IMPLEMENTATION OF GENOMICS IN AUSTRALIAN DAIRY CATTLE

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SUMMARY

Genomic estimated breeding values were calculated for 32 traits and 2 indices for young bulls and well-recorded cows. On average, the reliability at least doubled in young bulls compared to the parent average, while in the cows reliabilities increased by about 10 to 20% relative to the traditional breeding value, as a result of including the genomic information. Traditional and genomic breeding values were of a similar magnitude on average in young bulls.

INTRODUCTION

The Australian Diary Herd Improvement Scheme (ADHIS) calculated the first genomic estimated breeding values for Holstein bulls for a limited number of traits in 2010. In collaboration with DPI Victoria this system was further developed and validated to include all the traits for which ADHIS performs routine genetic evaluations and both sexes.

This paper describes the methods applied and details the implementation for all ADHIS traits except calving ease. It shows the difference in reliability and range between the traditional and genomic breeding values for young bulls and well-recorded cows.

MATERIAL AND METHODS

At the end of 2010 a total of 3150 Holstein animals had been genotyped in Australia, of which 2617 were bulls born between 1955 and 2010 and 533 cows born between 1992 and 2006. A total of 320 bulls born in 2009 and 2010 were submitted by breeding companies for genomic evaluation as young bull, they had no daughters recorded for any trait. Of the 553 cows that had been genotyped, 549 were used based on the quality of their phenotypes. The current analysis is based on Australian data and Interbull proofs obtained up to December 2010, with Daughter Trait Deviations (DTD, equivalent to Daughter Yield Deviations for yield traits) estimated from data received by October 2010. Details on the traits analysed and indices calculated by ADHIS are on the FAQ page of www.adhis.com.au. Non-yield traits are expressed as relative breeding values. Within the group of yield traits and within the workability group all traits have the same reliability.

The method used for genomic evaluations at ADHIS is largely as described in detail for six traits by Nieuwhof *et al.* (2010). In short; QA checks are applied to genotypes, missing genotypes are imputed, Direct Genomics Breeding Values (DGV) are calculated using Ridge Regression-BLUP and DGVs are blended with traditional breeding values (ABV) to obtain Genomically Enhanced Breeding Values (GEBV). Adjustments made to this general approach include:

Imputation. Beagle software (Browning and Browning 2009) is used for the imputation of missing markers, mainly because of its much higher speed.

Interbull proofs. ADHIS incorporates results of international genetic evaluations for yield, conformation, somatic cell count, survival and calving ease performed by Interbull in the two official ABV runs. In between these runs ADHIS performs evaluation for breeding companies based on Australian data only called Provisional Breeding Values (PBV). For yield traits a bull would either get the Interbull or the Australian only proof. Breeding companies submit young sons of foreign bulls for genomic testing, and for these animals there can be a large discrepancy

between Interbull proofs and Australian only figures. In order to adjust for this, survival and conformation traits PBVs were also based on the latest Interbull analysis. This is still to be extended to somatic cell count and to calving ease once it is included in genomic analyses.

Reference set. The concept of genomic selection is based on the existence of a reference set of animals with a genotype and good quality phenotypes to estimate marker effects. The original approach of using a fixed reference population for all analyses does not make best use of the variety of existing data across a large number of traits though. The reference set is now defined specifically for each trait and consists of all bulls that have the trait recorded for at least 10 daughters. DTDs are not weighted according to number of daughters or reliability.

For yield traits in Holstein, the reference set consisted of 2231 bulls with an average of 618 daughters each. The reference set also exceeded 2000 bulls for fertility, workability traits, SCC and survival albeit with lower numbers of daughters. For most type traits there were 1470 reference bulls with 144 daughters on average. The lowest number of reference bulls was for teat placement rear; 526 with 133 daughters. Cows were not included in the reference set.

Blending. The blending procedure developed by Harris and Johnson (2010) corrects the weighted sum of the ABV and the DGV for the genetic variation that is captured by both the ABV and DGV (called $\hat{a}_N$) under the assumption that the DGV fully includes $\hat{a}_N$. Recent work at DPI Victoria shows that this is not the case and that for instance for yield only about 80% of $\hat{a}_N$ is included in the DGV (Haile-Mariam *et al.* in preparation). Subsequently, the blending procedure from Harris and Johnson (2010) was modified to subtract only the appropriate proportion of $\hat{a}_N$ in the calculation of the GEBV and its reliability.

