GENOMIC ESTIMATED BREEDING VALUES FOR METHANE PRODUCTION IN AUSTRALIAN BEEF CATTLE

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SUMMARY

Methane emissions for beef cattle are heritable, whether measured as methane production, methane yield (methane production/dry matter intake), or residual methane (observed methane production – expected methane production). This suggests methane emissions could be reduced by selection. Genomic selection is perhaps the most feasible approach to implement for the beef industry, given the high cost of measuring methane production from individual cattle. Here we derive genomic estimated breeding values (GEBV) for methane traits from a reference set of 747 Angus animals measured for methane traits, and genotyped for 630K SNPs. The accuracy of GEBV was evaluated in a cohort of 273 Angus animals. Accuracies ranged from 0.29, for methane yield, to 0.35 for residual methane. Selection on GEBV using the genomic prediction equations derived here could reduce emissions for beef cattle by roughly 5% over 10 years.

INTRODUCTION

Methane emission levels, whether measured as methane production, methane yield (methane production/dry matter intake), or residual methane (difference between actual and predicted methane production) are all heritable traits (Donoghue *et al.* 2013; Herd *et al.* 2014). Selection for reduced emissions could therefore result in likely small annual but cumulative and permanent changes in emission levels. Residual methane production (RMP) or methane yield (MY) are more attractive targets for selection than methane production (MPR), as they are not unfavourably correlated with production traits (Donoghue *et al*. 2015).

Unfortunately given the cost and difficulty of measuring these traits, it is unlikely that either MY or RMP could be measured on the scale that would be necessary to calculate estimated breeding values (EBV) on an ongoing basis for the beef industry. An alternative is to use genomic selection for these traits. This entails measuring a large reference population for MY or RMP, genotyping the reference population for a large number of SNP markers, and then using the information to derive a genomic prediction equation, that can be used to calculate genomic estimated breeding values (GEBV) for any selection candidate that is genotyped. Here we use a large group of Angus animals measured for methane emission levels (as described by Donoghue *et al*. 2015), and real or imputed genotypes for 632,003 SNPs were used, to derive GEBV for MPR, MY and RMP. The accuracy of the GEBV was demonstrated to be moderate, enabling selection for reduced methane emission levels for Australian beef cattle.

MATERIALS AND METHODS

Phenotypes. For a full description of phenotypes, see Donoghue *et al*. (2015), in this proceedings. Briefly, 1,020 Angus animals were measured for methane production in 10 respiration chambers on the University of New England campus, Armidale NSW (Herd *et al.* 2014a) provides details on the management of animals and methane measurement procedure. The animals were progeny of 73 sires (average 14 progeny per sire, range 1-30), born across 4 drops.

Progeny of individual sires were stratified across groups and cohorts. Methane production was measured over 2 x 24h consecutive periods. For animals born from 2011 to 2013 these measurements were taken at approximately yearling age (mean = 339 days). However, for animals born in 2009, these measurements were taken at approximately two years of age (mean = 738 days). Traits measured (Table 1) included pre-test weight (TWT), dry matter intake (DMI), daily methane production (MPR) and methane production per unit feed intake (methane yield: MY). Four different forms of residual MPR (RMP) were defined to target MPR independent of feed intake, with RMP defined as actual MPR minus expected MPR (expMPR). For RMP_J, expMPR was calculated using a published prediction equation (Johnson *et al.*, 1995), while for RMP_R, the residuals from a simple regression of MPR on DMI were used.

Table 1. Definition of traits

Trait name	Abbrev-iation	Units	Definition
Test Weight	TWT	Kg	Pre-test weight
Dry matter intake	DMI	kg/day	Dry matter intake during methane measurement
Methane production rate	MPR	g/day	Methane produced
Methane intensity	MI	g/kg	MPR per unit TWT (MPR ÷ TWT)
Methane yield	MY	g/kg	MPR per unit DMI (MPR ÷ DMI)
Residual $methane_B$	RMP_B	g/day	MPR net of expected MPR (expMPR) from the DMI, with expMPR obtained by formula of Blaxter and Clapperton (1965)
Residual $methane_J$	RMP_J	g/day	MPR net of expected MPR from DMI, with expMPR obtained by formula of Johnson *et al*. (1995)
Residual $methane_I$	RMP_I	g/day	MPR net of expected MPR from DMI, with expMPR obtained by formula of IPCC (2006)
Residual $methane_R$	RMP_R	g/day	MPR net of expected MPR from the DMI, with expMPR obtained by regression of MPR on DMI

Genotypes. 1,020 Angus cattle, that have been measured for methane traits, were genotyped with either 777,000 SNPs Illumina Bovine HD Array (847 animals) or the Bovine 54,000 SNP50 array (173 animals). The SNP positions used were from bovine genome assembly UMD 3.1 (University of Maryland, College Park, MD). Stringent quality control procedures were applied to the data. Monomorphic SNPs and SNPs with less than 5 copies of the rare allele were removed. Then genotype calls with GenTrain score (GenCall) > 0.6 are high quality; below this value they were excluded. For the animals genotyped with the HD array, there were 650,934 SNPs genotyped at GenCall > 0.6. Furthermore, 343 mitochondrial SNPs, 1,124 Y chromosome SNPs, and 1,735 unmapped SNPs were excluded. SNPs with duplicate positions or dubious positions given linkage disequilibrium with surrounding SNPs were also removed. 632,003 SNPs remained. Samples (animals) were checked for excess heterozygosity (>0.4 is a sign of sample contamination), and had to have more than 90% of SNP with GenCall scores >0.6. All 1,020 samples passed these quality control criteria, and 97.9 % of SNPs were genotyped at GenCall > 0.6. Missing genotypes for animals genotyped with the 777K were imputed using Beagle3 (Browning and Browning 2009), and the same program was used to impute the animals genotyped for the 50K to 632,003 genotypes, after quality control on 50K genotypes as for the 777K genotypes

