

## Including cow information in genomic prediction of Holstein dairy cattle in the US

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**ABSTRACT:** The number of females genotyped in the US has increased to 12,650 per month comprising 74% of the total genotypes received in 2013. The objective of this study was to evaluate the accuracy of cow and bull traditional information in the genomic evaluation system. Cutoff studies to determine gains in reliability due to the addition of genomic information were compared for three predictor populations, cows only, bulls only and cows and bulls. The addition of cow information to that of bulls increased genomic reliability by 0.4 percentage points across all traits. The use of cow information only in the predictor population can be used for genomic predictions. However, the addition of cow data to data from the large number of high reliability bulls in the US system has only a small benefit.

**Keywords:** single nucleotide polymorphism; genomic evaluation; dairy cattle; genetics

### Introduction

Genomic testing of cows has increased since the first unofficial USDA genomic evaluations were released in 2008 (Wiggans et al., 2011a). The number of females genotyped monthly has increased from approximately 1,800 per month in 2010 to 12,650 per month in 2013. In addition to their increase in number, they are increasing as a proportion of total genotypes going from 38% in 2010 to 74% in 2013 (figure 1).

Many countries with genomic evaluations do not include cows in the predictor population (Schenkel et al., 2009; Reinhardt et al., 2009; Spelman et al., 2010). This reflects concern about bias in cow evaluations and complexity involved in using them.

To incorporate traditional evaluations of cows into the genomic evaluation system, two adjustments have been made to the traditional data. The first reduced the mean and variance of genomic cows to be similar to bull traditional evaluations (Wiggans et al., 2011b). The second adjustment applied to all cows to restore comparability of the two groups by reducing the deregressed Mendelian sampling within birth year groups (Wiggans et al., 2012).

In recent years, female genomic testing has become a way of making breeding decisions. In breeds other than Holstein, with few additional bulls with traditional evaluations to genotype the primary opportunity for the new data to improve genomic predictions is from

females. The objective of this study was to evaluate the accuracy of cow and bull traditional information in the genomic evaluation system.

### Materials and Methods

**Data.** The data collected for the December 2013 genomic evaluation was used in a cutoff study (VanRaden et al., 2009) to determine gains in reliability due to the addition of genomic information for three predictor populations. The first predictor population (cow only) included 30,852 cows, the second predictor population (bull only) included 21,883 bulls and the third (both) included 52,735 cows and bulls with traditional evaluations by August 2012. The validation set of bulls included animals with a traditional evaluation by December 2013. The number of bulls in the validation set varied by trait and ranged from 337 to 1486. Gains in reliability were calculated as the difference between genomic reliability of the validation set, which included SNP and polygenic effects estimated from the August 2012 predictor populations (genotyped animals with traditional evaluations) and August 2012 traditional parent averages, and parent average reliability.

### Results and Discussion

Table 1 shows gains in reliability over parent average for the three predictor populations. The addition of cow information increased genomic reliability by 0.4 percentage points across all traits excluding net merit. Type traits benefited the most from the additional information, increasing by 0.6 points followed by 0.5 for the yield traits. Overall, fitness traits were more accurately predicted using only bull information. This is especially true for net merit, which includes cow yield information that has not been adjusted by the second cow adjustments. Daughter pregnancy rate and heifer conception rate were most negatively influenced by the addition of cow information.

If the predictor population contains only cow information, genomic evaluation of young bulls is possible with an average gain in reliability of 20.4 percentage points across traits excluding daughter pregnancy rate and heifer conception rate. The inclusion of cow data becomes significantly less influential on genomic accuracy of predictions because the bulls have already provided the majority of the benefit that is attainable from genomics.

