DIVERGENT SELECTION FOR METHANE YIELD IN BEEF CATTLE

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SUMMARY

Genetic selection and breeding to reduce methane production is one option to reduce greenhouse gas emissions, but correlated responses in production traits also need to be considered. The objective of this study was to quantify the effect of divergent selection for methane yield (MY), on methane and body weight traits in Angus cattle. High and Low MY selection lines were created in each of two performance-recorded Angus research herds during the 2011 mating season. This study is a preliminary report on the divergence of these selection lines, as assessed by the performance of the 2013 born progeny. There was no significant selection line by herd interaction. Approximately half a generation of selection was achieved. There was a significant ($P<0.05$) divergence between the two lines in the selected trait, methane yield. This was also reflected in the significant ($P<0.05$) selection line differences in the residual methane (actual minus expected methane production) traits and also in the estimated breeding values for these traits. There were no significant selection line differences in birth, weaning and yearling weights.

INTRODUCTION

Ruminants emit methane, a potent greenhouse gas (GHG). Methane is the main GHG emitted by ruminants and is a by-product of enteric microbial fermentation of plant material mainly in the rumen (McAllister et al. 1996). Hence reducing enteric methane production is essential to any GHG emissions reduction strategy in livestock. Higher feed intake is associated with higher methane production in ruminants (Blaxter and Clapperton 1965; Pelchen and Peters 1998). Feed intake is highly correlated with growth and other production traits in ruminants (Arthur *et al.* 2001; Lancaster *et al.* 2009). Therefore, breeding animals for lower methane production *per se,* may have a detrimental impact on ruminant productivity due to reduced feed intake. Consequently there has been increased interest in the amount of methane produced per unit feed intake, also known as methane yield (MY).

In 2009, a research project was started at the Agricultural Research Centre at Trangie, NSW, Australia, to investigate the potential of genetic improvement to reduce methane GHG emissions in cattle. Details of the project have been reported by Donoghue et al. (2015). This study is one of the components of the main project, and it provides a preliminary report on the performance of cattle divergently selected for methane yield at yearling age. The objective of this study was to establish if breeding could be used to reduce methane production and what effect this would have on methane and body weight traits

MATERIALS AND METHODS

Cattle utilized in this study were from a performance recorded registered Angus stud, comprised of two research herds (an Autumn calving and a Spring calving herd), located at the Trangie Agricultural Research Centre, NSW. As part of the main project, cattle born in 2009, 2011, 2012 and 2013 were measured for methane production in 10 respiration chambers at the University of New England campus, Armidale, NSW. For cattle born in 2009, males from both herds and females from one of the herds were measured for methane at approximately two years of

age (mean=748 days) in 2011 due to delays in construction of the methane test facility. For cattle born in subsequent years, animals from both sexes in both herds were measured as yearlings. Animals were on a restricted (alfalfa and oaten hay chaff) ration of approximately 1.2 times their estimated daily energy requirement for maintenance, when measured for methane. Details on the methane measurement protocols have been published earlier by Herd *et al.* (2014).

This study commenced in 2011 with the establishment of High and Low MY selection lines in each of the 2 research herds, comprising 330 females. Due to the limited number of females tested for methane in each of the two herds, untested females were also randomly allocated to the selection lines and included as the foundation animals. Therefore the 2008, 2009 and 2011 born animals formed the foundation herd for this study. Foundation females were randomly allocated to the High MY line (High MY) (174 cows) and the Low MY line (Low MY) (156 cows), irrespective of their individual MY values. All 16 bulls used for mating had methane measurements. Within herds, the four bulls with the highest MY were allocated to the High MY line and the four bulls with the lowest MY to the Low MY line. The sole selection criterion for bulls in the High MY line and Low MY line was individual MY. Throughout the project bulls and heifers were mated at approximately 14 months of age, and bulls were used for only one mating season. Animals from each selection line were grazed together throughout the year, except during mating. Allocation of mates within selection line was completely random, except for the avoidance of half-sib and son-dam matings. All matings were by natural service and the breeding herd were on pasture all year round, with supplementary feed offered during times of limited pasture growth. A total of 304 and 264 (dams and 2013 drop progeny) animals were tested for MY in the high MY and Low MY selection lines respectively. The progeny of the selected sires were born in 2013. Calves (287) were reared by their dams until weaning and were on pasture all year except during methane measurement. Pastures comprised native and introduced perennial and annual grasses and forbs (Windmill grass, *Chloris truncate*; spear grass, *Stipa spp.*; barley grass, *Hordeum leporinum*; burr-medic, *Medicago spp.*; and crowsfoot, *Erodium spp.*).

