

RELATIONSHIP BETWEEN CHANGE IN TRAIT DEFINITION AND ACCURACY OF GENOMIC BREEDING VALUE OF TYPE TRAITS IN AUSTRALIAN HOLSTEIN

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SUMMARY

Data on type traits of Holstein cows scored between 1990 and 2014 were analysed to examine the extent of change in trait definition and to assess if these changes affect the accuracy of direct genomic values (DGV) of validation animals. The results showed that for 10 of the 20 traits, the genetic correlation of a trait that was scored before 2007 was less than 0.9 with the same trait scored after 2006. For 7 of the 10 traits, where the low genetic correlation suggested some level of change in trait definition, accuracy of their observed DGV were also markedly lower than the expected accuracy and accuracy predicted from the deterministic formula.

INTRODUCTION

Until recently type traits were not included directly in the economic index in Australia. However, from 2015, in the three new indexes (Balanced Performance Index, Health Weighted Index, Type Weighted Index), introduced by the Australian Dairy Herd Improvement Scheme (ADHIS) some type traits are included directly with their own economic values. Therefore these traits are now more important than they have been in the past. Recent results show that accuracy of direct genomic values (DGV) of type traits such as overall type and mammary system are lower than expected (Haile-Mariam *et al.* 2015). In addition, the accuracy of DGV for type traits varied considerably and explanations for such variation were not readily available (Haile-Mariam *et al.* 2013; 2015). Furthermore, results from ADHIS show that the variation in DGV among young bulls, particularly for overall type, is lower than expected. As part of the breed development program of Holstein Australia (HA) definition of some type traits has changed over time, and this may contribute to the lower than expected accuracy of DGVs for some traits.

This study explores if the low accuracies of DGVs observed for some type traits are related to changes in definitions of some type traits introduced in 2007 and we explore ways of minimising these effects on accuracy of DGVs. This is done in the following way: 1) for each type trait, estimating the genetic correlation for the trait scored on cows before 2007 and the trait scored after 2006, then assessing if the observed accuracy of DGV can be related to the genetic correlation of a trait in the two time periods; 2) for the two composite traits, namely overall type and mammary system, we assessed if predicting them from individual type traits can be used to increase genetic correlation between the two periods and thereby improve accuracy of DGVs.

MATERIALS AND METHODS

Data on Holstein cows type scored between 1990 and 2014 were obtained from the ADHIS. Cows were type scored by classifiers once during the first lactation. Details of the data used for this study is given by Haile-Mariam and Pryce (2015). The traits considered are those with relatively large amounts of data in the two periods (Table 1). The data included 18 linear traits scored on a scale of 1 to 9 and two composite traits scored on a scale of 1 to 16. In 2007 HA introduced some changes in the way type traits are scored. To assess the effect the change, data of cows scored before 2007 (period 1) and after 2006 (period 2) were split into two groups. Table 1

shows the numbers of cows scored with the mean and standard deviation for 20 traits in each period. Of the 2,724 bulls, with progeny in the second period 32% were also sires of 46% of the cows scored in the first period reflecting a good level of connectedness between the datasets.

Table 1. Number of cows classified, mean and standard deviation (SD) for type traits scored before 2007 and after 2006

Traits	Scored before 2007			Scored after 2006		
	No.	Mean	SD	No.	Mean	SD
Overall type	434,207	9.47	1.79	101,189	10.08	1.59
Mammary system	433,770	9.81	1.75	100,720	10.36	1.60
Stature	434,207	5.99	1.42	101,189	6.74	1.53
Udder texture	434,207	6.04	1.13	101,188	5.97	1.29
Bone quality	434,207	6.11	1.25	101,189	6.82	1.26
Angularity	434,207	5.46	1.14	101,189	5.84	1.10
Muzzle width	434,207	5.68	1.05	101,189	6.03	1.12
Body depth	356,080	6.25	1.12	101,189	5.59	1.32
Chest width	434,207	5.68	1.01	101,189	5.48	1.28
Pin width	434,207	5.75	1.19	101,189	6.67	1.30
Pin set	434,200	4.23	1.39	101,189	3.98	1.22
Foot angle	356,083	4.92	1.09	101,189	5.23	0.99
Rear leg set	434,203	5.47	1.01	101,189	5.28	1.07
Udder depth	356,068	5.89	1.15	101,188	5.18	1.59
Fore attachment	434,207	5.51	1.08	101,189	5.55	1.33
Rear attachment height	434,206	5.84	1.08	101,189	6.58	1.30
Rear attachment width	434,207	5.34	1.11	101,189	5.64	1.46
Central ligament	434,201	6.09	1.08	101,188	6.46	1.18
Teat placement fore	434,204	5.04	1.19	101,189	5.18	1.30
Teat length	356,025	4.44	1.46	101,188	4.55	1.35

