MATERNAL PRODUCTIVITY IN INDUSTRY HERDS: PRELIMINARY RESULTS

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SUMMARY

This paper presents results of analyses of 60% of the data from the initial 3 years of a large maternal productivity study involving 8 Angus co-operator herds. The genetic parameter estimates for weight and body composition measured repeatedly in Angus females at different time points during the first 2 parities tended to be consistent with expectations based on previous single point estimates reported in the literature. Further analyses of these data, together with information on early life performance as yearlings and subsequent measures of maternal productivity, will provide unique information on the likely consequences of selection for traits associated with body composition.

INTRODUCTION

Growth and carcase traits have received much attention in beef genetic improvement programs, and Australian beef producers have been successful in achieving significant genetic gains in these traits (Johnston 2007). The Cooperative Research Centre for Beef Genetic Technologies (Beef CRC) is investing in the development of new DNA based tools to enable beef producers to achieve genetic improvement from their breeding programs in "difficult to measure" traits eg. feed efficiency, meat tenderness. However, breeders may not fully utilise new opportunities for genetic improvement without better knowledge about the potential impacts on performance traits of the breeding cow herd, here termed maternal productivity.

This paper describes the preliminary results of a Beef CRC project designed to address concerns about the potential negative impacts on maternal productivity that may accompany genetic selection for traits associated with body composition (e.g. feed conversion efficiency and carcase traits). The project will determine genetic relationships between body composition and components of breeding herd productivity and explore potential new early-life selection criteria for improving maternal traits. This paper describes results from analyses of a subset of the data from the initial 3 years of the project, where body composition measurements have been recorded in 8 Angus co-operator herds.

MATERIALS AND METHODS

Data. A total of 7,226 liveweight and ultrasound body composition measurements were made on 3,775 Angus females in 8 co-operator herds. These measurements were taken at 2 points during the annual production cycle (Pre-Calving and Weaning) during the first and second parities and represent approximately 60% of the final data expected. In this analysis, four traits were considered: weight (Wt); P8 (P8) and rib (Rib) fat measures; and eye muscle area (EMA). Each female could have up to 4 measurements of these traits: Pre-Calving (PC1) and Weaning (W1) in Parity 1, and Pre-Calving (PC2) and Weaning (W2) in Parity 2. There were various reasons for females not having a complete set of measurements; age of animal (Parity 2 not yet recorded), disposal from herd, missing on measurement day. Animals with incomplete pedigrees, missing birth date and trait measurements greater than 3 standard deviations from the contemporary group mean were removed from the analysis.

Model of analysis. Variance components were estimated using ASReml (Gilmour *et al.* 2006). The fixed effect of contemporary group (CG) was included in the model and single record contemporary groups were excluded from the analysis. Contemporary group definition included herd, calving season (spring or autumn), date of measurement and breeder-defined management group. Age of the animal on the date of first measurement was included as a covariate. Random effects fitted included a term for direct genetic effects. Pedigree records for all animals with records and 2 further generations of ancestors were used. Multivariate analyses of the same trait across the 4 different time points were conducted separately for each trait. In addition, multivariate analyses among the four different traits were conducted separately for each of the time points.

RESULTS AND DISCUSSION

Data. Table 1 contains summary statistics of the data for each parity. Phenotypic variance and trait averages for P8 fat increased steadily over the 4 time points. There was a trend in the other traits, however, for decreased phenotypic variance and/or trait average at Pre-Calving in Parity 2 compared to Weaning in Parity 1.

Table 1. Descriptive statistics, phenotypic variances (σ^2_p) and heritabilities (h^2) for traits of females recorded at Pre-Calving and Weaning in 1st and 2nd parities

	Average (SD)	Minimum	Maximum	σ^2_p *(SE)*	h^2 *(SE)*
Parity 1					
Pre-Calving (n=3,016)					
Age (days)	685 (35)	585	905	-	-
P8 fat (mm)	5.2 (2.6)	1	21	3.1 *(0.10)*	0.47 *(0.06)*
Rib fat (mm)	4.1 (1.9)	1	13	1.7 *(0.06)*	0.54 *(0.07)*
Weight (kg)	476 (68)	291	748	1,115 *(37)*	0.48 *(0.06)*
Eye Muscle Area (cm^2)	56 (11)	20	89	39 *(1.1)*	0.28 *(0.05)*
Weaning (n=1,527)					
Age (days)	895 (52)	785	1,151	-	-
P8 fat (mm)	6.2 (2.7)	1	28	5.8 *(0.25)*	0.40 *(0.09)*
Rib fat (mm)	5.5 (2.1)	1	24	3.7 *(0.16)*	0.34 *(0.08)*
Weight (kg)	530 (64)	303	760	2,117 *(83)*	0.21 *(0.07)*
Eye Muscle Area (cm^2)	63 (8)	30	89	38 *(1.5)*	0.26 *(0.07)*
Parity 2					
Pre-Calving (n=1,755)					
Age (days)	1,049 (38)	884	1,261	-	-
P8 fat (mm)	6.4 (3.3)	2	26	6.6 *(0.25)*	0.32 *(0.07)*
Rib fat (mm)	5.0 (2.3)	2	20	3.2 *(0.12)*	0.19 *(0.06)*
Weight (kg)	562 (65)	351	774	1,913 *(71)*	0.23 *(0.06)*
Eye Muscle Area (cm^2)	62 (10)	33	94	47 *(1.7)*	0.24 *(0.06)*
Weaning (n=924)					
Age (days)	1,258 (53)	1,129	1,454	-	-
P8 fat (mm)	9.1 (4.1)	2	26	9.3 *(0.51)*	0.43 *(0.11)*
Rib fat (mm)	7.6 (3.1)	2	20	5.6 *(0.31)*	0.39 *(0.11)*
Weight (kg)	597 (74)	402	846	2,673 *(139)*	0.31 *(0.10)*
Eye Muscle Area (cm^2)	67 (10)	37	97	41 *(2.1)*	0.23 *(0.09)*

Heritabilities (h^2) for P8 fat and EMA across the 4 time points were relatively stable and are similar to published estimates for yearling ultrasound scan measurements (eg. Meyer *et al.* 2004). The heritabilities for rib fat and weight fluctuated across the time points, with very high estimates

for both traits at the first time point (Pre-Calving in Parity 1). All heritabilities had large associated standard errors, particularly traits measured at Weaning in Parity 2.

