

PRELIMINARY GENETIC PARAMETERS FOR METHANE PRODUCTION IN AUSTRALIAN BEEF CATTLE

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SUMMARY

This paper reports the first heritability estimates for methane traits in beef cattle, using records from 530 young Angus bulls and heifers measured for methane production in respiration chambers. Weight (WT) and ultrasound scan traits (eye muscle area: EMA; rump fat depth: P8; rib fat depth: RIB; intramuscular fat percentage: IMF) were also recorded on these animals in order to investigate the relationships between methane and production traits. Heritabilities for daily methane production (MP), methane production per unit feed intake (methane yield: MY) and methane production per unit weight (methane intensity: MI) were low to moderate (0.21, 0.19 and 0.23, respectively). Methane traits (MP, MY and MI) were not correlated, either phenotypically or genetically, with the body composition traits. These preliminary results show that there may be some potential to use genetic improvement to reduce methane emissions in beef cattle.

INTRODUCTION

Cattle and sheep emit methane, a potent greenhouse gas, but currently there are few technologies available to mitigate methane emissions in extensive beef production systems. Genetic improvement is capable of producing small but permanent and cumulative changes in performance, and is particularly useful in extensive production systems as found in majority of Australian beef herds. Thus, genetic improvement is an attractive approach for the mitigation of methane emissions in Australian beef cattle. In order to assess the viability of this mitigation approach, genetic variation in methane traits along with relationships with important production traits must be quantified. This paper provides preliminary heritability estimates for methane traits, along with estimates of phenotypic and genetic relationships with production traits.

MATERIALS AND METHODS

Progeny born in 2009 (n=218) and 2011 (n=312) from Angus cows in 2 research herds at the Agricultural Research Centre, Trangie NSW, were measured for methane production in 2011 and 2012 in 10 respiration chambers on the University of New England campus, Armidale NSW. For progeny born in 2009, males from both herds and females from one of the herds were measured for methane, while for progeny born in 2011, animals from both sexes in both herds were measured. Each year, animals were allocated into cohorts within herd and sex (n=40), fed a restricted diet (1.2-times the estimated energy requirement for maintenance) and groups of 10 animals were individually measured in the respiration chambers. The 530 animals were progeny of 38 sires (average 14 progeny per sire, range 1-33). Progeny of individual sires were stratified across groups and cohorts. Herd *et al.* (2013) provides details on the diet and measurement procedure.

Data. Methane production was measured over 2 x 24h consecutive periods. For animals born in 2011 these measurements were taken at approximately yearling age (mean=369 days). However, for animals born in 2009, these measurements were taken at approximately two years of

age (mean=748 days) due to delays in construction of the facility. Traits measured included pre-test weight (WT), dry matter intake (DMI), daily methane production (MP; litres of methane per day), methane production per unit feed intake (methane yield: MY) and methane production per unit weight (methane intensity: MI). Editing of records included removal of animals with incomplete pedigrees, missing birth date and trait measurements greater than 4 standard deviations from the contemporary group mean.

Live animal ultrasound scans were collected on all animals in the research herds at approximately 600 days of age by a certified ultrasound technician, including animals which had not been measured for methane. There were ultrasound scan records available on 750 animals, who were the progeny of 38 sires (average 20 progeny per sire, range 1-38). Traits recorded included eye muscle area (EMA), fat depth at the rump (P8) and rib (RIB) sites and intramuscular fat percentage (IMF).

Model of analysis. Variance components were estimated using ASReml (Gilmour *et al.* 2009). For methane and scan traits, the fixed effect of contemporary group (CG) was included in the model and single record contemporary groups were excluded from the analysis. For methane traits, CG definition included cohort and methane group and management group. Age of the animal on the date of measurement was included as a covariate for all methane traits, and WT was also included for the MP trait. For scan traits, CG definition was the same as for methane traits for those animals with a methane record. For animals without a methane record, CG definition included birth year, sex and management group. Age of the animal on the date of measurement was included as a covariate for all scan traits. 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. Bivariate analyses of all trait combinations were also conducted.

RESULTS AND DISCUSSION

Table 1 contains summary statistics for the methane test and body composition scan data. A large amount of variation was observed for both WT and age of methane measurement due to the older age of measurement of the animals born in 2009. The methane traits (MP, MY and MI) exhibited substantial phenotypic variation even after adjustments for DMI (MY) and WT (MI).