Genomic heritabilities and genomic breeding values. The models fitted to the data were as described by Donoghue *et al*. (2015), except that genomic relationships were used to describe relationships between animals:

$\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Zg} + \boldsymbol{e}$, where **y** is a vector of trait records (WT, DMI, CH4, MY, MI, RMP_B, RMP_J, RMP_I or RMP_R), **b** is a vector of fixed effects including contemporary group, age and dam age, **X** is a design matrix allocating records to fixed effects, **g** is a vector of genomic estimated breeding values (GEBV), **Z** is a design matrix allocating records to breeding values, and **e** is a vector of random residuals ~ N(0, $\mathbf{I}\sigma^2_e$), where σ^2_e is the error variance. The **g** were assumed distributed N(0, $\mathbf{G}\sigma^2_{gen}$), where σ^2_{gen} is the additive genetic variance and **G** is the genomic relationship matrix constructed from the 632,003 SNP markers genotypes, following Yang *et al.* (2010). Variance components were estimated on the full data set (1,020 records) using ASReml (Gilmour *et al.* 2009). Genomic heritabilities were then calculated as:

$$h^2 = \frac{\widehat{\sigma^2_{gen}}}{\widehat{\sigma^2_{gen}} + \widehat{\sigma^2_e}}.$$

The accuracy of genomic estimated breeding values (GEBV) was evaluated by predicting the youngest cohort of animals, those screened in 2014 (273). The reference population were then all the other animals (747). The accuracy of prediction was taken as for the animals in the validation set, the correlation of their genomic estimated breeding values and their phenotypes (corrected for fixed effects), divided by the pedigree heritability of the trait: $r(GEBV, y*)/\sqrt{h^2}$.

RESULTS AND DISCUSSION

The estimates of genomic heritabilities were very similar to those previously calculated using pedigree data (Donoghue *et al*. 2015) for most traits, and were within one standard error for all traits (Table 2).

Table 2. Estimates of heritability from analysis using either pedigree or genomic information to construct relationships between animals, and accuracy of genomic estimated breeding values in a validation cohort. Standard errors are in brackets.

Trait name	h^2 pedigree*	h^2 genomic	Proportion of genetic variance explained by SNP	Accuracy of GEBV
Weight (kg)	0.43 (0.08)	0.42 (0.07)	0.96	0.37
Dry matter intake	0.44 (0.08)	0.37 (0.07)	0.82	0.35
Methane Production	0.27 (0.06)	0.28 (0.06)	1.05	0.35
Methane Yield	0.22 (0.06)	0.20 (0.05)	0.92	0.29
Methane Intensity	0.28 (0.06)	0.25 (0.06)	0.83	0.29
Residual $methane_B$	0.19 (0.06)	0.18 (0.05)	0.97	0.30
Residual $methane_J$	0.19 (0.05)	0.18 (0.05)	0.98	0.34
Residual $methane_I$	0.19 (0.05)	0.18 (0.05)	0.96	0.34
Residual $methane_R$	0.19 (0.05)	0.18 (0.05)	0.94	0.35

*From Donoghue *et al*. (2015) using the same data.

The proportion of the additive genetic variance captured by the SNP (the estimated genetic variance from the SNP divided by the genetic variance estimated from pedigree) ranged from 0.82 to 1, and was close to 1 for most traits. This is encouraging, indicating the SNPs are picking up most of the genetic variation for the traits (the proportion of genetic variation explained by the SNP sets an upper limit on the accuracy of GEBV that can be achieved).

The accuracies of GEBV from GBLUP were moderate, and quite similar across traits (Table 2). Accuracies were all significantly different to zero - the standard error of the correlation between GEBV and phenotypes (which divided by square root of heritability gives the accuracy) was 0.06, and for all traits the correlation was positive and at least twice this standard error. The accuracies of GEBV are similar to those for methane traits in sheep (Rowe et al. 2014).

In conclusion, results were encouraging – accuracies of GEBV for all traits were moderate, even though no SNPs with large effects for any of the methane traits was observed. Given an accuracy of GEBV of 0.3 (e.g. for methane yield and methane intensity), we can calculate response to selection for these traits that could be achieved per year (very roughly) as:

$$\Delta G = \frac{ir\sigma_{gen}}{L}$$

where i is the intensity of selection (assume 1.5), L is the generation interval (assume 3.5), r = 0.3 is the accuracy of genomic breeding values, σ_{gen} is the genetic standard deviation for the trait. The selection response for methane yield and methane intensity would be 0.084 g/kg DMI and 0.002 g/kg live weight respectively. This is 0.4 % and 0.5 % of the mean for these traits – suggesting 10 years of selection could lead to a 4 % reduction in methane yield, or a 5 % reduction in methane intensity, using the genomic breeding values derived with the data set used here. This compares not too unfavourably with for example milk yield in dairy cattle, a much easier trait to measure, where roughly a 1.5 % gain per year is achieved.

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