

Using single-step genetic evaluation for type traits in the Nordic countries

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Abstract

In the Nordic Cattle Genetic Evaluation NAV (Denmark, Finland and Sweden) we are studying the use of the single-step approach to estimate genomic breeding values for Nordic Holstein cattle. The method used is a single-step GTBLUP model with blending of foreign information, and the traits in this report are the two type traits: chest width and udder depth. Breeding values estimated from single-step models using a full and a reduced dataset are compared and validated by Interbull validation and the Legarra Reverter Regression method. The mean GEBV's by birth year shows similar level for single-step full and single-step reduced and the correlation between those GEBV's are high. The validation results are as expected, and the results do not show any indication of GEBV inflation. The single-step model included a polygenic effect and two levels of polygenic effects (10% and 30%) were analyzed using a regression model for domestic AI bulls that were divided into groups based on number of daughters. It was found that polygenic effect of 30% were fitting best for the type traits with single-step approach for Nordic cattle.

Key-words: Nordic Holstein Cattle, Single-step, Type traits, Model validation, Polygenic effect

Introduction

The implementation of single-step in genetic evaluations is of high priority in many countries, since current two step methods cannot take the genomic pre-selection into account (Aguilar, et al., 2010). In this study breeding values (GEBV's) from a single-step approach are studied and compared with the current animal model (EBV's) and the current Nordic two-step SNP-BLUP model with 10% polygenic effect.

This study focuses on two traits: chest width and udder depth. These traits are chosen to check if the results of the single-step approach differ for traits with different selection pressure. Chest width was selected as a representative for a trait having no genetic trend in the past 20 years and udder depth as a representative for a trait with significant genetic trend. The purpose of this study is to examine genetic trends and to validate chest width and

udder depth GEBV's for Nordic Holstein cattle when using single-step approach.

Materials and methods

Conformation observations

This study is based on 2,225,000 first parity type phenotypes from Danish, Finnish and Swedish Holstein cows.

Genotypes

The reference population included 23,900 cows, 5,600 domestic AI bulls and 26,200 foreign AI bulls, which were mainly Eurogenomics bulls. Furthermore, 207,300 genotypes of male and female candidates were included in the analyses.

Statistical model

The method used to estimate GEBV's was a single-step GTBLUP model (Mäntysaari, Evans, & Strandén, 2017). Foreign information was integrated to non-Nordic reference bulls using the deregressed MACE EBV's included as pseudo phenotypes with weights in the evaluation (Pitkänen, 2020). Weights were the difference of information in MACE evaluation and in domestic evaluations (if bull had daughters in DFS).

A polygenic effect was included in the single-step model, and two levels (10% and 30%) of polygenic effect were tested in this study.

Validation

For validation purposes, two runs were conducted: a full model (single-step_full) where all

phenotypic information were included, and a reduced model (single-step_reduced) where records of daughters after domestic AI bulls born after 2011 were excluded. Furthermore, we used the Interbull validation (Mäntysaari, Liu, & VanRaden, 2010) and the Legarra Reverter Regression (Legarra & Reverter, 2018) to validate the predicted GEBVs from the single-step model.

Results and discussion

Genetic trend

Genetic trends and GEBV correlations between single-step full and single-step reduced GTBLUP models for udder depth are presented in Table 1.

Udder depth showed a positive genetic trend, which was expected. The genetic trends for single-step_full and single-step_reduced were nearly the same, and therefore there was no indication of GEBV inflation for domestic AI bulls (Table 1). The standard deviations of GEBV's were at the same magnitude for both single-step_full and single-step_reduced up to birth year 2011. AI bulls born in 2012-2016 had, as expected, higher standard deviations of GEBV's for the single-step_full than for single-step_reduced, since these bulls did not have daughters with records in the reduced dataset. The correlation between GEBV's from single-step_full and single-step_reduced was more than 0.99 for all birth year classes including daughter phenotypes in both evaluations (Table 1).

Table1. Mean and standard deviation of GEBV* for udder depth and correlation between single-step_full and single-step_reduced for domestic AI bulls by birth year**. For single-step the polygenic effect was 30%

Birth year	N	Single-step_full	Single-step_reduced	Corr(full,reduc)
2005	334	86.6 (10.5)	86.6 (10.5)	0.999
2006	383	89.0 (9.7)	89.1 (9.8)	0.999
2007	334	91.1 (9.8)	91.1 (9.8)	0.998
2008	293	93.7 (9.0)	93.8 (8.9)	0.997
2009	269	94.7 (9.6)	94.8 (9.7)	0.996
2010	226	98.8 (10.4)	98.8 (10.3)	0.994
2011	167	99.3 (9.6)	98.8 (9.6)	0.995
2012	172	101.2 (8.9)	101.3 (8.1)	0.899
2013	120	106.6 (8.8)	106.2 (8.1)	0.892
2014	104	107.0 (10.9)	107.5 (9.3)	0.914
2015	80	112.4 (11.4)	113.3 (10.2)	0.888
2016	66	114.0 (8.4)	114.4 (8.0)	0.953
2017	65	115.4 (9.5)	115.5 (8.8)	0.941
2018	89	116.0 (9.1)	116.1 (8.4)	0.957
2019	42	117.2 (8.9)	116.6 (8.3)	0.936

* Relative GEBV's on the Nordic scale with a standard deviation of 10

** For bulls born after 2015 there was no daughter information

Genetic trends from the single-step GTBLUP model, the current animal model (EBV's) and the current Nordic two-step model were at the same level up to birth year 2012 for progeny tested bulls (Table 2). For birth years 2013-2015 the genetic level of progeny tested bulls was slightly higher for the single-step model than for the current animal model. From 2016 onwards the bulls did not have daughter information included, and as expected, the genetic level from single-step and two-step models were higher than the pedigree index from the current animal model.

