

Progress toward Incorporating Residual Feed Intake into the New Zealand National Breeding Objective for Dairy Cattle: Genetic Parameters in Half-Sib 6-9 Month Old Friesian Bulls and Heifers

M. E. Olayemi¹, M. D. Camara¹, K. A. Macdonald, B. Dow, S. Meier and J. R. Bryant
DairyNZ Limited, Private Bag 3221, Hamilton 3240, New Zealand

¹Corresponding author; Mark.Camara@Dairynz.co.nz

Abstract

To investigate the potential to select for feed conversion efficiency in dairy cattle, we measured daily feed intake and body liveweight on 73 bull and 246 half sib heifer calves in a feeding trial using *ad libitum* Lucerne cube feed at the Westpac Taranaki Agricultural Research Station in Hawera, New Zealand. We measured feed consumption using automated systems, weighed all animals thrice weekly, and estimated residual feed intake (RFI) as the residual from a regression of daily dry matter intake (DMI) on average daily gain (ADG) and metabolic body weight ($MBW^{0.75}$). Using ASReml, we estimated the sex-specific additive genetic variances and heritabilities using univariate animal models as 0.05 and 0.13 ± 0.14 for the heifers, and 0.09 and 0.18 ± 0.57 for the young bulls. We also used a bivariate animal model that treated the RFI of the two sexes as different traits to estimate the genetic correlation between young bulls and heifers as 0.93 ± 1.46 . Despite the high standard errors around the genetic parameter estimates due to small sample size, our results provide a preliminary indication that RFI is largely controlled by the same genes in both sexes and that genetic variation in RFI in Friesian dairy cattle is sufficient to support a response to selection in female relatives of elite young bulls.

Key words: Residual feed intake, Friesian calves, genetic correlation, heritability, dairy cattle, New Zealand

Introduction

Residual feed intake (RFI) is defined as the difference between the feed intake of an individual and the expected feed intake of an average animal with the same maintenance requirements and weight gain in a specific population (Koch *et al.*, 1963). More efficient animals have negative RFI values and eat less than expected, whereas inefficient animals have a positive or high RFI and eat more than expected. Previous studies have reported low to moderate heritabilities of 0.07 to 0.62 for RFI in beef cattle (Archer *et al.*, 1999, Schenkel *et al.*, 2004, Arthur and Herd 2008, Arthur and Herd 2012, Berry and Crowley 2013), 0.22 to 0.38 in dairy cattle (Williams *et al.*, 2011, Pryce *et al.*, 2012) and 0.16 to 0.23 in pigs (Saintilan *et al.*, 2012). Saintilan *et al.* (2012) also reported high genetic correlations (0.88-0.99) between the sexes for RFI. These studies suggest that RFI should respond to selection and that selection on males should produce a correlated response in females.

Incorporating selection for RFI into the New Zealand national breeding objective, expressed as Breeding Worth, and developing a testing strategy, however, requires genetic parameter estimates for RFI in the New Zealand national dairy herd. In addition, the high costs and complexity of measuring RFI make it desirable to restrict testing to bulls that rank highly for other economically important traits. The aims of this study were to estimate the heritability of RFI in bull calves and their female half sibs and the between-sex genetic correlation for RFI.

Materials and Methods

Animal management and data collection

The feeding trials were conducted at Westpac Taranaki Agricultural Research Station in Hawera, New Zealand. Seventy-three Friesian bulls and 246 of their half-sib heifers with 9 common sires were randomly allocated to groups of 5-8, with each group assigned to one

