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Prepared by: Dr Robert Herd

New South Wales Department of Primary Industries

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Meat & Livestock Australia Limited
Locked Bag 991
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Genetic improvement of beef cattle for GHG outcomes

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Abstract

Methane yield (MY) has been adopted internationally to compare natural variation between animals in the amount of methane they produce relative to their feed intake. This project measured MY on young Angus bulls and heifers in two pedigreed, performance-recording research herds. Animals were recorded for MY over a minimum of two days on a controlled intake of a high roughage-content diet. Results for 339 animals were obtained. The results show substantial natural variation in methane emissions between individual animals and significant differences between sires in methane production by their progeny. Compared to the sires whose progeny had the lowest average MY, there were sires whose progeny had an average MY that were 24%, 24%, 16%, 19% and 11% higher across the five groups of cattle tested. A preliminary estimate for the heritability of MY was moderate, being approximately 0.3, and similar to animal weight at the age of test. Methane yield was not strongly associated with phenotypic or genetic variation in standard animal weight, body composition or fertility traits used the Australian beef cattle genetic improvement system BREEDPLAN®. These results show that a breeding solution to reduce methane emissions from beef cattle appears to be possible.

Executive summary

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 CO_2-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.

The aim of this project was to discover if there was sufficient natural variation between animals in a methane production trait, like MY, that could enable producers to breed beef cattle with significantly reduced methane emissions. This was a collaborative program of research between the NSW Department of Primary Industries (DPI) and the University of New England (UNE) on methane emissions from ruminants with funding from the Australian Government under its Climate Change Research Program and additional funding support from Meat & Livestock Australia.

The project used two pedigreed, performance-recording research herds of Angus cattle located at the NSW DPI Trangie and Glen Innes research centres, with methane measurements on individual cattle being conducted in the cattle animal houses at the DPI Grafton research centre and on the UNE campus. Young bulls and heifers were measured for methane production over a minimum of two days, on a controlled intake of a high roughage-content diet. Standard animal weight, body composition and fertility measurements used the Australian beef cattle genetic improvement system BREEDPLAN® were recorded on the tested cattle and their relatives in the research herds.

Following the methane production test the animals are ranked on MY, and bulls with low or high MY were selected for breeding to establish unique replicated, divergent selection lines in Australian beef cattle for evaluation of associations between MY and other production traits.

The project went to considerable effort to standardise the test protocol. Animals were prepared for testing on the same ration at all sites and were tested on this ration. The ration chosen had a high content of roughage and a modest content of energy: choices made to make the restricted feeding pattern in the test resemble the pasture intake pattern encountered by grazing cattle in Australia.

Results for 339 animals were obtained. The results show substantial natural variation in methane emissions between individual animals and that it is possible to find sires whose progeny naturally produce less methane. Compared to the sires whose progeny had the lowest average MY, there were sires whose progeny had an average MY that were 24%, 24%, 16%, 19% and 11% higher across the five groups of cattle tested. The sire differences provide evidence that there exists genetic variation in methane yield and demonstrate that sires exist that can be used in cattle breeding to produce progeny with lower methane emissions.

A preliminary estimate for the heritability of methane yield is presented. In this small dataset the heritability of MY was moderate, being approximately 0.3, and similar to animal weight at the age of test. Methane yield was not strongly associated with

phenotypic or genetic variation in standard animal weight, body composition or fertility traits used the Australian beef cattle genetic improvement system BREEDPLAN.

One implication from these results is that it is unlikely to be possible to predict MY for individual cattle based on simple phenotypic measurements such as weight or scanned body composition information. Further, selection using current BREEDPLAN EBV to reduce methane production, particularly MY, in the next generation of cattle will not lead to a predictable change in MY.

The corollary is that to be able to select to predictably reduce methane emiisions will require a new breeding value for a methane-related trait, such as MY, to become available to cattle breeders.

These results show that a breeding solution to reduce methane emissions from beef cattle appears to be possible. Methane yield appeared to be moderately heritable, similar to that for animal weight at test age. To use animal breeding to predictably reduce methane yield may require a new breeding value for a methane-related trait to become available through the BREEDPLAN system to cattle breeders.

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Background

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 (methane production per unit of animal product such as weight; MP_WT) and methane yield (methane produced per unit of feed intake; MY) can measure the methane mitigation achieved independent of animal size and feed intake. For genetic improvement, the magnitude of phenotypic and genetic variation in these traits and their phenotypic and genetic associations with other important production traits need to be determined.

The aim of this project was to discover if there was sufficient natural variation between animals in a methane production trait, like MY, that could enable producers to breed beef cattle with significantly reduced methane emissions while maintaining livestock productivity. This is a collaborative program of research between the NSW Department of Primary Industries (DPI) and the University of New England (UNE) on methane emissions from ruminants with funding from the Australian Government under its Climate Change Research Program and additional funding support from Meat and Livestock Australia.

Project objectives

1. By 1 September 2009 have defined the trait to be internationally accepted as the low methane phenotype for Angus cattle
2. By 1 September 2011 have initial estimates of heritability for the methane trait based on two generations of genetic improvement
3. By 1 December 2011 have identified positive and negative genotypic associations between the low methane phenotype and feed intake, growth and body composition traits

By agreement with MLA in December 2011 the due dates for these objectives and related milestones have been extended, to 1 November 2011 for objective 2, and 1 March 2012 for objective 3. These changes were agreed to recognising the unavoidable delay in completion of the new cattle animal house on the UNE campus and consequent delay in commencement of measuring methane production on large numbers of cattle.

Methodology

The project needed to measure the extent of natural phenotypic variation and underlying genetic variation in methane production traits in beef cattle. In addition, the project needed to measure these methane production traits and all standard production traits recorded in Australia's genetic improvement system BREEDPLAN® on cattle with known pedigrees.

For these reasons the project choose to use Angus cows in pedigree- and performance-recorded research herds at the NSW DPI research centres at Grafton and Trangie NSW. In 2010 it was necessary to relocate the research cow herd from Grafton to the NSW DPI Glen Innes Research Centre. The Trangie research herd had a history of breeding for differences in growth rate (Parnell et al., 1997) and net (or residual) feed intake (feed efficiency; (Arthur et al., 2001)). The Grafton/Glen Innes research herd had had been formed by retaining female progeny born 2002-2004 in an Australian Angus Society progeny test program.

The cows had been 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 net 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 bull calves from the Trangie herd, and then heifer calves from the Grafton herd 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 rate of methane production per day. After adaptation to diet (14 days), methane production was measured over 5 x 24h consecutive periods. Some photographs of the Grafton facility and cattle in the measurement chambers are attached in Appendix 2.

The bulls, then heifers, were split into 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, data from that cohort was not used. Table 1 shows the numbers of animals with valid methane production records obtained.

Table 1. Progress in testing animals to end February 2012.
Numbers shown in italics represent numbers yet to be tested.

Year of test	Method	Animals	Gen. Seln.	Rumen and faecal samples for RELRP network
2010	SF6	62 TR bulls	0	Faeces only
		73 GI heifers	0	Faeces only
		135		
2011	Chamber	75 TR bulls	0	Both
		64 GI bulls	.75	Both
		65 GI heifers	*.75*	Both
		204		
2012	Chamber	80 GI bulls	.75, some 2	Both
Total tested to end Feb. 2012		**419**		
2012	*Chamber*	*80 GI heifers*	*.75, some 2*	*Both*
		80 TR bulls	*.75*	*Both*
		80 TR heifers	*.75*	*Both*
To be tested		*240*		
End of June 2012		*659*		

Explanation:
SF6 and Chamber refer to the method used for methane production measurement
TR refers to the southern (Trangie) research herd
GI refers to the northern (Glen Innes) research herd
Gen. Seln. refers to approximate number of generations of selection.

In 2008 the same bulls and cows were mated but with different assignment of bull to cows. The progeny were born in 2009 and were to be tested in 2010 in new, purpose-built respiration chambers on the University of New England (UNE) campus, Armidale. The project had considerable delays resulting from the slow progress in completion of the new methane measurement facility on the UNE campus. The facility opened for methane measurement in April 2011. Some photographs of the UNE facility and cattle in the measurement chambers are attached in Appendix 3.

In 2011 progeny from both research herds were tested through the UNE chambers. Table 1 shows the numbers of animals tested in 2011. Preparation of animals for testing followed the same protocol as used previously. There were 10 test chambers in the UNE facility. Ten animals at a time were tested over 2 days, with daily feed intake and MPR in the chambers recorded.

Because of the delay in testing cattle, no matings were made in 2009. In 2010, matings using new bulls were conducted in both research herds. For both herds, sires were selected on the basis of high or low MY during their test in 2010. Progeny were born in 2011 and will be tested for methane traits in 2012. The use of bulls with low or high MY in separate herds has enabled the project to establish unique replicated, divergent selection lines in Australian beef cattle for evaluation of associations between MY and other production traits.

The project went to considerable effort to standardise the test protocol. Animals were prepared for methane testing on the same ration at all sites and were tested on this ration. The ration chosen has a high content of roughage and a relatively low content of metabolizable energy (9 MJ/kg DM; see Figure 1). It was offered at a restricted level of feeding (just above maintenance). Choice of a restricted feeding pattern of a modest energy feed was chosen to resemble the pasture intake pattern encountered by grazing cattle in Australia.

Figure 1. The test ration was uniformly Manuka "Blue Ribbon" Chaff® (Quirindi NSW)

In addition to methane produced during test (MP; L/day), the traits recorded were age at start of test (Age; days), animal weight just before start of test (WT; kg), feed dry-matter intake during test (DMI; kg/day), methane produced per unit of animal WT (MP_WT; L/kg) and methane yield (MY; L/kg DMI).

Fixed effects analyses were undertaken to identify significant fixed effects for these traits (year, cohort, sire), with age and weight at start of measurement fitted as covariates.

Results

Progress in testing animals

Progress in testing pedigreed Angus cattle from two NSW DPI research herds to end February 2012 is shown in Table 1, along with indicative numbers for cattle to be tested through to end of June 2012. In addition to the methane and animal production traits being measured, samples of rumen fluid and faeces were collected for sharing across the RELRP network.

Means and descriptive statistics for the 339 cattle with valid methane test data measured in 2010 and 2011 are presented in Table 2.

Table 2. Means and descriptive statistics for the N=339 animals tested for methane production traits.

The animals are Angus heifers in 2010 and heifers and bulls in 2011 from the NSW DPI Glen Innes research herd, and Angus bulls in 2010 and 2011 from the NSW DPI Trangie research herd.

Trait	Mean	Std Dev	Maximum	Minimum	N
Age	691	77	822	537	339
WT	483	73	670	316	339
DMI	7.7	1.0	9.5	4.8	339
MP	229	51	516	70	339
MP_WT	0.48	0.10	0.88	0.21	339
MY	30.1	6.5	58	22	339
EMA	62.6	6.1	80	35	266
Fat_p8	4.7	4.7	32	1	266
Fat_12_13	3.3	3.0	18	1	266
IMF	3.3	1.3	7.2	1.6	264
EBV_BthWt	4.1	1.9	10.6	-0.2	305
EBV_GestLgth	-1.1	1.0	1.8	-3.2	190
EBV_200WT	25.2	7.0	47	3.0	305
EBV_400WT	46.7	12.1	80	4.0	305
EBV_600WT	58.7	16.1	103	7	305
EBV_200Milk	9.1	2.5	16	2.0	297
EBV_DC	-0.6	1.6	4.7	-4.3	168
EBV_CarcWt	28.6	9.3	55.0	-7.0	305
EBV_CarcRib	0.9	1.8	6.2	-3.1	274
EBV_CarcRmp	0.8	1.8	6.4	-2.3	274
EBV_CarcRBY	-0.3	0.9	1.2	-3.2	274
EBV_CarcIMF	0.2	0.6	1.9	-0.9	230
EBV_CarcEMA	0.3	1.3	3.6	-3.3	274
EBV_NFI	0.0	0.5	1.4	-1.1	274

Abbreviations:

Age	age at start of test (days)
WT	animal weight just before start of test (kg)
DMI	feed dry-matter intake during test (kg/day)
MP	Methane produced during test (L/day)
MP_WT	Methane produced per unit of animal weight WT; L/kg)
MY	Methane yield, methane produced per unit of DMI (L/kg)
EMA	cross-sectional area of the ribeye-muscle determined by ultrasound scanning prior to test (cm^2)
Fat_p8	depth of subcutaneous fat at the rump p8 site, determined by ultrasound scan (mm)
Fat_rib	depth of subcutaneous fat at the 12/13th rib site, determined by ultrasound scan (mm)
IMF	“marbling” fat content of the ribeye muscle, determined by ultrasound scan (%)
EBV	estimated breeding value: an estimate of genetic merit for an animal produced by Australia’s Breedplan system. Must attain prescribed min. accuracy before an animals EBV is published, uses measurements on the animal and its relatives
EBV_BthWt	EBV for birth weight (kg)
EBV_GestLgth	EBV for gestation length (days), shorter usually considered better
EBV_200WT	EBV for weight at 200days of age (usually near weaning, kg)
EBV_400WT	EBV for weight at 400days of age (kg)
EBV_600WT	EBV for weight at 600days of age (kg)
EBV_200Milk	EBV for additional weight at 200days due to extra milk (kg)

EBV_DC	EBV for days to calving, from when bull goes to cows to when calf born, shorter usually considered battered (days)
EBV_CarcWt	EBV for weight of carcase after slaughter (kg)
EBV_CarcRib	EBV for depth of fat at 12/13 ribs on carcase (mm)
EBV_CarcRmp	EBV for depth of fat at rump p8 site on carcase (mm)
EBV_CarcRBY	EBV for estimated retail beef yield from carcase (kg)
EBV_CarcIMF	EBV for “marbling” fat in rib-eye on carcase (%)
EBV_CarcEMA	EBV for cross-sectional area of rib-eye muscle on carcase (cm^2)
EBV_NFI	Midparent EBV for postweaning NFI, a measure of feed efficiency, lower is better (more efficient, kg/day).

Progress against Objective 1: Definition of low methane phenotype for Angus cattle

Methane yield (MY) is the principal methane phenotype that has been adopted internationally to compare natural variation between animals in the amount of methane they produce relative to their feed intake (Vlaming et al., 2008). Methane yield is defined as the amount of methane produced per unit of feed consumed, and is usually recorded over periods of 24-hour duration or longer to account for any diurnal variation in methane production.

By breeding for low methane phenotype cattle, we seek to identify those individuals that eat well and grow well, but simply produce less methane per unit of feed intake or weight gained. The relationships between daily methane production (MP) and daily feed intake (DMI), and between DMI and average daily gain in weight (ADG), are known to be strong. The strength of the relationship between MP and DMI was firmly established by (Blaxter and Clapperton, 1965).

It is well established that there exists genetic variation in both DMI and ADG, and as a consequence it is likely that there is genetic variation in MP, but this remains to be demonstrated in beef cattle. Selection of animals with low MP for breeding purposes is likely to be effective in reducing MP in the next generation. However animals selected solely for low MP are likely to be those with lower DMI and ADG. That is, selection to reduce MP could inadvertently favour smaller, less productive, and generally less profitable animals.

In this project with Angus cattle the strong phenotypic associations between MP and DMI and animal size (WT) are apparent. The correlations between MP and DMI (r=0.33) and MP and WT (r=0.40; Table 3) show that generally animals with lower feed intake and smaller, lighter animals have the lowest MP.

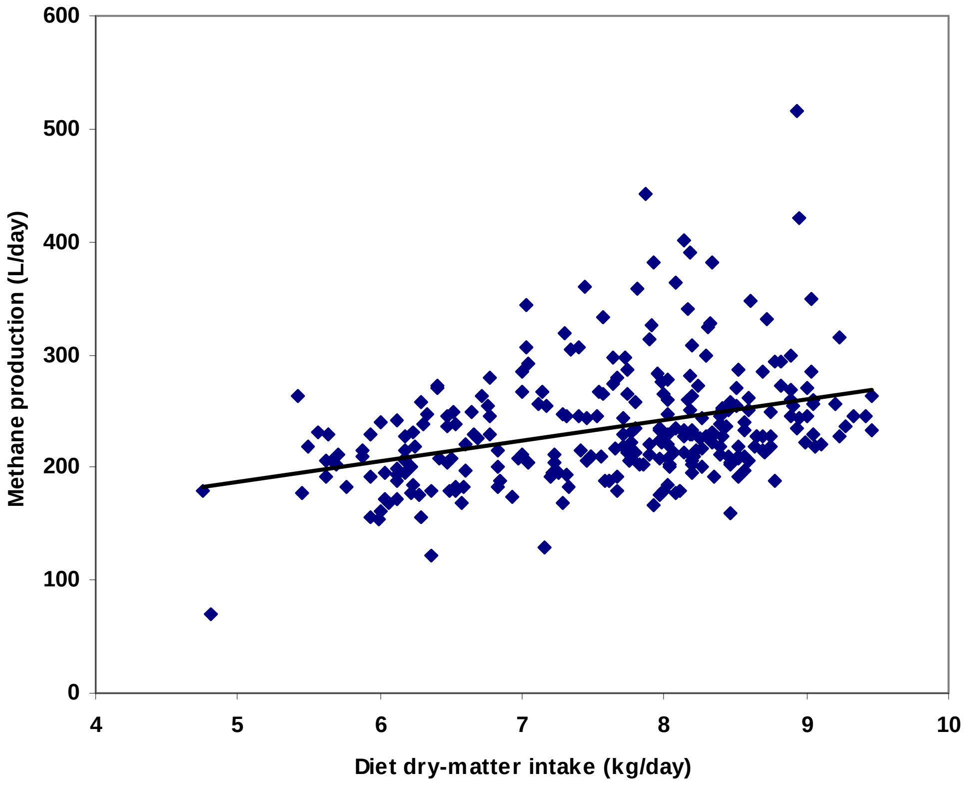
Table 3. Phenotypic correlations for methane test traits for N=339 animals tested for methane production traits.
The animals are Angus heifers in 2010 and heifers and bulls in 2011 from the NSW DPI Glen Innes research herd, and Angus bulls in 2010 and 2011 from the NSW DPI Trangie research herd.

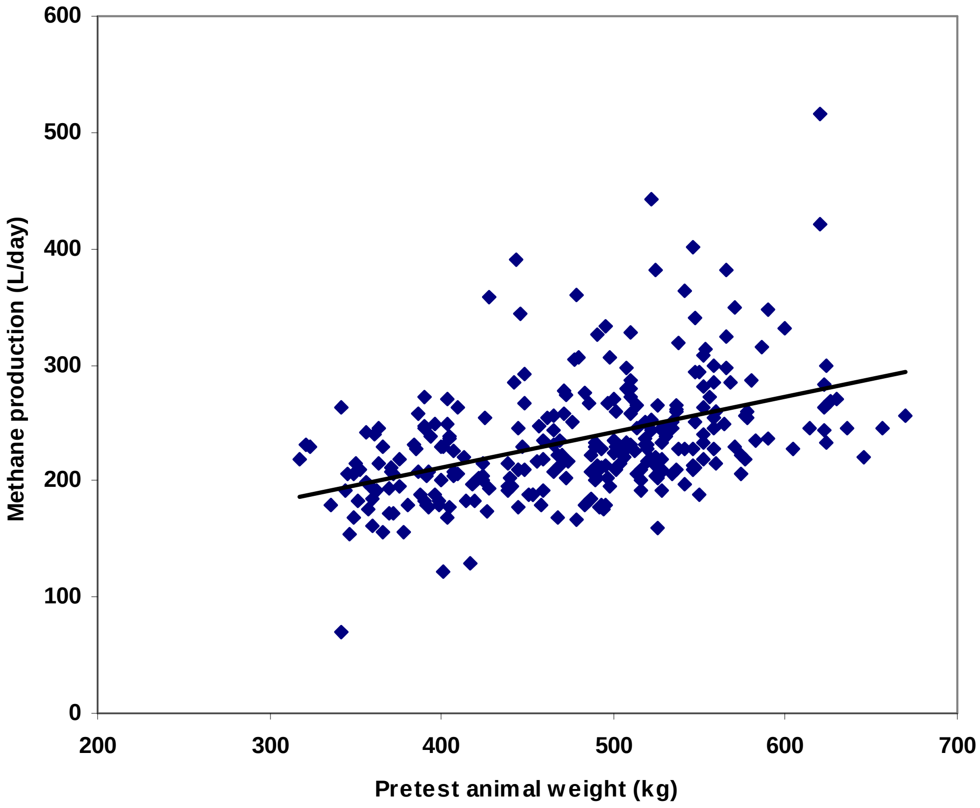
	DMI	MP	MP_WT	MY (L/kg)
WT (kg)	0.91*	0.40*	-0.33*	-0.15*
DMI (kg/day)		0.33*	-0.33*	-0.26*
MP (L/day)			0.72*	0.81*
MP_WT (L/kg)				0.95*

Abbreviations are explained under Table 2
* Correlation is different to zero at P<0.05.