Results were shown for udder depth for domestic AI bulls, and the results were similar for females. Results for chest width were not shown, but the conclusions were the same as for udder depth.

Validation

For udder depth the interbull validation of domestic AI bulls born in 2012-2015 showed a regression coefficient of 0.90 ($R^2=0.68$, $N=363$ bulls). The Legarra Reverter regression for those bulls showed a regression coefficient of 0.99 ($R^2=0.80$). These validations of the single-step model were therefor as expected.

Table2. Mean and standard deviation of EBV and GEBV for udder depth for domestic AI bulls by birth year*. For single-step the polygenic effect was 30%.

Birth year	N	Single-step_full	Two-step	Animal model (EBV)
2005	334	86.6 (10.5)	87.5 (10.2)	86.8 (10.0)
2006	383	89.0 (9.7)	89.9 (9.5)	89.2 (9.2)
2007	334	91.1 (9.8)	91.7 (9.4)	91.4 (9.2)
2008	293	93.7 (9.0)	94.5 (8.7)	93.9 (8.3)
2009	269	94.7 (9.6)	95.3 (9.5)	94.6 (8.5)
2010	226	98.8 (10.4)	98.9 (10.0)	98.6 (9.1)
2011	167	99.3 (9.6)	99.3 (8.8)	99.3 (8.9)
2012	172	101.2 (8.9)	101.1 (8.4)	100.1 (8.6)
2013	120	106.6 (8.8)	105.6 (8.1)	105.2 (8.4)
2014	104	107.0 (10.9)	105.0 (9.8)	104.1 (10.3)
2015	80	112.4 (11.4)	109.5 (10.5)	108.4 (10.8)
2016	66	114.0 (8.4)	111.3 (8.0)	105.5 (6.5)
2017	65	115.4 (9.5)	112.3 (9.0)	107.4 (6.8)
2018	89	116.0 (9.1)	113.6 (8.7)	107.6 (5.4)
2019	42	117.2 (8.9)	114.0 (8.8)	107.7 (5.7)

* For bulls born after 2015 there was no daughter information

10% or 30% of polygenic effect

In this part it was tested whether a polygenic effect of 10% or 30% were the most appropriate for the single-step evaluation of udder depth. Both polygenic effect alternatives tested showed nearly the same genetic trend and the correlations between GEBV's for polygenic effect 10% and 30% were above 0.99 for all birth year classes for domestic AI bulls.

The standard deviations of GEBV's were at similar level no matter if polygenic effect was set to 10% or 30%. However, the standard deviation of selection candidates decreased when polygenic effect was increased (i.e. from 10% to 30%), and this was expected, since more weight was put on the pedigree and less on the genomic information.

The genomic prediction had a reliability of 68% for udder depth (based on results from the

Interbull validation). We expected approximately the same reliability for bulls with 20-30 daughters with phenotypes for udder depth. To test this, the bulls were divided into five groups based on the number of daughters ([0-9], [10-45], [46-70], [71-100] and [101-]) and within groups we regressed the full data single-step evaluations on reduced data single-step evaluations and full data EBV:

$$GEBV_{SS_full} = \mu + b_1 * GEBV_{SS_red} + b_2 * EBV + e$$

For the group with 10-45 daughters, it was expected that those bulls would have about half the information from genomic information and about half the information from progeny testing - leading to the expectation that $b_1 \approx b_2$ for this group of bulls. The regression coefficients b_1 and b_2 for polygenic effect of 10% and 30% are shown in Table 3.

Table3. Regression coefficients b_1 and b_2 for polygenic effect of 10% or 30% for udder depth for domestic AI bulls grouped by number of daughters

Group	Polygenic effect 10%		Polygenic effect 30%	
	b_1	b_2	b_1	b_2
[0 - 9]	0.88	0.19	0.84	0.28
[10 - 45]	0.67	0.43	0.56	0.58
[46 - 70]	0.53	0.57	0.35	0.76
[71 - 100]	0.44	0.66	0.28	0.83
[101 -]	0.22	0.84	0.15	0.92

The results show that for the group of bulls with 10-45 daughters, the information was most equally coming from progeny testing and from the genomic information when the polygenic effect was 30% (Table 3). Thus, for the single-step approach the polygenic effect of 30% seemed more appropriate.

Conclusion

The single-step GTBLUP approach gave promising results for the Nordic Holstein cattle when applied on chest width and udder depth. The single-step_full and single-step_reduced models showed similar genetic trends and thus, there was no indication of GEBV inflation. For young animals the single-step model showed higher genetic trend than the current animal model and slightly higher than the current two-step approach, where a post processing is applied in order to reduce the standard deviations of the GEBV's.

Furthermore, this study showed that the polygenic effect of 30% better agrees with the expectations than the polygenic effect of 10%.

Genetic trend analyses and the results from the validation studies seem to fulfill the

requirements for implementing the single-step GTBLUP approach (with polygenic effect of 30%) to the official genetic evaluation of type traits in Nordic Holstein cattle.

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