

Comparison of single-step and multi-step evaluations for U.S. milk, fat, and protein

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Abstract

Predictive abilities of single-step (SS) and multi-step (MS) evaluations were compared using current and truncated domestic phenotypes for U.S. yield traits. Accuracy from SS was several percentage points higher than MS to predict either MS or SS current genomic estimated breeding values (GEBV) of 2,619 Holstein and 345 Jersey bulls from 4-year earlier data. Regressions for GEBV were close to 1.0 and similar for MS and SS for all traits and both breeds. Accuracy advantages of SS have increased since a previous study, perhaps indicating more bias from genomic preselection in MS. The MS methods put too much weight on pedigree evaluation, whereas the SS model had no polygenic effect and was more stable because new phenotypes have little influence on marker effects. Further testing will include more traits, foreign data from Interbull, and crossbreds to determine the potential to use SS methods.

Introduction

Most dairy cattle genomic evaluations still use MS methods, but recent research has improved both efficiency and accuracy of SS methods, and genomic preselection may increasingly bias MS methods. This study compares SS methods to official MS methods applied to the current or truncated domestic U.S. yield records. Previous reports (Masuda et al., 2018a; 2018b) included only Holstein records and less recent data than in the all-breed dataset now available. Masuda et al. (2018a) predicted 2015 protein daughter yield deviations from 2011 truncated Holstein phenotypes. They found little difference between SS and MS accuracy and regressions when unknown parent groups were applied only to pedigree but not to genomic relationships. Those earlier comparisons reported R^2 of 52% for SS and 51% for MS with corresponding regressions of 0.78 for SS and 0.81 for MS. Masuda et al. (2018b) compared SS vs. MS trends and observed underestimation for the latter due to preselection in traditional PTA, especially for young bulls. The authors predicted that differences would further increase for genotyped bulls with the accumulation of preselection bias over the years, which would become more evident with shorter generation intervals and more recent data. Thus, comparisons were updated to determine if the theoretical advantages of SS (Aguilar et al., 2010) now give larger actual advantages over MS when applied to national data.

Materials & Methods

Genotypes were available from 5.1 million purebreds; genotypes of crossbreds were excluded from both SS and MS methods. The SS GEBV were estimated using APY method with 45,000 core animals: 15,000 each for Holstein (HO) and Jersey (JE) and 5,000 each for Ayrshire, Brown Swiss, Guernsey, with genotypes and phenotypes for all 5 breeds together (Cesarani et al., 2022). The MS GEBV used current official methods with separate marker effects for each breed. During iteration, the MS used 0.6 million genotyped animals that had phenotypes or descendants with phenotypes, and the SS used 3.9 million genotyped animals that had phenotypes, descendants with phenotypes, or non-genotyped parents; for efficiency GEBVs of the remaining animals are computed only after convergence. Phenotypes were 305-d milk, fat,

and protein lactation records solved in multi-trait models in SS and the first step of MS followed by single-trait marker effects in MS. The complete dataset included 99 million lactations beginning in 1960 for MS, whereas SS used a subset of lactations beginning in 2000. For both SS and MS, the complete dataset included calving dates up to June 2021, while the reduced dataset included calving dates only to June 2017 after truncating the last 4 years. The EBV from Interbull were not included. Thus, validation comparisons were limited to 2,619 U.S. HO and 345 U.S. JE bulls that had ≥ 100 daughters in the complete but no daughters in the reduced dataset. Other breeds had fewer than 25 such bulls and are not reported here. The unknown parent groups defined for MS were also used in SS but were not optimal after removing the first 40 and last four years of phenotypes; MS software automatically condenses groups outside the minimum and maximum year with phenotypes for each trait. The final GEBVs from both SS and MS were predicted from the earlier SS and MS GEBVs with simple regressions and with extra regressions (SS+ and MS+) on birth year and pedigree EBV from the respective SS or MS evaluation (VanRaden, 2021). Direct genomic values (DGV) from the MS evaluation were also examined because the SS did not include a polygenic effect and thus effectively only solved for a DGV. A MS evaluation with only 1% polygenic variance and no extra weight on pedigree EBV in the final blending step was computed for comparison.