Table 1. Descriptive statistics for methane and body composition scan traits

	No. records	Average (SD)	Minimum	Maximum
<i>Methane traits</i>				
Age (days)	530	525 (192)	264	822
WT (kg)	530	410 (93)	229	670
DMI (kg/d)	530	6.9 (1.2)	4.6	9.5
MP (L/d)	530	205 (30)	122	350
MY (L/kg DMI)	530	29.9 (4.2)	15.9	41.2
MI (L/kg WT)	530	51.6 (9.4)	25.8	67.8
<i>Scan traits</i>				
Age (days)	750	613 (83)	483	791
EMA (cm ²)	750	59.9 (7.6)	35.0	96.0
P8 (mm)	750	5.5 (3.9)	1.0	32.0
RIB (mm)	750	3.8 (2.6)	1.0	18.0
IMF (%)	730	3.5 (1.2)	1.5	8.1

Genetic parameters for methane and scan traits are reported in Table 2. This study provides the first heritability estimates for methane traits in beef cattle. Heritabilities for methane traits (MP, MY and MI) were low to moderate (0.19-0.23), with relatively large associated standard errors.

Robinson *et al.* (2010) reported a low heritability (0.13) for MI in sheep, while Pinares-Patino *et al.* (2011) reported a moderate heritability (0.30) for MY, also in sheep. Several dairy studies have predicted MP using DMI, and heritabilities reported range from 0.12 (Cassandro *et al.*, 2010) to 0.35 (de Haas *et al.*, 2011) for MP and 0.58 (de Haas *et al.*, 2011) for MP adjusted for milk production (similar to MI in this study). Results from this study, along with other published estimates, indicate that there may be some potential to use genetic improvement to reduce methane emissions in livestock. However, further investigations involving larger numbers of animals are needed.

Heritabilities reported in this study for WT, EMA, P8 and IMF were very similar to published estimates in Australian Angus animals (Jeyaruban *et al.*, 2009; Meyer, 2005). While the heritability for RIB (0.63) was higher than reported estimates in young Angus animals (0.28-0.45; Meyer, 2005), it was similar to published estimates in Angus cows (Donoghue *et al.*, 2009).

Table 2. Genetic parameters (SE) for weight, methane and scan traits

	σ_a^2 (SE)	σ_e^2 (SE)	σ_p^2 (SE)	h^2 (SE)
WT	612 (210)	803 (172)	1,415 (101)	0.43 (0.13)
MP	72 (38)	271 (37)	343 (23)	0.21 (0.11)
MY	1.1 (0.6)	4.6 (0.6)	5.7 (0.4)	0.19 (0.10)
MI	4.1 (1.9)	13.7 (1.9)	17.8 (1.2)	0.23 (0.10)
EMA	13.0 (4.1)	18.5 (3.3)	31.5 (1.9)	0.41 (0.12)
P8	3.7 (0.9)	3.2 (0.7)	6.9 (0.4)	0.53 (0.12)
RIB	1.8 (0.4)	1.1 (0.3)	2.9 (0.2)	0.63 (0.12)
IMF	0.24 (0.07)	0.40 (0.06)	0.63 (0.04)	0.37 (0.10)

Phenotypic (r_p) and genetic (r_g) correlations and their associated standard errors between all traits are reported in Table 3. Large positive r_p (0.89-0.96) were observed among methane traits, indicating that, phenotypically, animals with higher MP also had higher MY and MI. Heavier animals had higher MP (0.58) and lower MI (-0.28), but no difference in MY (0.05) than lighter animals. In a dairy study, de Haas *et al.* (2011) reported a phenotypic correlation between predicted MP and milk production of 0.26. As expected, large positive phenotypic relationships were observed between the two measures of external fat (0.91; P8-RIB) and between external and internal fat measures (0.73-0.75; P8/RIB-IMF). Results from this study indicate that, phenotypically, there was no relationship between methane traits (MP, MY and MI) and scan traits (-0.16 to 0.07).