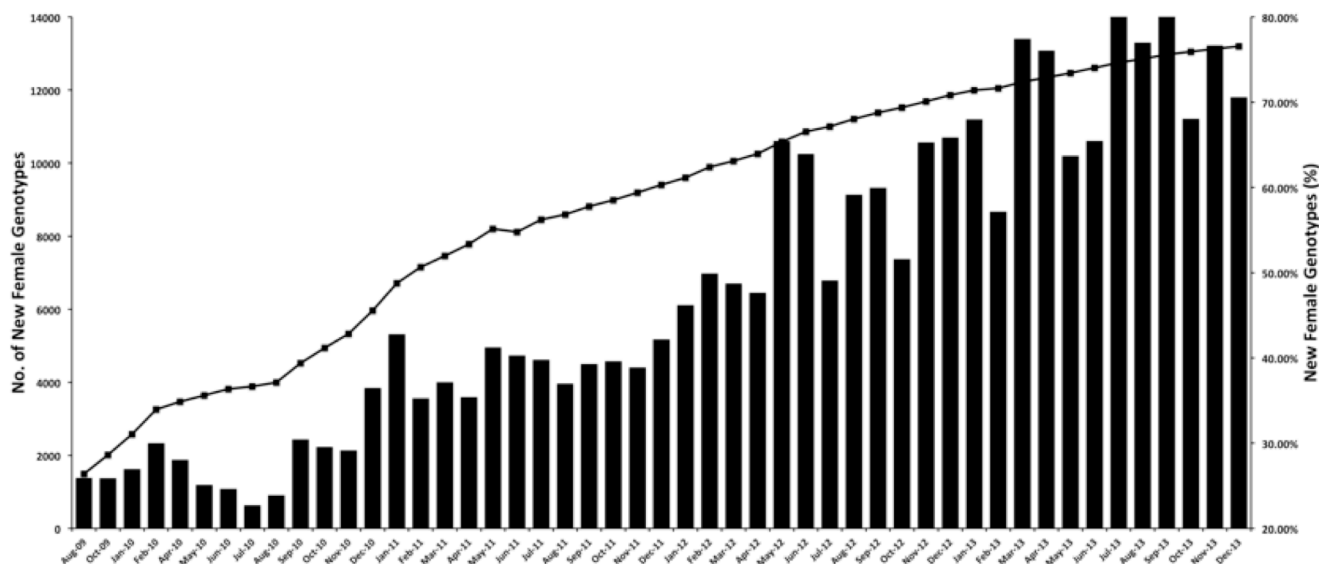


Figure 1. Number of female genotypes received monthly and percentage of total data received from females.

Table 1. Observed reliabilities in December 2013 for traditional parent average and gains in reliability over parent average reliability by trait for predictor populations<sup>1</sup> including cows only, bulls only and bulls and cows.

Trait	Validation Bulls (no.) <sup>2</sup>	Parent Average	Gain <sup>3</sup>		
			Cows <sup>4</sup>	Bulls <sup>5</sup>	Both <sup>6</sup>
Milk	1486	40.5	26.2	34.9	35.8*
Fat	1486	40.5	21.9	33.9*	33.3
Protein	1486	40.5	16.8	25.8	26.0*
Fat percent	1486	40.5	51.0	58.5	59.3*
Protein percent	1486	40.5	40.4	49.2	50.3*
Net merit	1486	35.1	20.9	55.1*	46.0
Productive life	1486	35.3	21.4	54.9	55.2*
Somatic cell score	1484	37.5	16.9	30.3	31.1*
Daughter pregnancy rate	1287	34.9	-5.0	23.3*	22.6
Heifer conception rate	1377	28.2	-3.2	28.3*	25.1
Cow conception rate	1063	28.6	19.5	56.9	57.4*
Single trait productive life	337	34.4	1.8	6.5	7.4*
Final score	934	36.3	17.7	27.0*	26.0
Stature	934	37.9	24.0	33.3	34.0*
Strength	934	37.2	21.8	29.5	31.3*
Dairy form	932	37.1	24.1	37.7*	36.9
Foot Angle	934	36.5	11.9	15.9	19.0*
Rear legs (side view)	934	37.0	13.9	20.3	21.5*
Body depth	934	37.5	23.6	32.6	34.0*
Rump angle	934	37.5	20.7	34.7*	34.1
Rump width	934	36.8	19.7	30.7	31.7*
Fore udder attachment	934	37.3	23.1	40.5*	39.4
Rear udder height	934	37.1	14.3	20.4*	19.8
Udder depth	934	37.8	26.3	44.0	44.2*
Udder cleft	934	37.0	19.0	21.0	23.6*
Front teat placement	934	37.4	17.9	29.3	29.9*
Teat length	934	37.6	15.4	26.3	26.8*
Rear legs (rear view)	934	36.3	10.6	23.8*	23.7
Feet and legs	934	36.4	9.6	18.3	18.7*
Rear teat placement	932	37.6	20.0	30.5	32.0*

<sup>1</sup>Includes SNP and polygenic effects estimated from bulls and/or cows with traditional evaluations by August 2012.

<sup>2</sup>Received traditional evaluation by December 2013 and have ten or more daughters.

<sup>3</sup>Genomic REL – parent average REL.

<sup>4</sup>Cows with traditional information by August 2012 in predictor population.

<sup>5</sup>Bulls with traditional information by August 2012 in predictor population.

<sup>6</sup>Bulls and Cows with traditional information by August 2012 in predictor population.

\*Trait with the highest reliability in the predictor population.

## Conclusion

Female genotypes have become a significant source of data collected each month for genomic evaluations. The use of cow information only in the predictor population can be used for genomic predictions. However, the inclusion of cow data with the large number of high reliability bulls in the US system has only a small benefit.

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