Results

The pedigree models using SS or MS software had similar correlations of initial with later EBV as expected. The correlations ranged from 0.58 to 0.73 and were consistent with the large gain in reliability (REL) when bulls became proven. The GEBV correlations were much higher than for EBV as expected. Correlations from SS were higher than MS model for all traits and both breeds but correlations of the DGV from MS software were higher than from SS for traits of HO (Table 1). Regressions for pedigree models were all below the desired value of 1.0 and were similar using MS or SS software. Genomic preselection can reduce the regressions on pedigree EBVs because selection intensity may be much higher for animals with lower EBV, whereas GEBVs should be much less biased by preselection. Regressions for GEBV were close to 1.0 and similar for MS and SS for all traits and breeds. Regressions were also close to 1.0 for the MS DGV for HO but were lower for JE (Table 2). The standard deviations (SD) were similar for pedigree EBVs from MS and SS software, as expected. The SD were higher from final than truncated EBVs, also consistent with the large gains in EBV REL. The final GEBV had higher SD than the truncated GEBV in the SS and MS models, as expected.

Predictions of final MS or SS GEBV or DYD using truncated GEBV from the other software or with extra regressions provides more information about the benefits and biases, with results for milk shown as an example (Table 3). The reduced SS had higher R^2 than the reduced MS GEBV to predict either the MS or SS final GEBV for both HO and JE breeds; differences in R^2 were larger when predicting SS than MS. The extra regressions improved MS+ predictions compared to MS more than SS+ compared to SS, indicating smaller biases in SS as desired. The extra regressions were significant in SS but smaller in magnitude. The R^2 for MS+ and SS+ were very similar with the extra regressions included. The b_1 regression estimates were a little closer to 1.0 for MS than for SS in both breeds, but the MS+ estimates were very high for b_1 as previously shown (VanRaden, 2021) with the extra regressions included.

The SS and MS final GEBVs for milk were correlated by 0.98 and the reduced GEBVs were correlated by 0.96 for the 2,619 U.S. HO bulls that had ≥ 100 in 2021 but no daughters in 2017. The pedigree EBV from SS and MS software were correlated by 0.99 for final and 0.96 for the reduced EBV. Those differences are likely due to the known biases detected by the extra regressions, inclusion of polygenic effects, and slight differences in input records. The

corresponding correlations for the 345 JE bulls were 0.98 for final GEBVs, 0.94 for reduced GEBVs, 0.98 for final EBVs, and 0.98 for reduced EBVs.

Table 1. Squared correlations (x100) of final and truncated EBVs within the same evaluation system.

Breed	Trait	Genomic EBVs			Pedigree EBVs	
		MS	SS	MS DGV	MS	SS
Holstein	Milk	74	81	93	37	34
	Fat	78	83	95	42	34
	Protein	75	83	94	45	37
Jersey	Milk	78	83	86	53	45
	Fat	70	78	78	39	34
	Protein	73	83	80	49	46

Table 2. Regressions of final on truncated EBVs within the same evaluation system.

Breed	Trait	Genomic EBVs			Pedigree EBVs	
		MS	SS	MS DGV	MS	SS
Holstein	Milk	0.95	0.96	0.97	0.75	0.72
	Fat	0.96	0.96	0.95	0.85	0.76
	Protein	0.91	0.95	0.94	0.80	0.73
Jersey	Milk	1.05	0.95	0.94	0.91	0.84
	Fat	0.94	0.91	0.84	0.75	0.67
	Protein	1.00	0.98	0.88	0.86	0.82

Table 3. Squared correlations (x100) and regressions to predict final MS and SS GEBV and MS DYD for milk from truncated MS and SS GEBV or with extra regressions on birth year and PA included (SS+ and MS+).

