

Increased Reliability of Genetic Evaluations for Dairy Cattle in the United States from Use of Genomic Information

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Introduction

Genomic evaluations have been official in the United States since January 2009 for Holsteins and Jerseys and since August 2009 for Brown Swiss. Those evaluations are considered accurate enough to allow bulls with only genomic information to be marketed routinely. Accuracy of the evaluations is largely a function of the number of bulls with genotypes and traditional evaluations because their data are used to estimate effects of single-nucleotide polymorphisms (SNP). VanRaden *et al.* (2009) reported reliability (REL) gains over traditional parent averages for evaluations that included SNP effects based on 3,576 Holstein predictor bulls with evaluations in 2004; those gains are expected to increase through the use of a 2006 cutoff, which would increase the number of predictor bulls. A 10% polygenic effect was applied for all animals starting in January 2009, which also affected REL gains. Cows also can contribute to accuracy, but they are not used by most countries because their evaluations usually have lower REL and may be biased upward. Wiggans *et al.* (2010a) have shown that adjusting traditional evaluations for yield traits of US cows can increase their usefulness in estimating SNP effects. The purpose of this study was to determine gain in evaluation REL from using the most recent genomic information and evaluation methods. Because genetic evaluations for type traits were significantly changed in April 2007 for overall conformation and in August 2008 for all linear traits, they were not included in the study. Genomic evaluation for the lifetime net merit index is now calculated from genomic evaluations for its component traits and no longer is processed as a separate trait.

Material and methods

Data. Table 1 shows numbers of genotyped Holstein, Jersey and Brown Swiss animals available for February 2010 evaluations. Those numbers result from collaboration of the US and Canadian dairy industries on a shared set of genotypes and over 500 Brown Swiss bull genotypes from Switzerland. Data from the predictor population of genotyped animals with traditional evaluations in August 2006 were used to estimate SNP effects as described by VanRaden (2008). The predicted animals have a traditional domestic evaluation in January 2010 but not in 2006. The total number of genotyped animals includes many young animals without a traditional evaluation that therefore did not contribute to this study. Evaluations of Holstein and Jerseys cows for milk, fat and protein yields were adjusted (Wiggans *et al.*

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Table 1: Number of genotyped animals and sizes of predictor and predicted populations by breed

Breed	Genotyped animals ^a	Predictor population ^b	Predicted population ^c	
			Bulls	Cows
Holstein	37,412	7,173	2,226	1,659
Jersey	3,825	1,819	370	181
Brown Swiss	1,416	1,010	117	0

^aAs of February 2010.

^bCows and bulls with official evaluations for yield traits as of August 2006.

^cAnimals with a January 2010 domestic traditional evaluation.

(2010a)) so that deregressed values had means and variances similar to those of bulls. Parent averages of all animals were recalculated using updated cow evaluations, and those revised parent averages were used to revise predicted transmitting abilities (**PTA**). As reported in Wiggans *et al.* (2010b), 43,385 SNP were used in the evaluation; the same SNP set was used across breeds.

Bias. Bias in accuracy determination because of selection was investigated. Selection on the independent variable (genomic evaluation) does not bias regression coefficients, but selection on the dependent variable (deregressed evaluation) does bias estimates (Henderson *et al.* (1959)). Genotyping more genetically superior bulls than inferior bulls has not been a concern because best linear unbiased prediction accounts for selective genotyping. However, in tests to determine the effectiveness of genomic selection, estimated regression coefficients and REL may be biased downwards because bulls in the predicted population (the dependent variable) were selectively genotyped after their phenotypes were observed. Bias was examined by splitting the predicted bulls into three groups based on their traditional evaluations for protein yield. Selection intensity in the predicted population was quantified by comparing means of 2,304 genotyped Holstein bulls with all 5,594 Holstein bulls born from October 2001 through October 2005 that were progeny tested by major North American artificial-insemination companies and available for genotyping. The birth date range was chosen to match the birth dates of the bulls that were being predicted.

Gains in REL. Squared correlations were calculated between August 2006 genomic evaluations and 2010 deregressed values and adjusted for REL of the 2010 evaluation (VanRaden *et al.* (2009)). Those were compared with similar values based on 2006 parent averages. Gains in REL were calculated for bulls. The benefit of adjustment of cow evaluations was determined through comparison with 2006 genomic evaluations without cow adjustment. All analyses were done within breed.

