

Genetic Variation for Methane Traits in Beef Cattle

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ABSTRACT: Records on 777 young, performance tested Angus bulls and heifers measured for methane emissions in open circuit respiratory chambers were used to estimate variance components of methane traits in beef cattle. The mean age at methane measurement was 448 d. Traits studied included yearling weight (YWT), dry matter intake (DMI), daily methane production (MP), methane intensity (MI; MP/pre-test weight), methane yield (MY; MP/DMI) and residual MP (RMP_R; actual minus predicted MP). Heritability estimates for YWT, DMI, MP, MI, MY, RMP_R were 0.42, 0.46, 0.26, 0.29, 0.23 and 0.19, respectively. MP was positively correlated with YWT and DMI. The other methane traits were either not correlated or only weakly correlated with YWT and DMI. These results show that there is the potential reduce methane emissions in beef cattle through selective breeding.

Keywords: beef cattle; methane emissions; genetics

Introduction

A recent FAO report estimates that globally livestock are responsible for 14.5% of greenhouse gas (GHG) emissions, and cattle are responsible of 66% of livestock GHG (Gerber et al. 2013). Ruminant livestock produce methane and nitrous oxide, both of which are GHGs. In grazing cattle, methane is the main source of GHGs and is produced as a by-product of enteric microbial fermentation of plant material in their rumen. Reduction of methane production must therefore be a prime target in any strategy to reduce GHG emissions in cattle, but currently there are few technologies available to mitigate methane emissions in extensive beef production systems. Genetic improvement is a proven approach to produce small but cumulative and permanent change in performance of cattle, and is therefore an attractive approach for the mitigation of methane emissions. 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 report provides interim results from a major project to estimate the natural genetic variation in methane emission traits in beef cattle.

Materials and Methods

A total of 777 Angus cattle born in 2009, 2011 and 2012 in two research herds at the Agricultural Research Centre, Trangie NSW, were used in this study. Each year, within each herd and sex, cohorts of 40 head in 4 groups of 10 were formed and prepared for measurement. Progeny of individual sires were stratified across groups and cohorts. The cohort of 40 animals were weighed and then fed in their groups of 10 an amount calculated to provide 1.2 to 1.5 times their estimated energy requirement for

maintenance. The test ration was a commercial lucerne and oaten hay chaff which had an average of 88% dry matter (DM), 14% crude protein (DM basis) and 9 MJ/kg DM metabolizable energy content. After 10 days the animals were weighed again, with this weight used as their pretest weight (TWT), and then transported to the test facility at the University of New England campus, Armidale NSW, which had 10 open circuit respiration chambers. The cattle were kept in their groups of 10 and fed the same amount of the same chaff ration for a minimum of 4 days. Then the first of the 4 groups was moved into the animal house and each animal fed in an individual pen at 1.2 times maintenance based on its TWT (SCA (2000)). Animals were placed in their chambers by 10.00h, with their daily feed allowance in a feed bin and water available from a drinker inside the chamber. Methane production was measured over 2 x 24h consecutive periods. Details on animals and methane measurements have been reported by Herd et al. (2013).

Data and traits. Animals born in 2009 were measured for methane in 2011 (n=210; mean age of 748 d), whereas those born in 2011 and 2012 were measured at yearling age in 2012 (n=316) and 2013 (n=251), respectively. Traits studied included yearling weight (YWT), dry matter intake (DMI), daily methane production (MP; litres of methane per day), methane intensity (MI; MP per unit TWT), and methane yield (MY; MP per unit DMI). Four different forms of residual methane production (RMP), which is a measure of actual minus predicted MP were examined. For the first three forms, predicted MP was calculated using formulae by Blaxter and Clapperton 1965 (RMP_B), Johnson et al. 1995 (RMP_J), and IPCC 2006 (RMP_I). For the last form (RMP_R) the residuals from a simple regression of MP on DMI performed within cohort were used, and these residuals are equivalent to actual MP minus predicted MP.

Statistical analyses. Variance and covariance components were estimated using ASReml (Gilmour *et al.* 2009). The standard model used included a fixed effect of contemporary group, random additive genetic and residual effects. For YWT the random genetic effects were fitted as additive direct and additive maternal genetic effects. Contemporary group included cohort, methane group and management group. The standard model was used for RMP_R, whereas for MI, MY, RMP_B, RMP_J and RMP_I a linear covariate for age was included in the model. For DMI, MP and YWT, age of the animal as well as age of dam were added to the model as linear covariates. Pedigree records for all animals and 2 further generations of ancestors were used. Bivariate analyses of all trait combinations were also conducted.

Results and Discussion

Descriptive statistics for the traits studied are presented in Table 1. A large amount of variation was observed in age because the 2009-born animals were measured for methane at an older age due to delays in completion of the respiratory chamber facilities. Estimates of variance components and heritability are presented in Table 2. The heritability estimates for YWT and DMI were moderate and in accordance with most published estimates. Heritability estimates for the methane traits (MP, MI and MY) were low to moderate and ranged from 0.23 to 0.29. Robinson et al. (2010) reported a low heritability estimate of 0.13 for MY in sheep, while Pinares-Patino et al. (2013) reported heritability estimates of 0.29 and 0.13 for MP and MI in sheep, respectively. The authors are not aware of any published genetic parameters for methane traits in beef cattle. The results from this study and the sheep studies indicate that there is the potential for genetic improvement to reduce methane emissions in cattle and sheep.