However the correlations between MP and DMI, and MP and animal WT, while high, are not unity. There exists natural variation in methane production above and below these general relationships. Figure 2 shows MP plotted against DMI and WT for the Angus cattle tested in this project.

Figure 2. Natural variation in methane production above and below general relationships with dry matter intake and animal pretest weight for the N=339 Angus cattle tested in this project.





It is apparent in Figure 2 that there are cattle that naturally produce less methane relative to their feed intake (that is, have a lower MY), and less methane relative to their size (weight). Unlike MP, MY is largely phenotypically independent of DMI and weight (correlations being -0.26 and -0.15 respectively; Table 3). Should these relationships hold at a genetic level, they indicate that selection for low MY need not favour smaller animals and lower DMI. Rather it should be possible to breed animals of a desired size that produce less methane from the feed they consume.

For these reasons MY has been chosen as the preferred methane phenotype trait to explore whether natural variation in methane production exists, such that it is possible to breed lower methane emitting cattle without comprising their growth performance and profitability.

Progress against Objective 2: Heritability of the low methane trait

Evidence from differences between sires

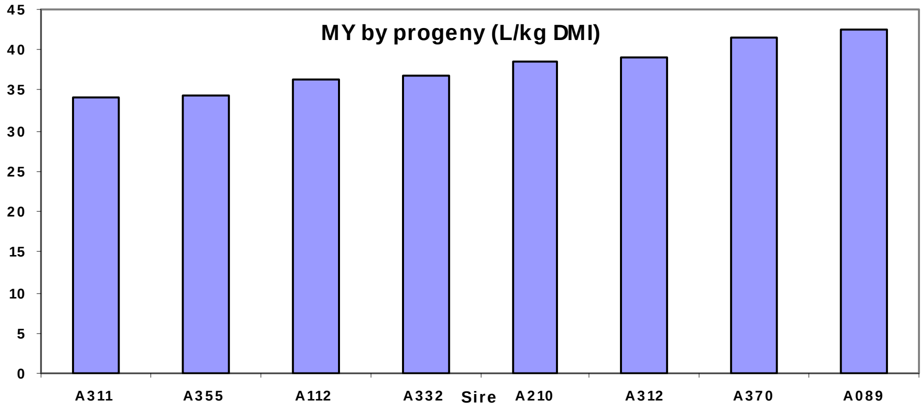
Early evidence for genetic variation in MY in Angus cattle is provided by the differences between sires in the MY by their progeny recorded in this project. Thus far, five groups of Angus bulls and heifers from the northern (Glen Innes) or the southern (Trangie) research herds have been tested for methane in 2010 and 2011 (see Table 1).

For each sire with progeny tested in this project, the average for MY of its progeny was calculated. These sire progeny averages (as LS-means) for MY for the first five groups of cattle tested in this project are shown in Figure 3. The LS-means for sires were determined using a linear model that first fitted age at test, pretest WT and then sire, with the LS-means for MY of their progeny calculated separately for each of the five tests.

There was a large range between the sires in the average MY of their progeny. Compared to the sires whose progeny had the lowest average MY in each test, the sires whose progeny had the highest average MY, had average MY that were 24%, 24%, 16%, 19% and 11% higher across the five groups of cattle tested. These results provide powerful evidence that there exist sires that can be used in cattle breeding to produce progeny with naturally lower MY.

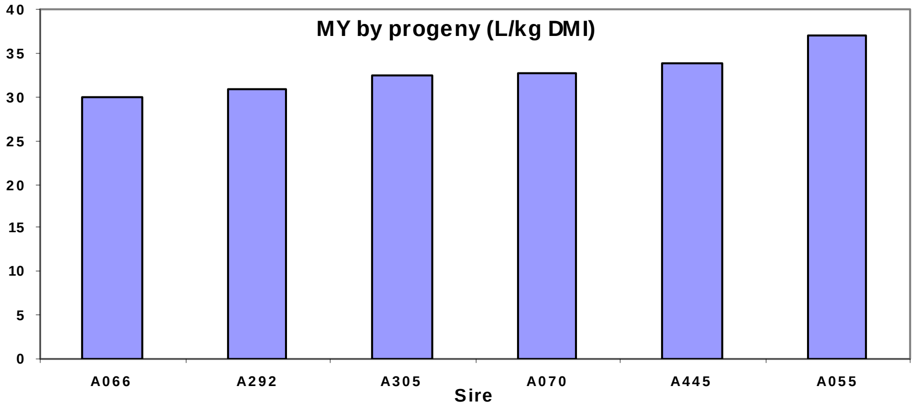
Figure 3. Sire progeny-group LS-means for MY for the sires of progeny in the first five groups of cattle tested in this project.

2010 tested Southern herd (Trangie) bulls



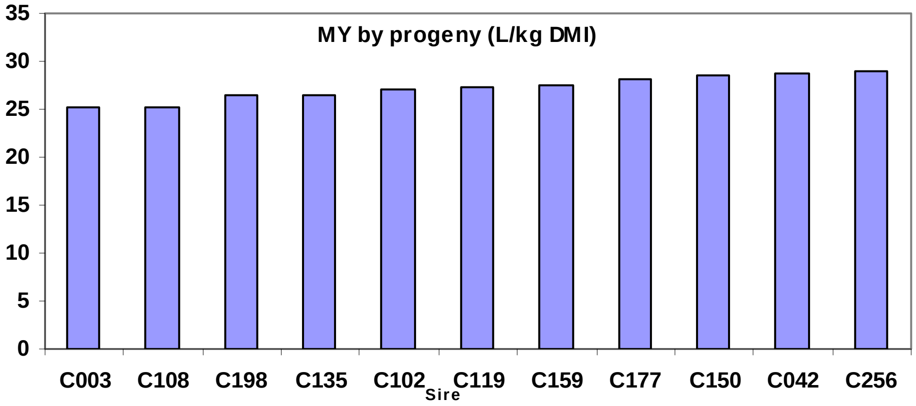
Progeny of A089 24% higher than progeny of A311; P<0.05

2010 tested Northern herd (Glen Innes) heifers



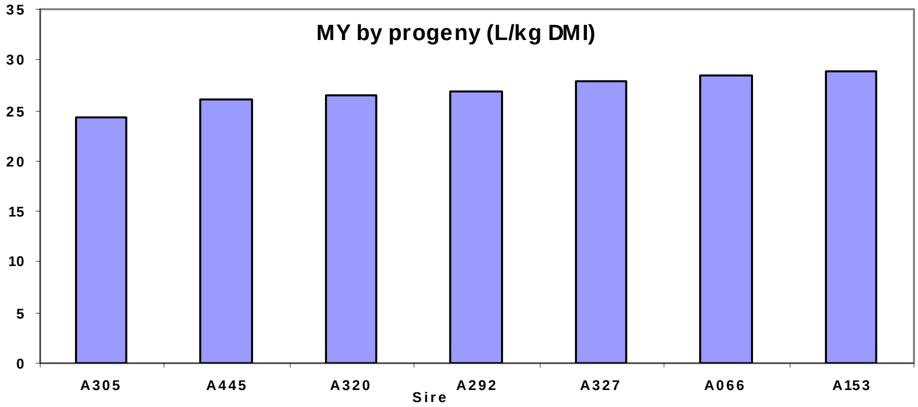
A055 24% higher than A066; P<0.05

2011 tested Southern herd (Trangie) bulls



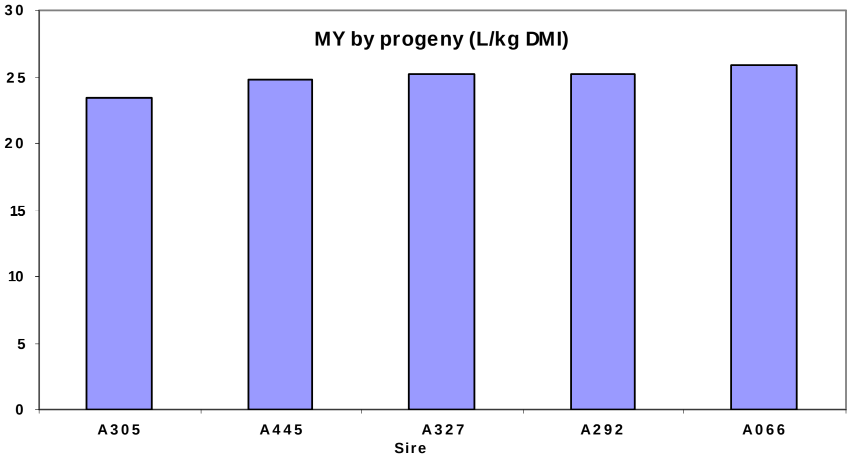
C256 16% higher than C003; P<0.05

2011 tested Northern herd (Glen Innes) bulls



A153 19% higher than A305; P<0.1

2011 tested Northern herd (Glen Innes) heifers



A066 11% higher than A305; P<0.05

Heritability

A preliminary estimate of the variance components and heritability for MY was calculated using the N=339 records collected to end of 2011, with 28 sires represented in these animals with records. Three generations of breeding records were used to build the pedigree, with a total of 1299 animals in the analysis pedigree.

Three models were fitted to estimate the additive, environmental and phenotypic variances and heritability for MY. The models: CG1 to CG3, included the following contemporary group (CG) definitions:
CG1 = cohort || year || run (within cohort); n=26
CG2 = cohort || year; n=8
CG3 = cohort || year || chamber n=61.

In these definitions: cohort refers to the group of cattle brought to the test facility (eg. typically 40 head at UNE); year is the year of test; run is the group of 10 measured at the same time at the UNE facility; and chamber is the number of the chamber in the UNE facility in which the animal was tested for methane.

For comparison, the variance components and heritability for pretest animal weight (WT) were also calculated, weight being a production trait whose heritability has been estimated before for the Trangie research herd (Arthur et al., 2001). The model fitted for weight also included a maternal genetic effect.

Table 4 shows the additive, environmental and phenotypic variances and heritability for MY and pretest animal weight (WT).

Table 4. Variance components and heritability for methane yield (MY) and pretest_wt (WT) (with standard errors). These must be considered PRELIMINARY ESTIMATES - CONFIDENTIAL, given the small dataset available for analysis.

	s^2_a	s^2_m	s^2_e	s^2_p	h^2_d	h^2_m
MY, CG1	4.1		18.6	22.7	0.18	
	(3.4)		(3.2)	(1.8)	(0.14)	
MY, CG2	4.7		17.5	22.2	0.21	
	(3.4)		(3.1)	(1.8)	(0.15)	
MY, CG3	6.1		15.2	21.3	0.29	
	(3.9)		(3.4)	(1.9)	(0.17)	
WT, CG1	979	-	839	1,818	0.54	-
	(404)		(318)	(166)	(0.19)	
WT, CG2	1,071	-	756	1,826	0.59	-
	(413)		(319)	(167)	(0.19)	
WT, CG3	1,233	-	605	1,839	0.67	-
	(467)		(356)	(184)	(0.21)	
WT, CG1	907	45	856	1,808	0.50	0.02
	(497)	(224)	(312)	(168)	(0.25)	(0.12)
WT, CG2	855	131	809	1,795	0.48	0.07
	(472)	(219)	(295)	(163)	(0.24)	(0.12)
WT, CG3	843	221	716	1,780	0.47	0.12
	(491)	(239)	(308)	(172)	(0.25)	(0.14)

Abbreviations:

CG1, CG2, CG3	Contemporary group definition used in the 3 models (see text above for further explanation)
s^2_a	Additive (genetic) variance
s^2_m	Maternal component of variance for WT only
s^2_e	Environmental variance
s^2_p	Phenotypic variance
h^2_d	Heritability of additive (genetic) variance
h^2_m	Heritability of maternal component of variance for Wt only.

The model with the more complex CG definition: CG3; best estimated the environmental variance and maximized the additive genetic variances for both traits. Examining the estimates for animal weight at start of test first, the heritability was 0.47 from the model that fitted CG3 and a maternal component. This value is high compared to that usually reported for seedstock industry Angus herds, being typically between 0.3 and 0.4.

We know from previous work with our DPI Angus herd that the herd has a higher genetic variation and heritability for liveweight traits than industry herds (Arthur et al., 2001). When adjusted for these inflated components of variance, the heritability of yearling (400-day-direct) weight in our herd was 0.27 ((Arthur et al., 2001)).

The heritability of the methane test trait (MY) was approximately 0.29 using the CG3 model (Table 4). As MY is calculated relative to feed intake, and hence to liveweight (because feed allocation in the test was based on liveweight), it is likely that the variance components for MY will not be inflated as those for weight. It is therefore likely that the heritability of MY is similar to that for growth traits, that is, it has a medium heritability.

Progress against Objective 3: Genotypic associations between methane phenotype and productivity

Relationships between the methane phenotype MY and selected live-animal traits, and with genetic merit for a range of production, fertility and carcase traits, are presented in Table 5. The production traits are those recorded in the Australian beef cattle genetic improvement system BREEDPLAN. The magnitude and direction of the regression coefficients were determined using a linear model that fitted age at test, animal weight (WT), year-of-test and research herd, and whether it was statistically significant (P<0.05) different from zero. The regression coefficients indicate how much phenotypic variation in MY is associated with phenotypic change in the live-animal traits or with a unit change in genetic merit of the production trait (as measured by estimated breeding values; EBV). Regression coefficients that were statistically different from zero provide evidence for phenotypic change in MY accompanying phenotypic or genetic variation in the production trait.

The analysis was based on data for 339 animals tested for methane production traits. The animals are Angus heifers in 2010 and heifers and bulls in 2011 from the NSW DPI Glen Innes research herd, and Angus bulls in 2010 and 2011 from the NSW DPI Trangie research herd.

Table 5. Regressions coefficients (b-values; with standard error) for methane yield (MY) with live animal weight and carcase traits, and with estimated breeding values (EBV) for a range of production traits for N=339 Angus bulls and heifers.

Live animal traits

WT	Fat_Rib	Fat_p8	IMF	EMA
0.002	0.04	0.07	0.09	-0.05
0.005	0.17	0.10	0.38	0.05

Production traits

EBV_BthWt	EBV_200WT	EBV_400WT	EBV_600WT	EBV_200Milk	EBV_NFI
-0.12	-0.04	-0.03	-0.02	-0.30*	-1.16†
0.15	0.05	0.03	0.02	0.12	0.65

Carcase traits

EBV_CarcWt	EBV_CarcRib	EBV_CarcRmp	EBV_CarcIMF	EBV_CarcEMA	EBV_CarcRBY
-0.01	-0.15	-0.17	-0.26	-0.42†	0.001
0.04	0.15	0.15	0.53	0.22	0.31

Fertility traits

EBV_GestLgth	EBV_DC
0.01	0.11
0.44	0.24

Abbreviations are explained under Table 2.
* Regression coefficient is different to zero at P<0.05; † trend to difference at P<0.1.

These results show that variation in weight attained on pasture prior to testing, and variation in scanned measurements of body composition on the live animal (subcutaneous fat over the ribs and rump, marbling fat (IMF) and size of the eye-muscle (EMA)) near the time of methane measurement had no association with variation observed in MY. This lack of significant phenotypic regressions in the sample of animals so far tested indicate that MY was independent of, that is not influenced by, animal weight and body composition when measured on restricted feed intake under the conditions of the test.

True genetic correlations between MY and the standard production traits could not be determined because of the small size of the dataset of records. However, phenotypic variation in MY does not appear to be associated with genetic variation in weight at birth, 200 days, 400 days and 600 days of age, or with genetic variation in carcase traits, except perhaps for genetic variation in carcase eye-muscle area (CarcEMA), or with genetic variation in the fertility traits (gestation length (GestLth) and days–to-calving (DC)) reported by BREEDPLAN. The association between variation in MY with genetic variation in extra weaning weight due to milk (200Milk) and genetic variation in carcase eye-muscle area is curious. It may reflect low MY being associated with genes favouring preferential diversion of feed energy from methane to extra milk from the cow and a more muscle growth. But this is just speculation until we have more data.

Methane yield tended to be negatively correlated with the NFI feed efficiency EBV. That is, genetic superiority for feed efficiency (as lower EBV_NFI) was associated with higher MY.

Discussion

This report good progress toward meeting the three objectives of this project.

Objective 1: Methane yield (MY) is defined as the methane phenotype that has now been accepted internationally for measurement of natural variation between animals in the amount of methane they produce relative to their feed intake. This methane phenotype has been adopted in this project to evaluate natural differences between animals in methane production. Large natural variation in MY between individual animals and differences between sires in MY by their progeny has provided early evidence that breeding for lower methane emissions is possible.

Objective 2: The unavoidable delay in commencement of measurement of cattle in the new beef cattle measurement facility on the UNE campus resulted in fewer records being collected in this project than originally planned. However, based on the MY records taken we report statistically significant differences between sires in MY by their progeny. This provides evidence that this methane production trait is under genetic control, and is an immediate demonstration that it is possible to find sires whose progeny have a naturally lower methane production. A preliminary estimate for the heritability for MY of approximately 0.3 is presented. A moderate heritability, similar to that for growth traits, is indicated, and if confirmed using a larger dataset, would indicate that breeding to reduce MY is possible.

Usually a minimum of one thousand records are required to calculate the heritability of a production trait with reasonable precision. This number of records had not been obtained at the time of this final report. More records for animals with MY are required and for this reason testing of animals for MY needs to continue after the date of this final report.

Objective 3: Preliminary results show that phenotypic associations are low, probably negotiable, for MY with weight gained on pasture and body composition (eye-muscle area, subcutaneous fat over the ribs and rump) and meat quality (marbling fat) taken near the time of methane measurement. While the magnitude of genetic correlations cannot be determined until more records for MY are collected, it does appear that phenotypic variation in MY does not appear to be associated with genetic variation in weight traits, important body composition and carcass traits, and fertility traits (as indicated by lack of associations with EBV).

The implication from these preliminary results are that it is unlikely to be possible to predict MY for individual cattle based on simple phenotypic measurements such as weight or scanned body composition information. Further, selection using current BREEDPLAN® EBV to change methane production, particularly MY, in the next generation of cattle will not lead to a predictable change in MY.

The corollary is that to be able to select to predictably change MY will require a new breeding value for a methane-related trait, such as MY, to become available to cattle breeders through the BREDPLAN system.