To explore if the low DGV accuracy that we observed (e.g. Haile-Mariam *et al.* 2013; Haile-Mariam *et al.* 2015) for some traits is related to the change in the definition of type traits over time the following analyses were performed. First, to assess the extent of change in trait definition, type data of cows scored in the two time period were analysed as two different but correlated traits in a bi-variate sire model to estimate heritability (h^2) for each period and genetic correlation between the two periods. Data were analysed fitting sire as a random effect and Herd-Classifer-Round as the main fixed effect. Age and days in milk at scoring were also fitted as covariates. For overall type and mammary system, the two composite traits, value for cows scored in period 1 were predicted from other type traits that were less affected by trait definition (Table 2). A genetic correlation of below 0.90 between the two periods was considered as criteria to designate a trait whose definition changed. For both traits, a linear prediction equation based on selected linear type traits and the composite traits was developed based on data of cows scored in period 2 and applied to data of cows scored in period 1, assuming the period 2 scores as ‘gold standard’. Secondly DGV for validation bulls born in 2004 and after were predicted and accuracy was calculated as a correlation between DGV and daughter trait deviation (DTD). These DGV accuracy were adjusted using the average accuracy of the DTDs (calculated from h^2 and number of daughters) and compared to expected accuracy calculated from the prediction error variance and to the accuracy calculated using deterministic formula (e.g. Hayes *et al.* 2009). For these analyses the DTD and

genotype data of 2,407 bulls were obtained from the ADHIS. Details on the DTD, genotype and methods for genomic prediction are provided elsewhere (e.g. Haile-Mariam *et al.* 2015). The parameters used for prediction of accuracy using the deterministic formula were the same as those assumed by Hayes *et al.* (2009). However, the reference population size was 2,056 bulls for 14 of the 20 traits and 1,860 bulls for udder depth, body depth, foot angle and teat length. The h^2 in Table 2 estimated based on the data in period 1 were used to calculate effective h^2 .

RESULTS AND DISCUSSION

The mean type score of cows increased from period 1 to period 2 for all traits except udder texture, body depth, chest width, pin set, rear leg set and udder depth (Table 1). The reason why the mean score of cows for udder texture and these other traits decreased could be related to the change in the way cows were scored, or to selection, if the optimum for the trait is a lower or intermediate score. For all traits, the h^2 was lower in cows scored in period 2 compared to those in period 1 (Table 2). The genetic correlation of cows scored in the two periods was very high for traits such as pin set, but was the lowest for mammary system followed by overall type (Table 2). When predicted overall type and mammary system were used for cows scored in period 1, instead of the scores by the classifiers, the genetic correlation between the two periods increased only marginally. In the case of mammary system, the correlation increased to 0.63 when 4 udder traits (udder depth, teat length, teat placement fore and fore attachment) were used as predictors. In the case of overall type, the use of 10 traits (teat length, teat placement fore, udder depth, rear set, foot angle, pin set, body depth, muzzle width, angularity, bone quality) increased the correlation to 0.68. This is slightly lower than the prediction using all type traits (0.70).

Table 2. Estimates of heritability (h^2), genetic correlation of a trait between scored before 2007 and after 2006, adjusted observed accuracy, expected accuracy and differences (Diff)