Breed	Predict: 2021	Squared correlation from 2017:				Regression (b1) from:			
		MS	SS	MS+	SS+	MS	SS	MS+	SS+
HO	MS	74	76	80	79	0.95	0.90	1.41	1.00
	SS	74	81	83	85	0.99	0.96	1.58	1.15
	DYD	60	63	69	68	0.93	0.90	1.52	1.08
JE	MS	78	80	80	81	1.05	0.96	1.47	0.96
	SS	74	83	79	84	0.99	0.95	1.58	1.09
	DYD	66	72	71	73	0.98	0.93	1.51	1.01

Genetic trend estimates were similar for MS and SS; correlations of birth year with GEBV for HO were 0.28 and 0.17 with reduced and final MS vs. 0.29 and 0.16 with reduced and final SS. Correlations in the final data may be lower because the young bulls were highly selected. To predict later MS or SS GEBVs, the extra regressions showed that parent average (PA) should be subtracted from the reduced MS GEBVs and that the birth year trend was steeper in young bulls than proven bulls. The trend was also too steep and of same magnitude in the reduced SS GEBVs. With SS, the extra regression on PA was positive to predict MS GEBV but near 0 to predict SS GEBV. When comparing only bulls with 1,000 daughters, 5 of the 10 largest differences of SS – MS were clones of famous bulls. Clones have identical DGVs, but their polygenic effects differ slightly due to being modelled as full sibs in the MS model. Thus, their GEBVs and daughter counts are copied to the clones in the official system. Different methods may be needed when using a genomic relationship matrix because clones make the matrix

singular. The SS and MS GEBVs had small differences for the highest ranking HO bulls for net merit with > 1,000 daughters, indicating little bias after bulls are widely used. Biases may occur with early daughters from highly selected mates. The selection and mating patterns for HO may be more extreme and cause more biases than for JE or smaller breeds. The MS model with 1% polygenic variance and no extra weight on pedigree EBV gave GEBV more similar to SS with correlation increased to 0.97, nearly identical prediction R^2 , and b_1 slightly closer to 1.0 than SS. Thus, previous revisions to the MS model to reduce overprediction of young animals (i.e., 10% polygenic variance and extra weight on PA) were a main difference between MS and SS predictions.

Discussion

The higher R^2 of SS to predict later MS or SS GEBV or DYD indicates better predictive ability than official MS for both HO and JE, but the b_1 regressions were a little closer to 1.0 for MS than for SS. The SS model without a polygenic effect may be too rigid and adapts less to new data of individual animals in large populations. Instead, new animals adjust the marker effects just a little, but their final GEBV mostly reflects the same historical marker effects they had when younger. For HO, the MS DGV were even more consistent than the SS GEBV. The earliest MS models in 2008 also used no polygenic effect but since 2010 have assumed 10% variance to avoid overprediction and obtain b_1 closer to 1.0. The MS model may now be assigning too much variance to the polygenic effect because recent enhancements and additions to the marker list should account for more of the genetic variance, but the SS model assigns too little polygenic variance (0%). Tests of German and Nordic SS models have assigned 30% polygenic variance to all traits (Alkhoder and Liu, 2021; Andersen et al., 2021). The U.S. MS model has put extra emphasis on pedigree EBV in the final blending step; those weights were decreased from 15% to 10% for yield traits in August 2021. Other model changes may be needed to prevent overprediction of final genetic trend that occurred in both the MS and SS GEBVs of young bulls. Negative values for the b_0 intercept are also a problem but were not yet compared in this validation. Future comparisons will include foreign data and more traits. Comparison of MS and SS results should lead to better understanding and improvements to both systems. The SS software could simplify and improve multi-trait modeling. Switching the current run flow to SS software for all the traits will take some effort and more computation but could be worthwhile.

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