

BREEDING ANGUS CATTLE THAT NATURALLY EMIT LESS METHANE

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SUMMARY

The aim of this experiment is to investigate and demonstrate genetic variation in daily methane production (MP; g/d), methane intensity (MI; MP per unit bodyweight; g/kg) and methane yield (MY; MP per unit feed intake; g/kg). Angus cows in pedigree- and performance-recorded research herds at Industry & Investment NSW research centres at Grafton and Trangie NSW were mated in 2007 to Angus bulls that had previously been recorded for MY. Bulls that had been identified as either phenotypically high or low for MY were used as sires in the Grafton herd; unselected sires were used in the Trangie herd. In 2010 the near 2-year-old bull progeny from Trangie and heifer progeny from Grafton were measured for MP, MI and MY. There were 8 sires with progeny represented in the Trangie bull data (n=63 progeny). A wide range in least-squares (LS) sire means was observed for MP (191g/d to 233g/d), MI (0.26g/kg to 0.63g/kg) and MY (24.3g/kg to 30.2g/kg). There were 6 sires with progeny represented in the Grafton heifer data (n=79 progeny). A wide range in LS sire means was observed for MP (133g/d to 165g/d), MP (0.15g/kg to 0.55g/kg) and MY (21.5g/kg to 27.0g/kg). The differences between sires for these traits that indicate that there may be genetic variation present and provide preliminary evidence that selection on a methane production trait may be possible.

INTRODUCTION

Cattle and sheep emit methane, a potent greenhouse gas (GHG), as part of the fermentation process in their stomach. Enteric emissions from Australian livestock were estimated to be 55.6 Mt CO₂-e or 10.4% of National GHG emissions in 2010. Over 90% of livestock emissions are from cattle and sheep, and currently beef cattle are Australia's largest single source of agricultural emissions. However, less than 5% of these emissions are amenable to nutritional modification by changes in feeding, (ie. largely restricted to cattle in feedlots). Traditional selective breeding is the most wide-reaching tool for lasting reduction in the other 95% of emissions from our national herd grazing extensive pastures.

In ruminants there is a strong positive relationship between feed intake and methane production. Hence, any animal breeding strategy that reduces feed intake per unit of product results in reduction of GHG emission intensity. Direct selection for lower daily methane production (MP) may not be desirable because it could favour lower feed intake and/or smaller, slower growing animals. Methane intensity (MI) and methane yield (MY), being methane produced per unit of bodyweight and per unit of feed intake, respectively, can measure methane mitigation achieved independent of size and feed intake. For genetic improvement, genetic variation in these traits and their phenotypic and genetic associations with other important production traits need to be determined.

The aim of this paper is to report preliminary results from an ongoing research project investigating phenotypic and genetic variation in methane production traits in Angus cattle.

MATERIALS AND METHODS

Angus cows in pedigree- and performance-recorded research herds at the Industry & Investment NSW research centres at Grafton and Trangie NSW were mated in 2007 to Angus bulls that some years previously had been recorded for residual feed intake and MY. Bulls that had been identified as either phenotypically high or low for MY were used as sires in the Grafton herd; sires that were high or low for residual feed intake were used in the Trangie herd. Methane production by the bulls had been measured using the SF₆ tracer method when being fed at *ad-libitum* feed intake a 70% grain-content feedlot ration in the Beef CRC “Tullimba” Research Feedlot as described by Hegarty *et al.* (2007). Progeny were born in 2008 and weaned in 2009.

As near 2-year-old animals in 2010, firstly the bull calves from Trangie (n=96), and then the heifer calves from Grafton (n=79), were measured for methane production at the Grafton Research Centre. There, in individual pens inside an animal house, each animal had methane production measured using the SF₆ method while being fed a fixed daily allowance of a roughage diet. The amount offered was calculated to provide 1.2-times the estimated energy requirement for maintenance based on the animal’s liveweight at the start of the measurement period. This was done to minimise day to day variation in daily methane production so increasing power to detect phenotype differences, and avoid ‘level of feeding’ effects on MI and MY. After adaptation to diet (14 days), methane production was measured over 5 x 24h consecutive periods.

