MEASUREMENT OF METHANE TRAITS IN THE BEEF INFORMATION NUCLEUS CATTLE

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SUMMARY

Methane is the main source of greenhouse gas (GHG) from ruminants. The focus of this study was to measure methane production (MPR) in industry cattle. The ultimate aim was to develop estimated breeding values (EBVs) for methane traits for use in genetic improvement to reduce GHG in cattle. A total of 548 Australian Angus and 102 Australian Charolais Beef Information Nucleus herd steers which were undertaking a net feed intake test at the University of New England "Tullimba" research feedlot, near Armidale NSW, were measured for MPR using GreenFeed Emission Monitoring (GEM) units. The units provide short term MPR measurement anytime an animal visits a unit. Two-thirds of the steers from each breed visited the GEM units; most of them more than 20 times within a period which ranged from 50 to 66 days. There were significant ($P < 0.05$) sire differences in MPR, MPR per unit feed intake, MPR per unit body weight and MPR per unit average daily gain in Angus cattle. The significant sire differences in the methane traits indicate the presence of genetic variation for methane traits when measured by GEM units.

INTRODUCTION

Across the globe the agricultural sector is a significant source of GHG emissions. A recent Food and Agriculture Organisation (FAO) study reported that livestock were responsible for 14.5% of global GHG emissions, and ruminants contribute about 80% of the livestock emissions (Gerber *et al*. 2013). Methane is the main source of GHG from ruminants, and is produced during the process of microbial fermentation of plant material, mainly in the rumen, which is then exhaled into the atmosphere. High methane production is associated with high feed intake in ruminants (Blaxter and Clapperton 1965; Pelchen and Peters 1998). Feed intake is highly correlated with growth and other productivity traits in ruminants (Arthur *et al*. 2001), hence any strategy to lower methane production *per se,* may have a detrimental impact on ruminant productivity through a correlated reduction in feed intake. Hence there has been increased interest in the amount of methane produced per unit feed intake, also known as methane yield (MY) and the amount of methane produced per unit of product, known as methane intensity (MI).

In the last decade there has been active development of methane measurement technologies to the stage where individual animal methane production (MPR) can now be measured on a large scale. The suitability and accuracies of these methane measurement technologies are currently being assessed, in conjunction with the development of standardised measurement protocols for livestock. For genetic improvement purposes it is essential to accurately measure the trait of interest (e.g. methane) in a large number of animals on a regular basis to estimate the genetic merit of each potential breeding animal for the trait. The focus of this study was to measure methane in large numbers of industry cattle from high-profile potentially elite sires that will contribute to future genetic improvement in Australian cattle breeds.. The ultimate aim was to develop estimated breeding values for methane traits for use in genetic improvement.

MATERIALS AND METHODS

Experimental animals. The Australian beef industry has developed a number of resource herds known as the Beef Information Nucleus (BIN) to underpin research and development of genomic selection. The BIN is a progeny testing scheme (Banks, 2011) and current participants include the Angus, Brahman, Charolais, Hereford and Limousin breed societies. Records on all economically important traits are collected on steers, heifers and cows, including difficult to measure traits like feed intake and feed efficiency. The steers from the Angus and Charolais BINs are measured for growth and net feed intake (NFI; the measure of feed efficiency) on a feedlot ration at the University of New England "Tullimba" research feedlot, near Armidale NSW. While being measured for NFI, the MPR of some cohorts of steers were measured. From December 2013 to January 2015, one cohort of Charolais and five cohorts of Angus BIN cattle had the opportunity to be measured for MPR. Each cohort is made up of approximately equal numbers of steers per sire used that in the progeny test for the year.

Measurement technology. The MPR of the cattle was measured using GreenFeed Emission Monitoring (GEM) units manufactured by C-Lock Inc. (U.S. Patent 7966971). The GEM units provide short term measurement of methane production made many times per day using portable breath collection and methane analyzer. The scientific principles underpinning the operation of the unit is explained by Zimmerman *et al*. (2013), and a detailed description is provided by Zimmerman (2013) at the company's website (http://c-lockinc.com/whatisgreenfeed.php). At the research feedlot the GEM units were located next to the feed intake recorders and the steers have the opportunity to voluntarily visit the GEM unit at any time to have their MPR measured.

Statistical analysis. The definitions of all the traits used in this report are provided in Table 1. The data used were from 102 Charolais (1 cohort) and 548 Angus (5 cohorts) steers who had the opportunity to visit the GEM units during their NFI test. The percentage and frequency of visits to the GEM units were calculated for both breeds. The number of records and progeny per sire in the Charolais data was limited and thus was not subjected to further analysis. The data from the Angus steers were analysed further to assess sire differences for the methane traits using records on the 356 steers with a minimum of 20 visits to the GEM units. A preliminary analysis was conducted to examine cohort effect on the traits with a full model which included the effects of cohort, sire, sire by cohort and residual error. All the terms in the model were assumed to have random effects and the errors were assumed to have a normal distribution with mean zero and variance. Cohort and sire effects were highly confounded hence cohort and sire by cohort were dropped in the final analysis. All parameters were estimated using residual maximum likelihood (REML) procedure and the sire means were adjusted using the best linear unbiased predictor (BLUP) due to their random nature. Least significant difference at 5% level was calculated and used to compare means between sires. All analyses were run on ASReml Release 3.00 (Gilmour *et al*, 2009).