Our results showed that MY tended to be negatively correlated with the NFI feed efficiency EBV. That is, genetic superiority for feed efficiency (as lower EBV_NFI) was associated with higher MY. When tested under conditions of ad-libitum feeding we have previously shown that lower EBV_NFI are associated with slightly lower DMI, lower MP and lower methane intensity (MP_WT) but not lower MY (Hegarty et al., 2007). We have previously shown that a greater ability to digest feed is one of the physiological mechanisms contributing to superior (lower) NFI (Richardson and Herd, 2004). In this project, cattle are offered a restricted feed allowance that is proportional to their weight. Under these conditions we might hypothesize that low EBV_NFI animals can extract more feed energy from their diet for growth, which is a good animal production outcome, but will also produce more methane, that is a higher MY.

This has implications for the use of genetic improvement in NFI as a breeding tool to reduce MP from cattle on pastures. It may be that on poor quality pastures, breeding for low NFI will result in cows with slightly higher daily MP and MY, but because they are more productive (better growth themselves or by their calves), they have the same or lower (better) methane intensity (L methane/unit weight) than unimproved cows. These relationships will need to be reviewed as more data becomes available if breeding for low NFI is to be recommended as a methane mitigation strategy in livestock.

Conclusion

Our results showed that there are cattle that naturally produce less methane relative to their feed intake, that is, cattle that have a naturally lower methane yield. Differences between sires in methane yield by their progeny were observed and were statistically significant. They provide evidence that there exists genetic variation in methane yield and demonstrate that sires exist that can be used in cattle breeding to produce progeny with lower methane emissions. A preliminary estimate for the heritability of methane yield is presented. In this small dataset methane yield appeared to be moderately heritable, similar to that for yearling weight.

It appears that methane yield is not strongly associated with phenotypic or genetic variation in standard animal weight, body composition or fertility traits used the Australian beef cattle genetic improvement system BREEDPLAN®. Our results indicate that to be able to use animal breeding to predictably reduce methane yield will require a new breeding value for a methane-related trait to become available to cattle breeders.

Acknowledgements

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Appendix 1

Publications arising from project

Journal Papers

Arthur, P. F., Herd, R. M. and Basarab, J. A. (2010). The role of cattle genetically efficient in feed utilisation in an Australian carbon trading environment. AFBM Journal 7: 5-13. See copy in Appendix 4.

Scientific Conferences

Arthur, P., Donoghue, K., Herd, R. and Hegarty, R. (2009). Can animal genetic improvement strategies assist in reducing greenhouse gas emissions from beef cattle? In Industry and Investment NSW Beef & Sheep Conference, pages14-18. Orange Agricultural Institute, Orange, NSW.

Arthur, P. F., Donoghue, K. A., Herd, R. M. and Hegarty, R. S. (2009). The role of animal genetic improvement in reducing greenhouse gas emissions from beef cattle. In Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics, Vol. 18, 472-475. See copy in Appendix 4.

Herd, R., Arthur, P., Hegarty, R., Bird, S. and Donoghue, K. (2011). Breeding cattle for lower greenhouse gas emissions in an Australian carbon trading environment. In Proceedings of the CCRSPI Conference, Melbourne, Victoria.

Herd, R., Bird, S., Donoghue, K., Hegarty, R. and Arthur, P. (2011). Breeding beef cattle for lower greenhouse gas emissions. In 4th Annual World Congress of Industrial Biotechnology, Dalian, China. See copy in Appendix 4.

Herd, R. M., Donoghue, K. A., Bird, S. H., Hegarty, R. F. and Arthur, P. A. (2011). Breeding Angus cattle that naturally emit less methane. In Proceedings of the Association for Advancement of Animal Breeding and Genetics, Vol. 19, 187-190. Perth WA. See copy in Appendix 4.

Herd, R. M., Bird, S. H., Donoghue, K. A., Hegarty, R. F. and Arthur, P. A. (2012). Sire differences in enteric methane emissions in Australian Angus cattle. In Proceedings of the 2nd Joint Conference of the Australian and New Zealand Societies of Animal Production, July 2012. Accepted. Lincoln, New Zealand.

Herd, R. M., Donoghue, K. A., Bird, S. H., Hegarty, R. F. and Arthur, P. A. (2012). Genetic improvement of Australian Angus cattle for lower methane emissions. In Proceedings of the Conference of the British Society of Animal Science, April 2012. Accepted. Nottingham, England.

Workshops, Field-days, Lectures, etc.

Arthur, P. F., Herd, R. M. and Basarab, J. A. (2010). The role of cattle genetically efficient in feed utilisation in an Australian carbon trading environment. In Abstract and Talk to I&I NSW Beef and Sheep Conference "Increasing the Steaks". Tamworth, NSW.

Hegarty, R. and Bird, S. (2012). Livestock Methane Research. Lecture and Beef Unit tour to the Agricultural and Environmental Science Teachers Professional Development Conference, UNE, Armidale, NSW. 2 March 2012.

Hegarty, R. S., Goopy, J. P., Bird, S. H. and Herd, R. M. (2010). Genetic control of methane production - current research. In Abstract and Talk to I&I NSW Beef and Sheep Conference "Increasing the Steaks". Tamworth, NSW.

Herd, R. (2010). Feed Efficiency and Methane Research: Briefing to I&I NSW Deputy-Director General George Davey, Beef Industry Centre. 9 July 2010. UNE, Armidale, NSW.

Herd, R. (2010). Genetic improvement of beef cattle for GHG outcomes. In I&I NSW

Climate in Primary Industries Meeting. 28-29 April 2010. Sydney, NSW.

Herd, R. (2011). BCCH 1006. Genetic improvement of beef cattle for GHG outcomes. Oral presentation to RELRP External Science Review, 1 August 2011, Brisbane Qld.

Herd, R. (2011). Breeding beef cattle for lower greenhouse gas emissions, and genetic improvement in feed efficiency in farm animals. Lectures to faculty and students of The Agricultural University of Inner Mongolia, Hohhot, China, 30 April 2011.

Herd, R. (2011). Breeding beef cattle for lower greenhouse gas emissions, and genetic improvement in feed efficiency in farm animals. Lectures to faculty and students of The Agricultural University of Shanxi, Taigu, China, 6 May 2011.

Herd, R. (2011). Breeding cattle and sheep for lower greenhouse gas emissions (2009–2012). In Primary Industries Science & Research Briefing Note-Climate in Primary Industries, Vol. Winter 2011(Ed G. Kelly). NSW Government - Primary Industries.

Herd, R. (2011). Breeding cattle for feed efficiency and Breeding cattle that naturally emit less methane. In UNE ANPR 440/540 Feedlot Management Course Lecture. 22 September 2011.

Herd, R. (2011). Host visit for 40 PICSE High School Science students and give lecture on cattle GHG research and inspect beef methane facility. UNE, Armidale, NSW.

Herd, R. (2012). Genetic improvement of beef cattle for GHG outcomes. Project Report for NSW DPI, 28 February 2012. 14 pages.

Herd, R. (2012). Livestock Methane. Lecture to the Catchment Management Authorities (CMA) workshop. 2 February 2012. Sydney, NSW.

Herd, R. (2012). Livestock Nutrition and Methane research at UNE. Lecture and animal house inspection to 55 visiting university students from Uruguay. 23 February 2012. UNE, Armidale, NSW.

Herd, R. (2012). Methodologies for benchmarking livestock methane emissions in southern Australia. Spoken and powerpoint report to DCCEE Livestock Technical Working Group. 22 February 2012. DCCEE, Canberra, ACT.

Herd, R. M. (2011). BCCH 1006. Genetic improvement of beef cattle for GHG outcomes. Project report to RELRP Technical Workshop. 19 October 2011, Perth WA.

Media

Herd, R. (2010). Low emission cattle. In Radio interview with David McGeoch, ABC NSW Rural Report, 8 July 2010.

Herd, R. and Hegarty, R. (2010). Clearing the air: Breed for less methane. In Agriculture Today (Newspaper), 1 July 2010, Pages 1 and 7. Sydney, NSW. See copy in Appendix 4.

Leader, T. C. (2010). Industry forced to adapt. In The Country Leader Newspaper 19 July 2010, 15 Armidale, NSW. –See copy in Appendix 4.

The Armidale Independent. (2010). Livestock researchers focus on future full of change. In The Armidale Independent Newspaper 28 July 2010, 5 and 8 Armidale, NSW.

The Armidale Independent. (2012). Good breeding reduces the burps. In The Armidale Independent Newspaper-Rural News, 15 February 2012, Armidale, NSW. See copy in Appendix 4.

The Methane Project. (2011). Bid to breed cattle with less 'burps'. In The Narromine News and Trangie Advocate, 16 December 2011. See copy in Appendix 4.

The Methane Project. (2012). Breeding reduces burps. In The Mudgee Guardian Newspaper, 10 February 2012, Mudgee, NSW. See copy in Appendix 4.

The Methane Project. (2012). David Mula's photo and Trangie project highlighted. In

NSW DPI Intranet Homepage - February 2012.

The Methane Project. (2012). Good breeding helps to reduce greenhouse burps. In The Grafton Daily Examiner Newspaper, 10 February 2012, Grafton, NSW. See copy in Appendix 4.

The Methane Project. (2012). Good breeding reduces greenhouse burps. In Max Express, NSW Trade & Investment, Orange, NSW, Vol. 95, 15 February 2012. See copy in Appendix 4.

The Methane Project. (2012). More research, less methane. In The Armidale Express, 20 February 2012, Armidale, NSW. See copy in Appendix 4.

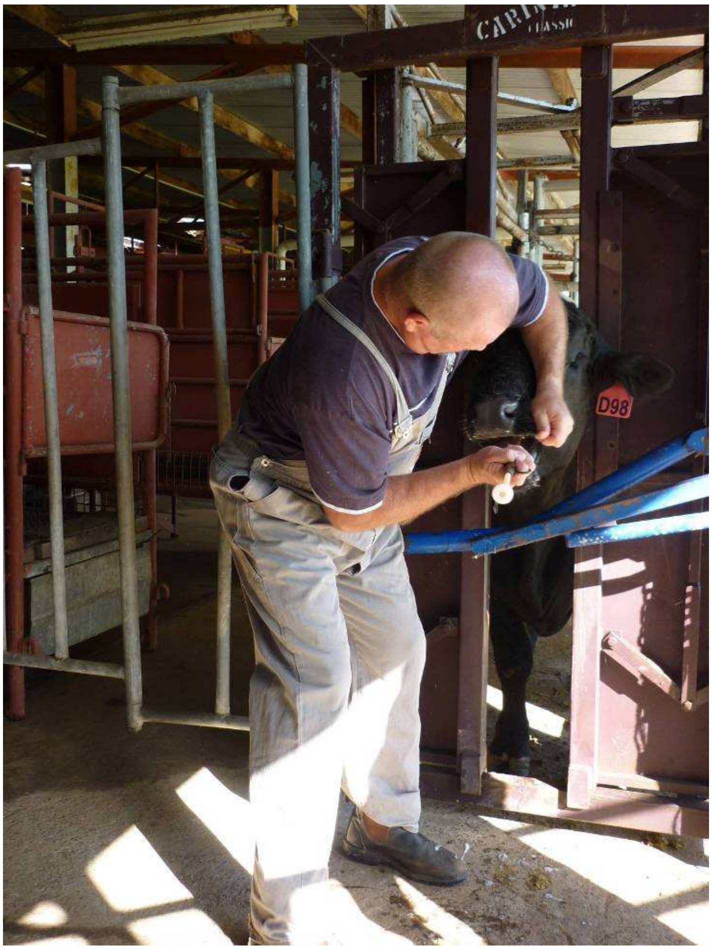
Scalan, J. and Herd, R. (2010). Livestock researchers focus on a future full of change. UNE Web News. 13 July 2010.

Appendix 2

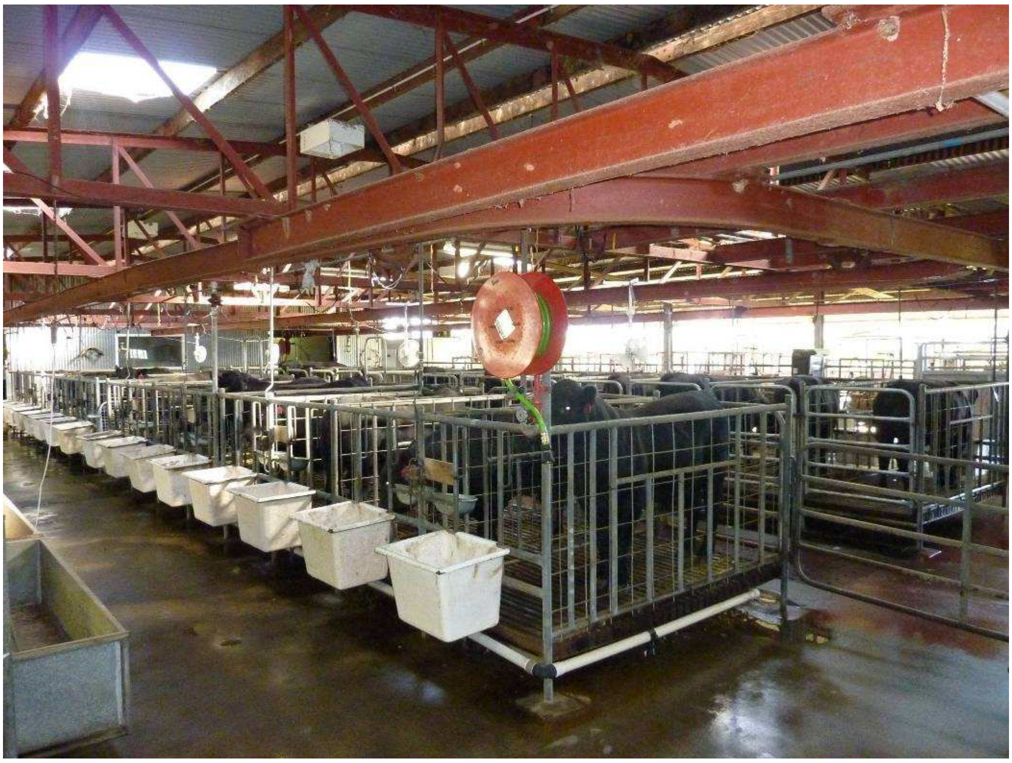
Grafton Agricultural Research Centre cattle animal house and methane measurement using the SF6 tracer method in 2010

The rumen bolus containing the SF6 tracer gas. The gas is released at a known, constant rate and mixes with the methane expired by the animal. From a sample of the expired air, and measurement of methane and SF6 concentrations, the methane produced by the animal can be calculated.

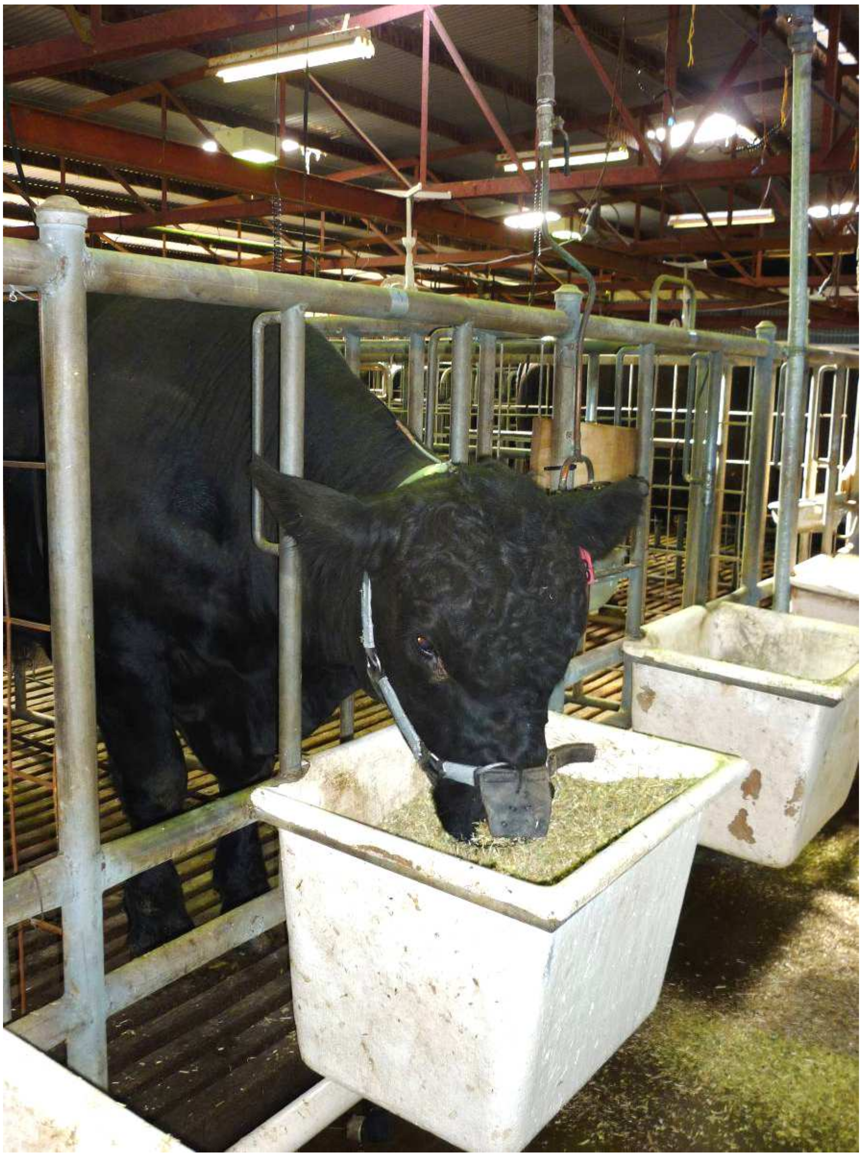
Placing the bolus into the rumen.



Cattle housed in individual pens. They are feed a known quantity of feed each day based on their bodyweight while methane production is being recorded.



The halter on the animals head holds plastic tubing in place over the animal’s nose. Through the tubing expired air is drawn and stored for later analysis of its methane and SF6 concentration.



Appendix 3

The Large Animal Facility, including cattle animal house and methane measurement chambers, opened on the UNE campus in April 2011

Front view of cattle animal house and methane measurement facility.

Methane chambers viewed from central laneway inside cattle animal house:

Methane chambers: two rows of five chambers with gas sample ducting.

Chamber opened to allow daily feed allowance to be provided

Angus bull inside methane measurement chamber with feed and water provided.

Appendix 4

Copies of selected project publications

AFBM Journal vol 7 - no 2

The role of cattle genetically efficient in feed utilisation in an Australian carbon trading environment

PF Arthur[1], RM Herd[2] and JA Basarab[3]
[1]Industry & Investment NSW, Elizabeth Macarthur Agricultural Institute, Narellan NSW 2567, Australia
[2]Industry & Investment NSW, Beef Industry Centre, Armidale NSW 2351, Australia
[3]Alberta Agriculture and Rural Development, Lacombe Research Centre, Lacombe AB, Canada T4L 1W1
paul.arthur@industry.nsw.gov.au

Abstract: Residual feed intake (RFI) is a measure of feed efficiency in beef cattle. It is a moderately heritable trait, and cattle with low RFI consume less feed than expected at the same level of growth relative to their high RFI contemporaries. Selection for RFI is a relatively new genetic improvement tool in beef cattle to reduce the cost of production, and currently has a low level of adoption in the industry. Selection for low RFI is associated with reduction in greenhouse gas (GHG) emissions, hence could play a role in any carbon trading scheme implemented in Australia. For any GHG reduction protocol to be acceptable in a carbon trading/offset environment, it needs to follow United Nations IPCC guidelines, be based on science, be quantifiable and be auditable. The beef industry already has quality assurance systems in place for RFI that can be fine-tuned to meet these criteria. Scientific information currently available is adequate for the development of GHG emission reduction protocols for cattle raised for slaughter. Selection for RFI also has an impact on GHG emissions from the breeding herd. However, information currently available lacks the degree of accuracy needed for protocol development. It is therefore recommended that funding be provided to continue the research on the relationships among RFI, cow feed intake and maternal productivity traits.

