INVESTIGATING RELATIONSHIP BETWEEN TRAITS ASSOCIATED WITH EATING QUALITY AND MARKET END POINT

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SUMMARY

BREEDPLAN reports estimated breeding values (EBVs) for many traits, but with the exception of carcass weight and rib fat, there are no EBVs specifically for the inputs into the Meat Standards Australia (MSA) Index that producers can use to make genetic progress in eating quality. Further it is not known how selection using BREEDPLAN EBVs influences the MSA Index and if these relationships are the same for different market endpoints. The motivation behind this study was to examine the extent to which MSA Index of commercial animals is related to EBVs of sires.

INTRODUCTION

With the development of Meat Standards Australia (MSA, Polkinghorne *et al.* 2008) and MSA Index, the interest by the industry to improve eating quality through genetic selection has been heightened. In investigating genetics underlying eating quality and carcass traits, Reverter *et al.* (2003), noted that it was important to determine whether there were significant genotype by environment (GxE) interactions for finishing systems (pasture- vs. feedlot-finished). Reverter *et al.* (2003) and Johnston *et al.* (2003) reported on genetic parameters for temperate cattle breeds for feedlot- vs. pasture-finished for a range of growth, body composition, carcass and meat quality traits. They reported generally increasing additive genetic variance with increasing carcass weight end points but minimal GxE and subsequent re-ranking of sires. In a study of 1.7M carcass records from 37,637 lots (slaughter groups) from the MSA database for cattle from nine processing plants in southern Australia from 2010-2013 Hebart *et al.* (2016) investigated the relationship between carcass end point defined either by weight or marbling and phenotypic variance. Hebart *et al.* (2016) found that increased lot mean carcass weight was associated with increasing phenotypic variance in carcass weight. Furthermore, higher lot mean MSA Marbling and carcass weight was associated with increased phenotypic variance in MSA Marbling. How eating quality traits respond to selection is a function of the selection intensity, heritability and the phenotypic variance of the traits. Currently producers can select for increased intramuscular fat (IMF) using BREEDPLAN estimated breeding values (EBVs) to improve marbling and in turn increase MSA Index. Differences in the phenotypic variance have the potential to change the magnitude of the regression coefficient for MSA Marbling on BREEDPLAN IMF EBV and, therefore, of the relationship between IMF EBV and MSA Index. The regression coefficient is calculated as:

$$b_{MSA,EBV} = r_G \times \frac{\sqrt{h^2} \times \sigma_P}{\sigma_{EBV}}$$

which is a function of the genetic correlation (r_G) between the traits (could be same trait at different endpoints), the heritability (h^2) of the trait, variation in the carcass trait (σ_P) and the variation in EBV (σ_{EBV}). Since the genetic correlation between traits, the heritability and the variation in EBV are likely to remain constant any scale effect observed in the variation of carcass traits is likely to have the greatest effect on the regression coefficient estimate. The motivation behind this study is to examine the extent to which MSA Index is related to estimated breeding values (EBVs) of sires for different market end points.

MATERIALS AND METHODS

Data from 12 industry or research data sets totalling 6,997 animals from four breeds (Angus, Charolais, Hereford and Limousin) and 433 sires have been included for analysis. The datasets are Maternal Productivity (MP – Vasse) (Pitchford *et al.* 2017), 4 x Regional Combinations (RC – NSW, RC – SA, RC – WA, RC – Vic.) animals (McKiernan *et al.* 2005), Rockdale (Herd *et al.* 2017) and Trangie (Arthur *et al.* 2005). In addition, three Beef Information Nucleus datasets (BIN, Angus BIN, Charolais BIN, and Hereford BIN) and data from two Team Te Mania herds (Central West NSW with calves born in early spring, and western Victorian autumn calving) were included. The datasets contain a range of growth paths (slow vs. fast), finishing regimes (Short feedlot <200 days, Long feedlot >200 days and Pasture) and carcass end point (200-500kg carcass weight) included in the analysis.

The carcass traits measured included hot standard carcass weight (HSCW, kg), rib fat (Rib, mm), intramuscular fat (IMF %, measured in the laboratory), MSA marbling (Marb), and MSA Index. Carcass traits (IMF, MSA marbling, MSA Index, Rib, and HSCW) were regressed on BREEDPLAN sire EBVs (IMF EBV, Rib EBV, 600 day weight EBV) after taking into account contemporary groups (a concatenation of dataset, management group and kill date), appropriate genetic "line" effects (high IMF, high yield, high RFI etc.) and management (Pasture, Short-fed, Long-fed) for each dataset. Sire BREEDPLAN EBVs were standardised by subtracting the mean sire EBV of a breed and dataset group within each breed within each dataset to allow for between breed comparisons and to account for EBVs being estimated at different times for each dataset. A general linear model was fitted in ASReml (Gilmour *et al.* 2009) which included dataset contemporary groups as fixed effects, standardised sire EBVs and interactions between finishing system, breed, dataset and the standardised sire EBVs to determine if there was a significant difference in the magnitude and or direction of the relationships between carcass traits and sire EBVs.

Sire variance components were estimated in ASReml (Gilmour *et al.* 2009) for each of the 12 datasets to determine whether the genetic variance in MSA index and its input traits changes with carcass weight. The same fixed effects as used for the regression analysis (excluding the sire EBVs and interactions) were fitted. Sire was included as a random effect in the benchmark model. Additional random effects were tested as interactions with sire: finish by sire, breed by sire and dataset by sire were included in separate models with separate sire variance components for finish regime, breed and dataset estimated. The log likelihood ratio test statistic was calculated to determine if the additional random terms significantly improved the model.

