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ASSESSMENT OF GENOMIC PREDICTIONS FOR FEEDLOT AND CARCASE TRAITS IN AUSTRALIAN ANGUS STEERS

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SUMMARY

Improving feedlot performance, carcase weight and quality is a primary goal of the beef industry globally. Here we used data from 3,408 Australian Angus steers from seven birth cohorts (2011 to 2017) with genotypes for 45,152 SNPs. We report genetic parameter estimates and accuracies of genomic estimated breeding values (GEBV) for feedlot and carcase traits, namely feedlot average daily gain (ADG), carcase weight (CWT) and carcase Meat Standard Australia marbling score (MBL). Prediction accuracies were estimated based on traditional method as well as method LR. The average prediction accuracies across cohorts assessed with the traditional method were 0.28 (ADG), 0.49 (CWT) and 0.50 (MBL), while method LR accuracies were 0.47 (ADG), 0.64 (CWT) and 0.59 (MBL). We found a strong correlation (0.74, P-value<0.001) between traditional accuracies and method LR accuracies. Heritability estimates were moderate to large (0.29 for ADG, 0.53 for CWT and 0.41 for MBL). The metrics of GEBV quality and heritabilities reported here suggest good potential for accurate genomic selection of Australian Angus for feedlot performance and carcase characteristics.

INTRODUCTION

Genomic selection represents a revolution in animal breeding. It enables the identification of superior animals through the estimation of genomic breeding values (GEBVs) for relevant quantitative traits (Goddard *et al*. 2010; Hayes *et al*. 2013). But the accuracy of GEBVs depends on several aspects including the size of the reference population and heritability of the trait (Goddard and Hayes 2009).

In this sense, Legarra and Reverter (2018) have proposed the method LR, which provides estimates of accuracy and biases by comparing genomic predictions based on partial and whole data. This method has been successfully applied to data from several different species (Aliakbari *et al.* 2020; Chu *et al.* 2019; Macedo *et al.* 2020; Silva *et al.* 2019).

Here we used method LR and a traditional method to evaluate the accuracy of genomic estimates in Australian Angus cattle. Angus is the dominant breed in the Australian cattle herd with an estimated 5.6 million females influenced by Angus genetics, accounting for 48% of the national female heard (Angus Australia 2019). Considering its importance, we aimed at determining the potential for accurate genomic selection of Australian Angus for feedlot performance and carcase characteristics.

MATERIALS AND METHODS

The dataset used for this study was collected as part of the Australian Angus Sire Benchmarking Program (ASBP). It includes phenotypes, genotypes, and fixed effect information of 3,408 Australian Angus steers from seven year of birth cohorts (YOB, 2011 to 2017) and imputed genotyped for 45,152 autosomal SNPs. The steers represent 12 breeding properties and 294 sires with an average of 11.5 progeny per sire, ranging from 1 to 27. The number of animals and sires (in

brackets) in YOB cohorts 2011 to 2017 are respectively 361 (35), 514 (48), 579 (44), 274 (25), 569 (49), 575 (63) and 536 (56).