Keywords: feed efficiency, residual feed intake, methane, greenhouse gas, emission, beef cattle.

Introduction

The agricultural sector is a source of greenhouse gas (GHG) emissions worldwide, with the magnitude of its contribution differing from country to country. A recent Food and Agriculture Organization (FAO) report estimates that globally livestock are responsible for 18 percent of greenhouse gas emissions (Steinfeld et al. 2006), though this report attributes all clearing of rain forests to livestock and does not account for carbon sequestration or for the substitution of biological nitrogen for fertiliser nitrogen. In Australia, emissions from the livestock industries are estimated at 62.8 Mt CO_2e, which represented 10.7% of the net national GHG emissions in 2008 (DCCEE 2010). More than 90% of the livestock emissions are from ruminants, predominantly sheep and cattle.

Greenhouse gases generated by cattle production include methane (CH_4) and nitrous oxide (N_2O), which have global warming potentials 21 and 310 times that of CO_2 respectively, making them potent GHGs. Methane primarily arises from enteric fermentation, but also small amounts derive from manure stores.

Some countries already have a carbon trading scheme, and Australia is currently in the process of putting a price on carbon. With this comes the need for all industries to examine and develop strategies to reduce their contribution to GHG emissions. The objectives of this paper were to provide the scientific information underpinning the use of selection for feed efficiency in beef cattle to reduce GHG emissions, to review the beef industries preparedness for selection for feed efficiency, and to outline a process that can be used to develop quantification protocols for any Australian carbon trading/offset scheme.

Feed efficiency in beef cattle

Providing feed to animals is a major input cost in most animal production systems. The utilisation of the feed consumed by an animal involves complex biological processes and interactions with the environment. In addition, it is complicated by the fact that feed intake is highly correlated with body size and level of production. To overcome these complexities and to relate feed intake to production system efficiency, several measures of feed efficiency have been developed and used, as described in detail by Archer et al. (1999).

In Australia residual feed intake (RFI) has been chosen as the feed efficiency trait for genetic improvement programs in beef cattle. It is also called net feed intake (NFI). Residual feed intake represents the amount of feed consumed, net of the animal's requirements for maintenance of body weight and production (Arthur et al. 2001b). It is measured as the difference between an animal's actual feed intake and its expected feed intake based on its size and growth over a specified period. Therefore, efficient animals are those that eat less than expected and have lower RFI values relative to inefficient animals.

Genetics of feed efficiency

The genetic control of RFI was one of the components of the review of feed efficiency in beef cattle by Archer et al. (1999), using pre-

1999 information. A summary of the results from Archer et al. (1999) has been combined with the results of a review by Arthur and Herd (2008) and presented in Table 1. The available estimates of genetic variation cover studies from several countries, different breed types of cattle, using different types of diets, and with different sources of ingredients (barley, oats, wheat, silage etc.).

These results indicate that there is genetic variation in RFI in most beef cattle breeds, and that the heritability is moderate; similar to that for growth. This indicates that there is the potential to genetically improve the efficiency of feed utilisation by beef cattle through selection for low RFI. RFI has strong positive genetic correlations with feed intake and other measures of feed efficiency (e.g. feed conversion ratio), and a weak to moderate correlation with fatness. The available information suggests that RFI is not genetically correlated with other traits of economic importance in beef cattle. Reviews by Arthur and Herd (2005, 2008) contain detailed information on the genetics of RFI, including genetic correlations with other economically important traits.

Proof of concept demonstration herds

At the Agricultural Research Centre at Trangie, Australia, Angus cattle have been divergently selected for low RFI and high RFI since 1994 (Arthur et al. 2001c). It is a single trait selection population, with the sole criterion for replacement bulls and heifers being RFI. Two generations of selection had been achieved by 1999 and there was evidence of a clear divergence between the two lines. The evaluation of the responses to selection by the RFI selection lines, up to the 1999-born progeny, clearly indicates that after two generations of selection the growth of young cattle and the maternal productivity of cows from the low RFI line were similar to those of the high RFI lines. However, the low RFI cattle consumed less feed to achieve this, and produced less methane (see Table 2). The quality of the meat of cattle from the two selection lines was also found to be similar. The only differences found were that low RFI cattle are slightly leaner and that low RFI cows tended to calve a few days later in the calving season (Arthur et al. 2005).

Summary of genetics of RFI

- There is genetic variation in RFI, and the trait is moderately heritable.
- Progeny of cattle selected for low RFI (high efficiency) consume less feed for the same level of growth as progeny of cattle selected for high RFI, irrespective of the source of the ingredients (e.g. wheat, oats or barley) of the diet.
- On lower quality nutrition, such as pasture, where daily feed energy intake is low, cattle selected for low RFI may exhibit higher growth rates than progeny of cattle selected for high RFI, at the same level of feed intake.
- Cattle tested as efficient (low RFI) during the post-weaning period remain efficient throughout their lives.
- Genetic improvement in feed efficiency in beef cattle can be achieved by selection for low RFI, with minimal level of correlated responses in growth and other economically important traits.

Residual feed intake and GHG emissions

The relationship between feed intake and methane production in ruminants has been known for many years, and is recognised in most algorithms predicting methane production rate (Blaxter and Clapperton 1965; Pelchen and Peters 1998). In general, the higher the feed intake, the higher the methane production per ruminant animal, on the same feedstuff.

Low RFI cattle have the same level of production as high RFI cattle, but they do so at a reduced level of feed intake (Arthur et al. 2001a; Nkrumah et al. 2007). This finding therefore offers the potential to reduce methane emission from cattle without compromising productivity. To explore this potential an Australian research group (Herd et al. 2002) and a Canadian group (Okine et al. 2001) used feed intake and production data from RFI projects to calculate methane production using standard algorithms (Blaxter and Clapperton 1965).

The Australian research group used the RFI selection line data (Arthur et al. 2001c) and estimated that cattle selected for low RFI produced 15% less enteric methane per animal per day than those selected for high RFI. Methane and nitrous oxide production from fermentation of faeces was 15% and 17% lower, respectively, in low RFI compared to high RFI cattle. It was concluded that the total greenhouse gas emission per unit liveweight gain was 16% lower in the low RFI cattle relative to the high RFI cattle.

The results from the Canadian study indicated that yearly methane emissions and manure production from high efficiency (low RFI) steers was 21% and 15% lower, respectively, than for low efficiency (high RFI) steers, with no significant difference in size and growth traits between the two groups. In both studies the GHG emissions were estimated, and not measured.

Empirical data

To obtain empirical data, where actual methane measurements have been taken to validate these findings, the Australian group used the progeny of cattle from the RFI selection lines (Arthur et al. 2001c). Ten steers from the low RFI and 10 from the high RFI selection lines were selected out of 76 steers. All steers had just completed RFI tests. Methane was measured by a marker-based method with the marker gas (SF_6) released from an intraruminal permeation device. All steers were fitted with a halter and gas collection apparatus, and gas sample collections were made over 10 days, after a five-day adaptation period. The gas analysis procedure is described in Hegarty et al. (2007). Methane production in the low RFI steers was 25% less than that in the high RFI steers (Hegarty et al. 2007).

The Canadian group used 11 extreme high and 8 extreme low and 8 medium RFI steers for calorimetry studies. These animals were obtained from 306 steers tested for RFI. The mean body weight (BW) as well as mean average daily gain (ADG) on the RFI test was similar between the low RFI (496 kg BW and 1.46 kg/day ADG) and high RFI (501 kg BW and 1.48 kg/day ADG) groups. However, the low RFI steers consumed 17% less feed than the high RFI group, resulting in mean RFI of -1.18 for the low RFI and +1.26 for the high RFI groups. Oxygen and methane production of the steers were measured in a four-chamber, open circuit, indirect calorimetry system. Methane production in the low RFI steers was 28% less than that in the high RFI steers (Nkrumah et al. 2006).

From the two studies it was not clear if there are differences between low RFI and high RFI steers in methane energy loss as a percentage of gross energy intake. However, the studies clearly show that low RFI cattle emit less methane, mainly through the fact that they have lower feed intake relative to high RFI cattle for the same level of production.

In studies where respiratory hoods have been used to measure methane, there is some evidence that low RFI animals also have improved DM digestibility due to a different rumen microbial population and/or host mediated processes (e.g. rate of passage, and rumen pH), thus resulting in less methane produced per unit of dry matter intake (DMI) or gross energy intake (Nkrumah et al., 2007). It is expected that these initial findings will be confirmed as more reports from studies using respiratory hoods are published.

Implications on various diets

The available information on the relationship between RFI and methane emission indicates that there is a direct association between feed intake and methane emissions. Basically, animals that consume less feed emit less methane. It therefore implies that where animals are fed diets of similar nutritive value (including similar digestibility), the type of ingredients used (e.g. wheat *versus* barley) is of little consequence.

Standard RFI testing protocols have been developed in Australia (Exton 2001) and they specify some standard nutritional quality of the test diet. For example, the diet for post-weaning RFI test should provide approximately 10 MJ metabolisable energy (ME)/kg dry matter (DM). For feedlot RFI tests the diet should provide approximately 12 MJ ME/kg DM. With such standardisation of testing, the magnitude of reduction in methane emission by low RFI cattle is dependent mainly on feed intake and not the source or type of ingredients in the diet.

Summary of the relationship between RFI and GHG emissions

- Low RFI cattle emit less methane than high RFI cattle in experiments where production data were used in the estimation of methane production (15-21%), and also where actual methane emission was measured (25-30%).
- Low RFI cattle produce less faecal DM than high RFI cattle.
- The reduction in methane production by low RFI cattle is achieved with no major impact on the growth of the cattle.
- The reduction in methane emissions by low RFI cattle is through reduction of feed intake.

Industry implementation of RFI technology

For genetic improvement of RFI to be implemented, animals superior for RFI need to be used for breeding. The first step is to measure potential breeding animals or their relatives for RFI. Seedstock breeders can then offer such animals for sale as breeding animals with reliable genetic merit information. The majority of potential breeding animals will be measured for other economically important traits. This is because these traits are relatively easy to measure and the cost of measurement is low. Residual feed intake, however, is an expensive trait to measure. Therefore seedstock breeders will not measure all their potential breeding stock for RFI. The results of the breeding systems design analysis done by Archer et al. (2004) indicate that for RFI there is no need to measure the whole cohort of potential breeding animals. Profitability is maximised when 10–20% of the potential breeding bulls are measured. After weaning, information on the calves themselves, and their relatives should be used to select those to be tested for RFI. In other words, if the genetic merit of a bull for other important traits is not good, then there is no need to test this bull for RFI. This is because bull buyers will not only look at the genetic merit for RFI; they will also look at the genetic merit for the other traits before making purchasing decisions.

Quality standards for RFI testing

Feed intake and its utilisation by cattle involve complex biological processes and interactions with the environment. In order to be able to compare RFI test results across time and across location, as required for genetic analyses, it is important to control as much as possible those factors that affect feed intake and its utilisation. There is therefore a need to standardise the methodologies and procedures associated with RFI testing. Testing standards and protocols for the measurement of RFI have been established based on scientific data published by Archer et al. (1997). In consultation with industry this scientific data has been used to develop a standards manual for testing cattle for RFI (Exton 2001). This ensures that data from tests conducted at different times and at different locations can be used for genetic improvement.

Standardised estimation of genetic merit

The genetic evaluation system for beef cattle in Australia is called BREEDPLAN and it handles all traits recorded in beef cattle for all breeds. Having a centralised system ensures that there is a single national database and the procedures for computation of the genetic merit (estimated breeding value, EBV) of an animal are standardised. In Australia, standardisation of computational procedures and result reporting are achieved because of the centralisation of the system.

Industry adoption

The beef research feedlot at Tullimba (near Armidale, NSW) is currently the major RFI testing facility for cattle in Australia. More than 10,000 cattle have been tested for RFI at Tullimba and other locations in Australia, with Angus breed having the most cattle tested. Since 2002, Australia's BREEDPLAN genetic improvement program has been providing trial EBVs for RFI. This means that there is opportunity for bull buyers to purchase bulls with known genetic merit for RFI to improve their herds.

Economic benefits Three integrated long-term research projects on the genetics of feed efficiency in beef cattle have been in progress in Australia since 1992, as reported by Arthur et al. (2004). Data from these projects formed the basis of the following economic analyses.

The first analysis (Exton et al., 2000) modelled a 100-cow herd run on native pasture, with progeny being grown on improved pastures. In the production system modelled, surplus heifers were sold at 18 months of age into the domestic market and 80% of the steers were sold for feedlot finishing and subsequent sale as heavy export steers. Gross margin budget and cashflow analyses for this herd showed that, despite the initial cost of purchasing bulls genetically superior for feed efficiency, over a 25-year investment period, the internal rate of return was a healthy 61% and the net present value (NPV) of surplus income over expenses was $21,907. This equates to an annual benefit per cow of $8.76.

In a second analysis (Archer et al. 2004), an evaluation of the benefit of recording RFI in industry breeding schemes using a model of investment and gene flow resulting from selection activities was conducted. The analysis considered breeding schemes targeting either the high quality Japanese export market (with steers fed for 210 days in the feedlot) or the grass-fed domestic market. A base scenario was modelled where a range of criteria (without feed intake data) were used. A second scenario incorporated selection of sires for the breeding unit using a two-stage selection process, with a proportion of bulls selected after weaning for measurement of feed intake. After accounting for the cost of measuring feed intake (ranging from $150 to $450), additional profit was generated from inclusion of feed intake measurement on a proportion of bulls, for all the breeding schemes considered. Profit was generally maximised where 10% to 20% of bulls were selected at weaning for measurement of feed intake.

It should be noted that in all the economic analyses presented, the genetic selection applied was not for the single trait, RFI. It was evaluated in a multi-trait selection index in representative genetic improvement schemes. The benefits presented are the marginal increase due to the inclusion of RFI and, therefore, it represents the additional benefits from genetic improvement in RFI.

Managing barriers to adoption A review by Arthur et al. (2004) highlighted some of the barriers to adoption. Research conducted since then has led to a better understanding of RFI and its benefits to seedstock and commercial beef producers. Some of the barriers and how they are being managed are as follows:

- The complexity of automatic feeders has limited the on-farm use of such equipment, and RFI testing is now predominantly done at centralised test stations.

- There was a general lack of appreciation in the beef industry of the importance of feed costs to enterprise profitability. However, Australian feedlot managers now have a good appreciation of the importance of the cost of feed to their enterprises. The recent droughts and high grain prices have strengthened the awareness of feedlot and cow-calf managers of feed costs, and increased their desire for more efficient cattle to feed.
- Accurate measurement of individual animal pasture feed intake is not available. Although it is still desirable to be able to accurately measure individual animal feed intake at pasture, a study by Herd et al. (2004) reporting that low RFI cattle (which are usually tested on prepared diets) are also efficient on pasture, has made this need less critical.
- The cost of identifying animals with superior RFI is high. The simplest solution is to bring down the RFI measurement cost. For most other economically important traits every potential breeding bull is measured. For RFI however, the high cost of measurement means that, in practice, not all potential breeding bulls will be measured. The finding by Archer et al. (2004) that profit was maximised where 10-20% of all potential breeding bulls were tested for RFI translates to a great cost saving to the individual seedstock breeder. The cost of testing for RFI has come down to about $150, much lower than the $300 used in previous estimates.
- There is currently intensive research on DNA markers for RFI in Australia and overseas. Some of these markers have been commercialised and others are to follow soon. The use of DNA information in genetic improvement is currently being developed and it is hoped that the price of identifying cattle that are genetically superior for RFI will come down even further.

Summary of industry implementation

- Quality standards for testing cattle for RFI have been developed and implemented.
- Standardised data processing and EBV computation have been implemented through BREEDPLAN.
- Inspite of the high initial capital outlay to invest in RFI technology, selection for low RFI is profitable at the individual farm level as well as at the national industry level.
- In spite of certain barriers to adoption, RFI technology is already being adopted by the beef industry, with more than 10,000 cattle tested for RFI.

Carbon trading environment

The economic benefit from the reduction of feed costs to the enterprise will be the driver for adoption of RFI technology in the beef industry. The potential financial benefit through the carbon trading system will be a welcome by-product of selection. Hence the estimation of this financial benefit from carbon trading does not take into account the cost of adopting the RFI technology.

Financial benefit from carbon trading

Using data from the Australian research projects on RFI, Alford et al. (2006) undertook to model the methane abatement resulting from the anticipated adoption of RFI in breeding programs within the Australian beef industry over a 25-year period. The expected reduction in methane emissions from the Australian beef herd resulting from using bulls identified as being more feed efficient as a result of having a low RFI was modelled, both in a single herd in southern Australia and in the national herd. A gene flow model was developed to simulate the spread of improved RFI genes through a breeding herd over 25 years. Based on the estimated gene flow, the voluntary feed intakes were revised annually for all beef classes using livestock populations taken from the Australian National Greenhouse Gas Inventory (NGGI). Changes in emissions (kg methane/animal/year) associated with the reduction in feed intake were then calculated using NGGI procedures. Annual enteric methane emissions from both the individual and national herd were calculated by multiplying the livestock numbers in each beef class by the revised estimates of emissions per animal.

For a representative 100-cow commercial herd in southern Australia, in which bulls of superior RFI were purchased in year 1, the cumulative total of enteric methane abatement during the 25-year simulation period was 24.5 t. This represents a 7.4% cumulative decrease in enteric methane production over the simulation period, compared with an unimproved herd. The annual saving in methane production over an unimproved herd by year 25 was 15.9%. The estimated 24.5 t of methane saved over 25 years by the representative southern Australian herd is equivalent to an annual average saving of 20.6 t (CO_2 E) which could be valued given access to a carbon trading scheme. Using a per tonne of CO_2 value of AU$10.50 (NSW Independent Pricing and Regulatory Tribunal 2005), a minimum value for the saved methane output due to adoption of RFI genetics for a 100-cow southern herd is on average $216 per annum. Therefore, enteric methane abatement resulting from selection for lower RFI is not at the expense of farm profit, as may be the case for some alternative abatement strategies. It should also be noted that the saving in feed costs from using low RFI cattle is likely to be more than five times the value of the carbon credits.

For the national herd, various adoption rates and adoption time lags were applied. At the base scenario of 0.76% rate of genetic improvement and 30% maximum adoption, the cumulative reduction in national emissions was 568,100 t of methane over 25 years, with annual emissions in year 25 being 3.1% lower than in year 1. Any increase in the rate of genetic improvement and/or the maximum adoption level increases the cumulative reduction in methane emission. For example, a 50% increase in the annual rate of genetic improvement in RFI for bulls used in the commercial herd, from 0.76% to 1.14% per year, would result in a decrease in annual enteric methane production of 84,400t, or 4.3% by year 25. Similarly, a 50% increase in the maximum level of adoption of the RFI technology would result in an increase in annual abatement of enteric methane to 91,300 t or 4.7% by year 25.

It was concluded that, despite the substantial time lag for most genetic improvement programs, such as that for RFI, selection for reduced RFI is expected to reduce greenhouse gas emissions from beef cattle. Residual feed intake offers a commercially attractive and practical abatement technology because it does not demand reductions in livestock numbers or level of production. The two particular aspects of selection for improved RFI that ensure its role in livestock greenhouse gas abatement are (i) the impact of the genetic improvement on the beef herd, not just finishing animals, and (ii) the cumulative nature of the response over time.

Procedures for quantification and auditing of emissions

For any GHG reduction protocol to be acceptable it has to follow IPCC (2006) guidelines, be based on science, be quantifiable and be auditable.

