Proc. Assoc. Advmt. Anim. Breed. Genet. 26: 134-137

ETHANE AND CARBON DIOXIDE EMISSIONS IN AUSTRALIAN ANGUS – PAST AND PRESENT

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SUMMARY

Methane production (MP) and carbon dioxide production (CP) records have been collected on Australian Angus cattle in both past and current projects. The historic records consisted of animals measured in respiration chamber (n=887 animals) and using Greenfeed Emission Monitor (GEM, n=318 animals), while recent records were collected using GEM units (n=892 animals). The aims of this study were to estimate variance components and genetic relationships between emission traits based on historic respiration chamber records, current GEM records, and combined current and historic GEM records. The heritabilities of MP were similar in the respiration chamber (0.39, SE 0.10), current GEM (0.38, SE 0.11), and combined current and historic GEM (0.36, SE 0.08) datasets. The heritability of CP was higher in the respiration chamber dataset (0.49-0.50, SE 0.26) than the current GEM (0.38, SE 0.10) or the combined current and historic GEM (0.33, SE 0.08) datasets. Low to moderate positive genetic correlations were observed between the respiration chamber records and either the current or combined current-historic GEM datasets. The large SEs were likely due to the relatively small data sizes, particularly for the respiration chamber CP records (263 records). The results indicated that including both historic and current records may be beneficial for the estimation of genetic parameters of emissions in Australian Angus cattle.

INTRODUCTION

Beef is considered a high-quality protein source, but also has a considerable environmental impact, particularly in the form of methane (CH_4) emissions. Consequently, research into increasing the sustainability of Australian beef production has been, and continues to be, a priority for the industry. Genetic selection and breeding of cattle that produce less CH_4 is a method offering a cumulative and permanent reduction in emissions from the beef industry.

Multiple projects have collected CH_4 and carbon dioxide (CO_2) emissions data on Australian Angus cattle over the last two decades, including the National Livestock Methane Program (NLMP) and the Low Methane Beef (LMB) project. Thus, records are available on both current and historic animals, and the potential value of including all available data in the genetic evaluation of emissions can be explored. The aims of the current study were to estimate variance components of emission traits based on current and historic records, and to examine the genetic correlations between emission traits based on records measured using different methods.

MATERIAL AND METHODS

Low methane beef dataset (CurGEM). The LMB records were collected in 2022-2024 on 892 genotyped Angus steers, comprising: 477 Angus Sire Benchmarking project (ASBP) and 415 Southern MultiBreed project (SMB) steers. All LMB data were collected using Greenfeed Emission Monitor (GEM) units (C-Lock Inc, USA) at the "Tullimba" research feedlot, near Armidale, NSW, Australia. The GEM units collect spot-samples of CH_4 and CO_2 when an animal visits the machine.

Only animals with a minimum of five CH_4 and CO_2 spot-samples of a minimum recording duration of 2 minutes were used. The spot-samples were averaged over the trial period to calculate CH_4 production (MP, g/day) and CO_2 production (CP, g/day) for each steer.

National livestock methane program datasets (RESP and HisGEM). The NLMP project produced two different emission datasets; one containing emission records measured using open-circuit respiration chambers (RESP), and one comprised of emission records obtained using GEM units (HisGEM). Detailed descriptions of cattle populations, management and recording procedures are provided in Herd *et al*. (2014) for RESP and Arthur *et al*. (2017) for HisGEM.

The RESP included MP on 887 Angus animals (517 bulls and 370 heifers), and 263 animals also had a CP record. Initial analysis showed genetic correlations of ~1.00 between bulls and heifers for both MP and CP and the traits were therefore treated as one trait for both bulls and heifers.

The HisGEM contained GEM emission records for 318 Angus steers collected at "Tullimba" feedlot. The dataset only included animals with a minimum of 30 spot-samples with a minimum recording duration of 3 minutes. The spot-samples were averaged over the trial period to calculate MP and CP.

Combined dataset (ComGEM). Analysing the records from the HisGEM dataset alone was not possible, due to the small data size. A dataset combining the HisGEM and CurGEM records were created (ComGEM), and it contained MP and CP records on 1,210 steers. Descriptive statistics for the four datasets can be found in Table 1. All animals were genotyped.