RESULTS AND DISCUSSION

The reliability of GEBVs is markedly higher than that of the ABVs for all traits, showing the benefits of genomic evaluations. The effect is stronger in the young bulls who have a lowly reliable ABV (parent average), and in these animals the DGV's reliability is almost as high as the GEBV's. The increases here are similar to those found in a group of validation bulls (Nieuwhof *et al.* 2010), but breeding values are not as high. The reliability of DGVs is on average higher in the cows than in the young bulls, showing that the cows are more closely related to the reference population. The figures in Table 1 are based on all animals, including those that had an ABV with 0% reliability. Excluding these animals increases the ABV reliability considerably (especially for young bulls and depending on the trait) but has only a small (few %) effect on the GEBV.

Table 1. Reliability of ABV, DGV and GEBV in 320 young bulls and 533 cows for selected traits and indices

	Young bulls			Cows		
	ABV	DGV	GEBV	ABV	DGV	GEBV
Yield	0.22	0.49	0.50	0.52	0.54	0.65
SCC	0.21	0.40	0.42	0.42	0.47	0.55
Fertility	0.06	0.31	0.31	0.29	0.40	0.43
Workability	0.13	0.45	0.45	0.37	0.51	0.56
Overall type	0.16	0.36	0.36	0.25	0.43	0.48
Survival index	0.16	0.30	0.32	0.33	0.40	0.44
APR	0.19	0.36	0.43	0.44	0.47	0.57

Table 2. Mean ABV(SD), DGV(SD) and GEBV(SD) for young bulls and correlation between the three breeding values for bulls with an ABV

Trait	N	ABV	(SD)	DGV	(SD)	GEBV	(SD)	ABV-DGV	ABV-GEBV	DGV-GEBV
Protein (kg)	320	24	(9)	32	(9)	32	(9)	0.05	0.42	0.84
Fat (kg)	320	26	(12)	19	(16)	24	(15)	0.18	0.45	0.89
Milk (l)	320	710	(375)	936	(424)	911	(432)	0.19	0.53	0.87
SCC	319	118	(13)	112	(13)	119	(17)	0.57	0.81	0.93
Fertility	193	99	(1)	99	(2)	99	(2)	0.44	0.55	0.97
Survival	312	103	(2)	102	(1)	104	(2)	0.24	0.77	0.74
Milk. speed	245	102	(0)	101	(1)	102	(1)	0.08	0.32	0.92
Temperament	245	101	(0)	101	(0)	101	(0)	0.26	0.57	0.86
Likeability	245	102	(1)	101	(0)	102	(1)	0.32	0.61	0.82
Angularity	306	102	(2)	101	(2)	102	(2)	0.34	0.54	0.65
Body depth	306	101	(3)	103	(4)	103	(5)	0.45	0.67	0.93
Bone quality	181	100	(2)	100	(2)	100	(2)	0.41	0.63	0.91
Central lig.	306	104	(3)	101	(2)	104	(2)	0.08	0.73	0.62
Chest width	306	100	(3)	101	(2)	101	(3)	0.49	0.66	0.93
Foot angle	306	102	(3)	100	(2)	102	(3)	0.29	0.83	0.73
Fore attachm	306	102	(2)	102	(3)	103	(3)	0.38	0.66	0.89
Loin strength	181	100	(3)	103	(3)	102	(4)	0.68	0.88	0.93
Mamm. score	320	104	(2)	103	(2)	105	(3)	0.31	0.64	0.86
Muzzle width	181	100	(4)	101	(2)	101	(3)	0.70	0.81	0.95
Overall type	306	103	(2)	104	(2)	105	(3)	0.27	0.56	0.87
Pin set	306	102	(3)	103	(3)	104	(5)	0.33	0.73	0.86
Pin width	306	104	(3)	104	(3)	106	(4)	0.47	0.76	0.86
Rear leg RV	306	100	(2)	101	(2)	101	(2)	0.47	0.71	0.91
Rear set	306	97	(2)	98	(1)	97	(2)	0.43	0.85	0.80
Rear AH	306	104	(3)	103	(3)	104	(4)	0.48	0.75	0.89
Rear AW	181	103	(2)	105	(3)	105	(3)	0.41	0.65	0.91
Stature	306	103	(5)	103	(4)	104	(6)	0.54	0.86	0.86
Teat length	306	96	(5)	97	(6)	96	(8)	0.48	0.75	0.91
Teat PF	306	106	(3)	104	(5)	106	(5)	0.27	0.63	0.86
Teat PR	306	103	(3)	101	(2)	103	(3)	0.34	0.82	0.75
Udder depth	306	105	(5)	100	(5)	103	(6)	0.28	0.77	0.74
Udder texture	181	101	(2)	103	(2)	102	(2)	0.37	0.61	0.87