Traits studied. The definitions of all the traits studied are provided in Table 1. Methane production was measured over 2 consecutive 24 hour periods. Traits measured included pre-test

Table 1. Definition of traits

Trait name	Abbreviation	Units	Definition
Pre-test weight	TWT	kg	Weight at time of methane test
Dry matter intake	DMI	kg/day	Dry matter intake during methane test
Methane production	MP	g/day	Methane produced
Methane yield	MY	g/kg	MP per unit DMI (MP/ DMI)
Residual methane$_B$	RMP$_B$	g/day	MP net of expected MP (expMP) from the DMI, with expMP obtained by formula of Blaxter and Clapperton (1965)
Residual methane$_J$	RMP$_J$	g/day	MP net of expected MP from the DMI, with expMP obtained by formula of Johnson et al. (1995)
Residual methane$_I$	RMP$_I$	g/day	MP net of expected MP from the DMI, with expMP obtained by formula of IPCC (2006)
Residual methane$_R$	RMP$_R$	g/day	MP net of the expected MP from the DMI, with expMP obtained by regression of MP on DMI
EBV for MY	EBV_MY	g/day	Estimated Breeding Value for methane yield
EBV for RMP$_R$	EBV_RMP$_R$	g/day	Estimated Breeding Value for residual methane RMP$_R$
Birth weight	BWT	kg	Weight at birth
Weaning weight	WWT	kg	Weight at weaning (~ 200 d of age)
Yearling weight	YWT	kg	Weight at one year of age (~ 400 d of age)

weight (TWT), dry matter intake (DMI), daily methane production (MP) and MY. Body weights were taken at birth and approximately every 3 months, for research and routine husbandry practices. Estimated breeding values (EBV) for MY and RMP_R, generated for all animals in the main project (Donoghue *et al.* 2015), were also evaluated.

Statistical analysis. Data from the 2013-born progeny were analysed to study the responses to selection as they were the most advanced generation of selection. Analyses were conducted using ASReml (Gilmour *et al*. 2014), fitting generalized linear mixed models to evaluate fixed effects and sire fitted as a random effect. Fixed effects included herd, selection line and sex, with dam age and age at measurement fitted as covariates. Herd by selection line, herd by sex and selection line by sex were fitted as interactions. For the methane traits, test cohort (management test group within herd and sex) was also fitted as an additional fixed effect.

RESULTS AND DISCUSSION
There was no significant selection line by herd or selection line by sex interactions for any of the traits studied in the 2013 born cattle. This implies that the selection line responses were similar across the two herds and sexes. Methane test cohort was not significant for any of the methane traits. The 2013-born progeny were the first generation, but were only half a selection generation, as only one parent (sire) was selected on methane tests, dams were not allocated to selection lines on methane tests. Selection line means for the traits studied are presented in Table 2. There was a significant (P<0.05) divergence between the two selection lines in methane yield. There were also significant (P<0.05) selection line differences in residual methane traits and the EBVs for these traits. This difference is important given that it was achieved in half a generation of selection. This simulates what could be achieved at a commercial level, where only introduced sires/bulls are used to make genetic progress within the herd. There were no significant selection line differences in body weight.