Table 1. Descriptive statistics for methane and carbon dioxide production (g/day) in the respiration chamber dataset (RESP) and the current (CurGEM), historic (HisGEM), and combined current and historic Greenfeed Emission Monitor (ComGEM) datasets

Trait	Statistic	RESP	CurGEM	HisGEM	ComGEM
Methane production	Records	887	892	318	1,210
	Mean (SD)	138 (24)	179 (34)	203 (31)	185 (35)
	Range	84-251	62-317	126-308	62-317
Carbon dioxide production	Records	263	892	318	1,210
	Mean (SD)	3,155 (643)	9,900 (1,350)	8,933 (1,214)	9,646 (1,382)
	Range	2,169-4,973	5,433-14,928	6,045-12,833	5,433-14,928

Statistical analysis. The data were analysed within trait using two bivariate genomic best linear unbiased prediction models, one model with RESP and CurGEM records and one model with RESP and ComGEM records. The models followed:

$\begin{bmatrix}\mathbf{y}_{\text{RESP}}\\ \mathbf{y}_{\text{j}}\end{bmatrix} = \begin{bmatrix}\mathbf{X}_{\text{RESP}} & 0\\ 0 & \mathbf{X}_{\text{j}}\end{bmatrix}\begin{bmatrix}\mathbf{b}_{\text{RESP}}\\ \mathbf{b}_{\text{j}}\end{bmatrix} + \begin{bmatrix}\mathbf{Z}_{\text{RESP}} & 0\\ 0 & \mathbf{Z}_{\text{j}}\end{bmatrix}\begin{bmatrix}\mathbf{a}_{\text{RESP}}\\ \mathbf{a}_{\text{j}}\end{bmatrix} + \begin{bmatrix}\mathbf{e}_{\text{RESP}}\\ \mathbf{e}_{\text{j}}\end{bmatrix}$, where the subscript RESP referred to the RESP datasets and subscript j referred to the CurGEM or ComGEM datasets. $\mathbf{y}$, $\mathbf{b}$, $\mathbf{a}$ and $\mathbf{e}$ were vectors containing the phenotypes (MP or CP), fixed effects, random genetic effects and random residuals for each dataset. Contemporary group and age were used as fixed effects for both traits in all datasets. Age of dam was included for both traits in the RESP dataset. The random genetic and residual effects were assumed multivariate normally distributed following $\begin{bmatrix}\mathbf{a}_{\text{RESP}}\\ \mathbf{a}_{\text{j}}\end{bmatrix} = MVN\left(\begin{bmatrix}0\\0\end{bmatrix}, \begin{bmatrix}\sigma^2_{a_{RESP}} & cov\\ cov & \sigma^2_{a_j}\end{bmatrix} \otimes G\right)$ and $\begin{bmatrix}\mathbf{e}_{\text{RESP}}\\ \mathbf{e}_{\text{j}}\end{bmatrix} = MVN\left(\begin{bmatrix}0\\0\end{bmatrix}, \begin{bmatrix}\sigma^2_{e_{RESP}} & 0\\ 0 & \sigma^2_{\epsilon_j}\end{bmatrix} \otimes \begin{bmatrix}\mathbf{I} & 0\\ 0 & \mathbf{W}_{\text{j}}\end{bmatrix}\right)$, respectively. σ^2_a and cov were the additive genetic variance within dataset and the covariance between the datasets, respectively. $\mathbf{G}$ was the genomic relationship matrix (VanRaden 2008) consisting of 2,103 animals. $\sigma^2_{e_{RESP}}$ was the residual variance of the RESP dataset. $\sigma^2_{\epsilon_j}$ was a scalar.

I was an identity matrix. $\mathbf{W}_j$ was a diagonal matrix used to weight the residuals based on the number of spot-samples used to calculate the trial average phenotype ($w_{ii} = 1 - \frac{1}{ns_i}$, where ns_i was the number of spot-samples for animal *i*). The residual variances in the CurGEM and ComGEM datasets were then calculated as $\frac{\sigma^2_{\epsilon_j}}{W_j}$. All analysis was completed using the DMUAI packet of DMU (Madsen and Jensen, 2013).

RESULTS AND DISCUSSION

The heritabilities of MP and CP were moderate for RESP, CurGEM, and ComGEM, with all three datasets showing considerable additive genetic variance for both traits (Table 2). The heritability of MP (0.39) and CP (0.49-0.50) in the RESP dataset differed from the previously reported heritabilities of 0.27-0.31 for MP (Donoghue *et al*. 2016; Donoghue *et al*. 2020; Hayes *et al*. 2016) and 0.53 for CP (Donoghue *et al*. 2020) which were estimated using the complete NLMP respiration chamber dataset. This differences in heritabilities were likely due to genotypes only being available for a subset of the NLMP historic respiration chamber dataset for this study (887 out of 1,096 animals).