Traits	h^2 before '07	h^2 after '06	Genetic correlation	Adj. accuracy	Exp. accuracy	Diff
Overall type	0.27±0.01	0.13±0.01	0.66±0.08	0.36	0.56	0.20
Mammary system	0.27±0.01	0.14±0.01	0.59±0.07	0.33	0.55	0.22
Stature	0.45±0.01	0.30±0.02	0.84±0.03	0.46	0.61	0.15
Udder texture	0.23±0.01	0.13±0.01	0.68±0.06	0.46	0.61	0.15
Bone quality	0.30±0.01	0.25±0.01	0.97±0.02	0.54	0.64	0.10
Angularity	0.26±0.01	0.18±0.01	0.93±0.03	0.55	0.61	0.06
Muzzle width	0.23±0.01	0.20±0.01	0.90±0.03	0.53	0.63	0.10
Body depth	0.38±0.01	0.28±0.02	0.95±0.02	0.70	0.64	-0.06
Chest width	0.25±0.01	0.21±0.01	0.81±0.04	0.53	0.66	0.13
Pin width	0.35±0.01	0.26±0.02	0.85±0.04	0.57	0.64	0.07
Pin set	0.37±0.01	0.29±0.01	0.99±0.01	0.51	0.61	0.10
Foot angle	0.20±0.01	0.17±0.01	0.93±0.03	0.55	0.61	0.06
Rear leg set	0.18±0.01	0.10±0.01	0.94±0.03	0.44	0.54	0.10
Udder depth	0.40±0.01	0.33±0.02	0.93±0.02	0.71	0.65	-0.06
Fore attachment	0.22±0.01	0.16±0.01	0.88±0.04	0.42	0.61	0.19
Rear attachment height	0.27±0.01	0.16±0.01	0.71±0.06	0.52	0.59	0.07
Rear attachment width	0.23±0.01	0.18±0.01	0.69±0.06	0.59	0.62	0.03
Central ligament	0.24±0.01	0.12±0.01	0.70±0.06	0.27	0.63	0.36
Teat placement fore	0.35±0.01	0.30±0.02	0.90±0.03	0.54	0.67	0.13
Teat length	0.44±0.01	0.34±0.02	0.94±0.02	0.52	0.66	0.14

For 18 of the 20 traits analysed the observed accuracy of DGV was lower than the expected accuracy (Table 2). The observed accuracy being lower compared to the expected accuracy could be a result of change in trait definition (Table 2) over the period. In fact Table 2 shows that for 7 of the 10 traits whose genetic correlations between the two periods were < 0.9 the observed accuracy was less than the expected accuracy by at least 0.1. However, for rear attachment height and rear attachment width where the genetic correlations between period 1 and 2 were low (Table 2) the observed accuracy was only marginally lower than the expected accuracy. For teat length, pin set, rear leg set and bone quality despite having genetic correlations of > 0.9 , the observed accuracy was lower than the expected accuracy by 0.1 to 0.14 (Table 2), suggesting that issues other than correlations that cover the current period may contribute to the difference.

The accuracy of prediction from the deterministic formula varied from 0.59 for foot angle (the lowest h^2) to 0.65 for stature (the highest h^2). The small variation in the formula predicted accuracy among traits is expected because all the parameters that influence accuracy, except the h^2 are the same. The highest differences between the formula predicted and the expected accuracy (0.07-0.08 in favour of the formula) were for mammary system, overall type and rear leg set. For all the other traits the difference was 0.04 or less. An additional evidence of the effect of change in trait definition detected as low genetic correlation of a trait over time on DGV accuracy was observed because the relationship of DGV accuracy with the product of h^2 and genetic correlation was stronger ($R^2 = 0.49$) than that of DGV with h^2 alone ($R^2 = 0.41$) based on all traits. Thus taking account of the genetic correlation improved agreement between observed DGV and expected accuracy.

The broader implications of these results are, when assessing the accuracy of DGV of traits that are subjectively scored the possible effects of changes in the trait definition should be considered. Overall changes in definition of traits may be important for valuing current cows according to current standards, but it should be done with care, considering its effect on genetic progress, accuracy of BV and trait harmonisation with Interbull member countries. The impact of change in trait definition on DGV accuracy could be more pronounced if the change in trait definition coincides with the subdivision of bulls into reference and validation set as was case in the current study. A gradual decrease in genetic correlations of a trait over time will most likely affect the data of all bulls and will be realised as low h^2 and consequently low DGV accuracy. For traits where there is marked change in trait definition that result in reduced accuracy of prediction of BV alternative genetic evaluation models including multi-variate and random regression models (Tsuruta *et al.* 2004; Haile-Mariam and Pryce 2015) or ignoring old data (Jamrozik and Schaeffer, 1991) should be considered.

In conclusion for most traits the discrepancy between the adjusted and expected accuracy of DGVs can be related to change in trait definitions. However, there were cases where differences between observed and expected accuracy could not be related to the absence or presence of change in trait definition that can be detected by calculating genetic correlations.

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