Temp, L., Pereira, L., Bussiman, F., Hidalgo, J., Lourenco, D., Baldi, F. (2026) Genomic evaluation of residual feed intake adjusted for rump fat in beef cattle: implications for selection strategies, *Proceedings 13th World Congress on Genetics Applied to Livestock Production* 23389: https://doi.org/10.31274/wcgalp.23389 ©2026 Temp, et al. CC BY-NC-ND

Genomic evaluation of residual feed intake adjusted for rump fat in beef cattle: implications for selection strategies

L. B. Temp[1*], L. S. Pereira[2], F. Bussiman[3], J. Hidalgo[3], D. Lourenco[3], and F. Baldi[4]

[1]Sao Paulo State University, Jaboticabal, Brazil; [2] Sustainable Livestock Research Center, Institute of Animal Science, Goiás, Brazil; [3] University of Georgia, Athens, United States; [3]Sao Paulo University, Pirassununga, Brazil. [*]Corresponding author: larissabordintemp@gmail.com

Introduction

Understanding the biological mechanisms underlying individual variation in feed efficiency is essential for optimizing the use of feed resources and mitigating environmental impacts, such as greenhouse gas emissions (Cantalapiedra-Hijar *et al*., 2018). Among the developmental stages, the post-weaning to yearling phase is particularly critical, as animals in this period can exhibit substantial feed efficiency, which directly impacts the economic viability of breeding and rearing practices in both males and females. (Cervieri *et al*., 2009). In this context, residual feed intake (RFI), defined as the difference between the observed and predicted feed intake (Koch *et al*., 1963), stands out as an effective metric to identify animals with below-average maintenance requirements and feed intake, without compromising performance (Sainz *et al*., 2024). These animals are considered more feed-efficient, as they require less maintenance energy while sustaining comparable levels of productivity (Sainz *et al*., 2024), thereby maximizing the potential for profitability (Pereira *et al*., 2023). Potential drawbacks associated with RFI selection have been identified by Leme and Gomes (2007) and Shaffer *et al*. (2011) reporting that animals with negative RFI tend to have leaner carcasses, lower fat deposition rates, and reduced carcass weight, which may lead to delayed puberty and reduced reproductive performance. To address these concerns, including rump fat thickness (RFT) as a covariate in the regression model used to calculate the RFI has been proposed as a strategy to mitigate potential unfavorable outcomes of selection. This adjustment aims to preserve carcass quality traits, such as marbling, flavor, and juiciness, by accounting for variation in fat deposition. Understanding the genetic relationships of RFI with RFT and with other traits, is essential for balanced breeding programs. In this study we aimed to 1) estimate variance components and genetic correlations between RFI—calculated with (RFI_F) and without (RFI_W) adjustment for RFT and growth, reproduction and carcass traits using genomic data in Nellore cattle, and 2) assess the accuracy, bias, and dispersion of genomic breeding values for RFI_F and RFI_W predicted via single-step genomic BLUP (ssGBLUP). We hypothesized that accounting for RFT would explain a small portion of RFI variation, with minimal impact on selection outcomes. To further support this, we analyzed the relationships between RFI traits and reproductive.

Materials & Methods

Phenotypic records were obtained from 9,094 Nellore cattle (3,253 females and 5,952 males) across 14 feed efficiency tests conducted between 2011 and 2024 from the Nellore improvement program database of the Brazilian Breeders and Researchers Association (ANCP). The evaluated traits (numbers of animals) were: rump fat thickness (RFT; 9,094), rib eye area (REA; 8,293), frame score (FRAME; 3,202), scrotal circumference adjusted to 365 days of age (SC365; 2,879), body weight adjusted to 365 (W365; 5,097) or 450 days of age

(W450; 5,113), age at first calving (AFC; 2,211), stayability (STAY; 1,516), and early heifer pregnancy probability (3P; 1,841). The pedigree comprised 17,407 animals, with 5,812 of them being genotyped using the GGP indicus panel from Neogen. Genotype quality control was performed using preGSF90 software (Misztal et al., 2014; Lourenco *et al*., 2022) with removal of SNPs or animals with a call rate lower than 0.90, minor allele frequency less than 0.05, a departure from Hardy-Weinberg equilibrium (difference between observed and expected heterozygous frequency) higher than 0.15 or monomorphic SNP. After quality control, 5,799 genotyped animals and 42,132 SNP markers were retained for subsequent analyses. Two RFI definitions were considered—RFI_W (residual feed intake without rump fat adjustment) and RFI_F (residual feed intake adjusted for rump fat thickness) within contemporary groups. Efficiency tests were conducted according to the guidelines of the manual "Procedures for measuring individual feed intake in beef cattle," consisting of a 21-day adaptation period followed by a 70-day testing phase (Mendes *et al*., 2020). The average age at the beginning of the performance test was 424.2 ± 126.89 days.