Table 2. Least squares means (± standard errors) for methane production and growth traits of 2013 born cattle from the methane yield (MY) selection lines

Trait[1]	Selection line		Significance[2]
	High MY line	Low MY line	
Number of animals	153	134	
Dry matter intake, kg/day	5.7 ± 0.1	5.7 ± 0.1	*ns*
Methane Production, g/day	127.4 ± 1.4	125.2 ± 1.5	*ns*
Methane yield, g/kg DMI	22.6 ± 0.1	22.1 ± 0.1	*
Residual methane$_B$, g/day	-13.5 ± 0.7	-16.7 ± 0.7	*
Residual methane$_J$, g/day	14.5 ± 0.7	11.4 ± 0.7	*
Residual methane$_I$, g/day	5.2 ± 0.7	2.1 ± 0.7	*
Residual methane$_R$, g/day	1.5 ± 0.7	-1.6 ± 0.7	*
EBV for MY, g/day	0.2 ± 0.1	-0.2 ± 0.1	*
EBV for RMP_R, g/day	0.8 ± 0.3	-1.4 ± 0.3	*
Birth weight, kg	31.3 ± 0.5	31.5 ± 0.5	*ns*
Weaning weight, kg	257.4 ± 3.8	259.9 ± 3.8	*ns*
Yearling weight, kg	416.2 ± 4.5	421.2 ± 4.5	*ns*

[1]See Table 1 for full trait names and definitions
[2] *ns* denotes non-significant difference (P>0.05); * denotes significant difference at P<0.05

Breeding cattle for lower methane production *per se,* may have a detrimental impact on productivity since low methane production is associated with a reduction in feed intake. Results

from this preliminary study support phenotypic and genetic correlation estimates between MY and live weight reported by Herd et al. (2014) and Pinares-Patino et al. (2013), through finding no significant difference between selection lines in live weight. Results of of this study reveal that selection for low methane yield (measured in respiration chambers, on restricted DMI) is possible and will result in a reduction in GHG emissions, which appear to have no impact on the growth of these Angus cattle. Further research is required to substantiate if these results are applicable to: unrestricted DMI of various feed types in cattle of various physiological state and breeds.

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REFERENCES

Arthur, P.F., Archer., J.A., Johnston, D.J., Herd, R.M., Richardson, E.C. et al. (2001) *J. Anim. Sci.* **79:** 2805.

Blaxter, K.L., and Clapperton, J.L. (1965) *Brit. J. Nutr*. **19:** 511.

Donoghue, K.A., Bird-Gardiner, T., Arthur, P.F., Herd, R.M. and Hegarty, R.F. (2015) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **21:** This proceedings.

Gilmour, A. R., Gogel, B. J., Cullis, B. R., Welham, S. J. and Thompson, R. (2014) 'ASReml User Guide Release 4.0' VSN International Ltd, Hemel Hempstead, HP1 1ES, UK www.vsni.co.uk.

Herd, R.M., Arthur, P.F., Donoghue, K.A., Bird, S.H., Bird-Gardiner, T. et al. (2014) *J. Anim. Sci.* **92:** 5267.

Intergovernmental Panel on Climate Change (IPCC) (2006) IPCC Guidelines for National Greenhouse Gas Inventories, **4:** (*10*) 1. IGES, Japan.

Johnson, D.E., Hill, T.M., Ward, G.M., Johnson, K.A., Branine, M.E., et al. (1995) In 'Atmospheric methane: sources, sinks and role in global change',. pp. 199-299, editor M.A.K. Khalil, Springer-Verlag, New York.

Lancaster, P.A., Carstens, G.E., Crews Jr., D.H., Welsh Jr., T.H., Forbes, et al. (2009) *J. Anim. Sci.* **87:** 3887.

McAllister, T.A., Okine, E.K., Mathison, G.W. and Cheng, K.J. (1996) *Can. J. Anim. Sci*. **76:**231.

Pelchen, A. and Peters, K.J. (1998) *Small Rumin. Res*. **27:** 137.

Pinares-Patino, C.S., Hickey, S.M., Young, E.A., Dodds, K.G., MacLean, S., *et al.* (2013) *Animal* 7: (s2) 316.