

## GENETIC PARAMETERS FOR METHANE PRODUCTION AND RELATIONSHIPS WITH PRODUCTION TRAITS IN AUSTRALIAN BEEF CATTLE

K.A. Donoghue<sup>1</sup>, T.L. Bird-Gardiner<sup>1</sup>, P.F. Arthur<sup>2</sup>, R.M. Herd<sup>3</sup> and R.F. Hegarty<sup>4</sup>

<sup>1</sup> NSW Department of Primary Industries, Agricultural Research Centre, Trangie, NSW 2823

<sup>2</sup> NSW Department of Primary Industries, EMAI, Menangle, NSW 2568

<sup>3</sup> NSW Department of Primary Industries, Beef Industry Centre, Armidale, NSW 2351

<sup>4</sup> Environmental and Rural Science, University of New England, Armidale, NSW 2351

### SUMMARY

This paper reports heritability estimates for methane traits and genetic relationships with production traits in beef cattle. Traits recorded during the methane test period included dry matter intake (DMI), test liveweight (TWT), methane production (MPR) and methane yield (MY; MPR/DMI). Two methods of calculating residual methane traits (RMP) were evaluated. Production traits included birth (BWT), weaning (WWT), yearling (YWT) and final (FWT) liveweight. Heritabilities for MPR, MY and RMP traits were moderate (0.19 to 0.27), indicating that there is potential to use genetic improvement to reduce methane emissions in Australian beef cattle. MPR was moderately genetically correlated with MY (0.50) and RMP traits (0.50 to 0.63). However, MPR was also moderately to highly genetically correlated (0.36 to 0.86) with weight traits. Methane yield and RMP traits, however, were lowly to moderately genetically correlated (-0.06 to 0.45) with weight traits. These results indicate that selection for lower MPR would have a negative impact on growth in beef cattle. Selection for reduced MY or RMP, however, would lead to reduced MPR with minimal impact on animal productivity. The use of a ratio trait, like MY, in animal breeding is generally undesirable, thus selection on RMP traits is a better alternative.

### INTRODUCTION

Livestock make a significant contribution (14.5%) to greenhouse gas (GHG) emissions worldwide, and ruminants are the primary source (Gerber *et al.*, 2013). The use of genetic improvement to reduce GHG emissions would produce small, cumulative and permanent changes and would be particularly useful in extensive beef production systems. Methane production (MPR) has been found to be moderately heritable in sheep (Pinares-Patino *et al.*, 2011), and in preliminary reports from this study (Donoghue *et al.*, 2013; Herd *et al.*, 2014b). However, preliminary results indicate that MPR is highly genetically correlated to production traits (Herd *et al.*, 2014b). Alternative methane traits studied include methane yield (MPR/dry matter intake) and residual methane (difference between actual and predicted MPR), with both found to be moderately heritable (Donoghue *et al.*, 2013; Herd *et al.*, 2014b). The objective of this study was to quantify whether genetic variation existed for several methane traits, and to gain better understanding of the relationships between methane and production traits.

### MATERIALS AND METHODS

Progeny born from Angus cows in 2 research herds at the New South Wales Department of Primary Industries Agricultural Research Centre, Trangie NSW, were measured for methane production in 10 respiration chambers on the University of New England campus, Armidale NSW. Herd *et al.* (2014a) provides details on the management of animals and methane measurement procedure. The 1,043 animals were progeny of 73 sires (average 14 progeny per sire, range 1-30), born across 4 drops. Each year, within herd and sex, cohorts of 40 head in 4 groups of 10 were formed, and progeny of individual sires were stratified across groups and cohorts.

**Data.** Methane production was measured over 2 x 24h consecutive periods. For animals born from 2011 to 2013 these measurements were taken at approximately yearling age (mean=339 days). However, for animals born in 2009, these measurements were taken at approximately two years of age (mean=738 days) due to delays in construction of the chamber facility. Traits measured included pre-test weight (TWT), dry matter intake (DMI), daily methane production (MPR) and methane production per unit feed intake (methane yield: MY). Two different forms of residual MPR (RMP) were defined to target MPR independent of feed intake, with RMP defined as actual MPR minus expected MPR (expMPR). For RMP<sub>I</sub>, expMPR was calculated using a published prediction equation (Johnson *et al.*, 1995), while for RMP<sub>R</sub>, the residuals from a simple regression of MPR on DMI were used.