RESULTS AND DISCUSSION

The regressions for all carcass traits regressed on their associated EBV were significant. There was a significant interaction demonstrating a different regression coefficient between the finish systems for all regressions. In all cases the regression coefficients were greater for the Long-fed cattle than the short and pasture which tended to be similar to each other. For Rib Fat on sire Rib EBV and IMF% regressed on sire IMF EBV the Long-finished coefficients were significantly greater than the Short and Pasture finished regression coefficients (Table 1). This difference was the greatest when IMF% was regressed on IMF EBV where there was a 6.5-fold difference between the Pasture and Long feeding regimes. Moreover, the effect of selecting for improved IMF EBV was almost 5 fold greater in long grain finished cattle than short for MSA marbling (Table 1). For every 1 % increase in sire IMF EBV the increase in MSA marbling was 36.7 MSA marbling scores in Long-fed cattle relative to 7.6 in Short-fed cattle. MSA index was most closely related to the IMF EBV with an increase in IMF EBV being associated with a significant increase in MSA Index with the Long finish almost 3 times greater than Pasture finished (Table 2). A 1 % increase in sire IMF EBV was worth 0.28 MSA Index points under a Long feedlot finishing regime relative to a 0.10 unit increase under Pasture

(Table 2). Similar results were observed for sire Rib and carcass weight EBVs where Long finished regression coefficients were significantly higher than pasture finished. There were no significant ($P<0.05$) differences between the breeds in their relationship between MSA Index and sire EBVs.

Including sire by finishing system and estimating separate sire variance components for each finishing system (i.e. placing a G structure on the data) resulted in a significant improvement to the model for all traits based on the likelihood ratio test statistic. For almost all traits the sire variance under a Long-fed finishing regime was significantly greater than both Short and Pasture (Table 3). The exception was MSA Index where the sire variance of the Short-fed cattle was higher than both Long and Pasture fed cattle. For HSCW, Rib Fat, and MSA marbling, the sire variance for Long-fed animals was between 4 and 6-fold higher than pasture finished cattle. The difference for IMF was even larger however there were fewer animals with IMF measured. The sire variances were larger than those estimated by Reverter *et al.* (2003) for temperate beef breeds.

Table 1. Finishing system regression coefficients for carcass traits on BREEDPLAN sire EBVs (± standard errors)

Finish	HSCW on CWT EBV	Rib Fat on Rib EBV	IMF% on IMF EBV	MSA Marbling on IMF EBV
Long	$0.72^a \pm 0.03$	$0.75^a \pm 0.04$	$1.08^a \pm 0.04$	$36.7^a \pm 1.9$
Short	$0.55^b \pm 0.06$	$0.21^b \pm 0.08$	$0.17^b \pm 0.13$	$7.6^b \pm 2.4$
Pasture	$0.48^b \pm 0.06$	$0.31^b \pm 0.09$	$0.15^b \pm 0.13$	$8.9^b \pm 2.8$
P-Value	0.009	<0.001	<0.001	<0.001

Different superscripts indicate significantly different regression coefficients between finishing systems.

Table 2. Finishing system regression coefficients for MSA Index on BREEDPLAN sire EBVs (± standard errors)

Finish	600D Wt EBV	CWT EBV	Rib EBV	IMF EBV
Long	0.012 ± 0.003	0.014 ± 0.002	0.003 ± 0.020	0.34 ± 0.03
Short	0.009 ± 0.003	0.010 ± 0.004	-0.085 ± 0.033	0.29 ± 0.06
Pasture	0.005 ± 0.003	0.002 ± 0.004	-0.023 ± 0.036	0.12 ± 0.07
P-Value	0.308	0.035	0.046	0.020

Table 3. Sire variances for each finishing system (± standard errors)

	HSCW	Rib Fat	IMF	Marbling	Index
Long	159 ± 27	3.03 ± 0.56	1.63 ± 0.27	1619 ± 286	0.34 ± 0.07
Short	82 ± 21	2.05 ± 0.42	0.22 ± 0.07	588 ± 112	0.63 ± 0.11
Pasture	39 ± 12	0.49 ± 0.19	0.04 ± 0.03	352 ± 107	0.07 ± 0.04

It was hypothesised that despite genetic correlations for marbling between various end points and finishing regimes being close to 1 the regression may change substantially depending on market end point. For example, where there is low variance, the regression coefficient of MSA marbling on IMF EBV is expected to be lower, in contrast where there is higher variance the regression coefficient

is expected to be higher. There appears to be systematic differences (increases) in variance of traits of interest such as MSA Marbling and IMF for heavier carcass weights (associated with Long fed feedlot) or faster growth paths. This highlights the importance of considering target market end point weight when reporting estimating breeding values.

CONCLUSIONS

This work has quantified relationships between carcass traits and sire BREEDPLAN EBVs with the regressions for all carcass traits regressed on their associated EBV being significant. Importantly, there was a significant interaction demonstrating a different regression coefficient between the finishing systems for regressions with greater regression coefficients observed for the Long-fed cattle than the Short and Pasture which tended to be similar to each other. At a commercial level, this will have major effects on the increase in MSA Index expected through genetic improvement for traits linked with eating quality depending on market end point.

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