



Department of  
Primary Industries

# Repeatability of methane emission measurements in Australian beef cattle

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# Genetic improvement of beef cattle for GHG outcomes

- Investigate whether genetic variation exists for methane traits
- Understand nature of relationships between methane traits and traits impacting \$\$\$\$\$\$\$\$

# First look-Journal of Animal Science

## **GENETIC AND PHENOTYPIC VARIANCE AND COVARIANCE COMPONENTS FOR METHANE EMISSION AND POSTWEANING TRAITS IN ANGUS CATTLE**

Kath Donoghue; Tracie Bird-Gardiner; Paul Arthur; Robert Herd; Roger Hegarty

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## **GENOMIC HERITABILITIES AND GENOMIC ESTIMATED BREEDING VALUES FOR METHANE TRAITS IN ANGUS CATTLE**

Ben Hayes; Kath Donoghue; Coralie Reich; Brett Mason; Tracie Bird-Gardiner; Robert Herd; Paul Arthur

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# Objective

Investigate repeatability of methane traits across various time frames:

- Consecutive days
- Within 60 days of first methane test
- 61-120 days after first methane test
- 121-450 days after first methane test

# Methodology

- Animals bred at Trangie in 2 separate herds
- Cohorts formed each year within herd & sex
- Each cohort had 40 head in 4 equal groups
- Animals fed 1.2 x maintenance
- Animals measured in Armidale in open circuit respiration chambers
- Measured over two consecutive 24 hour periods

# Data collection

- Live Weight (**WT**)
- Dry Matter Intake (**DMI**)
- Methane production (**MPR**): g CH<sub>4</sub>/day
- Methane yield (**MY**): g CH<sub>4</sub>/kg DMI
- Residual methane production (**RMP**): g CH<sub>4</sub>/day

# Residual Methane Traits

- $RMP_J = \text{Actual MPR} - \text{expected MPR}$
- Expected MPR using formula from Johnson et al. (2005)
- $RMP_R$ : Residuals obtained from simple regression of MPR on DMI performed within cohort

# Model of analysis

- Repeatabilities: repeated measures model in ASReml
- Phenotypic correlations: bivariate analyses
- Rank correlation between sire progeny means from first and repeat methane test



# Summary statistics (n=175)

Trait	First test		Repeat test	
	Mean	SD	Mean	SD
Age (days)	484	167	687	252
WT (kg)	392	97	514	147
DMI (kg/d)	6.58	1.49	7.76	1.99
MPR (g CH <sub>4</sub> /d)	130.6	30.3	163.5	41.0
MY (g CH <sub>4</sub> /kg DMI)	20.34	4.17	21.23	1.94
RMP <sub>J</sub> (g CH <sub>4</sub> /d)	-0.97	30.59	8.17	13.93
RMP <sub>R</sub> (g CH <sub>4</sub> /d)	-0.30	14.12	0.32	9.99

# Repeatabilities (SE)

Trait	Consecutive days (n=175)	Within 60 days (n=44)	61-120 days (n=30)	121-450 days (n=92)
MPR	0.94 (0.03)	0.91 (0.02)	0.27 (0.06)	0.27 (0.06)
MY	0.75 (0.05)	0.59 (0.10)	0.21 (0.05)	0.19 (0.05)
RMP <sub>J</sub>	0.89 (0.04)	0.83 (0.04)	0.20 (0.05)	0.16 (0.05)
RMP <sub>R</sub>	0.91 (0.04)	0.83 (0.04)	0.20 (0.05)	0.17 (0.05)

# Phenotypic correlations (SE)

Trait	Consecutive days (n=175)	Within 60 days (n=44)	61-120 days (n=30)	121-450 days (n=92)
MPR	0.95 (0.03)	0.78 (0.06)	0.27 (0.14)	0.26 (0.09)
MY	0.85 (0.05)	0.30 (0.15)	0.20 (0.14)	0.15 (0.10)
RMP <sub>J</sub>	0.91 (0.04)	0.39 (0.15)	0.13 (0.12)	0.12 (0.09)
RMP <sub>R</sub>	0.92 (0.04)	0.44 (0.14)	0.13 (0.11)	0.13 (0.09)

# Correlations for sire progeny means

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Trait

Correlation

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MPR

0.77

MY

0.55

RMP<sub>J</sub>

0.46

RMP<sub>R</sub>

0.19

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# Conclusions

- Methane traits:
  - Highly repeatable & highly phenotypically correlated in short term (~60 days)
  - Lowly repeatable & lowly phenotypically correlated over longer time frames
- Multiple measures required over animal's life time
- Knowledge of genetic correlations also needed

# National Livestock Methane Program



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