Three phenotypes were analysed, including feedlot average daily gain (ADG, 1.59 ± 0.33kg/d), carcase weight (CWT, 432.99 ± 65.60kg) and Meat Standard Australia marbling score (MLB, 494.66 ± 122.54). Variance components, heritabilities and genetic correlations were estimated using Qxpak5 (Pérez-Enciso and Misztal 2011). The linear mixed model used to analyse all traits contained the fixed effects of contemporary group (CG), including property of origin, year and month of birth, and date of measurement, age of dam (AOD) at birth of calf in years and the linear covariate of age at measurement. Contemporary groups were different for each phenotype due to the different measurement dates. The random additive polygenic and residual effects were fitted with assumed distributions N($\mathbf{0}$, $\mathbf{G}\otimes\mathbf{V_G}$) and N($\mathbf{0}$, $\mathbf{I}\otimes\mathbf{V_R}$), respectively, where $\mathbf{G}$ represents the genomic relationship matrix (GRM) generated using the first method of VanRaden (2008), $\mathbf{V_G}$ is the genetic covariance matrix, $\mathbf{I}$ is an identity matrix, $\mathbf{V_R}$ is the residual covariance matrix and $\otimes$ represents the Kronecker product. The analyses were undertaken in two stages. First, one multivariate (3-variate) analysis was performed with all traits. The resulting GEBV ($\hat{\mathbf{u}}_\mathbf{w}$) from this multivariate analysis, based on the whole dataset, was used as the calibration in the computation of accuracy and bias. Next, a series of single-trait analyses were undertaken where the values from animals from a given YOB cohort were treated as missing. The resulting GEBV ($\hat{\mathbf{u}}_\mathbf{p}$) from these univariate analyses based on partial data were used as the validation.

To ascertain the quality of the resulting GEBV in the validation population we used: 1) Traditional accuracy, calculated as the Pearson correlation between a GEBV and its associated phenotype adjusted for fixed effects for individuals in the validation population, divided by the square root of heritability (Bolormaa *et al*. 2013); 2) Method LR Bias, calculated as the difference between the average GEBV of individuals in the validation population minus that using the calibration data; 3) Method LR Dispersion, measured for individuals in the validation population from the slope of the regression of $\hat{\mathbf{u}}_\mathbf{w}$ on $\hat{\mathbf{u}}_\mathbf{p}$; and 4) Method LR accuracy, computed for individuals in the validation population according to Legarra and Reverter (2018) as follows:

$$\mathrm{ACC_{LR}} = \sqrt{\frac{cov(\hat{\boldsymbol{u}}_w, \hat{\boldsymbol{u}}_p)}{(1+\bar{F}-2\bar{f})\sigma^2_{g,\infty}}}$$

Where $\bar{F}$ is the average inbreeding coefficient, $2\bar{f}$ is the average relationship between individuals, and $\sigma^2_{g,\infty}$ is the genetic variance at equilibrium in a population under selection which, assuming the individuals in the validation population are not under selection, can be estimated by the additive genetic variance estimated from the partial dataset.

RESULTS AND DISCUSSION

Heritability estimates were 0.30 for ADG, 0.53 for CWT and 0.41 for MBL which are well within reported values in literature. For instance, Somavilla *et al.* (2017) using Bayesian GBLUP to evaluate feedlot ADG in Nellore cattle found a heritability of 0.31. For the carcase traits, Su *et al.* (2017) working with Hereford and admixed Simmental reported heritabilities of 0.48 and 0.43 for marbling score and 0.51 and 0.34 for CWT, respectively.

Genetic correlations were high and positive between ADG and CWT (0.64) and close to zero between those 2 traits and MBL (0.05 and 0.04, respectively). These results corroborate literature that have reported low correlations between live/carcass weight and traits such as fat deposition and marbling (Nkrumah *et al*. 2007).

The metrics of GEBV quality are presented in Table 1. Traditional accuracies were 0.28 (ADG), 0.49 (CWT) and 0.50 (MBL), while method LR accuracies were 0.47 (ADG), 0.64 (CWT) and 0.59

(MBL). This is in accordance with the literature that reports greater accuracy for carcase traits than for live animal body composition traits (Boerner *et al.* 2014) and increased accuracy for traits with a higher heritability (Fernandes Júnior *et al.* 2016). We found a strong correlation (0.74, P<0.001) between traditional accuracy and Method LR accuracy (Figure 1). Values of bias for all the traits were fairly close to zero, showing an absence of bias. In the absence of bias, the expected value of dispersion is 1, which was observed for all traits.