Data for growth traits were collected on all animals in the research herds, including animals that had not been measured for methane. Growth traits recorded included birth (BWT), weaning (WWT), yearling (YWT) and final (FWT) weight, which were measured at birth and at mean ( $\pm$ SD) age of 231 ( $\pm$ 23), 423 ( $\pm$ 28), and 606 ( $\pm$ 71) d, respectively. There were growth records available on 1,471 animals, who were the progeny of 75 sires (average 20 progeny per sire, range 1-38), though not all animals had all traits recorded. Editing of records included removal of animals with incomplete pedigree, missing birth date, large feed refusal during testing and trait measurements greater than 4 standard deviations from the contemporary group mean.

**Model of analysis.** Variance and covariance components were estimated with an animal model using ASReml (Gilmour *et al.* 2009). A fixed effect of contemporary group, random direct genetic effects, and residual effects were included in the standard model. Contemporary group was defined by cohort, methane group and management group. Covariates were added to the standard model where these variables were significant ( $P < 0.05$ ) for a particular trait. The standard model was used for RMP<sub>R</sub>. For BWT, age of dam (in years) was added to the model as a linear covariate, while for FWT, a linear covariate for age of animal (in days) was included. For the remaining traits (TWT, DMI, MPR, MY, RMP<sub>I</sub>, WWT and YWT), age of animal as well as age of dam were added to the model as linear covariates. For the traits of BWT, WWT and YWT, maternal genetic and maternal permanent environmental effects were also included in the model, with the direct-maternal genetic relationship fixed at zero. Pedigree records for all animals with records and 2 further generations of ancestors were used.

## RESULTS AND DISCUSSION

Table 1 contains summary statistics for the methane test and weight data.

**Table 1 Descriptive statistics for methane and growth traits**

Trait	No. records	Average (SD)	Minimum	Maximum
TWT (kg)	1,043	356.4 (89.6)	156	640
DMI (kg/d)	1,043	6.07 (1.31)	3.59	9.42
MPR (g/d)	1,043	132.2 (25.4)	78.9	251.0
MY (g/kg DMI)	1,043	22.0 (2.3)	13.1	29.5
RMP <sub>I</sub> (g/d)	1,043	10.7 (15.0)	-55.9	70.7
RMP <sub>R</sub> (g/d)	1,043	0 (9.5)	-39.6	64.0
BWT (kg)	1,471	34 (4.8)	19	50
WWT (kg)	1,456	242 (37)	110	355
YWT (kg)	1,377	370 (54)	172	592
FWT (kg)	1,011	450 (58)	265	648

Genetic parameters for methane and production traits are reported in Table 2. Heritabilities for methane traits were moderate (0.27 and 0.22) and are similar to estimates of Donoghue *et al.*

(2013) and Herd *et al.* (2014b) using a smaller subset of the animals in this study. Pinares-Patino *et al.* (2011) also reported a moderate heritability (0.30) for MY in sheep. Heritabilities for RMP were moderate (0.19), similar to preliminary estimates from this study (Herd *et al.*, 2014b) and offer the potential to make selection decisions to target MPR independent of feed intake while also avoiding using a ratio trait, such as MY. The results from this study, together with published estimates, indicate that there is potential to lower methane emissions from livestock through selection.

**Table 2 Genetic parameters (SE) for methane and growth traits**

Trait	$\sigma_d^2$	$\sigma_m^2$	$\sigma_c^2$	$\sigma_p^2$	$h_d^2$	$h_m^2$	$c^2$
TWT	446.9 (98)	-	-	1,016 (54)	0.44 (0.08)	-	-
DMI	0.080 (0.017)	-	-	0.175 (0.009)	0.46 (0.08)	-	-
MPR	44.0 (12)	-	-	164.3 (8)	0.27 (0.07)	-	-
MY	0.383 (0.111)	-	-	1.76 (0.09)	0.22 (0.06)	-	-
RMP <sub>J</sub>	15.7 (4.88)	-	-	84.1 (4.01)	0.19 (0.06)	-	-
RMP <sub>R</sub>	15.7 (4.79)	-	-	83.8 (3.96)	0.19 (0.05)	-	-
BWT	6.32 (1.60)	3.31 (1.10)	0.32 (0.90)	18.38 (0.84)	0.34 (0.08)	0.18 (0.06)	0.02 (0.05)
WWT	172.6 (49)	73.7 (35)	95.7 (35)	670.8 (29)	0.26 (0.07)	0.11 (0.05)	0.14 (0.05)
YWT	465.7 (94)	48.6 (45)	30.8 (48)	1,002 (47)	0.46 (0.08)	0.05 (0.05)	0.03 (0.05)
FWT	827.5 (147)	-	-	1,390 (77)	0.60 (0.08)	-	-

