

Comparison of genomic breeding values of Holstein in the Czech Republic

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Genomic evaluation by single-step procedure allows efficient implanting of genetic SNP markers into complicated procedure of random regression test-day-model of milk traits. Test-day records and pedigree files on nation-wide scale are combined with genomic relationship into common evaluation of both genotyped and ungenotyped animals. Due to strong import of foreign sperm into small national populations is the reliability of evaluation of young animals low. This is particularly seen in evaluation of young bulls, which frequently have both parents foreign. Genomic evaluation helps and notably improves reliability of evaluation. ssGBLUP procedure is advantageous especially for small populations. Domestic genomic evaluation of young animals has medium to high correlation with foreign Interbull values. Interbull conversion of values of bulls according MACE, which works with progeny tested bulls, is more reliable than conversion according GMACE procedure, which works with genomic evaluation of young animals.

Keywords: genomic breeding value, ssGBLUP, test day model, MACE, GMACE

1 Introduction

Small populations of dairy cattle are strongly influenced by import of foreign sperm and bulls. Import is frequently connected with some time delay, when already some evaluations about foreign animals are known. Therefore there is possibility to compare domestic evaluation with foreign values.

In a present period are globally introduced genomic evaluations using huge number of genetic SNP markers from genetic chips and genomic enhanced breeding values (GEBV) are calculated. Goal of genomic evaluation is higher reliability of evaluation for young animals without own phenotype and using them more early in breeding. Majority of countries are now using for GEBV calculation by multi-step procedures (Meuwissen et al., 2001), which works with preselected group of genotyped animals. Linear models according BLUP and Bayesian methodology are used. Input data in evaluation are "pseudo-phenotype data" daughter yield deviations (DYD) or deregressed proofs (DRP). More advanced is the single-step procedure (ssGBLUP) (Misztal et al., 2009; Christensen and Lund, 2010) which overcomes some disadvantages of previous methods. Namely works directly with recorded phenotypes of entire nation-wide population and directly compared

genotyped and ungenotyped animals, eliminates bias from preselection of genotyped animals and influences also breeding value of others ungenotyped animal in evaluated population.

Holstein population in Czech Republic is genomically evaluated by single-step procedure (ssGBLUP) for milk traits, conformation, reproduction and longevity. New results of genomic evaluation on Czech data are published in Bauer et al. (2014, 2015), Pešek et al. (2015), Příbyl et al. (2014, 2015) and Zavadilová et al. (2014).

Purpose of this study was to compare domestic GEBV of young bulls for milk traits with theirs foreign evaluation.

2 Material and methods

Milk traits are evaluated from test-day records using BLUP / ssGBLUP Animal model procedures. Evaluation (Plemdat 2015) is conducted utilizing 3-lactations-RRTDM with Legendre Polynomials (LP):

$$Y_k = \mathbf{X}_{TD} \beta_k + \mathbf{X}_{fg} \mathbf{f}_{fg,k} + \mathbf{Z}_{pe} \mathbf{f}_{pe,k} + \mathbf{Z}_{an} \mathbf{f}_{an,k} + \mathbf{e}_k$$

where:

Y – test-day record of milk yield of cow in lactation k
<1, 2, 3>

\mathbf{X}_{TD} – design matrix for herd-test-days

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- β – vector of herd-test-day contemporary groups within a herd in lactation k (fixed effect)
- $X_{fg,k}$ – design matrix for fixed average LP of lactation curve for groups of cows within management classes sharing similar environments (Zavadilová et al., 2005b)
- Z – design matrices for random LP of lactation curve for permanent environmental of cow and genetic effects of animal
- f – LP for fixed (**fg**), permanent environmental of cows (**pe**) and genetic effect of animal (**an**). With **pe** and **an** are connected covariance matrices of regression coefficients of LP (Zavadilová et al., 2005a)
- e – vector of random residuals of test day records within lactation k with weights according stage of lactation

In a BLUP evaluation for genetic animal effect pedigree relationship matrix **A** and in ssGBLUP combined relationship matrix **H** is used. Inversion H^{-1} , which is incorporated into system of equations for predicting GEBV, is constructed according Legarra et al. (2009):

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \lambda(G^{-1} - A_{22}^{-1}) \end{bmatrix}$$

where:

- A** – pedigree relationship matrix through five generations of ancestors
- H** – combined relationship matrix with weights $\lambda = 0.80$ (weights 0.20 for **A** and 0.80 for **G**)
- A_{22} – pedigree relationship matrix of genotyped animals only
- G** – genomic relationship matrix of genotyped animals based upon deviations from averages of observed allele frequencies for given loci in the analysed population standardized with respect to diagonal elements of **G** (Forni et al., 2011) and shifted such that the elements of A_{22} and elements of **G** have the same average (Vitezica et al., 2011)

Data for evaluation consisted of 19,435,367 test-day records of 1,086,267 cows for three first lactations of Holstein from 1995 till 2014 year. Together 3,260 bulls were genotyped, of which 552 were young in 2014.