Genetic correlations (r_g) and their associated standard errors between measurements of the same trait (weight, P8 fat, rib fat or EMA) across the 4 different time points are reported in Table 2. Very high positive r_g were observed among weight measurements at the 4 different time points, while r_g for P8 fat, rib fat and EMA were high to very high across all time points. For all traits, the highest r_g was observed between the same time point in different parities, while the lowest r_g occurred between Pre-Calving in Parity 1 and Weaning in Parity 2. For some traits, this latter r_g would indicate that significant re-ranking of animals would occur between those different time points, and that performance at Pre-Calving in Parity 1 for these traits is not a good indicator of performance at Weaning in Parity 2.

Table 2. Genetic correlations (SE) across time points for the same trait

Trait[*]	PC1-W1[**]	PC1-PC2[**]	PC1-W2[**]	W1-PC2	W1-W2	PC2-W2
Wt	0.91	0.98	0.90	0.92	0.90	0.92
	(0.06)	(0.03)	(0.07)	(0.06)	(0.10)	(0.05)
P8	0.78	0.91	0.73	0.85	0.94	0.87
	(0.08)	(0.06)	(0.09)	(0.06)	(0.05)	(0.06)
Rib	0.67	0.78	0.67	0.92	0.92	0.90
	(0.10)	(0.09)	(0.10)	(0.05)	(0.07)	(0.07)
EMA	0.76	0.93	0.64	0.84	0.89	0.82
	(0.11)	(0.07)	(0.16)	(0.09)	(0.14)	(0.12)

[*] Weight (Wt), P8 fat (P8), rib fat (Rib) and eye muscle area (EMA)
[**] Pre-Calving (PC1) and Weaning (W1) in Parity 1; Pre-Calving (PC2) and Weaning (W2) in Parity 2

Estimates of genetic correlations (and associated standard errors) between the 4 different traits within the same time point (Pre-Calving or Weaning in Parity 1, or Pre-Calving or Weaning in Parity 2) are reported in Table 3. The r_g between P8 and rib fat was consistently high across all time points and similar to earlier literature estimates (eg. Meyer *et al.* 2004). The r_g estimates between the fat traits and weight tended to be low and positive (highest at Weaning in both parities), except for weak negative correlations at Pre-Calving in Parity 2. Similar trends were observed for genetic correlation estimates between the fat measures and EMA. The r_g estimates between weight and EMA were low to moderate and positive, but fluctuated considerably across time.

Only approximately 60% of the target number of records for this project were available for this analysis. As more data become available, the parameter estimates reported above will be re-estimated with greater precision. In addition, further analyses will examine the phenotypic and genetic relationships between these measures and prior ultrasound and weight measurements taken at yearling age, and with subsequent maternal performance, including calf weaning weights, fertility (e.g. re-conception rates) and longevity (herd life). Genetic relationships between the present measures and structural soundness scores will also be examined on females that have been assessed for structural traits. All early-life measures will be examined especially for their usefulness as indicators of lifetime productivity.

Table 3. Genetic correlations (SE) between traits within time points

Time[*]	P8-Rib[**]	P8-Wt[**]	P8-EMA[**]	Rib-Wt	Rib-EMA	Wt-EMA
PC1	0.87	0.18	0.30	0.13	0.16	0.53
	(0.03)	(0.10)	(0.11)	(0.10)	(0.12)	(0.09)
W1	0.83	0.38	0.49	0.34	0.43	0.30
	(0.05)	(0.17)	(0.15)	(0.19)	(0.17)	(0.20)
PC2	0.82	-0.04	0.04	-0.12	-0.10	0.38
	(0.06)	(0.19)	(0.18)	(0.23)	(0.22)	(0.16)
W2	0.74	0.34	0.44	0.36	0.22	0.23
	(0.09)	(0.20)	(0.20)	(0.20)	(0.24)	(0.25)

[*] Pre-Calving (PC1) and Weaning (W1) in Parity 1; Pre-Calving (PC2) and Weaning (W2) in Parity 2
[**] Weight (Wt), P8 fat (P8), Rib fat (Rib) and eye muscle area (EMA)

CONCLUSIONS

Results of preliminary analyses of a large Beef CRC maternal productivity study showed genetic parameter estimates for traits of Angus females, measured at different time points during their first 2 parities, tended to be consistent with previous single point estimates from the literature. Further analyses of these data, together with measures of yearling performance and subsequent maternal productivity, will provide information on the likely consequences of selection for traits associated with body composition changes. In addition to identifying early indicators of lifetime maternal performance, this project will develop a comprehensive phenotypic database of breeding female performance and body composition on temperate genotypes which can be later used for evaluation and validation of the effect of future DNA markers.

ACKNOWLEDGMENTS

REFERENCES

Johnston, D. (2007) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **17**:8.

Gilmour, A.R., Gogel, B.J., Cullis, B.R., Welham, S.J. and Thompson, R. (2006) "ASReml User Guide Release 2.0" VSN International Ltd, Hemel Hempstead.

Meyer, K., Johnston, D. and Graser, H. (2004) *Aust. J. Agric. Res.* **55**:195.