Table 1. Traditional accuracy (ACC_T) and method LR accuracy (ACC_{LR}), bias ($Bias_{LR}$) and dispersion ($Disp_{LR}$) of GEBV for feedlot average daily gain (ADG), carcase weight (CWT) and marbling score (MBL), based on a 7-way cross-validation schema

	ADG				CWT				MBL			
	Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max
ACC_T	0.28	0.11	0.08	0.42	0.49	0.07	0.40	0.58	0.50	0.06	0.43	0.60
ACC_{LR}	0.47	0.04	0.42	0.53	0.64	0.05	0.57	0.67	0.59	0.05	0.53	0.67
$Bias_{LR}$	0.00	0.01	-0.01	0.01	0.27	0.61	-0.54	1.20	-0.08	1.71	-2.14	2.13
$Disp_{LR}$	0.97	0.15	0.74	1.17	0.99	0.09	0.83	1.10	0.98	0.09	0.88	1.13

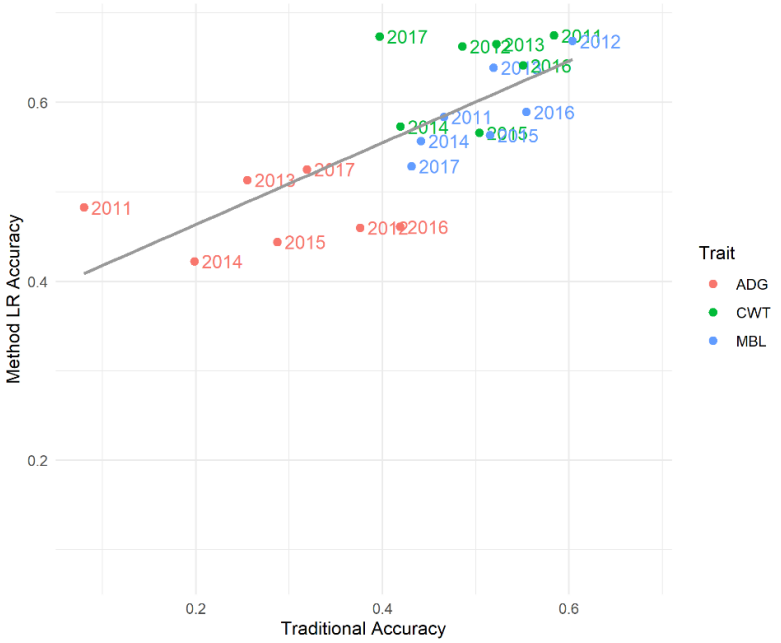

Figure 1. Relationship between traditional accuracy and Method LR accuracy for feedlot average daily gain (ADG), carcase weight (CWT) and carcase marbling score (MBL) according to the 7-way cross-validation scheme based on year of birth cohorts

The relationship between heritability and GEBV accuracy is also reflected in the phenotypic differences between validation animals in the highest and lowest GEBV quartile (Table 2). Based on SD units, ADG shows a Q1-Q4 difference of 0.35, CTW shows 0.93 and MBL 0.89. This demonstrates that the higher the GEBV accuracy, the higher the genetic gain expected when selecting elite bulls to sire the next generation.

Table 2. Difference between highest and lowest quartile for adjusted phenotypes (feedlot average daily gain - ADG, carcase weight - CWT and marbling score - MBL) based on GEBV ranking

Cohort	ADG	CWT	MBL
2011	0.00	33.57	103.47
2012	0.14	33.25	116.36
2013	0.08	34.44	99.20
2014	0.10	25.90	78.60
2015	0.08	28.36	85.45
2016	0.13	31.51	86.56
2017	0.09	20.53	60.19
Average	0.09	29.65	89.98
Average/SD*	0.35	0.94	0.89

*Standard deviation of adjusted phenotypes

CONCLUSIONS

The metrics of GEBV quality based on method LR, including accuracy, bias, and dispersion, as well as the heritabilities reported here, suggest good potential for accurate genomic selection of Australian Angus for the analysed traits. Further analyses are being undertaken to include other relevant feedlot and carcass traits.

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