The mean ABV (equivalent to the parent average in these bulls), DGV and GEBV in Table 2 were calculated for the young bulls that had an ABV with reliability greater than 0. For most traits, the mean ABV and GEBV are generally at a very similar level and show no indication that the ABVs for these young bulls were overestimated. The exceptions are protein and overall type where the GEBV is considerably higher than the ABV, this is different from earlier results (Nieuwhof *et al.* 2010) and may reflect a difference in the group of bulls; here we consider all

genotyped bulls, earlier only those that went on to get a good number of daughters were included in the analysis. As expected GEBVs have a larger standard deviation than ABVs for most traits.

The correlation between ABV (parent average) and DGV is very low for yield traits (< 0.2), and is higher for most other traits. The correlation between ABV and GEBV ranges from 0.32 for milking speed to 0.88 for loin, with yield traits again at the lower end. The DGV and GEBV are highly correlated for most traits. Because of the low reliability of ABVs, a low correlation between ABV and GEBV means that there is real value in adding genomic information to the evaluation. High correlations tend to occur where there are fewer reference bulls, indicating that the DGV is estimated less accurately. It must be noted that correlations are estimated in a small and selected sample and may poorly reflect correlations at population level.

For cows, means for selected traits are presented in Table 3. There is some tendency here for the GEBVs to be lower than the ABVs, which might indicate some selection, as is to be expected in older cows. The correlations between the various breeding values are higher than in the young bulls, which will be associated with the higher reliability of both the ABV and DGV. The mean ABV and GEBV for these cows is lower than for the considerably younger bulls with the exception of fertility, which is probably due to a combination of genetic progress and bull selection. The standard deviation of the GEBVs is slightly higher than for the ABVs for most traits.

Table 3. Mean ABV(SD), DGV(SD) and GEBV(SD) for cows and correlation between the three breeding values for bulls with an ABV

| Trait | N | Mean | | | | | | Correlation | | |
		ABV	(SD)	DGV	(SD)	GEBV	(SD)	ABV-DGV	ABV-GEBV	DGV-GEBV
Protein	533	2	(11)	1	(12)	-1	(13)	0.65	0.87	0.90
Fat	533	3	(16)	-4	(16)	-2	(18)	0.52	0.84	0.85
Milk	533	49	(424)	42	(504)	-26	(538)	0.63	0.86	0.90
SCC	533	101	(17)	97	(13)	98	(18)	0.62	0.90	0.88
Fertility	533	102	(2)	101	(2)	102	(3)	0.52	0.80	0.90
Survival	533	100	(2)	99	(2)	99	(3)	0.45	0.88	0.79
Milk Speed	533	100	(3)	100	(2)	100	(2)	0.55	0.89	0.83
Temperament	533	100	(2)	100	(1)	100	(2)	0.53	0.86	0.85
Likeability	533	100	(2)	99	(1)	99	(2)	0.52	0.85	0.85
Overall type	322	98	(4)	96	(4)	95	(5)	0.52	0.86	0.86

CONCLUSIONS

For the first time, genomic evaluations were conducted for all ADHIS traits except calving ease. In young bulls without daughters on average the reliabilities at least doubled compared to the parent average. In well-recorded cows the increase in reliability was about 10 to 20%. The average ABV (parent average) in young bulls is at a similar level as the GEBV.

REFERENCES

Browning B.L. and Browning S.R. (2009) *Am J Hum Genet* **84**:210.
Harris B.L. and Johnson D.L. (2010) *J. Dairy Sci.* **93**: 1243.
Nieuwhof G.J., Beard K.T., Konstantinov K.V., Bowman P.J, and Hayes B.J. (2010) *Interbull workshop Riga 2010.*