Variance components estimation. A linear animal model was used to estimate (co)variance components and genetic parameters for RFI_W, RFI_F, REA, FRAME, SC365, W365, W450, and AFC. For 3P and STAY a threshold model was implemented via Bayesian inference, considering the systematic effect of CG and the random animal additive effect. Genetic correlations were estimated using three-trait models. For all analyses, RFI_W and RFI_F were consistently included, whereas the third trait (REA, FRAME, SC365, W365, W450, AFC, STAY, or 3P) varied among the analyses. For analyses including only continuous traits, i.e., linear models, genetic correlations were estimated using restricted maximum likelihood (EM-REML) via the BLUPf90+ software. For analysis including a binary trait, linear-threshold models were fitted using Bayesian inference via Gibbs Sampling using the GIBBSf90+ software (Lourenco *et al*., 2022).

GEBV and validation. Single-trait models were used to predict the GEBV for RFI_W and RFI_F. The validation method used was the linear regression (Legarra and Reverter, 2018). The whole dataset (subscript *w*) included all sources of information (phenotypes, genotypes, and pedigrees) for all animals (N = 5,443). The partial dataset (subscript *p*) included all information but phenotypes for the last two years of data (N = 4,297). This was done to ensure enough focal animals for validation. Focal animals (N =1,146) were young, genotyped animals with progeny or own records in the whole dataset but without them in the partial dataset. The validation statistics were prediction accuracy ($acc = \sqrt{\frac{cov(\hat{\mathbf{u}}_w, \hat{\mathbf{u}}_p)}{(1-\bar{F})\hat{\sigma}_u^2}}$), bias ($\delta = \frac{\bar{\hat{\mathbf{u}}}_p - \bar{\hat{\mathbf{u}}}_w}{\hat{\sigma}_u}$), dispersion ($b_1 = \frac{cov(\hat{\mathbf{u}}_w, \hat{\mathbf{u}}_p)}{var(\hat{\mathbf{u}}_p)}$), and correlation (corr).

Results & Discussion

Heritability estimates ranged from 0.13 (AFC) to 0.42 (SC365). A low estimate was observed for AFC (0.13), whereas STAY (0.20) and 3P (0.29) presented moderate values. Moderate heritability estimates were obtained for REA, FRAME, APM, W365 and W450, ranging from 0.28 (REA) to 0.33 (FRAME; W450). Heritability estimates for RFI_W and RFI_F were low (0.16 and 0.17), highlighting the substantial influence of environmental effects on these traits. This suggests that RFI has a low to moderate heritability in Nellore cattle, contrasting with taurine breeds (e.g., Angus [0.30-0.40; Torres-Vázquez *et al*., 2018] and various continental breeds [0.50; Esfandyari and Jensen, 2021]), indicating that faster growing breeds have a higher heritability for feed efficiency than breeds well-adapted to harsh environments. Another relevant aspect to consider is that heritability estimates tend to vary depending on the statistical model used to predict RFI, as well as on the population structure analyzed and the methodology

applied to measure the trait. Including body fat measures helps ensure that differences in RFI reflect true feed efficiency rather than variation in fat deposition. This approach also minimizes the risk of selecting overly lean carcasses in slaughter cattle or compromising body condition in replacement heifers, thereby reducing bias in RFI caused by differences in energy partitioning. The R2 for the model without fat was 0.2337, while the R2 for the model adjusted for fat was 0.2287. These values indicate that both models explain a similar proportion of the phenotypic variance in feed intake, with only a marginal change in explained variance when the fat term is included. The genetic correlation between RFI_W and RFI_F was strong, with values above 0.96, indicating that including RFT as a covariate in the model has little impact on RFI. In this context, the strong correlation observed suggests that the genetic factors influencing RFI at earlier developmental stages and lower body weights remain consistently active throughout the animal's growth. The genetic correlation between RFI_W and RFT was weak (0.15), and the phenotypic correlation was 0.03.

These findings suggest that improvements in feed efficiency during the post-weaning phase can be achieved independently of changes in fat deposition. This independence allows for greater flexibility in selection strategies without compromising carcass fatness traits. Comparing breeding values by sex between RFI_W and RFI_F, high phenotypic correlations were observed for both, females ($r = 0.98$) and males ($r = 0.95$), with highly significant p-values ($p < 2.2 \times 10^{-16}$). In cow–calf production systems, fat reserves play a crucial role for females, as they are essential for simultaneously supporting body maintenance, pregnancy, and future lactation demands (Santana *et al*., 2014). This physiological requirement helps explain the results observed, where females showed substantially higher fat deposition compared to males.

From the slaughterhouse perspective, carcass yield is more strongly influenced by REA and fat deposition, particularly in strategic locations, such as the rump and rib regions. Genetic correlations between RFI_W or RFI_F and growth, reproductive and carcass traits ranged from -0.33 to 0.35 (Table 1).

Table 1. Genetic correlations between residual feed intake, with (RFI_F) and without adjustment (RFI_W) for rump fat thickness, and traits related to feed efficiency, carcass, growth, and reproduction in Nellore cattle.

