

## **Genomic prediction for feed efficiency: a validation of accuracy and its impact on methane emissions of dairy cows**

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### **Summary**

In 2015, the Feed Saved genomic breeding value was released in Australia. This breeding value was constructed using a genomic breeding value for residual feed intake (RFI) combined with an estimate of maintenance requirements. The objectives of this study were to evaluate the accuracy of the genomic prediction equation for RFI and to determine whether enteric methane emissions were reduced in more efficiency cows (low RFI). After correcting for the heritability, the accuracy of the genomic prediction equation for RFI was 0.35 and is consistent with that reported in the previous validation. The results also indicate that low RFI cows had significantly less methane production (471 vs 503 g/d) but not methane yield (19.3 vs. 18.6 g/kg of dry matter intake) and methane intensity (20.4 vs. 21.4 g/kg of milk).

*Keywords: Feed Saved, methane emissions, genomic selection, dairy cows*

### **Introduction**

Genomic selection for improved feed efficiency, defined as residual feed intake (RFI), and lower methane (CH<sub>4</sub>) emissions without compromising productivity have recently been a common topic in dairy cattle research (de Haas *et al.*, 2017). In Australia, a feed efficiency breeding value known as Feed Saved was released in 2015 which permits farmers to breed cows that produce the same amount of milk but eat less (Pryce *et al.*, 2015). One of the challenges with selecting for feed efficiency traits is that actual feed intake data is required, which generally limits the reference populations used for these traits to research herds. Due to the strong correlation between intake and methane production, cattle selected for low RFI (i.e. efficient) are expected to produce less methane compared to their counterparts.

This study aimed to validate the accuracy of the genomic estimated breeding values for RFI which is a major component of Feed Saved and to compare methane emissions of cows selected for divergent RFI.

### **Material and methods**

#### **Animal Data**

A 32-d experiment was conducted with 160 spring-calving Australian Holstein cows at the Ellinbank Centre of the Department of Economic Development, Jobs, Transport and Resources (Melbourne, Australia). Cows were assigned to 4 batches that were balanced for days in milk (DIM) and parity. Full details of animal management, the diets, the measurement

of dry matter intake (DMI) and other data have been described in Pryce *et al.* (2014). Methane production (g/d), methane yield (g/kg of DMI), and methane intensity (g/kg of milk) from individual cows were measured using the modified SF6 tracer technique. Genomic estimated breeding values (GEBV) for Feed Saved and RFI predicted using the reference population described by Pryce *et al.* (2015) were obtained from DataGene. Due to missing data for breeding values and methane measurements, data of only 112 cows could be used for analysis. It should be noted that the data is completely independent from that previously used for deriving genomic prediction equations for RFI and consequently Feed Saved. A summary of the data of the 112 cows is presented in Table 1.

Table 1. The lactation performance, residual feed intake and methane emissions by batch of 112 cows used in this study (mean  $\pm$  SD)

	Batch 1	Batch 2	Batch 3	Batch 4
Number of cows	28	33	31	20
Days in milk	79 $\pm$ 4	91 $\pm$ 7	80 $\pm$ 6	63 $\pm$ 22
Residual feed intake (kg/d)	-0.03 $\pm$ 0.9	0.05 $\pm$ 0.8	-0.005 $\pm$ 0.9	0.02 $\pm$ 0.5
Dry matter intake (kgDM/d)	22.0 $\pm$ 3.2	24.8 $\pm$ 2.9	23.1 $\pm$ 2.9	24.3 $\pm$ 2.2
Milk yield (kg/d)	22.5 $\pm$ 4.0	25.6 $\pm$ 4.6	23.2 $\pm$ 3.8	29.7 $\pm$ 4.2
Body weight (kg)	511 $\pm$ 73	544 $\pm$ 70	523 $\pm$ 51	569 $\pm$ 59
Methane production (g/d)	454 $\pm$ 60	450 $\pm$ 65	495 $\pm$ 66	543 $\pm$ 38
Methane yield (g/kgDMI)	19.5 $\pm$ 2.5	16.4 $\pm$ 1.9	20.5 $\pm$ 2.3	18.3 $\pm$ 1.4
Methane intensity (g/kgMY)	20.1 $\pm$ 3.6	21.5 $\pm$ 3.9	21.9 $\pm$ 3.4	20.8 $\pm$ 2.7

### Calculation of RFI

Phenotypes for RFI were derived using the model as follow:

$$y_{DMI} = \mu + b_1 \times DIM + b_2 \times ECM + b_3 \times BW + b_4 \times \Delta BW + X' \beta + e_{DMI}$$

where  $y_{DMI}$  is the average DMI over the experimental period,  $\mu$  is the overall mean,  $b_1$ ,  $b_2$ ,  $b_3$ , and  $b_4$  are partial regression coefficients, corresponding to DIM, ECM, BW, and  $\Delta BW$ , which are vectors of individual records for DIM at the beginning of the trial, energy corrected milk, mean body weight, and body weight change during the trial period, respectively. Then,  $\beta$  were the systematic environmental effect of parity (levels = 1 to 3+) and batch (level = 1 to 4). Finally, the residual term  $e_{DMI}$  became the vector of phenotypic records for RFI in cows.