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

Trait	TWT	DMI	MPR	MY	RMP <sub>J</sub>	RMP <sub>R</sub>	BWT	WWT	YWT	FWT
TWT		0.99 (0.01)	0.80 (0.07)	-0.10 (0.18)	0.05 (0.19)	-0.09 (0.19)	0.58 (0.13)	0.80 (0.07)	0.98 (0.02)	0.96 (0.02)
DMI	0.93 (0.01)		0.84 (0.06)	-0.04 (0.18)	0.10 (0.18)	-0.05 (0.18)	0.54 (0.14)	0.84 (0.06)	0.94 (0.03)	0.95 (0.03)
MPR	0.68 (0.02)	0.71 (0.02)		0.50 (0.14)	0.63 (0.11)	0.50 (0.14)	0.36 (0.18)	0.84 (0.09)	0.86 (0.06)	0.79 (0.08)
MY	0.04 (0.04)	-0.01 (0.04)	0.68 (0.02)		0.99 (0.01)	0.99 (0.01)	-0.01 (0.21)	0.27 (0.21)	0.21 (0.18)	0.05 (0.17)
RMP <sub>J</sub>	0.11 (0.03)	0.08 (0.04)	0.76 (0.01)	0.97 (0.01)		0.99 (0.01)	0.03 (0.22)	0.45 (0.20)	0.38 (0.17)	0.18 (0.17)
RMP <sub>R</sub>	0.02 (0.04)	-0.02 (0.04)	0.69 (0.02)	0.97 (0.01)	0.99 (0.01)		-0.06 (0.22)	0.32 (0.22)	0.23 (0.19)	0.06 (0.17)
BWT	0.43 (0.04)	0.39 (0.04)	0.26 (0.04)	-0.01 (0.04)	0.02 (0.04)	-0.03 (0.04)		0.53 (0.15)	0.56 (0.12)	0.54 (0.14)
WWT	0.71 (0.03)	0.71 (0.03)	0.53 (0.03)	0.03 (0.04)	0.11 (0.04)	0.04 (0.04)	0.36 (0.04)		0.92 (0.04)	0.92 (0.05)
YWT	0.85 (0.01)	0.80 (0.02)	0.61 (0.03)	0.09 (0.04)	0.16 (0.04)	0.08 (0.04)	0.40 (0.04)	0.66 (0.04)		0.99 (0.01)
FWT	0.84 (0.01)	0.79 (0.01)	0.56 (0.03)	0.10 (0.04)	0.13 (0.04)	0.07 (0.04)	0.39 (0.04)	0.62 (0.03)	0.84 (0.01)	

Phenotypic ( $r_p$ ) and genetic ( $r_g$ ) correlations and their associated standard errors between methane and growth traits are reported in Table 3. MPR was highly genetically correlated with both TWT (0.80) and DMI (0.84), indicating that reducing MPR would also lead to correlated reductions in TWT and DMI. In contrast, MY was not genetically correlated with TWT (-0.10) or DMI (-0.04), but was positively genetically correlated with MPR (0.50), indicating that reducing MY would have little impact on DMI or TWT, but have the correlated effect of reducing MPR. Large positive  $r_g$  (0.99) were observed between MY and the residual methane traits, indicating that, genetically, animals with higher MY also had higher RMP. Genetic relationships between the residual methane traits and TWT (-0.09, 0.05) and DMI (-0.05, 0.10) were low. This indicates that there is potential to select for reduced RMP with little impact on DMI and TWT, with the correlated effect of reducing MPR and the benefit of avoiding selection on a ratio trait. The genetic correlation between MPR and BWT (0.36) was moderate, while correlations with later growth traits (WWT, YWT and FWT) were large (0.79 to 0.86). These results are similar to those reported in sheep (Pinares-Patino *et al.*, 2013), where large genetic correlations were observed between MPR and WWT (0.71) and WT at 8 months of age (0.80). These correlations indicate that directly selecting for reduced MPR will also select for lighter animals. MY and residual methane traits were not genetically correlated with BWT or FWT (-0.06 to 0.18), but were lowly to moderately genetically correlated with WWT and YWT (0.21 to 0.45), however large standard errors were associated with all estimates. Pinares-Patino *et al.* (2013) reported little genetic relationship between MY and WWT (0.06) and WT at 8 months of age in sheep (0.06). The results in our study indicate that it may be possible to select for reduced MY or residual methane with minimal impact on animal productivity.

## CONCLUSIONS

Genetic variation in methane emissions is present in this population of Angus cattle, confirming the potential to use genetic improvement to reduce methane emissions in livestock. For Australian beef cattle herds, selection for lower methane production (MPR) may lead to selection for lower weight and have detrimental effects on animal productivity. In contrast, selection for lower MY or RMP would lead to lower MPR with minimal impact on herd productivity. The use of a ratio trait, like MY, in animal breeding is generally undesirable, and thus selection on either of the residual methane traits is a better alternative.

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