Paired trait	**RFI_W ± SD**	**RFI_F ± SD**
REA	-0.05 ± 0.07	-0.02 ± 0.07
FRAME	0.04 ± 0.04	0.14 ± 0.04
SC365	0.34 ± 0.10	0.35 ± 0.11
W365	0.15 ± 0.11	0.18 ± 0.12
W450	0.23 ± 0.10	0.27 ± 0.11
AFC	0.25 ± 0.15	0.28 ± 0.18
STAY*	0.21 (-0.24; 0.67)	0.12 (-0.33; 0.58)
3P*	-0.33 (-0.83; 0.15)	-0.24 (-0.75; 0.27)

REA, rib eye area; FRAME, frame score; SC365, adjusted scrotal circumference (cm) at 365 days; RFI, residual feed intake; W365, adjusted weight at 365 days; W450, adjusted weight at 450 days; AFC: age at first calving; STAY: stayability [dams with at least 3 calvings by 76 months of age, were classified as success (2), otherwise as failure (1)]; 3P: early heifer pregnancy probability [heifers who became pregnant by 20 months of age were classified as precocious (success: 2), otherwise, as conventional (failure: 1)]; RFI_W: residual feed intake without adjustment for rump fat thickness; RFI_F: residual feed intake adjusted for rump fat thickness; SD: standard deviation; *Confidence interval instead of SD.

In practical terms, the weak genetic association between RFI and REA, FRAME, and growth indicates that selection for RFI, as a complementary criterion, contributes to reducing feed consumption without compromising carcass, growth, and body composition traits. Correlations between RFI and STAY were positive but not significantly different from zero, as their

confidence intervals included zero. This indicates that selection for RFI is unlikely to compromise reproductive efficiency; however, selection should prioritize animals that balance reproductive and feed efficiency traits using a selection index that accounts for trait correlations. The correlations with 3P were negative in both models but not significantly different from zero, as their credibility intervals included zero. This indicates no clear genetic antagonism between feed efficiency and the ability of females to achieve three calvings by 30 months. Therefore, breeding programs combining sexual precocity and RFI should prioritize balanced animals to improve feed efficiency without compromising sexual precocity or fertility.

Prediction accuracy was similar for RFI_W (0.44) and RFI_F (0.43), with negligible differences in bias (−0.00 for both) and dispersion (0.05 for RFI_W and 0.03 for RFI_F). LR statistics indicated a slightly higher potential for genetic gain for RFI_F, although the difference was minimal. Overall, the results reinforce that using RFI_F instead of RFI_W does not result in meaningful differences in variance component estimation, genetic correlations, or predictive ability.

Conclusions

The results indicate that adjusting for rump fat thickness accounts for only a small portion of the variability in residual feed intake, as no significant differences in genetic parameters or prediction accuracy are observed between adjusted and unadjusted RFI. Correlations between RFI and traits related to growth, reproduction, and carcass are close to zero or moderate, suggesting that selection for RFI is unlikely to adversely affect these traits. Nevertheless, it remains important to consider the complete set of traits during the selection process to prevent potential negative impacts on the overall genetic progress of the herd.

References

Cantalapiedra-Hijar, G., Abo-Ismail, M., Carstens, G. E., *et al*. (2018) Animal, 12:s321-s335. 10.1017/S1751731118001489

Cervieri, R. C., Carvalho, J. C. F., and Martins, C. L. (2009) Simpósio Internacional de Nutrição de Ruminantes, 2:2-22.

Koch, R.M., Swiger, L.A., Chambers, D., et al. (1963) J. Anim. Sci. 22:486–94. 10.2527/jas1963.222486x

Legarra, A., and Reverter, A. (2018). Genet. Select. Evol. 50:53. 10.1186/s12711-018-0426-6

Leme P, Gomes R. (2007) Características de carcaça de novilhos Nelore com diferente consumo alimentar residual. In: XX Reunión Asociación Latinoamericana de Producion Animal (ALPA). Cuzco, Peru

Lourenco, D., Tsuruta, S., Masuda, Y., et al. (2022) Recent updates in the BLUPF90 software suite. World Congress on Genetics Applied to Livestock Production: 3 - 8 July

Misztal, I., Lourenco, D., Aguilar, I., et al. (2014) Manual for BLUPF90 family of programs. Available online at: http://nce.ads.uga.edu/wiki/lib/exe/fetch.php? media=blupf90_all.pdf

Pereira, L. S., Brunes, L. C., Baldi, et al. (2023) Trop. Anim He.alth and Prod. 55:132. 10.1007/s11250-023-03552-0

Sainz, R. D., Baldi, F., Temp, L. B., et al. (2024) J. Anim. Breed. Genet. 141:643-655. 10.1111/jbg.12870

Shaffer, K.S., Turk, P., Wagner, W.R., et al. (2011) J. Anim. Sci. 89:1028–34. 10.2527/jas.2010-3322

Torres-Vázquez, J. A., van der Werf, J. H., and Clark, S. A. (2018) J. Anim. Sci. 96:4521-4531. 10.1093/jas/sky325