

# Multiple Trait Genetic Evaluation Of Linear Type Traits Using Genomic And Phenotypic Data In US Holsteins

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## Introduction

The genomic selection of US Holsteins has currently been conducted with a multi-step procedure where regular EBVs are used to create genomic predictions (VanRaden, 2008). Later steps in the multi-step procedure involve only genotyped animals and use single-trait (ST) procedures.

Aguilar et al. (2010) obtained genomic EBV by a single-step procedure (SSP) for final score of US Holsteins, where a pedigree-based relationship matrix in the evaluation procedure is replaced by a matrix that combines pedigree and genomic relationships. From test results, the study found that the accuracy and inflation of genomic evaluation were improved by the SSP with small modifications. The accuracy became marginally higher as inflation decreased and approached zero. The need for modifications was probably due to incorrect scale of the genomic relationship matrix and preferential treatment of bull dams. Computing time of SSP with the ST model was very close to that of a regular BLUP procedure.

In chicken, Chen et al. (2010) used SSP for three traits in two populations. Despite similar heritability of each trait in the two populations, the degree of improvement in the accuracy after adding the genomic information varied by line. The variation in the accuracy was attributed to different multiple-trait (MT) selection in each line.

Currently, the standard evaluation for linear type traits in U.S. Holstein uses an MT model. However, the genomic selection of the traits is based on a multi-step procedure (VanRaden et al., 2009). There were three objectives of this study: 1) to determine computing feasibility of MT SSP for national evaluation; 2) to improve in accuracy by using the MT SSP and to determine accuracy variation by trait; 3) to investigate the variability in the accuracy increases and in the inflation of genomic breeding values after the modification of the combined relationship matrix.

## Material and methods

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Genetic markers from the Illumina BovineSNP50 genotyping Beadchip, consisting of 38,416 SNPs, were available for 6931 Holstein bulls. Genomic evaluation was conducted for five linear type traits with SSP where the inverse of the combined relationship matrix was

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - \omega \mathbf{A}_{22}^{-1} \end{bmatrix}$$

where  $\mathbf{A}$  is a pedigree-base relationship matrix,  $\mathbf{G}$  is a genomic relationship matrix,  $\mathbf{A}_{22}$  is a pedigree-based relationship matrix for genotyped animals, and  $\omega$  is a weight factor for the inverse of  $\mathbf{A}_{22}$  ( $\mathbf{A}^{-1}$ ). Three analyses of five linear type traits (stature, strength, body depth, dairy form, and rump angle) were conducted using 8,865,120 records from 2009 and 7,715,925 records from 2004. Using ST and MT models, EBV in 2009 were calculated with phenotypes and pedigree information (traditional genetic evaluation) while genomic EBV in 2004 were calculated with phenotypes and genotypes (SSP), varying the weight ( $\omega$ ) on the inverse numerator relationship matrix ( $\mathbf{A}_{22}^{-1}$ ) for genotyped animals. Regressions of daughter deviations from 2009 MT traditional evaluation on 2004 genomic EBV and its  $R^2$  were calculated for 1307 young bulls with at least 50 daughters in 2009. The EBV for 2004 traditional evaluation were used for parent average (PA). Table 1 shows heritability used in this analysis, and genetic and phenotypic correlations among five traits. Computation of EBV was done using the modified BLUP90IOD program (Tsuruta et al., 2001).

**Table 1: Heritability (diagonal), genetic (upper), and phenotypic (lower) correlations among five linear type traits used in genetic evaluation**

Trait	Stature	Strength	Body depth	Dairy form	Rump angle
Stature	0.45	0.71	0.80	0.34	0.15
Strength	0.55	0.27	0.89	-0.02	0.01
Body depth	0.63	0.74	0.34	0.38	0.02
Dairy form	0.22	-0.02	0.28	0.30	-0.03
Rump angle	0.11	0.00	0.02	0.01	0.34

## Results and discussion

Table 2 shows  $R^2$  values for multiple EBV. For PA, the change from using ST to MT increased  $R^2$  for Strength and Rump Angle but there was little to no improvement for the other traits. For genomic evaluations with  $\omega=1$ , the changes in  $R^2$  as a result of using MT instead of ST were similar to those for PA. The inflation of genomic evaluations ( $1/\delta$ ) were the same for ST and MT and were higher with genomic evaluations with  $\omega=1$  than for PA. Decreasing  $\omega$  reduced the inflation, but caused deflation for some traits, while marginally decreasing  $R^2$ . Differential increases of accuracies from ST to MT could be due to different genetic parameters as well as different selection pressure. Over the past 5 years, the relative gain in PTA for the traits in this study were 0.70., 0.45, 0.57, 0.72, and -0.09, respectively (Sire Summaries, 2010). The traits with the largest gain showed little or no improvement

from ST to MT. No body trait was directly selected, whereas dairy form has a negative weight in the TPI formula.