Results and discussion

Bull REL gains are shown in table 2 by breed. Largest gains were for fat and protein percentages, which reflects their higher heritability and the greater benefit of a nonlinear model for those traits. Gains were greatest for Holsteins, a reflection of their larger predictor population. Gains averaged across milk, fat, and protein yields, productive life (**PL**), somatic cell score (**SCS**) and daughter pregnancy rate (**DPR**) were 28.4% for Holsteins, 20.7% for

Table 2: Regression coefficients (b), squared correlations $\times 100$ (R^2) and observed REL gains from using August 2006 data to predict February 2010 bull evaluations by trait and breed

Breed	Trait ^a	Parent average		Genomic prediction			REL gain (%)	
		REL (%)	R^2	R^2	Bias ^b	b		REL (%)
Holstein	Milk (kg)	38.5	18.8	42.7	-35.4	0.90	71.0	32.5
	Fat (kg)	38.5	19.4	46.5	-1.5	0.97	75.6	37.1
	Protein (kg)	38.5	19.9	39.8	-0.6	0.87	65.6	27.2
	Fat (%)	38.5	27.3	65.5	0.0	0.98	90.8	52.3
	Protein (%)	38.5	31.6	61.5	0.0	0.88	78.5	40.0
	PL (months)	31.6	18.0	30.8	-1.1	1.03	60.4	28.7
	SCS	34.2	14.9	31.0	0.0	0.88	61.6	27.3
	DPR (%)	30.7	22.5	30.2	-0.2	1.09	48.1	17.4
	Sire CE	27.2	16.0	24.1	0.9	0.76	41.9	14.7
	Daughter CE	26.8	8.2	14.6	0.0	0.89	42.4	15.7
	Sire SB	23.4	7.5	9.9	1.1	0.86	30.3	7.0
Daughter SB	26.9	8.7	9.5	0.8	0.93	29.2	2.3	
Jersey	Milk (kg)	39.7	39.8	53.8	36.1	0.99	59.3	19.6
	Fat (kg)	39.7	28.2	41.1	2.5	0.83	57.9	18.2
	Protein (kg)	39.7	34.1	43.2	1.5	0.90	52.4	12.7
	Fat (%)	39.7	41.2	67.6	0.0	0.92	76.5	36.8
	Protein (%)	39.7	38.2	61.5	0.0	0.89	71.3	31.6
	PL (months)	31.9	8.5	18.7	-0.4	0.93	55.8	23.8
	SCS	35.5	11.5	21.9	0.1	0.79	54.2	18.6
	DPR (%)	30.6	7.8	20.5	-0.1	1.23	61.9	31.2
Brown Swiss	Milk (kg)	37.2	7.9	18.8	-207.3	0.70	54.3	17.1
	Fat (kg)	37.2	7.6	16.6	-9.5	0.57	51.3	14.1
Brown Swiss	Protein (kg)	37.2	7.0	17.8	-6.5	0.54	54.3	17.0
	Fat (%)	37.2	30.1	45.5	0.0	0.98	60.7	23.5
	Protein (%)	37.2	29.7	47.3	0.0	1.06	66.4	29.2
	PL (months)	28.2	11.6	20.6	-1.6	1.08	51.4	23.2
	SCS	32.3	11.9	16.1	0.0	0.84	40.3	7.9
	DPR (%)	25.5	4.5	3.7	0.2	0.46	23.0	-2.5

^aCE = calving ease and SB = stillbirth.

^b2010 deregressed value - 2006 genomic evaluation.

Jerseys, and 12.8% for Brown Swiss. Comparable gain based on 3,576 Holstein predictor bulls was 22.2% (VanRaden *et al.* (2009)). Adjustment of August 2006 cow evaluations increased REL gain by a mean of 2.7% for Holsteins and 8.6% for Jerseys across milk, fat, and protein yields. The larger gain for Jerseys reflects the higher heritability of yield traits used for Jerseys. Another benefit of cow adjustment was that SNP effects in the pseudo-autosomal region of the X chromosome that had extreme values without cow adjustment were in the expected range with adjustment. Regression coefficients ranged from 0.76 (sire calving ease) to 1.09 (DPR) for Holsteins. Jersey and Brown Swiss coefficients had wider

Table 3: Differences in mean PTA between genotyped and all progeny-tested Holstein bulls and standard deviations (SD) of PTA

Trait	PTA difference	SD of PTA	PTA difference/SD
Milk (kg)	34.0	293.0	0.12
Fat (kg)	1.5	10.6	0.15
Protein (kg)	1.1	7.5	0.15
PL (months)	0.6	2.2	0.29
SCS	0.0	0.2	-0.24
DPR (%)	0.3	1.4	0.20

ranges with the most extreme value for DPR. Regression coefficients close to 1 indicate that evaluations are successful in predicting the actual magnitude of differences among animals.

Table 3 shows that mean PTA and SD of genotyped Holstein bulls were similar to those of all Holstein bulls progeny tested at that time. Genotyped bulls were only superior genetically to progeny-tested bulls by <0.3 SD units.

Grouping the predicted bulls by their traditional protein evaluations did not have an effect on REL gain. The REL gain for each of the three groups was nearly the same as overall gain.

Conclusion

Genomic information provides a substantial increase in evaluation REL and has been the basis for large changes in acquisition of young bulls and marketing of semen before progeny testing. Genomic evaluations of young bulls have an average REL of >70% for yield traits. Validation tests show genomic predictions to be good predictors of future performance. Gains in REL will continue to increase as predictor animals are added. Cows contribute to increased evaluation accuracy if their traditional evaluations are adjusted.

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