Quantification of GHG reduction The production of methane from enteric fermentation in cattle can be measured directly in respiration chambers or indirectly using tracers such as sulphur hexafluoride. These are short duration techniques, and are expensive, cumbersome and not practical under normal farming conditions. But they can be, and have been, used to quantify the relationship between low RFI and reduction in methane production through reduction in feed intake. This reduction in feed intake is captured by RFI, since it is the reduction in feed intake relative to the expected feed intake for the size and growth of the animal. Measured as kg of feed (DM basis) per day, this should form the basis of any protocol development for GHG emission reduction from selection for low RFI.

Use of genetic merit information The protocol is based on genetic selection for low RFI, hence the genetic merit (expressed as EBV) of an animal for RFI (rather than the phenotypic measure) should be used for quantification of reductions in GHG emissions.

The beef industry is made up of a number of sectors. In broad terms the participants of each sector may contribute in the following manner:

- The seedstock breeder will be breeding low RFI animals for sale. It is expected that breeding stock for sale will have BREEDPLAN EBVs for RFI and accuracies as part of the sale information.
- The cow-calf manager will purchase breeding stock with BREEDPLAN EBVs for RFI from a seedtock breeder and use them in matings to produce progeny. The expectation is that the genetic merit of an offspring from such a mating by the cow-calf manager will be equivalent to half the genetic merit of its sire plus half that of its dam. Hence each progeny can be "assigned" a RFI EBV equal to the mean EBV of the parents, if the progeny does not have its own BREEDPLAN EBV for RFI. If one of the parents does not have a BREEDPLAN EBV, its EBV can be assumed to be zero. Selection for RFI is relatively new in the industry and has not been practised in most beef herds. As a consequence, the assumption of a value of zero (being breed average for RFI) for RFI EBV for non-BREEDPLAN animals is valid.

  Apart from those retained by the manager for replacement, it is expected that most of the progeny will be sold at the appropriate age/weight. At the time of sale the assigned RFI EBV should be provided as part of the sale information.
- The feedlot manager will purchase these cattle from the cow-calf manager and feed them for slaughter. These cattle will maintain their assigned RFI EBVs.
- The abattoir and wholesale/retail outlets process and sell the beef to the consumer. If any of the practitioners in this sector are eligible for carbon credits, the assigned EBVs of the slaughter animals can be used.

Estimating reduction in feed intake Estimated breeding values are computed using a specified year as the base. The mean EBV for a particular trait is set to zero for all the animals born in that year. This allows genetic improvement relative to the base year to be tracked over years ahead. This base year can also be used in the protocol to illustrate that practice change since that year has resulted in reductions in GHG emissions. For RFI it is also essential that the average DMI of animals during the RFI test period for the base year is calculated or estimated. For example, if for a participating herd 2004 is chosen as the base year, the average DMI of all cattle that were tested for RFI can be calculated or estimated at a standard ME content per kg DM. With this information the reduction in feed intake due to selection for RFI can be estimated using procedures similar to the reports by Exton et al. (2000) and Alford et al. (2006).

Estimating reductions in GHG emissions The estimates of DMI of the animals can then be used in standard equations (e.g. IPCC 2006) to estimate the greenhouse gas production from enteric fermentation and manure production. The greenhouse gas production of these animals can then be compared with those obtained from using the estimated mean DMI for the current year.

Verification strategies The phenotypic measure of RFI and EBVs for RFI will be used as the basis for any protocol development. As indicated, there are quality assurance standard protocols for RFI as they relate to measurement, data, computational method, and estimation of genetic merit of an animal. These QA standards lend themselves to auditing. The only other step that requires an audit trail is a system to verify that the breeding animal with the low RFI EBV was used to produce the progeny, for which the GHG emission credits are being claimed. It is therefore important that the identification of animals tested for RFI be linked into Australia's National Livestock Identification System (NLIS).

Cattle specific GHG protocol issues There are issues that unresolved will become barriers to adoption of GHG reduction protocols in cattle. These include:

- Ownership of the carbon credit. The beef cattle industry is made up of several sectors, and only few vertically integrated businesses. An animal will typically change ownership a number of times from conception to slaughter. The linkage of the protocol with the NLIS makes it easier to identify the owner of the cattle at any point in time. However, it is not easy to determine who owns the carbon credits. Is it the seedstock breeder who originally produced the parent(s), or the cow-calf manager who produced the progeny or the feedlot operator who fed the cattle but may not own them? The issue of ownership of the carbon credits needs to be worked through and agreed upon.
- Social barriers. The cattle community and the general public have some scepticism in relation to the science of climate change in general, and the government policies that drive GHG reductions. Efforts should be made to win the trust of these stakeholders.

General conclusion

Selection for RFI is a relatively new genetic improvement tool in beef cattle to reduce the cost of production. Currently it has a low level of adoption in the beef industry, but the rate and level of adoption has the potential to increase as the cost of identifying superior animals reduces.

Selection for low RFI is associated with reduction in GHG emissions by cattle and could play a role in any carbon trading scheme implemented in Australia.

The expectation is that the economic benefit from the reduction of feed costs to the enterprise will be the driver for adoption of RFI technology. The potential financial benefit through the carbon trading system will be a welcome by-product of selection.

In the province of Alberta in Canada, a GHG reduction protocol based on selection for RFI has been developed and it is in the final stages of the approval process (Climate Change Central 2010). After approval the protocol will be used in the carbon offset program of the province.

For any GHG reduction protocol to be acceptable in a carbon trading/offset environment, it needs to follow IPCC (2006) guidelines, be based on science, be quantifiable and be auditable. In the beef industry in Australia there are already quality assurance systems in place that can be fine-tuned to meet these criteria. Scientific information currently available is adequate for the development of GHG emission reduction protocols for cattle raised for slaughter. Selection for RFI also has an impact of GHG emissions from the breeding herd. However, information currently available lacks the degree of accuracy needed for protocol development. It is therefore recommended that funding be provided to continue the research on the relationships among RFI, cow feed intake and maternal productivity traits.

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Appendix

Table 1. Heritability estimates (± standard error) for residual feed intake in beef cattle

Breed type	Country	No. of animals	Heritability	Source
Pre 2000 reports	Various		0.14 to 0.28	Archer et al. (1999)
Hereford	Britain	540	0.16 ± 0.08	Herd and Bishop (2000)
Angus	Australia	1180	0.39 ± 0.03	Arthur et al. (2001a)
Charolais	France	792	0.39 ± 0.04	Arthur et al. (2001b)
Mixed	Australia	1481	0.18 ± 0.06	Robinson and Oddy (2004)
Mixed	Canada	2284	0.38 ± 0.07	Schenkel et al. (2004)
Wagyu	Japan	740	0.24 ± 0.11	Hoque et al. (2006)
Composite	Canada	464	0.21 ± 0.12	Nkrumah et al. (2007)
Brahman	Australia	680	0.24 ± 0.11	Barwick et al. (2009)
Tropical Composites	Australia	783	0.38 ± 0.12	Barwick et al. (2009)

Table 2. Least squares means (± standard errors) for growth, feed efficiency, reproduction, maternal productivity and methane production in beef cattle divergently selected for residual feed intake (RFI)

Traits	Generations of selection	Selection line		Significance
		Low RFI	High RFI	
Growth and feed efficiency	2.0			
Weaning weight (kg)		232.5 ± 3.1	228.3 ± 2.9	n.s.
Yearling weight (kg)		384.3 ± 6.9	380.7 ± 6.7	n.s.
Average daily gain (kg)		1.44 ± 0.03	1.40 ± 0.03	n.s.
P8 fat depth (mm)		6.7 ± 0.3	8.8 ± 0.3	*
Eye muscle area, (cm^2)		72.1 ± 0.8	74.2 ± 0.7	n.s.
Daily feed intake (kg)		9.4 ± 0.3	10.6 ± 0.3	*
Feed conversion ratio		6.6 ± 0.2	7.8 ± 0.2	*
Residual feed intake (kg/day)		-0.54 ± 0.12	0.71 ± 0.17	*
Maternal productivity[A,B]	1.5			
Calving rate (%)		89.2	88.3	n.s.
Weaning rate (%)		81.5	80.2	n.s.
Milk yield (kg/day)		7.5 ± 0.3	7.8 ± 0.3	n.s.
Wt of calf weaned (kg)		191.3 ± 8.4	198.4 ± 7.7	n.s.
Methane production in steers[C]	2.4			
Daily feed intake (kg)		8.38	14.13	*
Average daily gain (ADG ,kg)		1.13	1.23	n.s.
Methane (g/day)		142.3	190.2	*
Methane (g/kg of ADG)		131.8	173.0	P = 0.09

[A] Source: Arthur et al. 2005.
[B] Per cow exposed to bull.
[C] Source: Hegarty et al. 2007.
* $P<0.05$; n.s. $P>0.05$.

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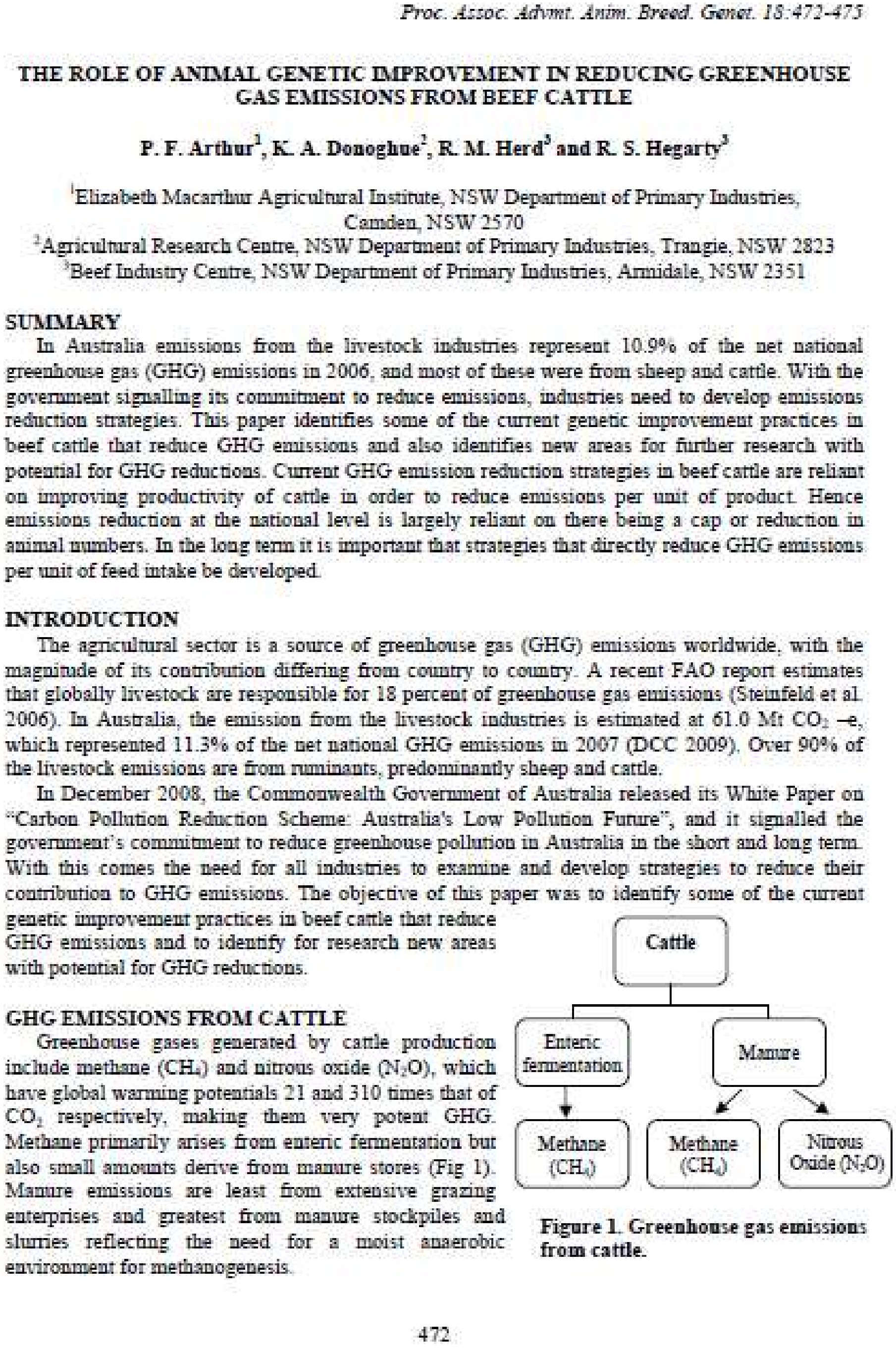

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THE ROLE OF ANIMAL GENETIC IMPROVEMENT IN REDUCING GREENHOUSE GAS EMISSIONS FROM BEEF CATTLE

P. F. Arthur[1], K. A. Donoghue[2], R. M. Herd[3] and R. S. Hegarty[3]

[1]Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries,
Camden, NSW 2570
[2]Agricultural Research Centre, NSW Department of Primary Industries, Trangie, NSW 2823
[3]Beef Industry Centre, NSW Department of Primary Industries, Armidale, NSW 2351

SUMMARY

In Australia emissions from the livestock industries represent 10.9% of the net national greenhouse gas (GHG) emissions in 2006, and most of these were from sheep and cattle. With the government signalling its commitment to reduce emissions, industries need to develop emissions reduction strategies. This paper identifies some of the current genetic improvement practices in beef cattle that reduce GHG emissions and also identifies new areas for further research with potential for GHG reductions. Current GHG emission reduction strategies in beef cattle are reliant on improving productivity of cattle in order to reduce emissions per unit of product. Hence emissions reduction at the national level is largely reliant on there being a cap or reduction in animal numbers. In the long term it is important that strategies that directly reduce GHG emissions per unit of feed intake be developed.

INTRODUCTION

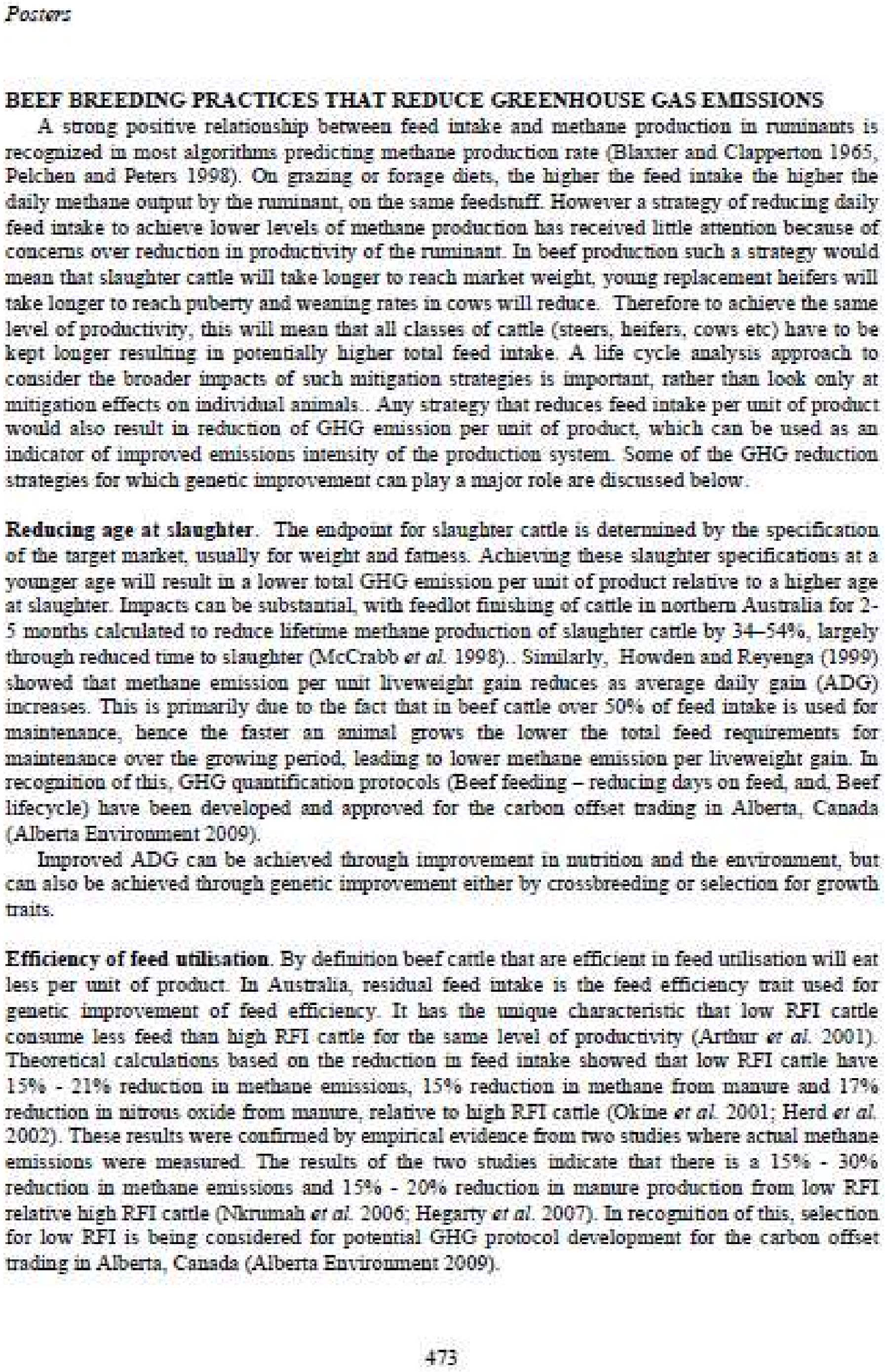
The agricultural sector is a source of greenhouse gas (GHG) emissions worldwide, with the magnitude of its contribution differing from country to country. A recent FAO report estimates that globally livestock are responsible for 18 percent of greenhouse gas emissions (Steinfeld et al. 2006). In Australia, the emission from the livestock industries is estimated at 61.0 Mt CO_2 –e, which represented 11.3% of the net national GHG emissions in 2007 (DCC 2009). Over 90% of the livestock emissions are from ruminants, predominantly sheep and cattle.

In December 2008, the Commonwealth Government of Australia released its White Paper on "Carbon Pollution Reduction Scheme: Australia's Low Pollution Future", and it signalled the government's commitment to reduce greenhouse pollution in Australia in the short and long term. With this comes the need for all industries to examine and develop strategies to reduce their contribution to GHG emissions. The objective of this paper was to identify some of the current genetic improvement practices in beef cattle that reduce GHG emissions and to identify for research new areas with potential for GHG reductions.

GHG EMISSIONS FROM CATTLE

Greenhouse gases generated by cattle production include methane (CH_4) and nitrous oxide (N_2O), which have global warming potentials 21 and 310 times that of CO_2 respectively, making them very potent GHG. Methane primarily arises from enteric fermentation but also small amounts derive from manure stores (Fig 1). Manure emissions are least from extensive grazing enterprises and greatest from manure stockpiles and slurries reflecting the need for a moist anaerobic environment for methanogenesis.

Figure 1. Greenhouse gas emissions from cattle.