Table 1. Definition of traits

Trait name	Abbreviation	Units	Definition
Body weight	BW	kg	Mid test BW (Start BW + End BW)/2
Average daily gain	ADG	kg	Daily BW gain (End BW – Start BW)/ days on test
Daily feed intake	FI	g/day	Average daily feed intake during the test
Methane production rate	MPR	g/day	Methane produced
Methane yield	MY	g/kg	MPR per unit FI (MPR ÷ FI)
Methane intensity$_{BW}$	MI$_B$	g/kg	MPR per unit BW (MPR ÷ BW)
Methane intensity$_{ADG}$	MI$_A$	g/kg	MPR per unit ADG (MPR ÷ ADG)

RESULTS AND DISCUSSION

About one third of the steers (33% of Angus and 34% of Charolais) did not visit the GEM units, hence did not have an MPR record. The percentage of steers with more than 20 visits to the GEM units was 56% for Angus and 63% for Charolais. Therefore, in order to obtained accurate data on as many progeny per sire as possible for the estimation of genetic parameters and EBVs for methane traits, the number of steers which use the GEM units and the frequency of visits need to increase. Measurement of MPR with the GEM units relies on the cattle visiting the units. In the feedlot environment the steers had *ad libitum* access to the high-energy feedlot ration. Although the GEM unit deliver a small amount of feed pellets to the steers on each visit, it did not appear to be a strong enough attractant for many steers. It is therefore important that other inducement strategies be investigated, especially in the feedlot environment. Most of the steers that used the GEM units visited more than 20 times during their NFI test period which were from 50 to 66 days.

The 356 Angus steers who had frequent visits (>20) to the GEM units were the progeny of 83 sires, with an average of 4.3, and a range of 1 to 14 steers per sire. The descriptive statistics for all the traits studied in the Angus steers are presented in Table 2. The steers were consuming an average of 15.8 kg of feed, growing at 1.95 kg and producing 217.6 g of methane per day.

Table 2. Descriptive statistics for production and methane traits of Angus steers

Trait[1]	Mean	SE	Min	Max
Body weight (BW), kg	601.9	3.7	438	830
Average daily gain (ADG), kg	1.95	0.02	0.72	3.53
Daily Feed intake (FI), kg	15.8	0.11	10.5	22.7
Methane Production rate, g/day	217.6	2.05	104.5	385
Methane yield, g/kg FI	13.86	0.14	6.41	26.93
Methane intensity$_{ADG}$, g/kg ADG	115.3	1.5	58.0	243.7
Methane intensity$_{BW}$, g/kg BW	0.363	0.003	0.166	0.640

[1]See Table 1 for full trait names and definitions

There were significant ($P < 0.05$) sire differences in all the methane traits (MPR, MY, MI_B and MI_A). Means for MY and MI_A of the top and bottom five sires are presented in Figure 1. In general, the sire differences were significant only between the top and bottom five sires for each of the methane traits, with no significant differences among the sires in the middle range. Donoghue *et al*. (2015) has shown that there is genetic variation, with moderate heritability for methane traits in Angus cattle when measured in respiration chambers. The presence of significant sire differences in the methane traits of the steers in the feedlot indicates the presence of genetic variation for methane traits when measured by GEM units. However, the number of animals measured is not adequate for comprehensive analyses to provide an accurate estimate of the genetic variation for these methane traits when measured in the GEM units. It is therefore essential that measurement of animals in the GEM units be continued in order to generate enough GEM based data for the estimation of genetic parameters and for the development of EBVs for industry cattle. The research on the measurement of methane traits on females at pasture is in its infancy and the use of GEM units to collect data from females at pasture needs to continue so that the relationship between feedlot measurements in steers and pasture measurement in females can be evaluated. Very few animals have been measured on pasture and measurement protocols are currently being developed and trialled. Continued funding is required to progress the work on measuring methane on females at pasture.
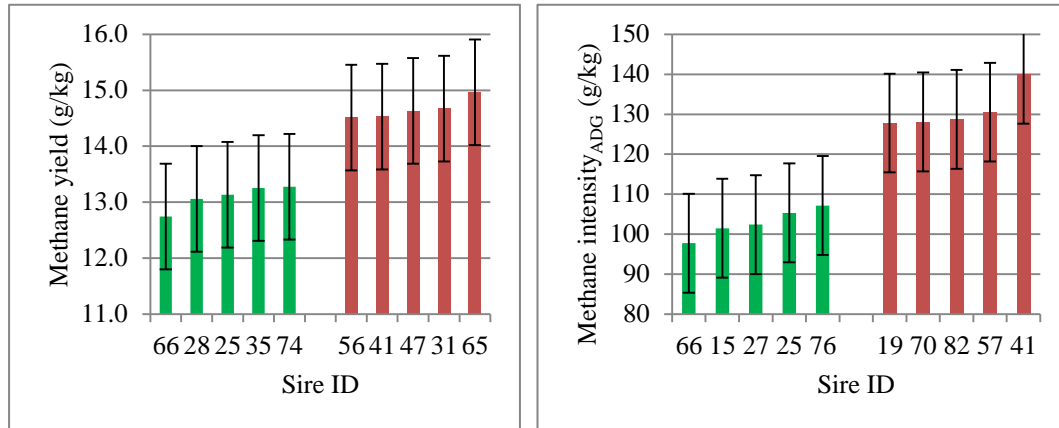
Figure 1. Mean methane yield and methane intensity$_{ADG}$, with standard error bars of steer progeny for the top (red) and bottom (green) five Angus sires

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