The bulls, then heifers, were split into 3 cohorts of 32 animals. Animals within a cohort were measured at the same time, with care taken to ensure sires were equally represented in each cohort. Due to equipment problems during measurement of the first cohort of Trangie bulls, only data from the second and third cohorts of bulls are used. Fixed effects analyses were undertaken to identify significant fixed effects for daily dry matter intake (DMI; kg); MP, MI and MY. Fixed effects fitted were sire of the animal and cohort, with age and weight at start of measurement fitted as covariates. The interaction of sire and cohort was not significant and not included.

RESULTS

Summary statistics from the measurement of the second and third cohorts of Trangie bulls and the 3 cohorts of Grafton heifers are presented in Table 1. There was substantial variation in all traits including in MP, MI and MY, with a four-fold and a three-fold difference observed in the latter trait for the bulls and in the heifers respectively.

Table 1. Summary statistics for Trangie bulls (n=63) and Grafton heifers (n=79)

Trait	Mean	SD	Minimum	Maximum
<i>Bulls:</i>				
Weight (kg)	522	46	428	622
Age (d)	582	16	537	614
DMI (kg/d)	7.83	0.53	6.77	8.95
MP (g/d)	209	46	98	368
MI (g/kg)	0.41	0.08	0.26	0.63
MY (g/kg)	26.8	5.4	10.9	41.2
<i>Heifers:</i>				
Weight (kg)	382	29	318	468
Age (d)	623	19	579	670
DMI (kg/d)	6.21	0.46	4.76	7.28
MP (g/d)	147	26	50	204
MI (g/kg)	0.39	0.07	0.15	0.55
MY (g/kg)	23.7	4.2	10.4	34.5

There were 8 sires with progeny represented in the Trangie bull data and 6 sires with progeny represented in the Grafton heifer data. Least-squares (LS) means for measurements made on the progeny of these sires are reported in Table 2. A wide range in sire LS-means was observed for MP, MI and MY in both the bull and heifer progeny providing evidence that there may be some genetic variation present for these traits. In the heifer progeny, differences observed between sires were significant for MP (at $P<0.1$), MI ($P<0.1$) and MY ($P<0.05$; Table 3). In the bull data, the differences between sires were not significant, presumably due to not enough records being available. The extent that difference in sex between the Trangie and Grafton progeny contributed to the observed results remains to be determined.

Table 2. Sire methane yield and least-squares means (SE) for bull progeny from Trangie and heifer progeny from Grafton

Sire	No. progeny	Sire MY (g/kg)	DMI (kg/d)	MP (g/d)	MI (g/kg)	MY (g/kg)
Bull progeny from Trangie						
1	7	19.1	7.75 (0.14) ^{a,b}	218 (16) ^a	0.418 (0.030) ^a	28.1 (1.9) ^{a,b}
2	8	19.4	7.59 (0.13) ^b	203 (15) ^a	0.391 (0.028) ^a	26.7 (1.8) ^{a,b}
3	10	21.0	7.67 (0.12) ^{a,b}	191 (14) ^a	0.363 (0.027) ^a	24.8 (1.7) ^{a,b}
4	7	22.0	7.70 (0.15) ^{a,b}	233 (17) ^a	0.448 (0.032) ^a	30.2 (2.0) ^a
5	8	23.9	7.97 (0.13) ^a	217 (15) ^a	0.417 (0.028) ^a	27.2 (1.7) ^{a,b}
6	7	24.7	7.94 (0.14) ^{a,b}	206 (16) ^a	0.397 (0.029) ^a	26.0 (1.8) ^{a,b}
7	7	29.0	7.97 (0.14) ^a	194 (16) ^a	0.379 (0.030) ^a	24.3 (1.8) ^b
8	8	na	7.95 (0.13) ^{a,b}	233 (15) ^a	0.453 (0.028) ^a	29.3 (1.7) ^{a,b}
Heifer progeny from Grafton						
9	9	10.3	6.17 (0.10) ^a	144 (8.5) ^{a,b}	0.380 (0.023) ^{a,b}	23.4 (1.3) ^b
10	15	12.0	6.18 (0.08) ^a	165 (7.3) ^b	0.437 (0.019) ^a	26.9 (1.1) ^a
11	7	12.4	6.25 (0.11) ^a	133 (9.8) ^a	0.353 (0.026) ^b	21.5 (1.5) ^b
12	16	12.6	6.23 (0.08) ^a	152 (6.8) ^{a,b}	0.396 (0.018) ^{a,b}	24.2 (1.1) ^{a,b}
13	13	28.5	6.16 (0.09) ^a	138 (7.6) ^a	0.363 (0.020) ^b	22.3 (1.2) ^b
14	13	30.8	6.20 (0.08) ^a	146 (7.1) ^{a,b}	0.383 (0.019) ^b	23.5 (1.1) ^b