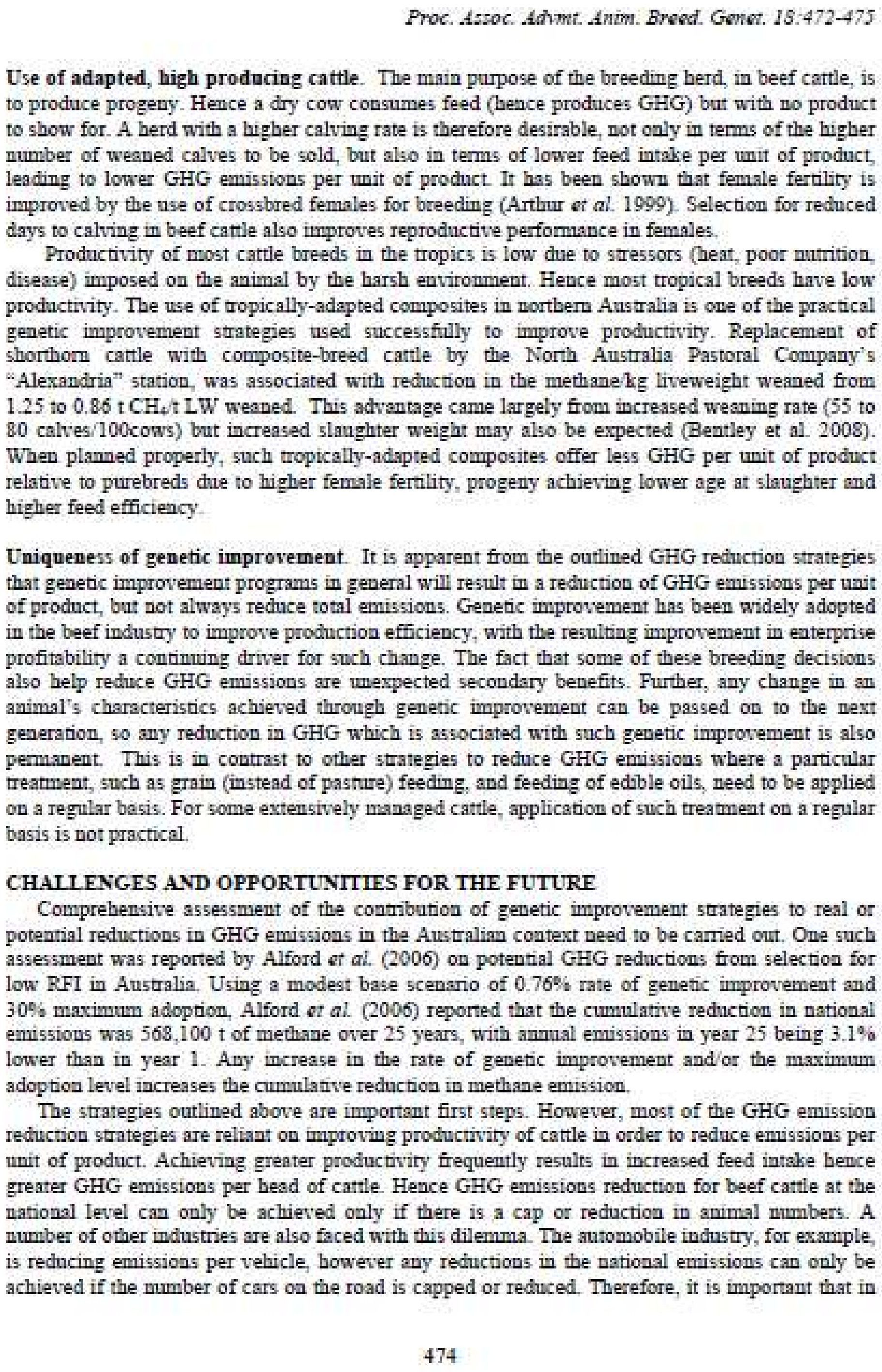
BEEF BREEDING PRACTICES THAT REDUCE GREENHOUSE GAS EMISSIONS

A strong positive relationship between feed intake and methane production in ruminants is recognized in most algorithms predicting methane production rate (Blaxter and Clapperton 1965, Pelchen and Peters 1998). On grazing or forage diets, the higher the feed intake the higher the daily methane output by the ruminant, on the same feedstuff. However a strategy of reducing daily feed intake to achieve lower levels of methane production has received little attention because of concerns over reduction in productivity of the ruminant. In beef production such a strategy would mean that slaughter cattle will take longer to reach market weight, young replacement heifers will take longer to reach puberty and weaning rates in cows will reduce. Therefore to achieve the same level of productivity, this will mean that all classes of cattle (steers, heifers, cows etc) have to be kept longer resulting in potentially higher total feed intake. A life cycle analysis approach to consider the broader impacts of such mitigation strategies is important, rather than look only at mitigation effects on individual animals.. Any strategy that reduces feed intake per unit of product would also result in reduction of GHG emission per unit of product, which can be used as an indicator of improved emissions intensity of the production system. Some of the GHG reduction strategies for which genetic improvement can play a major role are discussed below.

Reducing age at slaughter. The endpoint for slaughter cattle is determined by the specification of the target market, usually for weight and fatness. Achieving these slaughter specifications at a younger age will result in a lower total GHG emission per unit of product relative to a higher age at slaughter. Impacts can be substantial, with feedlot finishing of cattle in northern Australia for 2-5 months calculated to reduce lifetime methane production of slaughter cattle by 34–54%, largely through reduced time to slaughter (McCrabb *et al.* 1998).. Similarly, Howden and Reyenga (1999) showed that methane emission per unit liveweight gain reduces as average daily gain (ADG) increases. This is primarily due to the fact that in beef cattle over 50% of feed intake is used for maintenance, hence the faster an animal grows the lower the total feed requirements for maintenance over the growing period, leading to lower methane emission per liveweight gain. In recognition of this, GHG quantification protocols (Beef feeding – reducing days on feed, and, Beef lifecycle) have been developed and approved for the carbon offset trading in Alberta, Canada (Alberta Environment 2009).

Improved ADG can be achieved through improvement in nutrition and the environment, but can also be achieved through genetic improvement either by crossbreeding or selection for growth traits.

Efficiency of feed utilisation. By definition beef cattle that are efficient in feed utilisation will eat less per unit of product. In Australia, residual feed intake is the feed efficiency trait used for genetic improvement of feed efficiency. It has the unique characteristic that low RFI cattle consume less feed than high RFI cattle for the same level of productivity (Arthur *et al.* 2001). Theoretical calculations based on the reduction in feed intake showed that low RFI cattle have 15% - 21% reduction in methane emissions, 15% reduction in methane from manure and 17% reduction in nitrous oxide from manure, relative to high RFI cattle (Okine *et al.* 2001; Herd *et al.* 2002). These results were confirmed by empirical evidence from two studies where actual methane emissions were measured. The results of the two studies indicate that there is a 15% - 30% reduction in methane emissions and 15% - 20% reduction in manure production from low RFI relative high RFI cattle (Nkrumah *et al.* 2006; Hegarty *et al.* 2007). In recognition of this, selection for low RFI is being considered for potential GHG protocol development for the carbon offset trading in Alberta, Canada (Alberta Environment 2009).



Use of adapted, high producing cattle. The main purpose of the breeding herd, in beef cattle, is to produce progeny. Hence a dry cow consumes feed (hence produces GHG) but with no product to show for. A herd with a higher calving rate is therefore desirable, not only in terms of the higher number of weaned calves to be sold, but also in terms of lower feed intake per unit of product, leading to lower GHG emissions per unit of product. It has been shown that female fertility is improved by the use of crossbred females for breeding (Arthur *et al.* 1999). Selection for reduced days to calving in beef cattle also improves reproductive performance in females.

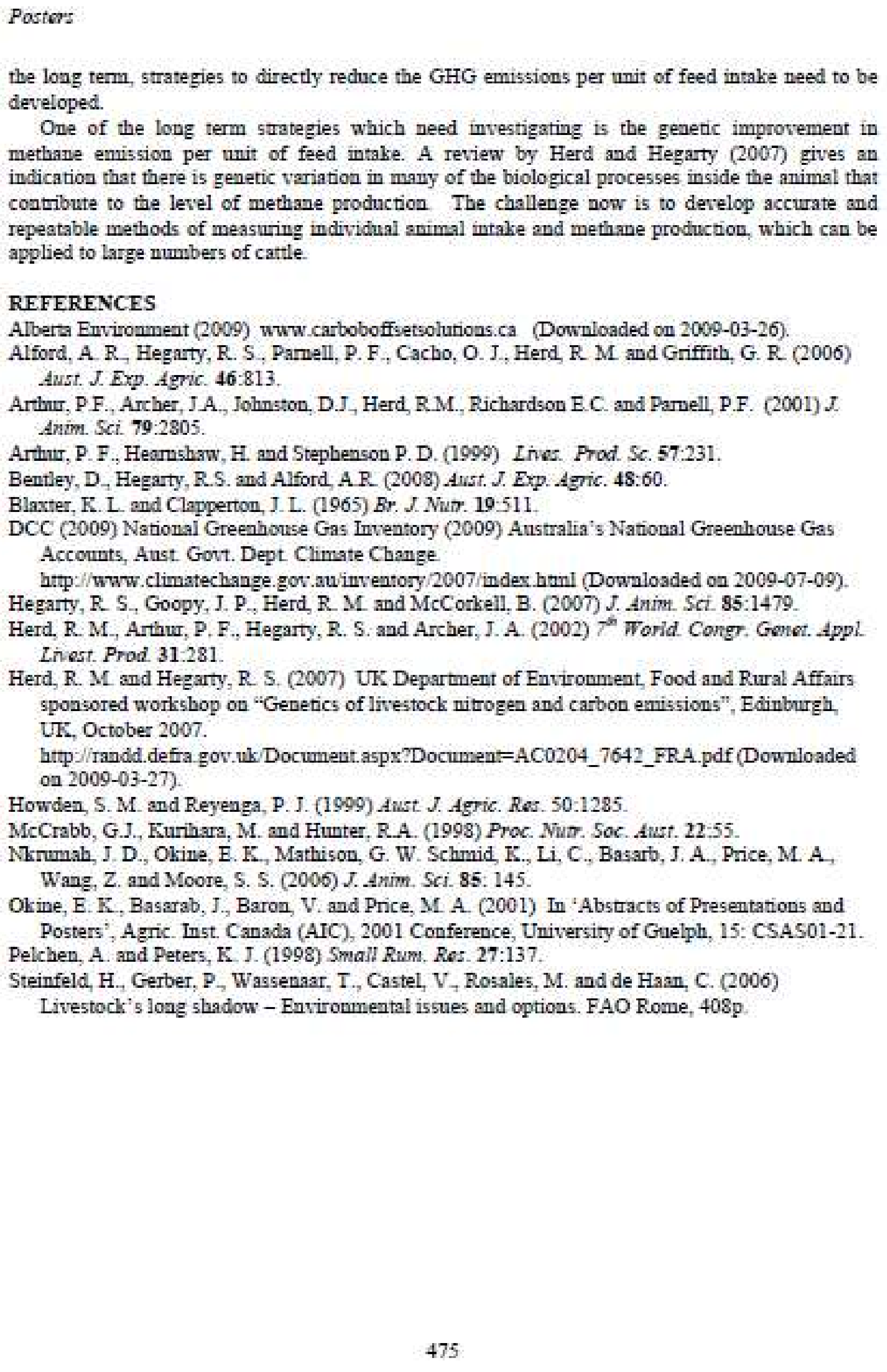
Productivity of most cattle breeds in the tropics is low due to stressors (heat, poor nutrition, disease) imposed on the animal by the harsh environment. Hence most tropical breeds have low productivity. The use of tropically-adapted composites in northern Australia is one of the practical genetic improvement strategies used successfully to improve productivity. Replacement of shorthorn cattle with composite-breed cattle by the North Australia Pastoral Company's "Alexandria" station, was associated with reduction in the methane/kg liveweight weaned from 1.25 to 0.86 t CH_4/t LW weaned. This advantage came largely from increased weaning rate (55 to 80 calves/100cows) but increased slaughter weight may also be expected (Bentley et al. 2008). When planned properly, such tropically-adapted composites offer less GHG per unit of product relative to purebreds due to higher female fertility, progeny achieving lower age at slaughter and higher feed efficiency.

Uniqueness of genetic improvement. It is apparent from the outlined GHG reduction strategies that genetic improvement programs in general will result in a reduction of GHG emissions per unit of product, but not always reduce total emissions. Genetic improvement has been widely adopted in the beef industry to improve production efficiency, with the resulting improvement in enterprise profitability a continuing driver for such change. The fact that some of these breeding decisions also help reduce GHG emissions are unexpected secondary benefits. Further, any change in an animal's characteristics achieved through genetic improvement can be passed on to the next generation, so any reduction in GHG which is associated with such genetic improvement is also permanent. This is in contrast to other strategies to reduce GHG emissions where a particular treatment, such as grain (instead of pasture) feeding, and feeding of edible oils, need to be applied on a regular basis. For some extensively managed cattle, application of such treatment on a regular basis is not practical.

CHALLENGES AND OPPORTUNITIES FOR THE FUTURE

Comprehensive assessment of the contribution of genetic improvement strategies to real or potential reductions in GHG emissions in the Australian context need to be carried out. One such assessment was reported by Alford *et al.* (2006) on potential GHG reductions from selection for low RFI in Australia. Using a modest base scenario of 0.76% rate of genetic improvement and 30% maximum adoption, Alford *et al.* (2006) reported that the cumulative reduction in national emissions was 568,100 t of methane over 25 years, with annual emissions in year 25 being 3.1% lower than in year 1. Any increase in the rate of genetic improvement and/or the maximum adoption level increases the cumulative reduction in methane emission.

The strategies outlined above are important first steps. However, most of the GHG emission reduction strategies are reliant on improving productivity of cattle in order to reduce emissions per unit of product. Achieving greater productivity frequently results in increased feed intake hence greater GHG emissions per head of cattle. Hence GHG emissions reduction for beef cattle at the national level can only be achieved only if there is a cap or reduction in animal numbers. A number of other industries are also faced with this dilemma. The automobile industry, for example, is reducing emissions per vehicle, however any reductions in the national emissions can only be achieved if the number of cars on the road is capped or reduced. Therefore, it is important that in



the long term, strategies to directly reduce the GHG emissions per unit of feed intake need to be developed.

One of the long term strategies which need investigating is the genetic improvement in methane emission per unit of feed intake. A review by Herd and Hegarty (2007) gives an indication that there is genetic variation in many of the biological processes inside the animal that contribute to the level of methane production. The challenge now is to develop accurate and repeatable methods of measuring individual animal intake and methane production, which can be applied to large numbers of cattle.

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BREEDING ANGUS CATTLE THAT NATURALLY EMIT LESS METHANE

R.M. Herd[1], K.A. Donoghue[2], S.H. Bird[1], R.F. Hegarty[3] and P.F. Arthur[4]

[1]Industry & Investment NSW Beef Industry Centre, Armidale, NSW 2351
[2]Industry & Investment NSW Agricultural Research Centre, Trangie, NSW 2823
[3]Environmental and Rural Science, University of New England, Armidale, NSW 2351
[4]Industry & Investment NSW Elizabeth Macarthur Agricultural institute, Menangle, NSW 2568

SUMMARY

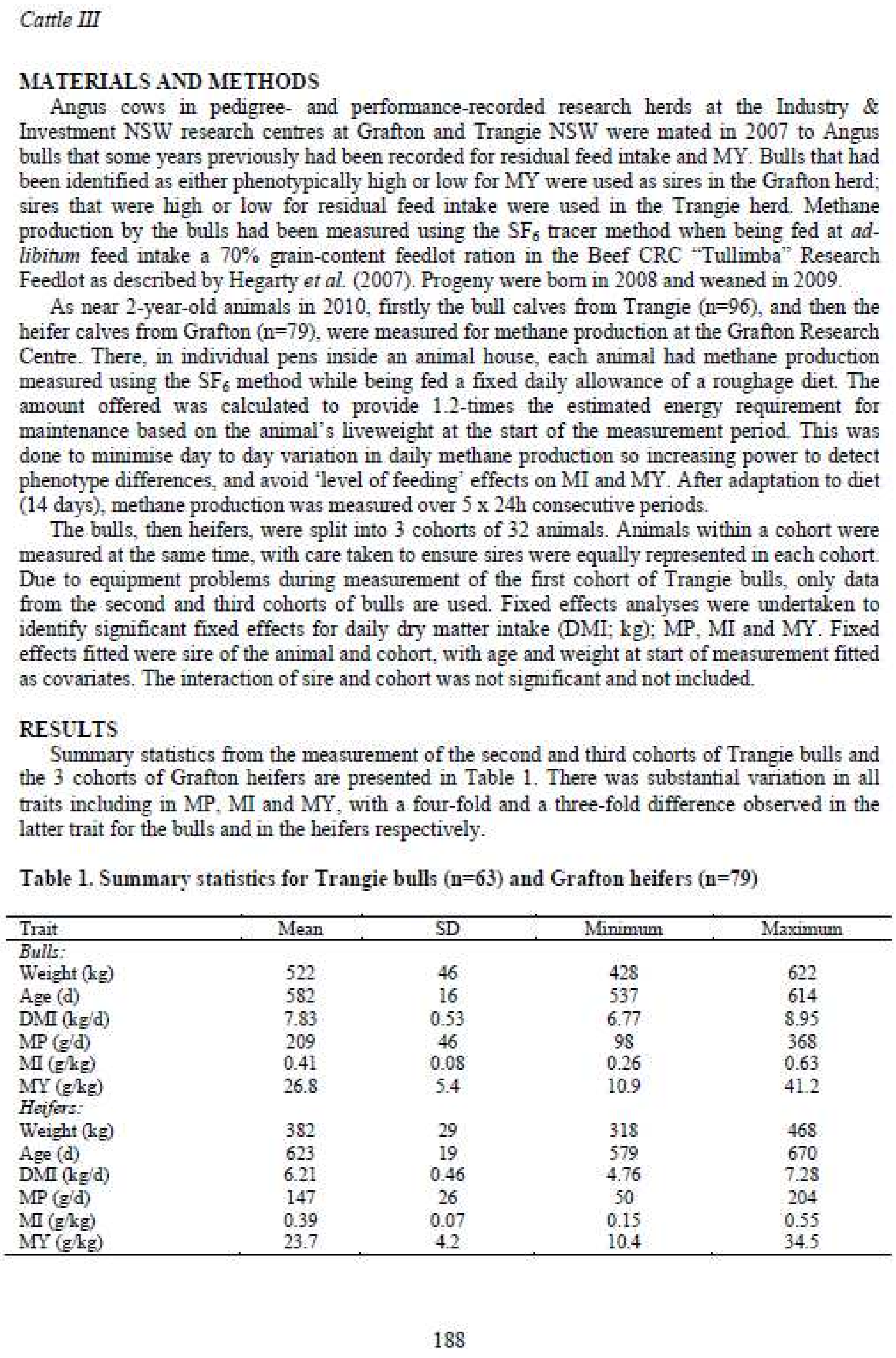
The aim of this experiment is to investigate and demonstrate genetic variation in daily methane production (MP; g/d), methane intensity (MI; MP per unit bodyweight; g/kg) and methane yield (MY; MP per unit feed intake; g/kg). Angus cows in pedigree- and performance-recorded research herds at Industry & 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 CO_2-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 SF_6 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 SF_6 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.