Large positive r_g (0.87-0.96) were observed among methane traits, indicating that, genetically, animals with higher MP also had higher MY and MI. While WT was highly positively correlated with MP (0.79), it was lowly positively correlated with MY (0.18) and lowly negatively correlated with MI (-0.23). Previous literature estimates for genetic correlations between predicted MP and milk production range from 0.31 (de Haas *et al.*, 2011) to 0.92 (Cassandro *et al.*, 2010), while de Haas *et al.* (2011) reported a large negative correlation (-0.87) between MI and milk production. As expected, large positive genetic relationships were observed between the two measures of subcutaneous fat (0.99; P8-RIB) and between subcutaneous and intramuscular fat measures (0.97-0.98; P8/RIB-IMF). In these preliminary results, no evidence of strong genetic relationships between methane traits and scan traits was observed (-0.23 to 0.29), indicating that selection for methane traits would have little impact on body composition. It should be noted that most of the genetic correlation estimates in this study have large standard errors and further investigations are warranted once more data are available. High correlations between the different methane traits (methane production, methane yield and methane intensity) indicate that, phenotypically and

Efficiency

genetically, methane is independent of feed intake.

Table 3. Genetic (above diagonal) and phenotypic (below diagonal) correlations (SE) for methane and scan traits

Trait	WT	MP	MY	MI	EMA	P8	RIB	IMF
WT	-	0.79 (0.12)	0.18 (0.30)	-0.23 (0.28)	0.55 (0.16)	-0.07 (0.21)	-0.01 (0.20)	0.08 (0.22)
MP	0.58 (0.03)	-	0.96 (0.04)	0.95 (0.04)	0.17 (0.29)	0.18 (0.25)	0.16 (0.25)	0.29 (0.27)
MY	0.05 (0.05)	0.93 (0.02)	-	0.87 (0.09)	-0.02 (0.30)	0.12 (0.26)	0.08 (0.26)	0.21 (0.28)
MI	-0.28 (0.05)	0.96 (0.03)	0.89 (0.01)	-	-0.23 (0.27)	0.15 (0.25)	0.14 (0.24)	0.21 (0.26)
EMA	0.44 (0.04)	-0.01 (0.05)	-0.03 (0.05)	-0.16 (0.05)	-	0.19 (0.19)	0.21 (0.18)	0.41 (0.18)
P8	0.18 (0.05)	0.04 (0.05)	0.06 (0.05)	-0.01 (0.05)	0.17 (0.04)	-	0.99 (0.01)	0.97 (0.04)
RIB	0.17 (0.05)	-0.004 (0.05)	0.01 (0.05)	-0.05 (0.05)	0.19 (0.04)	0.91 (0.01)	-	0.98 (0.03)
IMF	0.19 (0.05)	0.07 (0.05)	0.07 (0.05)	-0.01 (0.05)	0.19 (0.04)	0.75 (0.02)	0.73 (0.02)	-

CONCLUSIONS

These preliminary results show that genetic variation in methane emissions is present in these Angus cattle. No antagonistic phenotypic or genetic relationships between methane and body composition traits were identified. Thus, genetic improvement to reduce methane emissions may be possible, but further investigations involving larger numbers of animals are needed.

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REFERENCES

- Cassandro, M., Cecchinato, A., Battagin, M. and Penasa, M. (2010) Proc. 9th WCGALP, www.kongressband.de/wcgalp2010/assets/pdf/0837.pdf.
- de Haas, Y., Windig, J.J., Calus, M.P.L., Dijkstra, J., de Haan, M., Bannink, A. and Veerkamp, R.F. (2011) *J. Dairy Sci.* **94**:6122.
- Donoghue, K.A. and Parnell, P.F. (2009) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **18**: 117.
- Herd, R.M., Bird, S.H., Donoghue, K.A., Arthur, P.F. and Hegarty, R.F. (2013) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **20**: (This proceedings)
- Gilmour A.R., Cullis B.R., Welham S.J. and Thompson R. (2009) 'ASREML. Program user manual' NSW Agriculture, Orange Agricultural Institute, Forest Road, Orange, NSW, 2800, Australia.
- Jeyaruban, M.G., Johnston, D.J. and Graser, H.-U. (2009) *Anim. Prod. Sci.* **49**:1.
- Meyer, K. (2005) *Animal Science.* **81**:337.
- Pinares-Patino, C.S., McEwan, J.C., Dodds, K.G., Cardenas, E.A., Hegarty, R.S., Koolaard, J.P. and Clark, H. (2011) *Animal Feed Science and Technology.* **166-67**:210.
- Robinson, D.L., Goopy, J.P., Hegarty, R.S. and Vercoe, P.E. (2010) Proc. 9th WCGALP, www.kongressband.de/wcgalp2010/assets/pdf/0712.pdf.