Table 1. Descriptive statistics for methane and production traits in beef cattle

Trait [§]	Abb [¶]	Mean	SD	Min	Max
Age (d) [†]	Age	448	183	253	813
Yearling weight (kg)	YWT	357	45	172	526
Dry matter intake (kg/d)	DMI	6.2	1.4	3.6	9.4
Methane production (L/d)	MP	187	38	110	350
Methane intensity (Lx100/kg TWT)	MI	53.4	8.0	30.8	77.9
Methane yield (L/kg DMI)	MY	30.4	3.5	18.2	41.2
Residual MP – B&C (L/d) [‡]	RMP _B	-29.4	28.9	-133.4	36.5
Residual MP – J&Others (L/d) [‡]	RMP _J	13.5	23.8	-77.9	98.6
Residual MP – IPCC (L/d) [‡]	RMP _I	-0.8	25.2	-96.4	77.9
Residual MP – REG (L/d) [#]	RMP _R	0.0	15.1	-54.4	90.5

[§]Number of animals was 777 for all traits except for YWT which was 774.

[¶]Abbreviations for the traits.

[†]The Mean, SD, Min and Max age (d) for YWT were 416, 27, 311 and 478, respectively.

[‡]Residual methane calculated using formulae of Blaxter and Clapperton 1965 (RMP_B), Johnson et al. 1995 (RMP_J) and IPCC 2006 (RMP_I).

[#]Residual methane calculated by regression (RMP_R).

The use of ratio traits for genetic selection presents problems relating to prediction of the change in the component traits in future generations. This is due to the disproportionate fashion by which selection pressure is exerted on the component traits. Gunsett (1984) compared the efficiency of direct selection for a two-component trait with a linear index trait derived from the same two components. It was concluded that the use of a linear index increases selection responses as compared with direct selection on the ratio trait. As MI and MP are ratio traits,

this study explored the use of a linear index for MY, in the form of residual methane production (RMP). There was variation around the means of each of the four RMP traits (Table 1), and the heritability estimates [0.18 for RMP_I and 0.19 for each of the three other RMP traits] were close to that for MY, meaning that one of these could be used in place of MY for genetic improvement purposes. In the computation of the RMP traits, the prediction of MP by regression implies by definition that RMP_R will be independent of DMI, and thus is the RMP trait of choice, as independence of DMI is not guaranteed when standard formulae are used.

Table 2. Genetic parameters (SE) for weight, feed intake and methane traits in beef cattle

Trait [§]	σ_a^2 (SE)	σ_e^2 (SE)	σ_p^2 (SE)	h^2 (SE)
YWT [¶]		539 (88)	999 (59)	
YWT-d	418 (129)			0.42 (0.12)
YWT-m	42 (56)			0.04 (0.06)
DMI	0.09 (0.02)	0.10 (0.02)	0.19 (0.01)	0.46 (0.10)
MP	96 (31)	270 (28)	366 (21)	0.26 (0.08)
MI	4.47 (1.37)	11.15 (1.23)	15.62 (0.88)	0.29 (0.08)
MY	0.95 (0.33)	3.16 (0.31)	4.11 (0.23)	0.23 (0.08)
RMP _J	38 (14)	166 (15)	204 (11)	0.19 (0.07)
RMP _R	41 (15)	176 (16)	216 (12)	0.19 (0.07)

[§]See Table 1 for full trait names.

[¶]-d and -m represent direct and maternal genetic effects of YWT, respectively.

Estimates of genetic (r_g) and phenotypic (r_p) correlation among the traits studies are presented in Table 3. The four RMP traits were highly correlated (close to unity) with both r_g and r_p greater than 0.96, hence estimates of only two of them are presented in Tables 2 and 3. In general, estimates of r_g were higher than corresponding r_p values for all traits except MI where the reverse was observed. MP was positively correlated with all traits; the strongest being with YWT and DMI. The other methane traits (MI, MY and the four RMP traits) were either not correlated or lowly correlated with YWT and DMI. The positive correlations between MP and liveweight (YWT in this study) and the close to zero correlations between MY and liveweight are similar to those reported in sheep by Pinares-Patino et al. (2013). In an earlier report from the current project showed close to zero correlations for MP, MI and MY with scanned rib and rump fat depth and percent intramuscular (or marbling) fat (Donoghue et al. 2013). It is acknowledged that some of the genetic correlation estimates in the current study have large standard errors and more data are required for further analyses.

Table 3. Genetic (above diagonal) and phenotypic (below diagonal) correlations (SE) for weight, feed intake and methane traits in beef cattle

†	Trait [§]						
	YWT	DMI	MP	MI	MY	RMP _J	RMP _R
A	-		0.85 (0.09)	-0.09 (0.24)	0.26 (0.23)	0.44 (0.22)	0.31 (0.23)
B		-	0.79 (0.08)	-0.30 (0.18)	-0.05 (0.21)	0.10 (0.22)	-0.06 (0.22)
C	0.57 (0.03)	0.65 (0.02)	-	0.24 (0.20)	0.55 (0.15)	0.69 (0.12)	0.56 (0.15)
D	-0.19 (0.05)	-0.20 (0.04)	0.47 (0.03)	-	0.90 (0.06)	0.84 (0.08)	0.89 (0.07)
E	0.11 (0.05)	-0.02 (0.04)	0.72 (0.02)	0.85 (0.01)	-	0.99 (0.01)	*
F	0.16 (0.05)	0.06 (0.04)	0.79 (0.02)	0.80 (0.01)	0.97 (0.01)	-	0.97 (0.02)
G	0.12 (0.05)	-0.03 (0.04)	0.74 (0.02)	0.79 (0.01)	*	0.97 (0.01)	-

[§]See Table 1 for full trait names.

[†]The trait code A is YWT, B is DMI, C is MP, D is MI, E is MY, F is RMP_J and G is RMP_R.

* indicates convergence was not achieved.

Conclusion

This study has shown that there is some level of genetic control of methane emissions in beef cattle. Genetic variation in methane emission traits offers the potential reduce methane emissions in beef cattle through selective breeding.

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