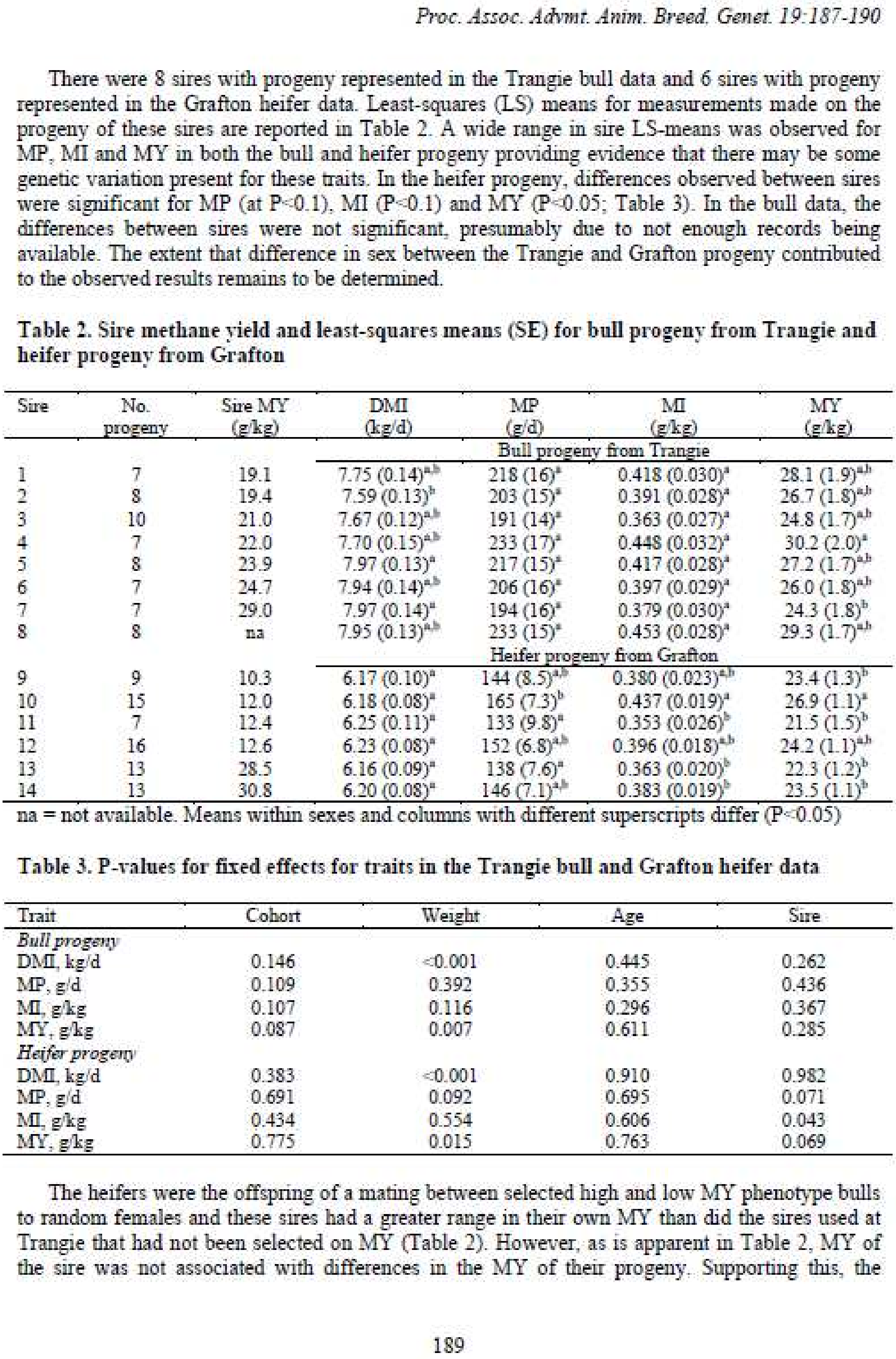
The bulls, then heifers, were split into 3 cohorts of 32 animals. Animals within a cohort were measured at the same time, with care taken to ensure sires were equally represented in each cohort. Due to equipment problems during measurement of the first cohort of Trangie bulls, only data from the second 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
Bulls:				
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
Heifers:				
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
Bull progeny				
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
Heifer progeny				
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 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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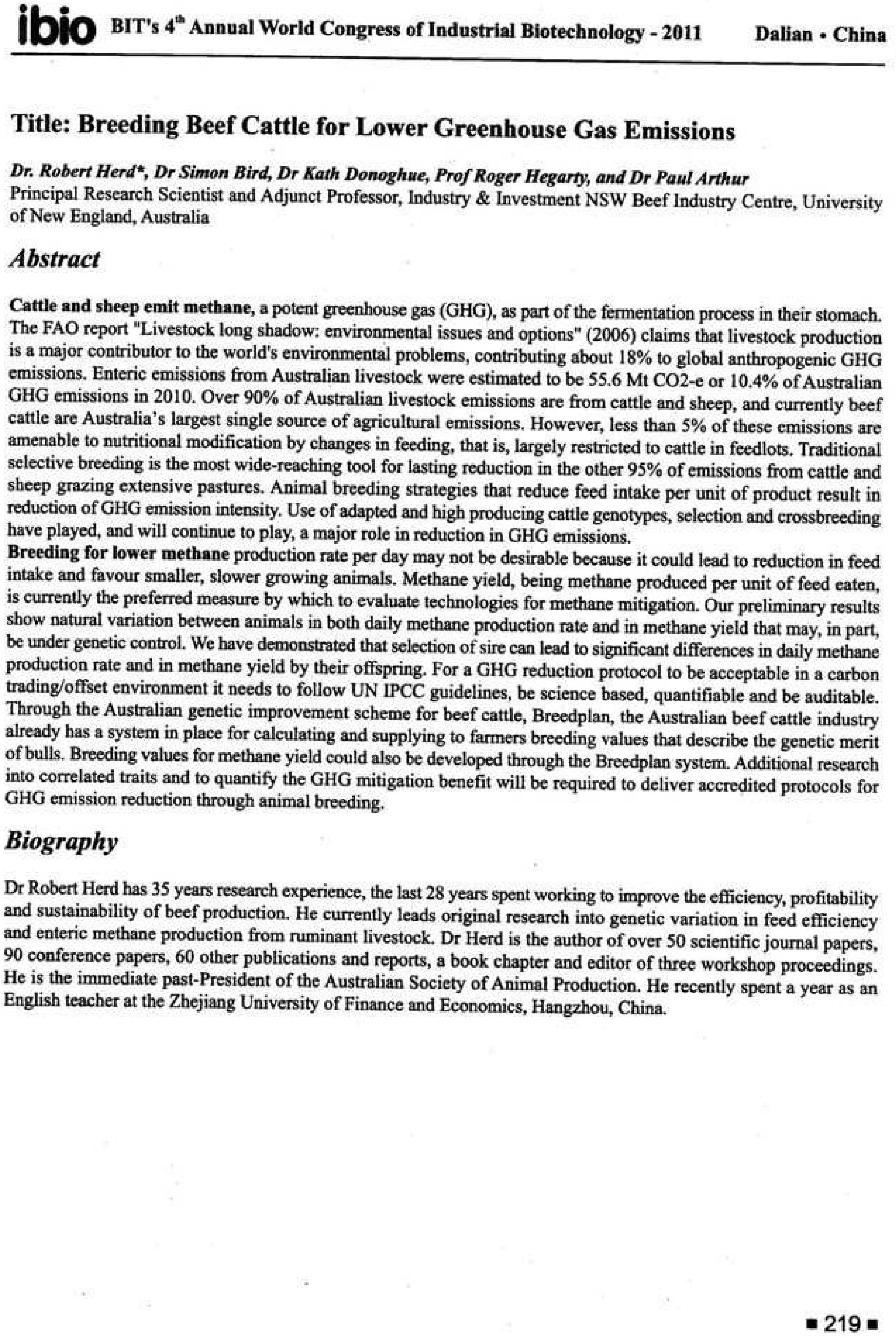

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Title: Breeding Beef Cattle for Lower Greenhouse Gas Emissions

Dr. Robert Herd, Dr Simon Bird, Dr Kath Donoghue, Prof Roger Hegarty, and Dr Paul Arthur*
Principal Research Scientist and Adjunct Professor, Industry & Investment NSW Beef Industry Centre, University of New England, Australia

Abstract

Cattle and sheep emit methane, a potent greenhouse gas (GHG), as part of the fermentation process in their stomach. The FAO report "Livestock long shadow: environmental issues and options" (2006) claims that livestock production is a major contributor to the world's environmental problems, contributing about 18% to global anthropogenic GHG emissions. Enteric emissions from Australian livestock were estimated to be 55.6 Mt CO2-e or 10.4% of Australian GHG emissions in 2010. Over 90% of Australian 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, that is, 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 cattle and sheep grazing extensive pastures. Animal breeding strategies that reduce feed intake per unit of product result in reduction of GHG emission intensity. Use of adapted and high producing cattle genotypes, selection and crossbreeding have played, and will continue to play, a major role in reduction in GHG emissions.

Breeding for lower methane production rate per day may not be desirable because it could lead to reduction in feed intake and favour smaller, slower growing animals. Methane yield, being methane produced per unit of feed eaten, is currently the preferred measure by which to evaluate technologies for methane mitigation. Our preliminary results show natural variation between animals in both daily methane production rate and in methane yield that may, in part, be under genetic control. We have demonstrated that selection of sire can lead to significant differences in daily methane production rate and in methane yield by their offspring. For a GHG reduction protocol to be acceptable in a carbon trading/offset environment it needs to follow UN IPCC guidelines, be science based, quantifiable and be auditable. Through the Australian genetic improvement scheme for beef cattle, Breedplan, the Australian beef cattle industry already has a system in place for calculating and supplying to farmers breeding values that describe the genetic merit of bulls. Breeding values for methane yield could also be developed through the Breedplan system. Additional research into correlated traits and to quantify the GHG mitigation benefit will be required to deliver accredited protocols for GHG emission reduction through animal breeding.

Biography

Dr Robert Herd has 35 years research experience, the last 28 years spent working to improve the efficiency, profitability and sustainability of beef production. He currently leads original research into genetic variation in feed efficiency and enteric methane production from ruminant livestock. Dr Herd is the author of over 50 scientific journal papers, 90 conference papers, 60 other publications and reports, a book chapter and editor of three workshop proceedings. He is the immediate past-President of the Australian Society of Animal Production. He recently spent a year as an English teacher at the Zhejiang University of Finance and Economics, Hangzhou, China.

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Clearing the air

INVISIBLE in the fog, the methane cattle burp and breathe out is a potent contributor to total greenhouse gas emissions from agriculture.

Industry and Investment NSW scientists are excited by new evidence that methane can, in part, be genetically controlled.

■ Story p7

Principal research scientist, Dr Roger Hegarty, hopes research will reveal cattle that eat well and grow well, but, at the same time, emit less methane per unit of feed intake.

Breed for less methane

EXCITEMENT is bubbling over Aussie cattle burps. New evidence proves agricultural production of the potent greenhouse gas, methane, can in part be genetically controlled, say scientists in the Primary Industries division of Industry and Investment NSW (I and I).

After determining this in a first generation of bulls, they are now at the stage of breeding a second generation of low and high methane emitting progeny, for measurement next year.

To bring it down to everybody's street level, the researchers make an interesting comparison between the greenhouse gas emissions of a six-cylinder family car and their highest methane emitters.

"Getting excited over cattle burps might seem strange to some people, but not to us," said Dr Robert Herd (pictured right), principal research scientist at the Armidale Beef Industry Centre of Excellence.

Methane in burps and in the air that cattle breathe out is a major contributor to total greenhouse emissions from agriculture.

Two years ago, the department's scientists had evidence that different bulls produced different volumes of methane.

So began their breeding program to produce low methane emitters.

Sons and daughters of those bulls, now "teenagers", have just been measured for their methane production.

Offspring of the "best" bull averaged 191 grams of methane emission per day, compared with 236g/day by the offspring of the "worst" bull.

"Grams of methane per day are a bit abstract to most of us," said Dr Herd.

"Climate scientists estimate that methane has a global warming potential about 21-times that of carbon dioxide.

"On this basis, the best group of cattle were producing the equivalent of four kilograms of carbon dioxide daily, about a quarter less than the worst, at about five kilograms a day.

"By comparison, a six-cylinder family car doing 20,000 kilometres a year produces about 12 kilograms of carbon dioxide a day."

Importantly, the project is targeting "methane yield".

The principal research scientist leading the project at Armidale, Dr Roger Hegarty, is quick to point out "methane produced per unit of feed intake must be reduced".

"We want cattle that eat well and grow well, but, at the same time, produce less methane," Dr Hegarty said.

Under Dr Hegarty's direction, the young cattle in the department's Angus research herd were measured for methane and feed intake simultaneously at the Grafton research station.

They were measured for methane production while consuming a roughage ration similar to good quality dry grass.

The animal's halter is fitted with a leather nose patch that holds the gas collection tubes above the nostril, allowing continuous sampling of exhaled gas. (Photo: Reg Woodgate.)

To measure methane production, researchers insert a small gas cylinder, a bit larger than a D-cell battery, into the rumen or forestomach of the animal.

Over the following days, the cylinder releases tracer gas.

Researchers measure the ratio of tracer gas to methane in the air breathed out, to calculate the rate of methane produced by the animal.

It is still early days but Dr Herd says the results "give real hope that it may be possible to breed cattle that produce less methane".

The research team has now reached another significant milestone.

In June, Dr Kath Donoghue, animal breeding researcher at the Trangie Agricultural Research Centre, designed the matings for the next generation of cattle.

She used the "best" and the "worst" new young bulls from among those measured at Grafton to join to 250 Angus cows at the Trangie centre, and to another 250 cows at I and I's Glen Innes research station.

"We are breeding a new generation of low and high methane emitting cattle," Dr Donoghue said.

"If we get the expected outcome, that of producing some truly unique low methane-emitting offspring, it will be a world-first demonstration of breeding cattle that produce less greenhouse gas without sacrificing growth performance."

The calves will be born early next year and will be measured for methane late in 2011.

Dr Hegarty says the project is doing much more than demonstrating the potential of conventional animal breeding to reduce methane emissions.

"In our lab, and in labs of collaborators in other States, we are investigating why some cattle are able to digest grass efficiently but seemingly produce much less methane than other cattle," he said.

"Is it the microbe bugs in their stomachs? Is it the way their stomachs function?

"Knowing may enable us to recommend feed supplements or pasture plants that change how much methane is produced."

Methane produced in bellies represents loss of feed energy, apart from being a greenhouse gas.

"Reducing methane production means improved efficiency of feed use, and better for the environment," Dr Herd said.

In recognition, the project is funded by Meat and Livestock Australia and the Australian Government's Climate Change Research Program.

■ Contact Dr Robert Herd, (02) 6770 1808, robert.herd@industry.nsw.gov.au, or Dr Roger Hegarty, (02) 6770 1806, roger.hegarty@industry.nsw.gov.au

LEFT: Some of the methane research team: Myles Light, Dr Robert Herd, Dr Kath Donoghue, Stuart McClelland, Reg Woodgate and Simon Bird.

Choose one of three field trips

THE Australian Society of Animal Production's 28th biennial conference will be held this month at the University of New England, Armidale.

"Producers and research and development providers from around Australia will come together, to discuss the application of science to the livestock industries of Australia," said one of the conference organisers, Robert Herd.

Dr Herd said Wednesday, July 14, would be a standout day.

The program will start with an animal welfare forum and the afternoon session will include a special showcase of science from the Sheep, Beef and Poultry Co-operative Research Centres (CRCs) which will include several tours.

Dr Herd, principal research scientist with Industry and Investment NSW at the Armidale Beef Industry Centre (below), said participants could choose one of three trips.

"They can tour Kirby Farm for Sheep CRC Information Nucleus flock demonstrations, join the Beef CRC for a trip to Tullimba beef research feedlot, or visit Kootingal to inspect a commercial turkey farm with the Poultry CRC," he said.

The tours will include lunch, presentations and demonstrations.

The conference starts with registration on July 11 and concludes on July 15 and Armidale district producers are being offered a special discounted day registration fee.

More information is available at www.asap.asn.au, or from Robert Herd, (02) 6770 1808, or robert.herd@industry.nsw.gov.au

■ Please register before the day with Geoff Hinch, (02) 6773 2202, or ghinch@une.edu.au

Getting excited over cattle burps might seem strange to some people, "but not to us", says Dr Robert Herd. A second generation of low and high methane emitting progeny is now being bred.

16 December 2011

Trangie Advocate
ISSN 1328-9683

Bid to breed cattle with less 'burps'

Researchers from the Trangie Agricultural Research Centre are contributing to a genetic research project which aims to reduce methane emissions from beef cattle.

NSW Department of Primary Industries research scientist, Kath Donoghue, said the project team was working to identify traits which could be selected to breed low methane-producing cattle.

"Beef cattle emit methane gas when they belch and are responsible for about 10 per cent of the nation's greenhouse emissions," Dr Donoghue said.

"Methane emissions from nearly 300 cattle have been measured to date and preliminary results indicate there is a genetic variation in methane emissions.

"That means we will be able to select bulls which can be used in breeding programs to produce progeny with naturally lower methane emissions."

Dr Donoghue said the project was recording methane emissions and collecting information on growth, carcase and fertility traits which have a significant impact on profitability in beef herds.

"We are taking measurements from Angus cattle which were bred as part of a methane selection line developed by NSW DPI at its Trangie and Glen Innes research stations," she said.

"These cattle are taken to a new facility at the University of New England in Armidale where their emissions are measured in 10 specially designed methane chambers.

"We are developing a better understanding of the relationships between methane emissions and important production traits, and the consequences of selection for low methane."

Dr Donoghue said the research was particularly significant and relevant to pasture-based extensive beef production which contributed 95 per cent of beef cattle methane emissions.

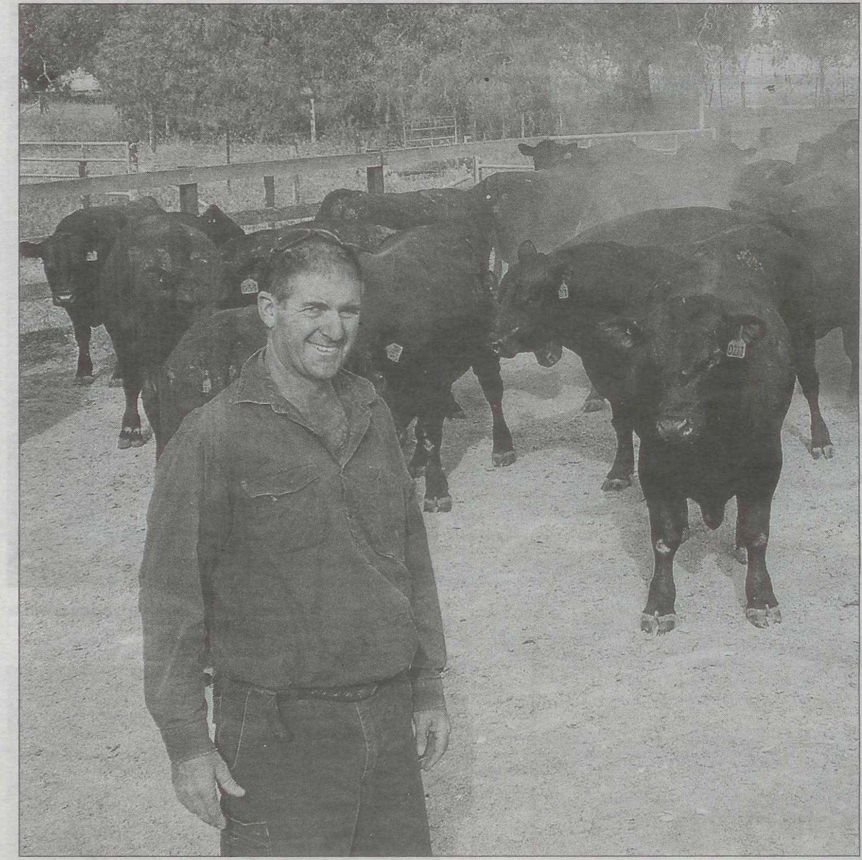
"Less than five per cent of beef cattle-generated methane emissions can be managed in controlled feeding situations, such as feedlots.

"Improvement of animals by traditional selective breeding is the most wide-reaching, permanent and simple tool to mitigate emissions from the extensive cattle sector," she said.

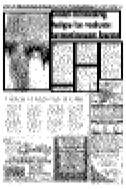
Calves born this year are due in Armidale to be monitored in the methane chambers in early 2012 as part of the 500 records to be collected by the end of the project next year.