Three comparisons were executed:

- a) Prediction of young genotyped bulls by data to 2009 with their progeny results in 2014.
- b) Genomic prediction of young bulls in 2014 with their foreign GMACE values.
- c) Genomic prediction of young bulls in 2014 with their foreign MACE values.

3 Results and discussion

Data until 2009 were evaluated by BLUP and ssGBLUP. Average validated reliability for young bulls was calculated according determination coefficient of predicted value in 2009 and DRP in 2014, divided by reliability of this DRP:

$$vrel = (r_{PV9, DRP14})^2 / rel14$$

Calculation was for 531 young bulls without daughter records until 2009 and with >20 daughters in 2014. Validated reliability according BLUP evaluation was 0.20 and according ssGBLUP evaluation 0.36. Reliability according BLUP was low. Reason is, that majority of young animals have foreign sires, and young bulls have frequently both parents foreign. Therefore these animals have weak connection to the domestic production records, which results in low reliability of genetic evaluation. (In other words, massive import of insemination doses suppresses domestic breeding.) Genomic evaluation notably improves value of validated reliability to 0.36.

Some of young bulls have also genomic evaluation abroad, which was incorporated by Interbull into GMACE evaluation, but without data from Czech Republic. Correlations of domestic GEBV with foreign GMACE value for Czech Republic according 158 bulls are in Figure 1. For milk production the correlation is 0.71, for kg of protein and kg of milk fat little lower and for contents in % little higher. Correlation for somatic cell score (SCS) was very low.

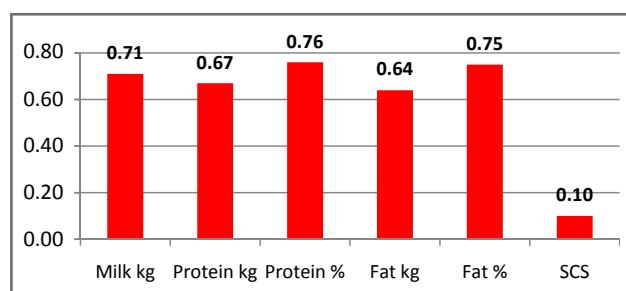


Figure 1 Correlation of domestic GEBV of young bulls with their GMACE evaluation according foreign data

Some of bulls evaluated in Czech Republic like young ones (i.e., those without progeny results) have already abroad daughters and are included by Interbull into MACE evaluation. Correlations of domestic GEBV with MACE value for Czech Republic according 73 bulls are in Figure 2. Correlations for milk and protein kg are higher than in Figure 1. Particularly correlation for SCS is much higher than in a case of correlation with GMACE. Those results show that GMACE values in year 2014 were not very accurate for transforming results of genomic evaluation

between countries. MACE values after progeny results were more reliable.

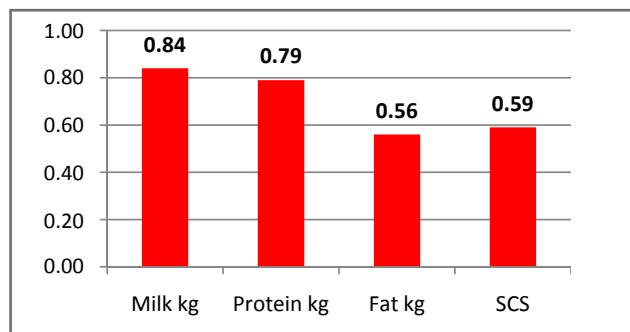


Figure 2 Correlation of domestic GEBV of young bulls with their MACE evaluation according foreign data

4 Conclusions

Due to persistent strong import of foreign sperm the reliability of domestic evaluation of young animals are low. This is particularly seen in evaluation of young bulls, which frequently have both parents foreign. Genomic evaluation by ssGBLUP procedure in a Czech condition helps and notably improves reliability of evaluation.

Genomic evaluation by ssGBLUP has several advantages and especially in a small populations. Increasing the reliability of evaluation according volume of information has curvilinear course. Inclusion of genomic data helps and reliability in a small population will approach to the situation in a big populations.

Domestic evaluation with foreign evaluations have medium to high correlations. Conversion of foreign EBV/GEBV according MACE procedure is more precise than according GMACE procedure.

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