The SEs of the estimated variance components were lower (both numerically and when expressed as a ratio of the estimate) for the ComGEM dataset compared to the CurGEM dataset. The lower SEs indicate that combining the CurGEM with the HisGEM improved the accuracy of estimation of variance components compared to using only the CurGEM dataset.

The genetic correlations between the RESP and either CurGEM or ComGEM dataset were moderately positive for MP and low to moderately positive for CP (Table 2) indicating that MP and CP collected via respiration chambers and GreenFeed units are different traits. The observed moderate genetic correlations between datasets were expected due to the differences in recording methods and environments. The SEs were large for all genetic correlations. However, the SEs of the genetic correlations between the RESP and ComGEM datasets were reduced compared to the SEs of the genetic correlations between the RESP and CurGEM datasets.

It was not surprising that more variation was observed in the GEM based datasets than the RESP dataset. For example, the variances of MP were at least 3.8 times larger in the GEM based datasets relative to the RESP dataset. For CP, the variances were at least 14.7 times larger in the GEM based datasets than the RESP dataset. The short duration spot-sampling done by GEM units is expected to contain more variability, even after averaging across the trial, than the continuous 24 to 48-hour measurement of emissions obtained from respiration chambers. In addition, feeding method and environmental differences may have contributed to the observed differences in estimated variance components. The RESP records were collected in single animal chambers, with temperature control, restricted feed intake and limited option for physical activity. In contrast, the GEM records were collected in open air pens with *ad lib* bunk feeding. Given the moderate genetic correlation between RESP and GEM, these datasets will be analysed separately for MP and CP in the future. The difference in data size likely also contributed to the differences between estimates from the RESP and the GEM based datasets. The number of CP records was less than a third in the RESP dataset relative to the GEM based datasets. This resulted in SEs-to-estimate ratios for CP that were 2 to 4 times larger in the RESP compared to the other two datasets. It also resulted in larger SEs of the genetic correlations between datasets for CP compared to the SEs of the genetic correlations of MP.

While this study indicates that inclusion of historic records could be beneficial for evaluation of emission traits, it did not examine the prediction ability of the different datasets. Further research should be conducted to assess the impacts of including the historic datasets on predictability of breeding values.

Table 2. Number of records and estimates and standard errors in parenthesis for additive genetic variance (σ_a^2), residual variance (σ_e^2) and heritability (h^2) of methane production and carbon dioxide production for the respiration chamber records (RESP), current Greenfeed Emission Monitor records (CurGEM) and combined historic and current Greenfeed Emission Monitor records (ComGEM), as well as the genetic correlation (r_g) between the RESP and either CurGEM or ComGEM datasets

Analysis	RESP and CurGEM		RESP and ComGEM	
	RESP	CurGEM	RESP	ComGEM
Methane production				
Records	887	892	887	1,210
σ_a^2	78 (16)	339 (78)	77 (16)	300 (59)
σ_e^2	120 (12)	551 (61)	120 (12)	542 (47)
h^2	0.39 (0.10)	0.38 (0.11)	0.39 (0.10)	0.36 (0.08)
r_g	0.55 (0.26)		0.39 (0.23)	
Carbon dioxide production				
Records	263	892	263	1,210
σ_a^2	19,806 (8,013)	365,755 (83,530)	20,155 (7,997)	295,414 (62,055)
σ_e^2	20,490 (5,588)	597,627 (65,735)	20,275 (5,548)	611,833 (51,464)
h^2	0.49 (0.26)	0.38 (0.10)	0.50 (0.26)	0.33 (0.08)
r_g	0.19 (0.40)		0.38 (0.38)	

CONCLUSION

The results of the current study suggest utilising all available data may be beneficial when evaluating emissions in Australian Angus cattle. However, further research is needed, particularly regarding the impact of including the historic records on the predictive ability of the models.

ACKNOWLEDGEMENT

The authors would like to thank the NLMP for providing historic emission records and the SMB and ASBP for providing animals for the LMB project. We would also like to thank all staff at Angus Australia and Rangers Valley Feedlot involved in the ASBP project, as well as the staff at Tullimba feedlot and New South Wales Department of Primary Industries involved in the NLMP, LMB and SMB projects.

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