of the 25 feeding pens and one of the two temporal cohorts. Bulls and heifers were tested in separate pens. The first temporal cohorts was on-test for 40 days and the second for 30 days, excluding a brief adjustment period to acclimate them to the facility. All calves were allowed unlimited, 24-hours access to Lucerne cube feed with their feed intake measured continuously by automated systems. We weighed them thrice weekly and calculated their average daily feed intake (DMI), average daily gain (ADG) and mid-trial body weight (MBW). We estimated residual feed intake (RFI) separately for heifers and young bulls as the residual error term from a regression of DMI on $MBW^{0.75}$ and ADG (Koch *et al.*, 1963) using the REG procedure of SAS software (SAS 2011) to fit the model $DMI = \mu + \beta_{MBW}^{0.75} + \beta_{ADG} + \varepsilon$, where DMI is the mean intake during the test period, μ is the intercept, $\beta_{MBW}^{0.75}$ is the regression coefficient on mid-trial metabolic body weight ($MBW^{0.75}$), β_{ADG} is the regression coefficient of average daily weight gain (ADG), and ε is the error term (residual intake).

Univariate genetic analysis

To estimate the additive genetic (σ_A^2), residual (σ_R^2), and phenotypic (σ_P^2) variance components for RFI, we fit a separate univariate animal model for each sex and for combined data using ASReml 4 (Gilmour *et al.*, 2015) and calculated the associated heritabilities and their standard errors using ASReml's native post-analysis procedures for calculating functions of variance components. The model terms are listed and described in Table 1.

Table 1. Terms in the mixed model.

Term	Type	Effect
mu	Fixed	Overall mean
Sex	Fixed	Sex (combined model only)
Cohort	Fixed	Time-based groups
Pen	Fixed	Feeding pens nested w/in cohort (and sex for combined model)
C_Group	Fixed	Contemporary groups (nested w/in sex for combined model)
Age	Fixed	Animal age (days)
Eczema	Fixed	Facial eczema (affected or not)
Animal	Random	Additive genetic effect (pedigree)

Bivariate genetic analysis

To estimate the genetic correlation between the RFI of young bulls and their half-sib heifers, we fit a cross-sex genetic model that treated the RFI of young bulls and heifers as separate traits using the multivariate equivalents of the univariate model terms (Table 1). However, because the male and female RFI traits were measured on different individuals in separate-sex pens, we constrained the residual covariance at zero, and the contemporary group and pen terms were trait/sex-specific. Furthermore, to obtain model convergence, we supplied the genetic variance estimates from the single-sex univariate models as starting values and constrained them at these values. This required ASReml to estimate only the genetic covariance and trait/sex-specific residual variances.

Results and Discussion

Table 2. shows the genetic parameter estimates for RFI from the single-sex and combined univariate animal models. The heritability estimates range from 0.12 to 0.18 indicating the potential existence of genetic variation for RFI, albeit with very large standard errors due to small sample size (9 sires with a range of 9 to 42 offspring). These heritability estimates are within the range of previously reported estimates (Berry & Crowley, 2013; Arthur and Herd 2012; Williams *et al.*, 2011; Pryce *et al.*, 2012).

Table 2. Additive genetic (σ_A^2), residual (σ_R^2), and phenotypic variances (σ_P^2), and heritability (h^2) estimates (\pm standard error [se]) for RFI from heifers, bulls, and combined data from univariate animal model.

Sex	σ_A^2	σ_R^2	σ_P^2	$h^2 \pm se$
Heifers only	0.05	0.37	0.42	0.13 ± 0.14
Bulls only	0.09	0.39	0.47	0.18 ± 0.57
Combined	0.05	0.35	0.39	0.12 ± 0.14

The bivariate analysis found a low phenotypic correlation of RFI between the sexes and a very high genetic correlation (Table 3). The genetic correlation estimate suggests that the same genes are largely responsible for the expression of RFI in both sexes, but again the standard errors are high due to the small sample size. This estimate of the between-sex genetic correlation for RFI is comparable to estimates of 0.88 to 0.99 in pigs (Saintilan *et al.*, 2012).

Table 3. Heritabilities and correlations between residual feed intake (RFI) in Friesian heifer and bull calves (\pm standard error (se)) Heritabilities on the diagonal, genetic correlations above; phenotypic below.