Selection lines for high and low methane production are continuing at TARC and Glen Innes with the breeding program due to produce another round of calves in 2012. This project is part of the Reducing Emissions from Livestock Research Program, which is supported by funding from the Australian Government's Department of Agriculture, Fisheries and Forestry as part of the Climate Change Research Program and Meat & Livestock Australia.

SNAPSHOT OF THE WEEK



❑ **NSW DPI technical officer, Dave Mula, oversees the herd from the methane selection line of Angus cattle at the Trangie Agricultural Research Centre. See story page 8.**



Grafton Daily Examiner
Friday, February 10, 2012
Page : 17
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Edition :
Region : NSW Regional

Page : 1 of 2
Circulation : 5,647
Area Of Clip : 447.49 sqcm
Clip ID : 3464073

Good breeding helps to reduce greenhouse burps

NSW Department of Primary Industries (DPI) researchers are contributing to a project which aims to reduce agricultural greenhouse emissions by reducing the amount of methane belched by beef cattle.

NSW DPI research scientist Kath Donoghue said the project team is working to identify traits which can be selected to breed low-methane-producing cattle.

"Cattle emit methane gas when they belch and beef cattle are responsible for about 10% of the nation's greenhouse emissions," Dr Donoghue said.

"Methane emissions from 400 cattle have been measured to date and preliminary results indicate that genetics account for a variation in the amount of methane cattle emit.

"That means we will be able to select bulls which can be used in breeding programs to produce progeny with naturally lower methane emissions."

Dr Donoghue said the project is also collecting information on growth, carcase and fertility traits which have a significant impact on profitability in beef herds.

"We are developing a better understanding of the relationships between methane emissions and important production traits, and the consequences of selection for low-methane traits," she said.

"This genetic research is particularly relevant to pasture-based extensive beef production systems which contribute 95% of beef cattle methane emissions.

"Improvement of animals by traditional selective breeding is the most wide-reaching, permanent and simple tool to mitigate emissions from the extensive cattle sector."

Beef cattle in feedlots make up most of the remaining 5% – those emissions can be managed by controlling feed intake.

NSW DPI has bred a selection line of angus cattle, with high- and low-methane production traits, at its Trangie and Glen Innes research stations.

These cattle are sent to the University of New England in Armidale where NSW DPI researchers use specially designed methane chambers to take precise measurements.

By the end of the project this year, records from the 500 cattle selected from the NSW DPI angus herd will have been collected and analysed.

This project is supported by funding from the Australian Government's Department of Agriculture, Fisheries and Forestry as part of the Climate Change Research Program and Meat & Livestock Australia.

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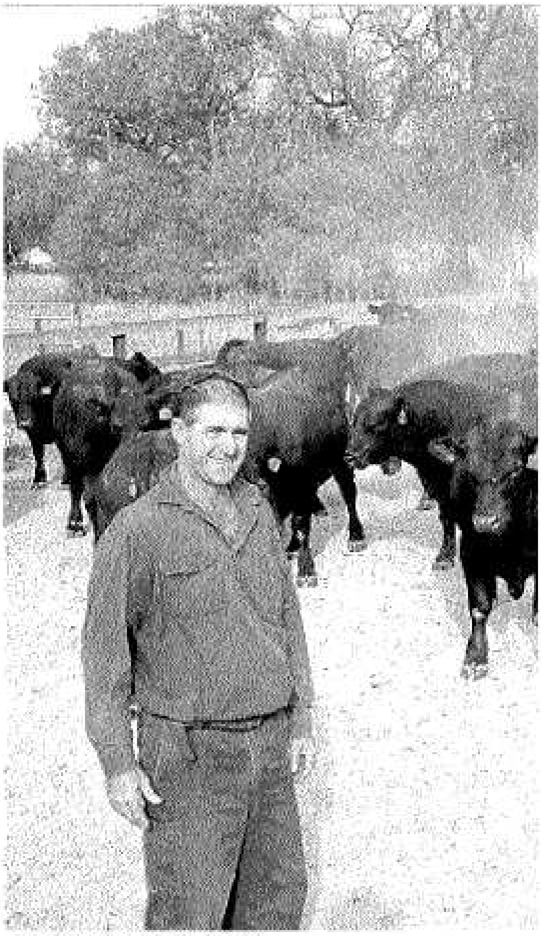
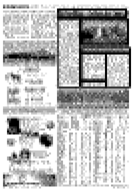


COOKING WITH GAS: Cattle with low-methane traits are being researched in an effort to help reduce greenhouse gas emissions.



Mudgee Guardian
Friday, February 10, 2012
Page : 36
Section :
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Region : NSW Regional

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Circulation : 3334
Area Of Clip : 247.31 sqcm
Clip ID : 3466671

Breeding reduces burps

NSW Department of Primary Industries (DPI) researchers are contributing to a project which aims to reduce agricultural greenhouse emissions by reducing the amount of methane belched by beef cattle.

NSW DPI research scientist, Kath Donoghue, said the project team is working to identify traits which can be selected to breed low methane producing cattle.

"Cattle emit methane gas when they belch and beef cattle are responsible for about 10 per cent of the nation's greenhouse emissions," Dr Donoghue said.

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Dr Donoghue said the project is also collecting information on growth, carcase and fertility traits which have a significant impact on profitability in beef herds.

"We are developing a better understanding of the relationships between methane emissions and important production traits, and the consequences of selection for low methane traits," she said.

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These cattle are sent to the University of New England in Armidale where NSW DPI researchers use specially designed methane chambers to take precise measurements.

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This project is supported by funding from the Australian Government's Department of Agriculture, Fisheries and Forestry as part of the Climate Change Research Program and Meat & Livestock Australia.

NEW: Department of Primary Industries researchers are looking at ways to reduce the amount of methane produced by beef cattle.
080212/RMCATTLE

THE ARMIDALE EXPRESS
MONDAY 20 FEBRUARY 2012

More research, less methane

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"Improvement of animals by traditional selective breeding is the most wide-reaching, permanent and simple tool to mitigate emissions from the extensive cattle sector.

"Beef cattle in feedlots make up most of the remaining five per cent, those emissions can be managed by controlling feed intake."

Good breeding reduces the burps

The reduction of agricultural greenhouse emissions by Beef cattle belching methane is the subject of researchers from the NSW Department of Primary Industries (DPI).

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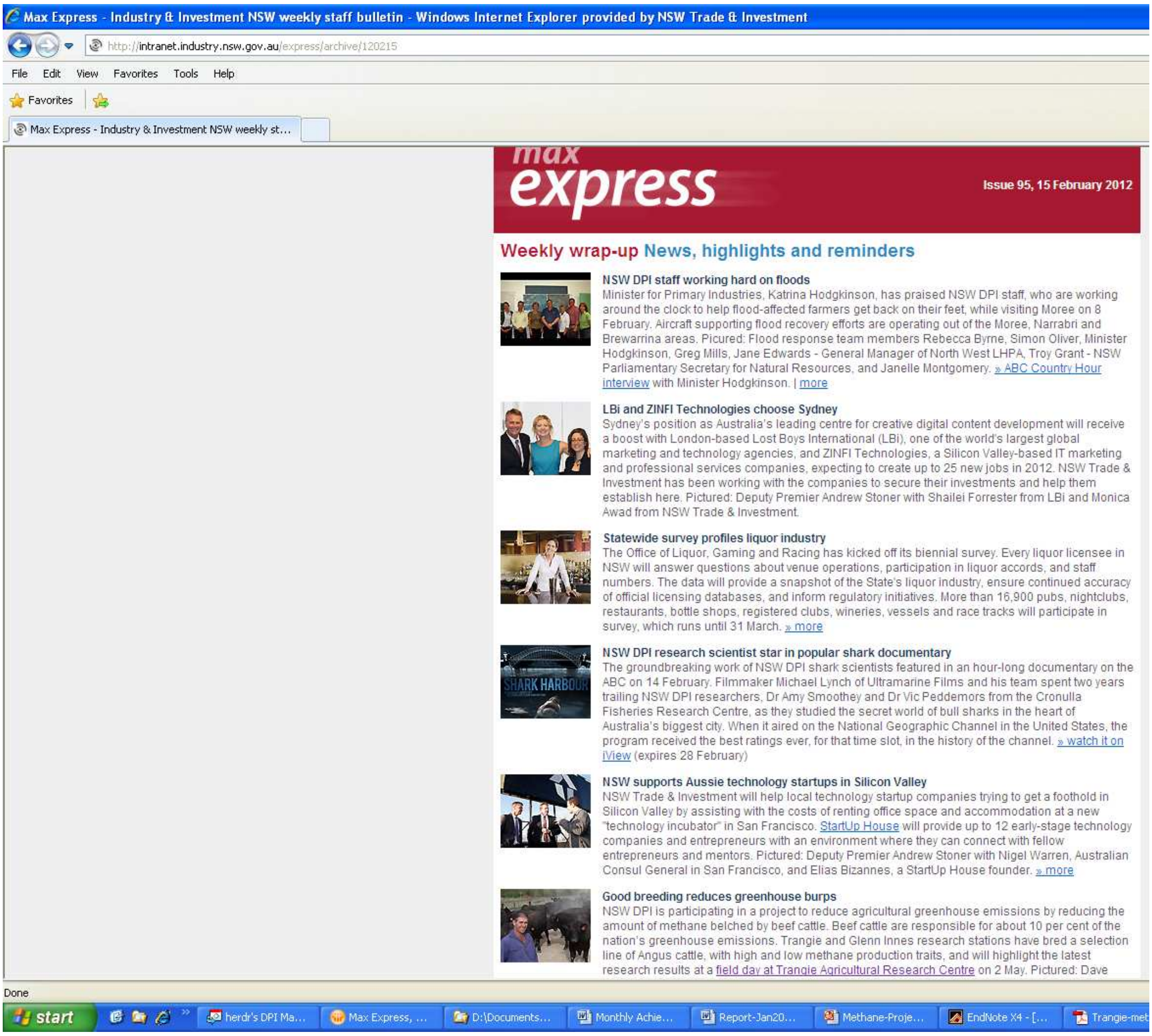
From The Armidale Independent Newspaper. 15 February 2012.



Issue 95, 15 February 2012

Weekly wrap-up News, highlights and reminders

NSW DPI staff working hard on floods
Minister for Primary Industries, Katrina Hodgkinson, has praised NSW DPI staff, who are working around the clock to help flood-affected farmers get back on their feet, while visiting Moree on 8 February. Aircraft supporting flood recovery efforts are operating out of the Moree, Narrabri and Brewarrina areas. Pictured: Flood response team members Rebecca Byrne, Simon Oliver, Minister Hodgkinson, Greg Mills, Jane Edwards - General Manager of North West LHPA, Troy Grant - NSW Parliamentary Secretary for Natural Resources, and Janelle Montgomery. » ABC Country Hour interview with Minister Hodgkinson. | more

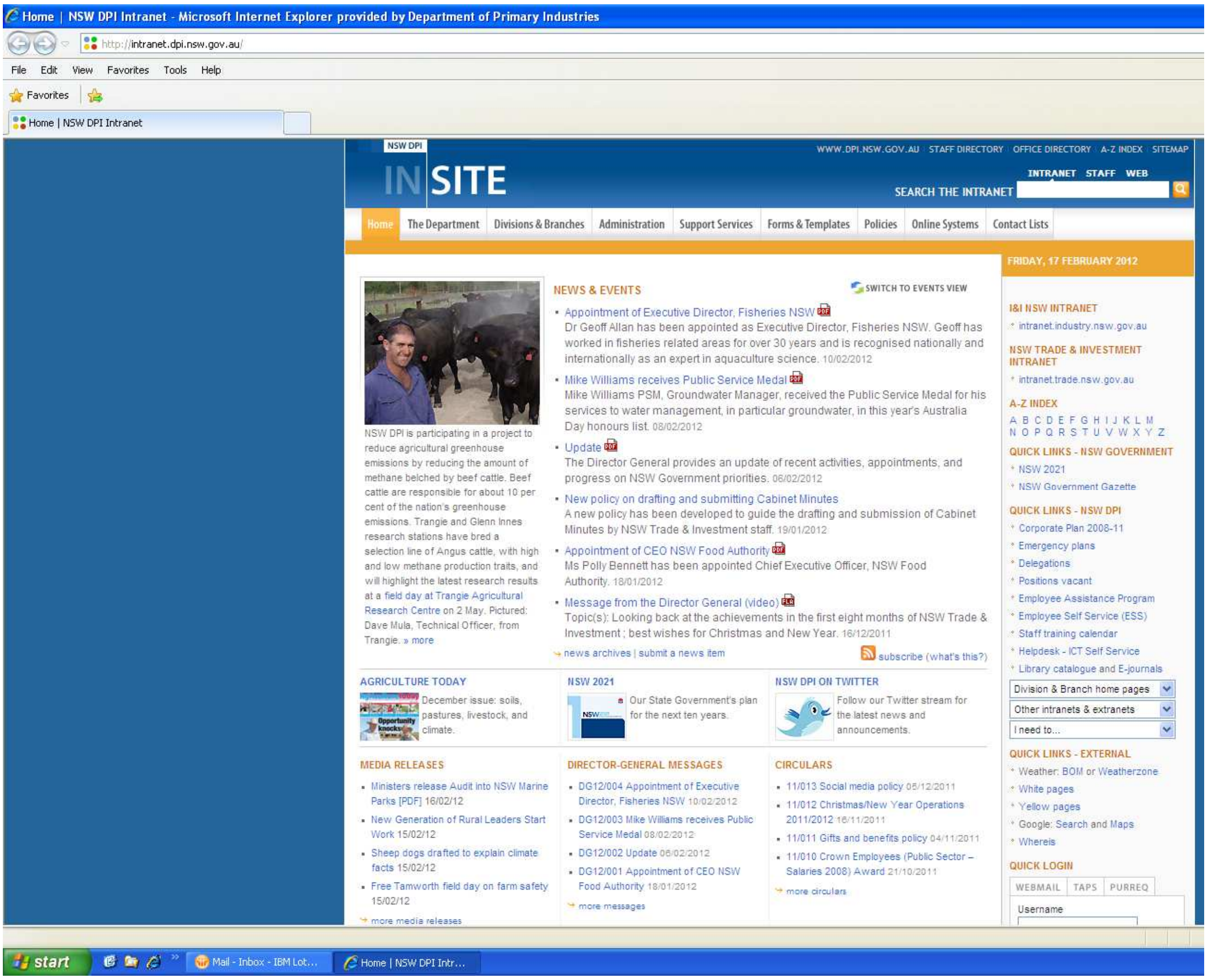
LBi and ZINFI Technologies choose Sydney
Sydney's position as Australia's leading centre for creative digital content development will receive a boost with London-based Lost Boys International (LBi), one of the world's largest global marketing and technology agencies, and ZINFI Technologies, a Silicon Valley-based IT marketing and professional services companies, expecting to create up to 25 new jobs in 2012. NSW Trade & Investment has been working with the companies to secure their investments and help them establish here. Pictured: Deputy Premier Andrew Stoner with Shailei Forrester from LBi and Monica Awad from NSW Trade & Investment.

Statewide survey profiles liquor industry
The Office of Liquor, Gaming and Racing has kicked off its biennial survey. Every liquor licensee in NSW will answer questions about venue operations, participation in liquor accords, and staff numbers. The data will provide a snapshot of the State's liquor industry, ensure continued accuracy of official licensing databases, and inform regulatory initiatives. More than 16,900 pubs, nightclubs, restaurants, bottle shops, registered clubs, wineries, vessels and race tracks will participate in survey, which runs until 31 March. » more

NSW DPI research scientist star in popular shark documentary
The groundbreaking work of NSW DPI shark scientists featured in an hour-long documentary on the ABC on 14 February. Filmmaker Michael Lynch of Ultramarine Films and his team spent two years trailing NSW DPI researchers, Dr Amy Smoothey and Dr Vic Peddemors from the Cronulla Fisheries Research Centre, as they studied the secret world of bull sharks in the heart of Australia's biggest city. When it aired on the National Geographic Channel in the United States, the program received the best ratings ever, for that time slot, in the history of the channel. » watch it on iView (expires 28 February)

NSW supports Aussie technology startups in Silicon Valley
NSW Trade & Investment will help local technology startup companies trying to get a foothold in Silicon Valley by assisting with the costs of renting office space and accommodation at a new "technology incubator" in San Francisco. StartUp House will provide up to 12 early-stage technology companies and entrepreneurs with an environment where they can connect with fellow entrepreneurs and mentors. Pictured: Deputy Premier Andrew Stoner with Nigel Warren, Australian Consul General in San Francisco, and Elias Bizannes, a StartUp House founder. » more

Good breeding reduces greenhouse burps
NSW DPI is participating in a project to reduce agricultural greenhouse emissions by reducing the amount of methane belched by beef cattle. Beef cattle are responsible for about 10 per cent of the nation's greenhouse emissions. Trangie and Glenn Innes research stations have bred a selection line of Angus cattle, with high and low methane production traits, and will highlight the latest research results at a field day at Trangie Agricultural Research Centre on 2 May. Pictured: Dave



FRIDAY, 17 FEBRUARY 2012

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NEWS & EVENTS

SWITCH TO EVENTS VIEW

- Appointment of Executive Director, Fisheries NSW
  Dr Geoff Allan has been appointed as Executive Director, Fisheries NSW. Geoff has worked in fisheries related areas for over 30 years and is recognised nationally and internationally as an expert in aquaculture science. 10/02/2012
- Mike Williams receives Public Service Medal
  Mike Williams PSM, Groundwater Manager, received the Public Service Medal for his services to water management, in particular groundwater, in this year's Australia Day honours list. 08/02/2012
- Update
  The Director General provides an update of recent activities, appointments, and progress on NSW Government priorities. 06/02/2012
- New policy on drafting and submitting Cabinet Minutes
  A new policy has been developed to guide the drafting and submission of Cabinet Minutes by NSW Trade & Investment staff. 19/01/2012
- Appointment of CEO NSW Food Authority
  Ms Polly Bennett has been appointed Chief Executive Officer, NSW Food Authority. 18/01/2012
- Message from the Director General (video)
  Topic(s): Looking back at the achievements in the first eight months of NSW Trade & Investment ; best wishes for Christmas and New Year. 16/12/2011

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AGRICULTURE TODAY

December issue: soils, pastures, livestock, and climate.

NSW 2021

Our State Government's plan for the next ten years.

NSW DPI ON TWITTER

Follow our Twitter stream for the latest news and announcements.

MEDIA RELEASES

- Ministers release Audit into NSW Marine Parks [PDF] 16/02/12
- New Generation of Rural Leaders Start Work 15/02/12
- Sheep dogs drafted to explain climate facts 15/02/12
- Free Tamworth field day on farm safety 15/02/12

more media releases

DIRECTOR-GENERAL MESSAGES

- DG12/004 Appointment of Executive Director, Fisheries NSW 10/02/2012
- DG12/003 Mike Williams receives Public Service Medal 08/02/2012
- DG12/002 Update 06/02/2012
- DG12/001 Appointment of CEO NSW Food Authority 18/01/2012

more messages

CIRCULARS

- 11/013 Social media policy 05/12/2011
- 11/012 Christmas/New Year Operations 2011/2012 16/11/2011
- 11/011 Gifts and benefits policy 04/11/2011
- 11/010 Crown Employees (Public Sector – Salaries 2008) Award 21/10/2011

more circulars

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- intranet.industry.nsw.gov.au

NSW TRADE & INVESTMENT INTRANET

- intranet.trade.nsw.gov.au

A-Z INDEX

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- NSW Government Gazette

QUICK LINKS - NSW DPI

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- Employee Self Service (ESS)
- Staff training calendar
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