in ssGBLUP (TD-GEBV); whereas in RRBLUP and GBLUP analyses, Interbull DRPs from 2,189 referenced bulls were utilized (rI-DGV and gI-DGV). In these cases DGVs of young bulls were combined in an index with EBVs predictions according to pedigree information from the domestic Holstein population (rI-GEBV and gI-GEBV), or parent average from Interbull file (rPA-GEBV and gPA-GEBV). Of all DRPs available from Interbull, a total of 112,880 were used in BLUP and ssGBLUP procedures (I-EBV and I-GEBV). This method corresponds to “one-step blending approach”. The combination of both domestic and

Interbull databases were analyzed by BLUP and ssGBLUP procedures (DI-EBV and DI-GEBV). To avoid the double counting in these combined analyses, Interbull DRPs were used only, when sires did not have daughters in the domestic population.

Procedures were validated by calculating correlations among predictors of genetic merit for 96 young bulls with theirs foreign Interbull values transformed by GMACE into domestic scale of the Czech Republic.

Own made programmes for routine evaluation, G-matrix (Su and Madsen, 2011), and the DMU (Madsen and Jensen (2010) and BLUPF90 (Misztal *et al.*, 2002) packages were used.

## Results and Discussion

Results of prediction of merit of young genotyped bulls are summarised in Table 2.

### Prediction by EBV

Predictions by EBVs according the domestic 1<sup>st</sup> lactation milk yield only (procedure D-EBV), have correlation with MACE value according foreign data 0.33. This reflect, that foreign bulls have only weak connection to the domestic population. Prediction according parent average calculated from Interbull file

(procedure I-PA) has correlation with GMACE value 0.41, which reflect, that sires of the bulls are usually well proven and used internationally. Prediction by EBVs according the blending procedure (I-EBV), which takes into account the entire Interbull file (II), has correlation 0.47. Prediction by EBVs according combination of domestic 1<sup>st</sup> lactation with entire Interbull file (DI-EBV) has correlation 0.60. Increasing the quantity of phenotype information (I-EBV and DI-EBV) improves the prediction, which is in agreement with our previous studies.

**Table 2.** Correlation of prediction for 96 young genotyped bulls with GMACE value.

| Sources of phenotype                             | Methods of prediction | Predicted value | Procedure | Correlation |
|--|-----------------------|-----------------|-----------|-------------|
| Domestic 1st lact.                               | a BLUP                | EBV             | D-EBV     | <b>0,33</b> |
| Domestic Test-Day                                | d ssGBLUP             | GEBV            | TD-GEBV   | 0,69        |
| Interbull DRP, only genotyped animals + pedigree | PA                    | EBV             | I-PA      | 0,41        |
|  | b RRBLUP              | DGV             | rI-DGV    | 0,60        |
|  | b RRBLUP              | GEBV            | rI-GEBV   | 0,67        |
|  | b RRBLUP              | GEBV            | rPA-GEBV  | 0,62        |
|  | c GBLUP               | DGV             | gI-DGV    | 0,62        |
|  | c GBLUP               | GEBV            | gI-GEBV   | 0,68        |
|  | c GBLUP               | GEBV            | gPA-GEBV  | 0,63        |
| Interbull DRP, all                               | e Blending            | EBV             | I-EBV     | 0,47        |
|  | e Blending            | GEBV            | I-GEBV    | 0,69        |
| <b>D + I all</b>                                 | f Combination         | EBV             | DI-EBV    | 0,60        |
|  | f Combination         | GEBV            | DI-GEBV   | <b>0,75</b> |

### Prediction by multi-step procedures

When using the genomic information, the correlations are more balanced. Predictions by DGVs according regression coefficients (rI-DGV procedure) has correlation with GMACE value 0.60, and calculated according GBLUP method (gI-DGV) correlation 0.62 respectively. These values are calculated according reference population of 2,189 old proven genotyped bulls. Predictions by GEBV calculated according selection indexes combining DGV with pedigree value from domestic population (rI-GEBV, gI-GEBV) have correlations 0.67 and 0.68 and correlations 0.62 and 0.63 in indexes combining DGV with parent average from Interbull (rPA-GEBV, gPA-GEBV). Higher correlation of combined value is in agreement with Liu *et al.* (2011). In indexes we used for all animals the overall weight 80% for DGV and 20% for pedigree value, which corresponds with combining the pedigree and

genomic relationship matrices into **H** in single-step procedures. Procedures rI-GEBV and gI-GEBV exploit both reflection of pedigree of foreign bulls in phenotypes of domestic population and sample of DRPs of reference bulls from Interbull file.

### Prediction by single-step procedures

Prediction by GEBV with ssGBLUP method from domestic test-day records using RRTDM (procedure TD-GEBV) has correlation 0.69 which is little better than selection indexes of GEBV in multi-step procedures. Prediction by GEBV according blending procedure, using all available Interbull DRP (I-GEBV) reached correlation also 0.69. It reflects large information power of file of internationally proven both genotyped and un-genotyped bulls. ssGBLUP on combined data (DI-GEBV) reached the highest correlation 0.75. Both single-step procedures with Interbull used

larger volume of input phenotype data, which are above all for sires considerably reliable.

All mentioned correlations are according pedigree values, which are in different procedures only differently intermediated in predictions. These are preliminary results. GMACE values, used here for comparing with predictions are of foreign bulls, without closer connection with domestic population. Changes of prediction for rank of animals are therefore expected after calving of daughters, because genetic correlations between countries are not unity. Nevertheless the rank of suitability of methods keeps the same like in previous studies (Příbyl *et al.*, 2013a, 2014), where methods were verified according progeny results. Volume of information is fluently growing therefore higher accuracy of prediction is expected in the future.

## Conclusion

Presented results, and results from previous studies agree and yield to the conjunct conclusions.

- A) All genomic predictions have higher accuracy than pedigree based breeding value.
- B) Addition of pedigree EBV to the DGV in Multi-step procedures increases accuracy.
- C) Single-step procedures have higher accuracy than Multi-step procedures.
- D) Inclusion of Interbull data into the domestic file of records increases accuracy of prediction both EBV and GEBV.
- E) Genetic Interbull correlation of foreign countries to the Czech Republic is about 0,85. It means, that merit of foreign bulls decreased after import to the approximately 72% of reliability in the country of origin. Breeding value is the regressed value, therefore effect of foreign bulls in importing country is reduced. The priority has therefore genetic evaluation according domestic production files.
- F) Our selection is the ssGBLUP method for Test-Day-Model, which reflect optimally domestic production conditions.

- G) For genotyped animals, which have not sufficient connection to the domestic population, the ssGBLUP, combining of domestic production with Interbull file of DRPs is optimal.

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