na = not available. Means within sexes and columns with different superscripts differ ($P<0.05$)

Table 3. P-values for fixed effects for traits in the Trangie bull and Grafton heifer data

Trait	Cohort	Weight	Age	Sire
<i>Bull progeny</i>				
DMI, kg/d	0.146	<0.001	0.445	0.262
MP, g/d	0.109	0.392	0.355	0.436
MI, g/kg	0.107	0.116	0.296	0.367
MY, g/kg	0.087	0.007	0.611	0.285
<i>Heifer progeny</i>				
DMI, kg/d	0.383	<0.001	0.910	0.982
MP, g/d	0.691	0.092	0.695	0.071
MI, g/kg	0.434	0.554	0.606	0.043
MY, g/kg	0.775	0.015	0.763	0.069

The heifers were the offspring of a mating between selected high and low MY phenotype bulls to random females and these sires had a greater range in their own MY than did the sires used at Trangie that had not been selected on MY (Table 2). However, as is apparent in Table 2, MY of the sire was not associated with differences in the MY of their progeny. Supporting this, the

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correlation of average MY for the progeny group with sire MY was not significant in either the heifer data ($r=0.30$; $P=0.57$) or the bull data ($r=0.53$; $P=0.22$).

DISCUSSION

Preliminary results from this research project show large natural variation between animals in MP, MI and MY. Some animals produced considerable less methane per day, per kg of weight and per kg of feed intake than the average for this sample of animals. Sire had a significant effect for MY, MI and approached significance for MP, in the heifer data, but not in the bull data. This is consistent with the finding in sheep of sire effects on methane production intensity (Robinson *et al.* 2010) and persistent between-animal differences in methane yield (Pinares-Pitino *et al.* 2003). These results provide preliminary evidence that selection for a methane production trait may be possible. However, that MY of the sires, measured on unrestricted feed-intake of a high grain-content feedlot ration, was not associated with differences in the MY of their progeny, tested on a restricted feeding allowance of roughage diet, means these two methane measurements may be different traits genetically.

This is an ongoing project. A team of the highest- and lowest-ranked Trangie bulls for MY measured on restricted intake at the Grafton Research Centre have now been used in both the Trangie and Grafton research herds to produce progeny that will be born autumn 2011 and measured for MY early in 2012. Cattle in both herds are routinely weighed and scanned using ultrasound for body composition traits. This data will be analysed to provide evidence of the magnitude of individual variation between animals in MP, MI and MY, on the extent of genetic variation and a preliminary estimate of heritability, and phenotypic correlations with size, growth and body composition traits.

There is potential opportunity under Australia's Carbon Farming Initiative (Combet 2011) to have genetic improvement feed efficiency and methane yield recognised as a carbon offset technology. Through the national genetic improvement scheme for beef cattle, BREEDPLAN, the Australian beef industry has a system for calculating breeding values that describe the genetic merit of bulls. Breeding values for a methane production trait will require additional research to deliver accredited protocols for GHG emission reduction through animal breeding.

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