

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

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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.

(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	σ_d^2	σ_m^2	σ_c^2	σ_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 _J	15.7 (4.88)	-	-	84.1 (4.01)	0.19 (0.06)	-	-
RMP _R	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 _J	RMP _R	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 _J	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 _R	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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