Sex	Heifer	Bull
Heifer	0.14 ± 0.01	0.93 ± 1.46
Bull	0.15 ± 0.23	0.19 ± 0.04

Conclusion

This study provides preliminary evidence for sufficient genetic variance and heritability for RFI in the New Zealand dairy herd to support a response to selection, and a very high genetic correlation between RFI in young bulls and heifers. We conclude that given these genetic parameter estimates, selection on bulls should produce a correlated response in heifers. However, due to limited sample size, all genetic parameter estimates have very high standard errors, and further research is required prior to incorporation of RFI into Breeding Worth, the New Zealand national breeding objective and routine national animal evaluation models.

Acknowledgements

The authors thank Dairy NZ technical staff in Newstead (Hamilton, New Zealand) and at the Westpac Taranaki Agricultural Research Station research facilities in Hawera (New Zealand), where animal feeding and measurements were carried out. This project is funded by the Transforming the Dairy Value Chain (TDVC) Primary Growth Partnership programme, a seven-year, \$170 million innovation programme led by commercial partners, including DairyNZ and Fonterra, in partnership with the New Zealand Ministry of Primary Industries .

References

- Archer, J.A., Richardson, E.C., Herd, R.M. & Arthur, P.F. 1999. Potential for selection to improve efficiency of feed use in beef cattle: A review. *Aust. J. Agric. Res.* 50, 147–161.
- Arthur, J.P.F. & Herd, R.M. 2008. Residual feed intake in beef cattle. *Revista Brasileira de Zootecnia* 37, 269-279.
- Arthur, P.F. & Herd, R.M. 2012. Genetic improvement of feed efficiency. In ‘. Pages 93–103 in R. Hill, editor. *Feed efficiency in the beef industry*. John Wiley & Sons, Cambridge, MA.

- Berry, D.P. & Crowley, J.J. 2013. Cell Biology Symposium: Genetics of feed efficiency in dairy and beef cattle. *Journal of Animal Science* 91, 1594-1613.
- Gilmour, A.R., Gogel, B.J., Cullis, B.R., Welham, S.J. & Thompson, R. 2015. *ASReml User Guide Release 4.1 Structural Specification*. VSN International Ltd, Hemel Hempstead, HP1 1ES, UK (www.vsnl.co.uk).
- Koch, R.M., Swiger, L.A., Chambers, D. & Gregory, K.E. 1963. Efficiency of Feed Use in Beef Cattle. *Journal of Animal Science* 22, 486-494.
- Pryce, J.E., Arias, J., Bowman, P.J., Davis, S.R., Macdonald, K.A., Waghorn, G.C., Wales, W.J., Williams, Y.J., Spelman, R.J. & Hayes, B.J. 2012. Accuracy of genomic predictions of residual feed intake and 250-day body weight in growing heifers using 625,000 single nucleotide polymorphism markers. *Journal of Dairy Science* 95, 2108-2119.
- Saintilan, R., Sellier, P., Billon, Y. & Gilbert, H. 2012. Genetic correlations between males, females and castrates for residual feed intake, feed conversion ratio, growth rate and carcass composition traits in Large White growing pigs. *Journal of Animal Breeding & Genetics* 129, 103-106.
- SAS. 2011. *SAS OnlineDoc®, Version 9.3*. <http://support.sas.com/documentation/93/>. SAS Institute Inc., Cary, NC.
- Schenkel, F.S., Miller, S.P. & Wilton, J.W. 2004. Genetic parameters and breed differences for feed efficiency, growth, and body composition traits of young beef bulls. *Canadian Journal of Animal Science* 84, 177-185.
- Williams, Y.J., Pryce, J.E., Grainger, C., Wales, W.J., Linden, N., Porker, M. & Hayes, B.J. 2011. Variation in residual feed intake in Holstein-Friesian dairy heifers in southern Australia. *Journal of Dairy Science* 94, 4715-4725.