Energy-corrected milk (kg/d) was calculated using average daily yields for milk, fat, and protein over the 32-d experimental period:

$$ECM = (\text{kg milk} \times (376 \times \text{fat}\% + 209 \times \text{protein}\% + 948)) \div 3138$$

### Statistical Analysis

The accuracy of the genomic prediction equation for RFI was evaluated using the correlation between the vector of RFI phenotypes and corresponding RFI GEBV. To compare methane emissions of cows with divergent RFI, data was first ranked on the RFI phenotypes and then 30 cows in each tail were selected and assigned to low and high RFI groups. The differences in methane emissions of cows in the low and high RFI groups were compared using a Welch's t-test (R Development Core Team, 2017).

### Results and discussion

The correlation between RFI phenotypes and RFI GEBV for lactating Australian cows was 0.16 (Figure 1). After correcting for the heritability (dividing by the squared-root of the heritability of RFI, 0.22 obtained from Pryce *et al.* (2012)), the accuracy was 0.35 which is very similar to the previous report of 0.37 of Pryce *et al.* (2015). This correction for the heritability estimate was to make the accuracy similar to the correlation between GEBV and true breeding values instead of phenotypes (Pryce *et al.*, 2012).

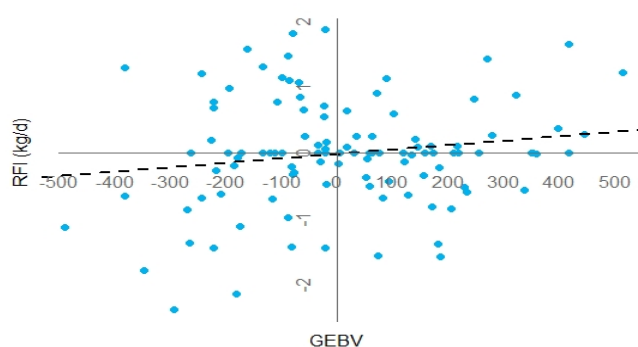


Figure 1. The correlation between residual feed intake (RFI) phenotypes and RFI genomic estimated breeding values (GEBV) for 112 cows estimated using the genomic prediction equation of Pryce *et al.* (2015).

In terms of methane emissions, the results show that at the same level of production, the 30 lowest RFI cows ate significantly less (21.9 vs. 24.5 kg of DM/d) and produced less methane (471 vs. 503 g/d) compared to their counterparts (Table 2). The averages of methane yield and methane intensity were, however, not different between the two groups (19.3 vs. 18.6 g/kg DMI and 20.4 vs. 21.4 g/kg of milk, respectively). These results are consistent with the previous findings on relationship between RFI and methane emissions in beef cattle (Alemu *et al.*, 2017). Conversely, other authors concluded beef cattle selected for low RFI do not necessarily produce less methane (Velazco *et al.*, 2017). Further, the significant difference in DMI between the low and high RFI cows and the correlation of 0.6 between DMI and methane production imply intake is a driver for divergent methane productions, which is in agreement with the conclusion of Alemu *et al.* (2017). The inherent variation in digestive efficiency between cows could also be a contributor (Herd & Arthur, 2009).

When the cows were ranked by Feed Saved or RFI GEBV instead of RFI phenotypes, no significant differences in average methane emissions could be observed (data not shown). This indicates that the current genomic estimated breeding values for feed efficiency are likely to be too low in reliability to detect divergence in methane emissions. de Haas *et al.* (2017) have discussed approaches for improving the accuracy of genomic selection of traits associated with feed intake including enlarging the reference population, optimizing the reference population with respect to the relationships between the animals, incorporating ungenotyped but phenotyped animals into the reference population, combining data sets internationally, and incorporating predictor traits into analyses.

Table 2. Performance and methane emissions (mean  $\pm$  SD) of low and high residual feed intake (RFI) cows

	Low RFI	High RFI	P-value
Number of cows	30	30	
Milk yield (kg/d)	23.9 ± 4.6	24.2 ± 4.7	NS
Dry matter intake (kg DM/d)	21.9 ± 2.5	24.5 ± 2.9	***
Body weight (kg)	520 ± 65	529 ± 60	NS
Residual feed intake (kg/d)	-1.0 ± 0.6	1.0 ± 0.4	***
Methane production (g/d)	471 ± 55	503 ± 67	*
Methane yield (g/kg DMI)	19.3 ± 2.6	18.6 ± 2.8	NS
Methane intensity (g/kg MY)	20.4 ± 3.3	21.4 ± 3.3	NS
Feed Saved (kg/year)	35.9 ± 92.3	15.3 ± 74.6	NS
RFI GEBV (kg/lifetime)	-51.6 ± 220.0	20.4 ± 230.2	NS

NS: non-significant; \*: level of statistical significance

## Conclusions

This study explored the potential of using genomic selection for improved feed efficiency to mitigate methane emissions in Australian dairy cattle. It was concluded that low RFI cows produced significantly less methane than high RFI cows. Dry matter intake was found to be the driver of varying methane production. More data is required to improve the reliability of the current genomic estimated breeding values for feed efficiency.

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