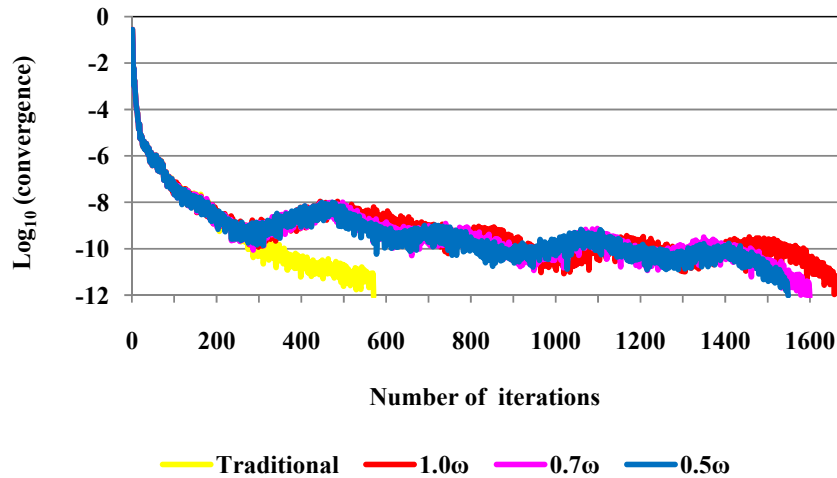
**Table 2: Coefficients of determination ( $R^2$ ) and regressions ( $\delta$ ) of daughter deviations in 2009 on genomic evaluations in 2004 using single and multiple trait models with 1.0, 0.7, and 0.5 weights ( $\omega$ ) on the A-inverse matrix for genotyped animals**

Trait	$\omega$	Single trait		Multiple trait	
		$R^2$ (%)	$\delta$	$R^2$ (%)	$\delta$
Stature	Parent average	34	0.86	34	0.86
	1.0	54	0.82	54	0.81
	0.7	54	0.95	54	0.94
	0.5	53	0.99	53	0.99
Strength	Parent average	25	0.78	29	0.80
	1.0	41	0.74	45	0.74
	0.7	40	0.87	44	0.87
	0.5	39	0.92	43	0.92
Body depth	Parent average	28	0.78	30	0.78
	1.0	45	0.74	47	0.74
	0.7	44	0.86	47	0.86
	0.5	44	0.91	46	0.91
Dairy form	Parent average	20	0.79	20	0.79
	1.0	38	0.76	38	0.77
	0.7	40	0.96	40	0.98
	0.5	39	1.04	40	1.05
Rump angle	Parent average	25	0.87	25	0.86
	1.0	45	0.91	45	0.90
	0.7	44	1.04	44	1.03
	0.5	43	1.08	43	1.07

**Table 3: Numbers of iterations (processing seconds per round) for genomic evaluation in 2004 using single trait and multiple trait models with 1.0, 0.7, and 0.5 weights ( $\omega$ ) on the A-inverse matrix for genotyped animals**

Evaluation method	$\omega$	Single trait					Multiple trait (seconds/round)
		Stature	Strength	Body depth	Dairy form	Rump angle	
Traditional	N/A	234 (9)	235 (9)	233 (9)	234 (10)	140 (10)	570 (36)
Genomic	1.0	435 (9)	501 (10)	439 (11)	657 (9)	146 (9)	1677 (45)
	0.7	430 (15)	485 (17)	545 (18)	642 (12)	147 (11)	1599 (56)
	0.5	430 (18)	434 (17)	432 (17)	600 (12)	152 (12)	1548 (56)

The MT model required 2-11 times more number of rounds (Table 3) and was 3-5 times slower per round than the ST model. With SSP, the number of rounds for the MT model increased 3 times (Figure 1) and the speed was 25-56% slower per round than with the traditional genetic evaluation.



**Figure1: Convergences for traditional and genomic evaluations with multiple trait model**

## Conclusion

Improvement of accuracy in the multiple trait model over the single trait model are trait dependent for linear type traits in US Holsteins. Accuracy gains in genomic EBV are similar to those in traditional EBV with pedigree information. Computations of genomic EBV using the multiple trait models increase as the number of traits increases.

## References

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